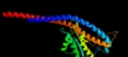
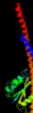
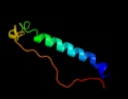
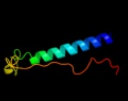
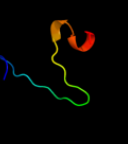
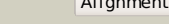


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c30aaO_	 Alignment		100.0	100	PDB header: hydrolase/transport protein Chain: O: PDB Molecule: atp synthase gamma chain; PDBTitle: structure of the e.coli f1-atp synthase inhibited by subunit epsilon
2	c2xokG_	 Alignment		100.0	24	PDB header: hydrolase Chain: G: PDB Molecule: atp synthase subunit gamma, mitochondrial; PDBTitle: refined structure of yeast f1c10 atpase complex to 3 a2 resolution
3	d1fs0g_	 Alignment		100.0	99	Fold: Pyruvate kinase C-terminal domain-like Superfamily: ATP synthase (F1-ATPase), gamma subunit Family: ATP synthase (F1-ATPase), gamma subunit
4	d2jdig1	 Alignment		100.0	39	Fold: Pyruvate kinase C-terminal domain-like Superfamily: ATP synthase (F1-ATPase), gamma subunit Family: ATP synthase (F1-ATPase), gamma subunit
5	c2qe7G_	 Alignment		100.0	42	PDB header: hydrolase Chain: G: PDB Molecule: atp synthase subunit gamma; PDBTitle: crystal structure of the f1-atpase from the thermoalkaliphilic2 bacterium bacillus sp. ta2.a1
6	c2w6jG_	 Alignment		100.0	41	PDB header: hydrolase Chain: G: PDB Molecule: atp synthase subunit gamma, mitochondrial; PDBTitle: low resolution structures of bovine mitochondrial f1-atpase2 during controlled dehydration: hydration state 5.
7	c3fksY_	 Alignment		100.0	32	PDB header: hydrolase Chain: Y: PDB Molecule: atp synthase subunit gamma, mitochondrial; PDBTitle: yeast f1 atpase in the absence of bound nucleotides
8	d1mabg_	 Alignment		100.0	51	Fold: Pyruvate kinase C-terminal domain-like Superfamily: ATP synthase (F1-ATPase), gamma subunit Family: ATP synthase (F1-ATPase), gamma subunit
9	c3re1B_	 Alignment		75.0	8	PDB header: lyase Chain: B: PDB Molecule: uroporphyrinogen-iii synthetase; PDBTitle: crystal structure of uroporphyrinogen iii synthase from pseudomonas2 syringae pv. tomato dc3000
10	d1wd7a_	 Alignment		61.9	18	Fold: HemD-like Superfamily: HemD-like Family: HemD-like
11	c3mw8A_	 Alignment		61.7	9	PDB header: lyase Chain: A: PDB Molecule: uroporphyrinogen-iii synthase; PDBTitle: crystal structure of an uroporphyrinogen-iii synthase (sama_3255) from2 shewanella amazonensis sb2b at 1.65 a resolution

12	c3d8tB_	 Alignment		60.4	15	PDB header: lyase Chain: B: PDB Molecule: uroporphyrinogen-iii synthase; PDBTitle: thermus thermophilus uroporphyrinogen iii synthase
13	c2qzuA_	 Alignment		59.4	13	PDB header: hydrolase Chain: A: PDB Molecule: putative sulfatase yidj; PDBTitle: crystal structure of the putative sulfatase yidj from bacteroides2 fragilis. northeast structural genomics consortium target bfr123
14	d1fsua_	 Alignment		54.0	15	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: Arylsulfatase
15	c3b5qB_	 Alignment		54.0	18	PDB header: hydrolase Chain: B: PDB Molecule: putative sulfatase yidj; PDBTitle: crystal structure of a putative sulfatase (np_810509.1)2 from bacteroides thetaiotaomicron vpi-5482 at 2.40 a3 resolution
16	d1hdha_	 Alignment		49.2	27	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: Arylsulfatase
17	c2xr9A_	 Alignment		46.8	21	PDB header: hydrolase Chain: A: PDB Molecule: ectonucleotide pyrophosphatase/phosphodiesterase family PDBTitle: crystal structure of autotaxin (enpp2)
18	c2kiIA_	 Alignment		44.1	15	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: nmr structure of the h103g mutant so2144 h-nox domain from2 shewanella oneidensis in the fe(ii)co ligation state
19	d1qw2a_	 Alignment		43.7	29	Fold: Hypothetical protein Ta1206 Superfamily: Hypothetical protein Ta1206 Family: Hypothetical protein Ta1206
20	c3k8vB_	 Alignment		42.9	13	PDB header: structural protein Chain: B: PDB Molecule: flagellin homolog; PDBTitle: crysatl structure of a bacterial cell-surface flagellin n20c20
21	c2xrgA_	 Alignment	not modelled	41.8	21	PDB header: hydrolase Chain: A: PDB Molecule: ectonucleotide pyrophosphatase/phosphodiesterase family PDBTitle: crystal structure of autotaxin (enpp2) in complex with the2 ha155 boronic acid inhibitor
22	d1auka_	 Alignment	not modelled	39.0	11	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: Arylsulfatase
23	d1p49a_	 Alignment	not modelled	37.2	17	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: Arylsulfatase
24	c3p9zA_	 Alignment	not modelled	36.5	15	PDB header: ligase Chain: A: PDB Molecule: uroporphyrinogen iii cosynthase (hemd); PDBTitle: crystal structure of uroporphyrinogen-iii synthetase from helicobacter2 pylori 26695
25	c2zktB_	 Alignment	not modelled	33.9	14	PDB header: isomerase Chain: B: PDB Molecule: 2,3-bisphosphoglycerate-independent phosphoglycerate PDBTitle: structure of ph0037 protein from pyrococcus horikoshii
26	c3ed4A_	 Alignment	not modelled	32.3	10	PDB header: transferase Chain: A: PDB Molecule: arylsulfatase; PDBTitle: crystal structure of putative arylsulfatase from escherichia coli
27	c2p1lF_	 Alignment	not modelled	32.0	39	PDB header: apoptosis Chain: F: PDB Molecule: beclin 1; PDBTitle: structure of the bcl-xl:beclin 1 complex
28	c2w8dB_	 Alignment	not modelled	27.6	11	PDB header: transferase Chain: B: PDB Molecule: processed glycerol phosphate lipoteichoic acid synthase 2; PDBTitle: distinct and essential morphogenic functions for wall-

						and2 lipo-teichoic acids in bacillus subtilis
29	c3q3qA_	Alignment	not modelled	27.5	15	PDB header: hydrolase Chain: A: PDB Molecule: alkaline phosphatase; PDBTitle: crystal structure of spap: an novel alkaline phosphatase from2 bacterium sphingomonas sp. strain bsar-1
30	d2pk8a1	Alignment	not modelled	26.8	14	Fold: Hypothetical protein PF0899 Superfamily: Hypothetical protein PF0899 Family: Hypothetical protein PF0899
31	c2vqrA_	Alignment	not modelled	25.9	16	PDB header: hydrolase Chain: A: PDB Molecule: putative sulfatase; PDBTitle: crystal structure of a phosphonate monoester hydrolase2 from rhizobium leguminosarum: a new member of the3 alkaline phosphatase superfamily
32	c3dvcU_	Alignment	not modelled	24.7	39	PDB header: viral protein/apoptosis Chain: C: PDB Molecule: beclin-1; PDBTitle: crystal structure of the complex of murine gamma-2 herpesvirus 68 bcl-2 homolog m11 and the beclin 1 bh33 domain
33	d1sfea2	Alignment	not modelled	24.2	42	Fold: Ribonuclease H-like motif Superfamily: Methylated DNA-protein cysteine methyltransferase domain Family: Methylated DNA-protein cysteine methyltransferase domain
34	c1o98A_	Alignment	not modelled	24.2	15	PDB header: isomerase Chain: A: PDB Molecule: 2,3-bisphosphoglycerate-independent PDBTitle: 1.4a crystal structure of phosphoglycerate mutase from2 bacillus stearothermophilus complexed with3 2-phosphoglycerate
35	c2i09A_	Alignment	not modelled	23.8	12	PDB header: isomerase Chain: A: PDB Molecule: phosphopentomutase; PDBTitle: crystal structure of putative phosphopentomutase from streptococcus2 mutans
36	c3lzcA_	Alignment	not modelled	23.8	23	PDB header: biosynthetic protein Chain: A: PDB Molecule: dph2; PDBTitle: crystal structure of dph2 from pyrococcus horikoshii
37	d2fefa1	Alignment	not modelled	22.6	32	Fold: Bromodomain-like Superfamily: PA2201 N-terminal domain-like Family: PA2201 N-terminal domain-like
38	c2w5tA_	Alignment	not modelled	22.6	13	PDB header: transferase Chain: A: PDB Molecule: processed glycerol phosphate lipoteichoic acid PDBTitle: structure-based mechanism of lipoteichoic acid synthesis by2 staphylococcus aureus ltas.
39	c3lxqB_	Alignment	not modelled	22.4	11	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein vp1736; PDBTitle: the crystal structure of a protein in the alkaline2 phosphatase superfamily from vibrio parahaemolyticus to3 1.95a
40	c2iucB_	Alignment	not modelled	19.7	13	PDB header: hydrolase Chain: B: PDB Molecule: alkaline phosphatase; PDBTitle: structure of alkaline phosphatase from the antarctic2 bacterium tab5
41	d1o98a2	Alignment	not modelled	18.2	15	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: 2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, catalytic domain
42	c3m8yC_	Alignment	not modelled	17.6	10	PDB header: isomerase Chain: C: PDB Molecule: phosphopentomutase; PDBTitle: phosphopentomutase from bacillus cereus after glucose-1,6-bisphosphate2 activation
43	c2ponA_	Alignment	not modelled	17.3	39	PDB header: apoptosis inhibitor Chain: A: PDB Molecule: beclin-1; PDBTitle: solution structure of the bcl-xl/beclin-1 complex
44	d1tlla2	Alignment	not modelled	17.1	22	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Cytochrome p450 reductase N-terminal domain-like
45	c3o3xA_	Alignment	not modelled	16.4	34	PDB header: viral protein Chain: A: PDB Molecule: gp41-5; PDBTitle: crystal structure of gp41-5, a single-chain 5-helix-bundle based on2 hiv gp41
46	d1kxpd3	Alignment	not modelled	16.2	21	Fold: Serum albumin-like Superfamily: Serum albumin-like Family: Serum albumin-like
47	d1ewsa_	Alignment	not modelled	14.7	50	Fold: Defensin-like Superfamily: Defensin-like Family: Defensin
48	c3cseA_	Alignment	not modelled	14.4	20	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrofolate reductase; PDBTitle: candida glabrata dihydrofolate reductase complexed with2 nadph and 2,4-diamino-5-(3-(2,5-dimethoxyphenyl)prop-1-3 ynyl)-6-ethylpyrimidine (ucp120b)
49	c3cu2A_	Alignment	not modelled	14.4	9	PDB header: isomerase Chain: A: PDB Molecule: ribulose-5-phosphate 3-epimerase; PDBTitle: crystal structure of ribulose-5-phosphate 3-epimerase (yp_718263.1)2 from haemophilus somnus 129pt at 1.91 a resolution
50	d2i09a1	Alignment	not modelled	13.9	13	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: DeoB catalytic domain-like
51	d1u55a_	Alignment	not modelled	13.7	14	Fold: Ligand-binding domain in the NO signalling and Golgi transport Superfamily: Ligand-binding domain in the NO signalling and Golgi transport Family: H-NOX domain
52	d1q77a_	Alignment	not modelled	13.3	19	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: Universal stress protein-like
53	c2dg2D_	Alignment	not modelled	13.0	10	PDB header: protein binding Chain: D: PDB Molecule: apolipoprotein a-i binding protein; PDBTitle: crystal structure of mouse apolipoprotein a-i binding2 protein

54	c2k2dA	Alignment	not modelled	12.9	25	PDB header: metal binding protein Chain: A: PDB Molecule: ring finger and chy zinc finger domain- PDBTitle: solution nmr structure of c-terminal domain of human pirh2.2 northeast structural genomics consortium (nesg) target ht2c
55	c2o0cB	Alignment	not modelled	12.4	15	PDB header: signaling protein Chain: B: PDB Molecule: air2278 protein; PDBTitle: crystal structure of the h-nox domain from nostoc sp. pcc 71202 complexed to no
56	d2ggfa1	Alignment	not modelled	10.5	57	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: HI0933 N-terminal domain-like
57	c3lmaC	Alignment	not modelled	10.1	15	PDB header: membrane protein Chain: C: PDB Molecule: stage v sporulation protein ad (spovad); PDBTitle: crystal structure of the stage v sporulation protein ad2 (spovad) from bacillus licheniformis. northeast structural3 genomics consortium target bir6.
58	c1jr2A	Alignment	not modelled	10.0	18	PDB header: lyase Chain: A: PDB Molecule: uroporphyrinogen-iii synthase; PDBTitle: structure of uroporphyrinogen iii synthase
59	d1jr2a	Alignment	not modelled	10.0	18	Fold: HemD-like Superfamily: HemD-like Family: HemD-like
60	c3k8wA	Alignment	not modelled	9.9	13	PDB header: structural protein Chain: A: PDB Molecule: flagellin homolog; PDBTitle: crysatl structure of a bacterial cell-surface flagellin n20c45
61	d2z06a1	Alignment	not modelled	9.9	29	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: TTHA0625-like
62	d1h3ob	Alignment	not modelled	9.7	15	Fold: Histone-fold Superfamily: Histone-fold Family: TBP-associated factors, TAFs
63	d1v10a3	Alignment	not modelled	9.3	40	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Multidomain cupredoxins
64	c1hucC	Alignment	not modelled	9.3	57	PDB header: thiol protease Chain: C: PDB Molecule: cathepsin b; PDBTitle: the refined 2.15 angstroms x-ray crystal structure of human2 liver cathepsin b: the structural basis for its specificity
65	d1yf2a2	Alignment	not modelled	8.8	13	Fold: DNA methylase specificity domain Superfamily: DNA methylase specificity domain Family: Type I restriction modification DNA specificity domain
66	d1m2da	Alignment	not modelled	8.8	19	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioredoxin-like 2Fe-2S ferredoxin
67	d1jeva2	Alignment	not modelled	8.7	10	Fold: vWA-like Superfamily: vWA-like Family: Ku70 subunit N-terminal domain
68	c3opyG	Alignment	not modelled	8.6	15	PDB header: transferase Chain: G: PDB Molecule: 6-phosphofructo-1-kinase alpha-subunit; PDBTitle: crystal structure of pichia pastoris phosphofructokinase in the t-2 state
69	c1skbA	Alignment	not modelled	8.4	67	PDB header: unknown function Chain: A: PDB Molecule: major prion protein 2; PDBTitle: n-terminal (1-30) of bovine prion protein
70	c2yruA	Alignment	not modelled	8.4	8	PDB header: apoptosis Chain: A: PDB Molecule: steroid receptor rna activator 1; PDBTitle: solution structure of mouse steroid receptor rna activator2 1 (sra1) protein
71	c3mxzA	Alignment	not modelled	8.2	21	PDB header: chaperone Chain: A: PDB Molecule: tubulin-specific chaperone a; PDBTitle: crystal structure of tubulin folding cofactor a from arabidopsis2 thaliana
72	c3opyH	Alignment	not modelled	8.2	18	PDB header: transferase Chain: H: PDB Molecule: 6-phosphofructo-1-kinase beta-subunit; PDBTitle: crystal structure of pichia pastoris phosphofructokinase in the t-2 state
73	c3opyB	Alignment	not modelled	8.2	18	PDB header: transferase Chain: B: PDB Molecule: 6-phosphofructo-1-kinase beta-subunit; PDBTitle: crystal structure of pichia pastoris phosphofructokinase in the t-2 state
74	c2bpoA	Alignment	not modelled	8.1	12	PDB header: reductase Chain: A: PDB Molecule: nadph-cytochrom p450 reductase; PDBTitle: crystal structure of the yeast cpr triple mutant: d74g,2 y75f, k78a.
75	c3igzB	Alignment	not modelled	8.0	18	PDB header: isomerase Chain: B: PDB Molecule: cofactor-independent phosphoglycerate mutase; PDBTitle: crystal structures of leishmania mexicana phosphoglycerate2 mutase at low cobalt concentration
76	c2ohcB	Alignment	not modelled	7.9	38	PDB header: hydrolase Chain: B: PDB Molecule: trna-splicing endonuclease; PDBTitle: structural and mutational analysis of trna-intron splicing2 endonuclease from thermoplasma acidophilum dsm1728
77	c2cseW	Alignment	not modelled	7.7	45	PDB header: virus Chain: W: PDB Molecule: major core protein lambda 1; PDBTitle: features of reovirus outer-capsid protein mu1 revealed by2 electron and image reconstruction of the virion at 7.0-a3 resolution
78	c3k1qB	Alignment	not modelled	7.5	36	PDB header: virus Chain: B: PDB Molecule: vp3a, the building block protein of inner shell; PDBTitle: backbone model of an aquareovirus virion by cryo-electron2 microscopy and bioinformatics
79	c1ew2A	Alianment	not modelled	7.4	4	PDB header: hydrolase Chain: A: PDB Molecule: phosphatase;

					PDBTitle: crystal structure of a human phosphatase
80	dlzeda1	Alignment	not modelled	7.4	4 Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: Alkaline phosphatase
81	c3d33B	Alignment	not modelled	7.3	27 PDB header: unknown function Chain: B: PDB Molecule: domain of unknown function with an immunoglobulin-like PDBTitle: crystal structure of a duf3244 family protein with an immunoglobulin-2 like beta-sandwich fold (bvu_0276) from bacteroides vulgatus atcc3 8482 at 1.70 a resolution
82	c2oipE	Alignment	not modelled	7.0	14 PDB header: transferase, oxidoreductase Chain: E: PDB Molecule: chain a, crystal structure of dhfr; PDBTitle: crystal structure of the s290g active site mutant of ts-2 dhfr from cryptosporidium hominis
83	cliqhA	Alignment	not modelled	7.0	33 PDB header: de novo protein Chain: A: PDB Molecule: chimeric peptide glytm1bzip: tropomyosin alpha PDBTitle: glytm1bzip: a chimeric peptide model of the n-terminus of a2 rat short alpha tropomyosin with the n-terminus encoded by3 exon 1b
84	c2i6sA	Alignment	not modelled	7.0	8 PDB header: hydrolase Chain: A: PDB Molecule: complement c2a fragment; PDBTitle: complement component c2a
85	c3k1qC	Alignment	not modelled	6.9	36 PDB header: virus Chain: C: PDB Molecule: vp3b, the building block protein of inner shell; PDBTitle: backbone model of an aquareovirus virion by cryo-electron2 microscopy and bioinformatics
86	c3n39D	Alignment	not modelled	6.7	9 PDB header: oxidoreductase Chain: D: PDB Molecule: protein nrdf; PDBTitle: ribonucleotide reductase di manganese(ii)-nrdf from escherichia coli in2 complex with nrdf
87	dly6va1	Alignment	not modelled	6.5	12 Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: Alkaline phosphatase
88	d1t70a	Alignment	not modelled	6.5	29 Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: DR1281-like
89	d1fpza	Alignment	not modelled	6.5	14 Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
90	dlucua	Alignment	not modelled	6.5	21 Fold: Phase 1 flagellin Superfamily: Phase 1 flagellin Family: Phase 1 flagellin
91	cliipeA	Alignment	not modelled	6.0	43 PDB header: electron transport Chain: A: PDB Molecule: dsbd-alpha; PDBTitle: crystal structure of dsbd-alpha; the n-terminal domain of2 dsbd
92	d1l6pa	Alignment	not modelled	6.0	43 Fold: Immunoglobulin-like beta-sandwich Superfamily: Thiol:disulfide interchange protein DsbD, N-terminal domain (DsbD-alpha) Family: Thiol:disulfide interchange protein DsbD, N-terminal domain (DsbD-alpha)
93	c3rg9A	Alignment	not modelled	5.9	16 PDB header: oxidoreductase/oxidoreductase inhibitor Chain: A: PDB Molecule: bifunctional dihydrofolate reductase-thymidylate synthase; PDBTitle: trypanosoma brucei dihydrofolate reductase (tdhfr) in complex with2 wr99210
94	d1c0aa2	Alignment	not modelled	5.8	13 Fold: DcoH-like Superfamily: GAD domain-like Family: GAD domain
95	c2fo1D	Alignment	not modelled	5.8	18 PDB header: gene regulation/signalling protein/dna Chain: D: PDB Molecule: protein lag-3; PDBTitle: crystal structure of the csl-notch-mastermind ternary2 complex bound to dna
96	d2fo1d1	Alignment	not modelled	5.8	18 Fold: Non-globular all-alpha subunits of globular proteins Superfamily: Lag-3 N-terminal region Family: Lag-3 N-terminal region
97	d1xo1a2	Alignment	not modelled	5.8	22 Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
98	c2j63B	Alignment	not modelled	5.7	43 PDB header: lyase Chain: B: PDB Molecule: ap-endonuclease; PDBTitle: crystal structure of ap endonuclease lmap from leishmania2 major
99	c2kxoA	Alignment	not modelled	5.7	12 PDB header: cell cycle Chain: A: PDB Molecule: cell division topological specificity factor; PDBTitle: solution nmr structure of the cell division regulator mine protein2 from neisseria gonorrhoeae