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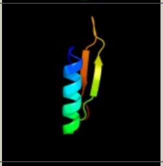
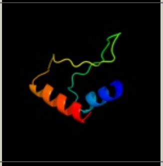
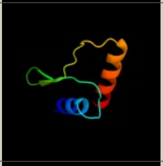
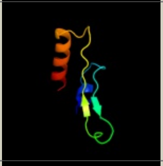
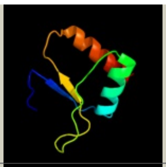
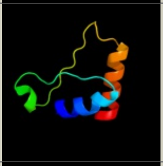
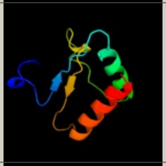
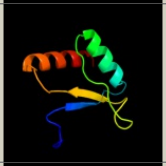
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1x60A_	Alignment		99.7	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sporulation-specific n-acetylmuramoyl-l-alanine **PDBTitle:** solution structure of the peptidoglycan binding domain of2 b. subtilis cell wall lytic enzyme cwlc
2	d1utaa_	Alignment		99.6	21	**Fold:**Ferredoxin-like **Superfamily:**Sporulation related repeat **Family:**Sporulation related repeat
3	d1wyua1	Alignment		78.2	12	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Glycine dehydrogenase subunits (GDC-P)
4	d1dq3a4	Alignment		77.6	14	**Fold:**Homing endonuclease-like **Superfamily:**Homing endonucleases **Family:**Intein endonuclease
5	d1m32a_	Alignment		75.5	16	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
6	d1js3a_	Alignment		71.7	8	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Pyridoxal-dependent decarboxylase
7	d1iuga_	Alignment		71.0	12	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
8	c3k40B_	Alignment		69.1	11	**PDB header:**lyase **Chain:** B: **PDB Molecule:**aromatic-l-amino-acid decarboxylase; **PDBTitle:** crystal structure of drosophila 3,4-dihydroxyphenylalanine2 decarboxylase
9	c2yrrA_	Alignment		68.8	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aminotransferase, class v; **PDBTitle:** hypothetical alanine aminotransferase (tth0173) from thermus2 thermophilus hb8
10	d1pmma_	Alignment		68.4	17	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Pyridoxal-dependent decarboxylase
11	c3caiA_	Alignment		67.8	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**possible aminotransferase; **PDBTitle:** crystal structure of mycobacterium tuberculosis rv3778c2 protein

12	c3f0hA_	Alignment		65.2	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aminotransferase; **PDBTitle:** crystal structure of aminotransferase (rer070207000802) from2 eubacterium rectale at 1.70 a resolution
13	c3ffrA_	Alignment		65.1	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoserine aminotransferase serc; **PDBTitle:** crystal structure of a phosphoserine aminotransferase serc (chu_0995)2 from cytophaga hutchinsonii atcc 33406 at 1.75 a resolution
14	d1bs0a_	Alignment		62.6	20	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
15	c2fyfB_	Alignment		60.0	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phosphoserine aminotransferase; **PDBTitle:** structure of a putative phosphoserine aminotransferase from2 mycobacterium tuberculosis
16	c2zxeG_	Alignment		59.1	48	**PDB header:**hydrolase/transport protein **Chain:** G: **PDB Molecule:**phospholemman-like protein; **PDBTitle:** crystal structure of the sodium - potassium pump in the e2.2k+.pi2 state
17	c2qmaB_	Alignment		57.5	8	**PDB header:**transferase **Chain:** B: **PDB Molecule:**diaminobutyrate-pyruvate transaminase and l-2,4- **PDBTitle:** crystal structure of glutamate decarboxylase domain of2 diaminobutyrate-pyruvate transaminase and l-2,4-diaminobutyrate3 decarboxylase from vibrio parahaemolyticus
18	d1m6sa_	Alignment		56.5	18	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
19	c2dr1A_	Alignment		52.0	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**386aa long hypothetical serine aminotransferase; **PDBTitle:** crystal structure of the ph1308 protein from pyrococcus horikoshii ot3
20	c3cq6E_	Alignment		51.5	11	**PDB header:**transferase **Chain:** E: **PDB Molecule:**histidinol-phosphate aminotransferase; **PDBTitle:** histidinol-phosphate aminotransferase from corynebacterium2 glutamicum holo-form (plp covalently bound)
21	d1fg7a_	Alignment	not modelled	49.5	16	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
22	c2jp3A_	Alignment	not modelled	49.5	26	**PDB header:**transcription **Chain:** A: **PDB Molecule:**fxyd domain-containing ion transport regulator 4; **PDBTitle:** solution structure of the human fxyd4 (chif) protein in sds2 micelles
23	d2ivda2	Alignment	not modelled	48.3	17	**Fold:**FAD-linked reductases, C-terminal domain **Superfamily:**FAD-linked reductases, C-terminal domain **Family:**L-aminoacid/polyamine oxidase
24	c2kncB_	Alignment	not modelled	48.2	32	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**integrin beta-3; **PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
25	c3hdoB_	Alignment	not modelled	46.8	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**histidinol-phosphate aminotransferase; **PDBTitle:** crystal structure of a histidinol-phosphate aminotransferase from2 geobacter metallireducens
26	d1qz9a_	Alignment	not modelled	46.4	13	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
27	c3hbxB_	Alignment	not modelled	46.1	21	**PDB header:**lyase **Chain:** B: **PDB Molecule:**glutamate decarboxylase 1; **PDBTitle:** crystal structure of gad1 from arabidopsis thaliana
28	d1elua_	Alignment	not modelled	45.0	16	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
						PDB header:cell adhesion

29	c2rmzA_	Alignment	not modelled	43.2	32	**Chain:** A: **PDB Molecule:**integrin beta-3; **PDBTitle:** bicelle-embedded integrin beta3 transmembrane segment
30	d1v72a1	Alignment	not modelled	43.1	13	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
31	d1t3ia_	Alignment	not modelled	42.8	9	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
32	d1jf9a_	Alignment	not modelled	41.4	11	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
33	c2jo1A_	Alignment	not modelled	40.3	13	**PDB header:**hydrolase regulator **Chain:** A: **PDB Molecule:**phospholemman; **PDBTitle:** structure of the na,k-atpase regulatory protein fxyd1 in2 micelles
34	d1seza2	Alignment	not modelled	39.8	26	**Fold:**FAD-linked reductases, C-terminal domain **Superfamily:**FAD-linked reductases, C-terminal domain **Family:**L-aminoacid/polyamine oxidase
35	d1oj4a2	Alignment	not modelled	39.2	14	**Fold:**Ferredoxin-like **Superfamily:**GHMP Kinase, C-terminal domain **Family:**4-(cytidine 5'-diphospho)-2C-methyl-D-erythritol kinase IspE
36	c3ly1C_	Alignment	not modelled	38.8	14	**PDB header:**transferase **Chain:** C: **PDB Molecule:**putative histidinol-phosphate aminotransferase; **PDBTitle:** crystal structure of putative histidinol-phosphate aminotransferase2 (yp_050345.1) from erwinia carotovora atroseptica scri1043 at 1.80 a3 resolution
37	d2erra1	Alignment	not modelled	38.4	7	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
38	c3getA_	Alignment	not modelled	37.9	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**histidinol-phosphate aminotransferase; **PDBTitle:** crystal structure of putative histidinol-phosphate aminotransferase2 (np_281508.1) from campylobacter jejuni at 2.01 a resolution
39	c3f9tB_	Alignment	not modelled	36.9	29	**PDB header:**lyase **Chain:** B: **PDB Molecule:**l-tyrosine decarboxylase mfna; **PDBTitle:** crystal structure of l-tyrosine decarboxylase mfna (ec 4.1.1.25)2 (np_247014.1) from methanococcus jannaschii at 2.11 a resolution
40	d1ztpa1	Alignment	not modelled	35.7	8	**Fold:**eIF4e-like **Superfamily:**eIF4e-like **Family:**BLES03-like
41	c3a2bA_	Alignment	not modelled	35.6	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**serine palmitoyltransferase; **PDBTitle:** crystal structure of serine palmitoyltransferase from sphingobacterium2 multivorum with substrate l-serine
42	c2okkA_	Alignment	not modelled	35.2	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**glutamate decarboxylase 2; **PDBTitle:** the x-ray crystal structure of the 65kda isoform of glutamic acid2 decarboxylase (gad65)
43	d2bwna1	Alignment	not modelled	34.9	13	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
44	c2huuA_	Alignment	not modelled	33.6	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**alanine glyoxylate aminotransferase; **PDBTitle:** crystal structure of aedes aegypti alanine glyoxylate2 aminotransferase in complex with alanine
45	d1eg5a_	Alignment	not modelled	33.5	15	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
46	d1nxia_	Alignment	not modelled	33.2	13	**Fold:**Ferredoxin-like **Superfamily:**Hypothetical protein VC0424 **Family:**Hypothetical protein VC0424
47	c2o01D_	Alignment	not modelled	32.7	13	**PDB header:**photosynthesis **Chain:** D: **PDB Molecule:**photosystem i reaction center subunit ii, **PDBTitle:** the structure of a plant photosystem i supercomplex at 3.42 angstrom resolution
48	c3hqtB_	Alignment	not modelled	32.4	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**cai-1 autoinducer synthase; **PDBTitle:** plp-dependent acyl-coa transferase cqsa
49	d3erja1	Alignment	not modelled	30.6	26	**Fold:**Peptidyl-tRNA hydrolase II **Superfamily:**Peptidyl-tRNA hydrolase II **Family:**Peptidyl-tRNA hydrolase II
50	d1x4ea1	Alignment	not modelled	30.6	20	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
51	d2gova1	Alignment	not modelled	30.1	7	**Fold:**Probable bacterial effector-binding domain **Superfamily:**Probable bacterial effector-binding domain **Family:**SOUL heme-binding protein
52	c2w8wA_	Alignment	not modelled	30.1	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**serine palmitoyltransferase; **PDBTitle:** n100y spt with plp-ser
53	c2k8eA_	Alignment	not modelled	29.4	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0339 protein yegp; **PDBTitle:** solution nmr structure of protein of unknown function yegp from e.2 coli. ontario center for structural proteomics target ec0640_1_1233 northeast structural genomics consortium target et102.
54	c2jisA_	Alignment	not modelled	28.9	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**cysteine sulfinic acid decarboxylase;

54	c2jisA_	Alignment	not modelled	28.9	15	**PDBTitle:** human cysteine sulfinic acid decarboxylase (csad) in2 complex with plp.
55	c2dh9A_	Alignment	not modelled	27.6	12	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**heterogeneous nuclear ribonucleoprotein m; **PDBTitle:** solution structure of the c-terminal rna binding domain in2 heterogeneous nuclear ribonucleoprotein m
56	d2f8ja1	Alignment	not modelled	26.4	21	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
57	d1h0ca_	Alignment	not modelled	26.1	19	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
58	c1xtyD_	Alignment	not modelled	25.8	19	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**peptidyl-trna hydrolase; **PDBTitle:** crystal structure of sulfolobus solfataricus peptidyl-trna2 hydrolase
59	c3r8kB_	Alignment	not modelled	25.5	12	**PDB header:**apoptosis **Chain:** B: **PDB Molecule:**heme-binding protein 2; **PDBTitle:** crystal structure of human soul protein (hexagonal form)
60	d1rk8a_	Alignment	not modelled	25.3	9	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
61	d2cpia1	Alignment	not modelled	23.7	4	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
62	c2hzpA_	Alignment	not modelled	23.1	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**kynureninase; **PDBTitle:** crystal structure of homo sapiens kynureninase
63	c3p3dA_	Alignment	not modelled	22.8	19	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**nucleoporin 53; **PDBTitle:** crystal structure of the nup53 rrm domain from pichia guilliermondii
64	c3bpqD_	Alignment	not modelled	22.4	31	**PDB header:**toxin **Chain:** D: **PDB Molecule:**toxin rele3; **PDBTitle:** crystal structure of relb-rele antitoxin-toxin complex from2 methanococcus jannaschii
65	c2zv3E_	Alignment	not modelled	22.1	23	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**peptidyl-trna hydrolase; **PDBTitle:** crystal structure of project mj0051 from methanocaldococcus2 jannaschii dsm 2661
66	c2d3kA_	Alignment	not modelled	21.9	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidyl-trna hydrolase; **PDBTitle:** structural study on project id ph1539 from pyrococcus2 horikoshii ot3
67	c2eqkA_	Alignment	not modelled	21.9	10	**PDB header:**transcription **Chain:** A: **PDB Molecule:**tudor domain-containing protein 4; **PDBTitle:** solution structure of the tudor domain of tudor domain-2 containing protein 4
68	d1mdoa_	Alignment	not modelled	21.9	17	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
69	c3eucB_	Alignment	not modelled	21.8	8	**PDB header:**transferase **Chain:** B: **PDB Molecule:**histidinol-phosphate aminotransferase 2; **PDBTitle:** crystal structure of histidinol-phosphate aminotransferase2 (yp_297314.1) from ralstonia eutropha jmp134 at 2.05 a resolution
70	d2c0ra1	Alignment	not modelled	20.2	7	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
71	c2z0rA_	Alignment	not modelled	19.7	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein ttha0547; **PDBTitle:** crystal structure of hypothetical protein ttha0547
72	d1rlka_	Alignment	not modelled	19.4	28	**Fold:**Peptidyl-tRNA hydrolase II **Superfamily:**Peptidyl-tRNA hydrolase II **Family:**Peptidyl-tRNA hydrolase II
73	c2q5cA_	Alignment	not modelled	18.7	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**ntrc family transcriptional regulator; **PDBTitle:** crystal structure of ntrc family transcriptional regulator from2 clostridium acetobutylicum
74	c2k49A_	Alignment	not modelled	18.7	4	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0339 protein so_3888; **PDBTitle:** solution nmr structure of upf0339 protein so3888 from shewanella2 oneidensis. northeast structural genomics consortium target sor190
75	c3ns5B_	Alignment	not modelled	18.6	18	**PDB header:**translation **Chain:** B: **PDB Molecule:**eukaryotic translation initiation factor 3 subunit b; **PDBTitle:** crystal structure of the rna recognition motif of yeast eif3b residues2 76-161
76	c3hdeA_	Alignment	not modelled	18.2	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lysozyme; **PDBTitle:** crystal structure of full-length endolysin r21 from phage 21
77	d1wi6a1	Alignment	not modelled	18.1	12	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
78	c1no8A_	Alignment	not modelled	17.8	11	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**aly; **PDBTitle:** solution structure of the nuclear factor aly rbd domain
79	d1no8a_	Alignment	not modelled	17.8	11	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD

80	c2wseD_	Alignment	not modelled	17.4	13	**PDB header:**photosynthesis **Chain:** D: **PDB Molecule:**photosystem i reaction center subunit ii, **PDBTitle:** improved model of plant photosystem i
81	c2jwaA_	Alignment	not modelled	17.4	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**receptor tyrosine-protein kinase erbb-2; **PDBTitle:** erbb2 transmembrane segment dimer spatial structure
82	c2pbiA_	Alignment	not modelled	17.3	9	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**regulator of g-protein signaling 9; **PDBTitle:** the multifunctional nature of gbeta5/rgs9 revealed from its crystal2 structure
83	c3ml6D_	Alignment	not modelled	16.8	12	**PDB header:**protein transport **Chain:** D: **PDB Molecule:**chimeric complex between protein dishevlled2 homolog dvl-2 **PDBTitle:** a complex between dishevlled2 and clathrin adaptor ap-2
84	d1gcca_	Alignment	not modelled	16.2	6	**Fold:**DNA-binding domain **Superfamily:**DNA-binding domain **Family:**GCC-box binding domain
85	c2divA_	Alignment	not modelled	16.0	10	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**trna selenocysteine associated protein; **PDBTitle:** solution structure of the rrm domain of trna selenocysteine2 associated protein
86	c3ht4B_	Alignment	not modelled	16.0	15	**PDB header:**lyase **Chain:** B: **PDB Molecule:**aluminum resistance protein; **PDBTitle:** crystal structure of the q81a77_baccr protein from bacillus2 cereus. northeast structural genomics consortium target3 bcr213
87	d1wg1a_	Alignment	not modelled	15.9	8	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
88	d1q7sa_	Alignment	not modelled	15.7	19	**Fold:**Peptidyl-tRNA hydrolase II **Superfamily:**Peptidyl-tRNA hydrolase II **Family:**Peptidyl-tRNA hydrolase II
89	c3ffhA_	Alignment	not modelled	15.6	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**histidinol-phosphate aminotransferase; **PDBTitle:** the crystal structure of histidinol-phosphate aminotransferase from2 listeria innocua clip11262.
90	d1jb0d_	Alignment	not modelled	15.0	10	**Fold:**Photosystem I subunit PsaD **Superfamily:**Photosystem I subunit PsaD **Family:**Photosystem I subunit PsaD
91	c2ordA_	Alignment	not modelled	15.0	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetylornithine aminotransferase; **PDBTitle:** crystal structure of acetylornithine aminotransferase (ec 2.6.1.11)2 (acoat) (tm1785) from thermotoga maritima at 1.40 a resolution
92	c3n23E_	Alignment	not modelled	14.6	24	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**na+/k+ atpase gamma subunit transcript variant a; **PDBTitle:** crystal structure of the high affinity complex between ouabain and the2 e2p form of the sodium-potassium pump
93	d2cqha1	Alignment	not modelled	14.6	15	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
94	d2ch1a1	Alignment	not modelled	14.4	13	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
95	d2cpea1	Alignment	not modelled	13.8	8	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
96	c2l9vA_	Alignment	not modelled	13.8	14	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**pre-mrna-processing factor 40 homolog a; **PDBTitle:** nmr structure of the ff domain l24a mutant's folding transition state
97	d2cpha1	Alignment	not modelled	13.8	19	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
98	c3e9kA_	Alignment	not modelled	13.7	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**kynureninase; **PDBTitle:** crystal structure of homo sapiens kynureninase-3-hydroxyhippuric acid2 inhibitor complex
99	d1fxla1	Alignment	not modelled	13.6	9	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD