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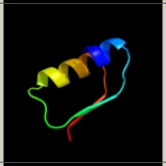
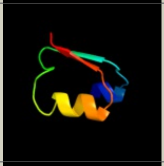
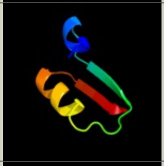
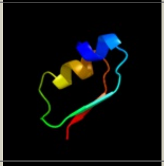
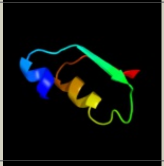
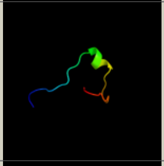
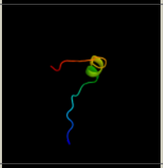
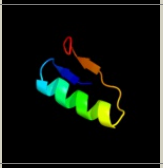
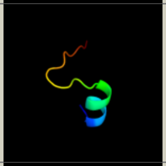
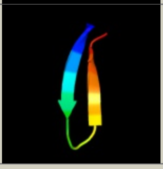
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2isba1	Alignment		100.0	38	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**FumA C-terminal domain-like **Family:**FumA C-terminal domain-like
2	c4a1oB_	Alignment		66.5	26	**PDB header:**transferase-hydrolase **Chain:** B: **PDB Molecule:**bifunctional purine biosynthesis protein purh; **PDBTitle:** crystal structure of mycobacterium tuberculosis purh complexed with2 aicar and a novel nucleotide cfair, at 2.48 a resolution.
3	c1zczA_	Alignment		65.9	26	**PDB header:**transferase/hydrolase **Chain:** A: **PDB Molecule:**bifunctional purine biosynthesis protein purh; **PDBTitle:** crystal structure of phosphoribosylaminoimidazolecarboxamide2 formyltransferase / imp cyclohydrolase (tm1249) from thermotoga3 maritima at 1.88 a resolution
4	d1zcza2	Alignment		64.6	26	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**AICAR transformylase domain of bifunctional purine biosynthesis enzyme ATIC
5	d1ed7a_	Alignment		48.5	19	**Fold:**WW domain-like **Superfamily:**Carbohydrate binding domain **Family:**Carbohydrate binding domain
6	d1g8ma2	Alignment		43.8	17	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**AICAR transformylase domain of bifunctional purine biosynthesis enzyme ATIC
7	d1pkxa2	Alignment		42.6	14	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**AICAR transformylase domain of bifunctional purine biosynthesis enzyme ATIC
8	d1o6aa_	Alignment		41.4	25	**Fold:**Surface presentation of antigens (SPOA) **Superfamily:**Surface presentation of antigens (SPOA) **Family:**Surface presentation of antigens (SPOA)
9	c1thzA_	Alignment		39.1	17	**PDB header:**transferase, hydrolase **Chain:** A: **PDB Molecule:**bifunctional purine biosynthesis protein purh; **PDBTitle:** crystal structure of avian aicar transformylase in complex2 with a novel inhibitor identified by virtual ligand3 screening
10	d1g8fa1	Alignment		35.3	15	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**ATP sulfurylase N-terminal domain
11	c3jviA_	Alignment		31.7	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein tyrosine phosphatase; **PDBTitle:** product state mimic crystal structure of protein tyrosine phosphatase2 from entamoeba histolytica

12	d1z5ye1	Alignment		31.3	23	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
13	d1x6va1	Alignment		29.4	12	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**ATP sulfurylase N-terminal domain
14	c3opyE_	Alignment		29.4	17	**PDB header:**transferase **Chain:** E: **PDB Molecule:**6-phosphofructo-1-kinase alpha-subunit; **PDBTitle:** crystal structure of pichia pastoris phosphofructokinase in the t-2 state
15	c3ibgF_	Alignment		28.3	33	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**atpase, subunit of the get complex; **PDBTitle:** crystal structure of aspergillus fumigatus get3 with bound2 adp
16	d1vkza2	Alignment		26.9	16	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
17	c3p9zA_	Alignment		26.6	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**uroporphyrinogen iii cosynthase (hemd); **PDBTitle:** crystal structure of uroporphyrinogen-iii synthetase from helicobacter2 pylori 26695
18	d1e32a1	Alignment		26.0	20	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Cdc48 N-terminal domain-like
19	d1jo0a_	Alignment		24.6	13	**Fold:**IF3-like **Superfamily:**YhbY-like **Family:**YhbY-like
20	d1aiwa_	Alignment		24.6	36	**Fold:**WW domain-like **Superfamily:**Carbohydrate binding domain **Family:**Carbohydrate binding domain
21	d12asa_	Alignment	not modelled	24.1	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
22	d1xnea_	Alignment	not modelled	22.8	27	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**ProFAR isomerase associated domain
23	d1o9ya_	Alignment	not modelled	22.7	10	**Fold:**Surface presentation of antigens (SPOA) **Superfamily:**Surface presentation of antigens (SPOA) **Family:**Surface presentation of antigens (SPOA)
24	c2d49A_	Alignment	not modelled	22.5	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chitinase c; **PDBTitle:** solution structure of the chitin-binding domain of2 streptomyces griseus chitinase c
25	c1r6xA_	Alignment	not modelled	22.3	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**atp:sulfate adenylyltransferase; **PDBTitle:** the crystal structure of a truncated form of yeast atp2 sulfurylase, lacking the c-terminal aps kinase-like domain,3 in complex with sulfate
26	c2qjfB_	Alignment	not modelled	21.2	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**bifunctional 3'-phosphoadenosine 5'- **PDBTitle:** crystal structure of atp-sulfurylase domain of human paps2 synthetase 1
27	d1goia1	Alignment	not modelled	21.2	14	**Fold:**WW domain-like **Superfamily:**Carbohydrate binding domain **Family:**Carbohydrate binding domain
28	d1s04a_	Alignment	not modelled	20.8	31	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**ProFAR isomerase associated domain

29	c1g8gB_	Alignment	not modelled	20.5	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**sulfate adenylyltransferase; **PDBTitle:** atp sulfurylase from s. cerevisiae: the binary product complex with2 aps
30	c1jr2A_	Alignment	not modelled	19.7	20	**PDB header:**lyase **Chain:** A: **PDB Molecule:**uroporphyrinogen-iii synthase; **PDBTitle:** structure of uroporphyrinogen iii synthase
31	d1jr2a_	Alignment	not modelled	19.7	20	**Fold:**HemD-like **Superfamily:**HemD-like **Family:**HemD-like
32	d2cp6a1	Alignment	not modelled	19.3	21	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
33	c2gksB_	Alignment	not modelled	19.3	23	**PDB header:**transferase **Chain:** B: **PDB Molecule:**bifunctional sat/aps kinase; **PDBTitle:** crystal structure of the bi-functional atp sulfurylase-aps kinase from2 aquifex aeolicus, a chemolithotrophic thermophile
34	c2zpmA_	Alignment	not modelled	18.6	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**regulator of sigma e protease; **PDBTitle:** crystal structure analysis of pdz domain b
35	c3stbC_	Alignment	not modelled	18.2	33	**PDB header:**rna binding protein/immune system **Chain:** C: **PDB Molecule:**rna-editing complex protein mp42; **PDBTitle:** a complex of two editosome proteins and two nanobodies
36	d2cpga_	Alignment	not modelled	18.0	35	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**CopG-like
37	d2dexx3	Alignment	not modelled	18.0	34	**Fold:**Pentein, beta/alpha-propeller **Superfamily:**Pentein **Family:**Peptidylarginine deiminase Pad4, catalytic C-terminal domain
38	d1tova_	Alignment	not modelled	17.9	26	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
39	c3kh7A_	Alignment	not modelled	15.6	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thiol:disulfide interchange protein dsbe; **PDBTitle:** crystal structure of the periplasmic soluble domain of reduced ccmg2 from pseudomonas aeruginosa
40	c3kojA_	Alignment	not modelled	15.3	43	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**uncharacterized protein ycf41; **PDBTitle:** crystal structure of the ssb domain of q5n255_synp6 protein2 from synechococcus sp. northeast structural genomics3 consortium target snr59a.
41	d1a3xa1	Alignment	not modelled	14.6	32	**Fold:**PK beta-barrel domain-like **Superfamily:**PK beta-barrel domain-like **Family:**Pyruvate kinase beta-barrel domain
42	c3opyG_	Alignment	not modelled	13.9	17	**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
43	c3en2A_	Alignment	not modelled	13.6	33	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**probable primosomal replication protein n; **PDBTitle:** three-dimensional structure of the protein prib from2 ralstonia solanacearum at the resolution 2.3a. northeast3 structural genomics consortium target rsr213c.
44	c3kw0D_	Alignment	not modelled	13.5	29	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**cysteine peptidase; **PDBTitle:** crystal structure of cysteine peptidase (np_982244.1) from bacillus2 cereus atcc 10987 at 2.50 a resolution
45	d1dcsa_	Alignment	not modelled	13.4	3	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**Penicillin synthase-like
46	d1xr4a2	Alignment	not modelled	12.6	18	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**CoA transferase alpha subunit-like
47	c2r47C_	Alignment	not modelled	12.5	17	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**uncharacterized protein mth_862; **PDBTitle:** crystal structure of mth_862 protein of unknown function from2 methanothermobacter thermautotrophicus
48	d1nq3a_	Alignment	not modelled	12.4	31	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YjgF-like **Family:**YjgF/L-PSP
49	c2jwlB_	Alignment	not modelled	12.1	27	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**protein tolr; **PDBTitle:** solution structure of periplasmic domain of tolr from h.2 influenzae with saxs data
50	d1b8aa1	Alignment	not modelled	12.1	13	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Anticodon-binding domain
51	c2l57A_	Alignment	not modelled	11.7	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution structure of an uncharacterized thioredoin-like protein from2 clostridium perfringens
52	d1j7ha_	Alignment	not modelled	11.7	21	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YjgF-like **Family:**YjgF/L-PSP
53	c2de0X_	Alignment	not modelled	11.5	29	**PDB header:**transferase **Chain:** X: **PDB Molecule:**alpha-(1,6)-fucosyltransferase; **PDBTitle:** crystal structure of human alpha 1,6-fucosyltransferase, fut8
54	c2pseA_	Alignment	not modelled	11.3	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**renilla-luciferin 2-monooxygenase; **PDBTitle:** crystal structures of the luciferase and green fluorescent2 protein from renilla reniformis

55	c3cr8C_	Alignment	not modelled	10.6	23	**PDB header:**transferase **Chain:** C: **PDB Molecule:**sulfate adenylyltranferase, adenylylsulfate **PDBTitle:** hexameric aps kinase from thiobacillus denitrificans
56	c3iuwA_	Alignment	not modelled	10.5	21	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**activating signal cointegrator; **PDBTitle:** crystal structure of activating signal cointegrator (np_814290.1) from2 enterococcus faecalis v583 at 1.58 a resolution
57	c3lzkC_	Alignment	not modelled	10.4	14	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**fumarylacetoacetate hydrolase family protein; **PDBTitle:** the crystal structure of a probably aromatic amino acid2 degradation protein from sinorhizobium meliloti 1021
58	d1y1la_	Alignment	not modelled	10.1	17	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**Phosphotyrosine protein phosphatases I **Family:**Low-molecular-weight phosphotyrosine protein phosphatases
59	d2grea1	Alignment	not modelled	10.1	29	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Aminopeptidase/glucanase lid domain **Family:**Aminopeptidase/glucanase lid domain
60	d2gqba1	Alignment	not modelled	10.1	11	**Fold:**RPA2825-like **Superfamily:**RPA2825-like **Family:**RPA2825-like
61	c2p4sA_	Alignment	not modelled	10.0	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**purine nucleoside phosphorylase; **PDBTitle:** structure of purine nucleoside phosphorylase from anopheles gambiae in2 complex with dadme-immh
62	c1xnjB_	Alignment	not modelled	9.9	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**bifunctional 3'-phosphoadenosine 5'-phosphosulfate **PDBTitle:** aps complex of human paps synthetase 1
63	c3qd7X_	Alignment	not modelled	9.9	19	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**uncharacterized protein ydal; **PDBTitle:** crystal structure of ydal, a stand-alone small muts-related protein2 from escherichia coli
64	c2hc8A_	Alignment	not modelled	9.8	21	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**cation-transporting atpase, p-type; **PDBTitle:** structure of the a. fulgidus copa a-domain
65	c3k81D_	Alignment	not modelled	9.8	26	**PDB header:**immune system, rna binding protein **Chain:** D: **PDB Molecule:**mp18 rna editing complex protein; **PDBTitle:** structure of the central interaction protein from the trypanosoma2 brucei editosome in complex with single domain antibodies
66	d1krta_	Alignment	not modelled	9.7	26	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Anticodon-binding domain
67	c3e7kF_	Alignment	not modelled	9.7	33	**PDB header:**membrane protein **Chain:** F: **PDB Molecule:**trpm7 channel; **PDBTitle:** crystal structure of an antiparallel coiled-coil tetramerization2 domain from trpm7 channels
68	c2e4hA_	Alignment	not modelled	9.5	26	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**restin; **PDBTitle:** solution structure of cytoskeletal protein in complex with2 tubulin tail
69	c2re2A_	Alignment	not modelled	9.4	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**uncharacterized protein ta1041; **PDBTitle:** crystal structure of a putative iron-molybdenum cofactor (femo-co)2 dinitrogenase (ta1041m) from thermoplasma acidophilum dsm 1728 at3 1.30 a resolution
70	c2fekA_	Alignment	not modelled	9.4	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**low molecular weight protein-tyrosine- **PDBTitle:** structure of a protein tyrosine phosphatase
71	d1bbua1	Alignment	not modelled	9.2	25	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Anticodon-binding domain
72	d1ln4a_	Alignment	not modelled	9.2	8	**Fold:**IF3-like **Superfamily:**YhbY-like **Family:**YhbY-like
73	d1p9ka_	Alignment	not modelled	9.1	24	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**YbcJ-like
74	d1jf8a_	Alignment	not modelled	9.1	17	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**Phosphotyrosine protein phosphatases I **Family:**Low-molecular-weight phosphotyrosine protein phosphatases
75	c2ju5A_	Alignment	not modelled	9.0	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin disulfide isomerase; **PDBTitle:** dsbh oxidoreductase
76	c3k3sG_	Alignment	not modelled	9.0	29	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**altronate hydrolase; **PDBTitle:** crystal structure of altronate hydrolase (fragment 1-84) from shigella2 flexneri.
77	d1bkba1	Alignment	not modelled	8.9	13	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**eIF5a N-terminal domain-like
78	d1pjqa3	Alignment	not modelled	8.8	21	**Fold:**Siroheme synthase middle domains-like **Superfamily:**Siroheme synthase middle domains-like **Family:**Siroheme synthase middle domains-like
79	c3fk8A_	Alignment	not modelled	8.8	21	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**disulphide isomerase; **PDBTitle:** the crystal structure of disulphide isomerase from xylella fastidiosa2 temecula1
80	d5pnta	Alignment	not modelled	8.8	11	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**Phosphotyrosine protein phosphatases I

80	d3pnta_	Alignment	not modelled	8.8	11	**Family:**Low-molecular-weight phosphotyrosine protein phosphatases
81	d1ueba1	Alignment	not modelled	8.7	29	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**eIF5a N-terminal domain-like
82	c2l18A_	Alignment	not modelled	8.7	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**arsenate reductase; **PDBTitle:** an arsenate reductase in the phosphate binding state
83	d2ewca1	Alignment	not modelled	8.7	33	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YjgF-like **Family:**YjgF/L-PSP
84	c2vw9B_	Alignment	not modelled	8.7	19	**PDB header:**dna-binding protein **Chain:** B: **PDB Molecule:**single-stranded dna binding protein; **PDBTitle:** single stranded dna binding protein complex from2 helicobacter pylori
85	c3fhwB_	Alignment	not modelled	8.6	29	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**primosomal replication protein n; **PDBTitle:** crystal structure of the protein prib from bordetella parapertussis.2 northeast structural genomics consortium target bpr162.
86	d1nvta1	Alignment	not modelled	8.6	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
87	c1y96D_	Alignment	not modelled	8.6	35	**PDB header:**rna binding protein **Chain:** D: **PDB Molecule:**gem-associated protein 7; **PDBTitle:** crystal structure of the gemin6/gemin7 heterodimer from the2 human smn complex
88	d1qaha_	Alignment	not modelled	8.4	24	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YjgF-like **Family:**YjgF/L-PSP
89	c3fw2A_	Alignment	not modelled	8.4	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thiol-disulfide oxidoreductase; **PDBTitle:** c-terminal domain of putative thiol-disulfide oxidoreductase from2 bacteroides thetaiotaomicron.
90	d1rq8a_	Alignment	not modelled	8.3	14	**Fold:**IF3-like **Superfamily:**YhbY-like **Family:**YhbY-like
91	d2eifa1	Alignment	not modelled	8.2	19	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**eIF5a N-terminal domain-like
92	d1onia_	Alignment	not modelled	8.1	21	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YjgF-like **Family:**YjgF/L-PSP
93	d1fdra1	Alignment	not modelled	8.0	19	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
94	c3tqyA_	Alignment	not modelled	7.9	33	**PDB header:**transferase **Chain:** A: **PDB Molecule:**single-stranded dna-binding protein; **PDBTitle:** structure of a single-stranded dna-binding protein (ssb), from2 coxiella burnetii
95	d1pk6a_	Alignment	not modelled	7.9	20	**Fold:**TNF-like **Superfamily:**TNF-like **Family:**TNF-like
96	c1o91B_	Alignment	not modelled	7.7	40	**PDB header:**collagen **Chain:** B: **PDB Molecule:**collagen alpha 1(viii) chain; **PDBTitle:** crystal structure of a collagen viii nc1 domain trimer
97	d1o91a_	Alignment	not modelled	7.7	40	**Fold:**TNF-like **Superfamily:**TNF-like **Family:**TNF-like
98	d1gsoa2	Alignment	not modelled	7.7	19	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
99	d1iz6a1	Alignment	not modelled	7.6	13	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**eIF5a N-terminal domain-like