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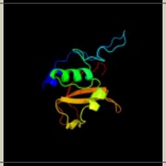
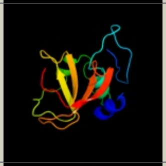
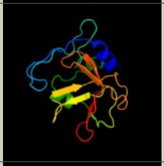
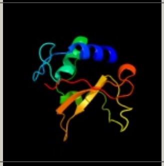
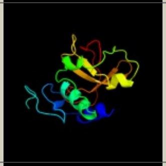
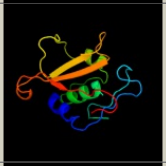
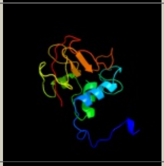
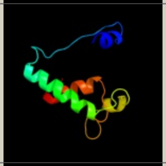
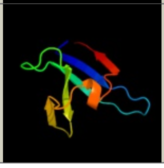
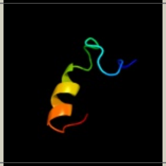
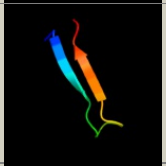
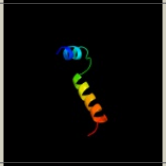
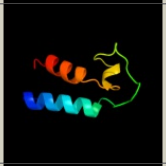
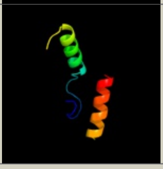
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2k1gA_	Alignment		96.6	26	**PDB header:**lipoprotein **Chain:** A: **PDB Molecule:**lipoprotein spr; **PDBTitle:** solution nmr structure of lipoprotein spr from escherichia coli k12.2 northeast structural genomics target er541-37-162
2	d2evra2	Alignment		95.4	22	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**NlpC/P60
3	c3pbiA_	Alignment		95.3	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**invasion protein; **PDBTitle:** structure of the peptidoglycan hydrolase ripb (rv1478) from2 mycobacterium tuberculosis at 1.6 resolution
4	c3gt2A_	Alignment		95.0	15	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of the p60 domain from m. avium2 paratuberculosis antigen map1272c
5	c3npfB_	Alignment		94.6	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative dipeptidyl-peptidase vi; **PDBTitle:** crystal structure of a putative dipeptidyl-peptidase vi (bacova_00612)2 from bacteroides ovatus at 1.72 a resolution
6	c3i86A_	Alignment		94.2	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of the p60 domain from m. avium subspecies2 paratuberculosis antigen map1204
7	c2xivA_	Alignment		93.6	25	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**hypothetical invasion protein; **PDBTitle:** structure of rv1477, hypothetical invasion protein of2 mycobacterium tuberculosis
8	c3h41A_	Alignment		93.5	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nlp/p60 family protein; **PDBTitle:** crystal structure of a nlpc/p60 family protein (bce_2878) from2 bacillus cereus atcc 10987 at 1.79 a resolution
9	c2fg0B_	Alignment		91.6	24	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cog0791: cell wall-associated hydrolases (invasion- **PDBTitle:** crystal structure of a putative gamma-d-glutamyl-l-diamino acid2 endopeptidase (npun_r0659) from nostoc punctiforme pcc 73102 at 1.793 a resolution
10	d2if6a1	Alignment		85.6	17	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**YiiX-like
11	c2p1gA_	Alignment		83.6	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative xylanase; **PDBTitle:** crystal structure of a putative xylanase from bacteroides fragilis

12	d2io8a2	Alignment		70.5	13	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**CHAP domain
13	c3kw0D_	Alignment		69.4	19	**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
14	c2vpmB_	Alignment		63.3	14	**PDB header:**ligase **Chain:** B: **PDB Molecule:**trypanothione synthetase; **PDBTitle:** trypanothione synthetase
15	c2k3aA_	Alignment		57.9	28	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chap domain protein; **PDBTitle:** nmr solution structure of staphylococcus saprophyticus chap2 (cysteine, histidine-dependent amidohydrolases/peptidases)3 domain protein. northeast structural genomics consortium4 target syr11
16	c3obcB_	Alignment		57.2	27	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**pyrophosphatase; **PDBTitle:** crystal structure of a pyrophosphatase (af1178) from archaeoglobus2 fulgidus at 1.80 a resolution
17	c3m1uB_	Alignment		55.9	24	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative gamma-d-glutamyl-l-diamino acid endopeptidase; **PDBTitle:** crystal structure of a putative gamma-d-glutamyl-l-diamino acid2 endopeptidase (dvu_0896) from desulfovibrio vulgaris hildenborough at3 1.75 a resolution
18	c2ioaA_	Alignment		53.7	18	**PDB header:**ligase, hydrolase **Chain:** A: **PDB Molecule:**bifunctional glutathionylspermidine **PDBTitle:** e. coli bifunctional glutathionylspermidine2 synthetase/amidase incomplex with mg2+ and adp and3 phosphinate inhibitor
19	c3isrB_	Alignment		53.3	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**transglutaminase-like enzymes, putative cysteine protease; **PDBTitle:** the crystal structure of a putative cysteine protease from cytophaga2 hutchinsonii to 1.9a
20	c1rqgA_	Alignment		53.3	29	**PDB header:**ligase **Chain:** A: **PDB Molecule:**methionyl-trna synthetase; **PDBTitle:** methionyl-trna synthetase from pyrococcus abyssi
21	d2a3qa1	Alignment	not modelled	49.5	34	**Fold:**all-alpha NTP pyrophosphatases **Superfamily:**all-alpha NTP pyrophosphatases **Family:**MazG-like
22	c2q4pA_	Alignment	not modelled	49.5	34	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**protein rs21-c6; **PDBTitle:** ensemble refinement of the crystal structure of protein from mus2 musculus mm.29898
23	d1nx4a_	Alignment	not modelled	46.5	22	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**gamma-Butyrobetaine hydroxylase
24	d1bqka_	Alignment	not modelled	42.5	13	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
25	c3r1jB_	Alignment	not modelled	40.9	33	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**alpha-ketoglutarate-dependent taurine dioxygenase; **PDBTitle:** crystal structure of alpha-ketoglutarate-dependent taurine dioxygenase2 from mycobacterium avium, native form
26	d1otja_	Alignment	not modelled	40.9	44	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**TauD/TfdA-like
27	c3pvjB_	Alignment	not modelled	38.9	33	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**alpha-ketoglutarate-dependent taurine dioxygenase; **PDBTitle:** crystal structure of the fe(ii)/alpha-ketoglutarate dependent taurine2 dioxygenase from pseudomonas putida kt2440
28	c2kytA_	Alignment	not modelled	38.0	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**group xvi phospholipase a2; **PDBTitle:** solution struture of the h-rev107 n-terminal domain

29	c3eatX_	Alignment	not modelled	36.2	22	**PDB header:**oxidoreductase **Chain:** X: **PDB Molecule:**pyoverdine biosynthesis protein pvcb; **PDBTitle:** crystal structure of the pvcb (pa2255) protein from2 pseudomonas aeruginosa
30	d1y0za_	Alignment	not modelled	35.3	33	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**gamma-Butyrobetaine hydroxylase
31	d1oiha_	Alignment	not modelled	35.2	44	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**TauD/TfdA-like
32	d1pmya_	Alignment	not modelled	34.9	17	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
33	d1ilea3	Alignment	not modelled	33.6	11	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
34	d1plaa_	Alignment	not modelled	32.6	16	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
35	c2x1lC_	Alignment	not modelled	32.3	30	**PDB header:**ligase **Chain:** C: **PDB Molecule:**methionyl-trna synthetase; **PDBTitle:** crystal structure of mycobacterium smegmatis methionyl-trna2 synthetase in complex with methionine and adenosine
36	c2ct8A_	Alignment	not modelled	32.1	26	**PDB header:**ligase/rna **Chain:** A: **PDB Molecule:**methionyl-trna synthetase; **PDBTitle:** crystal structure of aquifex aeolicus methionyl-trna2 synthetase complexed with trna(met) and methionyl-adenylate3 anologue
37	d2d5ba2	Alignment	not modelled	31.6	22	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
38	d1pfva2	Alignment	not modelled	31.4	30	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
39	d1kdja_	Alignment	not modelled	31.0	31	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
40	d1rqga2	Alignment	not modelled	30.7	31	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
41	c3kflA_	Alignment	not modelled	25.2	22	**PDB header:**ligase **Chain:** A: **PDB Molecule:**methionyl-trna synthetase; **PDBTitle:** leishmania major methionyl-trna synthetase in complex with2 methionyladenylate and pyrophosphate
42	d2jxma1	Alignment	not modelled	24.4	19	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
43	c2zouB_	Alignment	not modelled	24.4	15	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**spondin-1; **PDBTitle:** crystal struture of human f-spondin reeler domain (fragment 2)
44	d1pcsa_	Alignment	not modelled	23.5	21	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
45	d1wspa1	Alignment	not modelled	23.0	24	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**DIX domain
46	d7pcya_	Alignment	not modelled	22.4	25	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
47	d1bvp12	Alignment	not modelled	21.4	45	**Fold:**Viral protein domain **Superfamily:**Viral protein domain **Family:**Top domain of virus capsid protein
48	d9pcya_	Alignment	not modelled	20.8	19	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
49	d1ahsa_	Alignment	not modelled	20.5	26	**Fold:**Viral protein domain **Superfamily:**Viral protein domain **Family:**Top domain of virus capsid protein
50	d1h3na3	Alignment	not modelled	20.3	31	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
51	d1mgta2	Alignment	not modelled	19.7	23	**Fold:**Ribonuclease H-like motif **Superfamily:**Methylated DNA-protein cysteine methyltransferase domain **Family:**Methylated DNA-protein cysteine methyltransferase domain
52	d1bypa_	Alignment	not modelled	19.2	19	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
53	d1paza_	Alignment	not modelled	18.6	18	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
54	c1pfuA_	Alignment	not modelled	18.1	30	**PDB header:**ligase **Chain:** A: **PDB Molecule:**methionyl-trna synthetase; **PDBTitle:** methionyl-trna synthetase from escherichia coli complexed2 with methionine phosphinate
55	d2etna2	Alignment	not modelled	17.9	29	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**GreA transcript cleavage factor, C-terminal domain

56	d1ag6a_	Alignment	not modelled	17.9	19	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
57	d2oiea1	Alignment	not modelled	17.5	38	**Fold:**all-alpha NTP pyrophosphatases **Superfamily:**all-alpha NTP pyrophosphatases **Family:**MazG-like
58	c1woyA_	Alignment	not modelled	16.5	22	**PDB header:**ligase **Chain:** A: **PDB Molecule:**methionyl-trna synthetase; **PDBTitle:** crystal structure of methionyl trna synthetase y225f mutant2 from thermus thermophilus
59	c2im9A_	Alignment	not modelled	16.2	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of protein lpg0564 from legionella pneumophila str.2 philadelphia 1, pfam duf1460
60	d2im9a1	Alignment	not modelled	16.2	13	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Lpg0564-like
61	c2x35A_	Alignment	not modelled	15.8	20	**PDB header:**transcription **Chain:** A: **PDB Molecule:**peregrin; **PDBTitle:** molecular basis of histone h3k36me3 recognition by the pwwp2 domain of brpf1.
62	d1plca_	Alignment	not modelled	15.8	19	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
63	d1ivsa4	Alignment	not modelled	15.3	17	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
64	d2nlua1	Alignment	not modelled	15.1	14	**Fold:**SH3-like barrel **Superfamily:**Tudor/PWWP/MBT **Family:**PWWP domain
65	d2f23a2	Alignment	not modelled	15.1	29	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**GreA transcript cleavage factor, C-terminal domain
66	d1h3za_	Alignment	not modelled	15.0	15	**Fold:**SH3-like barrel **Superfamily:**Tudor/PWWP/MBT **Family:**PWWP domain
67	c2wbqA_	Alignment	not modelled	14.6	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**l-arginine beta-hydroxylase; **PDBTitle:** crystal structure of vioc in complex with (2s,3s)-2 hydroxyarginine
68	d1xcca_	Alignment	not modelled	14.5	19	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
69	c2og5A_	Alignment	not modelled	14.3	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative oxygenase; **PDBTitle:** crystal structure of asparagine oxygenase (asno)
70	c2etnA_	Alignment	not modelled	14.2	29	**PDB header:**transcription **Chain:** A: **PDB Molecule:**anti-cleavage anti-grea transcription factor **PDBTitle:** crystal structure of thermus aquaticus gfh1
71	d1iuza_	Alignment	not modelled	13.9	17	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
72	c3ms5A_	Alignment	not modelled	13.9	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**gamma-butyrobetaine dioxygenase; **PDBTitle:** crystal structure of human gamma-butyrobetaine,2-oxoglutarate2 dioxygenase 1 (bbox1)
73	c3lyiA_	Alignment	not modelled	13.9	9	**PDB header:**transcription **Chain:** A: **PDB Molecule:**bromodomain-containing protein 1; **PDBTitle:** pwwp domain of human bromodomain-containing protein 1
74	c3o82B_	Alignment	not modelled	13.8	14	**PDB header:**ligase **Chain:** B: **PDB Molecule:**peptide arylation enzyme; **PDBTitle:** structure of base n-terminal domain from acinetobacter baumannii bound2 to 5'-o-[n-(2,3-dihydroxybenzoyl)sulfamoyl] adenosine
75	c2l8kA_	Alignment	not modelled	13.0	35	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**non-structural protein 7; **PDBTitle:** nmr structure of the arterivirus nonstructural protein 7 alpha (nsp72 alpha)
76	c2v2gC_	Alignment	not modelled	12.9	26	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**peroxiredoxin 6; **PDBTitle:** crystal structure of the c45s mutant of the peroxiredoxin 62 of arenicola marina. monoclinic form
77	d1te7a_	Alignment	not modelled	12.8	31	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**yqfB-like
78	c3pfsA_	Alignment	not modelled	12.6	9	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**bromodomain and phd finger-containing protein 3; **PDBTitle:** pwwp domain of human bromodomain and phd finger-containing protein 3
79	c2q9lA_	Alignment	not modelled	12.4	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of imazg from vibrio dat 722: ctag-imazg (p43212)
80	d1ds1a_	Alignment	not modelled	12.3	22	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**Clavaminate synthase
81	d1ffya3	Alignment	not modelled	12.2	18	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
						PDB header:cytokine

82	c2l3oA_	Alignment	not modelled	11.7	33	**Chain:** A: **PDB Molecule:**interleukin 3; **PDBTitle:** solution structure of murine interleukin 3
83	c1u0bB_	Alignment	not modelled	11.6	28	**PDB header:**ligase/rna **Chain:** B: **PDB Molecule:**cysteinyl trna; **PDBTitle:** crystal structure of cysteinyl-trna synthetase binary2 complex with trnacys
84	c2wkdA_	Alignment	not modelled	11.5	57	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**orf34p2; **PDBTitle:** crystal structure of a double ile-to-met mutant of protein2 orf34 from lactococcus phage p2
85	d2q5ba1	Alignment	not modelled	11.5	31	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
86	d1em8a_	Alignment	not modelled	11.0	25	**Fold:**DNA polymerase III chi subunit **Superfamily:**DNA polymerase III chi subunit **Family:**DNA polymerase III chi subunit
87	c2l53B_	Alignment	not modelled	11.0	38	**PDB header:**ca-binding protein/proton transport **Chain:** B: **PDB Molecule:**voltage-gated sodium channel type v alpha isoform b **PDBTitle:** solution nmr structure of apo-calmodulin in complex with the iq motif2 of human cardiac sodium channel nav1.5
88	c2p4vA_	Alignment	not modelled	10.6	24	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription elongation factor greb; **PDBTitle:** crystal structure of the transcript cleavage factor, greb2 at 2.6a resolution
89	c3exmA_	Alignment	not modelled	10.1	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphatase sc4828; **PDBTitle:** crystal structure of the phosphatase sc4828 with the non-hydrolyzable2 nucleotide gpcp
90	c3ca8B_	Alignment	not modelled	9.6	25	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**protein ydcf; **PDBTitle:** crystal structure of escherichia coli ydcf, an s-adenosyl-l-methionine2 utilizing enzyme
91	d2cj3a1	Alignment	not modelled	9.0	18	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
92	d1qcsa1	Alignment	not modelled	8.7	30	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Cdc48 N-terminal domain-like
93	d1prxa_	Alignment	not modelled	8.5	26	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
94	c2kxwB_	Alignment	not modelled	8.3	33	**PDB header:**calcium-binding protein/metal transport **Chain:** B: **PDB Molecule:**sodium channel protein type 2 subunit alpha; **PDBTitle:** structure of the c-domain fragment of apo calmodulin bound to the iq2 motif of nav1.2
95	d1li5a2	Alignment	not modelled	8.2	31	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
96	c1obhA_	Alignment	not modelled	8.1	31	**PDB header:**synthetase **Chain:** A: **PDB Molecule:**leucyl-trna synthetase; **PDBTitle:** leucyl-trna synthetase from thermus thermophilus complexed2 with a pre-transfer editing substrate analogue in both3 synthetic active site and editing site
97	c2rfpA_	Alignment	not modelled	8.1	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative ntp pyrophosphohydrolase; **PDBTitle:** crystal structure of putative ntp pyrophosphohydrolase2 (yp_001813558.1) from exiguobacterium sibiricum 255-15 at 1.74 a3 resolution
98	c1ileA_	Alignment	not modelled	8.1	11	**PDB header:**aminoacyl-trna synthetase **Chain:** A: **PDB Molecule:**isoleucyl-trna synthetase; **PDBTitle:** isoleucyl-trna synthetase
99	d1bxua_	Alignment	not modelled	7.9	44	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like