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Description	P03961
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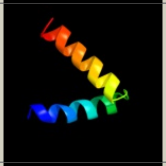
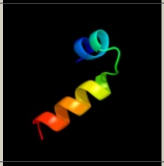
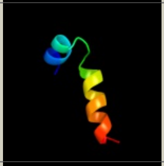
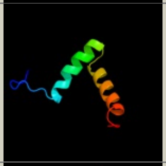
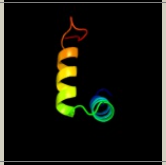
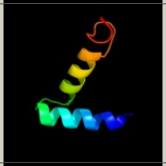
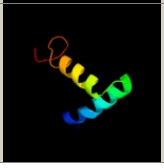
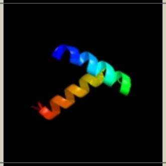
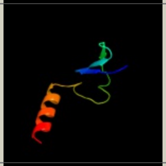
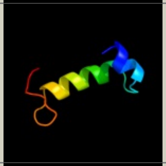
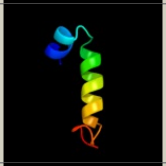
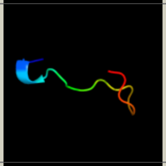
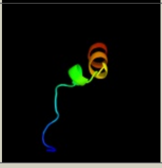
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1hq1a_	Alignment		56.0	17	**Fold:**Signal peptide-binding domain **Superfamily:**Signal peptide-binding domain **Family:**Signal peptide-binding domain
2	c3ipwA_	Alignment		54.7	8	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hydrolase tatd family protein; **PDBTitle:** crystal structure of hydrolase tatd family protein from entamoeba2 histolytica
3	d1dula_	Alignment		54.5	18	**Fold:**Signal peptide-binding domain **Superfamily:**Signal peptide-binding domain **Family:**Signal peptide-binding domain
4	d1qb2a_	Alignment		53.8	29	**Fold:**Signal peptide-binding domain **Superfamily:**Signal peptide-binding domain **Family:**Signal peptide-binding domain
5	c2jqeA_	Alignment		52.2	25	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**signal recognition 54 kda protein; **PDBTitle:** soution structure of af54 m-domain
6	d2ffha2	Alignment		49.4	25	**Fold:**Signal peptide-binding domain **Superfamily:**Signal peptide-binding domain **Family:**Signal peptide-binding domain
7	c3rcmA_	Alignment		47.0	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**tatd family hydrolase; **PDBTitle:** crystal structure of efi target 500140:tatd family hydrolase from2 pseudomonas putida
8	d1qzxa2	Alignment		46.0	32	**Fold:**Signal peptide-binding domain **Superfamily:**Signal peptide-binding domain **Family:**Signal peptide-binding domain
9	c3e2vA_	Alignment		45.3	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**3'-5'-exonuclease; **PDBTitle:** crystal structure of an uncharacterized amidohydrolase from2 saccharomyces cerevisiae
10	c3gg7A_	Alignment		42.2	8	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized metalloprotein; **PDBTitle:** crystal structure of an uncharacterized metalloprotein from2 deinococcus radiodurans
11	d1j6oa_	Alignment		35.0	3	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**TatD Mg-dependent DNase-like

12	d1xwya1	Alignment		33.9	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**TatD Mg-dependent DNase-like
13	c2xioA_	Alignment		27.1	8	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative deoxyribonuclease tatdn1; **PDBTitle:** structure of putative deoxyribonuclease tatdn1 isoform a
14	d1zoda1	Alignment		26.2	19	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
15	c3qllB_	Alignment		26.2	5	**PDB header:**lyase **Chain:** B: **PDB Molecule:**citrate lyase; **PDBTitle:** crystal structure of ripc from yersinia pestis
16	d1zzma1	Alignment		25.4	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**TatD Mg-dependent DNase-like
17	c2y1hA_	Alignment		24.7	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative deoxyribonuclease tatdn3; **PDBTitle:** crystal structure of the human tatd-domain protein 3 (tatdn3)
18	d2fp7b1	Alignment		23.6	33	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Viral proteases
19	c2gzxB_	Alignment		22.8	19	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative tatd related dnase; **PDBTitle:** crystal structure of the tatd deoxyribonuclease mw0446 from2 staphylococcus aureus. northeast structural genomics consortium3 target zr237.
20	c1toaA_	Alignment		22.1	8	**PDB header:**binding protein **Chain:** A: **PDB Molecule:**protein (periplasmic binding protein troa); **PDBTitle:** periplasmic zinc binding protein troa from treponema pallidum
21	d1toaa_	Alignment	not modelled	22.1	8	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**TroA-like
22	c3dxvA_	Alignment	not modelled	22.1	25	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**alpha-amino-epsilon-caprolactam racemase; **PDBTitle:** the crystal structure of alpha-amino-epsilon-caprolactam racemase from2 achromobacter obae
23	c2ordA_	Alignment	not modelled	22.0	24	**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
24	c1z7dE_	Alignment	not modelled	21.9	17	**PDB header:**transferase **Chain:** E: **PDB Molecule:**ornithine aminotransferase; **PDBTitle:** ornithine aminotransferase py00104 from plasmodium yoelii
25	d2ijob1	Alignment	not modelled	21.8	39	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Viral proteases
26	c2fvmA_	Alignment	not modelled	21.7	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dihydropyrimidinase; **PDBTitle:** crystal structure of dihydropyrimidinase from saccharomyces kluyveri2 in complex with the reaction product n-carbamyl-beta-alanine
27	c3e90B_	Alignment	not modelled	21.2	39	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**ns3 protease; **PDBTitle:** west nile virus ns2b-ns3protease in complexed with2 inhibitor naph-kkr-h
						PDB header:transferase **Chain:** B: **PDB Molecule:**acetylornithine/succinyldiaminopimelate

28	c2pb2B_	Alignment	not modelled	20.7	16	aminotransferase; **PDBTitle:** structure of biosynthetic n-acetylornithine aminotransferase from2 salmonella typhimurium: studies on substrate specificity and3 inhibitor binding
29	c2j37W_	Alignment	not modelled	20.4	29	**PDB header:**ribosome **Chain:** W: **PDB Molecule:**signal recognition particle 54 kda protein **PDBTitle:** model of mammalian srp bound to 80s rncs
30	c2v3cC_	Alignment	not modelled	20.0	17	**PDB header:**signaling protein **Chain:** C: **PDB Molecule:**signal recognition 54 kda protein; **PDBTitle:** crystal structure of the srp54-srp19-7s.s srp rna complex2 of m. jannaschii
31	c2ps3A_	Alignment	not modelled	19.5	13	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**high-affinity zinc uptake system protein znua; **PDBTitle:** structure and metal binding properties of znua, a2 periplasmic zinc transporter from escherichia coli
32	d1befa_	Alignment	not modelled	19.2	33	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Viral proteases
33	c3lkwA_	Alignment	not modelled	18.8	28	**PDB header:**viral protein,hydrolase **Chain:** A: **PDB Molecule:**fusion protein of nonstructural protein 2b and **PDBTitle:** crystal structure of dengue virus 1 ns2b/ns3 protease active2 site mutant
34	c3dm5A_	Alignment	not modelled	18.1	29	**PDB header:**rna binding protein, transport protein **Chain:** A: **PDB Molecule:**signal recognition 54 kda protein; **PDBTitle:** structures of srp54 and srp19, the two proteins assembling2 the ribonucleic core of the signal recognition particle3 from the archaeon pyrococcus furiosus.
35	c3mfqB_	Alignment	not modelled	17.9	5	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**high-affinity zinc uptake system protein znua; **PDBTitle:** a glance into the metal binding specificity of troa: where elaborate2 behaviors occur in the active center
36	d2byla1	Alignment	not modelled	17.7	16	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
37	d2fomb1	Alignment	not modelled	17.6	33	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Viral proteases
38	c2iy3A_	Alignment	not modelled	17.3	25	**PDB header:**rna-binding **Chain:** A: **PDB Molecule:**signal recognition particle protein ffh; **PDBTitle:** structure of the e. coli signal recognition particle2 bound to a translating ribosome
39	d1ohwa_	Alignment	not modelled	17.1	15	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
40	d2phcb1	Alignment	not modelled	16.2	29	**Fold:**Cyclophilin-like **Superfamily:**Cyclophilin-like **Family:**PH0987 C-terminal domain-like
41	c1oatB_	Alignment	not modelled	15.7	15	**PDB header:**aminotransferase **Chain:** B: **PDB Molecule:**ornithine aminotransferase; **PDBTitle:** ornithine aminotransferase
42	c3n5mD_	Alignment	not modelled	15.4	14	**PDB header:**transferase **Chain:** D: **PDB Molecule:**adenosylmethionine-8-amino-7-oxononanoate aminotransferase; **PDBTitle:** crystals structure of a bacillus anthracis aminotransferase
43	d1sffa_	Alignment	not modelled	15.4	13	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
44	c3fcrA_	Alignment	not modelled	15.1	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative aminotransferase; **PDBTitle:** crystal structure of putative aminotransferase (yp_614685.1) from2 silicibacter sp. tm1040 at 1.80 a resolution
45	d1vkoa1	Alignment	not modelled	14.9	24	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
46	c1qzwC_	Alignment	not modelled	14.6	29	**PDB header:**signaling protein/rna **Chain:** C: **PDB Molecule:**signal recognition 54 kda protein; **PDBTitle:** crystal structure of the complete core of archaeal srp and2 implications for inter-domain communication
47	c3i4jC_	Alignment	not modelled	14.6	17	**PDB header:**transferase **Chain:** C: **PDB Molecule:**aminotransferase, class iii; **PDBTitle:** crystal structure of aminotransferase, class iii from2 deinococcus radiodurans
48	d2pv4a1	Alignment	not modelled	14.5	29	**Fold:**Sama2622-like **Superfamily:**Sama2622-like **Family:**Sama2622-like
49	c2j289_	Alignment	not modelled	14.2	18	**PDB header:**ribosome **Chain:** 9: **PDB Molecule:**signal recognition particle 54; **PDBTitle:** model of e. coli srp bound to 70s rncs
50	d1yixa1	Alignment	not modelled	13.6	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**TatD Mg-dependent DNase-like
51	c2zp2B_	Alignment	not modelled	13.1	25	**PDB header:**transferase inhibitor **Chain:** B: **PDB Molecule:**kinase a inhibitor; **PDBTitle:** c-terminal domain of kipi from bacillus subtilis
52	d1s0aa_	Alignment	not modelled	13.1	17	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
						PDB header:high density lipoproteins

53	c1gw4A_	Alignment	not modelled	12.6	35	**Chain:** A: **PDB Molecule:**apoa-i; **PDBTitle:** the helix-hinge-helix structural motif in human2 apolipoprotein a-i determined by nmr spectroscopy, 13 structure
54	c3hjtB_	Alignment	not modelled	11.6	21	**PDB header:**cell adhesion, transport protein **Chain:** B: **PDB Molecule:**lmb; **PDBTitle:** structure of laminin binding protein (lmb) of streptococcus2 agalactiae a bifunctional protein with adhesin and metal3 transporting activity
55	c3oksB_	Alignment	not modelled	11.5	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**4-aminobutyrate transaminase; **PDBTitle:** crystal structure of 4-aminobutyrate transaminase from mycobacterium2 smegmatis
56	c3l44A_	Alignment	not modelled	11.5	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glutamate-1-semialdehyde 2,1-aminomutase 1; **PDBTitle:** crystal structure of bacillus anthracis heml-1, glutamate semialdehyde2 aminotransferase
57	d1z7da1	Alignment	not modelled	11.4	17	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
58	c3dodA_	Alignment	not modelled	11.2	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**adenosylmethionine-8-amino-7-oxononanoate aminotransferase; **PDBTitle:** crystal structure of plp bound 7,8-diaminopelargonic acid synthase in2 bacillus subtilis
59	c3nuiA_	Alignment	not modelled	11.0	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyruvate transaminase; **PDBTitle:** crystal structure of omega-transferase from vibrio fluvialis js17
60	c2eh6A_	Alignment	not modelled	10.6	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetylornithine aminotransferase; **PDBTitle:** crystal structure of acetylornithine aminotransferase from aquifex2 aeolicus vf5
61	d1afwa2	Alignment	not modelled	10.1	30	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Thiolase-related
62	d1d8ca_	Alignment	not modelled	10.1	36	**Fold:**TIM beta/alpha-barrel **Superfamily:**Malate synthase G **Family:**Malate synthase G
63	c1x3wB_	Alignment	not modelled	9.9	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**uv excision repair protein rad23; **PDBTitle:** structure of a peptide:n-glycanase-rad23 complex
64	d1e5pa_	Alignment	not modelled	9.8	25	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Retinol binding protein-like
65	c3ruyB_	Alignment	not modelled	9.8	8	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ornithine aminotransferase; **PDBTitle:** crystal structure of the ornithine-oxo acid transaminase rocd from2 bacillus anthracis
66	c3afhA_	Alignment	not modelled	9.8	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glutamyl-trna synthetase 2; **PDBTitle:** crystal structure of thermotoga maritima nondiscriminating glutamyl-2 trna synthetase in complex with a glutamyl-amp analog
67	d1ldma1	Alignment	not modelled	9.7	27	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
68	c2k9sA_	Alignment	not modelled	9.4	27	**PDB header:**transcription **Chain:** A: **PDB Molecule:**arabinose operon regulatory protein; **PDBTitle:** solution structure of dna binding domain of e. coli arac
69	d2v9va2	Alignment	not modelled	9.2	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**C-terminal fragment of elongation factor SelB
70	c2ee7A_	Alignment	not modelled	9.1	14	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**sperm flagellar protein 1; **PDBTitle:** solution structure of the ch domain from human sperm2 flagellar protein 1
71	d1gnsa_	Alignment	not modelled	9.1	17	**Fold:**Subtilisin-like **Superfamily:**Subtilisin-like **Family:**Subtilases
72	d1i0za1	Alignment	not modelled	8.9	24	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
73	d1tw3a1	Alignment	not modelled	8.9	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Plant O-methyltransferase, N-terminal domain
74	d1p1ja1	Alignment	not modelled	8.7	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
75	c3c19A_	Alignment	not modelled	8.5	0	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein mk0293; **PDBTitle:** crystal structure of protein mk0293 from methanopyrus kandleri av19
76	d2a1ja1	Alignment	not modelled	8.5	13	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Hef domain-like
77	c1u5vA_	Alignment	not modelled	8.4	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**cite; **PDBTitle:** structure of cite complexed with triphosphate group of atp2 form mycobacterium tuberculosis
78	c2ov3A_	Alignment	not modelled	8.1	25	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**periplasmic binding protein component of an abc **PDBTitle:** crystal structure of 138-173 znua deletion mutant plus

						zinc2 bound
79	c2kq5A_	Alignment	not modelled	8.0	14	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**avirulence protein; **PDBTitle:** solution nmr structure of a section of the repeat domain of the type2 iii effector protein ptha
80	d1psza_	Alignment	not modelled	7.9	14	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**TroA-like
81	c2xstA_	Alignment	not modelled	7.7	15	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**lipocalin 15; **PDBTitle:** crystal structure of the human lipocalin 15
82	c3rggD_	Alignment	not modelled	7.5	9	**PDB header:**lyase **Chain:** D: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase, pure protein; **PDBTitle:** crystal structure of treponema denticola pure bound to air
83	d1b8za_	Alignment	not modelled	7.5	24	**Fold:**IHF-like DNA-binding proteins **Superfamily:**IHF-like DNA-binding proteins **Family:**Prokaryotic DNA-bending protein
84	d1oqya3	Alignment	not modelled	7.4	23	**Fold:**XPC-binding domain **Superfamily:**XPC-binding domain **Family:**XPC-binding domain
85	d1z67a1	Alignment	not modelled	7.4	9	**Fold:**YidB-like **Superfamily:**YidB-like **Family:**YidB-like
86	c3ls1A_	Alignment	not modelled	7.3	26	**PDB header:**photosynthesis **Chain:** A: **PDB Molecule:**sll1638 protein; **PDBTitle:** crystal structure of cyanobacterial psbq from synechocystis2 sp. pcc 6803 complexed with zn2+
87	c2zc1A_	Alignment	not modelled	7.3	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphotriesterase; **PDBTitle:** organophosphorus hydrolase from deinococcus radiodurans
88	c2fw9A_	Alignment	not modelled	7.2	22	**PDB header:**lyase **Chain:** A: **PDB Molecule:**n5-carboxyaminoimidazole ribonucleotide mutase; **PDBTitle:** structure of pure (n5-carboxyaminoimidazole ribonucleotide mutase)2 h59f from the acidophilic bacterium acetobacter aceti, at ph 8
89	c2huoA_	Alignment	not modelled	7.2	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**inositol oxygenase; **PDBTitle:** crystal structure of mouse myo-inositol oxygenase in complex with2 substrate
90	d3bxda1	Alignment	not modelled	7.2	11	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**MioX-like
91	d1pq4a_	Alignment	not modelled	7.1	25	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**TroA-like
92	d1znda1	Alignment	not modelled	7.1	4	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Retinol binding protein-like
93	d1u11a_	Alignment	not modelled	7.1	22	**Fold:**Flavodoxin-like **Superfamily:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) **Family:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
94	d1hdgo2	Alignment	not modelled	7.1	19	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**GAPDH-like
95	d1x68a2	Alignment	not modelled	7.0	50	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
96	c1xvlC_	Alignment	not modelled	7.0	14	**PDB header:**metal transport **Chain:** C: **PDB Molecule:**mn transporter; **PDBTitle:** the three-dimensional structure of mntc from synechocystis2 6803
97	c3hmuA_	Alignment	not modelled	6.8	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aminotransferase, class iii; **PDBTitle:** crystal structure of a class iii aminotransferase from2 silicibacter pomeroyi
98	c1w1nA_	Alignment	not modelled	6.7	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphatidylinositol 3-kinase tor1; **PDBTitle:** the solution structure of the fatc domain of the protein2 kinase tor1 from yeast
99	c2e7uA_	Alignment	not modelled	6.7	14	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glutamate-1-semialdehyde 2,1-aminomutase; **PDBTitle:** crystal structure of glutamate-1-semialdehyde 2,1-aminomutase from2 thermus thermophilus hb8