



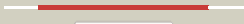









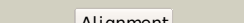

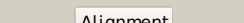

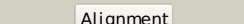

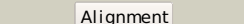



#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1h5ra_	 Alignment		100.0	100	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidyltransferase
2	d1mc3a_	 Alignment		100.0	65	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidyltransferase
3	d1fxoa_	 Alignment		100.0	76	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidyltransferase
4	d1iina_	 Alignment		100.0	92	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidyltransferase
5	d1lvwa_	 Alignment		100.0	61	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: glucose-1-phosphate thymidyltransferase
6	c2pa4B_	 Alignment		100.0	24	PDB header: transferase Chain: B: PDB Molecule: utp-glucose-1-phosphate uridylyltransferase; PDBTitle: crystal structure of udp-glucose pyrophosphorylase from corynebacteria2 glutamicum in complex with magnesium and udp-glucose
7	c2ux8G_	 Alignment		100.0	25	PDB header: transferase Chain: G: PDB Molecule: glucose-1-phosphate uridylyltransferase; PDBTitle: crystal structure of sphingomonas elodea atcc 31461 glucose-2 1-phosphate uridylyltransferase in complex with glucose-3 1-phosphate.
8	c2e3dB_	 Alignment		100.0	25	PDB header: transferase Chain: B: PDB Molecule: utp--glucose-1-phosphate uridylyltransferase; PDBTitle: crystal structure of e. coli glucose-1-phosphate2 uridylyltransferase
9	c2x5sB_	 Alignment		100.0	21	PDB header: transferase Chain: B: PDB Molecule: mannose-1-phosphate guanylyltransferase; PDBTitle: crystal structure of t. maritima gdp-mannose2 pyrophosphorylase in apo state.
10	c3jukA_	 Alignment		100.0	28	PDB header: transferase Chain: A: PDB Molecule: udp-glucose pyrophosphorylase (gal u); PDBTitle: the crystal structure of udp-glucose pyrophosphorylase complexed with2 udp-glucose
11	c1yp3C_	 Alignment		100.0	24	PDB header: transferase Chain: C: PDB Molecule: glucose-1-phosphate adenlyltransferase small PDBTitle: crystal structure of potato tuber adp-glucose2 pyrophosphorylase in complex with atp

12	c3hl3A_	Alignment		100.0	44	PDB header: transferase Chain: A: PDB Molecule: glucose-1-phosphate thymidyltransferase; PDBTitle: 2.76 angstrom crystal structure of a putative glucose-1-phosphate2 thymidyltransferase from bacillus anthracis in complex with a3 sucrose.
13	c3pnnA_	Alignment		100.0	18	PDB header: transferase Chain: A: PDB Molecule: conserved domain protein; PDBTitle: the crystal structure of a glycosyltransferase from porphyromonas2 gingivalis w83
14	c2cu2A_	Alignment		100.0	17	PDB header: transferase Chain: A: PDB Molecule: putative mannose-1-phosphate guanylyl transferase; PDBTitle: crystal structure of mannose-1-phosphate geranyltransferase from2 thermus thermophilus hb8
15	d1yp2a2	Alignment		100.0	22	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-di-phospho-sugar transferases Family: glucose-1-phosphate thymidyltransferase
16	c3brkX_	Alignment		100.0	20	PDB header: transferase Chain: X: PDB Molecule: glucose-1-phosphate adenyltransferase; PDBTitle: crystal structure of adp-glucose pyrophosphorylase from2 agrobacterium tumefaciens
17	c3d98A_	Alignment		100.0	20	PDB header: transferase Chain: A: PDB Molecule: bifunctional protein glmu; PDBTitle: crystal structure of glmu from mycobacterium tuberculosis, ligand-free2 form
18	c2qkxA_	Alignment		100.0	20	PDB header: transferase Chain: A: PDB Molecule: bifunctional protein glmu; PDBTitle: n-acetyl glucosamine 1-phosphate uridyltransferase from mycobacterium2 tuberculosis complex with n-acetyl glucosamine 1-phosphate
19	c1hm8A_	Alignment		100.0	23	PDB header: transferase Chain: A: PDB Molecule: udp-n-acetylglucosamine-1-phosphate uridyltransferase; PDBTitle: crystal structure of s.pneumoniae n-acetylglucosamine-1-phosphate2 uridyltransferase, glmu, bound to acetyl coenzyme a
20	d2cu2a2	Alignment		100.0	19	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-di-phospho-sugar transferases Family: mannose-1-phosphate guanylyl transferase
21	c2oi6A_	Alignment	not modelled	100.0	22	PDB header: transferase Chain: A: PDB Molecule: bifunctional protein glmu; PDBTitle: e. coli glmu- complex with udp-glcna, coa and glcn-1-po4
22	d1tzfa_	Alignment	not modelled	100.0	19	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-di-phospho-sugar transferases Family: Cytidyltransferase
23	c2v0hA_	Alignment	not modelled	100.0	24	PDB header: transferase Chain: A: PDB Molecule: bifunctional protein glmu; PDBTitle: characterization of substrate binding and catalysis of the2 potential antibacterial target n-acetylglucosamine-1-3 phosphate uridyltransferase (glmu)
24	c1fwyA_	Alignment	not modelled	100.0	19	PDB header: transferase Chain: A: PDB Molecule: udp-n-acetylglucosamine pyrophosphorylase; PDBTitle: crystal structure of n-acetylglucosamine 1-phosphate2 uridyltransferase bound to udp-glcna
25	d1g97a2	Alignment	not modelled	100.0	20	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-di-phospho-sugar transferases Family: UDP-glucose pyrophosphorylase
26	c2ggqA_	Alignment	not modelled	100.0	29	PDB header: transferase Chain: A: PDB Molecule: 401aa long hypothetical glucose-1-phosphate PDBTitle: complex of hypothetical glucose-1-phosphate thymidyltransferase from2 sulfobolus tokodaii
27	d2oi6a2	Alignment	not modelled	100.0	21	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-di-phospho-sugar transferases Family: UDP-glucose pyrophosphorylase
28	d1vica_	Alignment	not modelled	100.0	16	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-di-phospho-sugar transferases

						Family: Cytidyltransferase
29	c1jvLC	Alignment	not modelled	100.0	19	PDB header: transferase Chain: C: PDB Molecule: ctp:phosphocholine cytidyltransferase; PDBTitle: catalytic mechanism of ctp:phosphocholine2 cytidyltransferase from streptococcus pneumoniae (licc)
30	d1jyka	Alignment	not modelled	100.0	19	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidyltransferase
31	c3oamD	Alignment	not modelled	100.0	18	PDB header: transferase Chain: D: PDB Molecule: 3-deoxy-manno-octulosonate cytidyltransferase; PDBTitle: crystal structure of cytidyltransferase from vibrio cholerae
32	c2qh5B	Alignment	not modelled	100.0	17	PDB header: isomerase Chain: B: PDB Molecule: mannose-6-phosphate isomerase; PDBTitle: crystal structure of mannose-6-phosphate isomerase from helicobacter2 pylori
33	c2xmhB	Alignment	not modelled	100.0	18	PDB header: transferase Chain: B: PDB Molecule: ctp:inositol-1-phosphate cytidyltransferase; PDBTitle: the x-ray structure of ctp:inositol-1-phosphate2 cytidyltransferase from archaeoglobus fulgidus
34	c2xwlB	Alignment	not modelled	100.0	19	PDB header: transferase Chain: B: PDB Molecule: 2-c-methyl-d-erythritol 4-phosphate cytidyltransferase; PDBTitle: crystal structure of ispd from mycobacterium smegmatis in complex2 with ctp and mg
35	c3polA	Alignment	not modelled	100.0	19	PDB header: transferase Chain: A: PDB Molecule: 3-deoxy-manno-octulosonate cytidyltransferase; PDBTitle: 2.3 angstrom crystal structure of 3-deoxy-manno-octulosonate2 cytidyltransferase (kdsb) from acinetobacter baumannii.
36	d1vh1a	Alignment	not modelled	100.0	17	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidyltransferase
37	dli52a	Alignment	not modelled	100.0	16	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidyltransferase
38	d1h7ea	Alignment	not modelled	100.0	18	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidyltransferase
39	c3tqdA	Alignment	not modelled	100.0	17	PDB header: transferase Chain: A: PDB Molecule: 3-deoxy-manno-octulosonate cytidyltransferase; PDBTitle: structure of the 3-deoxy-d-manno-octulosonate cytidyltransferase2 (kdsb) from coxiella burnetii
40	c2y6pC	Alignment	not modelled	99.9	19	PDB header: transferase Chain: C: PDB Molecule: 3-deoxy-manno-octulosonate cytidyltransferase; PDBTitle: evidence for a two-metal-ion-mechanism in the2 kdsb cytidyltransferase kdsb
41	d1vpaa	Alignment	not modelled	99.9	16	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidyltransferase
42	d1eyra	Alignment	not modelled	99.9	15	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidyltransferase
43	d1vh3a	Alignment	not modelled	99.9	14	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidyltransferase
44	c3f1cB	Alignment	not modelled	99.9	18	PDB header: transferase Chain: B: PDB Molecule: putative 2-c-methyl-d-erythritol 4-phosphate PDBTitle: crystal structure of 2-c-methyl-d-erythritol 4-phosphate2 cytidyltransferase from listeria monocytogenes
45	d1qwja	Alignment	not modelled	99.9	14	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidyltransferase
46	d1w5a1	Alignment	not modelled	99.9	19	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidyltransferase
47	c3okrA	Alignment	not modelled	99.9	14	PDB header: transferase Chain: A: PDB Molecule: 2-c-methyl-d-erythritol 4-phosphate cytidyltransferase; PDBTitle: structure of mtb apo 2-c-methyl-d-erythritol 4-phosphate2 cytidyltransferase (ispd)
48	c2we9A	Alignment	not modelled	99.9	17	PDB header: unknown function Chain: A: PDB Molecule: moba-related protein; PDBTitle: crystal structure of rv0371c from mycobacterium2 tuberculosis h37rv
49	c2wawA	Alignment	not modelled	99.9	14	PDB header: unknown function Chain: A: PDB Molecule: moba relate protein; PDBTitle: crystal structure of mycobacterium tuberculosis rv0371c2 homolog from mycobacterium sp. strain jc1
50	d1e5ka	Alignment	not modelled	99.9	18	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Molybdenum cofactor biosynthesis protein MobA
51	c2vshB	Alignment	not modelled	99.9	15	PDB header: transferase Chain: B: PDB Molecule: 2-c-methyl-d-erythritol 4-phosphate PDBTitle: synthesis of cdp-activated ribitol for teichoic acid2 precursors in streptococcus pneumoniae
52	c3ngwA	Alignment	not modelled	99.9	13	PDB header: biosynthetic protein Chain: A: PDB Molecule: molybdopterin-guanine dinucleotide biosynthesis protein a PDBTitle: crystal structure of molybdopterin-guanine dinucleotide

						biosynthesis2 protein a from archaeoglobus fulgidus, northeast structural genomics3 consortium target gr189
53	c2px7A	Alignment	not modelled	99.8	13	PDB header: transferase Chain: A: PDB Molecule: 2-c-methyl-d-erythritol 4-phosphate PDBTitle: crystal structure of 2-c-methyl-d-erythritol 4-phosphate2 cytidyltransferase from thermus thermophilus hb8
54	d2dpwa1	Alignment	not modelled	99.8	18	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-di-phospho-sugar transferases Family: TTHA0179-like
55	d1w77a1	Alignment	not modelled	99.8	15	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-di-phospho-sugar transferases Family: Cytidylyltransferase
56	d1vgwa	Alignment	not modelled	99.8	16	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-di-phospho-sugar transferases Family: Cytidylyltransferase
57	c3rsbB	Alignment	not modelled	99.8	14	PDB header: transferase Chain: B: PDB Molecule: adenosylcobinamide-phosphate guanylyltransferase; PDBTitle: structure of the archaeal gtp:adocbi-p guanylyltransferase (coby) from2 methanocaldococcus jannaschii
58	c1w57A	Alignment	not modelled	99.8	18	PDB header: transferase Chain: A: PDB Molecule: ispd/ispf bifunctional enzyme; PDBTitle: structure of the bifunctional ispdf from campylobacter2 jejuni containing zn
59	c3okrC	Alignment	not modelled	99.7	17	PDB header: transferase Chain: C: PDB Molecule: 2-c-methyl-d-erythritol 4-phosphate cytidyltransferase; PDBTitle: structure of mtb apo 2-c-methyl-d-erythritol 4-phosphate2 cytidyltransferase (ispd)
60	c2e8bA	Alignment	not modelled	99.6	13	PDB header: biosynthetic protein Chain: A: PDB Molecule: probable molybdopterin-guanine dinucleotide biosynthesis PDBTitle: crystal structure of the putative protein (aq1419) from aquifex2 aeolicus vf5
61	c3d5nB	Alignment	not modelled	99.1	21	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: q97w15_sulso; PDBTitle: crystal structure of the q97w15_sulso protein from2 sulfolobus solfataricus. nesg target ssr125.
62	d1vm8a	Alignment	not modelled	99.0	18	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-di-phospho-sugar transferases Family: UDP-glucose pyrophosphorylase
63	c3oc9A	Alignment	not modelled	98.9	17	PDB header: transferase Chain: A: PDB Molecule: udp-n-acetylglucosamine pyrophosphorylase; PDBTitle: crystal structure of putative udp-n-acetylglucosamine2 pyrophosphorylase from entamoeba histolytica
64	d1jv1a	Alignment	not modelled	98.9	20	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-di-phospho-sugar transferases Family: UDP-glucose pyrophosphorylase
65	d2icya2	Alignment	not modelled	98.9	13	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-di-phospho-sugar transferases Family: UDP-glucose pyrophosphorylase
66	c2i5kB	Alignment	not modelled	98.8	14	PDB header: transferase Chain: B: PDB Molecule: utp--glucose-1-phosphate uridylyltransferase; PDBTitle: crystal structure of ugp1p
67	c2q4jB	Alignment	not modelled	98.8	10	PDB header: transferase Chain: B: PDB Molecule: probable utp-glucose-1-phosphate uridylyltransferase 2; PDBTitle: ensemble refinement of the protein crystal structure of gene product2 from arabidopsis thaliana at3g03250, a putative udp-glucose3 pyrophosphorylase
68	c2yqsA	Alignment	not modelled	98.7	19	PDB header: transferase Chain: A: PDB Molecule: udp-n-acetylglucosamine pyrophosphorylase; PDBTitle: crystal structure of uridine-diphospho-n-acetylglucosamine2 pyrophosphorylase from candida albicans, in the product-binding form
69	c3gueB	Alignment	not modelled	98.7	14	PDB header: transferase Chain: B: PDB Molecule: utp-glucose-1-phosphate uridylyltransferase 2; PDBTitle: crystal structure of udp-glucose phosphorylase from trypanosoma2 brucei, (tb10.389.0330)
70	c3ogzA	Alignment	not modelled	98.4	19	PDB header: transferase Chain: A: PDB Molecule: udp-sugar pyrophosphorylase; PDBTitle: protein structure of usp from l. major in apo-form
71	c2oefA	Alignment	not modelled	98.2	15	PDB header: transferase Chain: A: PDB Molecule: utp-glucose-1-phosphate uridylyltransferase 2, PDBTitle: open and closed structures of the udp-glucose2 pyrophosphorylase from leishmania major
72	c2d7iA	Alignment	not modelled	97.1	14	PDB header: transferase Chain: A: PDB Molecule: polypeptide n-acetylglactosaminyltransferase 10; PDBTitle: crsytal structure of pp-galnac-t10 with udp, galnac and mn2+
73	c1xhbA	Alignment	not modelled	96.3	11	PDB header: transferase Chain: A: PDB Molecule: polypeptide n-acetylglactosaminyltransferase 1; PDBTitle: the crystal structure of udp-galnac: polypeptide alpha-n-2 acetylglactosaminyltransferase-t1
74	c2ffuA	Alignment	not modelled	96.1	12	PDB header: transferase Chain: A: PDB Molecule: polypeptide n-acetylglactosaminyltransferase 2; PDBTitle: crystal structure of human ppgalnact-2 complexed with udp2 and ea2
						PDB header: transferase Chain: D: PDB Molecule: chondroitin synthase;

75	c2z86D_	Alignment	not modelled	95.6	13	PDBTitle: crystal structure of chondroitin polymerase from2 escherichia coli strain k4 (k4cp) complexed with udp-glucua3 and udp
76	d1omza_	Alignment	not modelled	95.1	9	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Exostosin
77	d1xhba2	Alignment	not modelled	95.0	10	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Polypeptide N-acetyl galactosaminyltransferase 1, N-terminal domain
78	c1omxB_	Alignment	not modelled	94.7	8	PDB header: transferase Chain: B: PDB Molecule: alpha-1,4-n-acetylhexosaminyltransferase extl2; PDBTitle: crystal structure of mouse alpha-1,4-n-2 acetylhexosaminyltransferase (extl2)
79	c3f1yC_	Alignment	not modelled	89.7	15	PDB header: transferase Chain: C: PDB Molecule: mannosyl-3-phosphoglycerate synthase; PDBTitle: mannosyl-3-phosphoglycerate synthase from rubrobacter xylanophilus
80	c2qgiA_	Alignment	not modelled	87.8	7	PDB header: transferase Chain: A: PDB Molecule: atp synthase subunits region orf 6; PDBTitle: the udp complex structure of the sixth gene product of the f1-atpase2 operon of rhodobacter blasticus
81	c3cgxA_	Alignment	not modelled	87.8	14	PDB header: transferase Chain: A: PDB Molecule: putative nucleotide-diphospho-sugar transferase; PDBTitle: crystal structure of putative nucleotide-diphospho-sugar transferase2 (yp_389115.1) from desulfovibrio desulfuricans g20 at 1.90 a3 resolution
82	c3ckvA_	Alignment	not modelled	86.6	14	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of a mycobacterial protein
83	c3bcvA_	Alignment	not modelled	82.0	14	PDB header: transferase Chain: A: PDB Molecule: putative glycosyltransferase protein; PDBTitle: crystal structure of a putative glycosyltransferase from bacteroides2 fragilis
84	d1qg8a_	Alignment	not modelled	77.1	14	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Spore coat polysaccharide biosynthesis protein SpsA
85	d2i5ea1	Alignment	not modelled	72.0	14	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: MM2497-like
86	d1oxza_	Alignment	not modelled	37.8	19	Fold: Spectrin repeat-like Superfamily: GAT-like domain Family: GAT domain
87	c1oxzA_	Alignment	not modelled	37.8	19	PDB header: membrane protein Chain: A: PDB Molecule: adp-ribosylation factor binding protein gga1; PDBTitle: crystal structure of the human gga1 gat domain
88	c1nafA_	Alignment	not modelled	32.4	19	PDB header: signaling protein, membrane protein Chain: A: PDB Molecule: adp-ribosylation factor binding protein gga1; PDBTitle: crystal structure of the human gga1 gat domain
89	d1j2jb_	Alignment	not modelled	27.0	13	Fold: Spectrin repeat-like Superfamily: GAT-like domain Family: GAT domain
90	c3uowB_	Alignment	not modelled	20.6	25	PDB header: ligase Chain: B: PDB Molecule: gmp synthetase; PDBTitle: crystal structure of pf10_0123, a gmp synthetase from plasmodium2 falciparum
91	d3bofa2	Alignment	not modelled	19.4	17	Fold: TIM beta/alpha-barrel Superfamily: Homocysteine S-methyltransferase Family: Homocysteine S-methyltransferase
92	c3zq4C_	Alignment	not modelled	16.9	11	PDB header: hydrolase Chain: C: PDB Molecule: ribonuclease j 1; PDBTitle: unusual, dual endo- and exo-nuclease activity in the degradosome2 explained by crystal structure analysis of rnase j1
93	d2i7na2	Alignment	not modelled	16.7	11	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Fumble-like
94	c1gpmD_	Alignment	not modelled	15.5	22	PDB header: transferase (glutamine amidotransferase) Chain: D: PDB Molecule: gmp synthetase; PDBTitle: escherichia coli gmp synthetase complexed with amp and pyrophosphate
95	c3lubE_	Alignment	not modelled	14.8	30	PDB header: hydrolase Chain: E: PDB Molecule: putative creatinine amidohydrolase; PDBTitle: crystal structure of putative creatinine amidohydrolase2 (yp_211512.1) from bacteroides fragilis nctc 9343 at 2.11 a3 resolution
96	c1ze2B_	Alignment	not modelled	13.0	14	PDB header: lyase/rna Chain: B: PDB Molecule: trna pseudouridine synthase b; PDBTitle: conformational change of pseudouridine 55 synthase upon its2 association with rna substrate
97	d2hk6a1	Alignment	not modelled	12.5	21	Fold: Chelatase-like Superfamily: Chelatase Family: Ferrochelatase
98	c3no4A_	Alignment	not modelled	11.7	12	PDB header: hydrolase Chain: A: PDB Molecule: creatinine amidohydrolase; PDBTitle: crystal structure of a creatinine amidohydrolase (npun_f1913) from2 nostoc punctiforme pcc 73102 at 2.00 a resolution
99	d2hrca1	Alignment	not modelled	11.7	13	Fold: Chelatase-like Superfamily: Chelatase Family: Ferrochelatase