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Value

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MGA_58017 Cabchydrates / Certinal cabchydrate metabolism / Dehydrogensse_complexes / Encyl-CoA hydratase [branched chain amino acid degradation] (EC 4.2.1.17)
MGA_57730 NA / NA / NA
MGA_1500S Carbohydrates / Fermentation / Acetyl-CoA fermentation, jo_Bulyrate / Probable electron transfer flavoprotein-quinone oxidoreductase FixC (EC 1.5.5.-)
MGA_1500S Insicellanous / YUSIC / Putative membrane-bound ClpP class protease associated with aq_911
MGA_77657 Carbohydrates / One-catron Metabolism / Serine-glycoylate_cycle / putative isocutyryl-CoA mutase, chain B
MGA_15141 Carbohydrates / One-catron Metabolism / Serine-glycoylate_cycle / putative isocutyryl-CoA mutase, chain B
MGA_56141 Carbohydrates / One-catron Metabolism / Serine-glycoylate_cycle / putative isocutyryl-CoA mutase, chain B
MGA_56141 Carbohydrates / One-catron Metabolism / Serine-glycoylate_cycle / putative isocutyryl-CoA mutase, chain B
MGA_56141 Carbohydrates / Caretabore / Lysine, threorine, methorine, and cystaine / Threorine and Homoseine_Biosynthesis / Aspar tate aminotransferase (EC 2.6.1.1)
MGA_14793 Amino Acids and Derivatives / Lysine, threorine, methorine, and cystaine / Threorine and Homoseine_Biosynthesis / Aspar tate aminotransferase (EC 2.6.1.1)
MGA_15630S Exists Response / Heat shock / Heat plock / Heat shock /

MGA, 3616 Me mbrane Transport / ABC transports is / ABC transport per branched chain, amino acid (TiC 3A.1.4.1) / High-affinity leucine-specific transport system, periplasmic bind MGA, 3616 Me mbrane Transport / ABC transports is / ABC transport by partnershin, amino acid (TiC 3A.1.4.1) / High-affinity leucine-specific transport system, periplasmic bind MGA, 1092 Citisering-based subsystems / Putative asociate of RNA polymerase sigma-54 factor gool / CBSS-316057.3peg 1308 / RNA polymerase sigma-70 factor MGA, 25916 Catchydrates / Certral catchydrate metablismic / Dehydrogenase, complexes / Encyl-CoA hydratase [branched-chain amino acid departdation] (EC 4.2.1.17) MGA, 57890 Cell Wall and Capsule / Gram Megative cell wall components / Outer, membrane / Dotter membrane protate membrane policies of Wall and Capsule / Gram Megative cell wall components / Outer, membrane / Dotter membrane policies with place / Wall protein MGA, 15940 Protein Metabolism / Protein biosynthesis / Ribosome | LSU bacterial / LSU ribosomal protein L36p MGA, 57847 Stoses Response / Outditive stress / Cilutathione. Nonechost, reactions / Unbranchetized glitathinore S transferase-like protein MGA, 10965 Amino Acids and Derivatives / Branchet-chain amino acids / Valine degradation / Predict transcriptional regulator of leucine degradation pathway, MerR family MGA, 39802 Cilustening beased subsystems / / Bacterial Cell_Division / rRNA small subunit methyltransferase-like protein MGA, 10963 / NOT FOUND MGA, 1519 Protein Metabolism / Protein biosynthesis / Translation initiation factors Sut1-related protein MGA, 26802 Croad Metabolism / Protein biosynthesis / Translation initiation factors Sut1-related protein MGA, 26802 Croad Metabolism / Protein biosynthesis / Translation leongation lactor LpA MGA, 26802 Croad Wall and Capsuse Life / Capsuse / Cap

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