Yjl068cp is an esterase with S-formylglutathione hydrolase activity which appears to be involved in formaldehyde detoxification. Purified Yjl068cp is able to hydroyze a variety of substrates, including S-formylglutathione, carboxyfluorescein diacetate, 4-methylumbelliferyl acetate, p-nitrophenyl acetate, and alpha-naphthyl acetate, but is unable to hydrolyze alpha-naphthyl laurate and alpha-naphthyl oleate. YJL068C is induced in response to methyl methanesulfonateand neocarzinostatin, which possesses a regulatory function on the metabolism of DNA and exhibits potent antiproliferative activity in mammalian cells and against gram-positive organisms. Null mutants in YJL068C are viable, but display reduced esterase activity and slow growth in the presence of formaldehyde. Yjl068cp exhibits similarity to the S-formylglutathione hydrolases of Paracoccus denitrificans, Haemophilus influenzae, Escherichia coli and humans.About glutathione-dependent formaldehyde oxidation Formaldehyde is formed by oxidative demethylation reactions in many plants and methylotrophic organisms, but Saccharomyces cerevisiae is a nonmethylotrophic yeast and cannot metabolize methanol to formaldehyde. However, S. cerevisiae is exposed to exogenous formaldehyde from plant material or in polluted air and water.Concentrations of formaldehyde of 1mM or higher are cytostatic or cytotoxic to haploid wild-type cells. Any free formaldehyde in vivo spontaneously reacts with glutathione to form S-hydroxymethylglutathione. The level of enzymes involved in the degradation of formaldehyde, such as Sfa1p and Yjl068p, determine the level of formaldehyde toxicity, and cells overproducing Sfa1p are resistant to formaldehyde and null mutants in either sfa1 or yjl068c are hypersensitive to formaldehyde. Sfa1p is induced in response to chemicals such as formaldehyde, ethanol and methyl methanesulphonate, and Yjl068p is also induced in response to chemical stresses.Formate dehydrogenase is encoded by FDH1/YOR388C and FDH2. In some strain backgrounds of S. cerevisiae, FDH2 is encoded by a continuous open reading frame comprised of YPL275W and YPL276W. However, in the systematic sequence of S288C, FDH2 is represented by these two separate open reading frames due to an in frame stop codon.