high throughput screening

	NCT Number	Title	Authors	Description	Identifier	Dates
1	pubmed:36087402	An enzymatic colorimetric whole-cell biosensor for high-throughput identification of lysine overproducers	Jie Liu Jian-Zhong Xu Zhi-Ming Rao Wei-Guo Zhang	L-lysine is a crucial nutrient for both humans and animals, and its main commercial use is as a supplement in animal feed to promote chicken and other animal growth. Fluorescence biosensors based on the transcriptional regulator have been developed for high-throughput screening of L-lysine producers. However, due to its inability to specifically detect lysine, this fluorescent biosensor cannot be employed to screen high-yielding strains. Here, we present a novel technique for observing L-lysine...	pmid:36087402 doi:10.1016/j.bios.2022.114681	Sat, 10 Sep 2022 06:00:00 -0400
2	pubmed:36087727	Molecular fingerprints of polar narcotic chemicals based on heterozygous essential gene knockout library in Saccharomyces cerevisiae	Miao Guan Wenya Ji Yue Xu Lu Yan Dong Chen Shengjie Li Xiaowei Zhang	Cytotoxicity of non-polar narcotic chemicals can be predicted by quantitative structure activity relationship (QSAR) models, but the polar narcotic chemicals' actual cytotoxicity exceeds the predicted values by their chemical structures. This discrepancy indicates that the molecular mechanism by which polar narcotic chemicals exert their toxicity is unclear. Taking advantage of Saccharomyces cerevisiae (yeast) functional genome-wide heterozygous essential gene knockout mutants, we here have...	pmid:36087727 doi:10.1016/j.chemosphere.2022.136343	Sat, 10 Sep 2022 06:00:00 -0400
3	pubmed:36087837	Development of a novel high-throughput screen for the identification of new inhibitors of protein S-acylation	Christine Salaun Hiroya Takizawa Alex Galindo Kevin R Munro Jayde McLellan Isamu Sugimoto Tomotaka Okino Nicholas C O Tomkinson Luke H Chamberlain	Protein S-acylation is a reversible post-translational modification that modulates the localization and function of many cellular proteins. S-acylation is mediated by a family of zinc finger DHHC domain-containing proteins encoded by 23 distinct ZDHHC genes in the human genome. These enzymes catalyze S-acylation in a two-step process involving "auto-acylation" of the cysteine residue in the catalytic DHHC motif followed by transfer of the acyl chain to a substrate cysteine. S-acylation is...	pmid:36087837 doi:10.1016/j.jbc.2022.102469	Sat, 10 Sep 2022 06:00:00 -0400