high throughput screening

	NCT Number	Title	Authors	Description	Identifier	Dates
1	pubmed:36071039	Multiomics approach reveals the ubiquitination-specific processes hijacked by SARS-CoV-2	Gang Xu Yezi Wu Tongyang Xiao Furong Qi Lujie Fan Shengyuan Zhang Jian Zhou Yanhua He Xiang Gao Hongxiang Zeng Yunfei Li Zheng Zhang	The Coronavirus Disease 2019 (COVID-19) caused by Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) is a global pandemic that seriously threatens health and socioeconomic development, but the existed antiviral drugs and vaccines still cannot yet halt the spread of the epidemic. Therefore, a comprehensive and profound understanding of the pathogenesis of SARS-CoV-2 is urgently needed to explore effective therapeutic targets. Here, we conducted a multiomics study of SARS-CoV-2-infected	pmid:36071039 doi:10.1038/s41392-022-01156-y	Wed, 07 Sep 2022 06:00:00 -0400
2	pubmed:36071458	Glucose transport engineering allows mimicking fed-batch performance in batch mode and selection of superior producer strains	Daniela Velazquez Juan-Carlos Sigala Luz María Martínez Paul Gaytán Guillermo Gosset Alvaro R Lara	conclusion: The combination of cell engineering and high throughput screening allowed the selection of a particular mutant that mimics fed-batch behavior in batch cultures. Moreover, the amount of GFP produced by the strain WHIC was substantially higher than that of W3110 under both, batch and fed-batch schemes. Therefore, our results represent a valuable technology for accelerated bioprocess development.	pmid:36071458 doi:10.1186/s12934-022-01906-1	Wed, 07 Sep 2022 06:00:00 -0400
3	pubmed:36073082	De-novo assembly and annotation of the CHOZN® GS ^{-/-} genome supports high-throughput genome-scale screening	Corey Kretzmer Rajagopalan Lakshmi Narasimhan Rahul Deva Lal Vincent Balassi James Ravellette K M Ajaya Kumar Jesvin Joy Koshy Marta Viano Serena Torre Valeria Maria Zanda Mausam Kumravat Keith Metelo Raul Saldanha Harikrishnan Chandranpillai Ifra Nihad Fei Zhong Yi Sun Jason Gustin Trissa Borgschulte JiaJian Liu David Razafsky	Chinese Hamster Ovary (CHO) cells have been used as the industry standard for the production of therapeutic monoclonal antibodies for several decades. Despite significant improvements in commercial scale production processes and media, the CHO cell has remained largely unchanged. Due to the cost and complexity of wholegenome sequencing and gene-editing it has been difficult to obtain the tools necessary to improve the CHO cell line. With the advent of next generation sequencing and the	pmid:36073082 doi:10.1002/bit.28226	Thu, 08 Sep 2022 06:00:00 -0400
4	pubmed:36074887	High-Throughput Generation, Manipulation, and Degradation of Magnetic Nanoparticleladen Alginate Core-shell Beads for Single Bacteria Culturing Analysis	Shuai Yuan Yulin Zhang Lang Nan P T Lai Tong Zhang Philip W T Pong Ho Cheung Shum	Microbes could be found almost everywhere around us and have significant impacts on our human society. The treatment of microorganisms has long been seen as a complex problem. Till now, most of the genetic and phenotypic information regarding rare species is buried in the bulk microbial colony due to a lack of efficient tools to screen live bacteria. Droplet microfluidics offers a powerful approach to address this problem. However, the interactions among bacteria and their living environment are	pmid:36074887 doi:10.1109/TNB.2022.3205057	Thu, 08 Sep 2022 06:00:00 -0400