Gur Pines

List of Publications by Year
in descending order

25 papers	1,975 citations	623188 14 h-index	676716 22 g-index
30 all docs	30 docs citations	30 times ranked	3607 citing authors

#	Article	IF	Citations
1	Differential Detection of the Tobamoviruses Tomato Mosaic Virus (ToMV) and Tomato Brown Rugose Fruit Virus (ToBRFV) Using CRISPR-Cas12a. Plants, 2021, 10, 1256.	1.6	36
2	Predicting Drug Resistance Using Deep Mutational Scanning. Molecules, 2020, 25, 2265.	1.7	8
3	SILAC identifies LAD1 as a filamin-binding regulator of actin dynamics in response to EGF and a marker of aggressive breast tumors. Science Signaling, 2018, 11, .	1.6	41
4	Genomic Deoxyxylulose Phosphate Reductoisomerase (DXR) Mutations Conferring Resistance to the Antimalarial Drug Fosmidomycin in <i>E. coli</i>. ACS Synthetic Biology, 2018, 7, 2824-2832.	1.9	11
5	Dynamic Management of Codon Compression for Saturation Mutagenesis. Methods in Molecular Biology, 2018, 1772, 171-189.	0.4	3
6	Quantitative Tracking of Combinatorially Engineered Populations with Multiplexed Binary Assemblies. ACS Synthetic Biology, 2017, 6, 619-627.	1.9	9
7	Genome-wide mapping of mutations at single-nucleotide resolution for protein, metabolic and genome engineering. Nature Biotechnology, 2017, 35, 48-55.	9.4	298
8	Refactoring the Genetic Code for Increased Evolvability. MBio, 2017, 8, .	1.8	17
9	A Web Interface for Codon Compression. ACS Synthetic Biology, 2016, 5, 1021-1023.	1.9	7
10	Interfering with the Dimerization of the ErbB Receptors by Transmembrane Domain-Derived Peptides Inhibits Tumorigenic Growth in Vitro and in Vivo. Biochemistry, 2016, 55, 5520-5530.	1.2	7
11	The Resistome: A Comprehensive Database of Escherichia coli Resistance Phenotypes. ACS Synthetic Biology, 2016, 5, 1566-1577.	1.9	17
12	Evolutionary Genomics: Supplement Aims and Scope. Evolutionary Bioinformatics, 2015, 11s2, EBO.S39729.	0.6	1
13	Multiplexed tracking of combinatorial genomic mutations in engineered cell populations. Nature Biotechnology, 2015, 33, 631-637.	9.4	49
14	Bacterial Recombineering: Genome Engineering via Phage-Based Homologous Recombination. ACS Synthetic Biology, 2015, 4, 1176-1185.	1.9	89
15	Codon Compression Algorithms for Saturation Mutagenesis. ACS Synthetic Biology, 2015, 4, 604-614.	1.9	45
16	The EGFR/ERBB Receptor Family. , 2015, , 107-164.		3
17	Deubiquitination of EGFR by Cezanne-1 contributes to cancer progression. Oncogene, 2012, 31, 4599-4608.	2.6	84
18	EGR1 and the ERK–ERF axis drive mammary cell migration in response to EGF. FASEB Journal, 2012, 26, 1582-1592.	0.2	88

#	ARTICLE	IF	CITATIONS
19	The ERBB network: at last, cancer therapy meets systems biology. Nature Reviews Cancer, 2012, 12, 553-563.	12.8	766
20	Oncogenic mutant forms of EGFR: Lessons in signal transduction and targets for cancer therapy. FEBS Letters, 2010, 584, 2699-2706.	1.3	141
21	EGFRvIV: a previously uncharacterized oncogenic mutant reveals a kinase autoinhibitory mechanism. Oncogene, 2010, 29, 5850-5860.	2.6	58
22	Kinase-mediated quasi-dimers of EGFR. FASEB Journal, 2010, 24, 4744-4755.	0.2	51
23	Kinaseâ€mediated quasiâ€dimers of EGFR. FASEB Journal, 2010, 24, 4744-4755.	0.2	8
24	Defective ubiquitinylation of EGFR mutants of lung cancer confers prolonged signaling. Oncogene, 2007, 26, 6968-6978.	2.6	131
25	Highly Efficient Libraries Design for Saturation Mutagenesis. Synthetic Biology, 0, , .	1.2	1