

Israel Steinfeld

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/10850623/publications.pdf>

Version: 2024-02-01

23
papers

6,446
citations

393982

19
h-index

642321

23
g-index

23
all docs

23
docs citations

23
times ranked

15304
citing authors

#	ARTICLE	IF	CITATIONS
1	Phosphonoacetate Modifications Enhance the Stability and Editing Yields of Guide RNAs for Cas9 Editors. <i>Biochemistry</i> , 2023, 62, 3512-3520.	1.2	2
2	Improving CRISPR-Cas specificity with chemical modifications in single-guide RNAs. <i>Nucleic Acids Research</i> , 2018, 46, 792-803.	6.5	206
3	Global Transcriptional Response to CRISPR/Cas9-AAV6-Based Genome Editing in CD34+ Hematopoietic Stem and Progenitor Cells. <i>Molecular Therapy</i> , 2018, 26, 2431-2442.	3.7	97
4	Serum N-glycan analysis in breast cancer patients – Relation to tumour biology and clinical outcome. <i>Molecular Oncology</i> , 2016, 10, 59-72.	2.1	34
5	Chemically modified guide RNAs enhance CRISPR-Cas genome editing in human primary cells. <i>Nature Biotechnology</i> , 2015, 33, 985-989.	9.4	882
6	ENViz: a Cytoscape App for integrated statistical analysis and visualization of sample-matched data with multiple data types. <i>Bioinformatics</i> , 2015, 31, 1683-1685.	1.8	12
7	Specific genomic and transcriptomic aberrations in tumors induced by partial hepatectomy of a chronically inflamed murine liver. <i>Oncotarget</i> , 2014, 5, 10318-10331.	0.8	15
8	Deregulation of cancer-related miRNAs is a common event in both benign and malignant human breast tumors. <i>Carcinogenesis</i> , 2014, 35, 76-85.	1.3	119
9	Association of N-Glycosylation with Breast Carcinoma and Systemic Features Using High-Resolution Quantitative UPLC. <i>Journal of Proteome Research</i> , 2014, 13, 2314-2327.	1.8	123
10	miRNA target enrichment analysis reveals directly active miRNAs in health and disease. <i>Nucleic Acids Research</i> , 2013, 41, e45-e45.	6.5	51
11	Identifying In-Trans Process Associated Genes in Breast Cancer by Integrated Analysis of Copy Number and Expression Data. <i>PLoS ONE</i> , 2013, 8, e53014.	1.1	54
12	Global Methylation Patterns in Idiopathic Pulmonary Fibrosis. <i>PLoS ONE</i> , 2012, 7, e33770.	1.1	169
13	miRNA-mRNA Integrated Analysis Reveals Roles for miRNAs in Primary Breast Tumors. <i>PLoS ONE</i> , 2011, 6, e16915.	1.1	278
14	EGF Decreases the Abundance of MicroRNAs That Restrain Oncogenic Transcription Factors. <i>Science Signaling</i> , 2010, 3, ra43.	1.6	100
15	Novel Rank-Based Statistical Methods Reveal MicroRNAs with Differential Expression in Multiple Cancer Types. <i>PLoS ONE</i> , 2009, 4, e8003.	1.1	150
16	GORilla: a tool for discovery and visualization of enriched GO terms in ranked gene lists. <i>BMC Bioinformatics</i> , 2009, 10, 48.	1.2	3,032
17	Developmental programming of CpG island methylation profiles in the human genome. <i>Nature Structural and Molecular Biology</i> , 2009, 16, 564-571.	3.6	345
18	The Fine-Scale and Complex Architecture of Human Copy-Number Variation. <i>American Journal of Human Genetics</i> , 2008, 82, 685-695.	2.6	315

#	ARTICLE	IF	CITATIONS
19	Clinically driven semi-supervised class discovery in gene expression data. <i>Bioinformatics</i> , 2008, 24, i90-i97.	1.8	15
20	Small Deletion Variants Have Stable Breakpoints Commonly Associated with Alu Elements. <i>PLoS ONE</i> , 2008, 3, e3104.	1.1	52
21	A genome-wide analysis in <i>Saccharomyces cerevisiae</i> demonstrates the influence of chromatin modifiers on transcription. <i>Nature Genetics</i> , 2007, 39, 303-309.	9.4	68
22	EXPANDER--an integrative program suite for microarray data analysis. <i>BMC Bioinformatics</i> , 2005, 6, 232.	1.2	283
23	Integrative analysis of genome-wide experiments in the context of a large high-throughput data compendium. <i>Molecular Systems Biology</i> , 2005, 1, 2005.0002.	3.2	44