

# 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

394421  
19  
h-index

642732  
23  
g-index

23  
all docs

23  
docs citations

23  
times ranked

15304  
citing authors

#	ARTICLE	IF	CITATIONS
1	GOrilla: a tool for discovery and visualization of enriched GO terms in ranked gene lists. BMC Bioinformatics, 2009, 10, 48.	2.6	3,032
2	Chemically modified guide RNAs enhance CRISPR-Cas genome editing in human primary cells. Nature Biotechnology, 2015, 33, 985-989.	17.5	882
3	Developmental programming of CpG island methylation profiles in the human genome. Nature Structural and Molecular Biology, 2009, 16, 564-571.	8.2	345
4	The Fine-Scale and Complex Architecture of Human Copy-Number Variation. American Journal of Human Genetics, 2008, 82, 685-695.	6.2	315
5	EXPANDER--an integrative program suite for microarray data analysis. BMC Bioinformatics, 2005, 6, 232.	2.6	283
6	miRNA-mRNA Integrated Analysis Reveals Roles for miRNAs in Primary Breast Tumors. PLoS ONE, 2011, 6, e16915.	2.5	278
7	Improving CRISPR-Cas specificity with chemical modifications in single-guide RNAs. Nucleic Acids Research, 2018, 46, 792-803.	14.5	206
8	Global Methylation Patterns in Idiopathic Pulmonary Fibrosis. PLoS ONE, 2012, 7, e33770.	2.5	169
9	Novel Rank-Based Statistical Methods Reveal MicroRNAs with Differential Expression in Multiple Cancer Types. PLoS ONE, 2009, 4, e8003.	2.5	150
10	Association of N-Glycosylation with Breast Carcinoma and Systemic Features Using High-Resolution Quantitative UPLC. Journal of Proteome Research, 2014, 13, 2314-2327.	3.7	123
11	Deregulation of cancer-related miRNAs is a common event in both benign and malignant human breast tumors. Carcinogenesis, 2014, 35, 76-85.	2.8	119
12	EGF Decreases the Abundance of MicroRNAs That Restrain Oncogenic Transcription Factors. Science Signaling, 2010, 3, ra43.	3.6	100
13	Global Transcriptional Response to CRISPR/Cas9-AAV6-Based Genome Editing in CD34+ Hematopoietic Stem and Progenitor Cells. Molecular Therapy, 2018, 26, 2431-2442.	8.2	97
14	A genome-wide analysis in Saccharomyces cerevisiae demonstrates the influence of chromatin modifiers on transcription. Nature Genetics, 2007, 39, 303-309.	21.4	68
15	Identifying In-Trans Process Associated Genes in Breast Cancer by Integrated Analysis of Copy Number and Expression Data. PLoS ONE, 2013, 8, e53014.	2.5	54
16	Small Deletion Variants Have Stable Breakpoints Commonly Associated with Alu Elements. PLoS ONE, 2008, 3, e3104.	2.5	52
17	miRNA target enrichment analysis reveals directly active miRNAs in health and disease. Nucleic Acids Research, 2013, 41, e45-e45.	14.5	51
18	Integrative analysis of genome-wide experiments in the context of a large high-throughput data compendium. Molecular Systems Biology, 2005, 1, 2005.0002.	7.2	44

#	ARTICLE	IF	CITATIONS
19	Serum N-glycan analysis in breast cancer patients – Relation to tumour biology and clinical outcome. Molecular Oncology, 2016, 10, 59-72.	4.6	34
20	Clinically driven semi-supervised class discovery in gene expression data. Bioinformatics, 2008, 24, i90-i97.	4.1	15
21	Specific genomic and transcriptomic aberrations in tumors induced by partial hepatectomy of a chronically inflamed murine liver. Oncotarget, 2014, 5, 10318-10331.	1.8	15
22	ENViz: a Cytoscape App for integrated statistical analysis and visualization of sample-matched data with multiple data types. Bioinformatics, 2015, 31, 1683-1685.	4.1	12
23	Phosphonoacetate Modifications Enhance the Stability and Editing Yields of Guide RNAs for Cas9 Editors. Biochemistry, 2023, 62, 3512-3520.	2.5	2