

Jan Hoinka

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2707161/publications.pdf>

Version: 2024-02-01

19
papers

603
citations

840776

11
h-index

888059

17
g-index

21
all docs

21
docs citations

21
times ranked

667
citing authors

#	ARTICLE	IF	CITATIONS
1	DNA Aptamers for Early Detection of Ebolavirus. <i>FASEB Journal</i> , 2021, 35, .	0.5	2
2	Immunotherapy using IgE or CAR T cells for cancers expressing the tumor antigen SLC3A2. , 2021, 9, e002140.		10
3	RepairSig: Deconvolution of DNA damage and repair contributions to the mutational landscape of cancer. <i>Cell Systems</i> , 2021, 12, 994-1003.e4.	6.2	6
4	Embedding gene sets in low-dimensional space. <i>Nature Machine Intelligence</i> , 2020, 2, 367-368.	16.0	2
5	Direct, Competitive Comparison of Linear, Monocyclic, and Bicyclic Libraries Using mRNA Display. <i>ACS Combinatorial Science</i> , 2020, 22, 306-310.	3.8	13
6	AptaBlocks Online: A Web-Based Toolkit for the In Silico Design of Oligonucleotide Sticky Bridges. <i>Journal of Computational Biology</i> , 2020, 27, 356-360.	1.6	0
7	Co-SELECT reveals sequence non-specific contribution of DNA shape to transcription factor binding in vitro. <i>Nucleic Acids Research</i> , 2019, 47, 6632-6641.	14.5	15
8	Subpopulation Detection and Their Comparative Analysis across Single-Cell Experiments with scPopCorn. <i>Cell Systems</i> , 2019, 8, 506-513.e5.	6.2	13
9	AptaSUITE: A Full-Featured Bioinformatics Framework for the Comprehensive Analysis of Aptamers from HT-SELEX Experiments. <i>Molecular Therapy - Nucleic Acids</i> , 2018, 11, 515-517.	5.1	54
10	AptaBlocks: Designing RNA complexes and accelerating RNA-based drug delivery systems. <i>Nucleic Acids Research</i> , 2018, 46, 8133-8142.	14.5	8
11	A 2â€²FY-RNA Motif Defines an Aptamer for Ebolavirus Secreted Protein. <i>Scientific Reports</i> , 2018, 8, 12373.	3.3	23
12	Highly Constrained Bicyclic Scaffolds for the Discovery of Protease-Stable Peptides <i>via</i> mRNA Display. <i>ACS Chemical Biology</i> , 2017, 12, 795-804.	3.4	53
13	AptaPLEX â€“ A dedicated, multithreaded demultiplexer for HT-SELEX data. <i>Methods</i> , 2016, 106, 82-85.	3.8	16
14	AptaTRACE Elucidates RNA Sequence-Structure Motifs from Selection Trends in HT-SELEX Experiments. <i>Cell Systems</i> , 2016, 3, 62-70.	6.2	55
15	AptaGUIâ€”A Graphical User Interface for the Efficient Analysis of HT-SELEX Data. <i>Molecular Therapy - Nucleic Acids</i> , 2015, 4, e257.	5.1	18
16	Identifying high-affinity aptamer ligands with defined cross-reactivity using high-throughput guided systematic evolution of ligands by exponential enrichment. <i>Nucleic Acids Research</i> , 2015, 43, e82-e82.	14.5	61
17	Large scale analysis of the mutational landscape in HT-SELEX improves aptamer discovery. <i>Nucleic Acids Research</i> , 2015, 43, 5699-5707.	14.5	97
18	AptaCluster â€“ A Method to Cluster HT-SELEX Aptamer Pools and Lessons from Its Application. <i>Lecture Notes in Computer Science</i> , 2014, 8394, 115-128.	1.3	71

#	ARTICLE	IF	CITATIONS
19	Identification of sequence-structure RNA binding motifs for SELEX-derived aptamers. <i>Bioinformatics</i> , 2012, 28, i215-i223.	4.1	85