Jan Hoinka

List of Publications by Year
in descending order

19	603	840776	888059
papers	citations	11	17
		h-index	g-index

21	21	21	667
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Large scale analysis of the mutational landscape in HT-SELEX improves aptamer discovery. Nucleic Acids Research, 2015, 43, 5699-5707.	14.5	97
2	Identification of sequence–structure RNA binding motifs for SELEX-derived aptamers. Bioinformatics, 2012, 28, i215-i223.	4.1	85
3	AptaCluster – A Method to Cluster HT-SELEX Aptamer Pools and Lessons from Its Application. Lecture Notes in Computer Science, 2014, 8394, 115-128.	1.3	71
4	Identifying high-affinity aptamer ligands with defined cross-reactivity using high-throughput guided systematic evolution of ligands by exponential enrichment. Nucleic Acids Research, 2015, 43, e82-e82.	14.5	61
5	AptaTRACE Elucidates RNA Sequence-Structure Motifs from Selection Trends in HT-SELEX Experiments. Cell Systems, 2016, 3, 62-70.	6.2	55
6	AptaSUITE: A Full-Featured Bioinformatics Framework for the Comprehensive Analysis of Aptamers from HT-SELEX Experiments. Molecular Therapy - Nucleic Acids, 2018, 11, 515-517.	5.1	54
7	Highly Constrained Bicyclic Scaffolds for the Discovery of Protease-Stable Peptides *via* mRNA Display. ACS Chemical Biology, 2017, 12, 795-804.	3.4	53
8	A 2′FY-RNA Motif Defines an Aptamer for Ebolavirus Secreted Protein. Scientific Reports, 2018, 8, 12373.	3.3	23
9	AptaGUI—A Graphical User Interface for the Efficient Analysis of HT-SELEX Data. Molecular Therapy - Nucleic Acids, 2015, 4, e257.	5.1	18
10	AptaPLEX – A dedicated, multithreaded demultiplexer for HT-SELEX data. Methods, 2016, 106, 82-85.	3.8	16
11	Co-SELECT reveals sequence non-specific contribution of DNA shape to transcription factor binding in vitro. Nucleic Acids Research, 2019, 47, 6632-6641.	14.5	15
12	Subpopulation Detection and Their Comparative Analysis across Single-Cell Experiments with scPopCorn. Cell Systems, 2019, 8, 506-513.e5.	6.2	13
13	Direct, Competitive Comparison of Linear, Monocyclic, and Bicyclic Libraries Using mRNA Display. ACS Combinatorial Science, 2020, 22, 306-310.	3.8	13
14	Immunotherapy using IgE or CAR T cells for cancers expressing the tumor antigen SLC3A2. , 2021, 9, e002140.		10
15	AptaBlocks: Designing RNA complexes and accelerating RNA-based drug delivery systems. Nucleic Acids Research, 2018, 46, 8133-8142.	14.5	8
16	RepairSig: Deconvolution of DNA damage and repair contributions to the mutational landscape of cancer. Cell Systems, 2021, 12, 994-1003.e4.	6.2	6
17	Embedding gene sets in low-dimensional space. Nature Machine Intelligence, 2020, 2, 367-368.	16.0	2
18	DNA Aptamers for Early Detection of Ebolavirus. FASEB Journal, 2021, 35, .	0.5	2

#	Article	IF	Citations
19	AptaBlocks Online: A Web-Based Toolkit for the In Silico Design of Oligonucleotide Sticky Bridges. Journal of Computational Biology, 2020, 27, 356-360.	1.6	0