

Abdullah Kahraman

List of Publications by Year in descending order

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Version: 2024-02-01

36
papers

3,841
citations

331538

21
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414303

32
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42
all docs

42
docs citations

42
times ranked

6713
citing authors

#	ARTICLE	IF	CITATIONS
1	Integrated Analysis Of Immunotherapy Treated Clear Cell Renal Cell Carcinomas: An Exploratory Study. <i>Journal of Immunotherapy</i> , 2022, 45, 35-42.	1.2	3
2	Frequency, molecular characteristics, and therapeutic targeting of ROS1 oncogenic fusions in colorectal cancer.. <i>Journal of Clinical Oncology</i> , 2022, 40, 160-160.	0.8	0
3	Editorial: Alternative Splicing in Health and Disease. <i>Frontiers in Molecular Biosciences</i> , 2022, 9, 878668.	1.6	0
4	Tracing Clonal Dynamics Reveals that Two- and Three-dimensional Patient-derived Cell Models Capture Tumor Heterogeneity of Clear Cell Renal Cell Carcinoma. <i>European Urology Focus</i> , 2021, 7, 152-162.	1.6	34
5	Clinicopathological and Genomic Profiles of Atypical Fibroxanthoma and Pleomorphic Dermal Sarcoma Identify Overlapping Signatures with a High Mutational Burden. <i>Genes</i> , 2021, 12, 974.	1.0	7
6	Establishing standardized immune phenotyping of metastatic melanoma by digital pathology. <i>Laboratory Investigation</i> , 2021, 101, 1561-1570.	1.7	15
7	Epithelial Wnt secretion drives the progression of inflammation-induced colon carcinoma in murine model. <i>IScience</i> , 2021, 24, 103369.	1.9	4
8	Probing Isoform Switching Events in Various Cancer Types: Lessons From Pan-Cancer Studies. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 726902.	1.6	4
9	Pathogenic impact of transcript isoform switching in 1,209 cancer samples covering 27 cancer types using an isoform-specific interaction network. <i>Scientific Reports</i> , 2020, 10, 14453.	1.6	27
10	Clonal Hematopoiesis in Hospitalized Elderly Patients With COVID-19. <i>HemaSphere</i> , 2020, 4, e453.	1.2	23
11	Pathway and network analysis of more than 2500 whole cancer genomes. <i>Nature Communications</i> , 2020, 11, 729.	5.8	73
12	Analyses of non-coding somatic drivers in 2,658 cancer whole genomes. <i>Nature</i> , 2020, 578, 102-111.	13.7	424
13	SCIM: universal single-cell matching with unpaired feature sets. <i>Bioinformatics</i> , 2020, 36, i919-i927.	1.8	37
14	<i>STRN</i> <i>ALK</i> Rearranged Malignant Peritoneal Mesothelioma With Dramatic Response Following Ceritinib Treatment. <i>JCO Precision Oncology</i> , 2019, 3, 1-6.	1.5	21
15	Therapy alteration of solid tumors based on FoundationOne comprehensive genome profiling assay.. <i>Journal of Clinical Oncology</i> , 2019, 37, e14742-e14742.	0.8	0
16	Cell-wide analysis of protein thermal unfolding reveals determinants of thermostability. <i>Science</i> , 2017, 355, .	6.0	313
17	Molecular Details Underlying Dynamic Structures and Regulation of the Human 26S Proteasome. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 840-854.	2.5	93
18	Measuring protein structural changes on a proteome-wide scale using limited proteolysis-coupled mass spectrometry. <i>Nature Protocols</i> , 2017, 12, 2391-2410.	5.5	171

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19	The SIB Swiss Institute of Bioinformaticsâ€™™ resources: focus on curated databases. <i>Nucleic Acids Research</i> , 2016, 44, D27-D37.	6.5	64
20	<i>xVis</i>: a web server for the schematic visualization and interpretation of crosslink-derived spatial restraints. <i>Nucleic Acids Research</i> , 2015, 43, W362-W369.	6.5	116
21	Proteomics beyond large-scale protein expression analysis. <i>Current Opinion in Biotechnology</i> , 2015, 34, 162-170.	3.3	56
22	Spin trapping combined with quantitative mass spectrometry defines free radical redistribution within the oxidized hemoglobin:haptoglobin complex. <i>Free Radical Biology and Medicine</i> , 2015, 85, 259-268.	1.3	18
23	Statistical methods for detecting differentially methylated loci and regions. <i>Frontiers in Genetics</i> , 2014, 5, 324.	1.1	99
24	Distance restraints from crosslinking mass spectrometry: Mining a molecular dynamics simulation database to evaluate lysineâ€™“lysine distances. <i>Protein Science</i> , 2014, 23, 747-759.	3.1	243
25	Global analysis of protein structural changes in complex proteomes. <i>Nature Biotechnology</i> , 2014, 32, 1036-1044.	9.4	288
26	Cross-Link Guided Molecular Modeling with ROSETTA. <i>PLoS ONE</i> , 2013, 8, e73411.	1.1	144
27	Structural Probing of a Protein Phosphatase 2A Network by Chemical Cross-Linking and Mass Spectrometry. <i>Science</i> , 2012, 337, 1348-1352.	6.0	357
28	Xwalk: computing and visualizing distances in cross-linking experiments. <i>Bioinformatics</i> , 2011, 27, 2163-2164.	1.8	130
29	On the diversity of physicochemical environments experienced by identical ligands in binding pockets of unrelated proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 1120-1136.	1.5	59
30	Heme proteinsâ€™”Diversity in structural characteristics, function, and folding. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 2349-2368.	1.5	147
31	Probing Native Protein Structures by Chemical Cross-linking, Mass Spectrometry, and Bioinformatics. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 1634-1649.	2.5	407
32	Shape Variation in Protein Binding Pockets and their Ligands. <i>Journal of Molecular Biology</i> , 2007, 368, 283-301.	2.0	188
33	Variation of geometrical and physicochemical properties in protein binding pockets and their ligands. <i>BMC Bioinformatics</i> , 2007, 8, .	1.2	4
34	PhenomicDB: a multi-species genotype/phenotype database for comparative phenomics. <i>Bioinformatics</i> , 2005, 21, 418-420.	1.8	66
35	Real spherical harmonic expansion coefficients as 3D shape descriptors for protein binding pocket and ligand comparisons. <i>Bioinformatics</i> , 2005, 21, 2347-2355.	1.8	170
36	IsoAligner: dynamic mapping of amino acid positions across protein isoforms. <i>F1000Research</i> , 0, 11, 382.	0.8	2