

Abdullah Kahraman

List of Publications by Year in descending order

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Version: 2024-02-01

36
papers

3,841
citations

331670
21
h-index

414414
32
g-index

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.	2.4	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.	1.6	0
3	Editorial: Alternative Splicing in Health and Disease. <i>Frontiers in Molecular Biosciences</i> , 2022, 9, 878668.	3.5	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.	3.1	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.	2.4	7
6	Establishing standardized immune phenotyping of metastatic melanoma by digital pathology. <i>Laboratory Investigation</i> , 2021, 101, 1561-1570.	3.7	15
7	Epithelial Wnt secretion drives the progression of inflammation-induced colon carcinoma in murine model. <i>IScience</i> , 2021, 24, 103369.	4.1	4
8	Probing Isoform Switching Events in Various Cancer Types: Lessons From Pan-Cancer Studies. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 726902.	3.5	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.	3.3	27
10	Clonal Hematopoiesis in Hospitalized Elderly Patients With COVID-19. <i>HemaSphere</i> , 2020, 4, e453.	2.7	23
11	Pathway and network analysis of more than 2500 whole cancer genomes. <i>Nature Communications</i> , 2020, 11, 729.	12.8	73
12	Analyses of non-coding somatic drivers in 2,658 cancer whole genomes. <i>Nature</i> , 2020, 578, 102-111.	27.8	424
13	SCIM: universal single-cell matching with unpaired feature sets. <i>Bioinformatics</i> , 2020, 36, i919-i927.	4.1	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.	3.0	21
15	Therapy alteration of solid tumors based on FoundationOne comprehensive genome profiling assay.. <i>Journal of Clinical Oncology</i> , 2019, 37, e14742-e14742.	1.6	0
16	Cell-wide analysis of protein thermal unfolding reveals determinants of thermostability. <i>Science</i> , 2017, 355, .	12.6	313
17	Molecular Details Underlying Dynamic Structures and Regulation of the Human 26S Proteasome. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 840-854.	3.8	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.	12.0	171

#	ARTICLE	IF	CITATIONS
19	The SIB Swiss Institute of Bioinformatics's™ resources: focus on curated databases. Nucleic Acids Research, 2016, 44, D27-D37.	14.5	64
20	<i>xVis</i>: a web server for the schematic visualization and interpretation of crosslink-derived spatial restraints. Nucleic Acids Research, 2015, 43, W362-W369.	14.5	116
21	Proteomics beyond large-scale protein expression analysis. Current Opinion in Biotechnology, 2015, 34, 162-170.	6.6	56
22	Spin trapping combined with quantitative mass spectrometry defines free radical redistribution within the oxidized hemoglobin:haptoglobin complex. Free Radical Biology and Medicine, 2015, 85, 259-268.	2.9	18
23	Statistical methods for detecting differentially methylated loci and regions. Frontiers in Genetics, 2014, 5, 324.	2.3	99
24	Distance restraints from crosslinking mass spectrometry: Mining a molecular dynamics simulation database to evaluate lysine's lysine distances. Protein Science, 2014, 23, 747-759.	7.6	243
25	Global analysis of protein structural changes in complex proteomes. Nature Biotechnology, 2014, 32, 1036-1044.	17.5	288
26	Cross-Link Guided Molecular Modeling with ROSETTA. PLoS ONE, 2013, 8, e73411.	2.5	144
27	Structural Probing of a Protein Phosphatase 2A Network by Chemical Cross-Linking and Mass Spectrometry. Science, 2012, 337, 1348-1352.	12.6	357
28	Xwalk: computing and visualizing distances in cross-linking experiments. Bioinformatics, 2011, 27, 2163-2164.	4.1	130
29	On the diversity of physicochemical environments experienced by identical ligands in binding pockets of unrelated proteins. Proteins: Structure, Function and Bioinformatics, 2010, 78, 1120-1136.	2.6	59
30	Heme proteins's'Diversity in structural characteristics, function, and folding. Proteins: Structure, Function and Bioinformatics, 2010, 78, 2349-2368.	2.6	147
31	Probing Native Protein Structures by Chemical Cross-linking, Mass Spectrometry, and Bioinformatics. Molecular and Cellular Proteomics, 2010, 9, 1634-1649.	3.8	407
32	Shape Variation in Protein Binding Pockets and their Ligands. Journal of Molecular Biology, 2007, 368, 283-301.	4.2	188
33	Variation of geometrical and physicochemical properties in protein binding pockets and their ligands. BMC Bioinformatics, 2007, 8, .	2.6	4
34	PhenomicDB: a multi-species genotype/phenotype database for comparative phenomics. Bioinformatics, 2005, 21, 418-420.	4.1	66
35	Real spherical harmonic expansion coefficients as 3D shape descriptors for protein binding pocket and ligand comparisons. Bioinformatics, 2005, 21, 2347-2355.	4.1	170
36	IsoAligner: dynamic mapping of amino acid positions across protein isoforms. F1000Research, 0, 11, 382.	1.6	2