

# Sangtae Kim

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1229156/publications.pdf>

Version: 2024-02-01

9  
papers

2,833  
citations

1163117

8  
h-index

1372567

10  
g-index

10  
all docs

10  
docs citations

10  
times ranked

6250  
citing authors

#	ARTICLE	IF	CITATIONS
1	MS1-Level Proteome Quantification Platform Allowing Maximally Increased Multiplexity for SILAC and In Vitro Chemical Labeling. <i>Analytical Chemistry</i> , 2020, 92, 4980-4989.	6.5	2
2	Strelka2: fast and accurate calling of germline and somatic variants. <i>Nature Methods</i> , 2018, 15, 591-594.	19.0	939
3	Informed-Proteomics: open-source software package for top-down proteomics. <i>Nature Methods</i> , 2017, 14, 909-914.	19.0	126
4	Reproducibility of Differential Proteomic Technologies in CPTAC Fractionated Xenografts. <i>Journal of Proteome Research</i> , 2016, 15, 691-706.	3.7	44
5	MS-GF+ makes progress towards a universal database search tool for proteomics. <i>Nature Communications</i> , 2014, 5, 5277.	12.8	945
6	The Generating Function of CID, ETD, and CID/ETD Pairs of Tandem Mass Spectra: Applications to Database Search. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 2840-2852.	3.8	226
7	Spectral Profiles, a Novel Representation of Tandem Mass Spectra and Their Applications for de Novo Peptide Sequencing and Identification. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 1391-1400.	3.8	37
8	Spectral Dictionaries. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 53-69.	3.8	87
9	Spectral Probabilities and Generating Functions of Tandem Mass Spectra: A Strike against Decoy Databases. <i>Journal of Proteome Research</i> , 2008, 7, 3354-3363.	3.7	426