## Jihun Lee

## List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/6608378/publications.pdf

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30	3,305	361045	476904
papers	citations	h-index	g-index
31 all docs	31 docs citations	31 times ranked	5306 citing authors
an does	does citations	times ranked	citing authors

#	Article	IF	CITATIONS
1	A therapeutic neutralizing antibody targeting receptor binding domain of SARS-CoV-2 spike protein. Nature Communications, 2021, 12, 288.	5.8	224
2	Ab initio folding of a trefoilâ $\in$ fold motif reveals structural similarity with a $\hat{I}^2\hat{a}\in$ propeller blade motif. Protein Science, 2020, 29, 1172-1185.	3.1	12
3	Analytical similarity assessment of rituximab biosimilar CT-P10 to reference medicinal product. MAbs, 2018, 10, 380-396.	2.6	50
4	Evaluation of analytical similarity between trastuzumab biosimilar CT-P6 and reference product using statistical analyses. MAbs, 2018, 10, 547-571.	2.6	32
5	Higherâ€order oligomerization promotes localization of <scp>SPOP</scp> to liquid nuclear speckles. EMBO Journal, 2016, 35, 1254-1275.	3.5	172
6	Multiple Weak Linear Motifs Enhance Recruitment and Processivity in SPOP-Mediated Substrate Ubiquitination. Journal of Molecular Biology, 2016, 428, 1256-1271.	2.0	44
7	The Role of Higher-Order SPOP Oligomers for Localization to Cellular "Bodies―and Ubiquitination Activity. Biophysical Journal, 2015, 108, 390a.	0.2	O
8	The Role of Protein Disorder and Self-Association in the Formation of Cellular Bodies. Biophysical Journal, 2015, 108, 6a.	0.2	1
9	Phase Separation by Low Complexity Domains Promotes Stress Granule Assembly and Drives Pathological Fibrillization. Cell, 2015, 163, 123-133.	13.5	2,053
10	Alternative Folding Nuclei Definitions Facilitate the Evolution of a Symmetric Protein Fold from a Smaller Peptide Motif. Structure, 2013, 21, 2042-2050.	1.6	13
11	Simplified protein design biased for prebiotic amino acids yields a foldable, halophilic protein.  Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 2135-2139.	3.3	96
12	Experimental support for the foldability–function tradeoff hypothesis: Segregation of the folding nucleus and functional regions in fibroblast growth factorâ€1. Protein Science, 2012, 21, 1911-1920.	3.1	21
13	Designing proteins from simple motifs: opportunities in Top-Down Symmetric Deconstruction. Current Opinion in Structural Biology, 2012, 22, 442-450.	2.6	24
14	Emergence of symmetric protein architecture from a simple peptide motif: evolutionary models. Cellular and Molecular Life Sciences, 2012, 69, 3999-4006.	2.4	19
15	An empirical phase diagram approach to investigate conformational stability of "secondâ€generation― functional mutants of acidic fibroblast growth factorâ€1. Protein Science, 2012, 21, 418-432.	3.1	24
16	A Polypeptide "Building Block―for the β-Trefoil Fold Identified by "Top-Down Symmetric Deconstruction― Journal of Molecular Biology, 2011, 407, 744-763.	2.0	43
17	Experimental support for the evolution of symmetric protein architecture from a simple peptide motif. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 126-130.	3.3	101
18	Engineering an improved crystal contact across a solvent-mediated interface of human fibroblast growth factor 1. Acta Crystallographica Section F: Structural Biology Communications, 2009, 65, 1136-1140.	0.7	4

#	Article	IF	Citations
19	X-ray structure and biophysical properties of rabbit fibroblast growth factor 1. Acta Crystallographica Section F: Structural Biology Communications, 2009, 65, 1097-1104.	0.7	1
20	Structural Basis of Conserved Cysteine in the Fibroblast Growth Factor Family: Evidence for a Vestigial Half-Cystine. Journal of Molecular Biology, 2009, 393, 128-139.	2.0	21
21	The Interaction between Thermodynamic Stability and Buried Free Cysteines in Regulating the Functional Half-Life of Fibroblast Growth Factor-1. Journal of Molecular Biology, 2009, 393, 113-127.	2.0	33
22	Analysis of the Dynamics of Assembly and Structural Impact for a Histidine Tagged FGF1â^'1.5 nm Au Nanoparticle Bioconjugate. Bioconjugate Chemistry, 2009, 20, 2106-2113.	1.8	22
23	A Logical OR Redundancy within the Asx-Pro-Asx-Gly Type I Î <sup>2</sup> -Turn Motif. Journal of Molecular Biology, 2008, 377, 1251-1264.	2.0	24
24	Activation Profiles and Regulatory Cascades of the Human Kallikrein-related Peptidases. Journal of Biological Chemistry, 2007, 282, 31852-31864.	1.6	135
25	Spackling the Crack: Stabilizing Human Fibroblast Growth Factor-1 by Targeting the N and C terminus Î <sup>2</sup> -Strand Interactions. Journal of Molecular Biology, 2007, 371, 256-268.	2.0	31
26	Sequence swapping does not result in conformation swapping for the $\hat{A}4/\hat{A}5$ and $\hat{A}8/\hat{A}9$ $\hat{A}$ -hairpin turns in human acidic fibroblast growth factor. Protein Science, 2005, 14, 351-359.	3.1	7
27	Redesigning symmetry-related "mini-core―regions of FGF-1 to increase primary structure symmetry: Thermodynamic and functional consequences of structural symmetry. Protein Science, 2005, 14, 2315-2323.	3.1	23
28	Conversion of type I 4:6 to 3:5 $\hat{I}^2$ -turn types in human acidic fibroblast growth factor: Effects upon structure, stability, folding, and mitogenic function. Proteins: Structure, Function and Bioinformatics, 2005, 62, 686-697.	1.5	5
29	Symmetric Primary and Tertiary Structure Mutations within a Symmetric Superfold: A Solution, not a Constraint, to Achieve a Foldable Polypeptide. Journal of Molecular Biology, 2004, 344, 769-780.	2.0	34
30	Identification of a Key Structural Element for Protein Folding Within $\hat{I}^2$ -Hairpin Turns. Journal of Molecular Biology, 2003, 328, 951-961.	2.0	33