

Byungkook Lee

List of Publications by Year in descending order

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Version: 2024-02-01

24
papers

1,159
citations

471509

17
h-index

677142

22
g-index

24
all docs

24
docs citations

24
times ranked

1298
citing authors

#	ARTICLE	IF	CITATIONS
1	Engineering antibody Fv fragments for cancer detection and therapy: Disulfide-stabilized Fv fragments. <i>Nature Biotechnology</i> , 1996, 14, 1239-1245.	17.5	143
2	Stabilization of the Fv fragments in recombinant immunotoxins by disulfide bonds engineered into conserved framework regions. <i>Biochemistry</i> , 1994, 33, 5451-5459.	2.5	134
3	Recombinant immunotoxin for cancer treatment with low immunogenicity by identification and silencing of human T-cell epitopes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 8571-8576.	7.1	104
4	Protein structure alignment using environmental profiles. <i>Protein Engineering, Design and Selection</i> , 2000, 13, 535-543.	2.1	103
5	Engineering interchain disulfide bonds into conserved framework regions of Fv fragments: improved biochemical characteristics of recombinant immunotoxins containing disulfide-stabilized Fv. <i>Protein Engineering, Design and Selection</i> , 1994, 7, 697-704.	2.1	94
6	Assessment of template-free modeling in CASP10 and ROLL. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 57-83.	2.6	79
7	A Frizzled-Like Cysteine-Rich Domain in Glypican-3 Mediates Wnt Binding and Regulates Hepatocellular Carcinoma Tumor Growth in Mice. <i>Hepatology</i> , 2019, 70, 1231-1245.	7.3	74
8	Circularly permuted proteins in the protein structure database. <i>Protein Science</i> , 2001, 10, 1881-1886.	7.6	67
9	Disulfide stabilization of antibody Fv: computer predictions and experimental evaluation. <i>Protein Engineering, Design and Selection</i> , 1995, 8, 1323-1331.	2.1	51
10	Antigen Shedding May Improve Efficiencies for Delivery of Antibody-Based Anticancer Agents in Solid Tumors. <i>Cancer Research</i> , 2012, 72, 3143-3152.	0.9	40
11	Cavities of α 1-antitrypsin that play structural and functional roles. <i>Protein Science</i> , 2008, 10, 1446-1453.	7.6	38
12	PRAC: A novel small nuclear protein that is specifically expressed in human prostate and colon. <i>Prostate</i> , 2001, 47, 125-131.	2.3	36
13	GDEP, a new gene differentially expressed in normal prostate and prostate cancer. <i>Prostate</i> , 2001, 48, 231-241.	2.3	31
14	A recombinant immunotoxin engineered for increased stability by adding a disulfide bond has decreased immunogenicity. <i>Protein Engineering, Design and Selection</i> , 2012, 25, 1-6.	2.1	30
15	Crystal structure of the disulfide-stabilized Fv fragment of anticancer antibody B1: Conformational influence of an engineered disulfide bond. <i>Proteins: Structure, Function and Bioinformatics</i> , 1998, 31, 128-138.	2.6	26
16	Poor correlation between T-cell activation assays and HLA-DR binding prediction algorithms in an immunogenic fragment of <i>Pseudomonas</i> exotoxin A. <i>Journal of Immunological Methods</i> , 2015, 425, 10-20.	1.4	23
17	SymD webserver: a platform for detecting internally symmetric protein structures. <i>Nucleic Acids Research</i> , 2014, 42, W296-W300.	14.5	19
18	Construction of a functional disulfide-stabilized TCR Fv indicates that antibody and tcr fv frameworks are very similar in structure. <i>Immunity</i> , 1995, 2, 281-287.	14.3	17

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19	Modeling Recombinant Immunotoxin Efficacies in Solid Tumors. <i>Annals of Biomedical Engineering</i> , 2008, 36, 486-512.	2.5	13
20	Effect of Antigen Shedding on Targeted Delivery of Immunotoxins in Solid Tumors from a Mathematical Model. <i>PLoS ONE</i> , 2014, 9, e110716.	2.5	13
21	Protein domain assignment from the recurrence of locally similar structures. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 853-866.	2.6	12
22	Molecular Models of STAT5A Tetramers Complexed to DNA Predict Relative Genome-Wide Frequencies of the Spacing between the Two Dimer Binding Motifs of the Tetramer Binding Sites. <i>PLoS ONE</i> , 2016, 11, e0160339.	2.5	8
23	A survey of recent work on evolutionary approaches to the protein folding problem. , 0, , .		4
24	A New Efficient Conformational Search Method for <i>ab initio</i> Protein Folding Study: Window Growth Evolutionary Algorithm. <i>Bulletin of the Korean Chemical Society</i> , 2016, 37, 1971-1976.	1.9	0