

Shiou-Ru Tzeng

List of Publications by Year in descending order

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31
papers

2,095
citations

394421

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33
all docs

33
docs citations

33
times ranked

3033
citing authors

#	ARTICLE	IF	CITATIONS
1	Molecular insights into substrate recognition and discrimination by the N-terminal domain of Lon AAA+ protease. <i>ELife</i> , 2021, 10, .	6.0	15
2	Mitochondrial <i>UQCRC1</i> mutations cause autosomal dominant parkinsonism with polyneuropathy. <i>Brain</i> , 2020, 143, 3352-3373.	7.6	37
3	A Celecoxib Derivative Eradicates Antibiotic-Resistant <i>Staphylococcus aureus</i> and Biofilms by Targeting YidC2 Translocase. <i>International Journal of Molecular Sciences</i> , 2020, 21, 9312.	4.1	6
4	Two separate functions of NME3 critical for cell survival underlie a neurodegenerative disorder. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 566-574.	7.1	36
5	Structural basis of adaptor-mediated protein degradation by the tail-specific PDZ-protease Prc. <i>Nature Communications</i> , 2017, 8, 1516.	12.8	46
6	SMYD3-Mediated H2A.Z.1 Methylation Promotes Cell Cycle and Cancer Proliferation. <i>Cancer Research</i> , 2016, 76, 6043-6053.	0.9	48
7	Importance of the C-terminal histidine residues of <i>Helicobacter pylori</i> GroES for Toll-like receptor 4 binding and interleukin-8 cytokine production. <i>Scientific Reports</i> , 2016, 6, 37367.	3.3	4
8	Exploiting <i>E. coli</i> auxotrophs for leucine, valine, and threonine specific methyl labeling of large proteins for NMR applications. <i>Journal of Biomolecular NMR</i> , 2016, 65, 99-108.	2.8	29
9	The role of slow and fast protein motions in allosteric interactions. <i>Biophysical Reviews</i> , 2015, 7, 251-255.	3.2	11
10	Structural basis of antizyme-mediated regulation of polyamine homeostasis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 11229-11234.	7.1	62
11	Allosteric inhibition through suppression of transient conformational states. <i>Nature Chemical Biology</i> , 2013, 9, 462-465.	8.0	92
12	Protein activity regulation by conformational entropy. <i>Nature</i> , 2012, 488, 236-240.	27.8	451
13	NMR Studies of Large Protein Systems. <i>Methods in Molecular Biology</i> , 2012, 831, 133-140.	0.9	36
14	Structural basis for regulation of the Crk signaling protein by a proline switch. <i>Nature Chemical Biology</i> , 2011, 7, 51-57.	8.0	79
15	Protein dynamics and allostery: an NMR view. <i>Current Opinion in Structural Biology</i> , 2011, 21, 62-67.	5.7	224
16	Structural basis for cAMP-mediated allosteric control of the catabolite activator protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 6927-6932.	7.1	197
17	Dynamic activation of an allosteric regulatory protein. <i>Nature</i> , 2009, 462, 368-372.	27.8	349
18	Solution Structure of the Ubp-M BUZ Domain, a Highly Specific Protein Module that Recognizes the C-terminal Tail of Free Ubiquitin. <i>Journal of Molecular Biology</i> , 2007, 370, 290-302.	4.2	52

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19	Structure of the ubiquitin-binding zinc finger domain of human DNA Y-polymerase $\hat{\text{I}}$. EMBO Reports, 2007, 8, 247-251.	4.5	123
20	Solution structure and phosphopeptide binding of the SH2 domain from the human Bruton's tyrosine kinase. Journal of Biomolecular NMR, 2006, 36, 73-78.	2.8	16
21	Solution Structure of a Novel Tryptophan-Rich Peptide with Bidirectional Antimicrobial Activity. Journal of Bacteriology, 2006, 188, 328-334.	2.2	57
22	^1H , ^{15}N and ^{13}C resonance assignments of the tetratricopeptide repeat (TPR) domain of hSGT. Journal of Biomolecular NMR, 2003, 26, 381-382.	2.8	2
23	^1H , ^{15}N and ^{13}C resonance assignments of the SH2 domain of Bruton's tyrosine kinase. Journal of Biomolecular NMR, 2002, 24, 163-164.	2.8	1
24	Stability and binding of SH3 domain of Bruton's tyrosine kinase. , 2002, , 565-566.		0
25	Structure and Peptide Binding Specificity of the SH3 and SH2 Domain from a Self-Regulated Protein Tyrosine Kinase " BTK. , 2001, , 695-696.		0
26	Solution structure of the human BTK SH3 domain complexed with a proline-rich peptide from p120cbl. Journal of Biomolecular NMR, 2000, 16, 303-312.	2.8	20
27	Stability and peptide binding specificity of Btk SH2 domain: Molecular basis for X-linked agammaglobulinemia. Protein Science, 2000, 9, 2377-2385.	7.6	35
28	Solution Structure and Dynamics of G1TE, a Nonphosphorylated Cyclic Peptide Inhibitor for the Grb2 SH2 Domain. Archives of Biochemistry and Biophysics, 1999, 372, 309-314.	3.0	17
29	SH3 domain of Bruton's tyrosine kinase can bind to proline-rich peptides of TH domain of the kinase and p120cbl. , 1997, 29, 545-552.		19
30	Stability and folding of the SH3 domain of bruton's tyrosine kinase. Proteins: Structure, Function and Bioinformatics, 1996, 26, 465-471.	2.6	29
31	Stability and folding of the SH3 domain of bruton's tyrosine kinase. Proteins: Structure, Function and Bioinformatics, 1996, 26, 465-471.	2.6	1