Xianchi Dong

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/10670875/publications.pdf

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21	1,533	516710 16	713466 21
papers	citations	h-index	g-index

25	25	25	2695
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	N501Y mutation of spike protein in SARS-CoV-2 strengthens its binding to receptor ACE2. ELife, 2021, 10, .	6.0	262
2	Force interacts with macromolecular structure in activation of TGF-Î². Nature, 2017, 542, 55-59.	27.8	222
3	GARP regulates the bioavailability and activation of TGFÎ². Molecular Biology of the Cell, 2012, 23, 1129-1139.	2.1	153
4	Structure of human MRG15 chromo domain and its binding to Lys36-methylated histone H3. Nucleic Acids Research, 2006, 34, 6621-6628.	14.5	138
5	Structural determinants of integrin Î²-subunit specificity for latent TGF-Î². Nature Structural and Molecular Biology, 2014, 21, 1091-1096.	8.2	115
6	Rules of engagement between Î±vÎ²6 integrin and foot-and-mouth disease virus. Nature Communications, 2017, 8, 15408.	12.8	75
7	Î±_VÎ²₃ Integrin Crystal Structures and Their Functional Implications. Biochemistry, 2012, 51, 8814-8828.	2.5	66
8	Molecular Basis of the Acceleration of the GDP-GTP Exchange of Human Ras Homolog Enriched in Brain by Human Translationally Controlled Tumor Protein. Journal of Biological Chemistry, 2009, 284, 23754-23764.	3.4	60
9	Molecular Basis of the Interaction of Saccharomyces cerevisiae Eaf3 Chromo Domain with Methylated H3K36. Journal of Biological Chemistry, 2008, 283, 36504-36512.	3.4	59
10	The von Willebrand factor Dâ€²D3 assembly and structural principles for factor VIII binding and concatemer biogenesis. Blood, 2019, 133, 1523-1533.	1.4	55
11	A novel calcium-binding site of von Willebrand factor A2 domain regulates its cleavage by ADAMTS13. Blood, 2011, 117, 4623-4631.	1.4	47
12	Fusion surface structure, function, and dynamics of gamete fusogen HAP2. ELife, 2018, 7, .	6.0	37
13	Catalytic mechanism of the tryptophan activation reaction revealed by crystal structures of human tryptophanyl-tRNA synthetase in different enzymatic states. Nucleic Acids Research, 2008, 36, 1288-1299.	14.5	34
14	Atypical interactions of integrin Î±VÎ²8 with pro-TGF-Î²1. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E4168-E4174.	7.1	34
15	Prodomainâ€“growth factor swapping in the structure of pro-TGF-Î²1. Journal of Biological Chemistry, 2018, 293, 1579-1589.	3.4	31
16	Crystal structures of Saccharomyces cerevisiae tryptophanyl-tRNA synthetase: new insights into the mechanism of tryptophan activation and implications for anti-fungal drug design. Nucleic Acids Research, 2010, 38, 3399-3413.	14.5	17
17	Specific high affinity interaction of HelicobacterÂpylori CagL with integrin Î±_VÎ²₆ promotes type <scp>IV</scp> secretion of CagA into human cells. FEBS Journal, 2019, 286, 3980-3997.	4.7	16
18	High integrin Î± _V Î² ₆ affinity reached by hybrid domain deletion slows ligand-binding on-rate. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E1429-E1436.	7.1	14

#	Article	IF	Citations
19	Disulfide exchange in multimerization of von Willebrand factor and gel-forming mucins. Blood, 2021, 137, 1263-1267.	1.4	14
20	Crystal structure of Pyrococcus horikoshii tryptophanyl-tRNA synthetase and structure-based phylogenetic analysis suggest an archaeal origin of tryptophanyl-tRNA synthetase. Nucleic Acids Research, 2010, 38, 1401-1412.	14.5	13
21	Structural basis of malaria transmission blockade by a monoclonal antibody to gamete fusogen HAP2. ELife, 2021, 10, .	6.0	7