Sebastian Kelm

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/1027490/publications.pdf

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29	1,235	471509	552781
papers	citations	17	26
		h-index	g-index

34	34	34	2044
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	A multi-crystal method for extracting obscured crystallographic states from conventionally uninterpretable electron density. Nature Communications, 2017, 8, 15123.	12.8	186
2	Observed Antibody Space: A Resource for Data Mining Next-Generation Sequencing of Antibody Repertoires. Journal of Immunology, 2018, 201, 2502-2509.	0.8	165
3	SAbPred: a structure-based antibody prediction server. Nucleic Acids Research, 2016, 44, W474-W478.	14.5	155
4	Computational approaches to therapeutic antibody design: established methods and emerging trends. Briefings in Bioinformatics, 2020, 21, 1549-1567.	6.5	126
5	MEDELLER: homology-based coordinate generation for membrane proteins. Bioinformatics, 2010, 26, 2833-2840.	4.1	103
6	Length-independent structural similarities enrich the antibody CDR canonical class model. MAbs, 2016, 8, 751-760.	5.2	49
7	Sphinx: merging knowledge-based and ab initio approaches to improve protein loop prediction. Bioinformatics, 2017, 33, 1346-1353.	4.1	49
8	Memoir: template-based structure prediction for membrane proteins. Nucleic Acids Research, 2013, 41, W379-W383.	14.5	38
9	Structurally Mapping Antibody Repertoires. Frontiers in Immunology, 2018, 9, 1698.	4.8	36
10	Crystal structure of dopamine D1 receptor in complex with G protein and a non-catechol agonist. Nature Communications, 2021, 12, 3305.	12.8	34
11	Insight into small molecule binding to the neonatal Fc receptor by X-ray crystallography and 100 kHz magic-angle-spinning NMR. PLoS Biology, 2018, 16, e2006192.	5.6	31
12	iMembrane: homology-based membrane-insertion of proteins. Bioinformatics, 2009, 25, 1086-1088.	4.1	29
13	SCALOP: sequence-based antibody canonical loop structure annotation. Bioinformatics, 2019, 35, 1774-1776.	4.1	29
14	B-cell epitopes: Discontinuity and conformational analysis. Molecular Immunology, 2019, 114, 643-650.	2.2	28
15	Structural diversity of B-cell receptor repertoires along the B-cell differentiation axis in humans and mice. PLoS Computational Biology, 2020, 16, e1007636.	3.2	27
16	Reconstruction of apo A2A receptor activation pathways reveal ligand-competent intermediates and state-dependent cholesterol hotspots. Scientific Reports, 2019, 9, 14199.	3.3	24
17	Environment specific substitution tables improve membrane protein alignment. Bioinformatics, 2011, 27, i15-i23.	4.1	20
18	Examining the Conservation of Kinks in Alpha Helices. PLoS ONE, 2016, 11, e0157553.	2.5	20

#	Article	IF	Citations
19	Electrostatic interactions modulate the differential aggregation propensities of IgG1 and IgG4P antibodies and inform charged residue substitutions for improved developability. Protein Engineering, Design and Selection, 2019, 32, 277-288.	2.1	19
20	Fragment-based modeling of membrane protein loops: Successes, failures, and prospects for the future. Proteins: Structure, Function and Bioinformatics, 2014, 82, 175-186.	2.6	15
21	Filtering Next-Generation Sequencing of the Ig Gene Repertoire Data Using Antibody Structural Information. Journal of Immunology, 2018, 201, 3694-3704.	0.8	11
22	The Chemical Synthesis of Knob Domain Antibody Fragments. ACS Chemical Biology, 2021, 16, 1757-1769.	3.4	10
23	Co-evolutionary distance predictions contain flexibility information. Bioinformatics, 2021, , .	4.1	9
24	The Aminotriazole Antagonist Cmpdâ€1 Stabilises a Distinct Inactive State of the Adenosine 2A Receptor. Angewandte Chemie - International Edition, 2019, 58, 9399-9403.	13.8	3
25	PANDDAs:Âmulti-dataset methods for finding hits from fragment screening by X-ray crystallography. Acta Crystallographica Section A: Foundations and Advances, 2015, 71, s258-s258.	0.1	2
26	Protein Modeling and Structural Prediction. , 2014, , 171-182.		1
27	Investigating Cotranslational Folding in Membrane Proteins using Fragment-Based Structure Prediction. Biophysical Journal, 2017, 112, 61a.	0.5	1
28	The Aminotriazole Antagonist Cmpdâ€1 Stabilises a Distinct Inactive State of the Adenosine 2A Receptor. Angewandte Chemie, 2019, 131, 9499-9503.	2.0	1
29	Efficient Sampling for the Prediction of Long and Multidomain Protein Structures. Biophysical Journal, 2018, 114, 574a.	0.5	0