

# Julia Brasch

## List of Publications by Year in descending order

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Version: 2024-02-01

24  
papers

2,623  
citations

430874

18  
h-index

713466

21  
g-index

24  
all docs

24  
docs citations

24  
times ranked

3546  
citing authors

#	ARTICLE	IF	CITATIONS
1	Visualizing cadherin intermembrane adhesion assemblies using cryo-electron tomography. <i>Microscopy and Microanalysis</i> , 2021, 27, 284-287.	0.4	0
2	Computational model of E-cadherin clustering under force. <i>Biophysical Journal</i> , 2021, 120, 4944-4954.	0.5	11
3	Family-wide Structural and Biophysical Analysis of Binding Interactions among Non-clustered $\hat{\Gamma}$ -Protocadherins. <i>Cell Reports</i> , 2020, 30, 2655-2671.e7.	6.4	35
4	TOPAZ: A Positive-Unlabeled Convolutional Neural Network CryoEM Particle Picker that can Pick Any Size and Shape Particle. <i>Microscopy and Microanalysis</i> , 2019, 25, 986-987.	0.4	14
5	Visualization of clustered protocadherin neuronal self-recognition complexes. <i>Nature</i> , 2019, 569, 280-283.	27.8	86
6	Positive-unlabeled convolutional neural networks for particle picking in cryo-electron micrographs. <i>Nature Methods</i> , 2019, 16, 1153-1160.	19.0	693
7	Pathogenic IgG4 autoantibodies from endemic pemphigus foliaceus recognize a desmoglein-1 conformational epitope. <i>Journal of Autoimmunity</i> , 2018, 89, 171-185.	6.5	19
8	CryoET of Single Particle CryoEM Grids Reveals Widespread Particle Adsorption to the Air-Water Interface, Which May be Reduced with New Plunging Techniques. <i>Microscopy and Microanalysis</i> , 2018, 24, 872-873.	0.4	0
9	Intrinsic DNA Shape Accounts for Affinity Differences between Hox-Cofactor Binding Sites. <i>Cell Reports</i> , 2018, 24, 2221-2230.	6.4	31
10	Homophilic and Heterophilic Interactions of Type II Cadherins Identify Specificity Groups Underlying Cell-Adhesive Behavior. <i>Cell Reports</i> , 2018, 23, 1840-1852.	6.4	54
11	Positive-unlabeled convolutional neural networks for particle picking in cryo-electron micrographs. <i>Microscopy and Microanalysis</i> , 2018, 24, 245-247.		12
12	Mammalian O-mannosylation of cadherins and plexins is independent of protein O-mannosyltransferases 1 and 2. <i>Journal of Biological Chemistry</i> , 2017, 292, 11586-11598.	3.4	39
13	Discovery of an O-mannosylation pathway selectively serving cadherins and protocadherins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 11163-11168.	7.1	83
14	Structural basis of adhesive binding by desmocollins and desmogleins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 7160-7165.	7.1	137
15	Structural and energetic determinants of adhesive binding specificity in type I cadherins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E4175-84.	7.1	78
16	Nectin ectodomain structures reveal a canonical adhesive interface. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 906-915.	8.2	104
17	Structures from Anomalous Diffraction of Native Biological Macromolecules. <i>Science</i> , 2012, 336, 1033-1037.	12.6	154
18	Thinking outside the cell: how cadherins drive adhesion. <i>Trends in Cell Biology</i> , 2012, 22, 299-310.	7.9	296

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19	Structure and Binding Mechanism of Vascular Endothelial Cadherin: A Divergent Classical Cadherin. <i>Journal of Molecular Biology</i> , 2011, 408, 57-73.	4.2	76
20	Crystal Structure of the Ligand Binding Domain of Netrin G2. <i>Journal of Molecular Biology</i> , 2011, 414, 723-734.	4.2	19
21	The Extracellular Architecture of Adherens Junctions Revealed by Crystal Structures of Type I Cadherins. <i>Structure</i> , 2011, 19, 244-256.	3.3	347
22	T-cadherin structures reveal a novel adhesive binding mechanism. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 339-347.	8.2	118
23	Two-step adhesive binding by classical cadherins. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 348-357.	8.2	184
24	Crystal Structures of $\hat{I}^2$ -Neurexin 1 and $\hat{I}^2$ -Neurexin 2 Ectodomains and Dynamics of Splice Insertion Sequence 4. <i>Structure</i> , 2008, 16, 410-421.	3.3	33