

Riccardo Pellarin

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2900138/publications.pdf>

Version: 2024-02-01

23
papers

2,184
citations

361413

20
h-index

642732

23
g-index

24
all docs

24
docs citations

24
times ranked

3183
citing authors

#	ARTICLE	IF	CITATIONS
1	Advanced <i>In Vivo</i> Cross-Linking Mass Spectrometry Platform to Characterize Proteome-Wide Protein Interactions. <i>Analytical Chemistry</i> , 2021, 93, 4166-4174.	6.5	22
2	Genetic interaction mapping informs integrative structure determination of protein complexes. <i>Science</i> , 2020, 370, .	12.6	24
3	Role of integrative structural biology in understanding transcriptional initiation. <i>Methods</i> , 2019, 159-160, 4-22.	3.8	10
4	<i>In situ</i> and high-resolution cryo-EM structure of a bacterial type VI secretion system membrane complex. <i>EMBO Journal</i> , 2019, 38, .	7.8	72
5	Bayesian Weighing of Electron Cryo-Microscopy Data for Integrative Structural Modeling. <i>Structure</i> , 2019, 27, 175-188.e6.	3.3	50
6	Simultaneous Determination of Protein Structure and Dynamics Using Cryo-Electron Microscopy. <i>Biophysical Journal</i> , 2018, 114, 1604-1613.	0.5	88
7	Integrative structure and functional anatomy of a nuclear pore complex. <i>Nature</i> , 2018, 555, 475-482.	27.8	435
8	Integrative structure modeling with the Integrative Modeling Platform. <i>Protein Science</i> , 2018, 27, 245-258.	7.6	92
9	Biogenesis and structure of a type VI secretion baseplate. <i>Nature Microbiology</i> , 2018, 3, 1404-1416.	13.3	76
10	A Residue-Resolved Bayesian Approach to Quantitative Interpretation of Hydrogen-Deuterium Exchange from Mass Spectrometry: Application to Characterizing Protein-Ligand Interactions. <i>Journal of Physical Chemistry B</i> , 2017, 121, 3493-3501.	2.6	52
11	Structure and Function of the Nuclear Pore Complex Cytoplasmic mRNA Export Platform. <i>Cell</i> , 2016, 167, 1215-1228.e25.	28.9	148
12	Structure of Complement C3(H2O) Revealed By Quantitative Cross-Linking/Mass Spectrometry And Modeling. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 2730-2743.	3.8	59
13	A strategy for dissecting the architectures of native macromolecular assemblies. <i>Nature Methods</i> , 2015, 12, 1135-1138.	19.0	113
14	Architecture of the Human and Yeast General Transcription and DNA Repair Factor TFIIF. <i>Molecular Cell</i> , 2015, 59, 794-806.	9.7	91
15	Molecular architecture of the yeast Mediator complex. <i>ELife</i> , 2015, 4, .	6.0	136
16	Structural Characterization by Cross-linking Reveals the Detailed Architecture of a Coatomer-related Heptameric Module from the Nuclear Pore Complex. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 2927-2943.	3.8	152
17	Determining Protein Complex Structures Based on a Bayesian Model of <i>In Vivo</i> Förster Resonance Energy Transfer (FRET) Data. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 2812-2823.	3.8	29
18	Molecular Architecture and Function of the SEA Complex, a Modulator of the TORC1 Pathway. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 2855-2870.	3.8	64

#	ARTICLE	IF	CITATIONS
19	Elucidating the Mechanism of Substrate Recognition by the Bacterial Hsp90 Molecular Chaperone. <i>Journal of Molecular Biology</i> , 2014, 426, 2393-2404.	4.2	45
20	Uncertainty in integrative structural modeling. <i>Current Opinion in Structural Biology</i> , 2014, 28, 96-104.	5.7	91
21	Molecular Architecture of Photoreceptor Phosphodiesterase Elucidated by Chemical Cross-Linking and Integrative Modeling. <i>Journal of Molecular Biology</i> , 2014, 426, 3713-3728.	4.2	37
22	Cys-Scanning Disulfide Crosslinking and Bayesian Modeling Probe the Transmembrane Signaling Mechanism of the Histidine Kinase, PhoQ. <i>Structure</i> , 2014, 22, 1239-1251.	3.3	103
23	Molecular Architecture of the 40Sâ€¦eIF1â€¦eIF3 Translation Initiation Complex. <i>Cell</i> , 2014, 158, 1123-1135.	28.9	193