

Grigore D Pintilie

List of Publications by Year in descending order

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Version: 2024-02-01

49
papers

2,339
citations

331670

21
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302126

39
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64
all docs

64
docs citations

64
times ranked

3188
citing authors

#	ARTICLE	IF	CITATIONS
1	Cryo-EM analysis of Ebola virus nucleocapsid-like assembly. STAR Protocols, 2022, 3, 101030.	1.2	0
2	Cryo-EM, Protein Engineering, and Simulation Enable the Development of Peptide Therapeutics against Acute Myeloid Leukemia. ACS Central Science, 2022, 8, 214-222.	11.3	7
3	Cryo-ET of <i>Toxoplasma</i> parasites gives subnanometer insight into tubulin-based structures. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	26
4	The N-terminus of varicella-zoster virus glycoprotein B has a functional role in fusion. PLoS Pathogens, 2021, 17, e1008961.	4.7	12
5	Evolution of standardization and dissemination of cryo-EM structures and data jointly by the community, PDB, and EMDb. Journal of Biological Chemistry, 2021, 296, 100560.	3.4	18
6	Cryo-EM model validation recommendations based on outcomes of the 2019 EMDDataResource challenge. Nature Methods, 2021, 18, 156-164.	19.0	73
7	CryoEM Map-Model Scores: From Average Density to Q-scores. Microscopy and Microanalysis, 2021, 27, 1382-1384.	0.4	1
8	High Resolution Data Collection at S2C2, a National CryoEM Center. Microscopy and Microanalysis, 2021, 27, 1152-1154.	0.4	0
9	Validation, analysis and annotation of cryo-EM structures. Acta Crystallographica Section D: Structural Biology, 2021, 77, 1142-1152.	2.3	14
10	Cryo-EM and antisense targeting of the 28-kDa frameshift stimulation element from the SARS-CoV-2 RNA genome. Nature Structural and Molecular Biology, 2021, 28, 747-754.	8.2	91
11	Cryo-EM structures of full-length Tetrahymena ribozyme at 3.1 Å resolution. Nature, 2021, 596, 603-607.	27.8	59
12	Molecular basis for ATPase-powered substrate translocation by the Lon AAA+ protease. Journal of Biological Chemistry, 2021, 297, 101239.	3.4	12
13	Complete three-dimensional structures of the Lon protease translocating a protein substrate. Science Advances, 2021, 7, eabj7835.	10.3	7
14	Mapping the catalytic conformations of an assembly-line polyketide synthase module. Science, 2021, 374, 729-734.	12.6	41
15	The N-terminus of varicella-zoster virus glycoprotein B has a functional role in fusion. , 2021, 17, e1008961.		0
16	The N-terminus of varicella-zoster virus glycoprotein B has a functional role in fusion. , 2021, 17, e1008961.		0
17	The N-terminus of varicella-zoster virus glycoprotein B has a functional role in fusion. , 2021, 17, e1008961.		0
18	The N-terminus of varicella-zoster virus glycoprotein B has a functional role in fusion. , 2021, 17, e1008961.		0

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19	Cryo-EM and MD infer water-mediated proton transport and autoinhibition mechanisms of V_o complex. Science Advances, 2020, 6, .	10.3	51
20	Full-length three-dimensional structure of the influenza A virus M1 protein and its organization into a matrix layer. PLoS Biology, 2020, 18, e3000827.	5.6	20
21	A glycoprotein B-neutralizing antibody structure at 2.8Å... uncovers a critical domain for herpesvirus fusion initiation. Nature Communications, 2020, 11, 4141.	12.8	23
22	A 3.4Å... cryo-electron microscopy structure of the human coronavirus spike trimer computationally derived from vitrified NL63 virus particles. QRB Discovery, 2020, 1, e11.	1.6	10
23	Resolving individual atoms of protein complex by cryo-electron microscopy. Cell Research, 2020, 30, 1136-1139.	12.0	69
24	Accelerated cryo-EM-guided determination of three-dimensional RNA-only structures. Nature Methods, 2020, 17, 699-707.	19.0	119
25	Measurement of atom resolvability in cryo-EM maps with Q-scores. Nature Methods, 2020, 17, 328-334.	19.0	230
26	Inhibition mechanisms of AcrF9, AcrF8, and AcrF6 against type I-F CRISPR-Cas complex revealed by cryo-EM. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 7176-7182.	7.1	35
27	Title is missing!. , 2020, 18, e3000827.		0
28	Title is missing!. , 2020, 18, e3000827.		0
29	Title is missing!. , 2020, 18, e3000827.		0
30	Title is missing!. , 2020, 18, e3000827.		0
31	Segmentation and Comparative Modeling in an 8.6Å... Cryo-EM Map of the Singapore Grouper Iridovirus. Structure, 2019, 27, 1561-1569.e4.	3.3	10
32	Cryo-EM structures of <i>Helicobacter pylori</i> vacuolating cytotoxin A oligomeric assemblies at near-atomic resolution. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 6800-6805.	7.1	33
33	Coupling of ssRNA cleavage with DNase activity in type III-A CRISPR-Csm revealed by cryo-EM and biochemistry. Cell Research, 2019, 29, 305-312.	12.0	40
34	Structural basis of amino acid surveillance by higher-order tRNA-mRNA interactions. Nature Structural and Molecular Biology, 2019, 26, 1094-1105.	8.2	52
35	Cryo-EM structure of a 40kDa SAM-IV riboswitch RNA at 3.7Å... resolution. Nature Communications, 2019, 10, 5511.	12.8	90
36	Structure of Calcarisporiella thermophila Hsp104 Disaggregase that Antagonizes Diverse Proteotoxic Misfolding Events. Structure, 2019, 27, 449-463.e7.	3.3	29

#	ARTICLE	IF	CITATIONS
37	Electron Cryo-microscopy Structure of Ebola Virus Nucleoprotein Reveals a Mechanism for Nucleocapsid-like Assembly. <i>Cell</i> , 2018, 172, 966-978.e12.	28.9	51
38	The 3.5-Å... CryoEM Structure of Nanodisc-Reconstituted Yeast Vacuolar ATPase Vo Proton Channel. <i>Molecular Cell</i> , 2018, 69, 993-1004.e3.	9.7	103
39	Assessment of structural features in Cryo-EM density maps using SSE and side chain Z-scores. <i>Journal of Structural Biology</i> , 2018, 204, 564-571.	2.8	23
40	The first single particle analysis Map Challenge: A summary of the assessments. <i>Journal of Structural Biology</i> , 2018, 204, 291-300.	2.8	17
41	Structural and Functional Impacts of ER Coactivator Sequential Recruitment. <i>Molecular Cell</i> , 2017, 67, 733-743.e4.	9.7	69
42	Resolution and Probabilistic Models of Components in CryoEM Maps of Mature P22 Bacteriophage. <i>Biophysical Journal</i> , 2016, 110, 827-839.	0.5	43
43	EMDataBank unified data resource for 3DEM. <i>Nucleic Acids Research</i> , 2016, 44, D396-D403.	14.5	230
44	Resolution and Probabilistic Structural Models of Subcomponents Derived from CryoEM Maps of Mature P22 Bacteriophage. <i>Biophysical Journal</i> , 2016, 110, 158a.	0.5	0
45	Structure of a Biologically Active Estrogen Receptor-Coactivator Complex on DNA. <i>Molecular Cell</i> , 2015, 57, 1047-1058.	9.7	137
46	Emdatabank: Unified Data Resource for 3DEM. <i>Biophysical Journal</i> , 2013, 104, 351a.	0.5	3
47	Comparison of <i>Segger</i> and other methods for segmentation and rigid-body docking of molecular components in Cryo-EM density maps. <i>Biopolymers</i> , 2012, 97, 742-760.	2.4	68
48	Acquisition of the 3D surface of the palate by in-vivo digitization with Wave. <i>Speech Communication</i> , 2012, 54, 923-931.	2.8	11
49	Quantitative analysis of cryo-EM density map segmentation by watershed and scale-space filtering, and fitting of structures by alignment to regions. <i>Journal of Structural Biology</i> , 2010, 170, 427-438.	2.8	352