

# Grigore D Pintilie

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2801092/publications.pdf>

Version: 2024-02-01

49  
papers

2,339  
citations

331670

21  
h-index

302126

39  
g-index

64  
all docs

64  
docs citations

64  
times ranked

3188  
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	EMDataBank unified data resource for 3DEM. <i>Nucleic Acids Research</i> , 2016, 44, D396-D403.	14.5	230
3	Measurement of atom resolvability in cryo-EM maps with Q-scores. <i>Nature Methods</i> , 2020, 17, 328-334.	19.0	230
4	Structure of a Biologically Active Estrogen Receptor-Coactivator Complex on DNA. <i>Molecular Cell</i> , 2015, 57, 1047-1058.	9.7	137
5	Accelerated cryo-EM-guided determination of three-dimensional RNA-only structures. <i>Nature Methods</i> , 2020, 17, 699-707.	19.0	119
6	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
7	Cryo-EM and antisense targeting of the 28-kDa frameshift stimulation element from the SARS-CoV-2 RNA genome. <i>Nature Structural and Molecular Biology</i> , 2021, 28, 747-754.	8.2	91
8	Cryo-EM structure of a 40ÅkDa SAM-IV riboswitch RNA at 3.7Å resolution. <i>Nature Communications</i> , 2019, 10, 5511.	12.8	90
9	Cryo-EM model validation recommendations based on outcomes of the 2019 EMDataResource challenge. <i>Nature Methods</i> , 2021, 18, 156-164.	19.0	73
10	Structural and Functional Impacts of ER Coactivator Sequential Recruitment. <i>Molecular Cell</i> , 2017, 67, 733-743.e4.	9.7	69
11	Resolving individual atoms of protein complex by cryo-electron microscopy. <i>Cell Research</i> , 2020, 30, 1136-1139.	12.0	69
12	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
13	Cryo-EM structures of full-length Tetrahymena ribozyme at 3.1Å resolution. <i>Nature</i> , 2021, 596, 603-607.	27.8	59
14	Structural basis of amino acid surveillance by higher-order tRNA-mRNA interactions. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 1094-1105.	8.2	52
15	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
16	Cryo-EM and MD infer water-mediated proton transport and autoinhibition mechanisms of V <sub>o</sub> complex. <i>Science Advances</i> , 2020, 6, .	10.3	51
17	Resolution and Probabilistic Models of Components in CryoEM Maps of Mature P22 Bacteriophage. <i>Biophysical Journal</i> , 2016, 110, 827-839.	0.5	43
18	Mapping the catalytic conformations of an assembly-line polyketide synthase module. <i>Science</i> , 2021, 374, 729-734.	12.6	41

#	ARTICLE	IF	CITATIONS
19	Coupling of ssRNA cleavage with DNase activity in type III-A CRISPR-Csm revealed by cryo-EM and biochemistry. <i>Cell Research</i> , 2019, 29, 305-312.	12.0	40
20	Inhibition mechanisms of AcrF9, AcrF8, and AcrF6 against type I-F CRISPR-Cas complex revealed by cryo-EM. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 7176-7182.	7.1	35
21	Cryo-EM structures of <i>Helicobacter pylori</i> vacuolating cytotoxin A oligomeric assemblies at near-atomic resolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 6800-6805.	7.1	33
22	Structure of <i>Calcarisporiella thermophila</i> Hsp104 Disaggregase that Antagonizes Diverse Proteotoxic Misfolding Events. <i>Structure</i> , 2019, 27, 449-463.e7.	3.3	29
23	Cryo-ET of <i>Toxoplasma</i> parasites gives subnanometer insight into tubulin-based structures. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	26
24	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
25	A glycoprotein B-neutralizing antibody structure at 2.8 Å... uncovers a critical domain for herpesvirus fusion initiation. <i>Nature Communications</i> , 2020, 11, 4141.	12.8	23
26	Full-length three-dimensional structure of the influenza A virus M1 protein and its organization into a matrix layer. <i>PLoS Biology</i> , 2020, 18, e3000827.	5.6	20
27	Evolution of standardization and dissemination of cryo-EM structures and data jointly by the community, PDB, and EMDB. <i>Journal of Biological Chemistry</i> , 2021, 296, 100560.	3.4	18
28	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
29	Validation, analysis and annotation of cryo-EM structures. <i>Acta Crystallographica Section D: Structural Biology</i> , 2021, 77, 1142-1152.	2.3	14
30	The N-terminus of varicella-zoster virus glycoprotein B has a functional role in fusion. <i>PLoS Pathogens</i> , 2021, 17, e1008961.	4.7	12
31	Molecular basis for ATPase-powered substrate translocation by the Lon AAA+ protease. <i>Journal of Biological Chemistry</i> , 2021, 297, 101239.	3.4	12
32	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
33	Segmentation and Comparative Modeling in an 8.6-Å... Cryo-EM Map of the Singapore Grouper Iridovirus. <i>Structure</i> , 2019, 27, 1561-1569.e4.	3.3	10
34	A 3.4-Å... cryo-electron microscopy structure of the human coronavirus spike trimer computationally derived from vitrified NL63 virus particles. <i>QRB Discovery</i> , 2020, 1, e11.	1.6	10
35	Complete three-dimensional structures of the Lon protease translocating a protein substrate. <i>Science Advances</i> , 2021, 7, eabj7835.	10.3	7
36	Cryo-EM, Protein Engineering, and Simulation Enable the Development of Peptide Therapeutics against Acute Myeloid Leukemia. <i>ACS Central Science</i> , 2022, 8, 214-222.	11.3	7

#	ARTICLE	IF	CITATIONS
37	Emdatabank: Unified Data Resource for 3DEM. Biophysical Journal, 2013, 104, 351a.	0.5	3
38	CryoEM Map-Model Scores: From Average Density to Q-scores. Microscopy and Microanalysis, 2021, 27, 1382-1384.	0.4	1
39	Resolution and Probabilistic Structural Models of Subcomponents Derived from CryoEM Maps of Mature P22 Bacteriophage. Biophysical Journal, 2016, 110, 158a.	0.5	0
40	High Resolution Data Collection at S2C2, a National CryoEM Center. Microscopy and Microanalysis, 2021, 27, 1152-1154.	0.4	0
41	Cryo-EM analysis of Ebola virus nucleocapsid-like assembly. STAR Protocols, 2022, 3, 101030.	1.2	0
42	Title is missing!. , 2020, 18, e3000827.		0
43	Title is missing!. , 2020, 18, e3000827.		0
44	Title is missing!. , 2020, 18, e3000827.		0
45	Title is missing!. , 2020, 18, e3000827.		0
46	The N-terminus of varicella-zoster virus glycoprotein B has a functional role in fusion. , 2021, 17, e1008961.		0
47	The N-terminus of varicella-zoster virus glycoprotein B has a functional role in fusion. , 2021, 17, e1008961.		0
48	The N-terminus of varicella-zoster virus glycoprotein B has a functional role in fusion. , 2021, 17, e1008961.		0
49	The N-terminus of varicella-zoster virus glycoprotein B has a functional role in fusion. , 2021, 17, e1008961.		0