

Dmitry Lyumkis

List of Publications by Year in descending order

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Version: 2024-02-01

43
papers

5,646
citations

257357

24
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276775

41
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55
docs citations

55
times ranked

6898
citing authors

#	ARTICLE	IF	CITATIONS
1	Quantitative mining of compositional heterogeneity in cryo-EM datasets of ribosome assembly intermediates. <i>Structure</i> , 2022, 30, 498-509.e4.	1.6	14
2	Pretransition state and apo structures of the filament-forming enzyme SgrAI elucidate mechanisms of activation and substrate specificity. <i>Journal of Biological Chemistry</i> , 2022, 298, 101760.	1.6	3
3	Structures, Mechanism, and Functional Relevance of Filament Formation by SgrAI. <i>FASEB Journal</i> , 2022, 36, .	0.2	0
4	Multivalent interactions essential for lentiviral integrase function. <i>Nature Communications</i> , 2022, 13, 2416.	5.8	12
5	Tools for visualizing and analyzing Fourier space sampling in Cryo-EM. <i>Progress in Biophysics and Molecular Biology</i> , 2021, 160, 53-65.	1.4	15
6	HIV-1 Integrase Inhibitors with Modifications That Affect Their Potencies against Drug Resistant Integrase Mutants. <i>ACS Infectious Diseases</i> , 2021, 7, 1469-1482.	1.8	14
7	Integrase Strand Transfer Inhibitors Are Effective Anti-HIV Drugs. <i>Viruses</i> , 2021, 13, 205.	1.5	42
8	Evaluating Local and Directional Resolution of Cryo-EM Density Maps. <i>Methods in Molecular Biology</i> , 2021, 2215, 161-187.	0.4	19
9	Retroviral integrase: Structure, mechanism, and inhibition. <i>The Enzymes</i> , 2021, 50, 249-300.	0.7	8
10	Non-uniformity of projection distributions attenuates resolution in Cryo-EM. <i>Progress in Biophysics and Molecular Biology</i> , 2020, 150, 160-183.	1.4	35
11	SrmB Rescues Trapped Ribosome Assembly Intermediates. <i>Journal of Molecular Biology</i> , 2020, 432, 978-990.	2.0	21
12	Molecular determinants for dsDNA translocation by the transcription-repair coupling and evolvability factor Mfd. <i>Nature Communications</i> , 2020, 11, 3740.	5.8	21
13	Structural Biology of HIV Integrase Strand Transfer Inhibitors. <i>Trends in Pharmacological Sciences</i> , 2020, 41, 611-626.	4.0	25
14	HIV-1 Integrase Inhibitors That Are Active against Drug-Resistant Integrase Mutants. <i>Antimicrobial Agents and Chemotherapy</i> , 2020, 64, .	1.4	21
15	Structural basis for strand-transfer inhibitor binding to HIV intasomes. <i>Science</i> , 2020, 367, 810-814.	6.0	74
16	Cryo-EM Structures of a Group II Intron Reverse Splicing into DNA. <i>Cell</i> , 2019, 178, 612-623.e12.	13.5	41
17	Mechanism of Filamentation-Induced Allosteric Activation of the SgrAI Endonuclease. <i>Structure</i> , 2019, 27, 1497-1507.e3.	1.6	13
18	Challenges and opportunities in cryo-EM single-particle analysis. <i>Journal of Biological Chemistry</i> , 2019, 294, 5181-5197.	1.6	273

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19	Analysis of discrete local variability and structural covariance in macromolecular assemblies using Cryo-EM and focused classification. <i>Ultramicroscopy</i> , 2019, 203, 170-180.	0.8	35
20	HIV-1 integrase tetramers are the antiviral target of pyridine-based allosteric integrase inhibitors. <i>ELife</i> , 2019, 8, .	2.8	41
21	Sub-2Å... Ewald curvature corrected structure of an AAV2 capsid variant. <i>Nature Communications</i> , 2018, 9, 3628.	5.8	73
22	Structural Basis for the RNA-Guided Ribonuclease Activity of CRISPR-Cas13d. <i>Cell</i> , 2018, 175, 212-223.e17.	13.5	195
23	Cryo-EM structures and atomic model of the HIV-1 strand transfer complex intasome. <i>Science</i> , 2017, 355, 89-92.	6.0	166
24	Open and closed structures reveal allostery and pliability in the HIV-1 envelope spike. <i>Nature</i> , 2017, 547, 360-363.	13.7	217
25	Addressing preferred specimen orientation in single-particle cryo-EM through tilting. <i>Nature Methods</i> , 2017, 14, 793-796.	9.0	708
26	Modular Assembly of the Bacterial Large Ribosomal Subunit. <i>Cell</i> , 2016, 167, 1610-1622.e15.	13.5	163
27	Structural Basis for the Activation of IKK1/β. <i>Cell Reports</i> , 2016, 17, 1907-1914.	2.9	47
28	Cryo-EM reveals a novel octameric integrase structure for betaretroviral intasome function. <i>Nature</i> , 2016, 530, 358-361.	13.7	88
29	Large-Scale 3D Heterogeneity Analysis of CryoEM Data Using Likelihood-Based Classification in FREALIGN. <i>Microscopy and Microanalysis</i> , 2015, 21, 1201-1202.	0.2	0
30	Model Building and Refinement of a Natively Glycosylated HIV-1 Env Protein by High-Resolution Cryoelectron Microscopy. <i>Structure</i> , 2015, 23, 1943-1951.	1.6	93
31	Single-particle cryoEM analysis at near-atomic resolution from several thousand asymmetric subunits. <i>Journal of Structural Biology</i> , 2015, 192, 235-244.	1.3	9
32	Structural basis for translational surveillance by the large ribosomal subunit-associated protein quality control complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 15981-15986.	3.3	111
33	A combined quantitative mass spectrometry and electron microscopy analysis of ribosomal 30S subunit assembly in <i>E. coli</i> . <i>ELife</i> , 2014, 3, .	2.8	65
34	Optimod – An automated approach for constructing and optimizing initial models for single-particle electron microscopy. <i>Journal of Structural Biology</i> , 2013, 184, 417-426.	1.3	22
35	Crystal Structure of a Soluble Cleaved HIV-1 Envelope Trimer. <i>Science</i> , 2013, 342, 1477-1483.	6.0	793
36	Cryo-EM Structure of a Fully Glycosylated Soluble Cleaved HIV-1 Envelope Trimer. <i>Science</i> , 2013, 342, 1484-1490.	6.0	662

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37	Allosteric Regulation of DNA Cleavage and Sequence-Specificity through Run-On Oligomerization. <i>Structure</i> , 2013, 21, 1848-1858.	1.6	23
38	Likelihood-based classification of cryo-EM images using FREALIGN. <i>Journal of Structural Biology</i> , 2013, 183, 377-388.	1.3	241
39	Single-particle EM reveals extensive conformational variability of the Ltn1 E3 ligase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 1702-1707.	3.3	38
40	Movies of Ice-Embedded Particles Enhance Resolution in Electron Cryo-Microscopy. <i>Structure</i> , 2012, 20, 1823-1828.	1.6	277
41	Automation in Single-Particle Electron Microscopy. <i>Methods in Enzymology</i> , 2010, 483, 291-338.	0.4	22
42	A Toolbox for ab initio 3-D reconstructions in single-particle electron microscopy. <i>Journal of Structural Biology</i> , 2010, 169, 389-398.	1.3	46
43	Appion: An integrated, database-driven pipeline to facilitate EM image processing. <i>Journal of Structural Biology</i> , 2009, 166, 95-102.	1.3	848