

# Gabriel C Lander

## List of Publications by Year in descending order

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89  
papers

9,742  
citations

61984  
43  
h-index

51608  
86  
g-index

122  
all docs

122  
docs citations

122  
times ranked

12628  
citing authors

#	ARTICLE	IF	CITATIONS
1	Appion: An integrated, database-driven pipeline to facilitate EM image processing. Journal of Structural Biology, 2009, 166, 95-102.	2.8	848
2	The Arabidopsis Information Resource (TAIR): a model organism database providing a centralized, curated gateway to Arabidopsis biology, research materials and community. Nucleic Acids Research, 2003, 31, 224-228.	14.5	761
3	High-Resolution Microtubule Structures Reveal the Structural Transitions in $\alpha$ -Tubulin upon GTP Hydrolysis. Cell, 2014, 157, 1117-1129.	28.9	582
4	Complete subunit architecture of the proteasome regulatory particle. Nature, 2012, 482, 186-191.	27.8	542
5	A novel cereblon modulator recruits GSPT1 to the CRL4CRBN ubiquitin ligase. Nature, 2016, 535, 252-257.	27.8	414
6	Functional Annotation of the Arabidopsis Genome Using Controlled Vocabularies. Plant Physiology, 2004, 135, 745-755.	4.8	410
7	Structures of the RNA-guided surveillance complex from a bacterial immune system. Nature, 2011, 477, 486-489.	27.8	355
8	The Structure of an Infectious P22 Virion Shows the Signal for Headful DNA Packaging. Science, 2006, 312, 1791-1795.	12.6	276
9	Cryo-electron microscopy structure of the TRPV2 ion channel. Nature Structural and Molecular Biology, 2016, 23, 180-186.	8.2	251
10	Structure of the cold- and menthol-sensing ion channel TRPM8. Science, 2018, 359, 237-241.	12.6	234
11	Conformational switching of the 26S proteasome enables substrate degradation. Nature Structural and Molecular Biology, 2013, 20, 781-788.	8.2	227
12	Substrate-engaged 26S proteasome structures reveal mechanisms for ATP-hydrolysis-driven translocation. Science, 2018, 362, .	12.6	226
13	Molecular architecture of human polycomb repressive complex 2. ELife, 2012, 1, e00005.	6.0	218
14	Structure Reveals Mechanisms of Viral Suppressors that Intercept a CRISPR RNA-Guided Surveillance Complex. Cell, 2017, 169, 47-57.e11.	28.9	191
15	Structure of the mitochondrial inner membrane AAA+ protease YME1 gives insight into substrate processing. Science, 2017, 358, .	12.6	179
16	The molecular principles governing the activity and functional diversity of AAA+ proteins. Nature Reviews Molecular Cell Biology, 2020, 21, 43-58.	37.0	173
17	High-resolution structure determination of sub-100 kDa complexes using conventional cryo-EM. Nature Communications, 2019, 10, 1032.	12.8	170
18	Unnatural Amino Acid Incorporation into Virus-Like Particles. Bioconjugate Chemistry, 2008, 19, 866-875.	3.6	164

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19	Insights into autophagosome biogenesis from structural and biochemical analyses of the ATG2A-WIP1 complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E9792-E9801.	7.1	159
20	Structural organization of the dynein–dynactin complex bound to microtubules. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 345-347.	8.2	158
21	Bacteriophage Lambda Stabilization by Auxiliary Protein gpD: Timing, Location, and Mechanism of Attachment Determined by Cryo-EM. <i>Structure</i> , 2008, 16, 1399-1406.	3.3	150
22	Achieving better-than-3-Å... resolution by single-particle cryo-EM at 200 keV. <i>Nature Methods</i> , 2017, 14, 1075-1078.	19.0	136
23	Cryo-electron tomography reveals that dynactin recruits a team of dyneins for processive motility. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 203-207.	8.2	122
24	Ubp6 deubiquitinase controls conformational dynamics and substrate degradation of the 26S proteasome. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 712-719.	8.2	116
25	Cryo-EM structure of a mitochondrial calcium uniporter. <i>Science</i> , 2018, 361, 506-511.	12.6	116
26	Cryo-electron microscopy structure of the lysosomal calcium-permeable channel TRPML3. <i>Nature</i> , 2017, 550, 411-414.	27.8	104
27	Peering Down the Barrel of a Bacteriophage Portal: The Genome Packaging and Release Valve in P22. <i>Structure</i> , 2011, 19, 496-502.	3.3	101
28	Conformational ensemble of the human TRPV3 ion channel. <i>Nature Communications</i> , 2018, 9, 4773.	12.8	100
29	Atomic structure of the 26S proteasome lid reveals the mechanism of deubiquitinase inhibition. <i>ELife</i> , 2016, 5, e13027.	6.0	88
30	Automated cryoEM data acquisition and analysis of 284742 particles of GroEL. <i>Journal of Structural Biology</i> , 2006, 155, 470-481.	2.8	84
31	Multivalent Microtubule Recognition by Tubulin Tyrosine Ligase-like Family Glutamylases. <i>Cell</i> , 2015, 161, 1112-1123.	28.9	83
32	Structure Reveals a Mechanism of CRISPR-RNA-Guided Nuclease Recruitment and Anti-CRISPR Viral Mimicry. <i>Molecular Cell</i> , 2019, 74, 132-142.e5.	9.7	79
33	Cas1 and the Csy complex are opposing regulators of Cas2/3 nuclease activity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E5113-E5121.	7.1	74
34	The P22 Tail Machine at Subnanometer Resolution Reveals the Architecture of an Infection Conduit. <i>Structure</i> , 2009, 17, 789-799.	3.3	63
35	Small Terminase Couples Viral DNA Binding to Genome-Packaging ATPase Activity. <i>Structure</i> , 2012, 20, 1403-1413.	3.3	60
36	Capsid Conformational Sampling in HK97 Maturation Visualized by X-Ray Crystallography and Cryo-EM. <i>Structure</i> , 2006, 14, 1655-1665.	3.3	58

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37	Unique Structural Features of the Mitochondrial AAA+ Protease AFG3L2 Reveal the Molecular Basis for Activity in Health and Disease. <i>Molecular Cell</i> , 2019, 75, 1073-1085.e6.	9.7	58
38	Structural basis for piRNA targeting. <i>Nature</i> , 2021, 597, 285-289.	27.8	57
39	A Multi-model Approach to Assessing Local and Global Cryo-EM Map Quality. <i>Structure</i> , 2019, 27, 344-358.e3.	3.3	55
40	Structural basis for distinct operational modes and protease activation in AAA+ protease Lon. <i>Science Advances</i> , 2020, 6, eaba8404.	10.3	55
41	Molecular Architecture and Connectivity of the Budding Yeast Mtw1 Kinetochore Complex. <i>Journal of Molecular Biology</i> , 2011, 405, 548-559.	4.2	53
42	Characterization of virus-like particles in GARDASIL® by cryo transmission electron microscopy. <i>Human Vaccines and Immunotherapeutics</i> , 2014, 10, 734-739.	3.3	53
43	The Pex1/Pex6 Complex Is a Heterohexameric AAA + Motor with Alternating and Highly Coordinated Subunits. <i>Journal of Molecular Biology</i> , 2015, 427, 1375-1388.	4.2	53
44	An allosteric network in spastin couples multiple activities required for microtubule severing. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 671-678.	8.2	51
45	The peroxisomal AAA-ATPase Pex1/Pex6 unfolds substrates by processive threading. <i>Nature Communications</i> , 2018, 9, 135.	12.8	50
46	Dynamics at the serine loop underlie differential affinity of cryptochromes for CLOCK:BMAL1 to control circadian timing. <i>ELife</i> , 2020, 9, .	6.0	50
47	Solid-to-fluid-like DNA transition in viruses facilitates infection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 14675-14680.	7.1	48
48	Assembly Architecture and DNA Binding of the Bacteriophage P22 Terminase Small Subunit. <i>Journal of Molecular Biology</i> , 2008, 383, 494-501.	4.2	46
49	A Toolbox for ab initio 3-D reconstructions in single-particle electron microscopy. <i>Journal of Structural Biology</i> , 2010, 169, 389-398.	2.8	46
50	Isolation of yeast complex IV in native lipid nanodiscs. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2016, 1858, 2984-2992.	2.6	45
51	Present and Emerging Methodologies in Cryo-EM Single-Particle Analysis. <i>Biophysical Journal</i> , 2020, 119, 1281-1289.	0.5	43
52	Sub-2 Angstrom resolution structure determination using single-particle cryo-EM at 200 keV. <i>Journal of Structural Biology: X</i> , 2020, 4, 100020.	1.3	43
53	Exploring icosahedral virus structures with VIPER. <i>Nature Reviews Microbiology</i> , 2005, 3, 809-817.	28.6	42
54	Genomic and functional analysis of <i>Vibrio</i> phage SIO-2 reveals novel insights into ecology and evolution of marine siphoviruses. <i>Environmental Microbiology</i> , 2012, 14, 2071-2086.	3.8	42

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55	Development of Bacteriophage P22 as a Platform for Molecular Display: Genetic and Chemical Modifications of the Procapsid Exterior Surface. <i>ChemBioChem</i> , 2008, 9, 514-518.	2.6	41
56	Current outcomes when optimizing “standard” sample preparation for single-particle cryo-EM. <i>Journal of Microscopy</i> , 2019, 276, 39-45.	1.8	41
57	How low can we go? Structure determination of small biological complexes using single-particle cryo-EM. <i>Current Opinion in Structural Biology</i> , 2020, 64, 9-16.	5.7	40
58	Structures of the human LONP1 protease reveal regulatory steps involved in protease activation. <i>Nature Communications</i> , 2021, 12, 3239.	12.8	40
59	The endoplasmic reticulum <scp>HSP</scp>40 co-chaperone <scp>ER</scp>dj3/<scp>DNAJB</scp>11 assembles and functions as a tetramer. <i>EMBO Journal</i> , 2017, 36, 2296-2309.	7.8	38
60	Go hybrid: EM, crystallography, and beyond. <i>Current Opinion in Structural Biology</i> , 2012, 22, 627-635.	5.7	37
61	Visualizing structural transitions of ligand-dependent gating of the TRPM2 channel. <i>Nature Communications</i> , 2019, 10, 3740.	12.8	34
62	A test-bed for optimizing high-resolution single particle reconstructions. <i>Journal of Structural Biology</i> , 2008, 163, 29-39.	2.8	33
63	The proteasome under the microscope: the regulatory particle in focus. <i>Current Opinion in Structural Biology</i> , 2013, 23, 243-251.	5.7	33
64	Architecture of the Complex Formed by Large and Small Terminase Subunits from Bacteriophage P22. <i>Journal of Molecular Biology</i> , 2015, 427, 3285-3299.	4.2	30
65	AcrIF9 tethers non-sequence specific dsDNA to the CRISPR RNA-guided surveillance complex. <i>Nature Communications</i> , 2020, 11, 2730.	12.8	27
66	Specific lid-base contacts in the 26s proteasome control the conformational switching required for substrate degradation. <i>ELife</i> , 2019, 8, .	6.0	27
67	Capsomer Dynamics and Stabilization in the T=12 Marine Bacteriophage SIO-2 and Its Procapsid Studied by CryoEM. <i>Structure</i> , 2012, 20, 498-503.	3.3	26
68	Drosophila A virus is an unusual RNA virus with a T=3 icosahedral core and permuted RNA-dependent RNA polymerase. <i>Journal of General Virology</i> , 2009, 90, 2191-2200.	2.9	25
69	DNA bending-induced phase transition of encapsidated genome in phage $\phi$ . <i>Nucleic Acids Research</i> , 2013, 41, 4518-4524.	14.5	25
70	Polyvalent Display of Heme on Hepatitis B Virus Capsid Protein through Coordination to Hexahistidine Tags. <i>Chemistry and Biology</i> , 2008, 15, 513-519.	6.0	24
71	Characterization of Large Conformational Changes and Autoproteolysis in the Maturation of a T=4 Virus Capsid. <i>Journal of Virology</i> , 2009, 83, 1126-1134.	3.4	19
72	Subunits fold at position-dependent rates during maturation of a eukaryotic RNA virus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 14111-14115.	7.1	19

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73	The Rod-Shaped ATG2A-WIPI4 Complex Tethers Membranes In Vitro. Contact (Thousand Oaks (Ventura) Tj ETQq1 1 0.784314rgBT /Ov	1.3	18
74	Protein domain mapping by internal labeling and single particle electron microscopy. Journal of Structural Biology, 2015, 192, 159-162.	2.8	16
75	Ab initio maximum likelihood reconstruction from cryo electron microscopy images of an infectious virion of the tailed bacteriophage P22 and maximum likelihood versions of Fourier Shell Correlation appropriate for measuring resolution of spherical or cylindrical objects. Journal of Structural Biology, 2009, 167, 185-199.	2.8	15
76	Exploring applications of crowdsourcing to cryo-EM. Journal of Structural Biology, 2018, 203, 37-45.	2.8	14
77	Thermodynamic Interrogation of the Assembly of a Viral Genome Packaging Motor Complex. Biophysical Journal, 2015, 109, 1663-1675.	0.5	13
78	Setting the dynein motor in motion: New insights from electron tomography. Journal of Biological Chemistry, 2019, 294, 13202-13217.	3.4	12
79	The YÎ motif defines the structure-activity relationships of human 20S proteasome activators. Nature Communications, 2022, 13, 1226.	12.8	10
80	An automated procedure for detecting protein folds from sub-nanometer resolution electron density. Journal of Structural Biology, 2010, 170, 513-521.	2.8	8
81	Setting up the Talos Arctica electron microscope and Gatan K2 direct detector for high-resolution cryogenic single-particle data acquisition. Protocol Exchange, 0, , .	0.3	7
82	Cryo-EM structure of hexameric yeast Lon protease (PIM1) highlights the importance of conserved structural elements. Journal of Biological Chemistry, 2022, 298, 101694.	3.4	6
83	A guided approach for subtomogram averaging of challenging macromolecular assemblies. Journal of Structural Biology: X, 2020, 4, 100041.	1.3	5
84	Site-specific labeling of proteins for electron microscopy. Journal of Structural Biology, 2015, 192, 151-158.	2.8	4
85	Conquer by cryo-EM without physically dividing. Biochemical Society Transactions, 2021, 49, 2287-2298.	3.4	4
86	A case for glycerol as an acceptable additive for single-particle cryoEM samples. Acta Crystallographica Section D: Structural Biology, 2022, 78, 124-135.	2.3	3
87	Allosteric differences dictate GroEL complementation of Â <i>E.Âcoli</i>. FASEB Journal, 2022, 36, e22198.	0.5	1
88	The Injectosome of Bacteriophage P22. Microscopy and Microanalysis, 2006, 12, 394-395.	0.4	0
89	Obtaining 3 Å... Resolution Structures of Biomedical Targets at 200 keV. Microscopy and Microanalysis, 2017, 23, 1198-1199.	0.4	0