

Gabriel C Lander

List of Publications by Year in descending order

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Version: 2024-02-01

89
papers

9,742
citations

61857

43
h-index

51492

86
g-index

122
all docs

122
docs citations

122
times ranked

12628
citing authors

#	ARTICLE	IF	CITATIONS
1	A case for glycerol as an acceptable additive for single-particle cryoEM samples. <i>Acta Crystallographica Section D: Structural Biology</i> , 2022, 78, 124-135.	1.1	3
2	Cryo-EM structure of hexameric yeast Lon protease (PIM1) highlights the importance of conserved structural elements. <i>Journal of Biological Chemistry</i> , 2022, 298, 101694.	1.6	6
3	Allosteric differences dictate GroEL complementation of <i>E. coli</i> . <i>FASEB Journal</i> , 2022, 36, e22198.	0.2	1
4	The Y1 motif defines the structure-activity relationships of human 20S proteasome activators. <i>Nature Communications</i> , 2022, 13, 1226.	5.8	10
5	Structures of the human LONP1 protease reveal regulatory steps involved in protease activation. <i>Nature Communications</i> , 2021, 12, 3239.	5.8	40
6	Structural basis for piRNA targeting. <i>Nature</i> , 2021, 597, 285-289.	13.7	57
7	Conquer by cryo-EM without physically dividing. <i>Biochemical Society Transactions</i> , 2021, 49, 2287-2298.	1.6	4
8	The molecular principles governing the activity and functional diversity of AAA+ proteins. <i>Nature Reviews Molecular Cell Biology</i> , 2020, 21, 43-58.	16.1	173
9	Present and Emerging Methodologies in Cryo-EM Single-Particle Analysis. <i>Biophysical Journal</i> , 2020, 119, 1281-1289.	0.2	43
10	A guided approach for subtomogram averaging of challenging macromolecular assemblies. <i>Journal of Structural Biology: X</i> , 2020, 4, 100041.	0.7	5
11	AcrIF9 tethers non-sequence specific dsDNA to the CRISPR RNA-guided surveillance complex. <i>Nature Communications</i> , 2020, 11, 2730.	5.8	27
12	Structural basis for distinct operational modes and protease activation in AAA+ protease Lon. <i>Science Advances</i> , 2020, 6, eaba8404.	4.7	55
13	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.	2.6	40
14	Sub-2 Angstrom resolution structure determination using single-particle cryo-EM at 200 keV. <i>Journal of Structural Biology: X</i> , 2020, 4, 100020.	0.7	43
15	Dynamics at the serine loop underlie differential affinity of cryptochromes for CLOCK:BMAL1 to control circadian timing. <i>ELife</i> , 2020, 9, .	2.8	50
16	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.	4.5	58
17	An allosteric network in spastin couples multiple activities required for microtubule severing. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 671-678.	3.6	51
18	Setting the dynein motor in motion: New insights from electron tomography. <i>Journal of Biological Chemistry</i> , 2019, 294, 13202-13217.	1.6	12

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19	Current outcomes when optimizing “standard” sample preparation for single-particle cryo-EM. <i>Journal of Microscopy</i> , 2019, 276, 39-45.	0.8	41
20	Visualizing structural transitions of ligand-dependent gating of the TRPM2 channel. <i>Nature Communications</i> , 2019, 10, 3740.	5.8	34
21	High-resolution structure determination of sub-100 kDa complexes using conventional cryo-EM. <i>Nature Communications</i> , 2019, 10, 1032.	5.8	170
22	Structure Reveals a Mechanism of CRISPR-RNA-Guided Nuclease Recruitment and Anti-CRISPR Viral Mimicry. <i>Molecular Cell</i> , 2019, 74, 132-142.e5.	4.5	79
23	A Multi-model Approach to Assessing Local and Global Cryo-EM Map Quality. <i>Structure</i> , 2019, 27, 344-358.e3.	1.6	55
24	Specific lid-base contacts in the 26s proteasome control the conformational switching required for substrate degradation. <i>ELife</i> , 2019, 8, .	2.8	27
25	Exploring applications of crowdsourcing to cryo-EM. <i>Journal of Structural Biology</i> , 2018, 203, 37-45.	1.3	14
26	The peroxisomal AAA-ATPase Pex1/Pex6 unfolds substrates by processive threading. <i>Nature Communications</i> , 2018, 9, 135.	5.8	50
27	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.	3.6	122
28	Structure of the cold- and menthol-sensing ion channel TRPM8. <i>Science</i> , 2018, 359, 237-241.	6.0	234
29	Conformational ensemble of the human TRPV3 ion channel. <i>Nature Communications</i> , 2018, 9, 4773.	5.8	100
30	The Rod-Shaped ATG2A-WIPI4 Complex Tethers Membranes In Vitro. <i>Contact (Thousand Oaks (Ventura) Tj ETQq0 0.0 rgBT /Qverlock 10</i>	0.4	18
31	Substrate-engaged 26 S proteasome structures reveal mechanisms for ATP-hydrolysis-driven translocation. <i>Science</i> , 2018, 362, .	6.0	226
32	Insights into autophagosome biogenesis from structural and biochemical analyses of the ATG2A-WIPI4 complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E9792-E9801.	3.3	159
33	Cryo-EM structure of a mitochondrial calcium uniporter. <i>Science</i> , 2018, 361, 506-511.	6.0	116
34	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.	3.3	74
35	Structure Reveals Mechanisms of Viral Suppressors that Intercept a CRISPR RNA-Guided Surveillance Complex. <i>Cell</i> , 2017, 169, 47-57.e11.	13.5	191
36	Structure of the mitochondrial inner membrane AAA+ protease YME1 gives insight into substrate processing. <i>Science</i> , 2017, 358, .	6.0	179

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37	Achieving better-than-3-Å... resolution by single-particle cryo-EM at 200 keV. <i>Nature Methods</i> , 2017, 14, 1075-1078.	9.0	136
38	Cryo-electron microscopy structure of the lysosomal calcium-permeable channel TRPML3. <i>Nature</i> , 2017, 550, 411-414.	13.7	104
39	The endoplasmic reticulum <sc>HSP</sc>40 co-chaperone <sc>ER</sc>dj3/<sc>DNAJB</sc>11 assembles and functions as a tetramer. <i>EMBO Journal</i> , 2017, 36, 2296-2309.	3.5	38
40	Obtaining 3 Å... Resolution Structures of Biomedical Targets at 200 keV. <i>Microscopy and Microanalysis</i> , 2017, 23, 1198-1199.	0.2	0
41	Isolation of yeast complex IV in native lipid nanodiscs. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2016, 1858, 2984-2992.	1.4	45
42	A novel cereblon modulator recruits GSPT1 to the CRL4CRBN ubiquitin ligase. <i>Nature</i> , 2016, 535, 252-257.	13.7	414
43	Cryo-electron microscopy structure of the TRPV2 ion channel. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 180-186.	3.6	251
44	Atomic structure of the 26S proteasome lid reveals the mechanism of deubiquitinase inhibition. <i>ELife</i> , 2016, 5, e13027.	2.8	88
45	Protein domain mapping by internal labeling and single particle electron microscopy. <i>Journal of Structural Biology</i> , 2015, 192, 159-162.	1.3	16
46	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.	2.0	53
47	Structural organization of the dynein-dynactin complex bound to microtubules. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 345-347.	3.6	158
48	Multivalent Microtubule Recognition by Tubulin Tyrosine Ligase-like Family Glutamylases. <i>Cell</i> , 2015, 161, 1112-1123.	13.5	83
49	Thermodynamic Interrogation of the Assembly of a Viral Genome Packaging Motor Complex. <i>Biophysical Journal</i> , 2015, 109, 1663-1675.	0.2	13
50	Ubp6 deubiquitinase controls conformational dynamics and substrate degradation of the 26S proteasome. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 712-719.	3.6	116
51	Architecture of the Complex Formed by Large and Small Terminase Subunits from Bacteriophage P22. <i>Journal of Molecular Biology</i> , 2015, 427, 3285-3299.	2.0	30
52	Site-specific labeling of proteins for electron microscopy. <i>Journal of Structural Biology</i> , 2015, 192, 151-158.	1.3	4
53	Characterization of virus-like particles in GARDASIL® by cryo transmission electron microscopy. <i>Human Vaccines and Immunotherapeutics</i> , 2014, 10, 734-739.	1.4	53
54	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.	3.3	48

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55	High-Resolution Microtubule Structures Reveal the Structural Transitions in β -Tubulin upon GTP Hydrolysis. <i>Cell</i> , 2014, 157, 1117-1129.	13.5	582
56	The proteasome under the microscope: the regulatory particle in focus. <i>Current Opinion in Structural Biology</i> , 2013, 23, 243-251.	2.6	33
57	Conformational switching of the 26S proteasome enables substrate degradation. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 781-788.	3.6	227
58	DNA bending-induced phase transition of encapsidated genome in phage λ . <i>Nucleic Acids Research</i> , 2013, 41, 4518-4524.	6.5	25
59	Complete subunit architecture of the proteasome regulatory particle. <i>Nature</i> , 2012, 482, 186-191.	13.7	542
60	Small Terminase Couples Viral DNA Binding to Genome-Packaging ATPase Activity. <i>Structure</i> , 2012, 20, 1403-1413.	1.6	60
61	Go hybrid: EM, crystallography, and beyond. <i>Current Opinion in Structural Biology</i> , 2012, 22, 627-635.	2.6	37
62	Molecular architecture of human polycomb repressive complex 2. <i>ELife</i> , 2012, 1, e00005.	2.8	218
63	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.	1.6	26
64	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.	1.8	42
65	Structures of the RNA-guided surveillance complex from a bacterial immune system. <i>Nature</i> , 2011, 477, 486-489.	13.7	355
66	Molecular Architecture and Connectivity of the Budding Yeast Mtw1 Kinetochore Complex. <i>Journal of Molecular Biology</i> , 2011, 405, 548-559.	2.0	53
67	Peering Down the Barrel of a Bacteriophage Portal: The Genome Packaging and Release Valve in P22. <i>Structure</i> , 2011, 19, 496-502.	1.6	101
68	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.	3.3	19
69	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
70	An automated procedure for detecting protein folds from sub-nanometer resolution electron density. <i>Journal of Structural Biology</i> , 2010, 170, 513-521.	1.3	8
71	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.	1.3	25
72	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.	1.5	19

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73	The P22 Tail Machine at Subnanometer Resolution Reveals the Architecture of an Infection Conduit. <i>Structure</i> , 2009, 17, 789-799.	1.6	63
74	Appion: An integrated, database-driven pipeline to facilitate EM image processing. <i>Journal of Structural Biology</i> , 2009, 166, 95-102.	1.3	848
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. <i>Journal of Structural Biology</i> , 2009, 167, 185-199.	1.3	15
76	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.	1.3	41
77	Polyvalent Display of Heme on Hepatitis B Virus Capsid Protein through Coordination to Hexahistidine Tags. <i>Chemistry and Biology</i> , 2008, 15, 513-519.	6.2	24
78	Unnatural Amino Acid Incorporation into Virus-Like Particles. <i>Bioconjugate Chemistry</i> , 2008, 19, 866-875.	1.8	164
79	Bacteriophage Lambda Stabilization by Auxiliary Protein gpD: Timing, Location, and Mechanism of Attachment Determined by Cryo-EM. <i>Structure</i> , 2008, 16, 1399-1406.	1.6	150
80	A test-bed for optimizing high-resolution single particle reconstructions. <i>Journal of Structural Biology</i> , 2008, 163, 29-39.	1.3	33
81	Assembly Architecture and DNA Binding of the Bacteriophage P22 Terminase Small Subunit. <i>Journal of Molecular Biology</i> , 2008, 383, 494-501.	2.0	46
82	Automated cryoEM data acquisition and analysis of 284742 particles of GroEL. <i>Journal of Structural Biology</i> , 2006, 155, 470-481.	1.3	84
83	The Injectosome of Bacteriophage P22. <i>Microscopy and Microanalysis</i> , 2006, 12, 394-395.	0.2	0
84	Capsid Conformational Sampling in HK97 Maturation Visualized by X-Ray Crystallography and Cryo-EM. <i>Structure</i> , 2006, 14, 1655-1665.	1.6	58
85	The Structure of an Infectious P22 Virion Shows the Signal for Headful DNA Packaging. <i>Science</i> , 2006, 312, 1791-1795.	6.0	276
86	Exploring icosahedral virus structures with VIPER. <i>Nature Reviews Microbiology</i> , 2005, 3, 809-817.	13.6	42
87	Functional Annotation of the Arabidopsis Genome Using Controlled Vocabularies. <i>Plant Physiology</i> , 2004, 135, 745-755.	2.3	410
88	The Arabidopsis Information Resource (TAIR): a model organism database providing a centralized, curated gateway to Arabidopsis biology, research materials and community. <i>Nucleic Acids Research</i> , 2003, 31, 224-228.	6.5	761
89	Setting up the Talos Arctica electron microscope and Gatan K2 direct detector for high-resolution cryogenic single-particle data acquisition. <i>Protocol Exchange</i> , 0, , .	0.3	7