

Nikolaus Grigorieff

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3116908/publications.pdf>

Version: 2024-02-01

116
papers

21,893
citations

18887

64
h-index

22488

117
g-index

158
all docs

158
docs citations

158
times ranked

24109
citing authors

#	ARTICLE	IF	CITATIONS
1	Locating macromolecular assemblies in cells by 2D template matching with cisTEM. <i>ELife</i> , 2021, 10, .	2.8	55
2	Cryo-TEM simulations of amorphous radiation-sensitive samples using multislice wave propagation. <i>IUCr</i> , 2021, 8, 943-953.	1.0	22
3	Structure of the Vesicular Stomatitis Virus L Protein in Complex with Its Phosphoprotein Cofactor. <i>Cell Reports</i> , 2020, 30, 53-60.e5.	2.9	51
4	In situ structure determination at nanometer resolution using TYGRESS. <i>Nature Methods</i> , 2020, 17, 201-208.	9.0	59
5	Structure and assembly of calcium homeostasis modulator proteins. <i>Nature Structural and Molecular Biology</i> , 2020, 27, 150-159.	3.6	55
6	Location and Identification of Macromolecular Complexes within Cellular Environments by High-Resolution Template Matching. <i>Biophysical Journal</i> , 2020, 118, 3a.	0.2	0
7	mRNA stem-loops can pause the ribosome by hindering A-site tRNA binding. <i>ELife</i> , 2020, 9, .	2.8	40
8	In situ Structure of Rotavirus VP1 RNA-Dependent RNA Polymerase. <i>Journal of Molecular Biology</i> , 2019, 431, 3124-3138.	2.0	45
9	High-resolution cryo-EM structures of outbreak strain human norovirus shells reveal size variations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 12828-12832.	3.3	53
10	Cryo-EM fibril structures from systemic AA amyloidosis reveal the species complementarity of pathological amyloids. <i>Nature Communications</i> , 2019, 10, 1104.	5.8	113
11	New Developments in the cisTEM Software Package. <i>Biophysical Journal</i> , 2019, 116, 11a.	0.2	0
12	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
13	Structural Mechanism of Functional Modulation by Gene Splicing in NMDA Receptors. <i>Neuron</i> , 2018, 98, 521-529.e3.	3.8	57
14	Physical basis of amyloid fibril polymorphism. <i>Nature Communications</i> , 2018, 9, 699.	5.8	133
15	cisTEM, user-friendly software for single-particle image processing. <i>ELife</i> , 2018, 7, .	2.8	792
16	Atomic Resolution Cryo-EM Structure of β -Galactosidase. <i>Structure</i> , 2018, 26, 848-856.e3.	1.6	115
17	Severing enzymes amplify microtubule arrays through lattice GTP-tubulin incorporation. <i>Science</i> , 2018, 361, .	6.0	180
18	Conformational States of a Soluble, Uncleaved HIV-1 Envelope Trimer. <i>Journal of Virology</i> , 2017, 91, .	1.5	19

#	ARTICLE	IF	CITATIONS
19	CryoEM Structure of an Influenza Virus Receptor-Binding Site Antibody Antigen Interface. <i>Journal of Molecular Biology</i> , 2017, 429, 1829-1839.	2.0	21
20	Ensemble cryo-EM elucidates the mechanism of translation fidelity. <i>Nature</i> , 2017, 546, 113-117.	13.7	151
21	Structure of RNA polymerase bound to ribosomal 30S subunit. <i>ELife</i> , 2017, 6, .	2.8	87
22	Expression, purification, and contaminant detection for structural studies of <i>Ralstonia metallidurance</i> CIC protein rm1. <i>PLoS ONE</i> , 2017, 12, e0180163.	1.1	4
23	Mechanism of ribosome rescue by ArfA and RF2. <i>ELife</i> , 2017, 6, .	2.8	50
24	Single-protein detection in crowded molecular environments in cryo-EM images. <i>ELife</i> , 2017, 6, .	2.8	65
25	Ribosome RelA structures reveal the mechanism of stringent response activation. <i>ELife</i> , 2016, 5, .	2.8	143
26	Cryo-EM reveals the steric zipper structure of a light chain-derived amyloid fibril. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 6200-6205.	3.3	61
27	Activation of NMDA receptors and the mechanism of inhibition by ifenprodil. <i>Nature</i> , 2016, 534, 63-68.	13.7	173
28	Frealign. <i>Methods in Enzymology</i> , 2016, 579, 191-226.	0.4	169
29	Structure of a Holliday junction complex reveals mechanisms governing a highly regulated DNA transaction. <i>ELife</i> , 2016, 5, .	2.8	21
30	Ensemble cryo-EM uncovers inchworm-like translocation of a viral IRES through the ribosome. <i>ELife</i> , 2016, 5, .	2.8	116
31	Structure of the transporter associated with antigen processing trapped by herpes simplex virus. <i>ELife</i> , 2016, 5, .	2.8	78
32	Evaluation of super-resolution performance of the K2 electron-counting camera using 2D crystals of aquaporin-0. <i>Journal of Structural Biology</i> , 2015, 192, 163-173.	1.3	26
33	Structure and conformational states of the bovine mitochondrial ATP synthase by cryo-EM. <i>ELife</i> , 2015, 4, e10180.	2.8	264
34	Measuring the optimal exposure for single particle cryo-EM using a 2.6 Å reconstruction of rotavirus VP6. <i>ELife</i> , 2015, 4, e06980.	2.8	748
35	Structure of the L Protein of Vesicular Stomatitis Virus from Electron Cryomicroscopy. <i>Cell</i> , 2015, 162, 314-327.	13.5	211
36	A Primer to Single-Particle Cryo-Electron Microscopy. <i>Cell</i> , 2015, 161, 438-449.	13.5	478

#	ARTICLE	IF	CITATIONS
37	Peptide dimer structure in an A ² (1 ⁴²) fibril visualized with cryo-EM. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 11858-11863.	3.3	196
38	Automatic estimation and correction of anisotropic magnification distortion in electron microscopes. Journal of Structural Biology, 2015, 192, 204-208.	1.3	124
39	CTFFIND4: Fast and accurate defocus estimation from electron micrographs. Journal of Structural Biology, 2015, 192, 216-221.	1.3	3,894
40	Taura syndrome virus IRES initiates translation by binding its tRNA-mRNA ^{â€} like structural element in the ribosomal decoding center. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 9139-9144.	3.3	59
41	Structures of Yeast 80S Ribosome-tRNA Complexes in the Rotated and Nonrotated Conformations. Structure, 2014, 22, 1210-1218.	1.6	88
42	Molecular Basis for Age-Dependent Microtubule Acetylation by Tubulin Acetyltransferase. Cell, 2014, 157, 1405-1415.	13.5	181
43	Frealix: Model-based refinement of helical filament structures from electron micrographs. Journal of Structural Biology, 2014, 186, 234-244.	1.3	26
44	Structure of the ribosome with elongation factor G trapped in the pretranslocation state. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 20994-20999.	3.3	125
45	Location of the dsRNA-Dependent Polymerase, VP1, in Rotavirus Particles. Journal of Molecular Biology, 2013, 425, 124-132.	2.0	69
46	Likelihood-based classification of cryo-EM images using FREALIGN. Journal of Structural Biology, 2013, 183, 377-388.	1.3	241
47	Quantitative characterization of electron detectors for transmission electron microscopy. Journal of Structural Biology, 2013, 184, 385-393.	1.3	183
48	Direct detection pays off for electron cryo-microscopy. ELife, 2013, 2, e00573.	2.8	53
49	Insights into splicing: structure of the yeast U1 snRNP. FASEB Journal, 2013, 27, 988.5.	0.2	0
50	Nucleotide excision repair (NER) machinery recruitment by the transcription-repair coupling factor involves unmasking of a conserved intramolecular interface. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 3353-3358.	3.3	42
51	Optimal noise reduction in 3D reconstructions of single particles using a volume-normalized filter. Journal of Structural Biology, 2012, 180, 26-38.	1.3	33
52	Maturation in Action: CryoEM Study of a Viral Capsid Caught during Expansion. Structure, 2012, 20, 1384-1390.	1.6	20
53	Beam-induced motion of vitrified specimen on holey carbon film. Journal of Structural Biology, 2012, 177, 630-637.	1.3	366
54	Movies of Ice-Embedded Particles Enhance Resolution in Electron Cryo-Microscopy. Structure, 2012, 20, 1823-1828.	1.6	277

#	ARTICLE	IF	CITATIONS
55	Interplay of DNA repair with transcription: from structures to mechanisms. Trends in Biochemical Sciences, 2012, 37, 543-552.	3.7	12
56	An adaptation of the Wiener filter suitable for analyzing images of isolated single particles. Journal of Structural Biology, 2011, 176, 60-74.	1.3	33
57	Tilt-Pair Analysis of Images from a Range of Different Specimens in Single-Particle Electron Cryomicroscopy. Journal of Molecular Biology, 2011, 413, 1028-1046.	2.0	138
58	Atomic model of an infectious rotavirus particle. EMBO Journal, 2011, 30, 408-416.	3.5	254
59	Recent progress in understanding Alzheimer's β -amyloid structures. Trends in Biochemical Sciences, 2011, 36, 338-345.	3.7	146
60	Near-atomic resolution reconstructions of icosahedral viruses from electron cryo-microscopy. Current Opinion in Structural Biology, 2011, 21, 265-273.	2.6	148
61	Structural Complexity of a Composite Amyloid Fibril. Journal of the American Chemical Society, 2011, 133, 14686-14698.	6.6	88
62	Nanoscale Flexibility Parameters of Alzheimer Amyloid Fibrils Determined by Electron Cryo-EM. Angewandte Chemie - International Edition, 2010, 49, 1321-1323.	7.2	65
63	Structure of clathrin coat with bound Hsc70 and auxilin: mechanism of Hsc70-facilitated disassembly. EMBO Journal, 2010, 29, 655-665.	3.5	114
64	The Ndc80 kinetochore complex forms oligomeric arrays along microtubules. Nature, 2010, 467, 805-810.	13.7	277
65	Adenomatous polyposis coli protein nucleates actin assembly and synergizes with the formin mDia1. Journal of Cell Biology, 2010, 189, 1087-1096.	2.3	154
66	GPU-enabled FREALIGN: Accelerating single particle 3D reconstruction and refinement in Fourier space on graphics processors. Journal of Structural Biology, 2010, 172, 407-412.	1.3	41
67	Subunit interactions in bovine papillomavirus. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 6298-6303.	3.3	134
68	Molecular interactions in rotavirus assembly and uncoating seen by high-resolution cryo-EM. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 10644-10648.	3.3	135
69	Actin filament labels for localizing protein components in large complexes viewed by electron microscopy. Rna, 2009, 15, 244-248.	1.6	13
70	Structural polymorphism of Alzheimer β and other amyloid fibrils. Prion, 2009, 3, 89-93.	0.9	234
71	β (1-40) Fibril Polymorphism Implies Diverse Interaction Patterns in Amyloid Fibrils. Journal of Molecular Biology, 2009, 386, 869-877.	2.0	280
72	Pentameric Assembly of Potassium Channel Tetramerization Domain-Containing Protein 5. Journal of Molecular Biology, 2009, 387, 175-191.	2.0	68

#	ARTICLE	IF	CITATIONS
73	Comparison of Alzheimer A β (1-40) and A β (1-42) amyloid fibrils reveals similar protofilament structures. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 19813-19818.	3.3	251
74	Increased sulfate uptake by E. coli overexpressing the SLC26-related SulP protein Rv1739c from Mycobacterium tuberculosis. Comparative Biochemistry and Physiology Part A, Molecular & Integrative Physiology, 2008, 149, 255-266.	0.8	40
75	A dose-rate effect in single-particle electron microscopy. Journal of Structural Biology, 2008, 161, 92-100.	1.3	47
76	Paired β -sheet structure of an A β (1-40) amyloid fibril revealed by electron microscopy. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 7462-7466.	3.3	194
77	Near-atomic resolution using electron cryomicroscopy and single-particle reconstruction. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 1867-1872.	3.3	347
78	Electron Diffraction of a Bacterial ClC-Type Chloride Channel. Novartis Foundation Symposium, 2008, , 193-206.	1.2	2
79	FREALIGN: High-resolution refinement of single particle structures. Journal of Structural Biology, 2007, 157, 117-125.	1.3	468
80	SIGNATURE: A single-particle selection system for molecular electron microscopy. Journal of Structural Biology, 2007, 157, 168-173.	1.3	150
81	Ab initio resolution measurement for single particle structures. Journal of Structural Biology, 2007, 157, 201-210.	1.3	102
82	A maximum likelihood approach to two-dimensional crystals. Journal of Structural Biology, 2007, 160, 362-374.	1.3	37
83	High-resolution Electron Microscopy of Helical Specimens: A Fresh Look at Tobacco Mosaic Virus. Journal of Molecular Biology, 2007, 371, 812-835.	2.0	231
84	Single Particle Reconstructions of the Transferrin-Transferrin Receptor Complex Obtained with Different Specimen Preparation Techniques. Journal of Molecular Biology, 2006, 355, 1048-1065.	2.0	57
85	The Three-dimensional Architecture of the EJC Core. Journal of Molecular Biology, 2006, 360, 743-749.	2.0	32
86	Quaternary Structure of a Mature Amyloid Fibril from Alzheimer's A β (1-40) Peptide. Journal of Molecular Biology, 2006, 362, 347-354.	2.0	69
87	Structure determination of clathrin coats to subnanometer resolution by single particle cryo-electron microscopy. Journal of Structural Biology, 2006, 156, 453-460.	1.3	35
88	Ewald sphere correction for single-particle electron microscopy. Ultramicroscopy, 2006, 106, 376-382.	0.8	61
89	Conformational changes in the Arp2/3 complex leading to actin nucleation. Nature Structural and Molecular Biology, 2005, 12, 26-31.	3.6	159
90	Ito Channels Are Octomeric Complexes with Four Subunits of Each Kv4.2 and K ⁺ Channel-interacting Protein 2. Journal of Biological Chemistry, 2004, 279, 5549-5554.	1.6	52

#	ARTICLE	IF	CITATIONS
91	Three-dimensional structure of C complex spliceosomes by electron microscopy. <i>Nature Structural and Molecular Biology</i> , 2004, 11, 265-269.	3.6	74
92	Structure of an auxilin-bound clathrin coat and its implications for the mechanism of uncoating. <i>Nature</i> , 2004, 432, 649-653.	13.7	159
93	Molecular model for a complete clathrin lattice from electron cryomicroscopy. <i>Nature</i> , 2004, 432, 573-579.	13.7	464
94	Noise bias in the refinement of structures derived from single particles. <i>Ultramicroscopy</i> , 2004, 102, 67-84.	0.8	125
95	Three-Dimensional Structure of Ito. <i>Neuron</i> , 2004, 41, 513-519.	3.8	80
96	Electron cryomicroscopy structure of N-ethyl maleimide sensitive factor at 11 Å resolution. <i>EMBO Journal</i> , 2003, 22, 4365-4374.	3.5	54
97	Low-resolution structure refinement in electron microscopy. <i>Journal of Structural Biology</i> , 2003, 144, 144-151.	1.3	49
98	Visualization of the Domain Structure of an L-type Ca ²⁺ Channel Using Electron Cryo-microscopy. <i>Journal of Molecular Biology</i> , 2003, 332, 171-182.	2.0	103
99	Accurate determination of local defocus and specimen tilt in electron microscopy. <i>Journal of Structural Biology</i> , 2003, 142, 334-347.	1.3	1,355
100	Conformational changes in the C terminus of Shaker K ⁺ channel bound to the rat Kv ^{2.1} -subunit. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 12607-12612.	3.3	53
101	Purification and characterization of native spliceosomes suitable for three-dimensional structural analysis. <i>Rna</i> , 2002, 8, 426-439.	1.6	316
102	A Common Mechanism Underlying Promiscuous Inhibitors from Virtual and High-Throughput Screening. <i>Journal of Medicinal Chemistry</i> , 2002, 45, 1712-1722.	2.9	1,013
103	Projection structure of a ClC-type chloride channel at 6.5 Å resolution. <i>Nature</i> , 2001, 409, 219-223.	13.7	120
104	Three-Dimensional Structure of a Voltage-Gated Potassium Channel at 2.5 nm Resolution. <i>Structure</i> , 2001, 9, 215-220.	1.6	144
105	Molecular Machines. <i>Journal of Cell Biology</i> , 2001, 152, F1-F10.	2.3	56
106	Resolution measurement in structures derived from single particles. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000, 56, 1270-1277.	2.5	108
107	Structure of the respiratory NADH:ubiquinone oxidoreductase (complex I). <i>Current Opinion in Structural Biology</i> , 1999, 9, 476-484.	2.6	93
108	Direct visualisation of micelles of Pluronic block copolymers in aqueous solution by cryo-TEM. <i>Physical Chemistry Chemical Physics</i> , 1999, 1, 3331-3334.	1.3	91

#	ARTICLE	IF	CITATIONS
109	Clathrin coats at 21Å resolution: a cellular assembly designed to recycle multiple membrane receptors. EMBO Journal, 1998, 17, 4943-4953.	3.5	129
110	Three-dimensional structure of bovine NADH:ubiquinone oxidoreductase (complex I) at 22 Å in ice. Journal of Molecular Biology, 1998, 277, 1033-1046.	2.0	332
111	Electron Crystallography of Two-Dimensional Crystals of Membrane Proteins. Journal of Structural Biology, 1998, 121, 142-161.	1.3	87
112	Electron-crystallographic Refinement of the Structure of Bacteriorhodopsin. Journal of Molecular Biology, 1996, 259, 393-421.	2.0	945
113	Comparison of calculated and observed dynamical diffraction from purple membrane: implications. Ultramicroscopy, 1996, 65, 101-107.	0.8	10
114	Diffuse scattering in electron diffraction data from protein crystals. Ultramicroscopy, 1995, 60, 295-309.	0.8	12
115	Lipid Location in Deoxycholate-treated Purple Membrane at 2.6 Å... Journal of Molecular Biology, 1995, 254, 404-415.	2.0	53
116	Electron microscopy of ultra-thin buried layers in InP and InGaAs. Philosophical Magazine A: Physics of Condensed Matter, Structure, Defects and Mechanical Properties, 1993, 68, 121-136.	0.8	11