

Raimond B G Ravelli

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/505550/publications.pdf>

Version: 2024-02-01

110
papers

11,360
citations

46918

47
h-index

30010

103
g-index

123
all docs

123
docs citations

123
times ranked

16488
citing authors

#	ARTICLE	IF	CITATIONS
1	Mycobacteriaâ€‘host interactions in human bronchiolar airway organoids. <i>Molecular Microbiology</i> , 2022, 117, 682-692.	1.2	32
2	Endocytosed nanogold fiducials for improved in-situ cryoâ€‘electron tomography tilt-series alignment. <i>Journal of Structural Biology</i> , 2021, 213, 107698.	1.3	5
3	Structure of the <i>Yersinia</i> injectosome in intracellular host cell phagosomes revealed by cryo FIB electron tomography. <i>Journal of Structural Biology</i> , 2021, 213, 107701.	1.3	28
4	<i>Mycobacterium tuberculosis</i> ferritin: a suitable workhorse protein for cryo-EM development. <i>Acta Crystallographica Section D: Structural Biology</i> , 2021, 77, 1077-1083.	1.1	6
5	Single-particle cryo-EM: alternative schemes to improve dose efficiency. <i>Journal of Synchrotron Radiation</i> , 2021, 28, 1343-1356.	1.0	5
6	An organoidâ€‘derived bronchioalveolar model for SARSâ€‘CoVâ€‘2 infection of human alveolar type IIâ€‘like cells. <i>EMBO Journal</i> , 2021, 40, e105912.	3.5	153
7	Priming mycobacterial ESX-secreted protein B to form a channel-like structure. <i>Current Research in Structural Biology</i> , 2021, 3, 153-164.	1.1	15
8	Structural Analysis of the Partially Disordered Protein EspK from <i>Mycobacterium Tuberculosis</i> . <i>Crystals</i> , 2021, 11, 18.	1.0	2
9	Efficient molecule discrimination in electron microscopy through an optimized orbital angular momentum sorter. <i>Physical Review A</i> , 2020, 102, .	1.0	8
10	Sub-pixel electron detection using a convolutional neural network. <i>Ultramicroscopy</i> , 2020, 218, 113091.	0.8	19
11	Structural dynamics of the GluK3-kainate receptor neurotransmitter binding domains revealed by cryo-EM. <i>International Journal of Biological Macromolecules</i> , 2020, 149, 1051-1058.	3.6	11
12	Architecture of the flexible tail tube of bacteriophage SPP1. <i>Nature Communications</i> , 2020, 11, 5759.	5.8	37
13	Vitrojet: Bridging the Gap in Sample Prep. <i>Microscopy and Microanalysis</i> , 2020, 26, 328-328.	0.2	1
14	Cryo-EM structure of islet amyloid polypeptide fibrils reveals similarities with amyloid-Î² fibrils. <i>Nature Structural and Molecular Biology</i> , 2020, 27, 660-667.	3.6	120
15	Could Egg White Lysozyme be Solved by Single Particle Cryo-EM?. <i>Journal of Chemical Information and Modeling</i> , 2020, 60, 2605-2613.	2.5	11
16	SARS-CoV-2 productively infects human gut enterocytes. <i>Science</i> , 2020, 369, 50-54.	6.0	1,347
17	Cryo-EM structures from sub-nl volumes using pin-printing and jet vitrification. <i>Nature Communications</i> , 2020, 11, 2563.	5.8	85
18	How the Observation in a New Custom Basis Based on Orbital Angular Momentum Space Could Improve Our Dose Effective Reconstruction of the Protein Structure.. <i>Microscopy and Microanalysis</i> , 2020, 26, 1168-1169.	0.2	0

#	ARTICLE	IF	CITATIONS
19	Atomic structure of PI3-kinase SH3 amyloid fibrils by cryo-electron microscopy. <i>Nature Communications</i> , 2019, 10, 3754.	5.8	32
20	Exemplar-based inpainting as a solution to the missing wedge problem in electron tomography. <i>Ultramicroscopy</i> , 2018, 191, 1-10.	0.8	11
21	Calibration of rotation axes for multi-axis goniometers in macromolecular crystallography. <i>Journal of Applied Crystallography</i> , 2018, 51, 1421-1427.	1.9	3
22	Fibril structure of amyloid- β (1-42) by cryo-electron microscopy. <i>Science</i> , 2017, 358, 116-119.	6.0	801
23	Single-particle cryo-EM using alignment by classification (ABC): the structure of <i>Lumbricus terrestris</i> haemoglobin. <i>IUCr</i> , 2017, 4, 678-694.	1.0	30
24	A posteriori correction of camera characteristics from large image data sets. <i>Scientific Reports</i> , 2015, 5, 10317.	1.6	22
25	Radiation damage to nucleoprotein complexes in macromolecular crystallography. <i>Journal of Synchrotron Radiation</i> , 2015, 22, 213-224.	1.0	21
26	Replication of <i>Plasmodium</i> in reticulocytes can occur without hemozoin formation, resulting in chloroquine resistance. <i>Journal of Experimental Medicine</i> , 2015, 212, 893-903.	4.2	62
27	Accounting for partiality in serial crystallography using ray-tracing principles. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 1799-1811.	2.5	18
28	Conversion of Mature Human β -Cells Into Glucagon-Producing α -Cells. <i>Diabetes</i> , 2013, 62, 2471-2480.	0.3	115
29	Glomerular Endothelial Surface Layer Acts as a Barrier against Albumin Filtration. <i>American Journal of Pathology</i> , 2013, 182, 1532-1540.	1.9	99
30	Destruction of Tissue, Cells and Organelles in Type 1 Diabetic Rats Presented at Macromolecular Resolution. <i>Scientific Reports</i> , 2013, 3, 1804.	1.6	46
31	Localization of fluorescently labeled structures in frozen-hydrated samples using integrated light electron microscopy. <i>Journal of Structural Biology</i> , 2013, 181, 283-290.	1.3	61
32	Image formation modeling in cryo-electron microscopy. <i>Journal of Structural Biology</i> , 2013, 183, 19-32.	1.3	90
33	Non-rigid image registration to reduce beam-induced blurring of cryo-electron microscopy images. <i>Journal of Synchrotron Radiation</i> , 2013, 20, 58-66.	1.0	5
34	The use of a mini-goniometer head in macromolecular crystallography diffraction experiments. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 1241-1251.	2.5	42
35	Design and Characterization of Modular Scaffolds for Tubulin Assembly. <i>Journal of Biological Chemistry</i> , 2012, 287, 31085-31094.	1.6	22
36	Large Multimeric Assemblies of Nucleosome Assembly Protein and Histones Revealed by Small-angle X-ray Scattering and Electron Microscopy. <i>Journal of Biological Chemistry</i> , 2012, 287, 26657-26665.	1.6	12

#	ARTICLE	IF	CITATIONS
37	Virtual nanoscopy: Generation of ultra-large high resolution electron microscopy maps. <i>Journal of Cell Biology</i> , 2012, 198, 457-469.	2.3	110
38	Precise and unbiased estimation of astigmatism and defocus in transmission electron microscopy. <i>Ultramicroscopy</i> , 2012, 116, 115-134.	0.8	22
39	Non-Random mtDNA Segregation Patterns Indicate a Metastable Heteroplasmic Segregation Unit in m.3243A>G Cybrid Cells. <i>PLoS ONE</i> , 2012, 7, e52080.	1.1	21
40	A new approach to improve the quality of ultrathin cryo-sections; its use for immunogold EM and correlative electron cryo-tomography. <i>Journal of Structural Biology</i> , 2011, 175, 62-72.	1.3	29
41	Defocus estimation from stroboscopic cryo-electron microscopy data. <i>Ultramicroscopy</i> , 2011, 111, 1592-1598.	0.8	6
42	Translation calibration of inverse-kappa goniometers in macromolecular crystallography. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2011, 67, 219-228.	0.3	15
43	Radiation damage in single-particle cryo-electron microscopy: effects of dose and dose rate. <i>Journal of Synchrotron Radiation</i> , 2011, 18, 398-412.	1.0	88
44	Cartilage ultrastructure in proteoglycan-deficient zebrafish mutants brings to light new candidate genes for human skeletal disorders. <i>Journal of Pathology</i> , 2011, 223, 531-542.	2.1	38
45	Infrared protein crystallography. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2011, 1814, 760-777.	1.1	24
46	PS13 - 65. Correlated microscopy and nanotomy to analyze complete cross sections of Islets of Langerhans in Type I diabetes. <i>Nederlands Tijdschrift Voor Diabetologie</i> , 2011, 9, 135-135.	0.0	0
47	A toolkit for the characterization of CCD cameras for transmission electron microscopy. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2010, 66, 97-109.	2.5	31
48	<i>MxCuBE</i> : a synchrotron beamline control environment customized for macromolecular crystallography experiments. <i>Journal of Synchrotron Radiation</i> , 2010, 17, 700-707.	1.0	193
49	Estimation of defocus and astigmatism in transmission electron microscopy. , 2010, , .		1
50	Structure of SRP14 from the <i>Schizosaccharomyces pombe</i> signal recognition particle. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2009, 65, 421-433.	2.5	10
51	Improving diffraction by humidity control: a novel device compatible with X-ray beamlines. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2009, 65, 1237-1246.	2.5	109
52	Colouring cryo-cooled crystals: online microspectrophotometry. <i>Journal of Synchrotron Radiation</i> , 2009, 16, 163-172.	1.0	69
53	A decade of user operation on the macromolecular crystallography MAD beamline ID14-4 at the ESRF. <i>Journal of Synchrotron Radiation</i> , 2009, 16, 803-812.	1.0	54
54	Strain relief at the active site of phosphoserine aminotransferase induced by radiation damage. <i>Protein Science</i> , 2009, 14, 1498-1507.	3.1	50

#	ARTICLE	IF	CITATIONS
55	Variations in the colchicine-binding domain provide insight into the structural switch of tubulin. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 13775-13779.	3.3	239
56	Radiation stability of proteinase K crystals grown by LB nanotemplate method. Journal of Structural Biology, 2009, 168, 409-418.	1.3	23
57	Complexes of tubulin with inhibitors that bind to the colchicine domain. Acta Crystallographica Section A: Foundations and Advances, 2009, 65, s25-s26.	0.3	0
58	Differential specific radiation damage in the Cu ^{II} -bound and Pd ^{II} -bound forms of an α -helical foldamer: a case study of crystallographic phasing by RIP and SAD. Acta Crystallographica Section D: Biological Crystallography, 2008, 64, 264-272.	2.5	7
59	X-ray tomographic reconstruction of macromolecular samples. Journal of Applied Crystallography, 2008, 41, 1057-1066.	1.9	28
60	Structural insight into the inhibition of tubulin by vinca domain peptide ligands. EMBO Reports, 2008, 9, 1101-1106.	2.0	140
61	Microtubule-Destabilizing Agents: Structural and Mechanistic Insights from the Interaction of Colchicine and Vinblastine with Tubulin. Topics in Current Chemistry, 2008, 286, 259-278.	4.0	51
62	The 1.8-Å... Crystal Structure of α 1-Acid Glycoprotein (Orosomucoid) Solved by UV RIP Reveals the Broad Drug-Binding Activity of This Human Plasma Lipocalin. Journal of Molecular Biology, 2008, 384, 393-405.	2.0	142
63	Structural analysis of the genetic switch that regulates the expression of restriction-modification genes. Nucleic Acids Research, 2008, 36, 4778-4787.	6.5	34
64	Quickly Getting the Best Data from Your Macromolecular Crystals with a New Generation of Beamline Instruments. AIP Conference Proceedings, 2007, , .	0.3	15
65	Structural insights into the Slit-Robo complex. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 14923-14928.	3.3	159
66	Structure of Dimeric SecA, the Escherichia coli Preprotein Translocase Motor. Journal of Molecular Biology, 2007, 366, 1545-1557.	2.0	127
67	The Solution and Crystal Structures of a Module Pair from the Staphylococcus aureus-Binding Site of Human Fibronectin—A Tale with a Twist. Journal of Molecular Biology, 2007, 368, 833-844.	2.0	34
68	3-D Structure of Serum Paraoxonase 1 Sheds Light on Its Activity, Stability, Solubility and Crystallizability. Arhiv Za Higijenu Rada I Toksikologiju, 2007, 58, 347-353.	0.4	30
69	Plastic-embedded protein crystals. Journal of Synchrotron Radiation, 2007, 14, 128-132.	1.0	6
70	X-ray radiation-induced damage in DNA monitored by online Raman. Journal of Synchrotron Radiation, 2007, 14, 99-108.	1.0	40
71	Crystal Structure of the Rabies Virus Nucleoprotein-RNA Complex. Science, 2006, 313, 360-363.	6.0	299
72	Structural Basis for Budding by the ESCRT-III Factor CHMP3. Developmental Cell, 2006, 10, 821-830.	3.1	220

#	ARTICLE	IF	CITATIONS
73	Is radiation damage dependent on the dose rate used during macromolecular crystallography data collection?. Acta Crystallographica Section D: Biological Crystallography, 2006, 62, 125-132.	2.5	51
74	C3D: a program for the automated centring of cryocooled crystals. Acta Crystallographica Section D: Biological Crystallography, 2006, 62, 1348-1357.	2.5	29
75	Radiation damage in macromolecular cryocrystallography. Current Opinion in Structural Biology, 2006, 16, 624-629.	2.6	134
76	Biochemical Characterization and Crystal Structure of Synechocystis Arogenate Dehydrogenase Provide Insights into Catalytic Reaction. Structure, 2006, 14, 767-776.	1.6	31
77	Phasing Macromolecular Structures with UV-Induced Structural Changes. Structure, 2006, 14, 791-800.	1.6	42
78	Structural basis for the regulation of tubulin by vinblastine. Nature, 2005, 435, 519-522.	13.7	651
79	X-Ray Crystallographic and NMR Studies of the Third KH Domain of hnRNP K in Complex with Single-Stranded Nucleic Acids. Structure, 2005, 13, 1055-1067.	1.6	90
80	Automation of macromolecular crystallography beamlines. Progress in Biophysics and Molecular Biology, 2005, 89, 124-152.	1.4	46
81	Improving radiation-damage substructures for RIP. Acta Crystallographica Section D: Biological Crystallography, 2005, 61, 1227-1237.	2.5	82
82	Parameters affecting the X-ray dose absorbed by macromolecular crystals. Journal of Synchrotron Radiation, 2005, 12, 268-275.	1.0	70
83	Phasing in the presence of radiation damage. Journal of Synchrotron Radiation, 2005, 12, 276-284.	1.0	47
84	Supercooled liquid-like solvent in trypsin crystals: implications for crystal annealing and temperature-controlled X-ray radiation damage studies. Journal of Synchrotron Radiation, 2005, 12, 310-317.	1.0	30
85	Initial Events in the Photocycle of Photoactive Yellow Protein. Journal of Biological Chemistry, 2004, 279, 26417-26424.	1.6	63
86	Structure and evolution of the serum paraoxonase family of detoxifying and anti-atherosclerotic enzymes. Nature Structural and Molecular Biology, 2004, 11, 412-419.	3.6	569
87	Insight into tubulin regulation from a complex with colchicine and a stathmin-like domain. Nature, 2004, 428, 198-202.	13.7	1,441
88	Crystallization, microPIXE and preliminary crystallographic analysis of the complex between the third KH domain of hnRNP K and single-stranded DNA. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 784-787.	2.5	10
89	Expression, crystallization and crystallographic analysis of DegS, a stress sensor of the bacterial periplasm. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 1429-1431.	2.5	5
90	X-ray absorption by macromolecular crystals: the effects of wavelength and crystal composition on absorbed dose. Journal of Applied Crystallography, 2004, 37, 513-522.	1.9	178

#	ARTICLE	IF	CITATIONS
91	Structure of an Activated Dictyostelium STAT in Its DNA-Unbound Form. <i>Molecular Cell</i> , 2004, 13, 791-804.	4.5	60
92	Specific Radiation Damage Can Be Used to Solve Macromolecular Crystal Structures. <i>Structure</i> , 2003, 11, 217-224.	1.6	141
93	Zero-dose extrapolation as part of macromolecular synchrotron data reduction. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 903-909.	2.5	66
94	The Structure of Bovine Lysosomal α -Mannosidase Suggests a Novel Mechanism for Low-pH Activation. <i>Journal of Molecular Biology</i> , 2003, 327, 631-644.	2.0	82
95	Tryparedoxins from <i>Crithidia fasciculata</i> and <i>Trypanosoma brucei</i> . <i>Journal of Biological Chemistry</i> , 2003, 278, 25919-25925.	1.6	43
96	Characterization of Photocycle Intermediates in Crystalline Photoactive Yellow Protein. <i>Photochemistry and Photobiology</i> , 2003, 78, 131.	1.3	19
97	Crystallization and preliminary X-ray analysis of the <i>Escherichia coli</i> adaptor protein ClpS, free and in complex with the N-terminal domain of ClpA. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 1207-1210.	2.5	6
98	Unit-cell volume change as a metric of radiation damage in crystals of macromolecules. <i>Journal of Synchrotron Radiation</i> , 2002, 9, 355-360.	1.0	63
99	Evidence for the formation of disulfide radicals in protein crystals upon X-ray irradiation. <i>Journal of Synchrotron Radiation</i> , 2002, 9, 342-346.	1.0	63
100	Structural analysis of the adaptor protein ClpS in complex with the N-terminal domain of ClpA. <i>Nature Structural Biology</i> , 2002, 9, 906-911.	9.7	115
101	Specific protein dynamics near the solvent glass transition assayed by radiation-induced structural changes. <i>Protein Science</i> , 2001, 10, 1953-1961.	3.1	64
102	The "fingerprint" that X-rays can leave on structures. <i>Structure</i> , 2000, 8, 315-328.	1.6	302
103	Specific chemical and structural damage to proteins produced by synchrotron radiation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2000, 97, 623-628.	3.3	438
104	Ab initio structure determination of low-molecular-weight compounds using synchrotron radiation Laue diffraction. <i>Journal of Synchrotron Radiation</i> , 1999, 6, 19-28.	1.0	4
105	Static Laue Diffraction Studies on Acetylcholinesterase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1998, 54, 1359-1366.	2.5	29
106	Activity of <i>Torpedo Californica</i> Acetylcholinesterase in the Crystalline State. , 1998, , 230-231.		0
107	STRATEGY: a program to optimize the starting spindle angle and scan range for X-ray data collection. <i>Journal of Applied Crystallography</i> , 1997, 30, 551-554.	1.9	55
108	Towards Automatic Indexing of the Laue Diffraction Pattern. <i>Journal of Applied Crystallography</i> , 1996, 29, 270-278.	1.9	22

#	ARTICLE	IF	CITATIONS
109	Soluble monomeric acetylcholinesterase from mouse: Expression, purification, and crystallization in complex with fasciculin. <i>Protein Science</i> , 1996, 5, 672-679.	3.1	56
110	Crystal structure of an acetylcholinesteraseâ€ƒfasciculin complex: interaction of a three-fingered toxin from snake venom with its target. <i>Structure</i> , 1995, 3, 1355-1366.	1.6	232