

Raimond B G Ravelli

List of Publications by Year in descending order

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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	Insight into tubulin regulation from a complex with colchicine and a stathmin-like domain. <i>Nature</i> , 2004, 428, 198-202.	13.7	1,441
2	SARS-CoV-2 productively infects human gut enterocytes. <i>Science</i> , 2020, 369, 50-54.	6.0	1,347
3	Fibril structure of amyloid- β (1-42) by cryo-electron microscopy. <i>Science</i> , 2017, 358, 116-119.	6.0	801
4	Structural basis for the regulation of tubulin by vinblastine. <i>Nature</i> , 2005, 435, 519-522.	13.7	651
5	Structure and evolution of the serum paraoxonase family of detoxifying and anti-atherosclerotic enzymes. <i>Nature Structural and Molecular Biology</i> , 2004, 11, 412-419.	3.6	569
6	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
7	The "fingerprint" that X-rays can leave on structures. <i>Structure</i> , 2000, 8, 315-328.	1.6	302
8	Crystal Structure of the Rabies Virus Nucleoprotein-RNA Complex. <i>Science</i> , 2006, 313, 360-363.	6.0	299
9	Variations in the colchicine-binding domain provide insight into the structural switch of tubulin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 13775-13779.	3.3	239
10	Crystal structure of an acetylcholinesterase-fasciculin complex: interaction of a three-fingered toxin from snake venom with its target. <i>Structure</i> , 1995, 3, 1355-1366.	1.6	232
11	Structural Basis for Budding by the ESCRT-III Factor CHMP3. <i>Developmental Cell</i> , 2006, 10, 821-830.	3.1	220
12	<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
13	X-ray absorption by macromolecular crystals: the effects of wavelength and crystal composition on absorbed dose. <i>Journal of Applied Crystallography</i> , 2004, 37, 513-522.	1.9	178
14	Structural insights into the Slit-Robo complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 14923-14928.	3.3	159
15	An organoid-derived bronchioalveolar model for SARS-CoV-2 infection of human alveolar type II-like cells. <i>EMBO Journal</i> , 2021, 40, e105912.	3.5	153
16	The 1.8-Å... Crystal Structure of β 1-Acid Glycoprotein (Orosomucoid) Solved by UV RIP Reveals the Broad Drug-Binding Activity of This Human Plasma Lipocalin. <i>Journal of Molecular Biology</i> , 2008, 384, 393-405.	2.0	142
17	Specific Radiation Damage Can Be Used to Solve Macromolecular Crystal Structures. <i>Structure</i> , 2003, 11, 217-224.	1.6	141
18	Structural insight into the inhibition of tubulin by vinca domain peptide ligands. <i>EMBO Reports</i> , 2008, 9, 1101-1106.	2.0	140

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19	Radiation damage in macromolecular cryocrystallography. <i>Current Opinion in Structural Biology</i> , 2006, 16, 624-629.	2.6	134
20	Structure of Dimeric SecA, the Escherichia coli Preprotein Translocase Motor. <i>Journal of Molecular Biology</i> , 2007, 366, 1545-1557.	2.0	127
21	Cryo-EM structure of islet amyloid polypeptide fibrils reveals similarities with amyloid- β fibrils. <i>Nature Structural and Molecular Biology</i> , 2020, 27, 660-667.	3.6	120
22	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
23	Conversion of Mature Human β -Cells Into Glucagon-Producing β -Cells. <i>Diabetes</i> , 2013, 62, 2471-2480.	0.3	115
24	Virtual nanoscopy: Generation of ultra-large high resolution electron microscopy maps. <i>Journal of Cell Biology</i> , 2012, 198, 457-469.	2.3	110
25	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
26	Glomerular Endothelial Surface Layer Acts as a Barrier against Albumin Filtration. <i>American Journal of Pathology</i> , 2013, 182, 1532-1540.	1.9	99
27	X-Ray Crystallographic and NMR Studies of the Third KH Domain of hnRNP K in Complex with Single-Stranded Nucleic Acids. <i>Structure</i> , 2005, 13, 1055-1067.	1.6	90
28	Image formation modeling in cryo-electron microscopy. <i>Journal of Structural Biology</i> , 2013, 183, 19-32.	1.3	90
29	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
30	Cryo-EM structures from sub-nl volumes using pin-printing and jet vitrification. <i>Nature Communications</i> , 2020, 11, 2563.	5.8	85
31	The Structure of Bovine Lysosomal β -Mannosidase Suggests a Novel Mechanism for Low-pH Activation. <i>Journal of Molecular Biology</i> , 2003, 327, 631-644.	2.0	82
32	Improving radiation-damage substructures for RIP. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 1227-1237.	2.5	82
33	Parameters affecting the X-ray dose absorbed by macromolecular crystals. <i>Journal of Synchrotron Radiation</i> , 2005, 12, 268-275.	1.0	70
34	Colouring cryo-cooled crystals: online microspectrophotometry. <i>Journal of Synchrotron Radiation</i> , 2009, 16, 163-172.	1.0	69
35	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
36	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

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37	Unit-cell volume change as a metric of radiation damage in crystals of macromolecules. Journal of Synchrotron Radiation, 2002, 9, 355-360.	1.0	63
38	Evidence for the formation of disulfide radicals in protein crystals upon X-ray irradiation. Journal of Synchrotron Radiation, 2002, 9, 342-346.	1.0	63
39	Initial Events in the Photocycle of Photoactive Yellow Protein. Journal of Biological Chemistry, 2004, 279, 26417-26424.	1.6	63
40	Replication of Plasmodium in reticulocytes can occur without hemozoin formation, resulting in chloroquine resistance. Journal of Experimental Medicine, 2015, 212, 893-903.	4.2	62
41	Localization of fluorescently labeled structures in frozen-hydrated samples using integrated light electron microscopy. Journal of Structural Biology, 2013, 181, 283-290.	1.3	61
42	Structure of an Activated Dictyostelium STAT in Its DNA-Unbound Form. Molecular Cell, 2004, 13, 791-804.	4.5	60
43	Soluble monomeric acetylcholinesterase from mouse: Expression, purification, and crystallization in complex with fasciculin. Protein Science, 1996, 5, 672-679.	3.1	56
44	STRATEGY: a program to optimize the starting spindle angle and scan range for X-ray data collection. Journal of Applied Crystallography, 1997, 30, 551-554.	1.9	55
45	A decade of user operation on the macromolecular crystallography MAD beamline ID14-4 at the ESRF. Journal of Synchrotron Radiation, 2009, 16, 803-812.	1.0	54
46	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
47	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
48	Strain relief at the active site of phosphoserine aminotransferase induced by radiation damage. Protein Science, 2009, 14, 1498-1507.	3.1	50
49	Phasing in the presence of radiation damage. Journal of Synchrotron Radiation, 2005, 12, 276-284.	1.0	47
50	Automation of macromolecular crystallography beamlines. Progress in Biophysics and Molecular Biology, 2005, 89, 124-152.	1.4	46
51	Destruction of Tissue, Cells and Organelles in Type 1 Diabetic Rats Presented at Macromolecular Resolution. Scientific Reports, 2013, 3, 1804.	1.6	46
52	Tryparedoxins from Crithidia fasciculata and Trypanosoma brucei. Journal of Biological Chemistry, 2003, 278, 25919-25925.	1.6	43
53	Phasing Macromolecular Structures with UV-Induced Structural Changes. Structure, 2006, 14, 791-800.	1.6	42
54	The use of a mini-goniometer head in macromolecular crystallography diffraction experiments. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 1241-1251.	2.5	42

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55	X-ray radiation-induced damage in DNA monitored by online Raman. <i>Journal of Synchrotron Radiation</i> , 2007, 14, 99-108.	1.0	40
56	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
57	Architecture of the flexible tail tube of bacteriophage SPP1. <i>Nature Communications</i> , 2020, 11, 5759.	5.8	37
58	The Solution and Crystal Structures of a Module Pair from the <i>Staphylococcus aureus</i> -Binding Site of Human Fibronectin—A Tale with a Twist. <i>Journal of Molecular Biology</i> , 2007, 368, 833-844.	2.0	34
59	Structural analysis of the genetic switch that regulates the expression of restriction-modification genes. <i>Nucleic Acids Research</i> , 2008, 36, 4778-4787.	6.5	34
60	Atomic structure of PI3-kinase SH3 amyloid fibrils by cryo-electron microscopy. <i>Nature Communications</i> , 2019, 10, 3754.	5.8	32
61	<i>Mycobacteria</i> –host interactions in human bronchiolar airway organoids. <i>Molecular Microbiology</i> , 2022, 117, 682-692.	1.2	32
62	Biochemical Characterization and Crystal Structure of <i>Synechocystis</i> Arogenate Dehydrogenase Provide Insights into Catalytic Reaction. <i>Structure</i> , 2006, 14, 767-776.	1.6	31
63	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
64	Supercooled liquid-like solvent in trypsin crystals: implications for crystal annealing and temperature-controlled X-ray radiation damage studies. <i>Journal of Synchrotron Radiation</i> , 2005, 12, 310-317.	1.0	30
65	3-D Structure of Serum Paraoxonase 1 Sheds Light on Its Activity, Stability, Solubility and Crystallizability. <i>Arhiv Za Higijenu Rada I Toksikologiju</i> , 2007, 58, 347-353.	0.4	30
66	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
67	Static Laue Diffraction Studies on Acetylcholinesterase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1998, 54, 1359-1366.	2.5	29
68	C3D: a program for the automated centring of cryocooled crystals. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006, 62, 1348-1357.	2.5	29
69	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
70	X-ray tomographic reconstruction of macromolecular samples. <i>Journal of Applied Crystallography</i> , 2008, 41, 1057-1066.	1.9	28
71	Structure of the <i>Yersinia</i> injectisome in intracellular host cell phagosomes revealed by cryo FIB electron tomography. <i>Journal of Structural Biology</i> , 2021, 213, 107701.	1.3	28
72	Infrared protein crystallography. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2011, 1814, 760-777.	1.1	24

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73	Radiation stability of proteinase K crystals grown by LB nanotemplate method. <i>Journal of Structural Biology</i> , 2009, 168, 409-418.	1.3	23
74	Towards Automatic Indexing of the Laue Diffraction Pattern. <i>Journal of Applied Crystallography</i> , 1996, 29, 270-278.	1.9	22
75	Design and Characterization of Modular Scaffolds for Tubulin Assembly. <i>Journal of Biological Chemistry</i> , 2012, 287, 31085-31094.	1.6	22
76	Precise and unbiased estimation of astigmatism and defocus in transmission electron microscopy. <i>Ultramicroscopy</i> , 2012, 116, 115-134.	0.8	22
77	A posteriori correction of camera characteristics from large image data sets. <i>Scientific Reports</i> , 2015, 5, 10317.	1.6	22
78	Radiation damage to nucleoprotein complexes in macromolecular crystallography. <i>Journal of Synchrotron Radiation</i> , 2015, 22, 213-224.	1.0	21
79	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
80	Characterization of Photocycle Intermediates in Crystalline Photoactive Yellow Protein. <i>Photochemistry and Photobiology</i> , 2003, 78, 131.	1.3	19
81	Sub-pixel electron detection using a convolutional neural network. <i>Ultramicroscopy</i> , 2020, 218, 113091.	0.8	19
82	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
83	Quickly Getting the Best Data from Your Macromolecular Crystals with a New Generation of Beamline Instruments. <i>AIP Conference Proceedings</i> , 2007, , .	0.3	15
84	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
85	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
86	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
87	Exemplar-based inpainting as a solution to the missing wedge problem in electron tomography. <i>Ultramicroscopy</i> , 2018, 191, 1-10.	0.8	11
88	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
89	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
90	Crystallization, microPIXE and preliminary crystallographic analysis of the complex between the third KH domain of hnRNP K and single-stranded DNA. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 784-787.	2.5	10

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91	Structure of SRP14 from the <i>Schizosaccharomyces pombe</i> signal recognition particle. Acta Crystallographica Section D: Biological Crystallography, 2009, 65, 421-433.	2.5	10
92	Efficient molecule discrimination in electron microscopy through an optimized orbital angular momentum sorter. Physical Review A, 2020, 102, .	1.0	8
93	Differential specific radiation damage in the Cu ^{II} -bound and Pd ^{II} -bound forms of an Î±-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
94	Crystallization and preliminary X-ray analysis of the Escherichia coli adaptor protein ClpS, free and in complex with the N-terminal domain of ClpA. Acta Crystallographica Section D: Biological Crystallography, 2002, 58, 1207-1210.	2.5	6
95	Plastic-embedded protein crystals. Journal of Synchrotron Radiation, 2007, 14, 128-132.	1.0	6
96	Defocus estimation from stroboscopic cryo-electron microscopy data. Ultramicroscopy, 2011, 111, 1592-1598.	0.8	6
97	<i>Mycobacterium tuberculosis</i> ferritin: a suitable workhorse protein for cryo-EM development. Acta Crystallographica Section D: Structural Biology, 2021, 77, 1077-1083.	1.1	6
98	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
99	Non-rigid image registration to reduce beam-induced blurring of cryo-electron microscopy images. Journal of Synchrotron Radiation, 2013, 20, 58-66.	1.0	5
100	Endocytosed nanogold fiducials for improved in-situ cryo-electron tomography tilt-series alignment. Journal of Structural Biology, 2021, 213, 107698.	1.3	5
101	Single-particle cryo-EM: alternative schemes to improve dose efficiency. Journal of Synchrotron Radiation, 2021, 28, 1343-1356.	1.0	5
102	Ab initio structure determination of low-molecular-weight compounds using synchrotron radiation Laue diffraction. Journal of Synchrotron Radiation, 1999, 6, 19-28.	1.0	4
103	Calibration of rotation axes for multi-axis goniometers in macromolecular crystallography. Journal of Applied Crystallography, 2018, 51, 1421-1427.	1.9	3
104	Structural Analysis of the Partially Disordered Protein EspK from Mycobacterium Tuberculosis. Crystals, 2021, 11, 18.	1.0	2
105	Estimation of defocus and astigmatism in transmission electron microscopy. , 2010, , .		1
106	Vitrojet: Bridging the Gap in Sample Prep. Microscopy and Microanalysis, 2020, 26, 328-328.	0.2	1
107	PS13 - 65. Correlated microscopy and nanotomography to analyze complete cross sections of Islets of Langerhans in Type I diabetes. Nederlands Tijdschrift Voor Diabetologie, 2011, 9, 135-135.	0.0	0
108	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

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109	Activity of Torpedo Californica Acetylcholinesterase in the Crystalline State. , 1998, , 230-231.		0
110	How the Observation in a New Custom Basis Based on Orbital Angular Momentum Space Could Improve Our Dose Effective Reconstruction of the Protein Structure.. Microscopy and Microanalysis, 2020, 26, 1168-1169.	0.2	0