

Janet Vonck

List of Publications by Year in descending order

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76
papers

4,820
citations

70961

41
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98622

67
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86
all docs

86
docs citations

86
times ranked

4724
citing authors

#	ARTICLE	IF	CITATIONS
1	The molybdenum storage protein forms and deposits distinct polynuclear tungsten oxygen aggregates. <i>Journal of Inorganic Biochemistry</i> , 2022, 234, 111904.	1.5	1
2	High-resolution structure and dynamics of mitochondrial complex I—Insights into the proton pumping mechanism. <i>Science Advances</i> , 2021, 7, eabj3221.	4.7	65
3	A hybrid approach reveals the allosteric regulation of GTP cyclohydrolase I. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 31838-31849.	3.3	7
4	Respiratory complex I— structure, mechanism and evolution. <i>Current Opinion in Structural Biology</i> , 2020, 63, 1-9.	2.6	79
5	Analysis of the co-translational assembly of the fungal fatty acid synthase (FAS). <i>Scientific Reports</i> , 2020, 10, 895.	1.6	18
6	Structural basis of proton-coupled potassium transport in the KUP family. <i>Nature Communications</i> , 2020, 11, 626.	5.8	60
7	The resolution revolution in cryoEM requires high-quality sample preparation: a rapid pipeline to a high-resolution map of yeast fatty acid synthase. <i>IUCr</i> , 2020, 7, 220-227.	1.0	16
8	Respiratory supercomplexes III ₂ IV ₂ come into focus. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 87-89.	3.6	10
9	High-resolution cryo-EM structures of respiratory complex I: Mechanism, assembly, and disease. <i>Science Advances</i> , 2019, 5, eaax9484.	4.7	109
10	Molybdate pumping into the molybdenum storage protein via an ATP-powered piercing mechanism. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 26497-26504.	3.3	8
11	A comparative study of single-particle cryo-EM with liquid-nitrogen and liquid-helium cooling. <i>IUCr</i> , 2019, 6, 1099-1105.	1.0	14
12	Mitochondrial Respiratory Chain Complexes. <i>Sub-Cellular Biochemistry</i> , 2018, 87, 167-227.	1.0	122
13	Structural basis for energy transduction by respiratory alternative complex III. <i>Nature Communications</i> , 2018, 9, 1728.	5.8	38
14	Cryo-EM structure of respiratory complex I at work. <i>ELife</i> , 2018, 7, .	2.8	98
15	Bayesian inference of rotor ring stoichiometry from electron microscopy images of archaeal ATP synthase. <i>Microscopy (Oxford, England)</i> , 2018, 67, 266-273.	0.7	8
16	Structure, mechanism, and regulation of the chloroplast ATP synthase. <i>Science</i> , 2018, 360, .	6.0	308
17	The PomXYZ Proteins Self-Organize on the Bacterial Nucleoid to Stimulate Cell Division. <i>Developmental Cell</i> , 2017, 41, 299-314.e13.	3.1	62
18	Regioselective <i>para</i> -Carboxylation of Catechols with a Prenylated Flavin Dependent Decarboxylase. <i>Angewandte Chemie - International Edition</i> , 2017, 56, 13893-13897.	7.2	64

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19	Advances in high-resolution cryo-EM of oligomeric enzymes. <i>Current Opinion in Structural Biology</i> , 2017, 46, 48-54.	2.6	26
20	Cryo-EM structure of the bifunctional secretin complex of <i>Thermus thermophilus</i> . <i>ELife</i> , 2017, 6, .	2.8	27
21	Helical jackknives control the gates of the double-pore K ⁺ uptake system KtrAB. <i>ELife</i> , 2017, 6, .	2.8	23
22	Structure and in situ organisation of the <i>Pyrococcus furiosus</i> archaeellum machinery. <i>ELife</i> , 2017, 6, .	2.8	83
23	The nucleotide-dependent interaction of FlaH and FlaI is essential for assembly and function of the archaeellum motor. <i>Molecular Microbiology</i> , 2016, 99, 674-685.	1.2	47
24	A bacterial hydrogen-dependent CO ₂ reductase forms filamentous structures. <i>FEBS Journal</i> , 2016, 283, 1311-1322.	2.2	22
25	Structure of a Complete ATP Synthase Dimer Reveals the Molecular Basis of Inner Mitochondrial Membrane Morphology. <i>Molecular Cell</i> , 2016, 63, 445-456.	4.5	230
26	The obligate respiratory supercomplex from Actinobacteria. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2016, 1857, 1705-1714.	0.5	41
27	Cryo-EM structure of respiratory complex I reveals a link to mitochondrial sulfur metabolism. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2016, 1857, 1935-1942.	0.5	27
28	Topology and Structure/Function Correlation of Ring- and Gate-forming Domains in the Dynamic Secretin Complex of <i>Thermus thermophilus</i> . <i>Journal of Biological Chemistry</i> , 2016, 291, 14448-14456.	1.6	14
29	Structure of Alcohol Oxidase from <i>Pichia pastoris</i> by Cryo-Electron Microscopy. <i>PLoS ONE</i> , 2016, 11, e0159476.	1.1	28
30	Functional asymmetry and electron flow in the bovine respirasome. <i>ELife</i> , 2016, 5, .	2.8	130
31	Cryo-EM structure of fatty acid synthase (FAS) from <i>Rhodosporidium toruloides</i> provides insights into the evolutionary development of fungal FAS. <i>Protein Science</i> , 2015, 24, 987-995.	3.1	28
32	Horizontal membrane-intrinsic Î±-helices in the stator a-subunit of an F-type ATP synthase. <i>Nature</i> , 2015, 521, 237-240.	13.7	293
33	Atomic model of the F420-reducing [NiFe] hydrogenase by electron cryo-microscopy using a direct electron detector. <i>ELife</i> , 2014, 3, e01963.	2.8	132
34	Production of fully assembled and active Aquifex aeolicus F1FO ATP synthase in <i>Escherichia coli</i> . <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2014, 1840, 34-40.	1.1	1
35	Structure and Conformational Variability of the <i>Mycobacterium tuberculosis</i> Fatty Acid Synthase Multienzyme Complex. <i>Structure</i> , 2013, 21, 1251-1257.	1.6	39
36	De novo modeling of the F420-reducing [NiFe]-hydrogenase from a methanogenic archaeon by cryo-electron microscopy. <i>ELife</i> , 2013, 2, e00218.	2.8	66

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37	Using 2D Crystals to Analyze the Structure of Membrane Proteins. <i>Methods in Molecular Biology</i> , 2013, 1033, 47-65.	0.4	1
38	Choice and Maintenance of Equipment for Electron Crystallography. <i>Methods in Molecular Biology</i> , 2013, 955, 331-351.	0.4	0
39	FlaX, A Unique Component of the Crenarchaeal Archaellum, Forms Oligomeric Ring-shaped Structures and Interacts with the Motor ATPase FlaI. <i>Journal of Biological Chemistry</i> , 2012, 287, 43322-43330.	1.6	36
40	Structural study on the architecture of the bacterial ATP synthase F _o motor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, E2050-6.	3.3	29
41	Unusual N-terminal β -Sheet Fold of PilQ from <i>Thermus thermophilus</i> Mediates Ring Formation and Is Essential for Piliation. <i>Journal of Biological Chemistry</i> , 2012, 287, 8484-8494.	1.6	23
42	Supramolecular Organization of the Respiratory Chain. , 2012, , 247-277.		2
43	Engineering rotor ring stoichiometries in the ATP synthase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, E1599-608.	3.3	89
44	Structure of the SecY Complex Unlocked by a Preprotein Mimic. <i>Cell Reports</i> , 2012, 1, 21-28.	2.9	63
45	Cell-Free Expression and Assembly of ATP Synthase. <i>Journal of Molecular Biology</i> , 2011, 413, 593-603.	2.0	81
46	Structure of the archaeal Na ⁺ /H ⁺ antiporter NhaP1 and functional role of transmembrane helix 1. <i>EMBO Journal</i> , 2011, 30, 439-449.	3.5	54
47	Structure and Function of PilQ, a Secretin of the DNA Transporter from the Thermophilic Bacterium <i>Thermus thermophilus</i> HB27. <i>Journal of Biological Chemistry</i> , 2011, 286, 9977-9984.	1.6	53
48	Prion Protein Amyloid Formation Involves Structural Rearrangements in the C-terminal Domain. <i>ChemBioChem</i> , 2010, 11, 1208-1213.	1.3	22
49	Direct structural insight into the substrate-shuttling mechanism of yeast fatty acid synthase by electron cryomicroscopy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 9164-9169.	3.3	62
50	Ultrathin conductive carbon nanomembranes as support films for structural analysis of biological specimens. <i>Physical Chemistry Chemical Physics</i> , 2010, 12, 4345.	1.3	14
51	Supramolecular organization of protein complexes in the mitochondrial inner membrane. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2009, 1793, 117-124.	1.9	130
52	The c13 Ring from a Thermoalkaliphilic ATP Synthase Reveals an Extended Diameter Due to a Special Structural Region. <i>Journal of Molecular Biology</i> , 2009, 388, 611-618.	2.0	79
53	Three-dimensional Structure of A1A0 ATP Synthase from the Hyperthermophilic Archaeon <i>Pyrococcus furiosus</i> by Electron Microscopy. <i>Journal of Biological Chemistry</i> , 2009, 284, 10110-10119.	1.6	68
54	An intermediate step in the evolution of ATPases â€” a hybrid F _o â€”V _o rotor in a bacterial Na ⁺ F ₁ F _o ATP synthase. <i>FEBS Journal</i> , 2008, 275, 1999-2007.	2.2	48

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55	Inhibition of the fungal fatty acid synthase type I multienzyme complex. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 12803-12808.	3.3	111
56	Proteorhodopsin: Characterisation of 2D crystals by electron microscopy and solid state NMR. Biochimica Et Biophysica Acta - Biomembranes, 2007, 1768, 3012-3019.	1.4	41
57	Three-Dimensional Structure of the Respiratory Chain Supercomplex I ₁ III ₂ IV ₁ from Bovine Heart Mitochondria. Biochemistry, 2007, 46, 12579-12585.	1.2	140
58	The Structural Basis for Unidirectional Rotation of Thermoalkaliphilic F ₁ -ATPase. Structure, 2007, 15, 904-914.	1.6	48
59	Structural Investigations of the Membrane-Embedded Rotor Ring of the F-ATPase from Clostridium paradoxum. Journal of Bacteriology, 2006, 188, 7759-7764.	1.0	59
60	Architecture of Active Mammalian Respiratory Chain Supercomplexes. Journal of Biological Chemistry, 2006, 281, 15370-15375.	1.6	234
61	The c 15 ring of the Spirulina platensis F ₁ /F ₀ ATP synthase: F ₁ /F ₀ symmetry mismatch is not obligatory. EMBO Reports, 2005, 6, 1040-1044.	2.0	173
62	Evidence for Structural Integrity in the Undecameric c-Rings Isolated from Sodium ATP Synthases. Journal of Molecular Biology, 2003, 325, 389-397.	2.0	80
63	Molecular Architecture of the Undecameric Rotor of a Bacterial Na ⁺ -ATP Synthase. Journal of Molecular Biology, 2002, 321, 307-316.	2.0	118
64	Projection structure of the monomeric porin OmpG at 6 Å resolution. Journal of Molecular Biology, 2001, 305, 71-77.	2.0	41
65	Parameters affecting specimen flatness of two-dimensional crystals for electron crystallography. Ultramicroscopy, 2000, 85, 123-129.	0.8	45
66	Structure of the bacteriorhodopsin mutant F219L N intermediate revealed by electron crystallography. EMBO Journal, 2000, 19, 2152-2160.	3.5	125
67	A Three-Dimensional Difference Map of the N Intermediate in the Bacteriorhodopsin Photocycle: Part of the F Helix Tilts in the M to N Transition. Biochemistry, 1996, 35, 5870-5878.	1.2	126
68	Specimen flatness of glucose-embedded biological materials for electron crystallography is affected significantly by the choice of carbon evaporation stock. Ultramicroscopy, 1994, 55, 1-5.	0.8	19
69	Two progressive substrates of the M-intermediate can be identified in glucose-embedded, wild-type bacteriorhodopsin. Biophysical Journal, 1994, 67, 1173-1178.	0.2	29
70	The bacteriorhodopsin photocycle: direct structural study of two substrates of the M-intermediate. Biophysical Journal, 1994, 67, 1179-1186.	0.2	55
71	Electron microscopic analysis and structural characterization of novel NADP(H)-containing methanol: N,N'-dimethyl-4-nitrosoaniline oxidoreductases from the gram-positive methylotrophic bacteria Amycolatopsis methanolica and Mycobacterium gastris MB19. Journal of Bacteriology, 1993, 175, 1814-1822.	1.0	52
72	Purification and characterization of an oxygen-labile, NAD-dependent alcohol dehydrogenase from Desulfovibrio gigas. Journal of Bacteriology, 1993, 175, 2859-2863.	1.0	50

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73	Determination of the molecular packing of three-dimensional crystals of alcohol oxidase from <i>Pichia pastoris</i> by electron microscopy and image analysis. <i>Journal of Structural Biology</i> , 1992, 109, 78-85.	1.3	3
74	Architecture of peroxisomal alcohol oxidase crystals from the methylotrophic yeast <i>Hansenula polymorpha</i> as deduced by electron microscopy. <i>Journal of Bacteriology</i> , 1992, 174, 5391-5399.	1.0	18
75	In vivo crystal formation in <i>Escherichia coli</i> of an over-expressed soluble form of penicillin-binding protein 5. <i>FEMS Microbiology Letters</i> , 1992, 99, 117-123.	0.7	1
76	Electron microscopy and image analysis of two-dimensional crystals and single molecules of alcohol oxidase from <i>Hansenula polymorpha</i> . <i>BBA - Proteins and Proteomics</i> , 1990, 1038, 74-79.	2.1	46