

# Janet Vonck

## List of Publications by Year in descending order

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76  
papers

4,820  
citations

70961

41  
h-index

98622

67  
g-index

86  
all docs

86  
docs citations

86  
times ranked

4724  
citing authors

#	ARTICLE	IF	CITATIONS
1	Structure, mechanism, and regulation of the chloroplast ATP synthase. <i>Science</i> , 2018, 360, .	6.0	308
2	Horizontal membrane-intrinsic $\pm$ -helices in the stator a-subunit of an F-type ATP synthase. <i>Nature</i> , 2015, 521, 237-240.	13.7	293
3	Architecture of Active Mammalian Respiratory Chain Supercomplexes. <i>Journal of Biological Chemistry</i> , 2006, 281, 15370-15375.	1.6	234
4	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
5	The c 15 ring of the <i>Spirulina platensis</i> F <sub>1</sub> /F <sub>0</sub> ATP synthase: F <sub>1</sub> /F <sub>0</sub> symmetry mismatch is not obligatory. <i>EMBO Reports</i> , 2005, 6, 1040-1044.	2.0	173
6	Three-Dimensional Structure of the Respiratory Chain Supercomplex I <sub>3</sub> II <sub>2</sub> IV <sub>1</sub> from Bovine Heart Mitochondria. <i>Biochemistry</i> , 2007, 46, 12579-12585.	1.2	140
7	Atomic model of the F <sub>420</sub> -reducing [NiFe] hydrogenase by electron cryo-microscopy using a direct electron detector. <i>ELife</i> , 2014, 3, e01963.	2.8	132
8	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
9	Functional asymmetry and electron flow in the bovine respirasome. <i>ELife</i> , 2016, 5, .	2.8	130
10	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. <i>Biochemistry</i> , 1996, 35, 5870-5878.	1.2	126
11	Structure of the bacteriorhodopsin mutant F219L N intermediate revealed by electron crystallography. <i>EMBO Journal</i> , 2000, 19, 2152-2160.	3.5	125
12	Mitochondrial Respiratory Chain Complexes. <i>Sub-Cellular Biochemistry</i> , 2018, 87, 167-227.	1.0	122
13	Molecular Architecture of the Undecameric Rotor of a Bacterial Na <sup>+</sup> -ATP Synthase. <i>Journal of Molecular Biology</i> , 2002, 321, 307-316.	2.0	118
14	Inhibition of the fungal fatty acid synthase type I multienzyme complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 12803-12808.	3.3	111
15	High-resolution cryo-EM structures of respiratory complex I: Mechanism, assembly, and disease. <i>Science Advances</i> , 2019, 5, eaax9484.	4.7	109
16	Cryo-EM structure of respiratory complex I at work. <i>ELife</i> , 2018, 7, .	2.8	98
17	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
18	Structure and in situ organisation of the <i>Pyrococcus furiosus</i> archaeellum machinery. <i>ELife</i> , 2017, 6, .	2.8	83

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19	Cell-Free Expression and Assembly of ATP Synthase. <i>Journal of Molecular Biology</i> , 2011, 413, 593-603.	2.0	81
20	Evidence for Structural Integrity in the Undecameric c-Rings Isolated from Sodium ATP Synthases. <i>Journal of Molecular Biology</i> , 2003, 325, 389-397.	2.0	80
21	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
22	Respiratory complex I " structure, mechanism and evolution. <i>Current Opinion in Structural Biology</i> , 2020, 63, 1-9.	2.6	79
23	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
24	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
25	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
26	Regioselective " Carboxylation of Catechols with a Prenylated Flavin Dependent Decarboxylase. <i>Angewandte Chemie - International Edition</i> , 2017, 56, 13893-13897.	7.2	64
27	Structure of the SecY Complex Unlocked by a Preprotein Mimic. <i>Cell Reports</i> , 2012, 1, 21-28.	2.9	63
28	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
29	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
30	Structural basis of proton-coupled potassium transport in the KUP family. <i>Nature Communications</i> , 2020, 11, 626.	5.8	60
31	Structural Investigations of the Membrane-Embedded Rotor Ring of the F-ATPase from <i>Clostridium paradoxum</i> . <i>Journal of Bacteriology</i> , 2006, 188, 7759-7764.	1.0	59
32	The bacteriorhodopsin photocycle: direct structural study of two substrates of the M-intermediate. <i>Biophysical Journal</i> , 1994, 67, 1179-1186.	0.2	55
33	Structure of the archaeal Na <sup>+</sup> /H <sup>+</sup> antiporter NhaP1 and functional role of transmembrane helix 1. <i>EMBO Journal</i> , 2011, 30, 439-449.	3.5	54
34	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
35	Electron microscopic analysis and structural characterization of novel NADP(H)-containing methanol: N,N'-dimethyl-4-nitrosoaniline oxidoreductases from the gram-positive methylotrophic bacteria <i>Amycolatopsis methanolica</i> and <i>Mycobacterium gastris</i> MB19. <i>Journal of Bacteriology</i> , 1993, 175, 1814-1822.	1.0	52
36	Purification and characterization of an oxygen-labile, NAD-dependent alcohol dehydrogenase from <i>Desulfovibrio gigas</i> . <i>Journal of Bacteriology</i> , 1993, 175, 2859-2863.	1.0	50

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37	The Structural Basis for Unidirectional Rotation of Thermoalkaliphilic F <sub>1</sub> -ATPase. <i>Structure</i> , 2007, 15, 904-914.	1.6	48
38	An intermediate step in the evolution of ATPases â€” a hybrid F <sub>0</sub> â€”V <sub>0</sub> rotor in a bacterial Na <sup>+</sup> F <sub>1</sub> F <sub>0</sub> ATP synthase. <i>FEBS Journal</i> , 2008, 275, 1999-2007.	2.2	48
39	The nucleotideâ€”dependent interaction of FlaH and FlaI is essential for assembly and function of the archaeum motor. <i>Molecular Microbiology</i> , 2016, 99, 674-685.	1.2	47
40	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
41	Parameters affecting specimen flatness of two-dimensional crystals for electron crystallography. <i>Ultramicroscopy</i> , 2000, 85, 123-129.	0.8	45
42	Projection structure of the monomeric porin OmpG at 6 Å resolution. <i>Journal of Molecular Biology</i> , 2001, 305, 71-77.	2.0	41
43	Proteorhodopsin: Characterisation of 2D crystals by electron microscopy and solid state NMR. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2007, 1768, 3012-3019.	1.4	41
44	The obligate respiratory supercomplex from Actinobacteria. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2016, 1857, 1705-1714.	0.5	41
45	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
46	Structural basis for energy transduction by respiratory alternative complex III. <i>Nature Communications</i> , 2018, 9, 1728.	5.8	38
47	FlaX, A Unique Component of the Crenarchaeal Archaeum, 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
48	Two progressive substrates of the M-intermediate can be identified in glucose-embedded, wild-type bacteriorhodopsin. <i>Biophysical Journal</i> , 1994, 67, 1173-1178.	0.2	29
49	Structural study on the architecture of the bacterial ATP synthase F <sub>0</sub> motor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, E2050-6.	3.3	29
50	Cryoâ€”EM structure of fatty acid synthase (FAS) from <i>Rhodospiridium toruloides</i> provides insights into the evolutionary development of fungal FAS. <i>Protein Science</i> , 2015, 24, 987-995.	3.1	28
51	Structure of Alcohol Oxidase from <i>Pichia pastoris</i> by Cryo-Electron Microscopy. <i>PLoS ONE</i> , 2016, 11, e0159476.	1.1	28
52	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
53	Cryo-EM structure of the bifunctional secretin complex of <i>Thermus thermophilus</i> . <i>ELife</i> , 2017, 6, .	2.8	27
54	Advances in high-resolution cryo-EM of oligomeric enzymes. <i>Current Opinion in Structural Biology</i> , 2017, 46, 48-54.	2.6	26

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55	Unusual N-terminal $\beta$ -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
56	Helical jackknives control the gates of the double-pore K <sup>+</sup> uptake system KtrAB. <i>ELife</i> , 2017, 6, .	2.8	23
57	Prion Protein Amyloid Formation Involves Structural Rearrangements in the C-terminal Domain. <i>ChemBioChem</i> , 2010, 11, 1208-1213.	1.3	22
58	A bacterial hydrogen-dependent CO <sub>2</sub> reductase forms filamentous structures. <i>FEBS Journal</i> , 2016, 283, 1311-1322.	2.2	22
59	Specimen flatness of glucose-embedded biological materials for electron crystallography is affected significantly by the choice of carbon evaporation stock. <i>Ultramicroscopy</i> , 1994, 55, 1-5.	0.8	19
60	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
61	Analysis of the co-translational assembly of the fungal fatty acid synthase (FAS). <i>Scientific Reports</i> , 2020, 10, 895.	1.6	18
62	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
63	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
64	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
65	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
66	Respiratory supercomplexes III <sub>2</sub> IV <sub>2</sub> come into focus. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 87-89.	3.6	10
67	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
68	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
69	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
70	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
71	Supramolecular Organization of the Respiratory Chain. , 2012, , 247-277.		2
72	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

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73	Production of fully assembled and active Aquifex aeolicus F1FO ATP synthase in Escherichia coli. Biochimica Et Biophysica Acta - General Subjects, 2014, 1840, 34-40.	1.1	1
74	Using 2D Crystals to Analyze the Structure of Membrane Proteins. Methods in Molecular Biology, 2013, 1033, 47-65.	0.4	1
75	The molybdenum storage protein forms and deposits distinct polynuclear tungsten oxygen aggregates. Journal of Inorganic Biochemistry, 2022, 234, 111904.	1.5	1
76	Choice and Maintenance of Equipment for Electron Crystallography. Methods in Molecular Biology, 2013, 955, 331-351.	0.4	0