

# Marin Van Heel

## List of Publications by Year in descending order

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82  
papers

9,598  
citations

66250

44  
h-index

93651

72  
g-index

83  
all docs

83  
docs citations

83  
times ranked

7270  
citing authors

#	ARTICLE	IF	CITATIONS
1	A New Generation of the IMAGIC Image Processing System. <i>Journal of Structural Biology</i> , 1996, 116, 17-24.	1.3	1,182
2	Fourier shell correlation threshold criteria. <i>Journal of Structural Biology</i> , 2005, 151, 250-262.	1.3	682
3	Use of multivariate statistics in analysing the images of biological macromolecules. <i>Ultramicroscopy</i> , 1981, 6, 187-194.	0.8	610
4	Single-particle electron cryo-microscopy: towards atomic resolution. <i>Quarterly Reviews of Biophysics</i> , 2000, 33, 307-369.	2.4	535
5	Angular reconstitution: A posteriori assignment of projection directions for 3D reconstruction. <i>Ultramicroscopy</i> , 1987, 21, 111-123.	0.8	520
6	Structure of the AAA ATPase p97. <i>Molecular Cell</i> , 2000, 6, 1473-1484.	4.5	394
7	Visualization of elongation factor Tu on the Escherichia coli ribosome. <i>Nature</i> , 1997, 389, 403-406.	13.7	342
8	Similarity measures between images. <i>Ultramicroscopy</i> , 1987, 21, 95-100.	0.8	331
9	Large-Scale Movement of Elongation Factor G and Extensive Conformational Change of the Ribosome during Translocation. <i>Cell</i> , 2000, 100, 301-309.	13.5	294
10	Multivariate statistical classification of noisy images (randomly oriented biological) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 382 Td (macro	0.8	254
11	Arrangement of tRNAs in Pre- and Posttranslocational Ribosomes Revealed by Electron Cryomicroscopy. <i>Cell</i> , 1997, 88, 19-28.	13.5	247
12	The 70S Escherichia coli ribosome at 23 Å resolution: fitting the ribosomal RNA. <i>Structure</i> , 1995, 3, 815-821.	1.6	237
13	IMAGIC: A fast, flexible and friendly image analysis software system. <i>Ultramicroscopy</i> , 1981, 7, 113-129.	0.8	211
14	Structure of keyhole limpet hemocyanin type 1 (KLH1) at 15 Å... resolution by electron cryomicroscopy and angular reconstitution â€ 1 â€ This article is dedicated to the memory of Anneke van Heel. 1Edited by M.F. Moody. <i>Journal of Molecular Biology</i> , 1997, 271, 417-437.	2.0	202
15	Structure of the Escherichia coli ribosomal termination complex with release factor 2. <i>Nature</i> , 2003, 421, 90-94.	13.7	191
16	Electron cryomicroscopy and angular reconstitution used to visualize the skeletal muscle calcium release channel. <i>Nature Structural Biology</i> , 1995, 2, 18-24.	9.7	185
17	3D map of the plant photosystem II supercomplex obtained by cryoelectron microscopy and single particle analysis. <i>Nature Structural Biology</i> , 2000, 7, 44-47.	9.7	172
18	Two structural configurations of the skeletal muscle calcium release channel. <i>Nature Structural and Molecular Biology</i> , 1996, 3, 547-552.	3.6	161

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19	Structure of lactococcal phage p2 baseplate and its mechanism of activation. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 6852-6857.	3.3	143
20	Visualization of release factor 3 on the ribosome during termination of protein synthesis. Nature, 2004, 427, 862-865.	13.7	131
21	Structure of alpha-latrotoxin oligomers reveals that divalent cation-dependent tetramers form membrane pores. Nature Structural Biology, 2000, 7, 48-53.	9.7	128
22	The Escherichia coli large ribosomal subunit at 7.5 Å... resolution. Structure, 1999, 7, 1575-1583.	1.6	127
23	Structure of a viral DNA gatekeeper at 10 Å resolution by cryo-electron microscopy. EMBO Journal, 2003, 22, 1255-1262.	3.5	124
24	Structure of Lumbricus terrestris Hemoglobin at 30 Å... Resolution Determined Using Angular Reconstitution. Journal of Structural Biology, 1995, 114, 28-40.	1.3	119
25	Hexameric ring structure of the full-length archaeal MCM protein complex. EMBO Reports, 2003, 4, 1079-1083.	2.0	112
26	Ribosome interactions of aminoacyl-tRNA and elongation factor Tu in the codon-recognition complex. Nature Structural Biology, 2002, 9, 849-54.	9.7	108
27	The 3D arrangement of the 23 S and 5 S rRNA in the Escherichia coli 50 S ribosomal subunit based on a cryo-electron microscopic reconstruction at 7.5 Å... resolution. Journal of Molecular Biology, 2000, 298, 35-59.	2.0	106
28	[2] Statistical image analysis of electron micrographs of ribosomal subunits. Methods in Enzymology, 1988, 164, 35-49.	0.4	93
29	Correlation functions revisited. Ultramicroscopy, 1992, 46, 307-316.	0.8	91
30	Structure of influenza haemagglutinin at neutral and at fusogenic pH by electron cryo-microscopy. FEBS Letters, 1999, 463, 255-259.	1.3	90
31	Invariant classification of molecular views in electron micrographs. Ultramicroscopy, 1990, 32, 255-264.	0.8	85
32	A new model for the three-dimensional folding of Escherichia coli 16 s ribosomal RNA. III . The topography of the functional centre 1 . Paper II in this series is an accompanying paper, Mueller & Brimacombe (1997b). Edited by D. E. Draper. Journal of Molecular Biology, 1997, 271, 566-587.	2.0	76
33	A new family of powerful multivariate statistical sequence analysis techniques. Journal of Molecular Biology, 1991, 220, 877-887.	2.0	68
34	Correlation of the expansion segments in mammalian rRNA with the fine structure of the 80 s ribosome; a cryoelectron microscopic reconstruction of the rabbit reticulocyte ribosome at 21 Å resolution. Journal of Molecular Biology, 1998, 279, 403-421.	2.0	62
35	Structure of the 13-fold symmetric portal protein of bacteriophage SPP1. Nature Structural Biology, 1999, 6, 842-846.	9.7	62
36	Detection of objects in quantum-noise-limited images. Ultramicroscopy, 1982, 7, 331-341.	0.8	61

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37	Hexameric ring structure of the full-length archaeal MCM protein complex. EMBO Reports, 2003, 4, 1079-1083.	2.0	61
38	Finding trimeric HIV-1 envelope glycoproteins in random noise. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E4175-7.	3.3	56
39	Structure and Molecular Assignment of Lactococcal Phage TP901-1 Baseplate. Journal of Biological Chemistry, 2010, 285, 39079-39086.	1.6	55
40	Visualizing a Complete Siphoviridae Member by Single-Particle Electron Microscopy: the Structure of Lactococcal Phage TP901-1. Journal of Virology, 2013, 87, 1061-1068.	1.5	55
41	Classification of image data in conjugate representation spaces. Journal of the Optical Society of America A: Optics and Image Science, and Vision, 1990, 7, 601.	0.8	53
42	Multivariate Analysis of Single-Molecule Spectra: Surpassing Spectral Diffusion. Physical Review Letters, 2005, 94, 195501.	2.9	53
43	The 80S rat liver ribosome at 25 Å resolution by electron cryomicroscopy and angular reconstitution. Structure, 1998, 6, 389-399.	1.6	49
44	Structural studies of the archaeal MCM complex in different functional states. Journal of Structural Biology, 2006, 156, 210-219.	1.3	46
45	Stacked bilayer helices: a new structural organization of amphiphilic molecules. Ultramicroscopy, 1996, 62, 133-139.	0.8	43
46	Structure of the ATP synthase from chloroplasts studied by electron microscopy and image processing. Biochimica Et Biophysica Acta - Bioenergetics, 1988, 933, 365-371.	0.5	42
47	Elucidating the medium-resolution structure of ribosomal particles: an interplay between electron cryo-microscopy and X-ray crystallography. Structure, 1999, 7, 931-941.	1.6	41
48	Tetramerisation of Î±-latrotoxin by divalent cations is responsible for toxin-induced non-vesicular release and contributes to the Ca <sup>2+</sup> -dependent vesicular exocytosis from synaptosomes. Biochimie, 2000, 82, 453-468.	1.3	41
49	Voltage-gated K <sup>+</sup> Channel from Mammalian Brain: 3D Structure at 18Å.. of the Complete (Î±) <sub>4</sub> (Î²) <sub>4</sub> Complex. Journal of Molecular Biology, 2003, 326, 1005-1012.	2.0	39
50	Molecular shape of Lumbricus terrestris erythrocrucorin studied by electron microscopy and image analysis. BBA - Proteins and Proteomics, 1988, 957, 370-379.	2.1	36
51	Imaging protein three-dimensional nanocrystals with cryo-EM. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 852-859.	2.5	33
52	Unveiling ribosomal structures: the final phases. Current Opinion in Structural Biology, 2000, 10, 259-264.	2.6	30
53	Single-particle cryo-EM using alignment by classification (ABC): the structure of <i>Lumbricus terrestris</i> haemoglobin. IUCr, 2017, 4, 678-694.	1.0	30
54	Invariant recognition of molecular projections in vitreous ice preparations. Ultramicroscopy, 1992, 45, 15-22.	0.8	29

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55	Quaternary structure of multihexameric arthropod hemocyanins. <i>Micron</i> , 1994, 25, 387-418.	1.1	29
56	Characteristic views of prokaryotic 50S ribosomal subunits. <i>Journal of Molecular Evolution</i> , 1987, 26, 347-357.	0.8	24
57	Three-dimensional reconstruction of a human metaphase chromosome from electron micrographs. <i>Chromosoma</i> , 1987, 95, 366-374.	1.0	24
58	Stereographic representation of three-dimensional density distributions. <i>Ultramicroscopy</i> , 1983, 11, 307-313.	0.8	23
59	Multivariate analysis of single unit cells in electron crystallography. <i>Ultramicroscopy</i> , 1998, 74, 179-199.	0.8	23
60	A posteriori correction of camera characteristics from large image data sets. <i>Scientific Reports</i> , 2015, 5, 10317.	1.6	22
61	The SPP1 connection. <i>FEMS Microbiology Reviews</i> , 1995, 17, 47-56.	3.9	20
62	Three-Dimensional Structure of Keyhole Limpet Hemocyanin by Cryoelectron Microscopy and Angular Reconstitution. <i>Journal of Structural Biology</i> , 1995, 115, 226-232.	1.3	20
63	Packing of the 30 nm chromatin fiber in the human metaphase chromosome. <i>Chromosoma</i> , 1988, 97, 159-163.	1.0	16
64	A fast algorithm for transposing large multidimensional image data sets. <i>Ultramicroscopy</i> , 1991, 38, 75-83.	0.8	14
65	Direct localization by cryo-electron microscopy of secondary structural elements in <i>Escherichia coli</i> 23 S rRNA which differ from the corresponding regions in <i>Haloarcula marismortui</i> Edited by D. E. Draper. <i>Journal of Molecular Biology</i> , 2001, 307, 1341-1349.	2.0	13
66	Magnification variations due to illumination curvature and object defocus in transmission electron microscopy. <i>Optics Express</i> , 2005, 13, 9085.	1.7	7
67	Direct 3D Reconstruction from Projections with Initially Unknown Angles. , 1985, , 649-653.		7
68	Electron cryomicroscopy and digital image processing of lipoprotein(a). <i>Chemistry and Physics of Lipids</i> , 1994, 67-68, 81-89.	1.5	5
69	FINDING THE CHARACTERISTIC VIEWS OF MACROMOLECULES IN EXTREMELY NOISY ELECTRON MICROGRAPHS. , 1986, , 291-299.		5
70	Determination of <i>Escherichia coli</i> RNA Polymerase Structure by Single Particle Cryoelectron Microscopy. <i>Methods in Enzymology</i> , 2003, 370, 24-42.	0.4	4
71	Conformational Changes of <i>Escherichia coli</i> $\sigma$ <sup>54</sup> -RNA-Polymerase upon Closed Promoter Complex Formation. <i>Journal of Molecular Biology</i> , 2005, 354, 201-205.	2.0	4
72	DIRECT 3D RECONSTRUCTION FROM PROJECTIONS WITH INITIALLY UNKNOWN ANGLES. , 1986, , 279-288.		3

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73	The Skeletal Muscle Calcium-Release Channel Visualised By Electron Cryomicroscopy and Angular Reconstitution. , 1998, , 23-46.		2
74	Oblique sampling of projections for direct three-dimensional reconstruction. Computer Vision, Graphics, and Image Processing, 1987, 38, 81-89.	1.1	1
75	Addendum to "angular reconstitution: A posteriori assignment of projection directions for 3D reconstruction" Ultramicroscopy, 1988, 24, 62.	0.8	1
76	Visualization of the Translational Elongation Cycle by Cryo-Electron Microscopy. , 0, , 35-44.		1
77	Structure analysis of biological macromolecules using pattern recognition. Ultramicroscopy, 1984, 15, 379-380.	0.8	0
78	Ribosome structure and function by single-particle cryo-EM. Biochemical Society Transactions, 2002, 30, A17-A17.	1.6	0
79	Advance Techniques in Biophysics. , 2017, , 245-274.		0
80	Single Molecule Electron Crystallography. , 1987, , 89-99.		0
81	Angular reconstitution of ice embedded macromolecules with arbitrary point group symmetry. Proceedings Annual Meeting Electron Microscopy Society of America, 1994, 52, 90-91.	0.0	0
82	3-D structure of single macromolecules at 15Å... resolution by cryo-microscopy and angular reconstitution. Proceedings Annual Meeting Electron Microscopy Society of America, 1995, 53, 838-839.	0.0	0