

Edward Morris

List of Publications by Year in descending order

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80
papers

5,465
citations

81743

39
h-index

82410

72
g-index

84
all docs

84
docs citations

84
times ranked

5766
citing authors

#	ARTICLE	IF	CITATIONS
1	Concerted Loading of Mcm2â€™7 Double Hexamers around DNA during DNA Replication Origin Licensing. <i>Cell</i> , 2009, 139, 719-730.	13.5	560
2	Three-dimensional structure of the plant photosystem II reaction centre at 8â€™Å... resolution. <i>Nature</i> , 1998, 396, 283-286.	13.7	340
3	A new look at thin filament regulation in vertebrate skeletal muscle. <i>FASEB Journal</i> , 1998, 12, 761-771.	0.2	210
4	Molecular Model of the Human 26S Proteasome. <i>Molecular Cell</i> , 2012, 46, 54-66.	4.5	195
5	Structures of APC/CCdh1 with substrates identify Cdh1 and Apc10 as the D-box co-receptor. <i>Nature</i> , 2011, 470, 274-278.	13.7	176
6	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
7	Two-dimensional structure of plant photosystem II at 8-Å... resolution. <i>Nature</i> , 1997, 389, 522-526.	13.7	159
8	Phosphatidylglycerol Is Involved in the Dimerization of Photosystem II. <i>Journal of Biological Chemistry</i> , 2000, 275, 6509-6514.	1.6	158
9	Atomic model of the human cardiac muscle myosin filament. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 318-323.	3.3	153
10	Structural basis for the subunit assembly of the anaphase-promoting complex. <i>Nature</i> , 2011, 470, 227-232.	13.7	150
11	Structural Basis for a Reciprocal Regulation between SCF and CSN. <i>Cell Reports</i> , 2012, 2, 616-627.	2.9	145
12	IP3 receptors: the search for structure. <i>Trends in Biochemical Sciences</i> , 2004, 29, 210-219.	3.7	144
13	Human Condensin I and II Drive Extensive ATP-Dependent Compaction of Nucleosome-Bound DNA. <i>Molecular Cell</i> , 2020, 79, 99-114.e9.	4.5	129
14	The structure, function and dynamics of photosystem two. <i>Physiologia Plantarum</i> , 1997, 100, 817-827.	2.6	127
15	Revealing the structure of the oxygen-evolving core dimer of photosystem II by cryoelectron crystallography. <i>Nature Structural Biology</i> , 1999, 6, 560-564.	9.7	123
16	Structural basis of RNA polymerase III transcription initiation. <i>Nature</i> , 2018, 553, 301-306.	13.7	123
17	Origin Licensing Requires ATP Binding and Hydrolysis by the MCM Replicative Helicase. <i>Molecular Cell</i> , 2014, 55, 666-677.	4.5	104
18	Three-dimensional reconstruction of the <i>Shigella</i> T3SS transmembrane regions reveals 12-fold symmetry and novel features throughout. <i>Nature Structural and Molecular Biology</i> , 2009, 16, 477-485.	3.6	100

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19	3D structure of EspA filaments from enteropathogenic Escherichia coli. <i>Molecular Microbiology</i> , 2003, 49, 301-308.	1.2	91
20	Visualization of a DNA-PK/PARP1 complex. <i>Nucleic Acids Research</i> , 2012, 40, 4168-4177.	6.5	89
21	Three-Dimensional Structure of the Photosystem II Core Dimer of Higher Plants Determined by Electron Microscopy. <i>Journal of Structural Biology</i> , 2001, 135, 262-269.	1.3	88
22	Domain organization of the type 1 inositol 1,4,5-trisphosphate receptor as revealed by single-particle analysis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 3936-3941.	3.3	88
23	Structure of the Human 26S Proteasome. <i>Journal of Biological Chemistry</i> , 2008, 283, 23305-23314.	1.6	86
24	Oligomeric structure of $\hat{1}\pm$ -calmodulin-dependent protein kinase II11 Edited by A. R. Fersht. <i>Journal of Molecular Biology</i> , 2001, 308, 1-8.	2.0	81
25	Subunit positioning and transmembrane helix organisation in the core dimer of photosystem II. <i>FEBS Letters</i> , 2001, 504, 142-151.	1.3	80
26	Prereplicative complexes assembled in vitro support origin-dependent and independent DNA replication. <i>EMBO Journal</i> , 2014, 33, 605-620.	3.5	76
27	Tankyrase Requires SAM Domain-Dependent Polymerization to Support Wnt- $\hat{1}^2$ -Catenin Signaling. <i>Molecular Cell</i> , 2016, 63, 498-513.	4.5	72
28	Structural Insights into the COP9 Signalosome and Its Common Architecture with the 26S Proteasome Lid and eIF3. <i>Structure</i> , 2010, 18, 518-527.	1.6	68
29	Localisation of the PsbH subunit in photosystem II: a new approach using labelling of his-tags with a Ni ²⁺ -NTA gold cluster and single particle analysis. <i>Journal of Molecular Biology</i> , 2001, 312, 371-379.	2.0	66
30	The three-dimensional structure of a photosystem II core complex determined by electron crystallography. <i>Structure</i> , 1997, 5, 837-849.	1.6	62
31	Structural Analysis of the Photosystem I Supercomplex of Cyanobacteria Induced by Iron Deficiencyâ€¢. <i>Biochemistry</i> , 2003, 42, 3180-3188.	1.2	60
32	The Structure of the 26S Proteasome Subunit Rpn2 Reveals Its PC Repeat Domain as a Closed Toroid of Two Concentric $\hat{1}\pm$ -Helical Rings. <i>Structure</i> , 2012, 20, 513-521.	1.6	60
33	Biochemical and structural analyses of a higher plant photosystem II supercomplex of a photosystem II-less mutant of barley. <i>FEBS Journal</i> , 2006, 273, 4616-4630.	2.2	58
34	Nanostructures from Synthetic Genetic Polymers. <i>ChemBioChem</i> , 2016, 17, 1107-1110.	1.3	57
35	The 4-stranded helical arrangement of myosin heads on insect (<i>Lethocerus</i>) flight muscle thick filaments. <i>Journal of Structural Biology</i> , 1991, 107, 237-249.	1.3	53
36	Subunit positioning in photosystem II revisited. <i>Trends in Biochemical Sciences</i> , 1999, 24, 43-45.	3.7	52

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37	RET Recognition of GDNF-GFR α 1 Ligand by a Composite Binding Site Promotes Membrane-Proximal Self-Association. <i>Cell Reports</i> , 2014, 8, 1894-1904.	2.9	51
38	Structure of human RNA polymerase III. <i>Nature Communications</i> , 2020, 11, 6409.	5.8	50
39	Molecular Characterization of the Inositol 1,4,5-Trisphosphate Receptor Pore-forming Segment. <i>Journal of Biological Chemistry</i> , 2008, 283, 2939-2948.	1.6	49
40	Recombinant expression, reconstitution and structure of human anaphase-promoting complex (APC/C). <i>Biochemical Journal</i> , 2013, 449, 365-371.	1.7	48
41	Cryo-EM reveals the conformation of a substrate analogue in the human 20S proteasome core. <i>Nature Communications</i> , 2015, 6, 7573.	5.8	40
42	Structural basis of Cullin 2 RING E3 ligase regulation by the COP9 signalosome. <i>Nature Communications</i> , 2019, 10, 3814.	5.8	40
43	Interaction of the allophycocyanin core complex with photosystem II Dedicated to the memory of Nobel Laureate, Lord George Porter FRSC FRS OM.. <i>Photochemical and Photobiological Sciences</i> , 2003, 2, 536.	1.6	37
44	Myosin filament 3D structure in mammalian cardiac muscle. <i>Journal of Structural Biology</i> , 2008, 163, 117-126.	1.3	36
45	Superhelical Architecture of the Myosin Filament-Linking Protein Myomesin with Unusual Elastic Properties. <i>PLoS Biology</i> , 2012, 10, e1001261.	2.6	35
46	3D structure of relaxed fish muscle myosin filaments by single particle analysis. <i>Journal of Structural Biology</i> , 2006, 155, 202-217.	1.3	32
47	Structure and Orientation of Troponin in the Thin Filament. <i>Journal of Biological Chemistry</i> , 2009, 284, 15007-15015.	1.6	31
48	Three-Dimensional Structure of Vertebrate Muscle Z-Band: The Small-Square Lattice Z-Band in Rat Cardiac Muscle. <i>Journal of Molecular Biology</i> , 2015, 427, 3527-3537.	2.0	29
49	Myosin and Actin Filaments in Muscle: Structures and Interactions. <i>Sub-Cellular Biochemistry</i> , 2017, 82, 319-371.	1.0	28
50	Single particle analysis of filamentous and highly elongated macromolecular assemblies. <i>Journal of Structural Biology</i> , 2004, 148, 236-250.	1.3	26
51	The 7-stranded structure of relaxed scallop muscle myosin filaments: Support for a common head configuration in myosin-regulated muscles. <i>Journal of Structural Biology</i> , 2009, 166, 183-194.	1.3	26
52	The Structure of F-actin. <i>Journal of Molecular Biology</i> , 1994, 240, 138-154.	2.0	25
53	Identification of Functionally Critical Residues in the Channel Domain of Inositol Trisphosphate Receptors. <i>Journal of Biological Chemistry</i> , 2012, 287, 43674-43684.	1.6	25
54	Cryo-EM structures of the XPF-ERCC1 endonuclease reveal how DNA-junction engagement disrupts an auto-inhibited conformation. <i>Nature Communications</i> , 2020, 11, 1120.	5.8	24

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55	Relaxed and active thin filament structures; a new structural basis for the regulatory mechanism. <i>Journal of Structural Biology</i> , 2017, 197, 365-371.	1.3	23
56	Nse5/6 is a negative regulator of the ATPase activity of the Smc5/6 complex. <i>Nucleic Acids Research</i> , 2021, 49, 4534-4549.	6.5	22
57	Three-Dimensional Structure of the M-region (Bare Zone) of Vertebrate Striated Muscle Myosin Filaments by Single-Particle Analysis. <i>Journal of Molecular Biology</i> , 2010, 403, 763-776.	2.0	21
58	Single Particle Analysis: A new approach to solving the 3D structure of myosin filaments. <i>Journal of Muscle Research and Cell Motility</i> , 2004, 25, 635-644.	0.9	20
59	Evidence for a remodelling of DNA-PK upon autophosphorylation from electron microscopy studies. <i>Nucleic Acids Research</i> , 2011, 39, 5757-5767.	6.5	20
60	Three-dimensional structure of recombinant type I inositol 1,4,5-trisphosphate receptor. <i>Biochemical Journal</i> , 2010, 428, 483-489.	1.7	19
61	Three-dimensional structure of the basketweave Z-band in midshipman fish sonic muscle. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 15534-15539.	3.3	19
62	Structural Insights into the Mechanism of Phosphoregulation of the Retinoblastoma Protein. <i>PLoS ONE</i> , 2013, 8, e58463.	1.1	14
63	Calcium-dependent Conformational Changes in Inositol Trisphosphate Receptors. <i>Journal of Biological Chemistry</i> , 2010, 285, 25085-25093.	1.6	13
64	Organisation and Properties of the Striated Muscle Sarcomere. , 1990, , 1-48.		13
65	The Interacting Head Motif Structure Does Not Explain the X-Ray Diffraction Patterns in Relaxed Vertebrate (Bony Fish) Skeletal Muscle and Insect (<i>Lethocerus</i>) Flight Muscle. <i>Biology</i> , 2019, 8, 67.	1.3	12
66	Cryoultramicrotomy of muscle: improved preservation and resolution of muscle ultrastructure using negatively stained ultrathin cryosections. <i>Journal of Microscopy</i> , 1991, 163, 29-42.	0.8	11
67	A novel approach to the structural analysis of partially decorated actin based filaments. <i>Journal of Structural Biology</i> , 2010, 170, 278-285.	1.3	10
68	A closed conformation of the <i>Caenorhabditis elegans</i> separase–securin complex. <i>Open Biology</i> , 2016, 6, 160032.	1.5	10
69	High-resolution cryo-EM proteasome structures in drug development. <i>Acta Crystallographica Section D: Structural Biology</i> , 2017, 73, 522-533.	1.1	10
70	Cryoelectron microscopy of refrozen cryosections. <i>Journal of Structural Biology</i> , 2003, 142, 233-240.	1.3	9
71	A Measure for the Angle Between Projections Based on the Extent of Correlation Between Corresponding Central Sections. <i>Journal of Molecular Biology</i> , 2004, 344, 707-724.	2.0	9
72	Crystallisation of CP43, a Chlorophyll Binding Protein of Photosystem II: An Electron Microscopy Analysis of Molecular Packing. <i>Journal of Structural Biology</i> , 2000, 131, 181-186.	1.3	7

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73	How to build a proteasome. <i>Nature Structural and Molecular Biology</i> , 2021, 28, 409-410.	3.6	4
74	Electron Crystallography in Photosynthesis Research. <i>Advances in Photosynthesis and Respiration</i> , 2008, , 125-150.	1.0	3
75	3-Dimensional Structure of Human Cardiac Muscle Myosin Filaments by Electron Microscopy and Single Particle Analysis. <i>Biophysical Journal</i> , 2012, 102, 149a-150a.	0.2	2
76	The distribution of the charged residues in myosin hinge region and its relationship to the distribution of charged residues in the rest of myosin rod. <i>Journal of Muscle Research and Cell Motility</i> , 1987, 8, 297-302.	0.9	1
77	Cryo-EM Studies of Cullin-Ring Ubiquitin E3 Ligase (CRL)2 Regulation by the COP9 Signalosome. <i>Biophysical Journal</i> , 2017, 112, 578a.	0.2	1
78	On the other hand <i>Nature</i> , 1990, 345, 116-117.	13.7	0
79	THREE-DIMENSIONAL STRUCTURE OF PHOTOSYSTEM II DETERMINED BY ELECTRON CRYSTALLOGRAPHY. <i>Biochemical Society Transactions</i> , 2000, 28, A79-A79.	1.6	0
80	Unravelling the structure of the human 26S proteasome: a hybrid approach. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2013, 69, s36-s36.	0.3	0