

# David A Agard

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8862331/publications.pdf>

Version: 2024-02-01

176  
papers

28,677  
citations

13068

68  
h-index

7136

153  
g-index

222  
all docs

222  
docs citations

222  
times ranked

33704  
citing authors

#	ARTICLE	IF	CITATIONS
1	MotionCor2: anisotropic correction of beam-induced motion for improved cryo-electron microscopy. <i>Nature Methods</i> , 2017, 14, 331-332.	9.0	6,166
2	A SARS-CoV-2 protein interaction map reveals targets for drug repurposing. <i>Nature</i> , 2020, 583, 459-468.	13.7	3,542
3	Electron counting and beam-induced motion correction enable near-atomic-resolution single-particle cryo-EM. <i>Nature Methods</i> , 2013, 10, 584-590.	9.0	1,707
4	Liquid droplet formation by HP1 suggests a role for phase separation in heterochromatin. <i>Nature</i> , 2017, 547, 236-240.	13.7	1,351
5	Microtubule nucleation by $\beta$ -tubulin complexes. <i>Nature Reviews Molecular Cell Biology</i> , 2011, 12, 709-721.	16.1	616
6	Microtubule nucleation by $\beta$ -tubulin-containing rings in the centrosome. <i>Nature</i> , 1995, 378, 638-640.	13.7	509
7	Comparative host-coronavirus protein interaction networks reveal pan-viral disease mechanisms. <i>Science</i> , 2020, 370, .	6.0	508
8	Three-dimensional architecture of a polytene nucleus. <i>Nature</i> , 1983, 302, 676-681.	13.7	432
9	Structural Analysis of <i>E. coli</i> hsp90 Reveals Dramatic Nucleotide-Dependent Conformational Rearrangements. <i>Cell</i> , 2006, 127, 329-340.	13.5	415
10	A molecular pore spans the double membrane of the coronavirus replication organelle. <i>Science</i> , 2020, 369, 1395-1398.	6.0	372
11	Atomic structure of Hsp90-Cdc37-Cdk4 reveals that Hsp90 traps and stabilizes an unfolded kinase. <i>Science</i> , 2016, 352, 1542-1547.	6.0	354
12	Glucocorticoid Receptor Function Regulated by Coordinated Action of the Hsp90 and Hsp70 Chaperone Cycles. <i>Cell</i> , 2014, 157, 1685-1697.	13.5	327
13	A protein-folding reaction under kinetic control. <i>Nature</i> , 1992, 356, 263-265.	13.7	318
14	Telomeres Cluster De Novo before the Initiation of Synapsis: A Three-dimensional Spatial Analysis of Telomere Positions before and during Meiotic Prophase. <i>Journal of Cell Biology</i> , 1997, 137, 5-18.	2.3	292
15	Conformational dynamics of the molecular chaperone Hsp90. <i>Quarterly Reviews of Biophysics</i> , 2011, 44, 229-255.	2.4	270
16	The catalytic protease pro-region does not require a physical linkage to activate the protease domain in vivo. <i>Nature</i> , 1989, 341, 462-464.	13.7	265
17	Structure of the $\beta$ -tubulin ring complex: a template for microtubule nucleation. <i>Nature Cell Biology</i> , 2000, 2, 365-370.	4.6	264
18	UCSF tomography: An integrated software suite for real-time electron microscopic tomographic data collection, alignment, and reconstruction. <i>Journal of Structural Biology</i> , 2007, 157, 138-147.	1.3	233

#	ARTICLE	IF	CITATIONS
19	Microtubule nucleating $\hat{\Gamma}^3$ -TuSC assembles structures with 13-fold microtubule-like symmetry. <i>Nature</i> , 2010, 466, 879-882.	13.7	231
20	Structural basis of mitochondrial receptor binding and constriction by DRP1. <i>Nature</i> , 2018, 558, 401-405.	13.7	219
21	The lattice as allosteric effector: Structural studies of $\hat{\Gamma}^2$ - and $\hat{\Gamma}^3$ -tubulin clarify the role of GTP in microtubule assembly. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 5378-5383.	3.3	216
22	Assembly of a nucleus-like structure during viral replication in bacteria. <i>Science</i> , 2017, 355, 194-197.	6.0	207
23	Unfolded conformations of $\hat{\Gamma}$ -lytic protease are more stable than its native state. <i>Nature</i> , 1998, 395, 817-819.	13.7	204
24	Species-Dependent Ensembles of Conserved Conformational States Define the Hsp90 Chaperone ATPase Cycle. <i>Molecular Cell</i> , 2008, 32, 631-640.	4.5	202
25	Direct Measurement of Interfacial Curvature Distributions in a Bicontinuous Block Copolymer Morphology. <i>Physical Review Letters</i> , 2000, 84, 518-521.	2.9	190
26	Large-scale chromatin structural domains within mitotic and interphase chromosomes in vivo and in vitro. <i>Chromosoma</i> , 1989, 98, 129-143.	1.0	189
27	GCP5 and GCP6: Two New Members of the Human $\hat{\Gamma}^3$ -Tubulin Complex. <i>Molecular Biology of the Cell</i> , 2001, 12, 3340-3352.	0.9	182
28	Fully automated, sequential tilt-series acquisition with Legimon. <i>Journal of Structural Biology</i> , 2009, 167, 11-18.	1.3	180
29	The Crystal Structure of the Carboxy-Terminal Dimerization Domain of htpG, the Escherichia coli Hsp90, Reveals a Potential Substrate Binding Site. <i>Structure</i> , 2004, 12, 1087-1097.	1.6	178
30	The role of pro regions in protein folding. <i>Current Opinion in Cell Biology</i> , 1993, 5, 966-970.	2.6	172
31	Structural plasticity broadens the specificity of an engineered protease. <i>Nature</i> , 1989, 339, 191-195.	13.7	170
32	Insights into microtubule nucleation from the crystal structure of human $\hat{\Gamma}^3$ -tubulin. <i>Nature</i> , 2005, 435, 523-527.	13.7	167
33	Energetic landscape of $\hat{\Gamma}$ -lytic protease optimizes longevity through kinetic stability. <i>Nature</i> , 2002, 415, 343-346.	13.7	165
34	Multiple Conformations of E. coli Hsp90 in Solution: Insights into the Conformational Dynamics of Hsp90. <i>Structure</i> , 2008, 16, 755-765.	1.6	154
35	Substrate Binding Drives Large-Scale Conformational Changes in the Hsp90 Molecular Chaperone. <i>Molecular Cell</i> , 2011, 42, 96-105.	4.5	147
36	Serine protease mechanism: structure of an inhibitory complex of $\alpha$ -lytic protease and a tightly bound peptide boronic acid. <i>Biochemistry</i> , 1987, 26, 7609-7614.	1.2	146

#	ARTICLE	IF	CITATIONS
37	A bacteriophage nucleus-like compartment shields DNA from CRISPR nucleases. <i>Nature</i> , 2020, 577, 244-248.	13.7	146
38	Structural Asymmetry in the Closed State of Mitochondrial Hsp90 (TRAP1) Supports a Two-Step ATP Hydrolysis Mechanism. <i>Molecular Cell</i> , 2014, 53, 330-343.	4.5	144
39	IVE (Image Visualization Environment): A Software Platform for All Three-Dimensional Microscopy Applications. <i>Journal of Structural Biology</i> , 1996, 116, 56-60.	1.3	142
40	Integration of Small-Angle X-Ray Scattering Data into Structural Modeling of Proteins and Their Assemblies. <i>Journal of Molecular Biology</i> , 2008, 382, 1089-1106.	2.0	139
41	Amorphous no more: subdiffraction view of the pericentriolar material architecture. <i>Trends in Cell Biology</i> , 2014, 24, 188-197.	3.6	134
42	Client-Loading Conformation of the Hsp90 Molecular Chaperone Revealed in the Cryo-EM Structure of the Human Hsp90:Hop Complex. <i>Molecular Cell</i> , 2011, 42, 771-781.	4.5	131
43	Three-dimensional structure of basal body triplet revealed by electron cryo-tomography. <i>EMBO Journal</i> , 2012, 31, 552-562.	3.5	125
44	Activation of a Retroviral Membrane Fusion Protein: Soluble Receptor-induced Liposome Binding of the ALSV Envelope Glycoprotein. <i>Journal of Cell Biology</i> , 1997, 139, 1455-1464.	2.3	123
45	Protease pro region required for folding is a potent inhibitor of the mature enzyme. <i>Proteins: Structure, Function and Bioinformatics</i> , 1992, 12, 339-344.	1.5	119
46	The Cancer Cell Map Initiative: Defining the Hallmark Networks of Cancer. <i>Molecular Cell</i> , 2015, 58, 690-698.	4.5	117
47	An improved strategy for automated electron microscopic tomography. <i>Journal of Structural Biology</i> , 2004, 147, 91-101.	1.3	116
48	Ring closure activates yeast $\hat{1}^3$ TuRC for species-specific microtubule nucleation. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 132-137.	3.6	115
49	Uncovering a Region of Heat Shock Protein 90 Important for Client Binding in <i>E.Âcoli</i> and Chaperone Function in Yeast. <i>Molecular Cell</i> , 2013, 49, 464-473.	4.5	112
50	The Psychiatric Cell Map Initiative: A Convergent Systems Biological Approach to Illuminating Key Molecular Pathways in Neuropsychiatric Disorders. <i>Cell</i> , 2018, 174, 505-520.	13.5	108
51	Focal points for chromosome condensation and decondensation revealed by three-dimensional in vivo time-lapse microscopy. <i>Nature</i> , 1989, 342, 293-296.	13.7	107
52	Structural analysis of specificity: .alpha.-lytic protease complexes with analogs of reaction intermediates. <i>Biochemistry</i> , 1989, 28, 7600-7609.	1.2	104
53	A simple and robust procedure for preparing graphene-oxide cryo-EM grids. <i>Journal of Structural Biology</i> , 2018, 204, 80-84.	1.3	101
54	Influence of electron dose rate on electron counting images recorded with the K2 camera. <i>Journal of Structural Biology</i> , 2013, 184, 251-260.	1.3	99

#	ARTICLE	IF	CITATIONS
55	A Phage Tubulin Assembles Dynamic Filaments by an Atypical Mechanism to Center Viral DNA within the Host Cell. <i>Cell</i> , 2012, 149, 1488-1499.	13.5	98
56	Subangstrom Crystallography Reveals that Short Ionic Hydrogen Bonds, and Not a His-Asp Low-Barrier Hydrogen Bond, Stabilize the Transition State in Serine Protease Catalysis. <i>Journal of the American Chemical Society</i> , 2006, 128, 9086-9102.	6.6	97
57	Mechanistic Studies of Sansalvamide A-Amide: An Allosteric Modulator of Hsp90. <i>ACS Medicinal Chemistry Letters</i> , 2010, 1, 4-8.	1.3	97
58	The Structure of the $\hat{\gamma}$ -Tubulin Small Complex: Implications of Its Architecture and Flexibility for Microtubule Nucleation. <i>Molecular Biology of the Cell</i> , 2008, 19, 207-215.	0.9	96
59	Hsp70 Forms Antiparallel Dimers Stabilized by Post-translational Modifications to Position Clients for Transfer to Hsp90. <i>Cell Reports</i> , 2015, 11, 759-769.	2.9	93
60	Intra- and Intermonomer Interactions Are Required to Synergistically Facilitate ATP Hydrolysis in Hsp90. <i>Journal of Biological Chemistry</i> , 2008, 283, 21170-21178.	1.6	92
61	Asynchronous data acquisition and on-the-fly analysis of dose fractionated cryoEM images by UCSFImage. <i>Journal of Structural Biology</i> , 2015, 192, 174-178.	1.3	92
62	Structure of Hsp90 $\hat{\alpha}$ -Hsp70 $\hat{\alpha}$ -Hop $\hat{\alpha}$ -GR reveals the Hsp90 client-loading mechanism. <i>Nature</i> , 2022, 601, 460-464.	13.7	90
63	Toward Fully Automated High-Resolution Electron Tomography. <i>Journal of Structural Biology</i> , 1996, 116, 181-189.	1.3	89
64	Kinetic properties of the binding of $\alpha$ -lytic protease to peptide boronic acids. <i>Biochemistry</i> , 1988, 27, 7682-7688.	1.2	86
65	Competing protein-protein interactions regulate binding of Hsp27 to its client protein tau. <i>Nature Communications</i> , 2018, 9, 4563.	5.8	82
66	Condensed Mitotic Chromosome Structure at Nanometer Resolution Using PALM and EGFP- Histones. <i>PLoS ONE</i> , 2010, 5, e12768.	1.1	80
67	Structure of Hsp90 $\hat{\alpha}$ -p23 $\hat{\alpha}$ -GR reveals the Hsp90 client-remodelling mechanism. <i>Nature</i> , 2022, 601, 465-469.	13.7	80
68	Crystal structure of $\hat{\gamma}$ -tubulin complex protein GCP4 provides insight into microtubule nucleation. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 915-919.	3.6	79
69	Enzyme specificity under dynamic control: A normal mode analysis of $\hat{\alpha}$ -lytic protease. <i>Journal of Molecular Biology</i> , 1999, 286, 267-278.	2.0	77
70	High-resolution restoration of 3D structures from widefield images with extreme low signal-to-noise-ratio. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 17344-17349.	3.3	77
71	How Hsp90 and Cdc37 Lubricate Kinase Molecular Switches. <i>Trends in Biochemical Sciences</i> , 2017, 42, 799-811.	3.7	77
72	Molecular Dynamics Simulations Reveal the Mechanisms of Allosteric Activation of Hsp90 by Designed Ligands. <i>Scientific Reports</i> , 2016, 6, 23830.	1.6	71

#	ARTICLE	IF	CITATIONS
73	General and robust covalently linked graphene oxide affinity grids for high-resolution cryo-EM. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 24269-24273.	3.3	71
74	Conformational substates in enzyme mechanism: The 120 K structure of $\hat{\mu}$ -lytic protease at 1.5 Å.. resolution. Protein Science, 1997, 6, 1375-1386.	3.1	70
75	Mind the gap: Micro-expansion joints drastically decrease the bending of FIB-milled cryo-lamellae. Journal of Structural Biology, 2019, 208, 107389.	1.3	70
76	Structure of $\hat{\mu}$ -lytic protease complexed with its pro region. Nature Structural Biology, 1998, 5, 945-950.	9.7	69
77	Symmetry broken and rebroken during the ATP hydrolysis cycle of the mitochondrial Hsp90 TRAP1. ELife, 2017, 6, .	2.8	67
78	Crystal structures of $\alpha$ -lytic protease complexes with irreversibly bound phosphonate esters. Biochemistry, 1991, 30, 2263-2272.	1.2	65
79	Activation of Hsp90 Enzymatic Activity and Conformational Dynamics through Rationally Designed Allosteric Ligands. Chemistry - A European Journal, 2015, 21, 13598-13608.	1.7	65
80	High-performance iterative electron tomography reconstruction with long-object compensation using graphics processing units (GPUs). Journal of Structural Biology, 2010, 171, 142-153.	1.3	64
81	Osmolyte-induced conformational changes in the Hsp90 molecular chaperone. Protein Science, 2010, 19, 57-65.	3.1	62
82	Viral Capsid Trafficking along Treadmilling Tubulin Filaments in Bacteria. Cell, 2019, 177, 1771-1780.e12.	13.5	62
83	A bacteriophage tubulin harnesses dynamic instability to center DNA in infected cells. ELife, 2014, 3, .	2.8	62
84	The 0.83Å.. Resolution Crystal Structure of $\hat{\mu}$ -Lytic Protease Reveals the Detailed Structure of the Active Site and Identifies a Source of Conformational Strain. Journal of Molecular Biology, 2004, 338, 999-1013.	2.0	60
85	MRC2014: Extensions to the MRC format header for electron cryo-microscopy and tomography. Journal of Structural Biology, 2015, 192, 146-150.	1.3	59
86	Structural basis for broad specificity in $\alpha$ -lytic protease mutants. Biochemistry, 1991, 30, 10388-10398.	1.2	56
87	The conserved arginine 380 of Hsp90 is not a catalytic residue, but stabilizes the closed conformation required for ATP hydrolysis. Protein Science, 2012, 21, 1162-1171.	3.1	56
88	The mitochondrial HSP90 paralog TRAP1 forms an OXPHOS-regulated tetramer and is involved in mitochondrial metabolic homeostasis. BMC Biology, 2020, 18, 10.	1.7	56
89	Pro Region C-Terminus:Protease Active Site Interactions Are Critical in Catalyzing the Folding of $\hat{\mu}$ -Lytic Protease. Biochemistry, 1998, 37, 12058-12067.	1.2	52
90	Probing the Flexibility of Large Conformational Changes in Protein Structures through Local Perturbations. PLoS Computational Biology, 2009, 5, e1000343.	1.5	52

#	ARTICLE	IF	CITATIONS
91	Grp94, the endoplasmic reticulum Hsp90, has a similar solution conformation to cytosolic Hsp90 in the absence of nucleotide. <i>Protein Science</i> , 2009, 18, 1815-1827.	3.1	52
92	pH-Dependent Conformational Changes in Bacterial Hsp90 Reveal a Grp94-Like Conformation at pH 6 That Is Highly Active in Suppression of Citrate Synthase Aggregation. <i>Journal of Molecular Biology</i> , 2009, 390, 278-291.	2.0	52
93	Comprehensive Analysis of Protein Folding Activation Thermodynamics Reveals a Universal Behavior Violated by Kinetically Stable Proteases. <i>Journal of Molecular Biology</i> , 2005, 347, 355-366.	2.0	50
94	The Structural Asymmetry of Mitochondrial Hsp90 (Trap1) Determines Fine Tuning of Functional Dynamics. <i>Journal of Chemical Theory and Computation</i> , 2018, 14, 1033-1044.	2.3	50
95	Insights into centriole geometry revealed by cryotomography of doublet and triplet centrioles. <i>ELife</i> , 2018, 7, .	2.8	50
96	The three-dimensional structure of in vitro reconstituted <i>Xenopus laevis</i> chromosomes by EM tomography. <i>Chromosoma</i> , 2007, 116, 349-372.	1.0	49
97	Structures of the HER2-HER3-NRG1 <sup>2</sup> complex reveal a dynamic dimer interface. <i>Nature</i> , 2021, 600, 339-343.	13.7	48
98	3D Nanometer-Scale Study of Coexisting Bicontinuous Morphologies in a Block Copolymer/Homopolymer Blend. <i>Macromolecular Rapid Communications</i> , 2006, 27, 1424-1429.	2.0	47
99	On the efficiency of iterative ordered subset reconstruction algorithms for acceleration on GPUs. <i>Computer Methods and Programs in Biomedicine</i> , 2010, 98, 261-270.	2.6	47
100	Functional Linkage Between the Active Site of $\beta$ -Lytic Protease and Distant Regions of Structure: Scanning Alanine Mutagenesis of a Surface Loop Affects Activity and Substrate Specificity. <i>Journal of Molecular Biology</i> , 1995, 251, 116-134.	2.0	45
101	Cross-Monomer Substrate Contacts Reposition the Hsp90 N-Terminal Domain and Prime the Chaperone Activity. <i>Journal of Molecular Biology</i> , 2012, 415, 3-15.	2.0	45
102	Elucidating the Mechanism of Substrate Recognition by the Bacterial Hsp90 Molecular Chaperone. <i>Journal of Molecular Biology</i> , 2014, 426, 2393-2404.	2.0	45
103	Amino and PEG-amino graphene oxide grids enrich and protect samples for high-resolution single particle cryo-electron microscopy. <i>Journal of Structural Biology</i> , 2020, 209, 107437.	1.3	45
104	Activity-Independent Discovery of Secondary Metabolites Using Chemical Elicitation and Cheminformatic Inference. <i>ACS Chemical Biology</i> , 2015, 10, 2616-2623.	1.6	43
105	Cryo-tomography tilt-series alignment with consideration of the beam-induced sample motion. <i>Journal of Structural Biology</i> , 2018, 202, 200-209.	1.3	43
106	Structural and Mechanistic Exploration of Acid Resistance: Kinetic Stability Facilitates Evolution of Extremophilic Behavior. <i>Journal of Molecular Biology</i> , 2007, 368, 870-883.	2.0	42
107	Kinetic and Structural Characterization of Mutations of Glycine 216 in $\beta$ -Lytic Protease: A New Target for Engineering Substrate Specificity. <i>Journal of Molecular Biology</i> , 1995, 254, 720-736.	2.0	41
108	The folding landscape of <i>Streptomyces griseus</i> protease B reveals the energetic costs and benefits associated with evolving kinetic stability. <i>Protein Science</i> , 2004, 13, 381-390.	3.1	41

#	ARTICLE	IF	CITATIONS
109	A novel N-terminal extension in mitochondrial TRAP1 serves as a thermal regulator of chaperone activity. <i>ELife</i> , 2014, 3, .	2.8	40
110	The Structure and Assembly Mechanism of a Novel Three-Stranded Tubulin Filament that Centers Phage DNA. <i>Structure</i> , 2014, 22, 539-548.	1.6	37
111	Inhibition of $\hat{\pm}$ -Lytic Protease by Pro Region C-Terminal Steric Occlusion of the Active Site. <i>Biochemistry</i> , 1997, 36, 3894-3902.	1.2	36
112	The Free Energy Profile of Tubulin Straight-Bent Conformational Changes, with Implications for Microtubule Assembly and Drug Discovery. <i>PLoS Computational Biology</i> , 2014, 10, e1003464.	1.5	35
113	Electron cryotomography of intact motile cilia defines the basal body to axoneme transition. <i>Journal of Cell Biology</i> , 2020, 219, .	2.3	35
114	Mesophile versus Thermophile: Insights Into the Structural Mechanisms of Kinetic Stability. <i>Journal of Molecular Biology</i> , 2007, 370, 784-795.	2.0	34
115	<title>PRIISM: an integrated system for display and analysis of 3-D microscope images</title>. , 1992, , .		33
116	Design of Allosteric Stimulators of the Hsp90 ATPase as New Anticancer Leads. <i>Chemistry - A European Journal</i> , 2017, 23, 5188-5192.	1.7	33
117	Practical considerations for using K3 cameras in CDS mode for high-resolution and high-throughput single particle cryo-EM. <i>Journal of Structural Biology</i> , 2021, 213, 107745.	1.3	33
118	Bacterial tubulin TubZ-Bt transitions between a two-stranded intermediate and a four-stranded filament upon GTP hydrolysis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 3407-3412.	3.3	32
119	$\hat{\pm}$ -Lytic Protease Precursor: A Characterization of a Structured Folding Intermediate. <i>Biochemistry</i> , 1999, 38, 4728-4735.	1.2	31
120	Disabling the folding catalyst is the last critical step in $\hat{\pm}$ -lytic protease folding. <i>Protein Science</i> , 2004, 13, 325-331.	3.1	30
121	How general is the nucleation "condensation" mechanism?. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 73, 754-764.	1.5	30
122	Higher-order oligomerization of Spc110p drives $\hat{\pm}$ -tubulin ring complex assembly. <i>Molecular Biology of the Cell</i> , 2016, 27, 2245-2258.	0.9	29
123	Hsp70 chaperone blocks $\hat{\pm}$ -synuclein oligomer formation via a novel engagement mechanism. <i>Journal of Biological Chemistry</i> , 2021, 296, 100613.	1.6	29
124	Relationship between Enzyme Specificity and the Backbone Dynamics of Free and Inhibited $\hat{\pm}$ -Lytic Protease. <i>Biochemistry</i> , 1998, 37, 7696-7707.	1.2	28
125	Interdependent Folding of the N- and C-Terminal Domains Defines the Cooperative Folding of $\hat{\pm}$ -Lytic Protease. <i>Biochemistry</i> , 2003, 42, 13212-13219.	1.2	28
126	Interaction of CK1 $\hat{\gamma}$ with $\hat{\pm}$ TuSC ensures proper microtubule assembly and spindle positioning. <i>Molecular Biology of the Cell</i> , 2015, 26, 2505-2518.	0.9	27



#	ARTICLE	IF	CITATIONS
127	The solution structure of the viral binding domain of Tva, the cellular receptor for subgroup A avian leukosis and sarcoma virus1. FEBS Letters, 2001, 509, 161-168.	1.3	26
128	Evaluation of super-resolution performance of the K2 electron-counting camera using 2D crystals of aquaporin-0. Journal of Structural Biology, 2015, 192, 163-173.	1.3	26
129	Internal Structure and Preferential Protein Binding of Colloidal Aggregates. ACS Chemical Biology, 2017, 12, 282-290.	1.6	26
130	Consideration of sample motion in cryo-tomography based on alignment residual interpolation. Journal of Structural Biology, 2019, 205, 1-6.	1.3	26
131	Localization and orientation of the $\beta$ -Tubulin Small Complex components using protein tags as labels for single particle EM. Journal of Structural Biology, 2009, 168, 571-574.	1.3	25
132	The Seckel syndrome and centrosomal protein Ninein localizes asymmetrically to stem cell centrosomes but is not required for normal development, behavior, or DNA damage response in Drosophila. Molecular Biology of the Cell, 2016, 27, 1740-1752.	0.9	25
133	Novel Small Molecules Targeting the Intrinsically Disordered Structural Ensemble of $\beta$ -Synuclein Protect Against Diverse $\beta$ -Synuclein Mediated Dysfunctions. Scientific Reports, 2019, 9, 16947.	1.6	25
134	Electron cryo-tomography provides insight into procentriole architecture and assembly mechanism. ELife, 2019, 8, .	2.8	25
135	Free energy calculations on binding and catalysis by $\beta$ -lytic protease: The role of substrate size in the P1 pocket. Proteins: Structure, Function and Bioinformatics, 1991, 10, 140-148.	1.5	24
136	Enzyme specificity under dynamic control II: Principal component analysis of $\beta$ -lytic protease using global and local solvent boundary conditions. Protein Science, 2008, 10, 1403-1414.	3.1	24
137	The Pro Region N-Terminal Domain Provides Specific Interactions Required for Catalysis of $\beta$ -Lytic Protease Folding. Biochemistry, 2002, 41, 8860-8867.	1.2	23
138	Microarray-based screening of heat shock protein inhibitors. Journal of Biotechnology, 2014, 180, 1-9.	1.9	23
139	Structure of $\beta$ -tubulin small complex based on a cryo-EM map, chemical cross-links, and a remotely related structure. Journal of Structural Biology, 2016, 194, 303-310.	1.3	23
140	XMAP215 and $\beta$ -tubulin additively promote microtubule nucleation in purified solutions. Molecular Biology of the Cell, 2020, 31, 2187-2194.	0.9	23
141	CM1-driven assembly and activation of yeast $\beta$ -tubulin small complex underlies microtubule nucleation. ELife, 2021, 10, .	2.8	23
142	Unfolding Simulations Reveal the Mechanism of Extreme Unfolding Cooperativity in the Kinetically Stable $\beta$ -Lytic Protease. PLoS Computational Biology, 2010, 6, e1000689.	1.5	21
143	Two energetically disparate folding pathways of alpha-lytic protease share a single transition state. , 2000, 7, 394-397.		20
144	Closed loop adaptive optics for microscopy without a wavefront sensor. , 2010, 7570, .		17

#	ARTICLE	IF	CITATIONS
145	Synthesis of Functionalized 2-(4-Hydroxyphenyl)-3-methylbenzofuran Allosteric Modulators of Hsp90 Activity. <i>European Journal of Organic Chemistry</i> , 2016, 2016, 3349-3364.	1.2	17
146	Electron cryo-tomography structure of axonemal doublet microtubule from <i>Tetrahymena thermophila</i> . <i>Life Science Alliance</i> , 2022, 5, e202101225.	1.3	17
147	Calcium binding to a remote site can replace magnesium as cofactor for mitochondrial Hsp90 (TRAP1) ATPase activity. <i>Journal of Biological Chemistry</i> , 2018, 293, 13717-13724.	1.6	16
148	Increased depth of field and stereo pairs of fluorescence micrographs via inverse filtering and maximum-likelihood estimation. <i>Journal of Microscopy</i> , 1991, 164, 217-237.	0.8	15
149	The folding landscape of an $\alpha$ -lytic protease variant reveals the role of a conserved $\beta$ -hairpin in the development of kinetic stability. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 61, 105-114.	1.5	15
150	Automated acquisition of electron microscopic random conical tilt sets. <i>Journal of Structural Biology</i> , 2007, 157, 148-155.	1.3	15
151	NMR characterization of HtpG, the <i>E. coli</i> Hsp90, using sparse labeling with $^{13}\text{C}$ -methyl alanine. <i>Journal of Biomolecular NMR</i> , 2017, 68, 225-236.	1.6	15
152	A small molecule that preferentially binds the closed conformation of Hsp90. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2011, 21, 7068-7071.	1.0	14
153	Dual-axis target mapping and automated sequential acquisition of dual-axis EM tomographic data. <i>Journal of Structural Biology</i> , 2009, 168, 323-331.	1.3	13
154	A distributed multi-GPU system for high speed electron microscopic tomographic reconstruction. <i>Ultramicroscopy</i> , 2011, 111, 1137-1143.	0.8	13
155	Proteomic analysis of microtubule inner proteins (MIPs) in Rib72 null <i>Tetrahymena</i> cells reveals functional MIPs. <i>Molecular Biology of the Cell</i> , 2021, 32, br8.	0.9	13
156	The centrosomin CM2 domain is a multi-functional binding domain with distinct cell cycle roles. <i>PLoS ONE</i> , 2018, 13, e0190530.	1.1	12
157	Entropy-regularized deconvolution of cellular cryotransmission electron tomograms. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	11
158	Three-dimensional light microscopy of diploid <i>Drosophila</i> chromosomes. <i>Cytoskeleton</i> , 1988, 10, 18-27.	4.4	10
159	Alterations in chemical shifts and exchange broadening upon peptide boronic acid inhibitor binding to $\alpha$ -lytic protease. <i>Journal of Biomolecular NMR</i> , 1997, 10, 21-27.	1.6	10
160	Functional modulation of a protein folding landscape via side-chain distortion. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 9414-9419.	3.3	8
161	Design and construction of an optimal illumination system for quantitative wide-field multi-dimensional microscopy. <i>Bioimaging</i> , 1993, 1, 71-81.	1.8	8
162	K3 - A First Look at The New Direct Electron Detection Camera from Gatan Company. <i>Microscopy and Microanalysis</i> , 2018, 24, 890-891.	0.2	6

#	ARTICLE	IF	CITATIONS
163	Microtubule Nucleation. , 2005, , 27-41.		4
164	Microtubules form by progressively faster tubulin accretion, not by nucleationâ€“elongation. Journal of Cell Biology, 2021, 220, .	2.3	4
165	Assessment of the Role of Computations in Structural Biology. Advances in Protein Chemistry, 2003, 66, 1-25.	4.4	3
166	Protein Expression and Purification of the Hsp90-Cdc37-Cdk4 Kinase Complex from Saccharomyces cerevisiae. Bio-protocol, 2017, 7, .	0.2	3
167	Use of surface affinity enrichment and cryo-embedding to prepare in vitro reconstituted mitotic chromosomes for EM tomography. Ultramicroscopy, 2005, 103, 261-274.	0.8	2
168	Î±-Lytic Protease. , 2013, , 2558-2565.		2
169	Bacterial extracellular secretion. Membrane Protein Transport, 1996, , 165-179.	0.2	1
170	Sub-100nm Axial Resolution in 3D Widefield Optical Microscopy Using Two Opposing Objective Lenses. Microscopy and Microanalysis, 1997, 3, 801-802.	0.2	0
171	Image Restoration of Thick Biological Specimens for Transmission Electron Microscope Tomography. , 1999, , 92-99.		0
172	Functional Analysis of Î²-Secretase Using Mutagenesis and Structural Homology Modeling. , 0, , 799-807.		0
173	Structural Insights into Hsp90 Function. , 2016, , 251-316.		0
174	Frontispiece: Design of Allosteric Stimulators of the Hsp90 ATPase as New Anticancer Leads. Chemistry - A European Journal, 2017, 23, .	1.7	0
175	CryoEM Reveals Multi-step Activation of Î³Tubulin and Assemblies to Optimize Microtubule Nucleation. Microscopy and Microanalysis, 2019, 25, 1298-1299.	0.2	0
176	The centrosome and the mechanism of microtubule nucleation. FASEB Journal, 2006, 20, A35.	0.2	0