

David A Agard

List of Publications by Year in descending order

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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	Structure of Hsp90â€“Hsp70â€“Hopâ€“GR reveals the Hsp90 client-loading mechanism. <i>Nature</i> , 2022, 601, 460-464.	13.7	90
2	Structure of Hsp90â€“p23â€“GR reveals the Hsp90 client-remodelling mechanism. <i>Nature</i> , 2022, 601, 465-469.	13.7	80
3	Electron cryo-tomography structure of axonemal doublet microtubule from <i>Tetrahymena thermophila</i> . <i>Life Science Alliance</i> , 2022, 5, e202101225.	1.3	17
4	Hsp70 chaperone blocks Î±-synuclein oligomer formation via a novel engagement mechanism. <i>Journal of Biological Chemistry</i> , 2021, 296, 100613.	1.6	29
5	Microtubules form by progressively faster tubulin accretion, not by nucleationâ€“elongation. <i>Journal of Cell Biology</i> , 2021, 220, .	2.3	4
6	CM1-driven assembly and activation of yeast Î³-tubulin small complex underlies microtubule nucleation. <i>ELife</i> , 2021, 10, .	2.8	23
7	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
8	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
9	Structures of the HER2â€“HER3â€“NRG1Î² complex reveal a dynamic dimer interface. <i>Nature</i> , 2021, 600, 339-343.	13.7	48
10	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
11	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
12	A bacteriophage nucleus-like compartment shields DNA from CRISPR nucleases. <i>Nature</i> , 2020, 577, 244-248.	13.7	146
13	Comparative host-coronavirus protein interaction networks reveal pan-viral disease mechanisms. <i>Science</i> , 2020, 370, .	6.0	508
14	XMAP215 and Î³-tubulin additively promote microtubule nucleation in purified solutions. <i>Molecular Biology of the Cell</i> , 2020, 31, 2187-2194.	0.9	23
15	A molecular pore spans the double membrane of the coronavirus replication organelle. <i>Science</i> , 2020, 369, 1395-1398.	6.0	372
16	General and robust covalently linked graphene oxide affinity grids for high-resolution cryo-EM. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 24269-24273.	3.3	71
17	A SARS-CoV-2 protein interaction map reveals targets for drug repurposing. <i>Nature</i> , 2020, 583, 459-468.	13.7	3,542
18	Electron cryotomography of intact motile cilia defines the basal body to axoneme transition. <i>Journal of Cell Biology</i> , 2020, 219, .	2.3	35

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19	The mitochondrial HSP90 paralog TRAP1 forms an OXPHOS-regulated tetramer and is involved in mitochondrial metabolic homeostasis. <i>BMC Biology</i> , 2020, 18, 10.	1.7	56
20	Viral Capsid Trafficking along Treadmilling Tubulin Filaments in Bacteria. <i>Cell</i> , 2019, 177, 1771-1780.e12.	13.5	62
21	CryoEM Reveals Multi-step Activation of $\hat{\gamma}$ Tubulin and Assemblies to Optimize Microtubule Nucleation. <i>Microscopy and Microanalysis</i> , 2019, 25, 1298-1299.	0.2	0
22	Mind the gap: Micro-expansion joints drastically decrease the bending of FIB-milled cryo-lamellae. <i>Journal of Structural Biology</i> , 2019, 208, 107389.	1.3	70
23	Consideration of sample motion in cryo-tomography based on alignment residual interpolation. <i>Journal of Structural Biology</i> , 2019, 205, 1-6.	1.3	26
24	Novel Small Molecules Targeting the Intrinsically Disordered Structural Ensemble of $\hat{\gamma}$ -Synuclein Protect Against Diverse $\hat{\gamma}$ -Synuclein Mediated Dysfunctions. <i>Scientific Reports</i> , 2019, 9, 16947.	1.6	25
25	Electron cryo-tomography provides insight into procentriole architecture and assembly mechanism. <i>ELife</i> , 2019, 8, .	2.8	25
26	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
27	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
28	Competing protein-protein interactions regulate binding of Hsp27 to its client protein tau. <i>Nature Communications</i> , 2018, 9, 4563.	5.8	82
29	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
30	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
31	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
32	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
33	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
34	Structural basis of mitochondrial receptor binding and constriction by DRP1. <i>Nature</i> , 2018, 558, 401-405.	13.7	219
35	Insights into centriole geometry revealed by cryotomography of doublet and triplet centrioles. <i>ELife</i> , 2018, 7, .	2.8	50
36	Assembly of a nucleus-like structure during viral replication in bacteria. <i>Science</i> , 2017, 355, 194-197.	6.0	207

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37	Design of Allosteric Stimulators of the Hsp90 ATPase as New Anticancer Leads. Chemistry - A European Journal, 2017, 23, 5188-5192.	1.7	33
38	MotionCor2: anisotropic correction of beam-induced motion for improved cryo-electron microscopy. Nature Methods, 2017, 14, 331-332.	9.0	6,166
39	Frontispiece: Design of Allosteric Stimulators of the Hsp90 ATPase as New Anticancer Leads. Chemistry - A European Journal, 2017, 23, .	1.7	0
40	Liquid droplet formation by HP1 suggests a role for phase separation in heterochromatin. Nature, 2017, 547, 236-240.	13.7	1,351
41	Internal Structure and Preferential Protein Binding of Colloidal Aggregates. ACS Chemical Biology, 2017, 12, 282-290.	1.6	26
42	How Hsp90 and Cdc37 Lubricate Kinase Molecular Switches. Trends in Biochemical Sciences, 2017, 42, 799-811.	3.7	77
43	NMR characterization of HtpG, the E. coli Hsp90, using sparse labeling with ¹³ C-methyl alanine. Journal of Biomolecular NMR, 2017, 68, 225-236.	1.6	15
44	Symmetry broken and rebroken during the ATP hydrolysis cycle of the mitochondrial Hsp90 TRAP1. ELife, 2017, 6, .	2.8	67
45	Protein Expression and Purification of the Hsp90-Cdc37-Cdk4 Kinase Complex from Saccharomyces cerevisiae. Bio-protocol, 2017, 7, .	0.2	3
46	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
47	Synthesis of Functionalized 2-(4-Hydroxyphenyl)-5-methylbenzofuran Allosteric Modulators of Hsp90 Activity. European Journal of Organic Chemistry, 2016, 2016, 3349-3364.	1.2	17
48	Structural Insights into Hsp90 Function. , 2016, , 251-316.		0
49	Molecular Dynamics Simulations Reveal the Mechanisms of Allosteric Activation of Hsp90 by Designed Ligands. Scientific Reports, 2016, 6, 23830.	1.6	71
50	Higher-order oligomerization of Spc110p drives β -tubulin ring complex assembly. Molecular Biology of the Cell, 2016, 27, 2245-2258.	0.9	29
51	Atomic structure of Hsp90-Cdc37-Cdk4 reveals that Hsp90 traps and stabilizes an unfolded kinase. Science, 2016, 352, 1542-1547.	6.0	354
52	Structure of β -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
53	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
54	Activation of Hsp90 Enzymatic Activity and Conformational Dynamics through Rationally Designed Allosteric Ligands. Chemistry - A European Journal, 2015, 21, 13598-13608.	1.7	65

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55	The Cancer Cell Map Initiative: Defining the Hallmark Networks of Cancer. <i>Molecular Cell</i> , 2015, 58, 690-698.	4.5	117
56	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
57	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
58	Interaction of CK1 $\hat{1}$ with $\hat{1}^3$ TuSC ensures proper microtubule assembly and spindle positioning. <i>Molecular Biology of the Cell</i> , 2015, 26, 2505-2518.	0.9	27
59	MRC2014: Extensions to the MRC format header for electron cryo-microscopy and tomography. <i>Journal of Structural Biology</i> , 2015, 192, 146-150.	1.3	59
60	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
61	Activity-Independent Discovery of Secondary Metabolites Using Chemical Elicitation and Cheminformatic Inference. <i>ACS Chemical Biology</i> , 2015, 10, 2616-2623.	1.6	43
62	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
63	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
64	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
65	Amorphous no more: subdiffraction view of the pericentriolar material architecture. <i>Trends in Cell Biology</i> , 2014, 24, 188-197.	3.6	134
66	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
67	Glucocorticoid Receptor Function Regulated by Coordinated Action of the Hsp90 and Hsp70 Chaperone Cycles. <i>Cell</i> , 2014, 157, 1685-1697.	13.5	327
68	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
69	Microarray-based screening of heat shock protein inhibitors. <i>Journal of Biotechnology</i> , 2014, 180, 1-9.	1.9	23
70	A bacteriophage tubulin harnesses dynamic instability to center DNA in infected cells. <i>ELife</i> , 2014, 3, .	2.8	62
71	A novel N-terminal extension in mitochondrial TRAP1 serves as a thermal regulator of chaperone activity. <i>ELife</i> , 2014, 3, .	2.8	40
72	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

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73	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
74	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
75	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
76	Î±-Lytic Protease. , 2013, , 2558-2565.		2
77	Three-dimensional structure of basal body triplet revealed by electron cryo-tomography. <i>EMBO Journal</i> , 2012, 31, 552-562.	3.5	125
78	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
79	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
80	The conserved arginine 380 of Hsp90 is not a catalytic residue, but stabilizes the closed conformation required for ATP hydrolysis. <i>Protein Science</i> , 2012, 21, 1162-1171.	3.1	56
81	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
82	Substrate Binding Drives Large-Scale Conformational Changes in the Hsp90 Molecular Chaperone. <i>Molecular Cell</i> , 2011, 42, 96-105.	4.5	147
83	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
84	Crystal structure of Î³-tubulin complex protein GCP4 provides insight into microtubule nucleation. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 915-919.	3.6	79
85	Microtubule nucleation by Î³-tubulin complexes. <i>Nature Reviews Molecular Cell Biology</i> , 2011, 12, 709-721.	16.1	616
86	A distributed multi-GPU system for high speed electron microscopic tomographic reconstruction. <i>Ultramicroscopy</i> , 2011, 111, 1137-1143.	0.8	13
87	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
88	Conformational dynamics of the molecular chaperone Hsp90. <i>Quarterly Reviews of Biophysics</i> , 2011, 44, 229-255.	2.4	270
89	Osmolyte-induced conformational changes in the Hsp90 molecular chaperone. <i>Protein Science</i> , 2010, 19, 57-65.	3.1	62
90	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

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91	Microtubule nucleating $\hat{\gamma}$ -TuSC assembles structures with 13-fold microtubule-like symmetry. <i>Nature</i> , 2010, 466, 879-882.	13.7	231
92	Condensed Mitotic Chromosome Structure at Nanometer Resolution Using PALM and EGFP- Histones. <i>PLoS ONE</i> , 2010, 5, e12768.	1.1	80
93	Closed loop adaptive optics for microscopy without a wavefront sensor. , 2010, 7570, .		17
94	Unfolding Simulations Reveal the Mechanism of Extreme Unfolding Cooperativity in the Kinetically Stable $\hat{\gamma}$ -Lytic Protease. <i>PLoS Computational Biology</i> , 2010, 6, e1000689.	1.5	21
95	High-performance iterative electron tomography reconstruction with long-object compensation using graphics processing units (GPUs). <i>Journal of Structural Biology</i> , 2010, 171, 142-153.	1.3	64
96	Mechanistic Studies of Sansalvamide A-Amide: An Allosteric Modulator of Hsp90. <i>ACS Medicinal Chemistry Letters</i> , 2010, 1, 4-8.	1.3	97
97	Probing the Flexibility of Large Conformational Changes in Protein Structures through Local Perturbations. <i>PLoS Computational Biology</i> , 2009, 5, e1000343.	1.5	52
98	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
99	Fully automated, sequential tilt-series acquisition with Legimon. <i>Journal of Structural Biology</i> , 2009, 167, 11-18.	1.3	180
100	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
101	Localization and orientation of the $\hat{\gamma}$ -Tubulin Small Complex components using protein tags as labels for single particle EM. <i>Journal of Structural Biology</i> , 2009, 168, 571-574.	1.3	25
102	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
103	How general is the nucleation "condensation mechanism?. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 73, 754-764.	1.5	30
104	Enzyme specificity under dynamic control II: Principal component analysis of $\hat{\gamma}$ -lytic protease using global and local solvent boundary conditions. <i>Protein Science</i> , 2008, 10, 1403-1414.	3.1	24
105	Multiple Conformations of <i>E. coli</i> Hsp90 in Solution: Insights into the Conformational Dynamics of Hsp90. <i>Structure</i> , 2008, 16, 755-765.	1.6	154
106	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
107	Species-Dependent Ensembles of Conserved Conformational States Define the Hsp90 Chaperone ATPase Cycle. <i>Molecular Cell</i> , 2008, 32, 631-640.	4.5	202
108	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

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109	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
110	The lattice as allosteric effector: Structural studies of $\hat{\alpha}$ - and $\hat{\beta}$ -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
111	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
112	Automated acquisition of electron microscopic random conical tilt sets. <i>Journal of Structural Biology</i> , 2007, 157, 148-155.	1.3	15
113	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
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	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
116	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
117	Structural Analysis of <i>E. coli</i> hsp90 Reveals Dramatic Nucleotide-Dependent Conformational Rearrangements. <i>Cell</i> , 2006, 127, 329-340.	13.5	415
118	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
119	The centrosome and the mechanism of microtubule nucleation. <i>FASEB Journal</i> , 2006, 20, A35.	0.2	0
120	Microtubule Nucleation. , 2005, , 27-41.		4
121	Insights into microtubule nucleation from the crystal structure of human $\hat{\beta}$ -tubulin. <i>Nature</i> , 2005, 435, 523-527.	13.7	167
122	Use of surface affinity enrichment and cryo-embedding to prepare in vitro reconstituted mitotic chromosomes for EM tomography. <i>Ultramicroscopy</i> , 2005, 103, 261-274.	0.8	2
123	The folding landscape of an $\hat{\alpha}$ -lytic protease variant reveals the role of a conserved $\hat{\beta}$ -hairpin in the development of kinetic stability. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 61, 105-114.	1.5	15
124	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
125	The Crystal Structure of the Carboxy-Terminal Dimerization Domain of htpG, the <i>Escherichia coli</i> Hsp90, Reveals a Potential Substrate Binding Site. <i>Structure</i> , 2004, 12, 1087-1097.	1.6	178
126	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

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127	An improved strategy for automated electron microscopic tomography. <i>Journal of Structural Biology</i> , 2004, 147, 91-101.	1.3	116
128	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. <i>Journal of Molecular Biology</i> , 2004, 338, 999-1013.	2.0	60
129	Disabling the folding catalyst is the last critical step in $\hat{\mu}$ -lytic protease folding. <i>Protein Science</i> , 2004, 13, 325-331.	3.1	30
130	Interdependent Folding of the N- and C-Terminal Domains Defines the Cooperative Folding of $\hat{\mu}$ -Lytic Protease. <i>Biochemistry</i> , 2003, 42, 13212-13219.	1.2	28
131	Assessment of the Role of Computations in Structural Biology. <i>Advances in Protein Chemistry</i> , 2003, 66, 1-25.	4.4	3
132	The Pro Region N-Terminal Domain Provides Specific Interactions Required for Catalysis of $\hat{\mu}$ -Lytic Protease Folding. <i>Biochemistry</i> , 2002, 41, 8860-8867.	1.2	23
133	Energetic landscape of $\hat{\mu}$ -lytic protease optimizes longevity through kinetic stability. <i>Nature</i> , 2002, 415, 343-346.	13.7	165
134	The solution structure of the viral binding domain of Tva, the cellular receptor for subgroup A avian leukosis and sarcoma virus1. <i>FEBS Letters</i> , 2001, 509, 161-168.	1.3	26
135	GCP5 and GCP6: Two New Members of the Human $\hat{\beta}$ -Tubulin Complex. <i>Molecular Biology of the Cell</i> , 2001, 12, 3340-3352.	0.9	182
136	Two energetically disparate folding pathways of alpha-lytic protease share a single transition state. , 2000, 7, 394-397.		20
137	Structure of the $\hat{\beta}$ -tubulin ring complex: a template for microtubule nucleation. <i>Nature Cell Biology</i> , 2000, 2, 365-370.	4.6	264
138	Direct Measurement of Interfacial Curvature Distributions in a Bicontinuous Block Copolymer Morphology. <i>Physical Review Letters</i> , 2000, 84, 518-521.	2.9	190
139	Image Restoration of Thick Biological Specimens for Transmission Electron Microscope Tomography. , 1999, , 92-99.		0
140	$\hat{\mu}$ -Lytic Protease Precursor: A Characterization of a Structured Folding Intermediate. <i>Biochemistry</i> , 1999, 38, 4728-4735.	1.2	31
141	Enzyme specificity under dynamic control: A normal mode analysis of $\hat{\mu}$ -lytic protease. <i>Journal of Molecular Biology</i> , 1999, 286, 267-278.	2.0	77
142	Structure of $\hat{\mu}$ -lytic protease complexed with its pro region. <i>Nature Structural Biology</i> , 1998, 5, 945-950.	9.7	69
143	Unfolded conformations of $\hat{\mu}$ -lytic protease are more stable than its native state. <i>Nature</i> , 1998, 395, 817-819.	13.7	204
144	Pro Region C-Terminus: Protease Active Site Interactions Are Critical in Catalyzing the Folding of $\hat{\mu}$ -Lytic Protease. <i>Biochemistry</i> , 1998, 37, 12058-12067.	1.2	52

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145	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
146	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
147	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
148	Sub-100nm Axial Resolution in 3D Widefield Optical Microscopy Using Two Opposing Objective Lenses. <i>Microscopy and Microanalysis</i> , 1997, 3, 801-802.	0.2	0
149	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
150	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
151	Conformational substates in enzyme mechanism: The 120 K structure of $\hat{\pm}$ -lytic protease at 1.5 Å... resolution. <i>Protein Science</i> , 1997, 6, 1375-1386.	3.1	70
152	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
153	Toward Fully Automated High-Resolution Electron Tomography. <i>Journal of Structural Biology</i> , 1996, 116, 181-189.	1.3	89
154	Bacterial extracellular secretion. <i>Membrane Protein Transport</i> , 1996, , 165-179.	0.2	1
155	Microtubule nucleation by $\hat{\pm}$ -tubulin-containing rings in the centrosome. <i>Nature</i> , 1995, 378, 638-640.	13.7	509
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