

Michel O Steinmetz

List of Publications by Year in descending order

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185
papers

15,820
citations

13827

67
h-index

19690

117
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209
all docs

209
docs citations

209
times ranked

16192
citing authors

#	ARTICLE	IF	CITATIONS
1	<i>In Vivo</i> Photocontrol of Microtubule Dynamics and Integrity, Migration and Mitosis, by the Potent GFP-Imaging-Compatible Photoswitchable Reagents SB _{Tub} A4P and SB _{Tub} 2M. <i>Journal of the American Chemical Society</i> , 2022, 144, 5614-5628.	6.6	24
2	Rational Design of a Novel Tubulin Inhibitor with a Unique Mechanism of Action. <i>Angewandte Chemie</i> , 2022, 134, .	1.6	1
3	Rational Design of a Novel Tubulin Inhibitor with a Unique Mechanism of Action. <i>Angewandte Chemie - International Edition</i> , 2022, 61, .	7.2	13
4	Crystallization Systems for the High-Resolution Structural Analysis of Tubulin-Ligand Complexes. <i>Methods in Molecular Biology</i> , 2022, 2430, 349-374.	0.4	3
5	Novel fragment-derived colchicine-site binders as microtubule-destabilizing agents. <i>European Journal of Medicinal Chemistry</i> , 2022, 241, 114614.	2.6	10
6	A Robust, GFP-Orthogonal Photoswitchable Inhibitor Scaffold Extends Optical Control over the Microtubule Cytoskeleton. <i>Cell Chemical Biology</i> , 2021, 28, 228-241.e6.	2.5	43
7	Centriole length control. <i>Current Opinion in Structural Biology</i> , 2021, 66, 89-95.	2.6	13
8	Surface tensiometry of phase separated protein and polymer droplets by the sessile drop method. <i>Soft Matter</i> , 2021, 17, 1655-1662.	1.2	32
9	The Mechanism of Selective Kinesin Inhibition by Kinesin Binding Protein. <i>Biophysical Journal</i> , 2021, 120, 6a.	0.2	0
10	Centrosomes in the spotlight: from organization to function to role in disease. <i>Current Opinion in Structural Biology</i> , 2021, 66, iii-v.	2.6	0
11	Comprehensive Analysis of Binding Sites in Tubulin. <i>Angewandte Chemie - International Edition</i> , 2021, 60, 13331-13342.	7.2	44
12	Comprehensive Analysis of Binding Sites in Tubulin. <i>Angewandte Chemie</i> , 2021, 133, 13443-13454.	1.6	7
13	Preclinical and Early Clinical Development of PTC596, a Novel Small-Molecule Tubulin-Binding Agent. <i>Molecular Cancer Therapeutics</i> , 2021, 20, 1846-1857.	1.9	13
14	1,3-Benzodioxole-Modified Noscapine Analogues: Synthesis, Antiproliferative Activity, and Tubulin-Bound Structure. <i>ChemMedChem</i> , 2021, 16, 2882-2894.	1.6	6
15	Structure and regulation of the microtubule plus-end tracking protein Kar9. <i>Structure</i> , 2021, 29, 1266-1278.e4.	1.6	5
16	Inhibiting parasite proliferation using a rationally designed anti-tubulin agent. <i>EMBO Molecular Medicine</i> , 2021, 13, e13818.	3.3	14
17	Taxanes convert regions of perturbed microtubule growth into rescue sites. <i>Nature Materials</i> , 2020, 19, 355-365.	13.3	44
18	Pharmaceutical-Grade Rigosertib Is a Microtubule-Destabilizing Agent. <i>Molecular Cell</i> , 2020, 79, 191-198.e3.	4.5	22

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19	Structural Basis of Noscapine Activation for Tubulin Binding. <i>Journal of Medicinal Chemistry</i> , 2020, 63, 8495-8501.	2.9	30
20	Structural Refinement of the Tubulin Ligand (+)-Discodermolide to Attenuate Chemotherapy-Mediated Senescence. <i>Molecular Pharmacology</i> , 2020, 98, 156-167.	1.0	4
21	Mechanisms of Motor-Independent Membrane Remodeling Driven by Dynamic Microtubules. <i>Current Biology</i> , 2020, 30, 972-987.e12.	1.8	30
22	Homodimerization of coronin A through the C-terminal coiled-coil domain is essential for multicellular differentiation of <i>Dictyostelium discoideum</i> . <i>FEBS Letters</i> , 2020, 594, 2116-2127.	1.3	1
23	Advances in long-wavelength native phasing at X-ray free-electron lasers. <i>IUCr</i> , 2020, 7, 965-975.	1.0	25
24	Structural model for differential cap maturation at growing microtubule ends. <i>ELife</i> , 2020, 9, .	2.8	44
25	WDR90 is a centriolar microtubule wall protein important for centriole architecture integrity. <i>ELife</i> , 2020, 9, .	2.8	31
26	The mechanism of kinesin inhibition by kinesin-binding protein. <i>ELife</i> , 2020, 9, .	2.8	15
27	VISAGE Reveals a Targetable Mitotic Spindle Vulnerability in Cancer Cells. <i>Cell Systems</i> , 2019, 9, 74-92.e8.	2.9	24
28	Crystal Structure of a Heterotetrameric Katanin p60:p80 Complex. <i>Structure</i> , 2019, 27, 1375-1383.e3.	1.6	11
29	Structural Basis of Colchicine-Site targeting Acylhydrazones active against Multidrug-Resistant Acute Lymphoblastic Leukemia. <i>IScience</i> , 2019, 21, 95-109.	1.9	4
30	GEF-H1 Signaling upon Microtubule Destabilization Is Required for Dendritic Cell Activation and Specific Anti-tumor Responses. <i>Cell Reports</i> , 2019, 28, 3367-3380.e8.	2.9	37
31	Structure, Thermodynamics, and Kinetics of Plinabulin Binding to Two Tubulin Isoforms. <i>CheM</i> , 2019, 5, 2969-2986.	5.8	33
32	Structural basis of tubulin detyrosination by the vasohibin-SVBP enzyme complex. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 571-582.	3.6	42
33	Microtubule minus-end regulation at a glance. <i>Journal of Cell Science</i> , 2019, 132, .	1.2	67
34	Conformational Properties of the Chemotherapeutic Drug Analogue Epothilone A: How to Model a Flexible Protein Ligand Using Scarcely Available Experimental Data. <i>Journal of Chemical Information and Modeling</i> , 2019, 59, 2218-2230.	2.5	4
35	Crystal Structure of the Cyclostreptin-Tubulin Adduct: Implications for Tubulin Activation by Taxane-Site Ligands. <i>International Journal of Molecular Sciences</i> , 2019, 20, 1392.	1.8	24
36	MAP7 family proteins regulate kinesin-1 recruitment and activation. <i>Journal of Cell Biology</i> , 2019, 218, 1298-1318.	2.3	114

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37	Structural determinants of microtubule minus end preference in CAMSAP CCK domains. <i>Nature Communications</i> , 2019, 10, 5236.	5.8	36
38	Tetrahydroisoquinoline Sulfamates as Potent Microtubule Disruptors: Synthesis, Antiproliferative and Antitubulin Activity of Dichlorobenzyl-Based Derivatives, and a Tubulin Cocrystal Structure. <i>ACS Omega</i> , 2019, 4, 755-764.	1.6	9
39	Structure-activity relationships, biological evaluation and structural studies of novel pyrrolonaphthoxazepines as antitumor agents. <i>European Journal of Medicinal Chemistry</i> , 2019, 162, 290-320.	2.6	31
40	Remote control of microtubule plus-end dynamics and function from the minus-end. <i>ELife</i> , 2019, 8, .	2.8	23
41	Structural Basis of Formation of the Microtubule Minus-End-Regulating CAMSAP-Katanin Complex. <i>Structure</i> , 2018, 26, 375-382.e4.	1.6	47
42	Cep120 promotes microtubule formation through a unique tubulin binding C2 domain. <i>Journal of Structural Biology</i> , 2018, 203, 62-70.	1.3	10
43	Interaction between the <i>Caenorhabditis elegans</i> centriolar protein SAS-5 and microtubules facilitates organelle assembly. <i>Molecular Biology of the Cell</i> , 2018, 29, 722-735.	0.9	8
44	Structure-Function Relationship of the Bik1-Bim1 Complex. <i>Structure</i> , 2018, 26, 607-618.e4.	1.6	18
45	High-affinity ligands of the colchicine domain in tubulin based on a structure-guided design. <i>Scientific Reports</i> , 2018, 8, 4242.	1.6	42
46	Quinazolinone-Based Anticancer Agents: Synthesis, Antiproliferative SAR, Antitubulin Activity, and Tubulin Co-crystal Structure. <i>Journal of Medicinal Chemistry</i> , 2018, 61, 1031-1044.	2.9	91
47	Combinatorial use of disulfide bridges and native sulfur-SAD phasing for rapid structure determination of coiled-coils. <i>Bioscience Reports</i> , 2018, 38, .	1.1	4
48	A fluorescence anisotropy assay to discover and characterize ligands targeting the maytansine site of tubulin. <i>Nature Communications</i> , 2018, 9, 2106.	5.8	41
49	CLASP Suppresses Microtubule Catastrophes through a Single TOG Domain. <i>Developmental Cell</i> , 2018, 46, 40-58.e8.	3.1	110
50	Sustainable Syntheses of (âˆ“)Jerantinines A & E and Structural Characterisation of the Jerantinine-Tubulin Complex at the Colchicine Binding Site. <i>Scientific Reports</i> , 2018, 8, 10617.	1.6	10
51	Microtubule-Targeting Agents: Strategies To Hijack the Cytoskeleton. <i>Trends in Cell Biology</i> , 2018, 28, 776-792.	3.6	340
52	Structural Basis of Microtubule Stabilization by Discodermolide. <i>ChemBioChem</i> , 2017, 18, 905-909.	1.3	30
53	Deconvolution of Buparlisib's mechanism of action defines specific PI3K and tubulin inhibitors for therapeutic intervention. <i>Nature Communications</i> , 2017, 8, 14683.	5.8	88
54	Structural Basis of cis- and trans-Combretastatin Binding to Tubulin. <i>Chem</i> , 2017, 2, 102-113.	5.8	164

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55	Microtubule minus-end regulation at spindle poles by an ASPM-katanin complex. <i>Nature Cell Biology</i> , 2017, 19, 480-492.	4.6	147
56	Short Linear Sequence Motif LxxPTPh Targets Diverse Proteins to Growing Microtubule Ends. <i>Structure</i> , 2017, 25, 924-932.e4.	1.6	37
57	Combined CRISPRi/a-Based Chemical Genetic Screens Reveal that Rigosertib Is a Microtubule-Destabilizing Agent. <i>Molecular Cell</i> , 2017, 68, 210-223.e6.	4.5	197
58	A structural model for microtubule minus-end recognition and protection by CAMSAP proteins. <i>Nature Structural and Molecular Biology</i> , 2017, 24, 931-943.	3.6	86
59	Serial millisecond crystallography for routine room-temperature structure determination at synchrotrons. <i>Nature Communications</i> , 2017, 8, 542.	5.8	203
60	Identification of Chlamydomonas Central Core Centriolar Proteins Reveals a Role for Human WDR90 in Ciliogenesis. <i>Current Biology</i> , 2017, 27, 2486-2498.e6.	1.8	53
61	Structural basis of katanin p60:p80 complex formation. <i>Scientific Reports</i> , 2017, 7, 14893.	1.6	24
62	Kinesin-4 KIF21B is a potent microtubule pausing factor. <i>ELife</i> , 2017, 6, .	2.8	51
63	Quinolin-6-Yloxyacetamides Are Microtubule Destabilizing Agents That Bind to the Colchicine Site of Tubulin. <i>International Journal of Molecular Sciences</i> , 2017, 18, 1336.	1.8	9
64	Antivascular and antitumor properties of the tubulin-binding chalcone TUB091. <i>Oncotarget</i> , 2017, 8, 14325-14342.	0.8	50
65	Pironetin Binds Covalently to Cys316 and Perturbs a Major Loop and Helix of α -Tubulin to Inhibit Microtubule Formation. <i>Journal of Molecular Biology</i> , 2016, 428, 2981-2988.	2.0	64
66	Structural Determinants of the Dictyostatin Chemotype for Tubulin Binding Affinity and Antitumor Activity Against Taxane- and Etoposide-Resistant Cancer Cells. <i>ACS Omega</i> , 2016, 1, 1192-1204.	1.6	22
67	Molecular basis of Kar9-Bim1 complex function during mating and spindle positioning. <i>Molecular Biology of the Cell</i> , 2016, 27, 3729-3745.	0.9	17
68	The Human Centriolar Protein CEP135 Contains a Two-Stranded Coiled-Coil Domain Critical for Microtubule Binding. <i>Structure</i> , 2016, 24, 1358-1371.	1.6	27
69	EB1 interacts with outwardly curved and straight regions of the microtubule lattice. <i>Nature Cell Biology</i> , 2016, 18, 1102-1108.	4.6	81
70	Biophysical and Structural Characterization of the Centriolar Protein Cep104 Interaction Network. <i>Journal of Biological Chemistry</i> , 2016, 291, 18496-18504.	1.6	31
71	The synthetic diazonamide DZ-2384 has distinct effects on microtubule curvature and dynamics without neurotoxicity. <i>Science Translational Medicine</i> , 2016, 8, 365ra159.	5.8	42
72	Structural basis for misregulation of kinesin KIF21A autoinhibition by CFEOM1 disease mutations. <i>Scientific Reports</i> , 2016, 6, 30668.	1.6	26

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73	Crystal Structures of the Human Doublecortin C- and N-terminal Domains in Complex with Specific Antibodies. <i>Journal of Biological Chemistry</i> , 2016, 291, 16292-16306.	1.6	16
74	Data-collection strategy for challenging native SAD phasing. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016, 72, 421-429.	1.1	42
75	Centriolar CPAP/SAS-4 Imparts Slow Processive Microtubule Growth. <i>Developmental Cell</i> , 2016, 37, 362-376.	3.1	90
76	Termination of Protofilament Elongation by Eribulin Induces Lattice Defects that Promote Microtubule Catastrophes. <i>Current Biology</i> , 2016, 26, 1713-1721.	1.8	97
77	SAS-6 engineering reveals interdependence between cartwheel and microtubules in determining centriole Architecture. <i>Nature Cell Biology</i> , 2016, 18, 393-403.	4.6	73
78	Kinesin-Binding Protein Controls Microtubule Dynamics and Cargo Trafficking by Regulating Kinesin Motor Activity. <i>Current Biology</i> , 2016, 26, 849-861.	1.8	82
79	Structural Basis of Microtubule Destabilization by Potent Auristatin Anti-Mitotics. <i>PLoS ONE</i> , 2016, 11, e0160890.	1.1	121
80	Abstract 1364: Novel 4-(pyrimidin-2-yl)morpholines targeting the colchicine-binding site of tubulin. , 2016, , .		0
81	Optochemistry to control the microtubule cytoskeleton. <i>EMBO Journal</i> , 2015, 34, 2114-2116.	3.5	4
82	Control of microtubule organization and dynamics: two ends in the limelight. <i>Nature Reviews Molecular Cell Biology</i> , 2015, 16, 711-726.	16.1	733
83	Fast native-SAD phasing for routine macromolecular structure determination. <i>Nature Methods</i> , 2015, 12, 131-133.	9.0	120
84	Abstract 671: BKM120-mediated G2 arrest: Structural and functional segregation of off-target action and PI3K inhibition. , 2015, , .		1
85	Strukturmodell: Structural Basis of Microtubule Stabilization by Laulimalide and Peloruside. <i>Angewandte Chemie - International Edition</i> , 2014, 53, 1621-1625.	1.6	0
86	Actin-microtubule coordination at growing microtubule ends. <i>Nature Communications</i> , 2014, 5, 4778.	5.8	126
87	In Vitro Reconstitution of Dynamic Microtubules Interacting with Actin Filament Networks. <i>Methods in Enzymology</i> , 2014, 540, 301-320.	0.4	24
88	Structural Basis of Microtubule Stabilization by Laulimalide and Peloruside. <i>Angewandte Chemie - International Edition</i> , 2014, 53, 1621-1625.	7.2	154
89	The Novel Microtubule-Destabilizing Drug BAL27862 Binds to the Colchicine Site of Tubulin with Distinct Effects on Microtubule Organization. <i>Journal of Molecular Biology</i> , 2014, 426, 1848-1860.	2.0	240
90	Structural basis for recognition of synaptic vesicle protein 2C by botulinum neurotoxin A. <i>Nature</i> , 2014, 505, 108-111.	13.7	103

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91	A missense mutation in the PISA domain of HsSAS-6 causes autosomal recessive primary microcephaly in a large consanguineous Pakistani family. <i>Human Molecular Genetics</i> , 2014, 23, 5940-5949.	1.4	63
92	A new tubulin-binding site and pharmacophore for microtubule-destabilizing anticancer drugs. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 13817-13821.	3.3	229
93	Reconstitution of a hierarchical +TIP interaction network controlling microtubule end tracking of dynein. <i>Nature Cell Biology</i> , 2014, 16, 804-811.	4.6	100
94	Localizing Chemical Groups while Imaging Single Native Proteins by High-Resolution Atomic Force Microscopy. <i>Nano Letters</i> , 2014, 14, 2957-2964.	4.5	48
95	Native Architecture of the Centriole Proximal Region Reveals Features Underlying Its 9-Fold Radial Symmetry. <i>Current Biology</i> , 2013, 23, 1620-1628.	1.8	113
96	Molecular Mechanism of Action of Microtubule-Stabilizing Anticancer Agents. <i>Science</i> , 2013, 339, 587-590.	6.0	436
97	<i>Caenorhabditis elegans</i> centriolar protein SAS-6 forms a spiral that is consistent with imparting a ninefold symmetry. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 11373-11378.	3.3	54
98	End-binding proteins sensitize microtubules to the action of microtubule-targeting agents. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 8900-8905.	3.3	101
99	Structural basis of tubulin tyrosination by tubulin tyrosine ligase. <i>Journal of Cell Biology</i> , 2013, 200, 259-270.	2.3	189
100	Structural Basis for the Oligomerization-State Switch from a Dimer to a Trimer of an Engineered Cortaxillin-1 Coiled-Coil Variant. <i>PLoS ONE</i> , 2013, 8, e63370.	1.1	2
101	End Binding Proteins Are Obligatory Dimers. <i>PLoS ONE</i> , 2013, 8, e74448.	1.1	32
102	ELM—the database of eukaryotic linear motifs. <i>Nucleic Acids Research</i> , 2012, 40, D242-D251.	6.5	290
103	Sequence Determinants of a Microtubule Tip Localization Signal (MtLS). <i>Journal of Biological Chemistry</i> , 2012, 287, 28227-28242.	1.6	44
104	Cooperative Stabilization of Microtubule Dynamics by EB1 and CLIP-170 Involves Displacement of Stably Bound P ₁ at Microtubule Ends. <i>Biochemistry</i> , 2012, 51, 3021-3030.	1.2	20
105	Influence of 63Ser Phosphorylation and Dephosphorylation on the Structure of the Stathmin Helical Nucleation Sequence: A Molecular Dynamics Study. <i>Biochemistry</i> , 2012, 51, 8455-8463.	1.2	7
106	Tyrosine-dependent capture of CAP-Gly domain-containing proteins in complex mixture by EB1 C-terminal peptidic probes. <i>Journal of Proteomics</i> , 2012, 75, 3605-3616.	1.2	3
107	Interaction of mammalian end binding proteins with CAP-Gly domains of CLIP-170 and p150glued. <i>Journal of Structural Biology</i> , 2012, 177, 160-167.	1.3	36
108	A Proteome-wide Screen for Mammalian SxIP Motif-Containing Microtubule Plus-End Tracking Proteins. <i>Current Biology</i> , 2012, 22, 1800-1807.	1.8	192

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109	Probing the Structure and Dynamics of Proteins by Combining Molecular Dynamics Simulations and Experimental NMR Data. <i>Journal of Chemical Theory and Computation</i> , 2012, 8, 3430-3444.	2.3	13
110	Structural Basis of the 9-Fold Symmetry of Centrioles. <i>Cell</i> , 2011, 144, 364-375.	13.5	317
111	Microtubule End Binding: EBs Sense the Guanine Nucleotide State. <i>Current Biology</i> , 2011, 21, R283-R285.	1.8	19
112	SLAIN2 links microtubule plus end tracking proteins and controls microtubule growth in interphase. <i>Journal of Cell Biology</i> , 2011, 193, 1083-1099.	2.3	116
113	Insights into EB1 structure and the role of its C-terminal domain for discriminating microtubule tips from the lattice. <i>Molecular Biology of the Cell</i> , 2011, 22, 2912-2923.	0.9	59
114	Methods of NMR structure refinement: molecular dynamics simulations improve the agreement with measured NMR data of a C-terminal peptide of GCN4-p1. <i>Journal of Biomolecular NMR</i> , 2010, 47, 221-235.	1.6	31
115	In Vitro Reconstitution of the Functional Interplay between MCAK and EB3 at Microtubule Plus Ends. <i>Current Biology</i> , 2010, 20, 1717-1722.	1.8	130
116	Automated seamless DNA co-transformation cloning with direct expression vectors applying positive or negative insert selection. <i>BMC Biotechnology</i> , 2010, 10, 56.	1.7	39
117	Exploring the trigger sequence of the GCN4 coiled-coil: Biased molecular dynamics resolves apparent inconsistencies in NMR measurements. <i>Protein Science</i> , 2010, 19, 2462-2474.	3.1	11
118	Microtubule +TIPs at a glance. <i>Journal of Cell Science</i> , 2010, 123, 3415-3419.	1.2	236
119	Molecular basis of coiled-coil oligomerization-state specificity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 19850-19855.	3.3	66
120	Molecular Insights into Mammalian End-binding Protein Heterodimerization. <i>Journal of Biological Chemistry</i> , 2010, 285, 5802-5814.	1.6	48
121	Drosophila Stathmins Bind Tubulin Heterodimers with High and Variable Stoichiometries. <i>Journal of Biological Chemistry</i> , 2010, 285, 11667-11680.	1.6	17
122	Insights into Peroxisome Function from the Structure of PEX3 in Complex with a Soluble Fragment of PEX19. <i>Journal of Biological Chemistry</i> , 2010, 285, 25410-25417.	1.6	46
123	Laminin chain assembly is regulated by specific coiled-coil interactions. <i>Journal of Structural Biology</i> , 2010, 170, 398-405.	1.3	41
124	Regulation of Microtubule Dynamic Instability in Vitro by Differentially Phosphorylated Stathmin. <i>Journal of Biological Chemistry</i> , 2009, 284, 15640-15649.	1.6	73
125	Solid State NMR Spectroscopy Reveals that <i>E. coli</i> Inclusion Bodies of HETs(218â€“289) are Amyloids. <i>Angewandte Chemie - International Edition</i> , 2009, 48, 4858-4860.	7.2	73
126	Automated unrestricted multigene recombineering for multiprotein complex production. <i>Nature Methods</i> , 2009, 6, 447-450.	9.0	98

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127	An EB1-Binding Motif Acts as a Microtubule Tip Localization Signal. <i>Cell</i> , 2009, 138, 366-376.	13.5	594
128	Mammalian end binding proteins control persistent microtubule growth. <i>Journal of Cell Biology</i> , 2009, 184, 691-706.	2.3	331
129	High-level Expression and Purification of a Designed Angiopoietin-1 Chimeric Protein, COMP-Ang1, Produced in Chinese Hamster Ovary Cells. <i>Protein Journal</i> , 2008, 27, 319-326.	0.7	16
130	Exploring the Conserved Water Site and Hydration of a Coiled-Coil Trimerisation Motif: A MD Simulation Study. <i>ChemBioChem</i> , 2008, 9, 1749-1756.	1.3	7
131	Polymorphism in an Amyloid-Like Fibril-Forming Model Peptide. <i>Angewandte Chemie - International Edition</i> , 2008, 47, 5842-5845.	7.2	53
132	Tracking the ends: a dynamic protein network controls the fate of microtubule tips. <i>Nature Reviews Molecular Cell Biology</i> , 2008, 9, 309-322.	16.1	908
133	STIM1 Is a MT-Plus-End-Tracking Protein Involved in Remodeling of the ER. <i>Current Biology</i> , 2008, 18, 177-182.	1.8	378
134	Capturing protein tails by CAP-Gly domains. <i>Trends in Biochemical Sciences</i> , 2008, 33, 535-545.	3.7	106
135	Atomic Models of De Novo Designed α -Met Amyloid-Like Fibrils. <i>Journal of Molecular Biology</i> , 2008, 376, 898-912.	2.0	34
136	Suppression of Microtubule Dynamic Instability by the +TIP Protein EB1 and Its Modulation by the CAP-Gly Domain of p150Glued. <i>Biochemistry</i> , 2008, 47, 779-786.	1.2	69
137	Motor Neuron Disease-Associated Mutant Vesicle-Associated Membrane Protein-Associated Protein (VAP) B Recruits Wild-Type VAPs into Endoplasmic Reticulum-Derived Tubular Aggregates. <i>Journal of Neuroscience</i> , 2007, 27, 9801-9815.	1.7	203
138	Molecular basis of coiled-coil formation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 7062-7067.	3.3	116
139	Structural basis for the specific inhibition of protein kinase G, a virulence factor of <i>Mycobacterium tuberculosis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 12151-12156.	3.3	152
140	Structure and thermodynamics of the tubulin-stathmin interaction. <i>Journal of Structural Biology</i> , 2007, 158, 137-147.	1.3	75
141	Production of in vitro amplified DNA pseudolibraries and high-throughput cDNA target amplification. <i>BMC Biotechnology</i> , 2007, 7, 31.	1.7	3
142	The <i>Caenorhabditis elegans</i> septin complex is nonpolar. <i>EMBO Journal</i> , 2007, 26, 3296-3307.	3.5	130
143	Structure of a VEGF-VEGF receptor complex determined by electron microscopy. <i>Nature Structural and Molecular Biology</i> , 2007, 14, 249-250.	3.6	137
144	Structure-function relationship of CAP-Gly domains. <i>Nature Structural and Molecular Biology</i> , 2007, 14, 959-967.	3.6	176

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145	Configurational entropy elucidates the role of salt-bridge networks in protein thermostability. <i>Protein Science</i> , 2007, 16, 1349-1359.	3.1	99
146	Key Interaction Modes of Dynamic +TIP Networks. <i>Molecular Cell</i> , 2006, 23, 663-671.	4.5	160
147	De novo design of a two-stranded coiled-coil switch peptide. <i>Journal of Structural Biology</i> , 2006, 155, 146-153.	1.3	41
148	¹³ C, ¹⁵ N Resonance Assignment of Parts of the HET-s Prion Protein in its Amyloid Form. <i>Journal of Biomolecular NMR</i> , 2006, 34, 75-87.	1.6	91
149	Control of Intrinsically Disordered Stathmin by Multisite Phosphorylation*. <i>Journal of Biological Chemistry</i> , 2006, 281, 16078-16083.	1.6	45
150	Structure of the Extracellular Domain of Tie Receptor Tyrosine Kinases and Localization of the Angiopoietin-binding Epitope. <i>Journal of Biological Chemistry</i> , 2006, 281, 28408-28414.	1.6	35
151	Structural insights into the EB1-APC interaction. <i>EMBO Journal</i> , 2005, 24, 261-269.	3.5	138
152	Structural insights into the EB1-APC interaction. <i>EMBO Journal</i> , 2005, 24, 872-872.	3.5	4
153	Structural basis for the regulation of tubulin by vinblastine. <i>Nature</i> , 2005, 435, 519-522.	13.7	651
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