

Maya Topf

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6312370/publications.pdf>

Version: 2024-02-01

115
papers

7,532
citations

41344

49
h-index

62596

80
g-index

141
all docs

141
docs citations

141
times ranked

9770
citing authors

#	ARTICLE	IF	CITATIONS
1	Structural mass spectrometry decodes domain interaction and dynamics of the full-length Human Histone Deacetylase 2. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2022, 1870, 140759.	2.3	0
2	The pore conformation of lymphocyte perforin. <i>Science Advances</i> , 2022, 8, eabk3147.	10.3	10
3	Stoichiometry-Selective Antagonism of $\alpha 4\beta 2$ Nicotinic Acetylcholine Receptors by Fluoroquinolone Antibiotics. <i>ACS Chemical Neuroscience</i> , 2022, 13, 1805-1817.	3.5	3
4	Assessment of protein-protein interfaces in cryo-EM derived assemblies. <i>Nature Communications</i> , 2021, 12, 3399.	12.8	20
5	Cryo-EM structure of a microtubule-bound parasite kinesin motor and implications for its mechanism and inhibition. <i>Journal of Biological Chemistry</i> , 2021, 297, 101063.	3.4	13
6	TopoStats - A program for automated tracing of biomolecules from AFM images. <i>Methods</i> , 2021, 193, 68-79.	3.8	23
7	Computational models in the service of X-ray and cryo-electron microscopy structure determination. <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 1633-1646.	2.6	37
8	Target highlights in CASP14: Analysis of models by structure providers. <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 1647-1672.	2.6	27
9	Cryo-EM targets in CASP14. <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 1949-1958.	2.6	11
10	Critical assessment of methods of protein structure prediction (CASP) - Round XIV. <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 1607-1617.	2.6	281
11	TEMPy 2: a Python library with improved 3D electron microscopy density-fitting and validation workflows. <i>Acta Crystallographica Section D: Structural Biology</i> , 2021, 77, 41-47.	2.3	32
12	Automated Modeling and Validation of Protein Complexes in Cryo-EM Maps. <i>Methods in Molecular Biology</i> , 2021, 2215, 189-223.	0.9	2
13	The prefusion structure of herpes simplex virus glycoprotein B. <i>Science Advances</i> , 2020, 6, .	10.3	50
14	KMT2B-related disorders: expansion of the phenotypic spectrum and long-term efficacy of deep brain stimulation. <i>Brain</i> , 2020, 143, 3242-3261.	7.6	57
15	Combining Information from Crosslinks and Monolinks in the Modeling of Protein Structures. <i>Structure</i> , 2020, 28, 1061-1070.e3.	3.3	17
16	Comparing Cryo-EM Reconstructions and Validating Atomic Model Fit Using Difference Maps. <i>Journal of Chemical Information and Modeling</i> , 2020, 60, 2552-2560.	5.4	29
17	Structure of Microtubule-Trapped Human Kinesin-5 and Its Mechanism of Inhibition Revealed Using Cryoelectron Microscopy. <i>Structure</i> , 2020, 28, 450-457.e5.	3.3	22
18	Modelling structures in cryo-EM maps. <i>Current Opinion in Structural Biology</i> , 2019, 58, 105-114.	5.7	53

#	ARTICLE	IF	CITATIONS
19	Cryo-electron microscopy targets in CASP13: Overview and evaluation of results. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019, 87, 1128-1140.	2.6	21
20	Structural transitions during the scaffolding-driven assembly of a viral capsid. <i>Nature Communications</i> , 2019, 10, 4840.	12.8	21
21	Critical assessment of methods of protein structure prediction (CASP) – Round XIII. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019, 87, 1011-1020.	2.6	380
22	Target highlights in CASP13: Experimental target structures through the eyes of their authors. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019, 87, 1037-1057.	2.6	12
23	Exome sequencing identifies variants in FKBP4 that are associated with recurrent fetal loss in humans. <i>Human Molecular Genetics</i> , 2019, 28, 3466-3474.	2.9	13
24	Protein interactions and consensus clustering analysis uncover insights into herpesvirus virion structure and function relationships. <i>PLoS Biology</i> , 2019, 17, e3000316.	5.6	18
25	Frequency and phenotypic spectrum of <i>KMT2B</i> dystonia in childhood: A single-center cohort study. <i>Movement Disorders</i> , 2019, 34, 1516-1527.	3.9	55
26	Modeling Protein Monomers and Complexes using Restraints from Crosslinking Mass Spectrometry. <i>Biophysical Journal</i> , 2019, 116, 330a.	0.5	0
27	The Cryo-EM Structure and Activity of Kinesin-5 from <i>Plasmodium falciparum</i> : Mechanistic Lessons from a Parasite Kinesin. <i>Biophysical Journal</i> , 2019, 116, 308a.	0.5	0
28	Conserved Central Intraviral Protein Interactome of the <i>Herpesviridae</i> Family. <i>MSystems</i> , 2019, 4, .	3.8	4
29	Cover Image, Volume 87, Issue 12. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019, 87, C4.	2.6	0
30	Mapping Aldehyde Dehydrogenase 1A1 Activity using an [¹⁸ F]Substrate-Based Approach. <i>Chemistry - A European Journal</i> , 2019, 25, 2345-2351.	3.3	2
31	Genetic diversity of CHC22 clathrin impacts its function in glucose metabolism. <i>ELife</i> , 2019, 8, .	6.0	22
32	Diversity of Nicotinic Acetylcholine Receptor Positive Allosteric Modulators Revealed by Mutagenesis and a Revised Structural Model. <i>Molecular Pharmacology</i> , 2018, 93, 128-140.	2.3	39
33	Disease-associated missense mutations in GluN2B subunit alter NMDA receptor ligand binding and ion channel properties. <i>Nature Communications</i> , 2018, 9, 957.	12.8	58
34	Clinical and molecular characterization of <i>KCNT1</i> -related severe early-onset epilepsy. <i>Neurology</i> , 2018, 90, e55-e66.	1.1	89
35	CryoEM reveals how the complement membrane attack complex ruptures lipid bilayers. <i>Nature Communications</i> , 2018, 9, 5316.	12.8	83
36	Analyses of Tissue Culture Adaptation of Human Herpesvirus-6A by Whole Genome Deep Sequencing Redefines the Reference Sequence and Identifies Virus Entry Complex Changes. <i>Viruses</i> , 2018, 10, 16.	3.3	7

#	ARTICLE	IF	CITATIONS
37	Structural Model for Preferential Microtubule Minus End Binding by CAMSAP CKK Domains. <i>Biophysical Journal</i> , 2018, 114, 507a-508a.	0.5	0
38	Jwalk and MNXL web server: model validation using restraints from crosslinking mass spectrometry. <i>Bioinformatics</i> , 2018, 34, 3584-3585.	4.1	23
39	Modeling Protein Complexes Using Restraints from Crosslinking Mass Spectrometry. <i>Structure</i> , 2018, 26, 1015-1024.e2.	3.3	50
40	Identification by virtual screening and functional characterisation of novel positive and negative allosteric modulators of the $\alpha 7$ nicotinic acetylcholine receptor. <i>Neuropharmacology</i> , 2018, 139, 194-204.	4.1	14
41	Mosaic RAS/MAPK variants cause sporadic vascular malformations which respond to targeted therapy. <i>Journal of Clinical Investigation</i> , 2018, 128, 1496-1508.	8.2	191
42	Improved metrics for comparing structures of macromolecular assemblies determined by 3D electron-microscopy. <i>Journal of Structural Biology</i> , 2017, 199, 12-26.	2.8	56
43	Unravelling the Mechanism of Membrane Attack Complex Pore Closure. <i>Biophysical Journal</i> , 2017, 112, 335a.	0.5	0
44	Mutations in the histone methyltransferase gene KMT2B cause complex early-onset dystonia. <i>Nature Genetics</i> , 2017, 49, 223-237.	21.4	186
45	A structural model for microtubule minus-end recognition and protection by CAMSAP proteins. <i>Nature Structural and Molecular Biology</i> , 2017, 24, 931-943.	8.2	86
46	Structural basis of human kinesin-8 function and inhibition. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E9539-E9548.	7.1	48
47	Structural pathway of regulated substrate transfer and threading through an Hsp100 disaggregase. <i>Science Advances</i> , 2017, 3, e1701726.	10.3	112
48	The Role of Disulfide Bond Replacements in Analogues of the Tarantula Toxin ProTx-II and Their Effects on Inhibition of the Voltage-Gated Sodium Ion Channel $Na_v1.7$. <i>Journal of the American Chemical Society</i> , 2017, 139, 13063-13075.	13.7	41
49	Integrative modelling of cellular assemblies. <i>Current Opinion in Structural Biology</i> , 2017, 46, 102-109.	5.7	15
50	Disruption of a Structurally Important Extracellular Element in the Glycine Receptor Leads to Decreased Synaptic Integration and Signaling Resulting in Severe Startle Disease. <i>Journal of Neuroscience</i> , 2017, 37, 7948-7961.	3.6	15
51	The divergent mitotic kinesin MKLP2 exhibits atypical structure and mechanochemistry. <i>ELife</i> , 2017, 6, .	6.0	39
52	HVint: A Strategy for Identifying Novel Protein-Protein Interactions in Herpes Simplex Virus Type 1. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 2939-2953.	3.8	17
53	The Importance of Non-accessible Crosslinks and Solvent Accessible Surface Distance in Modeling Proteins with Restraints From Crosslinking Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 2491-2500.	3.8	79
54	Refinement of atomic models in high resolution EM reconstructions using Flex-EM and local assessment. <i>Methods</i> , 2016, 100, 42-49.	3.8	101

#	ARTICLE	IF	CITATIONS
55	Two distinct trimeric conformations of natively membrane-anchored full-length herpes simplex virus 1 glycoprotein B. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 4176-4181.	7.1	93
56	Genetic and functional analyses demonstrate a role for abnormal glycinergic signaling in autism. <i>Molecular Psychiatry</i> , 2016, 21, 936-945.	7.9	85
57	$\hat{\text{i}}^3$ -TEMPy: Simultaneous Fitting of Components in 3D-EM Maps of Their Assembly Using a Genetic Algorithm. <i>Structure</i> , 2015, 23, 2365-2376.	3.3	34
58	Collaborative Computational Project for Electron cryo-Microscopy. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 123-126.	2.5	84
59	Outcome of the First wwPDB Hybrid/Integrative Methods Task Force Workshop. <i>Structure</i> , 2015, 23, 1156-1167.	3.3	159
60	Conformational Changes during Pore Formation by the Perforin-Related Protein Pleurotolysin. <i>PLoS Biology</i> , 2015, 13, e1002049.	5.6	114
61	Mutations in SLC12A5 in epilepsy of infancy with migrating focal seizures. <i>Nature Communications</i> , 2015, 6, 8038.	12.8	160
62	Novel Missense Mutation A789V in IQSEC2 Underlies X-Linked Intellectual Disability in the MRX78 Family. <i>Frontiers in Molecular Neuroscience</i> , 2015, 8, 85.	2.9	23
63	<i>i>TEMPy</i> : a Python library for assessment of three-dimensional electron microscopy density fits. <i>Journal of Applied Crystallography</i> , 2015, 48, 1314-1323.	4.5	75
64	Photo-antagonism of the GABAA receptor. <i>Nature Communications</i> , 2014, 5, 4454.	12.8	22
65	Combined approaches to flexible fitting and assessment in virus capsids undergoing conformational change. <i>Journal of Structural Biology</i> , 2014, 185, 427-439.	2.8	23
66	Allosteric signalling in the outer membrane translocation domain of PapC usher. <i>ELife</i> , 2014, 3, .	6.0	18
67	Conserved mechanisms of microtubule-stimulated ADP release, ATP binding, and force generation in transport kinesins. <i>ELife</i> , 2014, 3, e03680.	6.0	100
68	Stepwise visualization of membrane pore formation by suliyisin, a bacterial cholesterol-dependent cytolysin. <i>ELife</i> , 2014, 3, e04247.	6.0	145
69	Conformational States of Macromolecular Assemblies Explored by Integrative Structure Calculation. <i>Structure</i> , 2013, 21, 1500-1508.	3.3	29
70	Distinct phenotypes in zebrafish models of human startle disease. <i>Neurobiology of Disease</i> , 2013, 60, 139-151.	4.4	32
71	Novel missense mutations in the glycine receptor $\hat{\text{i}}^2$ subunit gene (GLRB) in startle disease. <i>Neurobiology of Disease</i> , 2013, 52, 137-149.	4.4	54
72	The Structure of Herpesvirus Fusion Glycoprotein B-Bilayer Complex Reveals the Protein-Membrane and Lateral Protein-Protein Interaction. <i>Structure</i> , 2013, 21, 1396-1405.	3.3	47

#	ARTICLE	IF	CITATIONS
73	Changes in Apaf-1 Conformation That Drive Apoptosome Assembly. <i>Biochemistry</i> , 2013, 52, 2319-2327.	2.5	53
74	Structure of a translocation signal domain mediating conjugative transfer by type <scp>IV</scp> secretion systems. <i>Molecular Microbiology</i> , 2013, 89, 324-333.	2.5	40
75	RIBFIND: a web server for identifying rigid bodies in protein structures and to aid flexible fitting into cryo EM maps. <i>Bioinformatics</i> , 2012, 28, 2391-2393.	4.1	19
76	Mutations in the GlyT2 Gene (SLC6A5) Are a Second Major Cause of Startle Disease. <i>Journal of Biological Chemistry</i> , 2012, 287, 28975-28985.	3.4	84
77	A Novel Dominant Hyperekplexia Mutation Y705C Alters Trafficking and Biochemical Properties of the Presynaptic Glycine Transporter GlyT2. <i>Journal of Biological Chemistry</i> , 2012, 287, 28986-29002.	3.4	42
78	Molecular mechanisms of glycine transporter GlyT2 mutations in startle disease. <i>Biological Chemistry</i> , 2012, 393, 283-289.	2.5	7
79	Finding rigid bodies in protein structures: Application to flexible fitting into cryoEM maps. <i>Journal of Structural Biology</i> , 2012, 177, 520-531.	2.8	33
80	ATP-Triggered Conformational Changes Delineate Substrate-Binding and -Folding Mechanics of the GroEL Chaperonin. <i>Cell</i> , 2012, 149, 113-123.	28.9	160
81	Structural Analysis of Coxsackievirus A7 Reveals Conformational Changes Associated with Uncoating. <i>Journal of Virology</i> , 2012, 86, 7207-7215.	3.4	41
82	Identification of congenital muscular dystonia 2 associated with an inherited GlyT2 defect in Belgian Blue cattle from the United Kingdom. <i>Animal Genetics</i> , 2012, 43, 267-270.	1.7	8
83	Exploring the spatial and temporal organization of a cell's proteome. <i>Journal of Structural Biology</i> , 2011, 173, 483-496.	2.8	36
84	Scoring functions for cryoEM density fitting. <i>Journal of Structural Biology</i> , 2011, 174, 333-343.	2.8	65
85	Structure of the Drosophila Apoptosome at 6.9Å Resolution. <i>Structure</i> , 2011, 19, 128-140.	3.3	73
86	Structure of an Apoptosome-Procaspase-9 CARD Complex. <i>Structure</i> , 2010, 18, 571-583.	3.3	118
87	RNA channelling by the eukaryotic exosome. <i>EMBO Reports</i> , 2010, 11, 936-942.	4.5	68
88	Mechanism of eIF6-mediated Inhibition of Ribosomal Subunit Joining. <i>Journal of Biological Chemistry</i> , 2010, 285, 14848-14851.	3.4	107
89	CHOYCE: a web server for constrained homology modelling with cryoEM maps. <i>Bioinformatics</i> , 2010, 26, 1673-1674.	4.1	7
90	TUBA1A mutations cause wide spectrum lissencephaly (smooth brain) and suggest that multiple neuronal migration pathways converge on alpha tubulins. <i>Human Molecular Genetics</i> , 2010, 19, 2817-2827.	2.9	176

#	ARTICLE	IF	CITATIONS
91	A fast mathematical programming procedure for simultaneous fitting of assembly components into cryoEM density maps. <i>Bioinformatics</i> , 2010, 26, i261-i268.	4.1	21
92	Comprehensive Molecular Structure of the Eukaryotic Ribosome. <i>Structure</i> , 2009, 17, 1591-1604.	3.3	140
93	Inferential Optimization for Simultaneous Fitting of Multiple Components into a CryoEM Map of Their Assembly. <i>Journal of Molecular Biology</i> , 2009, 388, 180-194.	4.2	117
94	Mechanism of lid closure in the eukaryotic chaperonin TRiC/CCT. <i>Nature Structural and Molecular Biology</i> , 2008, 15, 746-753.	8.2	91
95	A new tRNA intermediate revealed on the ribosome during EF4-mediated back-translocation. <i>Nature Structural and Molecular Biology</i> , 2008, 15, 910-915.	8.2	65
96	Protein Structure Fitting and Refinement Guided by Cryo-EM Density. <i>Structure</i> , 2008, 16, 295-307.	3.3	334
97	Structure of the Mammalian 80S Ribosome at 8.7 Å... Resolution. <i>Structure</i> , 2008, 16, 535-548.	3.3	135
98	The genetics of hyperekplexia: more than startle!. <i>Trends in Genetics</i> , 2008, 24, 439-447.	6.7	187
99	Crystallographic Conformers of Actin in a Biologically Active Bundle of Filaments. <i>Journal of Molecular Biology</i> , 2008, 375, 331-336.	4.2	37
100	Mapping a molecular link between allosteric inhibition and activation of the glycine receptor. <i>Nature Structural and Molecular Biology</i> , 2008, 15, 1084-1093.	8.2	33
101	Integrating Diverse Data for Structure Determination of Macromolecular Assemblies. <i>Annual Review of Biochemistry</i> , 2008, 77, 443-477.	11.1	204
102	Subnanometer-resolution electron cryomicroscopy-based domain models for the cytoplasmic region of skeletal muscle RyR channel. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 9610-9615.	7.1	106
103	Refinement of Protein Structures by Iterative Comparative Modeling and CryoEM Density Fitting. <i>Journal of Molecular Biology</i> , 2006, 357, 1655-1668.	4.2	104
104	Combining electron microscopy and comparative protein structure modeling. <i>Current Opinion in Structural Biology</i> , 2005, 15, 578-585.	5.7	73
105	Structural characterization of components of protein assemblies by comparative modeling and electron cryo-microscopy. <i>Journal of Structural Biology</i> , 2005, 149, 191-203.	2.8	92
106	A structural perspective on protein-protein interactions. <i>Current Opinion in Structural Biology</i> , 2004, 14, 313-324.	5.7	260
107	PREDICT modeling and in-silico screening for G-protein coupled receptors. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 57, 51-86.	2.6	99
108	Theoretical Studies on the Deacylation Step of Serine Protease Catalysis in the Gas Phase, in Solution, and in Elastase. <i>Journal of the American Chemical Society</i> , 2004, 126, 14631-14641.	13.7	54

#	ARTICLE	IF	CITATIONS
109	The Unusual Bifunctional Catalysis of Epimerization and Desaturation by Carbapenem Synthase. Journal of the American Chemical Society, 2004, 126, 9932-9933.	13.7	29
110	Crystal Structure of Carbapenem Synthase (CarC). Journal of Biological Chemistry, 2003, 278, 20843-20850.	3.4	90
111	Ab Initio QM/MM Dynamics Simulation of the Tetrahedral Intermediate of Serine Proteases: Insights into the Active Site Hydrogen-Bonding Network. Journal of the American Chemical Society, 2002, 124, 14780-14788.	13.7	81
112	Molecular dynamics simulations of the acyl-enzyme and the tetrahedral intermediate in the deacylation step of serine proteases. Proteins: Structure, Function and Bioinformatics, 2002, 47, 357-369.	2.6	23
113	Quantum mechanical/molecular mechanical study of three stationary points along the deacylation step of the catalytic mechanism of elastase. Theoretical Chemistry Accounts, 2001, 106, 146-151.	1.4	13
114	Modeling the 3D structure of GPCRs from sequence. Medicinal Research Reviews, 2001, 21, 472-483.	10.5	67
115	Combining Information from Crosslinks and Monolinks in the Modelling of Protein Structures. SSRN Electronic Journal, 0, , .	0.4	0