

# Tristan I Croll

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4078419/publications.pdf>

Version: 2024-02-01

64  
papers

13,829  
citations

186209

28  
h-index

118793

62  
g-index

79  
all docs

79  
docs citations

79  
times ranked

17591  
citing authors

#	ARTICLE	IF	CITATIONS
1	Catalytic trajectory of a dimeric nonribosomal peptide synthetase subunit with an inserted epimerase domain. <i>Nature Communications</i> , 2022, 13, 592.	5.8	16
2	Structural basis of SARS-CoV-2 Omicron immune evasion and receptor engagement. <i>Science</i> , 2022, 375, 864-868.	6.0	394
3	2.4-Å... structure of the double-ring <i>Gemmatimonas phototrophica</i> photosystem. <i>Science Advances</i> , 2022, 8, eabk3139.	4.7	16
4	How insulin-like growth factor I binds to a hybrid insulin receptor type 1 insulin-like growth factor receptor. <i>Structure</i> , 2022, 30, 1098-1108.e6.	1.6	16
5	The two-domain elevator-type mechanism of zinc-transporting ZIP proteins. <i>Science Advances</i> , 2022, 8, .	4.7	19
6	<scp>UCSF ChimeraX</scp>: Structure visualization for researchers, educators, and developers. <i>Protein Science</i> , 2021, 30, 70-82.	3.1	4,478
7	Phasertng: directed acyclic graphs for crystallographic phasing. <i>Acta Crystallographica Section D: Structural Biology</i> , 2021, 77, 1-10.	1.1	10
8	Adaptive Cartesian and torsional restraints for interactive model rebuilding. <i>Acta Crystallographica Section D: Structural Biology</i> , 2021, 77, 438-446.	1.1	16
9	Circulating SARS-CoV-2 spike N439K variants maintain fitness while evading antibody-mediated immunity. <i>Cell</i> , 2021, 184, 1171-1187.e20.	13.5	541
10	Molecular basis of ligand recognition and activation of human V2 vasopressin receptor. <i>Cell Research</i> , 2021, 31, 929-931.	5.7	38
11	Improving SARS-CoV-2 structures: Peer review by early coordinate release. <i>Biophysical Journal</i> , 2021, 120, 1085-1096.	0.2	21
12	Structure, Dynamics, Receptor Binding, and Antibody Binding of the Fully Glycosylated Full-Length SARS-CoV-2 Spike Protein in a Viral Membrane. <i>Journal of Chemical Theory and Computation</i> , 2021, 17, 2479-2487.	2.3	62
13	MyD88 TIR domain higher-order assembly interactions revealed by microcrystal electron diffraction and serial femtosecond crystallography. <i>Nature Communications</i> , 2021, 12, 2578.	5.8	55
14	Making the invisible enemy visible. <i>Nature Structural and Molecular Biology</i> , 2021, 28, 404-408.	3.6	18
15	SARS-CoV-2 RBD antibodies that maximize breadth and resistance to escape. <i>Nature</i> , 2021, 597, 97-102.	13.7	385
16	Cryo-EM structure of the monomeric <i>Rhodobacter sphaeroides</i> RCâ€‘LH1 core complex at 2.5â€‘Å... <i>Biochemical Journal</i> , 2021, 478, 3775-3790.	1.7	33
17	Structures of full-length glycoprotein hormone receptor signalling complexes. <i>Nature</i> , 2021, 598, 688-692.	13.7	52
18	Cryo-EM structure of the <i>Rhodospirillum rubrum</i> RCâ€‘LH1 complex at 2.5â€‘Å... <i>Biochemical Journal</i> , 2021, 478, 3253-3263.	1.7	23

#	ARTICLE	IF	CITATIONS
19	Ligand recognition and G-protein coupling selectivity of cholecystokinin A receptor. <i>Nature Chemical Biology</i> , 2021, 17, 1238-1244.	3.9	54
20	Cryo-EM Structure of the <i>Rhodobacter sphaeroides</i> Light-Harvesting $\hat{A}2$ Complex at 2.1 Å... <i>Biochemistry</i> , 2021, 60, 3302-3314.	1.2	38
21	Cryo-EM structure of the dimeric <i>Rhodobacter sphaeroides</i> RC-LH1 core complex at 2.9 Å...: the structural basis for dimerisation. <i>Biochemical Journal</i> , 2021, 478, 3923-3937.	1.7	26
22	Structure and ion-release mechanism of PIB-4-type ATPases. <i>ELife</i> , 2021, 10, .	2.8	8
23	Structures of fungal and plant acetoxyacid synthases. <i>Nature</i> , 2020, 586, 317-321.	13.7	37
24	Lig v 1 structure and the inflammatory response to the Ole e 1 protein family. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2020, 75, 2395-2398.	2.7	5
25	Developing a Fully Glycosylated Full-Length SARS-CoV-2 Spike Protein Model in a Viral Membrane. <i>Journal of Physical Chemistry B</i> , 2020, 124, 7128-7137.	1.2	240
26	How IGF-II Binds to the Human Type 1 Insulin-like Growth Factor Receptor. <i>Structure</i> , 2020, 28, 786-798.e6.	1.6	36
27	Structure of CD20 in complex with the therapeutic monoclonal antibody rituximab. <i>Science</i> , 2020, 367, 1224-1230.	6.0	113
28	Evaluation of template-based modeling in CASP13. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019, 87, 1113-1127.	1.5	56
29	Evaluation of model refinement in CASP13. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019, 87, 1249-1262.	1.5	28
30	Cryo-EM structures of the pore-forming A subunit from the <i>Yersinia entomophaga</i> ABC toxin. <i>Nature Communications</i> , 2019, 10, 1952.	5.8	40
31	Molecular basis of cullin-3 (Cul3) ubiquitin ligase subversion by vaccinia virus protein A55. <i>Journal of Biological Chemistry</i> , 2019, 294, 6416-6429.	1.6	14
32	Macromolecular structure determination using X-rays, neutrons and electrons: recent developments in <i>Phenix</i> . <i>Acta Crystallographica Section D: Structural Biology</i> , 2019, 75, 861-877.	1.1	4,060
33	Xanthine Oxidoreductase: A Novel Therapeutic Target for the Treatment of Chronic Wounds?. <i>Advances in Wound Care</i> , 2018, 7, 95-104.	2.6	19
34	Automating tasks in protein structure determination with the clipper python module. <i>Protein Science</i> , 2018, 27, 207-216.	3.1	6
35	Design of <i>Plasmodium vivax</i> Hypoxanthine-Guanine Phosphoribosyltransferase Inhibitors as Potential Antimalarial Therapeutics. <i>ACS Chemical Biology</i> , 2018, 13, 82-90.	1.6	22
36	<i>ISOLDE</i> : a physically realistic environment for model building into low-resolution electron-density maps. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 519-530.	1.1	1,115

#	ARTICLE	IF	CITATIONS
37	Prediction of a novel internal rearrangement of the insulin receptor. <i>Journal of Biomolecular Structure and Dynamics</i> , 2017, 35, 857-867.	2.0	0
38	Multiple functional self-association interfaces in plant TIR domains. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E2046-E2052.	3.3	103
39	Structural basis of TIR-domain-assembly formation in MAL- and MyD88-dependent TLR4 signaling. <i>Nature Structural and Molecular Biology</i> , 2017, 24, 743-751.	3.6	140
40	Improved Model of Proton Pump Crystal Structure Obtained by Interactive Molecular Dynamics Flexible Fitting Expands the Mechanistic Model for Proton Translocation in P-Type ATPases. <i>Frontiers in Physiology</i> , 2017, 8, 202.	1.3	29
41	A structural analysis of DNA binding by hSSB1 (NABP2/OBFC2B) in solution. <i>Nucleic Acids Research</i> , 2016, 44, 7963-7973.	6.5	26
42	Re-evaluation of low-resolution crystal structures via interactive molecular-dynamics flexible fitting (iMDFF): a case study in complement C4. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016, 72, 1006-1016.	1.1	43
43	The CC domain structure from the wheat stem rust resistance protein Sr33 challenges paradigms for dimerization in plant NLR proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 12856-12861.	3.3	105
44	Antagonists of IGF:Vitronectin Interactions Inhibit IGF-Induced Breast Cancer Cell Functions. <i>Molecular Cancer Therapeutics</i> , 2016, 15, 1602-1613.	1.9	5
45	Higher-Resolution Structure of the Human Insulin Receptor Ectodomain: Multi-Modal Inclusion of the Insert Domain. <i>Structure</i> , 2016, 24, 469-476.	1.6	129
46	A pre-clinical functional assessment of an acellular scaffold intended for the treatment of hard-to-heal wounds. <i>International Wound Journal</i> , 2015, 12, 160-168.	1.3	7
47	The rate of cis to trans conformation errors is increasing in low-resolution crystal structures. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 706-709.	2.5	17
48	Transglutaminases and receptor tyrosine kinases. <i>Amino Acids</i> , 2013, 44, 19-24.	1.2	7
49	Vitronectin: Master controller or micromanager?. <i>IUBMB Life</i> , 2013, 65, 807-818.	1.5	76
50	Lysine residues of IGF-I are substrates for transglutaminases and modulate downstream IGF-I signalling. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2013, 1833, 3176-3185.	1.9	3
51	A peptidomimetic inhibitor of matrix metalloproteinases containing a tetherable linker group. <i>Journal of Biomedical Materials Research - Part A</i> , 2011, 96A, 663-672.	2.1	13
52	Modeling the adhesion of human embryonic stem cells to poly(lactic-co-glycolic acid) surfaces in a 3D environment. <i>Journal of Biomedical Materials Research - Part A</i> , 2010, 92A, 683-692.	2.1	13
53	Controlled presentation of recombinant proteins via a zinc-binding peptide-linker in two and three dimensional formats. <i>Biomaterials</i> , 2009, 30, 6614-6620.	5.7	11
54	Nanoscale presentation of cell adhesive molecules via block copolymer self-assembly. <i>Biomaterials</i> , 2009, 30, 4732-4737.	5.7	56

#	ARTICLE	IF	CITATIONS
55	Engineering tissue tubes using novel multilayered scaffolds in the rat peritoneal cavity. Journal of Biomedical Materials Research - Part A, 2008, 87A, 719-727.	2.1	15
56	Analysis of the Phase Behavior of the Aqueous Poly(ethylene glycol)-Ficoll System. Biotechnology Progress, 2008, 19, 1269-1273.	1.8	7
57	Transplantation of 3D scaffolds seeded with human embryonic stem cells: biological features of surrogate tissue and teratoma-forming potential. Regenerative Medicine, 2007, 2, 289-300.	0.8	68
58	Systematic selection of solvents for the fabrication of 3D combined macro- and microporous polymeric scaffolds for soft tissue engineering. Journal of Biomaterials Science, Polymer Edition, 2006, 17, 369-402.	1.9	41
59	A Blank Slate? Layer-by-Layer Deposition of Hyaluronic Acid and Chitosan onto Various Surfaces. Biomacromolecules, 2006, 7, 1610-1622.	2.6	137
60	Modelling oxygen diffusion and cell growth in a porous, vascularising scaffold for soft tissue engineering applications. Chemical Engineering Science, 2005, 60, 4924-4934.	1.9	74
61	Scaffolds, Stem Cells, and Tissue Engineering: A Potent Combination!. Australian Journal of Chemistry, 2005, 58, 691.	0.5	23
62	Production and Surface Modification of Polylactide-Based Polymeric Scaffolds for Soft-Tissue Engineering. , 2004, 238, 87-112.		28
63	Controllable Surface Modification of Poly(lactic-co-glycolic acid) (PLGA) by Hydrolysis or Aminolysis I: Physical, Chemical, and Theoretical Aspects. Biomacromolecules, 2004, 5, 463-473.	2.6	373
64	Quantitative prediction of phase diagrams for polymer partitioning in aqueous two-phase systems. Journal of Polymer Science, Part B: Polymer Physics, 2003, 41, 437-443.	2.4	3