

Thomas R Schneider

List of Publications by Year in Descending Order

Source: <https://exaly.com/author-pdf/935871/thomas-r-schneider-publications-by-year.pdf>

Version: 2024-04-17

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

83
papers

8,360
citations

34
h-index

88
g-index

88
ext. papers

9,002
ext. citations

10.4
avg, IF

6.03
L-index

#	Paper	IF	Citations
83	Ground-state destabilization by electrostatic repulsion is not a driving force in orotidine-5?-monophosphate decarboxylase catalysis. <i>Nature Catalysis</i> , 2022 , 5, 332-341	36.5	1
82	Profiling cellular diversity in sponges informs animal cell type and nervous system evolution. <i>Science</i> , 2021 , 374, 717-723	33.3	15
81	Structural insights into the inhibition of glycine reuptake. <i>Nature</i> , 2021 , 591, 677-681	50.4	18
80	X-ray screening identifies active site and allosteric inhibitors of SARS-CoV-2 main protease. <i>Science</i> , 2021 , 372, 642-646	33.3	95
79	The structural bases for agonist diversity in an glutamate receptor-like channel. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 752-760	11.5	37
78	Liquid application method for time-resolved analyses by serial synchrotron crystallography. <i>Nature Methods</i> , 2019 , 16, 979-982	21.6	41
77	Optical performance and radiation stability of polymer X-ray refractive nano-lenses. <i>Journal of Synchrotron Radiation</i> , 2019 , 26, 714-719	2.4	6
76	MXCuBE2: the dawn of MXCuBE Collaboration. <i>Journal of Synchrotron Radiation</i> , 2019 , 26, 393-405	2.4	14
75	Long-wavelength Mesh&Collect native SAD phasing from microcrystals. <i>Acta Crystallographica Section D: Structural Biology</i> , 2019 , 75, 192-199	5.5	5
74	Visualization of protein crystals by high-energy phase-contrast X-ray imaging. <i>Acta Crystallographica Section D: Structural Biology</i> , 2019 , 75, 947-958	5.5	11
73	An NAD Phosphorylase Toxin Triggers Mycobacterium tuberculosis Cell Death. <i>Molecular Cell</i> , 2019 , 73, 1282-1291.e8	17.6	37
72	Clustering of atomic displacement parameters in bovine trypsin reveals a distributed lattice of atoms with shared chemical properties. <i>Scientific Reports</i> , 2019 , 9, 19281	4.9	4
71	The structure of the N-terminal module of the cell wall hydrolase RipA and its role in regulating catalytic activity. <i>Proteins: Structure, Function and Bioinformatics</i> , 2018 , 86, 912-923	4.2	16
70	Structural and Functional Characterization of the BcsG Subunit of the Cellulose Synthase in Salmonella typhimurium. <i>Journal of Molecular Biology</i> , 2018 , 430, 3170-3189	6.5	19
69	Microfluidic Chips for In Situ Crystal X-ray Diffraction and In Situ Dynamic Light Scattering for Serial Crystallography. <i>Journal of Visualized Experiments</i> , 2018 ,	1.6	14
68	Identification of the point of diminishing returns in high-multiplicity data collection for sulfur SAD phasing. <i>Journal of Synchrotron Radiation</i> , 2017 , 24, 19-28	2.4	4
67	Core Mediator structure at 3.4 Å extends model of transcription initiation complex. <i>Nature</i> , 2017 , 545, 248-251	50.4	74

66	P13, the EMBL macromolecular crystallography beamline at the low-emittance PETRA III ring for high- and low-energy phasing with variable beam focusing. <i>Journal of Synchrotron Radiation</i> , 2017 , 24, 323-332	2.4	84
65	Rat ceruloplasmin: a new labile copper binding site and zinc/copper mosaic. <i>Metallomics</i> , 2017 , 9, 1828-1838	4.3	13
64	A multicrystal diffraction data-collection approach for studying structural dynamics with millisecond temporal resolution. <i>IUCrJ</i> , 2016 , 3, 393-401	4.7	14
63	Data collection with a tailored X-ray beam size at 2.69 Å wavelength (4.6 keV): sulfur SAD phasing of Cdc23(Nterm). <i>Acta Crystallographica Section D: Structural Biology</i> , 2016 , 72, 403-12	5.5	8
62	Advances in experimental phasing. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016 , 72, 291-2	5.5	
61	The inhibition mechanism of human 20S proteasomes enables next-generation inhibitor design. <i>Science</i> , 2016 , 353, 594-8	33.3	123
60	3-Sulfino-propionyl-coenzyme A (3SP-CoA) desulfonase from <i>Advenella mimigardefordensis</i> DPN7(T): crystal structure and function of a desulfonase with an acyl-CoA dehydrogenase fold. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015 , 71, 1360-72		4
59	Terahertz radiation induces non-thermal structural changes associated with Fröhlich condensation in a protein crystal. <i>Structural Dynamics</i> , 2015 , 2, 054702	3.2	37
58	Serial crystallography on in vivo grown microcrystals using synchrotron radiation. <i>IUCrJ</i> , 2014 , 1, 87-94	4.7	164
57	A novel glycosidase structure from <i>Geobacillus thermoglucosidasius</i> : the first crystal structure of a glycoside hydrolase family GH52 enzyme reveals unpredicted similarity to other glycoside hydrolase folds. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014 , 70, 1366-74		14
56	Crystal structure of the gamma-2 herpesvirus LANA DNA binding domain identifies charged surface residues which impact viral latency. <i>PLoS Pathogens</i> , 2013 , 9, e1003673	7.6	25
55	SCEDS: protein fragments for molecular replacement in Phaser. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013 , 69, 2216-25		12
54	Alignment of protein structures in the presence of domain motions. <i>BMC Bioinformatics</i> , 2008 , 9, 352	3.6	41
53	RAPIDO: a web server for the alignment of protein structures in the presence of conformational changes. <i>Nucleic Acids Research</i> , 2008 , 36, W42-6	20.1	91
52	Synchrotron radiation: micrometer-sized x-ray beams as fine tools for macromolecular crystallography. <i>HFSP Journal</i> , 2008 , 2, 302-6		11
51	Crystal structure of the ubiquitin binding domains of rabex-5 reveals two modes of interaction with ubiquitin. <i>Cell</i> , 2006 , 124, 1183-95	56.2	233
50	Ultrahigh-resolution study of protein atomic displacement parameters at cryotemperatures obtained with a helium cryostat. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006 , 62, 1535-44		14
49	SITCOM: a program for comparing sites in macromolecular substructures. <i>Journal of Applied Crystallography</i> , 2006 , 39, 618-619	3.8	9

48	Mechanism of Aurora B activation by INCENP and inhibition by hesperadin. <i>Molecular Cell</i> , 2005 , 18, 379-391	1.6	321
47	Structure of Ecballium elaterium trypsin inhibitor II (EETI-II): a rigid molecular scaffold. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005 , 61, 1255-62		33
46	Structural basis for the autoinhibition and STI-571 inhibition of c-Kit tyrosine kinase. <i>Journal of Biological Chemistry</i> , 2004 , 279, 31655-63	5.4	470
45	Subatomic and atomic crystallographic studies of aldose reductase: implications for inhibitor binding. <i>Cellular and Molecular Life Sciences</i> , 2004 , 61, 763-73	10.3	28
44	Ultrahigh resolution drug design. II. Atomic resolution structures of human aldose reductase holoenzyme complexed with Fidarestat and Minalrestat: implications for the binding of cyclic imide inhibitors. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004 , 55, 805-13	4.2	66
43	Ultrahigh resolution drug design I: details of interactions in human aldose reductase-inhibitor complex at 0.66 Å. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004 , 55, 792-804	4.2	232
42	The crystallographic structure of the aldose reductase-IDD552 complex shows direct proton donation from tyrosine 48. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004 , 60, 1347-54		25
41	Domain identification by iterative analysis of error-scaled difference distance matrices. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004 , 60, 2269-75		31
40	HKL2MAP: a graphical user interface for macromolecular phasing with SHELX programs. <i>Journal of Applied Crystallography</i> , 2004 , 37, 843-844	3.8	599
39	Molecular basis for redox-Bohr and cooperative effects in cytochrome c3 from <i>Desulfovibrio desulfuricans</i> ATCC 27774: crystallographic and modeling studies of oxidized and reduced high-resolution structures at pH 7.6. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004 , 54, 135-52	4.2	17
38	Substrate and metal complexes of 3-deoxy-D-arabino-heptulosonate-7-phosphate synthase from <i>Saccharomyces cerevisiae</i> provide new insights into the catalytic mechanism. <i>Journal of Molecular Biology</i> , 2004 , 337, 675-90	6.5	37
37	Evolution of feedback-inhibited beta /alpha barrel isoenzymes by gene duplication and a single mutation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003 , 100, 862-7	11.5	94
36	Automatic solution of heavy-atom substructures. <i>Methods in Enzymology</i> , 2003 , 374, 37-83	1.7	31
35	Stereoselective Synthesis of the Two trans-(16-Hydroxymethyl)-3-methoxy-13 β -estra-1,3,5(10)-trien-17-ol Isomers. <i>Collection of Czechoslovak Chemical Communications</i> , 2003 , 68, 1141-1148		5
34	Use of multiple anomalous dispersion to phase highly merohedrally twinned crystals of interleukin-1beta. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003 , 59, 290-8		13
33	Structure of the alpha-amylase inhibitor tendamistat at 0.93 Å. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003 , 59, 1737-43		5
32	Optimization of selenium substructures as obtained from SHELXD. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003 , 59, 1987-94		6
31	Structural information content at high resolution: MAD versus native. <i>Methods in Enzymology</i> , 2003 , 374, 321-41	1.7	3

30	A genetic algorithm for the identification of conformationally invariant regions in protein molecules. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002 , 58, 195-208		113
29	Substructure solution with SHELXD. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002 , 58, 1772-9		1408
28	3-Methoxy-1 β -phenyl-4 β -dihydro-1H-pyrazolo[4 β ,3 γ :16,17]estra-1,3,5(10)-triene. <i>Acta Crystallographica Section E: Structure Reports Online</i> , 2002 , 58, o810-o811		2
27	Stereoselective synthesis of some novel heterocyclic estrone derivatives by intramolecular 1,3-dipolar cycloaddition. <i>Tetrahedron</i> , 2002 , 58, 6843-6849	2.4	34
26	Crystal structure of the endosomal SNARE complex reveals common structural principles of all SNAREs. <i>Nature Structural Biology</i> , 2002 , 9, 107-11		207
25	Silylhydrazine und dimere N,N'-Dilithium-N,N'-bis(silyl)hydrazide [Synthesen, Reaktionen, Isomerisierungen. <i>Zeitschrift Fur Anorganische Und Allgemeine Chemie</i> , 2001 , 627, 2581-2588	1.3	12
24	X-ray snapshots of serine protease catalysis reveal a tetrahedral intermediate. <i>Nature Structural Biology</i> , 2001 , 8, 689-94		89
23	The First Structurally Characterized Aluminum Compounds with Terminal Acetylide Groups This work was supported by the Deutsche Forschungsgemeinschaft. N.C.M.-Z. thanks the Schweizerischer Nationalfonds for a fellowship. <i>Angewandte Chemie - International Edition</i> , 2000 , 39, 3099-3101	16.4	31
22	Alumoxane Hydride and Aluminum Chalcogenide Hydride Compounds with Pyrazolato Ligands. <i>Angewandte Chemie - International Edition</i> , 2000 , 39, 4276-4279	16.4	32
21	A steroidal phenyldihydro-1,3-oxazine derivative. <i>Acta Crystallographica Section C: Crystal Structure Communications</i> , 2000 , 56, e363-e364		6
20	Ab initio structure determination of the lantibiotic mersacidin. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000 , 56, 705-13		25
19	Objective comparison of protein structures: error-scaled difference distance matrices. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000 , 56, 714-21		74
18	Protein-protein recognition, hydride transfer and proton pumping in the transhydrogenase complex. <i>Structure</i> , 2000 , 8, 809-15	5.2	53
17	Asymmetric Tris- and Cyclic Silylhydroxylamines from Trimeric and Tetrameric Lithium N,N-Bis(silyl)hydroxylamides. <i>Organometallics</i> , 2000 , 19, 5376-5383	3.8	25
16	1.7 A structure of the stabilized REIv mutant T39K. Application of local NCS restraints. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999 , 55, 1158-67		25
15	Crystallization and preliminary X-ray analysis of 3-deoxy-D-arabino-heptulosonate-7-phosphate synthase (tyrosine inhibitable) from <i>Saccharomyces cerevisiae</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999 , 55, 1586-8		2
14	Structure of catalase HPII from <i>Escherichia coli</i> at 1.9 A resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 1999 , 34, 155-66	4.2	51
13	Influence of internal dynamics on accuracy of protein NMR structures: derivation of realistic model distance data from a long molecular dynamics trajectory. <i>Journal of Molecular Biology</i> , 1999 , 285, 727-40 ^{6.5}		33

12	Structure of balhimycin and its complex with solvent molecules. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1998 , 54, 175-83		17
11	Refinement of triclinic hen egg-white lysozyme at atomic resolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1998 , 54, 522-46		85
10	Loop closure and intersubunit communication in tryptophan synthase. <i>Biochemistry</i> , 1998 , 37, 5394-406	3.2	135
9	[16] SHELXL: High-resolution refinement. <i>Methods in Enzymology</i> , 1997 , 319-343	1.7	194 ^o
8	X-ray crystallography reveals stringent conservation of protein fold after removal of the only disulfide bridge from a stabilized immunoglobulin variable domain. <i>Folding & Design</i> , 1997 , 2, 357-61		18
7	Macromolecular Cryocrystallography. <i>Journal of Applied Crystallography</i> , 1997 , 30, 211-237	3.8	220
6	X-ray structure determination of a metastable state of carbonmonoxy myoglobin after photodissociation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1996 , 93, 7013-6	11.5	131
5	Crystal structure of vancomycin. <i>Structure</i> , 1996 , 4, 1509-15	5.2	150
4	Contribution of the intramolecular disulfide bridge to the folding stability of REIv, the variable domain of a human immunoglobulin kappa light chain. <i>Folding & Design</i> , 1996 , 1, 431-40		59
3	Comparison of different X-ray data-collection systems using the crystal structure of octreotide. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1995 , 51, 60-8		3
2	Crystal structure of domain A of <i>Thermus flavus</i> 5S rRNA and the contribution of water molecules to its structure. <i>FEBS Letters</i> , 1994 , 351, 159-64	3.8	53
1	Structural insights into glycine reuptake inhibition		1