

# Zbyszek Otwinowski

## List of Publications by Citations

**Source:** <https://exaly.com/author-pdf/8924043/zbyszek-otwinowski-publications-by-citations.pdf>

**Version:** 2024-04-20

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.

104  
papers

36,760  
citations

41  
h-index

106  
g-index

106  
ext. papers

38,424  
ext. citations

11.1  
avg, IF

7.4  
L-index

#	Paper	IF	Citations
104	[20] Processing of X-ray diffraction data collected in oscillation mode. <i>Methods in Enzymology</i> , <b>1997</b> , 276, 307-326	1.7	24505
103	HKL-3000: the integration of data reduction and structure solution--from diffraction images to an initial model in minutes. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2006</b> , 62, 859-66		1457
102	Crystallographic analysis of the interaction of the glucocorticoid receptor with DNA. <i>Nature</i> , <b>1991</b> , 352, 497-505	50.4	1364
101	The crystal structure of the bacterial chaperonin GroEL at 2.8 A. <i>Nature</i> , <b>1994</b> , 371, 578-86	50.4	1250
100	Crystal structure of trp repressor/operator complex at atomic resolution. <i>Nature</i> , <b>1988</b> , 335, 321-9	50.4	906
99	Interfacial catalysis: the mechanism of phospholipase A2. <i>Science</i> , <b>1990</b> , 250, 1541-6	33.3	690
98	Multiparametric scaling of diffraction intensities. <i>Acta Crystallographica Section A: Foundations and Advances</i> , <b>2003</b> , 59, 228-34		529
97	Crystal structure of soybean lipoxygenase L-1 at 1.4 A resolution. <i>Biochemistry</i> , <b>1996</b> , 35, 10687-701	3.2	390
96	The three-dimensional structure of trp repressor. <i>Nature</i> , <b>1985</b> , 317, 782-6	50.4	352
95	A new generation of crystallographic validation tools for the protein data bank. <i>Structure</i> , <b>2011</b> , 19, 1395-412	5.412	335
94	Crystal structure of bee-venom phospholipase A2 in a complex with a transition-state analogue. <i>Science</i> , <b>1990</b> , 250, 1563-6	33.3	325
93	Structure and control of the actin regulatory WAVE complex. <i>Nature</i> , <b>2010</b> , 468, 533-8	50.4	324
92	Crystal structure of cobra-venom phospholipase A2 in a complex with a transition-state analogue. <i>Science</i> , <b>1990</b> , 250, 1560-3	33.3	305
91	The crystal structure of trp aporepressor at 1.8 A shows how binding tryptophan enhances DNA affinity. <i>Nature</i> , <b>1987</b> , 327, 591-7	50.4	257
90	Structural basis for CoREST-dependent demethylation of nucleosomes by the human LSD1 histone demethylase. <i>Molecular Cell</i> , <b>2006</b> , 23, 377-87	17.6	252
89	From nonpeptide toward noncarbon protease inhibitors: metallacarboranes as specific and potent inhibitors of HIV protease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2005</b> , 102, 15394-9	11.5	252
88	The 2.4 A crystal structure of the bacterial chaperonin GroEL complexed with ATP gamma S. <i>Nature Structural Biology</i> , <b>1996</b> , 3, 170-7		211

87	Secondary structure of Huntingtin amino-terminal region. <i>Structure</i> , <b>2009</b> , 17, 1205-12	5.2	199
86	Crystal structure of the human sterol transporter ABCG5/ABCG8. <i>Nature</i> , <b>2016</b> , 533, 561-4	50.4	185
85	Crystal structures of mitochondrial processing peptidase reveal the mode for specific cleavage of import signal sequences. <i>Structure</i> , <b>2001</b> , 9, 615-25	5.2	183
84	WASH and WAVE actin regulators of the Wiskott-Aldrich syndrome protein (WASP) family are controlled by analogous structurally related complexes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2010</b> , 107, 10442-7	11.5	160
83	Crystallographic determination of the active site iron and its ligands in soybean lipoxygenase L-1. <i>Biochemistry</i> , <b>1993</b> , 32, 6320-3	3.2	147
82	Structural basis for dsRNA recognition and interferon antagonism by Ebola VP35. <i>Nature Structural and Molecular Biology</i> , <b>2010</b> , 17, 165-72	17.6	145
81	Flexibility of the DNA-binding domains of trp repressor. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>1988</b> , 3, 18-31	4.2	134
80	The 2.4 Å crystal structure of cholera toxin B subunit pentamer: cholera toxin B subunit pentamer. <i>Journal of Molecular Biology</i> , <b>1995</b> , 251, 550-62	6.5	108
79	An Intrinsically Disordered Peptide from Ebola Virus VP35 Controls Viral RNA Synthesis by Modulating Nucleoprotein-RNA Interactions. <i>Cell Reports</i> , <b>2015</b> , 11, 376-89	10.6	106
78	Data publication with the structural biology data grid supports live analysis. <i>Nature Communications</i> , <b>2016</b> , 7, 10882	17.4	78
77	Structural basis for Marburg virus VP35-mediated immune evasion mechanisms. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2012</b> , 109, 20661-6	11.5	75
76	A tethered delivery mechanism explains the catalytic action of a microtubule polymerase. <i>ELife</i> , <b>2014</b> , 3, e03069	8.9	74
75	Strategies for macromolecular synchrotron crystallography. <i>Structure</i> , <b>2000</b> , 8, R105-10	5.2	70
74	Tiger Swallowtail Genome Reveals Mechanisms for Speciation and Caterpillar Chemical Defense. <i>Cell Reports</i> , <b>2015</b> , 10, 910-919	10.6	66
73	High-resolution timing of cell cycle-regulated gene expression. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2007</b> , 104, 16892-7	11.5	64
72	Crystal structure of the cohesin loader Scc2 and insight into cohesinopathy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2016</b> , 113, 12444-12449	11.5	61
71	In silico derived small molecules bind the filovirus VP35 protein and inhibit its polymerase cofactor activity. <i>Journal of Molecular Biology</i> , <b>2014</b> , 426, 2045-58	6.5	59
70	Measurement errors and their consequences in protein crystallography. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2003</b> , 59, 2031-8		55

69	Disruption of Wnt/ $\beta$ Catenin Signaling and Telomeric Shortening Are Inextricable Consequences of Tankyrase Inhibition in Human Cells. <i>Molecular and Cellular Biology</i> , <b>2015</b> , 35, 2425-35	4.8	50
68	Structure of cyanase reveals that a novel dimeric and decameric arrangement of subunits is required for formation of the enzyme active site. <i>Structure</i> , <b>2000</b> , 8, 505-14	5.2	50
67	Diffraction data analysis in the presence of radiation damage. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2010</b> , 66, 426-36		49
66	Structure of the human cohesin inhibitor Wapl. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2013</b> , 110, 11355-60	11.5	48
65	Extracellular architecture of the SYG-1/SYG-2 adhesion complex instructs synaptogenesis. <i>Cell</i> , <b>2014</b> , 156, 482-94	56.2	46
64	The many faces of radiation-induced changes. <i>Journal of Synchrotron Radiation</i> , <b>2007</b> , 14, 24-33	2.4	41
63	Structural genomics: keeping up with expanding knowledge of the protein universe. <i>Current Opinion in Structural Biology</i> , <b>2007</b> , 17, 347-53	8.1	40
62	Comparative genome sequencing reveals chemotype-specific gene clusters in the toxigenic black mold <i>Stachybotrys</i> . <i>BMC Genomics</i> , <b>2014</b> , 15, 590	4.5	38
61	Structural and biochemical basis for polyamine binding to the Tp0655 lipoprotein of <i>Treponema pallidum</i> : putative role for Tp0655 (TpPotD) as a polyamine receptor. <i>Journal of Molecular Biology</i> , <b>2007</b> , 373, 681-94	6.5	36
60	Complete genome of <i>Plutella</i> , a resilient alien, a cabbage pest, and a source of anti-cancer proteins. <i>F1000Research</i> , <b>2016</b> , 5, 2631	3.6	35
59	Complete genomes of Hairstreak butterflies, their speciation, and nucleo-mitochondrial incongruence. <i>Scientific Reports</i> , <b>2016</b> , 6, 24863	4.9	35
58	Speciation in Cloudless Sulphurs Gleaned from Complete Genomes. <i>Genome Biology and Evolution</i> , <b>2016</b> , 8, 915-31	3.9	33
57	Skipper genome sheds light on unique phenotypic traits and phylogeny. <i>BMC Genomics</i> , <b>2015</b> , 16, 639	4.5	32
56	Structure of the type III secretion effector protein ExoU in complex with its chaperone SpcU. <i>PLoS ONE</i> , <b>2012</b> , 7, e49388	3.7	31
55	When COI barcodes deceive: complete genomes reveal introgression in hairstreaks. <i>Proceedings of the Royal Society B: Biological Sciences</i> , <b>2017</b> , 284,	4.4	29
54	SCEPTRANS: an online tool for analyzing periodic transcription in yeast. <i>Bioinformatics</i> , <b>2007</b> , 23, 1559-61	7.2	28
53	The structural genomics experimental pipeline: insights from global target lists. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2004</b> , 56, 201-10	4.2	27
52	Identification of patterns in diffraction intensities affected by radiation exposure. <i>Journal of Synchrotron Radiation</i> , <b>2013</b> , 20, 37-48	2.4	24

51	Crystal structures of the effector-binding domain of repressor Central glycolytic gene Regulator from <i>Bacillus subtilis</i> reveal ligand-induced structural changes upon binding of several glycolytic intermediates. <i>Molecular Microbiology</i> , <b>2008</b> , 69, 895-910	4.1	24
50	Facing up to membranes: structure/function relationships in phospholipases. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , <b>1987</b> , 52, 441-52	3.9	24
49	To automate or not to automate: this is the question. <i>Journal of Structural and Functional Genomics</i> , <b>2010</b> , 11, 211-21		23
48	Crystal structure and putative function of small Toprim domain-containing protein from <i>Bacillus stearothermophilus</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2008</b> , 70, 311-9	4.2	22
47	Novel pyridazinone inhibitors for vascular adhesion protein-1 (VAP-1): old target-new inhibition mode. <i>Journal of Medicinal Chemistry</i> , <b>2013</b> , 56, 9837-48	8.3	21
46	Phylogeny Reconstruction with Alignment-Free Method That Corrects for Horizontal Gene Transfer. <i>PLoS Computational Biology</i> , <b>2016</b> , 12, e1004985	5	21
45	Complete Genome of , The First Representative of the Eudaminae Subfamily of Skippers. <i>Current Genomics</i> , <b>2017</b> , 18, 366-374	2.6	17
44	Crystal structures of the human elongation factor eEFSec suggest a non-canonical mechanism for selenocysteine incorporation. <i>Nature Communications</i> , <b>2016</b> , 7, 12941	17.4	15
43	The first complete genomes of Metalmarks and the classification of butterfly families. <i>Genomics</i> , <b>2017</b> , 109, 485-493	4.3	15
42	Autoinhibition of Mint1 adaptor protein regulates amyloid precursor protein binding and processing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2012</b> , 109, 3802-7	11.5	14
41	Bayesian statistical studies of the Ramachandran distribution. <i>Statistical Applications in Genetics and Molecular Biology</i> , <b>2005</b> , 4, Article35	1.2	14
40	Structure of <i>Escherichia coli</i> RutC, a member of the YjgF family and putative aminoacrylate peracid reductase of the rut operon. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , <b>2012</b> , 68, 1294-9		12
39	The crystal structure of the effector-binding domain of the trehalose repressor TreR from <i>Bacillus subtilis</i> 168 reveals a unique quaternary assembly. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2007</b> , 69, 679-82	4.2	12
38	Structure of the effector-binding domain of the arabinose repressor AraR from <i>Bacillus subtilis</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2012</b> , 68, 176-85		10
37	Crystallization and preliminary X-ray analysis of Ebola VP35 interferon inhibitory domain mutant proteins. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , <b>2010</b> , 66, 689-92		10
36	Crystal structure of native $\beta$ -L-rhamnosidase from <i>Aspergillus terreus</i> . <i>Acta Crystallographica Section D: Structural Biology</i> , <b>2018</b> , 74, 1078-1084	5.5	10
35	Methodology and applications of automatic electron-density map interpretation by six-dimensional rotational and translational search for molecular fragments. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2002</b> , 58, 275-83		9
34	X-ray diffraction experiment--the last experiment in the structure elucidation process. <i>Advances in Protein Chemistry and Structural Biology</i> , <b>2009</b> , 77, 23-40	5.3	8

33	The Bear Giant-Skipper genome suggests genetic adaptations to living inside yucca roots. <i>Molecular Genetics and Genomics</i> , <b>2019</b> , 294, 211-226	3.1	8
32	Crystal structure of native N-acetylhexosaminidase isolated from <i>Aspergillus oryzae</i> sheds light onto its substrate specificity, high stability, and regulation by propeptide. <i>FEBS Journal</i> , <b>2018</b> , 285, 580-598	5.7	8
31	The crystallographic fast Fourier transform. I. p3 symmetry. <i>Acta Crystallographica Section A: Foundations and Advances</i> , <b>2002</b> , 58, 574-9		7
30	Using surface-bound rubidium ions for protein phasing. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2001</b> , 57, 1008-12		7
29	Estimation of Uncertainties in the Global Distance Test (GDT_TS) for CASP Models. <i>PLoS ONE</i> , <b>2016</b> , 11, e0154786	3.7	7
28	Real-space analysis of radiation-induced specific changes with independent component analysis. <i>Journal of Synchrotron Radiation</i> , <b>2018</b> , 25, 451-467	2.4	6
27	Structure of the effector-binding domain of deoxyribonucleoside regulator DeoR from <i>Bacillus subtilis</i> . <i>FEBS Journal</i> , <b>2014</b> , 281, 4280-92	5.7	6
26	Structural characterization of V57D and V57P mutants of human cystatin C, an amyloidogenic protein. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2013</b> , 69, 577-86		6
25	The structure of pyogenecin immunity protein, a novel bacteriocin-like immunity protein from <i>Streptococcus pyogenes</i> . <i>BMC Structural Biology</i> , <b>2009</b> , 9, 75	2.7	6
24	High-resolution cryo-EM reconstructions in the presence of substantial aberrations. <i>IUCrJ</i> , <b>2020</b> , 7, 445-457	4.7	6
23	Structural basis for IFN antagonism by human respiratory syncytial virus nonstructural protein 2. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2021</b> , 118,	11.5	6
22	Mutation severity spectrum of rare alleles in the human genome is predictive of disease type. <i>PLoS Computational Biology</i> , <b>2020</b> , 16, e1007775	5	5
21	A multi-faceted analysis of RutD reveals a novel family of $\beta$ -hydrolases. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2012</b> , 80, 2359-68	4.2	5
20	Crystallization and preliminary X-ray diffraction analysis of Val57 mutants of the amyloidogenic protein human cystatin C. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , <b>2011</b> , 67, 1608-11		5
19	The crystallographic fast Fourier transform. Recursive symmetry reduction. <i>Acta Crystallographica Section A: Foundations and Advances</i> , <b>2007</b> , 63, 465-80		5
18	Optimal structure determination from sub-optimal diffraction data. <i>Protein Science</i> , <b>2021</b> ,	6.3	5
17	Crystal structure of cardiac troponin C regulatory domain in complex with cadmium and deoxycholic acid reveals novel conformation. <i>Journal of Molecular Biology</i> , <b>2011</b> , 413, 699-711	6.5	4
16	An efficient routine for computing symmetric real spherical harmonics for high orders of expansion. <i>Journal of Applied Crystallography</i> , <b>2005</b> , 38, 501-504	3.8	4

15	NMR and crystallographic structural studies of the extremely stable monomeric variant of human cystatin C with single amino acid substitution. <i>FEBS Journal</i> , <b>2020</b> , 287, 361-376	5.7	4
14	Refinement by shifting secondary structure elements improves sequence alignments. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2015</b> , 83, 411-27	4.2	3
13	Application of Maximum Entropy principle to modeling torsion angle probability distribution in proteins. <i>AIP Conference Proceedings</i> , <b>2004</b> ,	0	3
12	Coordinate transformations in modern crystallographic computing. <i>Acta Crystallographica Section A: Foundations and Advances</i> , <b>2004</b> , 60, 542-9		3
11	Expression, purification and X-ray crystallographic analysis of thioredoxin from <i>Streptomyces coelicolor</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , <b>2005</b> , 61, 164-8		3
10	Taking a look at the calibration of a CCD detector with a fiber-optic taper. <i>Journal of Applied Crystallography</i> , <b>2016</b> , 49, 415-425	3.8	2
9	The crystallographic fast Fourier transform. II. One-step symmetry reduction. <i>Acta Crystallographica Section A: Foundations and Advances</i> , <b>2003</b> , 59, 172-82		2
8	The crystallographic fast Fourier transform. III. Centred lattices. <i>Acta Crystallographica Section A: Foundations and Advances</i> , <b>2003</b> , 59, 183-92		2
7	High-resolution cryo-EM reconstructions in the presence of substantial aberrations		2
6	Kinetic control of eukaryotic chromatin structure by recursive topological restraints. <i>Nature Precedings</i> , <b>2008</b> ,		1
5	The crystallographic fast Fourier transform. IV. FFT-asymmetric units in the reciprocal space. <i>Acta Crystallographica Section A: Foundations and Advances</i> , <b>2004</b> , 60, 146-52		1
4	Everything Happens at Once [Deconvolving Systematic Effects in X-ray Data Processing. <i>NATO Science for Peace and Security Series A: Chemistry and Biology</i> , <b>2013</b> , 105-112	0.1	1
3	Synchrotron Radiation as a Tool for Macromolecular X-Ray Crystallography: a XXI Century Perspective. <i>Nuclear Instruments &amp; Methods in Physics Research B</i> , <b>2021</b> , 489, 30-40	1.2	1
2	2,5-Dibromo-6-isopropyl-3-methyl-p-benzoquinone. <i>Acta Crystallographica Section E: Structure Reports Online</i> , <b>2002</b> , 58, o170-o171		
1	Crystallization and preliminary X-ray analysis of nerve growth factor from <i>Vipera lebetina</i> . <i>Journal of Crystal Growth</i> , <b>1991</b> , 110, 214-219	1.6	