

# Zbyszek Otwinowski

## List of Publications by Year in Descending Order

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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	Optimal structure determination from sub-optimal diffraction data. <i>Protein Science</i> , <b>2021</b> ,	6.3	5
103	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
102	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
101	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
100	High-resolution cryo-EM reconstructions in the presence of substantial aberrations. <i>IUCrJ</i> , <b>2020</b> , 7, 445-457	4.7	6
99	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
98	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
97	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
96	Crystal structure of native N-acetylhexosaminidase isolated from <i>Aspergillus bryzae</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
95	Crystal structure of native $\beta$ -rhamnosidase from <i>Aspergillus terreus</i> . <i>Acta Crystallographica Section D: Structural Biology</i> , <b>2018</b> , 74, 1078-1084	5.5	10
94	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
93	The first complete genomes of Metalmarks and the classification of butterfly families. <i>Genomics</i> , <b>2017</b> , 109, 485-493	4.3	15
92	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
91	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
90	Data publication with the structural biology data grid supports live analysis. <i>Nature Communications</i> , <b>2016</b> , 7, 10882	17.4	78
89	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
88	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

87	Speciation in Cloudless Sulphurs Gleaned from Complete Genomes. <i>Genome Biology and Evolution</i> , <b>2016</b> , 8, 915-31	3.9	33
86	Complete genome of , a resilient alien, a cabbage pest, and a source of anti-cancer proteins. <i>F1000Research</i> , <b>2016</b> , 5, 2631	3.6	35
85	Phylogeny Reconstruction with Alignment-Free Method That Corrects for Horizontal Gene Transfer. <i>PLoS Computational Biology</i> , <b>2016</b> , 12, e1004985	5	21
84	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
83	Complete genomes of Hairstreak butterflies, their speciation, and nucleo-mitochondrial incongruence. <i>Scientific Reports</i> , <b>2016</b> , 6, 24863	4.9	35
82	Crystal structure of the human sterol transporter ABCG5/ABCG8. <i>Nature</i> , <b>2016</b> , 533, 561-4	50.4	185
81	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
80	Disruption of Wnt/ECatenin 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
79	Skipper genome sheds light on unique phenotypic traits and phylogeny. <i>BMC Genomics</i> , <b>2015</b> , 16, 639	4.5	32
78	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
77	Tiger Swallowtail Genome Reveals Mechanisms for Speciation and Caterpillar Chemical Defense. <i>Cell Reports</i> , <b>2015</b> , 10, 910-919	10.6	66
76	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
75	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
74	Extracellular architecture of the SYG-1/SYG-2 adhesion complex instructs synaptogenesis. <i>Cell</i> , <b>2014</b> , 156, 482-94	56.2	46
73	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
72	A tethered delivery mechanism explains the catalytic action of a microtubule polymerase. <i>ELife</i> , <b>2014</b> , 3, e03069	8.9	74
71	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
70	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

69	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
68	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
67	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
66	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
65	Structure of Escherichia coli 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
64	Structure of the effector-binding domain of the arabinose repressor AraR from Bacillus subtilis. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2012</b> , 68, 176-85		10
63	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
62	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
61	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
60	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
59	A new generation of crystallographic validation tools for the protein data bank. <i>Structure</i> , <b>2011</b> , 19, 1395-412	5.4	335
58	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
57	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
56	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
55	Structure and control of the actin regulatory WAVE complex. <i>Nature</i> , <b>2010</b> , 468, 533-8	50.4	324
54	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
53	Diffraction data analysis in the presence of radiation damage. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2010</b> , 66, 426-36		49
52	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

51	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
50	Secondary structure of Huntingtin amino-terminal region. <i>Structure</i> , <b>2009</b> , 17, 1205-12	5.2	199
49	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
48	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
47	Kinetic control of eukaryotic chromatin structure by recursive topological restraints. <i>Nature Precedings</i> , <b>2008</b> ,		1
46	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
45	The crystallographic fast Fourier transform. Recursive symmetry reduction. <i>Acta Crystallographica Section A: Foundations and Advances</i> , <b>2007</b> , 63, 465-80		5
44	The many faces of radiation-induced changes. <i>Journal of Synchrotron Radiation</i> , <b>2007</b> , 14, 24-33	2.4	41
43	The crystal structure of the effector-binding domain of the trehalose repressor TreR from <i>Bacillus subtilis</i> 168 reveals a unique quarternary assembly. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2007</b> , 69, 679-82	4.2	12
42	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
41	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
40	SCEPTRANS: an online tool for analyzing periodic transcription in yeast. <i>Bioinformatics</i> , <b>2007</b> , 23, 1559-61	7.2	28
39	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
38	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
37	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
36	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
35	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
34	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

33	Bayesian statistical studies of the Ramachandran distribution. <i>Statistical Applications in Genetics and Molecular Biology</i> , <b>2005</b> , 4, Article35	1.2	14
32	Application of Maximum Entropy principle to modeling torsion angle probability distribution in proteins. <i>AIP Conference Proceedings</i> , <b>2004</b> ,	0	3
31	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
30	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
29	Coordinate transformations in modern crystallographic computing. <i>Acta Crystallographica Section A: Foundations and Advances</i> , <b>2004</b> , 60, 542-9		3
28	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
27	The crystallographic fast Fourier transform. III. Centred lattices. <i>Acta Crystallographica Section A: Foundations and Advances</i> , <b>2003</b> , 59, 183-92		2
26	Multiparametric scaling of diffraction intensities. <i>Acta Crystallographica Section A: Foundations and Advances</i> , <b>2003</b> , 59, 228-34		529
25	Measurement errors and their consequences in protein crystallography. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2003</b> , 59, 2031-8		55
24	The crystallographic fast Fourier transform. I. p3 symmetry. <i>Acta Crystallographica Section A: Foundations and Advances</i> , <b>2002</b> , 58, 574-9		7
23	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
22	2,5-Dibromo-6-isopropyl-3-methyl-p-benzoquinone. <i>Acta Crystallographica Section E: Structure Reports Online</i> , <b>2002</b> , 58, o170-o171		
21	Using surface-bound rubidium ions for protein phasing. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2001</b> , 57, 1008-12		7
20	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
19	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
18	Strategies for macromolecular synchrotron crystallography. <i>Structure</i> , <b>2000</b> , 8, R105-10	5.2	70
17	[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
16	Crystal structure of soybean lipoxygenase L-1 at 1.4 Å resolution. <i>Biochemistry</i> , <b>1996</b> , 35, 10687-701	3.2	390

15	The 2.4 Å crystal structure of the bacterial chaperonin GroEL complexed with ATP gamma S. <i>Nature Structural Biology</i> , <b>1996</b> , 3, 170-7		211
14	The 2.4 Å crystal structure of cholera toxin B subunit pentamer: cholera toxin. <i>Journal of Molecular Biology</i> , <b>1995</b> , 251, 550-62	6.5	108
13	The crystal structure of the bacterial chaperonin GroEL at 2.8 Å. <i>Nature</i> , <b>1994</b> , 371, 578-86	50.4	1250
12	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
11	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	
10	Crystallographic analysis of the interaction of the glucocorticoid receptor with DNA. <i>Nature</i> , <b>1991</b> , 352, 497-505	50.4	1364
9	Interfacial catalysis: the mechanism of phospholipase A2. <i>Science</i> , <b>1990</b> , 250, 1541-6	33.3	690
8	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
7	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
6	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
5	Crystal structure of trp repressor/operator complex at atomic resolution. <i>Nature</i> , <b>1988</b> , 335, 321-9	50.4	906
4	The crystal structure of trp aporepressor at 1.8 Å shows how binding tryptophan enhances DNA affinity. <i>Nature</i> , <b>1987</b> , 327, 591-7	50.4	257
3	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
2	The three-dimensional structure of trp repressor. <i>Nature</i> , <b>1985</b> , 317, 782-6	50.4	352
1	High-resolution cryo-EM reconstructions in the presence of substantial aberrations		2