

Zygmunt S Derewenda

List of Publications by Year in descending order

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109
papers

9,026
citations

57631

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42291

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111
all docs

111
docs citations

111
times ranked

9308
citing authors

#	ARTICLE	IF	CITATIONS
1	On the centennials of the discoveries of the hydrogen bond and the structure of the water molecule: the short life and work of Eustace Jean Cuy (1897–1925). <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2021, 77, 362-378.	0.0	1
2	Ca ²⁺ hydrogen bonds in kinase-inhibitor interfaces. <i>IUBMB Life</i> , 2020, 72, 1233-1242.	1.5	7
3	Architecture of the Cellulose Synthase Outer Membrane Channel and Its Association with the Periplasmic TPR Domain. <i>Structure</i> , 2019, 27, 1855-1861.e3.	1.6	41
4	RSK2 contributes to myogenic vasoconstriction of resistance arteries by activating smooth muscle myosin and the Na ⁺ /H ⁺ exchanger. <i>Science Signaling</i> , 2018, 11, .	1.6	13
5	The structure of the C-terminal domain of the nucleoprotein from the Bundibugyo strain of the Ebola virus in complex with a pan-specific synthetic Fab. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 681-689.	1.1	9
6	The "Sticky Patch" Model of Crystallization and Modification of Proteins for Enhanced Crystallizability. <i>Methods in Molecular Biology</i> , 2017, 1607, 77-115.	0.4	17
7	Crystal structures of the methyltransferase and helicase from the ZIKA 1947 MR766 Uganda strain. <i>Acta Crystallographica Section D: Structural Biology</i> , 2017, 73, 767-774.	1.1	10
8	Molecular architecture of the nucleoprotein C-terminal domain from the Ebola and Marburg viruses. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016, 72, 49-58.	1.1	14
9	Bacterial Expression, Purification and In Vitro Phosphorylation of Full-Length Ribosomal S6 Kinase 2 (RSK2). <i>PLoS ONE</i> , 2016, 11, e0164343.	1.1	6
10	Adventures in cooperativity. <i>Postepy Biochemii</i> , 2016, 62, 286-297.	0.5	1
11	The structure of the C-terminal domain of the Zaire ebolavirus nucleoprotein. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 2420-2429.	2.5	39
12	Salvage or Recovery of Failed Targets by Mutagenesis to Reduce Surface Entropy. <i>Methods in Molecular Biology</i> , 2014, 1140, 201-209.	0.4	13
13	The unusual mechanism of inhibition of the p90 ribosomal S6 kinase (RSK) by flavonol rhamnosides. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2013, 1834, 1285-1291.	1.1	7
14	Agonist-induced Ca ²⁺ Sensitization in Smooth Muscle. <i>Journal of Biological Chemistry</i> , 2013, 288, 34030-34040.	1.6	21
15	Dynactin helps target Polo-like kinase 1 to kinetochores via its left-handed beta-helical p27 subunit. <i>EMBO Journal</i> , 2013, 32, 1023-1035.	3.5	46
16	Identification of quercitrin as an inhibitor of the p90 S6 ribosomal kinase (RSK): structure of its complex with the N-terminal domain of RSK2 at 1.8 Å resolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 266-275.	2.5	15
17	The p90 Ribosomal S6 Kinase (RSK) Is a Mediator of Smooth Muscle Contractility. <i>PLoS ONE</i> , 2013, 8, e58703.	1.1	14
18	Insights into the Inhibition of the p90 Ribosomal S6 Kinase (RSK) by the Flavonol Glycoside SL0101 from the 1.5 Å Crystal Structure of the N-Terminal Domain of RSK2 with Bound Inhibitor. <i>Biochemistry</i> , 2012, 51, 6499-6510.	1.2	39

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19	Structural Features and Chaperone Activity of the NudC Protein Family. <i>Journal of Molecular Biology</i> , 2011, 409, 722-741.	2.0	38
20	Abstractions, algorithms and data structures for structural bioinformatics in PyCogent. <i>Journal of Applied Crystallography</i> , 2011, 44, 424-428.	1.9	4
21	It's all in the crystals. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2011, 67, 243-248.	2.5	29
22	p63RhoGEF Couples G β -Mediated Signaling to Ca ²⁺ Sensitization of Vascular Smooth Muscle Contractility. <i>Circulation Research</i> , 2011, 109, 993-1002.	2.0	66
23	The N-terminal coiled-coil of Ndel1 is a regulated scaffold that recruits LIS1 to dynein. <i>Journal of Cell Biology</i> , 2011, 192, 433-445.	2.3	78
24	Insights into the Molecular Activation Mechanism of the RhoA-specific Guanine Nucleotide Exchange Factor, PDZRhoGEF. <i>Journal of Biological Chemistry</i> , 2011, 286, 35163-35175.	1.6	23
25	Application of protein engineering to enhance crystallizability and improve crystal properties. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2010, 66, 604-615.	2.5	98
26	The solution structure and dynamics of the DH ϵ PH module of PDZRhoGEF in isolation and in complex with nucleotide-free RhoA. <i>Protein Science</i> , 2009, 18, 2067-2079.	3.1	18
27	Structure of <i>Thermotoga maritima</i> TM0439: implications for the mechanism of bacterial GntR transcription regulators with Zn ²⁺ -binding FCD domains. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2009, 65, 356-365.	2.5	31
28	The role of entropy and polarity in intermolecular contacts in protein crystals. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2009, 65, 500-509.	2.5	31
29	On the mechanism of autoinhibition of the RhoA-specific nucleotide exchange factor PDZRhoGEF. <i>BMC Structural Biology</i> , 2009, 9, 36.	2.3	24
30	Structure and Function of <i>Bacillus subtilis</i> YphP, a Prokaryotic Disulfide Isomerase with a CXC Catalytic Motif. <i>Biochemistry</i> , 2009, 48, 8664-8671.	1.2	37
31	On wine, chirality and crystallography. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2008, 64, 246-258.	0.3	28
32	Degenerate specificity of PDZ domains from RhoA-specific nucleotide exchange factors PDZRhoGEF and LARG. <i>Acta Biochimica Polonica</i> , 2008, 55, 269-80.	0.3	3
33	Protein crystallization in drug design: towards a rational approach. <i>Expert Opinion on Drug Discovery</i> , 2007, 2, 1329-1340.	2.5	3
34	Bivalent Peptides as Models for Multimeric Targets of PDZ Domains. <i>ChemBioChem</i> , 2007, 8, 443-452.	1.3	19
35	Protein crystallization by surface entropy reduction: optimization of the SER strategy. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2007, 63, 636-645.	2.5	146
36	Structure of the <i>Bacillus subtilis</i> OhrB hydroperoxide-resistance protein in a fully oxidized state. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2007, 63, 1269-1273.	2.5	4

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37	The Structure of the Coiled-Coil Domain of Ndel1 and the Basis of Its Interaction with Lis1, the Causal Protein of Miller-Dieker Lissencephaly. <i>Structure</i> , 2007, 15, 1467-1481.	1.6	74
38	Toward rational protein crystallization: A Web server for the design of crystallizable protein variants. <i>Protein Science</i> , 2007, 16, 1569-1576.	3.1	247
39	The Dimerization Mechanism of LIS1 and its Implication for Proteins Containing the LisH Motif. <i>Journal of Molecular Biology</i> , 2006, 357, 621-631.	2.0	47
40	Entropy and surface engineering in protein crystallization. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006, 62, 116-124.	2.5	207
41	The DC-module of doublecortin: Dynamics, domain boundaries, and functional implications. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 64, 874-882.	1.5	15
42	The Molecular Basis of RhoA Specificity in the Guanine Nucleotide Exchange Factor PDZ-RhoGEF. <i>Journal of Biological Chemistry</i> , 2006, 281, 32891-32897.	1.6	40
43	Towards a high-resolution structure of dynactin. <i>FASEB Journal</i> , 2006, 20, A95.	0.2	0
44	Probing the Supramodular Architecture of a Multidomain Protein: The Structure of Syntenin in Solution. <i>Structure</i> , 2005, 13, 319-327.	1.6	19
45	<i>B. subtilis</i> ykuD protein at 2.0 Å... resolution: Insights into the structure and function of a novel, ubiquitous family of bacterial enzymes. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 62, 144-151.	1.5	94
46	The molecular structure and catalytic mechanism of a quorum-quenching N-acyl-L-homoserine lactone hydrolase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 17606-17611.	3.3	106
47	The Structure of <i>Yersinia pestis</i> V-Antigen, an Essential Virulence Factor and Mediator of Immunity against Plague. <i>Structure</i> , 2004, 12, 301-306.	1.6	100
48	Rational Protein Crystallization by Mutational Surface Engineering. <i>Structure</i> , 2004, 12, 529-535.	1.6	254
49	The Structure of the N-Terminal Domain of the Product of the Lissencephaly Gene Lis1 and Its Functional Implications. <i>Structure</i> , 2004, 12, 987-998.	1.6	106
50	The Crystal Structure of the Reduced, Zn ²⁺ -Bound Form of the <i>B. subtilis</i> Hsp33 Chaperone and Its Implications for the Activation Mechanism. <i>Structure</i> , 2004, 12, 1901-1907.	1.6	77
51	The Crystal Structure of RhoA in Complex with the DH/PH Fragment of PDZ-RhoGEF, an Activator of the Ca ²⁺ Sensitization Pathway in Smooth Muscle. <i>Structure</i> , 2004, 12, 1955-1965.	1.6	79
52	The impact of Lys ¹⁷ Arg surface mutations on the crystallization of the globular domain of RhoGDI. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 275-280.	2.5	38
53	Preliminary crystallographic analysis of the complex of the human GTPase RhoA with the DH/PH tandem of PDZ-RhoGEF. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 740-742.	2.5	9
54	Harvesting the high-hanging fruit: the structure of the YdeN gene product from <i>Bacillus subtilis</i> at 1.8 Å... resolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 1101-1107.	2.5	23

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55	The use of recombinant methods and molecular engineering in protein crystallization. <i>Methods</i> , 2004, 34, 354-363.	1.9	141
56	Coupling PAF Signaling to Dynein Regulation. <i>Neuron</i> , 2004, 44, 809-821.	3.8	72
57	The PDZ2 Domain of Syntenin at Ultra-high Resolution: Bridging the Gap Between Macromolecular and Small Molecule Crystallography. <i>Journal of Molecular Biology</i> , 2004, 338, 483-493.	2.0	47
58	The Structure and Ligand Binding Properties of the B.subtilis YkoF Gene Product, a Member of a Novel Family of Thiamin/HMP-binding Proteins. <i>Journal of Molecular Biology</i> , 2004, 343, 395-406.	2.0	43
59	Assignment of 1H, 13C and 15N resonances of the N-terminal microtubule-binding domain of human doublecortin. <i>Journal of Biomolecular NMR</i> , 2003, 25, 81-82.	1.6	2
60	PDZ Tandem of Human Syntenin. <i>Structure</i> , 2003, 11, 459-468.	1.6	90
61	Molecular Roots of Degenerate Specificity in Syntenin's PDZ2 Domain. <i>Structure</i> , 2003, 11, 845-853.	1.6	83
62	Purification and crystallization of the N-terminal domain from the human doublecortin-like kinase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 502-505.	2.5	8
63	Structure of a constitutively activated RhoA mutant (Q63L) at 1.55 Å resolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 876-880.	2.5	28
64	The DCX-domain tandems of doublecortin and doublecortin-like kinase. <i>Nature Structural and Molecular Biology</i> , 2003, 10, 324-333.	3.6	122
65	Molecular Basis of Mitomycin C Resistance in Streptomyces. <i>Structure</i> , 2002, 10, 933-942.	1.6	30
66	Substrate-selectivity in acylhydrolases: a cautionary tale. <i>Colloids and Surfaces B: Biointerfaces</i> , 2002, 26, 31-35.	2.5	2
67	The structure of the FERM domain of merlin, the neurofibromatosis type 2 gene product. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 381-391.	2.5	45
68	The impact of Glu ¹ Ala and Glu ¹ Asp mutations on the crystallization properties of RhoGDI: the structure of RhoGDI at 1.3 Å resolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 1983-1991.	2.5	64
69	Expression, Purification, and Crystallization of the RGS-like Domain from the Rho Nucleotide Exchange Factor, PDZ-RhoGEF, Using the Surface Entropy Reduction Approach. <i>Protein Expression and Purification</i> , 2001, 21, 412-416.	0.6	29
70	Protein crystallization by rational mutagenesis of surface residues: Lys to Ala mutations promote crystallization of RhoGDI. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 679-688.	2.5	104
71	Structure of the RGS-like Domain from PDZ-RhoGEF. <i>Structure</i> , 2001, 9, 559-569.	1.6	73
72	Preparation and crystal structure of the recombinant $\hat{I}\pm 1/\hat{I}\pm 2$ catalytic heterodimer of bovine brain platelet-activating factor acetylhydrolase Ib. <i>Protein Engineering, Design and Selection</i> , 2001, 14, 513-519.	1.0	19

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73	Homologs of the α - and β -subunits of mammalian brain platelet-activating factor acetylhydrolase Ib in the <i>Drosophila melanogaster</i> genome. , 2000, 39, 1-8.		25
74	Crystal structure of the <i>Escherichia coli</i> thioesterase II, a homolog of the human Nef binding enzyme. <i>Nature Structural Biology</i> , 2000, 7, 555-559.	9.7	105
75	Crystal Structure of the Human Acyl Protein Thioesterase I from a Single X-Ray Data Set to 1.5 Å... <i>Structure</i> , 2000, 8, 1137-1146.	1.6	124
76	Substrate Specificity in Glycoside Hydrolase Family 10. <i>Journal of Biological Chemistry</i> , 2000, 275, 23020-23026.	1.6	70
77	Structure of the BH Domain from Graf and Its Implications for Rho GTPase Recognition. <i>Journal of Biological Chemistry</i> , 2000, 275, 38605-38610.	1.6	22
78	Domain Identification of Hormone-sensitive Lipase by Circular Dichroism and Fluorescence Spectroscopy, Limited Proteolysis, and Mass Spectrometry. <i>Journal of Biological Chemistry</i> , 1999, 274, 15382-15388.	1.6	30
79	How RhoGDI binds Rho. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 1503-1515.	2.5	65
80	Crystal structure of brefeldin A esterase, a bacterial homolog of the mammalian hormone-sensitive lipase. <i>Nature Structural Biology</i> , 1999, 6, 340-345.	9.7	135
81	The name is bond-H bond. , 1999, 6, 403-406.		156
82	Biochemical and molecular biological characterization of a lipase produced by the fungus <i>Rhizopus delemar</i> . <i>Lipid - Fett</i> , 1999, 101, 364-370.	0.6	9
83	PAF-acetylhydrolases. <i>Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids</i> , 1999, 1441, 229-236.	1.2	30
84	Overcoming Expression and Purification Problems of RhoGDI Using a Family of α -Parallel-Expression Vectors. <i>Protein Expression and Purification</i> , 1999, 15, 34-39.	0.6	606
85	Structure of a microbial homologue of mammalian platelet-activating factor acetylhydrolases: <i>Streptomyces exfoliatus</i> lipase at 1.9 Å resolution. <i>Structure</i> , 1998, 6, 511-519.	1.6	107
86	Crystal structure of RhoA-GDP and its functional implications. <i>Nature Structural Biology</i> , 1997, 4, 699-703.	9.7	158
87	Brain acetylhydrolase that inactivates platelet-activating factor is a G-protein-like trimer. <i>Nature</i> , 1997, 385, 89-93.	13.7	180
88	Conversion of Serine-114 to Cysteine-114 and the Role of the Active Site Nucleophile in Acyl Transfer by Myristoyl-ACP Thioesterase from <i>Vibrio harveyi</i> . <i>Biochemistry</i> , 1996, 35, 9967-9973.	1.2	41
89	The <i>Escherichia coli</i> Malonyl-CoA:Acyl Carrier Protein Transacylase at 1.5-Å... Resolution.. <i>Journal of Biological Chemistry</i> , 1995, 270, 12961-12964.	1.6	165
90	Molecular mechanism of enantioselectivity by esterases. <i>Journal of the American Chemical Society</i> , 1995, 117, 2104-2105.	6.6	29

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91	The Occurrence of C α -H \cdots O Hydrogen Bonds in Proteins. <i>Journal of Molecular Biology</i> , 1995, 252, 248-262.	2.0	540
92	Structure and Function of Lipases. <i>Advances in Protein Chemistry</i> , 1994, 45, 1-52.	4.4	140
93	Crystallization and preliminary crystallographic studies of the precursor and mature forms of a neutral lipase from the fungus <i>Rhizopus delemar</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 1994, 18, 301-306.	1.5	12
94	Crystallization of Thioesterase II from <i>Escherichia coli</i> . <i>Journal of Molecular Biology</i> , 1994, 236, 660-662.	2.0	4
95	Crystallization of the Malonyl Coenzyme A-Acyl Carrier Protein Transacylase from <i>Escherichia coli</i> . <i>Journal of Molecular Biology</i> , 1994, 242, 99-102.	2.0	15
96	Crystallization of canine cardiac calsequestrin. <i>Journal of Molecular Biology</i> , 1994, 235, 357-360.	2.0	12
97	News from the interface: the molecular structures of triacylglyceride lipases. <i>Trends in Biochemical Sciences</i> , 1993, 18, 20-25.	3.7	197
98	The crystal and molecular structure of the <i>Rhizomucor miehei</i> triacylglyceride lipase at 1.9 \AA .. resolution. <i>Journal of Molecular Biology</i> , 1992, 227, 818-839.	2.0	253
99	High resolution crystal structures and comparisons of T-state deoxyhaemoglobin and two liganded T-State haemoglobins: T(\pm -oxy)haemoglobin and T(met)haemoglobin. <i>Journal of Molecular Biology</i> , 1992, 228, 551-579.	2.0	104
100	Crystallization and preliminary crystallographic data of a <i>Streptomyces scabies</i> extracellular esterase. <i>Journal of Molecular Biology</i> , 1992, 227, 569-571.	2.0	6
101	Expression, purification and crystallization of the <i>Vibrio harveyi</i> acyltransferase. <i>Journal of Molecular Biology</i> , 1992, 227, 572-574.	2.0	8
102	Relationships among serine hydrolases: evidence for a common structural motif in triacylglyceride lipases and esterases. <i>Biochemistry and Cell Biology</i> , 1991, 69, 842-851.	0.9	146
103	A serine protease triad forms the catalytic centre of a triacylglycerol lipase. <i>Nature</i> , 1990, 343, 767-770.	13.7	1,207
104	Initiating a crystallographic study of trypanothione reductase. <i>Journal of Molecular Biology</i> , 1990, 216, 235-237.	2.0	22
105	Stereochemistry of carbon monoxide binding to normal human adult and Cowtown haemoglobins. <i>Journal of Molecular Biology</i> , 1990, 211, 515-519.	2.0	76
106	High-resolution (1.5 \AA ..) crystal structure of phospholipase C from <i>Bacillus cereus</i> . <i>Nature</i> , 1989, 338, 357-360.	13.7	484
107	Structure of the liganded T state of haemoglobin identifies the origin of cooperative oxygen binding. <i>Nature</i> , 1988, 331, 725-728.	13.7	95
108	Crystallization of the periplasmic oligopeptide-binding protein of <i>Salmonella typhimurium</i> . <i>Journal of Molecular Biology</i> , 1988, 204, 493-494.	2.0	12

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109	Bonding of molecular oxygen to T state human haemoglobin. Nature, 1984, 307, 74-76.	13.7	106