Zygmunt S Derewenda

List of Publications by Year in descending order

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109 papers	9,026 citations	57758 44 h-index	42399 92 g-index
111	111	111	9308
all docs	docs citations	times ranked	citing authors

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#	Article	IF	CITATIONS
1	A serine protease triad forms the catalytic centre of a triacylglycerol lipase. Nature, 1990, 343, 767-770.	27.8	1,207
2	Overcoming Expression and Purification Problems of RhoGDI Using a Family of "Parallel―Expression Vectors. Protein Expression and Purification, 1999, 15, 34-39.	1.3	606
3	The Occurence of C–H · · · O Hydrogen Bonds in Proteins. Journal of Molecular Biology, 1995, 252, 248-262.	4.2	540
4	High-resolution (1.5 Ã) crystal structure of phospholipase C from Bacillus cereus. Nature, 1989, 338, 357-360.	27.8	484
5	Rational Protein Crystallization by Mutational Surface Engineering. Structure, 2004, 12, 529-535.	3.3	254
6	The crystal and molecular structure of the Rhizomucor miehei triacylglyceride lipase at 1.9 Ã resolution. Journal of Molecular Biology, 1992, 227, 818-839.	4.2	253
7	Toward rational protein crystallization: A Web server for the design of crystallizable protein variants. Protein Science, 2007, 16, 1569-1576.	7.6	247
8	Entropy and surface engineering in protein crystallization. Acta Crystallographica Section D: Biological Crystallography, 2006, 62, 116-124.	2.5	207
9	News from the interface: the molecular structures of triacyglyceride lipases. Trends in Biochemical Sciences, 1993, 18, 20-25.	7.5	197
10	Brain acetylhydrolase that inactivates platelet-activating factor is a G-protein-like trimer. Nature, 1997, 385, 89-93.	27.8	180
11	The Escherichia coli Malonyl-CoA:Acyl Carrier Protein Transacylase at 1.5-Ã Resolution Journal of Biological Chemistry, 1995, 270, 12961-12964.	3.4	165
12	Crystal structure of RhoA–GDP and its functional implications. Nature Structural Biology, 1997, 4, 699-703.	9.7	158
13	The name is bondH bond. , 1999, 6, 403-406.		156
14	Relationships among serine hydrolases: evidence for a common structural motif in triacylglyceride lipases and esterases. Biochemistry and Cell Biology, 1991, 69, 842-851.	2.0	146
15	Protein crystallization by surface entropy reduction: optimization of the SER strategy. Acta Crystallographica Section D: Biological Crystallography, 2007, 63, 636-645.	2.5	146
16	The use of recombinant methods and molecular engineering in protein crystallization. Methods, 2004, 34, 354-363.	3.8	141
17	Structure and Function of Lipases. Advances in Protein Chemistry, 1994, 45, 1-52.	4.4	140
18	Crystal structure of brefeldin A esterase, a bacterial homolog of the mammalian hormone-sensitive lipase. Nature Structural Biology, 1999, 6, 340-345.	9.7	135

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19	Crystal Structure of the Human Acyl Protein Thioesterase I from a Single X-Ray Data Set to 1.5 Ã Structure, 2000, 8, 1137-1146.	3.3	124
20	The DCX-domain tandems of doublecortin and doublecortin-like kinase. Nature Structural and Molecular Biology, 2003, 10, 324-333.	8.2	122
21	Structure of a microbial homologue of mammalian platelet-activating factor acetylhydrolases: Streptomyces exfoliatus lipase at 1.9 å resolution. Structure, 1998, 6, 511-519.	3.3	107
22	Bonding of molecular oxygen to T state human haemoglobin. Nature, 1984, 307, 74-76.	27.8	106
23	The Structure of the N-Terminal Domain of the Product of the Lissencephaly Gene Lis1 and Its Functional Implications. Structure, 2004, 12, 987-998.	3.3	106
24	The molecular structure and catalytic mechanism of a quorum-quenching N-acyl-L-homoserine lactone hydrolase. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 17606-17611.	7.1	106
25	Crystal structure of the Escherichia coli thioesterase II, a homolog of the human Nef binding enzyme. Nature Structural Biology, 2000, 7, 555-559.	9.7	105
26	High resolution crystal structures and comparisons of T-state deoxyhaemoglobin and two liganded T-State haemoglobins: T(α-oxy)haemoglobin and T(met)haemoglobin. Journal of Molecular Biology, 1992, 228, 551-579.	4.2	104
27	Protein crystallization by rational mutagenesis of surface residues: Lys to Ala mutations promote crystallization of RhoGDI. Acta Crystallographica Section D: Biological Crystallography, 2001, 57, 679-688.	2.5	104
28	The Structure of Yersinia pestis V-Antigen, an Essential Virulence Factor and Mediator of Immunity against Plague. Structure, 2004, 12, 301-306.	3.3	100
29	Application of protein engineering to enhance crystallizability and improve crystal properties. Acta Crystallographica Section D: Biological Crystallography, 2010, 66, 604-615.	2.5	98
30	Structure of the liganded T state of haemoglobin identifies the origin of cooperative oxygen binding. Nature, 1988, 331, 725-728.	27.8	95
31	B. subtilis ykuD protein at 2.0 Ã resolution: Insights into the structure and function of a novel, ubiquitous family of bacterial enzymes. Proteins: Structure, Function and Bioinformatics, 2005, 62, 144-151.	2.6	94
32	PDZ Tandem of Human Syntenin. Structure, 2003, 11, 459-468.	3.3	90
33	Molecular Roots of Degenerate Specificity in Syntenin's PDZ2 Domain. Structure, 2003, 11, 845-853.	3.3	83
34	The Crystal Structure of RhoA in Complex with the DH/PH Fragment of PDZRhoGEF, an Activator of the Ca2+ Sensitization Pathway in Smooth Muscle. Structure, 2004, 12, 1955-1965.	3.3	79
35	The N-terminal coiled-coil of Ndel1 is a regulated scaffold that recruits LIS1 to dynein. Journal of Cell Biology, 2011, 192, 433-445.	5.2	78
36	The Crystal Structure of the Reduced, Zn2+-Bound Form of the B. subtilis Hsp33 Chaperone and Its Implications for the Activation Mechanism. Structure, 2004, 12, 1901-1907.	3.3	77

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37	Stereochemistry of carbon monoxide binding to normal human adult and Cowtown haemoglobins. Journal of Molecular Biology, 1990, 211, 515-519.	4.2	76
38	The Structure of the Coiled-Coil Domain of Ndel1 and the Basis of Its Interaction with Lis1, the Causal Protein of Miller-Dieker Lissencephaly. Structure, 2007, 15, 1467-1481.	3.3	74
39	Structure of the RGS-like Domain from PDZ-RhoGEF. Structure, 2001, 9, 559-569.	3.3	73
40	Coupling PAF Signaling to Dynein Regulation. Neuron, 2004, 44, 809-821.	8.1	72
41	Substrate Specificity in Glycoside Hydrolase Family 10. Journal of Biological Chemistry, 2000, 275, 23020-23026.	3.4	70
42	p63RhoGEF Couples G _{αq/11} -Mediated Signaling to Ca ²⁺ Sensitization of Vascular Smooth Muscle Contractility. Circulation Research, 2011, 109, 993-1002.	4.5	66
43	How RhoGDI binds Rho. Acta Crystallographica Section D: Biological Crystallography, 1999, 55, 1503-1515.	2.5	65
44	The impact of Glu→Ala and Glu→Asp mutations on the crystallization properties of RhoGDI: the structure of RhoGDI at 1.3â€Ã resolution. Acta Crystallographica Section D: Biological Crystallography, 2002, 58, 1983-1991.	2.5	64
45	The PDZ2 Domain of Syntenin at Ultra-high Resolution: Bridging the Gap Between Macromolecular and Small Molecule Crystallography. Journal of Molecular Biology, 2004, 338, 483-493.	4.2	47
46	The Dimerization Mechanism of LIS1 and its Implication for Proteins Containing the LisH Motif. Journal of Molecular Biology, 2006, 357, 621-631.	4.2	47
47	Dynactin helps target Polo-like kinase 1 to kinetochores via its left-handed beta-helical p27 subunit. EMBO Journal, 2013, 32, 1023-1035.	7.8	46
48	The structure of the FERM domain of merlin, the neurofibromatosis type 2 gene product. Acta Crystallographica Section D: Biological Crystallography, 2002, 58, 381-391.	2.5	45
49	The Structure and Ligand Binding Properties of the B.subtilis YkoF Gene Product, a Member of a Novel Family of Thiamin/HMP-binding Proteins. Journal of Molecular Biology, 2004, 343, 395-406.	4.2	43
50	Conversion of Serine-114 to Cysteine-114 and the Role of the Active Site Nucleophile in Acyl Transfer by Myristoyl-ACP Thioesterase fromVibrio harveyiâ€. Biochemistry, 1996, 35, 9967-9973.	2.5	41
51	Architecture of the Cellulose Synthase Outer Membrane Channel and Its Association with the Periplasmic TPR Domain. Structure, 2019, 27, 1855-1861.e3.	3.3	41
52	The Molecular Basis of RhoA Specificity in the Guanine Nucleotide Exchange Factor PDZ-RhoGEF. Journal of Biological Chemistry, 2006, 281, 32891-32897.	3.4	40
53	Insights into the Inhibition of the p90 Ribosomal S6 Kinase (RSK) by the Flavonol Glycoside SL0101 from the 1.5 Ã Crystal Structure of the N-Terminal Domain of RSK2 with Bound Inhibitor. Biochemistry, 2012, 51, 6499-6510.	2.5	39
54	The structure of the C-terminal domain of the <i>Zaire ebolavirus</i> nucleoprotein. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 2420-2429.	2.5	39

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55	The impact of Lys→Arg surface mutations on the crystallization of the globular domain of RhoGDI. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 275-280.	2.5	38
56	Structural Features and Chaperone Activity of the NudC Protein Family. Journal of Molecular Biology, 2011, 409, 722-741.	4.2	38
57	Structure and Function of Bacillus subtilis YphP, a Prokaryotic Disulfide Isomerase with a CXC Catalytic Motif,. Biochemistry, 2009, 48, 8664-8671.	2.5	37
58	Structure of <i>Thermotoga maritima</i> TM0439: implications for the mechanism of bacterial GntR transcription regulators with Zn ²⁺ -binding FCD domains. Acta Crystallographica Section D: Biological Crystallography, 2009, 65, 356-365.	2.5	31
59	The role of entropy and polarity in intermolecular contacts in protein crystals. Acta Crystallographica Section D: Biological Crystallography, 2009, 65, 500-509.	2.5	31
60	Domain Identification of Hormone-sensitive Lipase by Circular Dichroism and Fluorescence Spectroscopy, Limited Proteolysis, and Mass Spectrometry. Journal of Biological Chemistry, 1999, 274, 15382-15388.	3.4	30
61	PAF-acetylhydrolases. Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids, 1999, 1441, 229-236.	2.4	30
62	Molecular Basis of Mitomycin C Resistance in Streptomyces. Structure, 2002, 10, 933-942.	3.3	30
63	Molecular mechanism of enantiorecognition by esterases. Journal of the American Chemical Society, 1995, 117, 2104-2105.	13.7	29
64	Expression, Purification, and Crystallization of the RGS-like Domain from the Rho Nucleotide Exchange Factor, PDZ-RhoGEF, Using the Surface Entropy Reduction Approach. Protein Expression and Purification, 2001, 21, 412-416.	1.3	29
65	It's all in the crystals…. Acta Crystallographica Section D: Biological Crystallography, 2011, 67, 243-248.	2.5	29
66	Structure of a constitutively activated RhoA mutant (Q63L) at 1.55â€Ã resolution. Acta Crystallographica Section D: Biological Crystallography, 2003, 59, 876-880.	2.5	28
67	On wine, chirality and crystallography. Acta Crystallographica Section A: Foundations and Advances, 2008, 64, 246-258.	0.3	28
68	Homologs of the ?- and ?-subunits of mammalian brain platelet-activating factor acetylhydrolase lb in theDrosophila melanogaster genome. , 2000, 39, 1-8.		25
69	On the mechanism of autoinhibition of the RhoA-specific nucleotide exchange factor PDZRhoGEF. BMC Structural Biology, 2009, 9, 36.	2.3	24
70	Harvesting the high-hanging fruit: the structure of theYdeNgene product fromBacillus subtilisat 1.8â€Ã resolution. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 1101-1107.	2.5	23
71	Insights into the Molecular Activation Mechanism of the RhoA-specific Guanine Nucleotide Exchange Factor, PDZRhoCEF. Journal of Biological Chemistry, 2011, 286, 35163-35175.	3.4	23
72	Initiating a crystallographic study of trypanothione reductase. Journal of Molecular Biology, 1990, 216, 235-237.	4.2	22

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73	Structure of the BH Domain from Graf and Its Implications for Rho GTPase Recognition. Journal of Biological Chemistry, 2000, 275, 38605-38610.	3.4	22
74	Agonist-induced Ca2+ Sensitization in Smooth Muscle. Journal of Biological Chemistry, 2013, 288, 34030-34040.	3.4	21
75	Preparation and crystal structure of the recombinant α1/α2 catalytic heterodimer of bovine brain platelet-activating factor acetylhydrolase lb. Protein Engineering, Design and Selection, 2001, 14, 513-519.	2.1	19
76	Probing the Supramodular Architecture of a Multidomain Protein: The Structure of Syntenin in Solution. Structure, 2005, 13, 319-327.	3.3	19
77	Bivalent Peptides as Models for Multimeric Targets of PDZ Domains. ChemBioChem, 2007, 8, 443-452.	2.6	19
78	The solution structure and dynamics of the DHâ€PH module of PDZRhoGEF in isolation and in complex with nucleotideâ€free RhoA. Protein Science, 2009, 18, 2067-2079.	7.6	18
79	The "Sticky Patch―Model of Crystallization and Modification of Proteins for Enhanced Crystallizability. Methods in Molecular Biology, 2017, 1607, 77-115.	0.9	17
80	Crystallization of the Malonyl Coenzyme A-Acyl Carrier Protein Transacylase from Escherichia coli. Journal of Molecular Biology, 1994, 242, 99-102.	4.2	15
81	The DC-module of doublecortin: Dynamics, domain boundaries, and functional implications. Proteins: Structure, Function and Bioinformatics, 2006, 64, 874-882.	2.6	15
82	ldentification of quercitrin as an inhibitor of the p90 S6 ribosomal kinase (RSK): structure of its complex with the N-terminal domain of RSK2 at 1.8â€Ã resolution. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 266-275.	2.5	15
83	Molecular architecture of the nucleoprotein C-terminal domain from the Ebola and Marburg viruses. Acta Crystallographica Section D: Structural Biology, 2016, 72, 49-58.	2.3	14
84	The p90 Ribosomal S6 Kinase (RSK) Is a Mediator of Smooth Muscle Contractility. PLoS ONE, 2013, 8, e58703.	2.5	14
85	RSK2 contributes to myogenic vasoconstriction of resistance arteries by activating smooth muscle myosin and the Na ⁺ /H ⁺ exchanger. Science Signaling, 2018, 11, .	3.6	13
86	Salvage or Recovery of Failed Targets by Mutagenesis to Reduce Surface Entropy. Methods in Molecular Biology, 2014, 1140, 201-209.	0.9	13
87	Crystallization of the periplasmic oligopeptide-binding protein of Salmonella typhimurium. Journal of Molecular Biology, 1988, 204, 493-494.	4.2	12
88	Crystallization and preliminary crystallographic studies of the precursor and mature forms of a neutral lipase from the fungusRhizopus delemar. Proteins: Structure, Function and Bioinformatics, 1994, 18, 301-306.	2.6	12
89	Crystallization of canine cardiac calsequestrin. Journal of Molecular Biology, 1994, 235, 357-360.	4.2	12
90	Crystal structures of the methyltransferase and helicase from the ZIKA 1947 MR766 Uganda strain. Acta Crystallographica Section D: Structural Biology, 2017, 73, 767-774.	2.3	10

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91	Biochemical and molecular biological characterization of a lipase produced by the fungusRhizopus delemar. Lipid - Fett, 1999, 101, 364-370.	0.4	9
92	Preliminary crystallographic analysis of the complex of the human GTPase RhoA with the DH/PH tandem of PDZ-RhoGEF. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 740-742.	2.5	9
93	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. Acta Crystallographica Section D: Structural Biology, 2018, 74, 681-689.	2.3	9
94	Expression, purification and crystallization of the Vibrio harveyi acyltransferase. Journal of Molecular Biology, 1992, 227, 572-574.	4.2	8
95	Purification and crystallization of the N-terminal domain from the human doublecortin-like kinase. Acta Crystallographica Section D: Biological Crystallography, 2003, 59, 502-505.	2.5	8
96	The unusual mechanism of inhibition of the p90 ribosomal S6 kinase (RSK) by flavonol rhamnosides. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2013, 1834, 1285-1291.	2.3	7
97	<scp>C─H</scp> â<¯O hydrogen bonds in kinaseâ€inhibitor interfaces. IUBMB Life, 2020, 72, 1233-1242.	3.4	7
98	Crystallization and preliminary crystallographic data of a Streptomyces scabies extracellular esterase. Journal of Molecular Biology, 1992, 227, 569-571.	4.2	6
99	Bacterial Expression, Purification and In Vitro Phosphorylation of Full-Length Ribosomal S6 Kinase 2 (RSK2). PLoS ONE, 2016, 11, e0164343.	2.5	6
100	Crystallization of Thioesterase II from Escherichia coli. Journal of Molecular Biology, 1994, 236, 660-662.	4.2	4
101	Structure of the <i>Bacillus subtilis</i> OhrB hydroperoxide-resistance protein in a fully oxidized state. Acta Crystallographica Section D: Biological Crystallography, 2007, 63, 1269-1273.	2.5	4
102	Abstractions, algorithms and data structures for structural bioinformatics inPyCogent. Journal of Applied Crystallography, 2011, 44, 424-428.	4.5	4
103	Protein crystallization in drug design: towards a rational approach. Expert Opinion on Drug Discovery, 2007, 2, 1329-1340.	5.0	3
104	Degenerate specificity of PDZ domains from RhoA-specific nucleotide exchange factors PDZRhoGEF and LARG. Acta Biochimica Polonica, 2008, 55, 269-80.	0.5	3
105	Substrate-selectivity in acylhydrolases: a cautionary tale. Colloids and Surfaces B: Biointerfaces, 2002, 26, 31-35.	5.0	2
106	Assignment of 1H, 13C and 15N resonances of the N-terminal microtubule-binding domain of human doublecortin. Journal of Biomolecular NMR, 2003, 25, 81-82.	2.8	2
107	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). Acta Crystallographica Section A: Foundations and Advances, 2021, 77, 362-378.	0.1	1
108	Adventures in cooperativity. Postepy Biochemii, 2016, 62, 286-297.	0.2	1

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109	Towards a highâ€resolution structure of dynactin. FASEB Journal, 2006, 20, A95.	0.5	0