

Eric Girard

List of Publications by Year in descending order

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73
papers

1,658
citations

236925

25
h-index

330143

37
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78
all docs

78
docs citations

78
times ranked

2079
citing authors

#	ARTICLE	IF	CITATIONS
1	Microbial diversity and adaptation to high hydrostatic pressure in deep-sea hydrothermal vents prokaryotes. <i>Extremophiles</i> , 2015, 19, 721-740.	2.3	117
2	Adaptation of the base-paired double-helix molecular architecture to extreme pressure. <i>Nucleic Acids Research</i> , 2007, 35, 4800-4808.	14.5	68
3	Bacteriophage T5 tail tube structure suggests a trigger mechanism for Siphoviridae DNA ejection. <i>Nature Communications</i> , 2017, 8, 1953.	12.8	64
4	High-pressure macromolecular crystallography and NMR: status, achievements and prospects. <i>Current Opinion in Structural Biology</i> , 2012, 22, 636-642.	5.7	58
5	Crystallophore: a versatile lanthanide complex for protein crystallography combining nucleating effects, phasing properties, and luminescence. <i>Chemical Science</i> , 2017, 8, 5909-5917.	7.4	58
6	Rational-Differential Design of Highly Specific Glycomimetic Ligands: Targeting DC-SIGN and Excluding Langerin Recognition. <i>ACS Chemical Biology</i> , 2018, 13, 600-608.	3.4	56
7	Structure-Function Perturbation and Dissociation of Tetrameric Urate Oxidase by High Hydrostatic Pressure. <i>Biophysical Journal</i> , 2010, 98, 2365-2373.	0.5	53
8	The First Crystal Structure of a Macromolecular Assembly under High Pressure: CpMV at 330 MPa. <i>Biophysical Journal</i> , 2005, 88, 3562-3571.	0.5	51
9	Advances in High-Pressure Biophysics: Status and Prospects of Macromolecular Crystallography. <i>Annual Review of Biophysics</i> , 2009, 38, 153-171.	10.0	46
10	Archaeal acetoacetyl-CoA thiolase/HMG-CoA synthase complex channels the intermediate via a fused CoA-binding site. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 3380-3385.	7.1	44
11	Crystal Structure of pb9, the Distal Tail Protein of Bacteriophage T5: a Conserved Structural Motif among All Siphophages. <i>Journal of Virology</i> , 2014, 88, 820-828.	3.4	43
12	High pressure macromolecular crystallography: The 140-MPa crystal structure at 2.3 Å... resolution of urate oxidase, a 135-kDa tetrameric assembly. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2006, 1764, 391-397.	2.3	42
13	Glycosaminoglycans Are Interactants of Langerin: Comparison with gp120 Highlights an Unexpected Calcium-Independent Binding Mode. <i>PLoS ONE</i> , 2012, 7, e50722.	2.5	42
14	Gradual Adaptive Changes of a Protein Facing High Salt Concentrations. <i>Journal of Molecular Biology</i> , 2010, 404, 493-505.	4.2	40
15	Toward fully fledged high-pressure macromolecular crystallography. <i>Journal of Applied Crystallography</i> , 2007, 40, 912-918.	4.5	38
16	An experimental point of view on hydration/solvation in halophilic proteins. <i>Frontiers in Microbiology</i> , 2014, 5, 66.	3.5	37
17	The Crystal Structure of the Anti-If Factor CnrY in Complex with the If Factor CnrH Shows a New Structural Class of Anti-If Factors Targeting Extracytoplasmic Function If Factors. <i>Journal of Molecular Biology</i> , 2014, 426, 2313-2327.	4.2	37
18	Opening the High-Pressure Domain beyond 2 kbar to Protein and Virus Crystallography—Technical Advance. <i>Structure</i> , 2002, 10, 1409-1414.	3.3	36

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19	Gd-HPDO3A, a complex to obtain high-phasing-power heavy-atom derivatives for SAD and MAD experiments: results with tetragonal hen egg-white lysozyme. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 1-9.	2.5	35
20	A new class of lanthanide complexes to obtain high-phasing-power heavy-atom derivatives for macromolecular crystallography. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 1914-1922.	2.5	35
21	The multicatalytic compartment of propionyl-CoA synthase sequesters a toxic metabolite. <i>Nature Chemical Biology</i> , 2018, 14, 1127-1132.	8.0	34
22	Structural Basis for Metal Sensing by CnrX. <i>Journal of Molecular Biology</i> , 2011, 408, 766-779.	4.2	32
23	SAXS/SANS on Supercharged Proteins Reveals Residue-Specific Modifications of the Hydration Shell. <i>Biophysical Journal</i> , 2016, 110, 2185-2194.	0.5	32
24	A segment of cold shock protein directs the folding of a combinatorial protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 1396-1401.	7.1	31
25	Reduction of radiation damage and other benefits of short wavelengths for macromolecular crystallography data collection. <i>Journal of Applied Crystallography</i> , 2012, 45, 652-661.	4.5	30
26	Structure of the Archaeal Pab87 Peptidase Reveals a Novel Self-Compartmentalizing Protease Family. <i>PLoS ONE</i> , 2009, 4, e4712.	2.5	23
27	A simple and versatile microfluidic device for efficient biomacromolecule crystallization and structural analysis by serial crystallography. <i>IUCr</i> , 2019, 6, 454-464.	2.2	23
28	Unique GMP-binding site in <i>Mycobacterium tuberculosis</i> guanosine monophosphate kinase. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 62, 489-500.	2.6	22
29	Metal sensing and signal transduction by CnrX from <i>Cupriavidus metallidurans</i> CH34: role of the only methionine assessed by a functional, spectroscopic, and theoretical study. <i>Metallomics</i> , 2014, 6, 263-273.	2.4	21
30	Protein crystal structure determination with the crystallophore, a nucleating and phasing agent. <i>Journal of Applied Crystallography</i> , 2019, 52, 722-731.	4.5	21
31	X-ray structure of the metal sensor CnrX in both the apo and copper bound forms. <i>FEBS Letters</i> , 2008, 582, 3954-3958.	2.8	20
32	High-Pressure Macromolecular Crystallography (HPMX): Status and prospects. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2006, 1764, 384-390.	2.3	19
33	Small-angle neutron scattering reveals the assembly mode and oligomeric architecture of TET, a large, dodecameric aminopeptidase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 2983-2993.	2.5	19
34	New insights into the mechanism of substrates trafficking in Glyoxylate/Hydroxypyruvate reductases. <i>Scientific Reports</i> , 2016, 6, 20629.	3.3	19
35	Unveiling the Binding Modes of the Crystallophore, a Terbium-based Nucleating and Phasing Molecular Agent for Protein Crystallography. <i>Chemistry - A European Journal</i> , 2018, 24, 9739-9746.	3.3	19
36	Equilibria between conformational states of the Ras oncogene protein revealed by high pressure crystallography. <i>Chemical Science</i> , 2022, 13, 2001-2010.	7.4	17

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37	Isothermal compressibility of macromolecular crystals and macromolecules derived from high-pressure X-ray crystallography. <i>Journal of Applied Crystallography</i> , 2010, 43, 407-416.	4.5	16
38	Structural Insight into Ubiquitin-Like Protein Recognition and Oligomeric States of JAMM/MPN+ Proteases. <i>Structure</i> , 2017, 25, 823-833.e6.	3.3	16
39	Medical contrast media as possible tools for SAXS contrast variation. <i>IUCr</i> , 2019, 6, 521-525.	2.2	16
40	Evidence for Conformational Changes upon Copper Binding to <i>Cupriavidus metallidurans</i> CzcE. <i>Biochemistry</i> , 2010, 49, 1913-1922.	2.5	13
41	Exploration of the supramolecular interactions involving tris-dipicolinate lanthanide complexes in protein crystals by a combined biostructural, computational and NMR study. <i>Physical Chemistry Chemical Physics</i> , 2013, 15, 18235.	2.8	13
42	The archaeal LDH-like malate dehydrogenase from <i>Ignicoccus islandicus</i> displays dual substrate recognition, hidden allostery and a non-canonical tetrameric oligomeric organization. <i>Journal of Structural Biology</i> , 2019, 208, 7-17.	2.8	13
43	Using a quasi-parallel X-ray beam of ultrashort wavelength for high-pressure virus crystallography: implications for standard macromolecular crystallography. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 1767-1772.	2.5	12
44	A new paradigm for macromolecular crystallography beamlines derived from high-pressure methodology and results. <i>Journal of Synchrotron Radiation</i> , 2011, 18, 31-36.	2.4	12
45	Using lanthanoid complexes to phase large macromolecular assemblies. <i>Journal of Synchrotron Radiation</i> , 2011, 18, 74-78.	2.4	11
46	<i>Pyrococcus horikoshii</i> TET2 Peptidase Assembling Process and Associated Functional Regulation. <i>Journal of Biological Chemistry</i> , 2013, 288, 22542-22554.	3.4	11
47	Interface Matters: The Stiffness Route to Stability of a Thermophilic Tetrameric Malate Dehydrogenase. <i>PLoS ONE</i> , 2014, 9, e113895.	2.5	11
48	The X-ray Structure of NccX from <i>Cupriavidus metallidurans</i> 31A Illustrates Potential Dangers of Detergent Solubilization When Generating and Interpreting Crystal Structures of Membrane Proteins. <i>Journal of Biological Chemistry</i> , 2014, 289, 31160-31172.	3.4	10
49	Krypton-derivatization highlights O ₂ -channeling in a four-electron reducing oxidase. <i>Chemical Communications</i> , 2020, 56, 10863-10866.	4.1	10
50	Resurrection of Ancestral Malate Dehydrogenases Reveals the Evolutionary History of Halobacterial Proteins: Deciphering Gene Trajectories and Changes in Biochemical Properties. <i>Molecular Biology and Evolution</i> , 2021, 38, 3754-3774.	8.9	10
51	Macromolecular crystallography at high pressure with pneumatic diamond anvil cells handled by a six-axis robotic arm. <i>Journal of Applied Crystallography</i> , 2010, 43, 762-768.	4.5	9
52	Biostructural analysis of the metal-sensor domain of CnrX from <i>Cupriavidus metallidurans</i> CH34. <i>Antonie Van Leeuwenhoek</i> , 2009, 96, 141-148.	1.7	8
53	Tuned by metals: the TET peptidase activity is controlled by 3 metal binding sites. <i>Scientific Reports</i> , 2016, 6, 20876.	3.3	8
54	Instrumentation for synchrotron-radiation macromolecular crystallography. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006, 62, 12-18.	2.5	7

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55	Clicked europium dipicolinate complexes for protein X-ray structure determination. <i>Chemical Communications</i> , 2012, 48, 11886.	4.1	7
56	Functional Sub-states by High-pressure Macromolecular Crystallography. <i>Sub-Cellular Biochemistry</i> , 2015, 72, 215-235.	2.4	7
57	Determinants of neuroglobin plasticity highlighted by joint coarse-grained simulations and high pressure crystallography. <i>Scientific Reports</i> , 2017, 7, 1858.	3.3	7
58	Experimental study of proteome halophilicity using nanoDSF: a proof of concept. <i>Extremophiles</i> , 2022, 26, 1.	2.3	6
59	Comparative study of the effects of high hydrostatic pressure <i>per se</i> and high argon pressure on urate oxidase ligand stabilization. <i>Acta Crystallographica Section D: Structural Biology</i> , 2022, 78, 162-173.	2.3	6
60	Pressure-induced activation of latent dihydroorotase from <i>Aquifex aeolicus</i> as revealed by high pressure protein crystallography. <i>FEBS Journal</i> , 2019, 286, 1204-1213.	4.7	5
61	Heavy-atom derivatives in lipidic cubic phases: results on hen egg-white lysozyme tetragonal derivative crystals with Gd-HPDO3A complex. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 1506-1508.	2.5	4
62	The C-terminal domain of <i>Corynebacterium glutamicum</i> mycolyltransferase A is composed of five repeated motifs involved in cell wall binding and stability. <i>Molecular Microbiology</i> , 2020, 114, 1-16.	2.5	4
63	Biochemical, structural and dynamical studies reveal strong differences in the thermal-dependent allosteric behavior of two extremophilic lactate dehydrogenases. <i>Journal of Structural Biology</i> , 2021, 213, 107769.	2.8	4
64	A new dimension in structural biology: fully fledged high-pressure macromolecular crystallography. <i>High Pressure Research</i> , 2004, 24, 173-182.	1.2	3
65	Characterization of a Glycyl-Specific TET Aminopeptidase Complex from <i>Pyrococcus horikoshii</i> . <i>Journal of Bacteriology</i> , 2018, 200, .	2.2	3
66	Monitoring the Production of High Diffraction-Quality Crystals of Two Enzymes in Real Time Using In Situ Dynamic Light Scattering. <i>Crystals</i> , 2020, 10, 65.	2.2	3
67	Influence of Divalent Cations in the Protein Crystallization Process Assisted by Lanthanide-Based Additives. <i>Inorganic Chemistry</i> , 2021, 60, 15208-15214.	4.0	3
68	Tracking Crystallophore Nucleating Properties: Setting Up a Database for Statistical Analysis. <i>Crystal Growth and Design</i> , 2020, 20, 5322-5329.	3.0	2
69	Behavior of B- and Z-DNA Crystals under High Hydrostatic Pressure. <i>Crystals</i> , 2022, 12, 871.	2.2	2
70	The prominent role of resonant elastic scattering for solving the X-ray structure of macromolecules. <i>European Physical Journal: Special Topics</i> , 2012, 208, 15-20.	2.6	1
71	X-ray Crystallography at High Pressure to Probe Conformational Fluctuations in Biological Macromolecules. <i>AIP Conference Proceedings</i> , 2007, , .	0.4	0
72	High-Pressure Crystallography of Biomolecules: Recent Achievements. I – Introduction, Materials and Methods. <i>NATO Science for Peace and Security Series B: Physics and Biophysics</i> , 2010, , 591-601.	0.3	0

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73	High-Pressure Crystallography of Biomolecules: Recent Achievements. II " Applications. NATO Science for Peace and Security Series B: Physics and Biophysics, 2010, , 603-612.	0.3	0