

# 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	Experimental study of proteome halophilicity using nanoDSF: a proof of concept. <i>Extremophiles</i> , 2022, 26, 1.	2.3	6
2	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
3	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
4	Behavior of B- and Z-DNA Crystals under High Hydrostatic Pressure. <i>Crystals</i> , 2022, 12, 871.	2.2	2
5	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
6	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
7	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
8	Tracking Crystallophore Nucleating Properties: Setting Up a Database for Statistical Analysis. <i>Crystal Growth and Design</i> , 2020, 20, 5322-5329.	3.0	2
9	Krypton-derivatization highlights O <sub>2</sub> -channeling in a four-electron reducing oxidase. <i>Chemical Communications</i> , 2020, 56, 10863-10866.	4.1	10
10	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
11	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
12	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
13	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
14	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
15	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
16	Medical contrast media as possible tools for SAXS contrast variation. <i>IUCr</i> , 2019, 6, 521-525.	2.2	16
17	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
18	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

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19	The multicatalytic compartment of propionyl-CoA synthase sequesters a toxic metabolite. <i>Nature Chemical Biology</i> , 2018, 14, 1127-1132.	8.0	34
20	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
21	Characterization of a Glycyl-Specific TET Aminopeptidase Complex from <i>Pyrococcus horikoshii</i> . <i>Journal of Bacteriology</i> , 2018, 200, .	2.2	3
22	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
23	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
24	Determinants of neuroglobin plasticity highlighted by joint coarse-grained simulations and high pressure crystallography. <i>Scientific Reports</i> , 2017, 7, 1858.	3.3	7
25	Bacteriophage T5 tail tube structure suggests a trigger mechanism for Siphoviridae DNA ejection. <i>Nature Communications</i> , 2017, 8, 1953.	12.8	64
26	New insights into the mechanism of substrates trafficking in Glyoxylate/Hydroxypyruvate reductases. <i>Scientific Reports</i> , 2016, 6, 20629.	3.3	19
27	SAXS/SANS on Supercharged Proteins Reveals Residue-Specific Modifications of the Hydration Shell. <i>Biophysical Journal</i> , 2016, 110, 2185-2194.	0.5	32
28	Tuned by metals: the TET peptidase activity is controlled by 3 metal binding sites. <i>Scientific Reports</i> , 2016, 6, 20876.	3.3	8
29	Microbial diversity and adaptation to high hydrostatic pressure in deep-sea hydrothermal vents prokaryotes. <i>Extremophiles</i> , 2015, 19, 721-740.	2.3	117
30	Functional Sub-states by High-pressure Macromolecular Crystallography. <i>Sub-Cellular Biochemistry</i> , 2015, 72, 215-235.	2.4	7
31	An experimental point of view on hydration/solvation in halophilic proteins. <i>Frontiers in Microbiology</i> , 2014, 5, 66.	3.5	37
32	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
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	The Crystal Structure of the Anti- $\beta$ Factor CnrY in Complex with the $\beta$ Factor CnrH Shows a New Structural Class of Anti- $\beta$ Factors Targeting Extracytoplasmic Function $\beta$ Factors. <i>Journal of Molecular Biology</i> , 2014, 426, 2313-2327.	4.2	37
35	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
36	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

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37	Interface Matters: The Stiffness Route to Stability of a Thermophilic Tetrameric Malate Dehydrogenase. PLoS ONE, 2014, 9, e113895.	2.5	11
38	Exploration of the supramolecular interactions involving tris-dipicolinate lanthanide complexes in protein crystals by a combined biostructural, computational and NMR study. Physical Chemistry Chemical Physics, 2013, 15, 18235.	2.8	13
39	Pyrococcus horikoshii TET2 Peptidase Assembling Process and Associated Functional Regulation. Journal of Biological Chemistry, 2013, 288, 22542-22554.	3.4	11
40	Clicked europium dipicolinate complexes for protein X-ray structure determination. Chemical Communications, 2012, 48, 11886.	4.1	7
41	The prominent role of resonant elastic scattering for solving the X-ray structure of macromolecules. European Physical Journal: Special Topics, 2012, 208, 15-20.	2.6	1
42	High-pressure macromolecular crystallography and NMR: status, achievements and prospects. Current Opinion in Structural Biology, 2012, 22, 636-642.	5.7	58
43	Glycosaminoglycans Are Interactants of Langerin: Comparison with gp120 Highlights an Unexpected Calcium-Independent Binding Mode. PLoS ONE, 2012, 7, e50722.	2.5	42
44	Reduction of radiation damage and other benefits of short wavelengths for macromolecular crystallography data collection. Journal of Applied Crystallography, 2012, 45, 652-661.	4.5	30
45	Structural Basis for Metal Sensing by CnrX. Journal of Molecular Biology, 2011, 408, 766-779.	4.2	32
46	Using lanthanoid complexes to phase large macromolecular assemblies. Journal of Synchrotron Radiation, 2011, 18, 74-78.	2.4	11
47	A new paradigm for macromolecular crystallography beamlines derived from high-pressure methodology and results. Journal of Synchrotron Radiation, 2011, 18, 31-36.	2.4	12
48	Isothermal compressibility of macromolecular crystals and macromolecules derived from high-pressure X-ray crystallography. Journal of Applied Crystallography, 2010, 43, 407-416.	4.5	16
49	Macromolecular crystallography at high pressure with pneumatic diamond anvil cells handled by a six-axis robotic arm. Journal of Applied Crystallography, 2010, 43, 762-768.	4.5	9
50	Structure-Function Perturbation and Dissociation of Tetrameric Urate Oxidase by High Hydrostatic Pressure. Biophysical Journal, 2010, 98, 2365-2373.	0.5	53
51	Evidence for Conformational Changes upon Copper Binding to <i>Cupriavidus metallidurans</i> CzcE. Biochemistry, 2010, 49, 1913-1922.	2.5	13
52	Gradual Adaptive Changes of a Protein Facing High Salt Concentrations. Journal of Molecular Biology, 2010, 404, 493-505.	4.2	40
53	High-Pressure Crystallography of Biomolecules: Recent Achievements. I " Introduction, Materials and Methods. NATO Science for Peace and Security Series B: Physics and Biophysics, 2010, , 591-601.	0.3	0
54	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

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55	Structure of the Archaeal Pab87 Peptidase Reveals a Novel Self-Compartmentalizing Protease Family. PLoS ONE, 2009, 4, e4712.	2.5	23
56	Biostructural analysis of the metal-sensor domain of CnrX from Cupriavidus metallidurans CH34. Antonie Van Leeuwenhoek, 2009, 96, 141-148.	1.7	8
57	Advances in High-Pressure Biophysics: Status and Prospects of Macromolecular Crystallography. Annual Review of Biophysics, 2009, 38, 153-171.	10.0	46
58	X-ray structure of the metal-sensor CnrX in both the apo- and copper-bound forms. FEBS Letters, 2008, 582, 3954-3958.	2.8	20
59	X-ray Crystallography at High Pressure to Probe Conformational Fluctuations in Biological Macromolecules. AIP Conference Proceedings, 2007, , .	0.4	0
60	Adaptation of the base-paired double-helix molecular architecture to extreme pressure. Nucleic Acids Research, 2007, 35, 4800-4808.	14.5	68
61	Toward fully fledged high-pressure macromolecular crystallography. Journal of Applied Crystallography, 2007, 40, 912-918.	4.5	38
62	Instrumentation for synchrotron-radiation macromolecular crystallography. Acta Crystallographica Section D: Biological Crystallography, 2006, 62, 12-18.	2.5	7
63	High pressure macromolecular crystallography: The 140-MPa crystal structure at 2.3 Å... resolution of urate oxidase, a 135-kDa tetrameric assembly. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2006, 1764, 391-397.	2.3	42
64	High-Pressure Macromolecular Crystallography (HPMX): Status and prospects. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2006, 1764, 384-390.	2.3	19
65	Unique GMP-binding site in Mycobacterium tuberculosis guanosine monophosphate kinase. Proteins: Structure, Function and Bioinformatics, 2005, 62, 489-500.	2.6	22
66	A segment of cold shock protein directs the folding of a combinatorial protein. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 1396-1401.	7.1	31
67	The First Crystal Structure of a Macromolecular Assembly under High Pressure: CpMV at 330 MPa. Biophysical Journal, 2005, 88, 3562-3571.	0.5	51
68	A new dimension in structural biology: fully fledged high-pressure macromolecular crystallography. High Pressure Research, 2004, 24, 173-182.	1.2	3
69	Heavy-atom derivatives in lipidic cubic phases: results on hen egg-white lysozyme tetragonal derivative crystals with Gd-HPDO3A complex. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 1506-1508.	2.5	4
70	Using a quasi-parallel X-ray beam of ultrashort wavelength for high-pressure virus crystallography: implications for standard macromolecular crystallography. Acta Crystallographica Section D: Biological Crystallography, 2003, 59, 1767-1772.	2.5	12
71	A new class of lanthanide complexes to obtain high-phasing-power heavy-atom derivatives for macromolecular crystallography. Acta Crystallographica Section D: Biological Crystallography, 2003, 59, 1914-1922.	2.5	35
72	Opening the High-Pressure Domain beyond 2 kbar to Protein and Virus Crystallography—Technical Advance. Structure, 2002, 10, 1409-1414.	3.3	36

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73	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