

Pietro Roversi

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2050709/publications.pdf>

Version: 2024-02-01

108
papers

7,194
citations

76294

40
h-index

69214

77
g-index

122
all docs

122
docs citations

122
times ranked

10622
citing authors

#	ARTICLE	IF	CITATIONS
1	Automated Structure Solution With autoSHARP. , 2007, 364, 215-230.		851
2	Antibody Multispecificity Mediated by Conformational Diversity. Science, 2003, 299, 1362-1367.	6.0	673
3	Refinement of severely incomplete structures with maximum likelihood inBUSTERâ€TNT. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 2210-2221.	2.5	666
4	Neisseria meningitidis recruits factor H using protein mimicry of host carbohydrates. Nature, 2009, 458, 890-893.	13.7	287
5	A conserved face of the Jagged/Serrate DSL domain is involved in Notch trans-activation and cis-inhibition. Nature Structural and Molecular Biology, 2008, 15, 849-857.	3.6	222
6	The complex of Arl2-GTP and PDEdelta: from structure to function. EMBO Journal, 2002, 21, 2095-2106.	3.5	206
7	Architecture of the major component of the type III secretion system export apparatus. Nature Structural and Molecular Biology, 2013, 20, 99-104.	3.6	200
8	Structural basis for complement factor Hâ€linked age-related macular degeneration. Journal of Experimental Medicine, 2007, 204, 2277-2283.	4.2	168
9	Structure of the TatC core of the twin-arginine protein transport system. Nature, 2012, 492, 210-214.	13.7	164
10	Assembly and Regulation of the Membrane Attack Complex Based on Structures of C5b6 and sC5b9. Cell Reports, 2012, 1, 200-207.	2.9	161
11	Molecular model of a type III secretion system needle: Implications for host-cell sensing. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 12529-12533.	3.3	149
12	Functional and structural characterization of the integrase from the prototype foamy virus. Nucleic Acids Research, 2009, 37, 243-255.	6.5	130
13	Self-chaperoning of the Type III Secretion System Needle Tip Proteins IpaD and BipD. Journal of Biological Chemistry, 2007, 282, 4035-4044.	1.6	129
14	What's the point of the type III secretion system needle?. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 6507-6513.	3.3	125
15	Crystal structure of Toll-like receptor adaptor MAL/TIRAP reveals the molecular basis for signal transduction and disease protection. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 14879-14884.	3.3	123
16	Structure of and influence of a tick complement inhibitor on human complement component 5. Nature Immunology, 2008, 9, 753-760.	7.0	121
17	Structural basis for complement factor I control and its disease-associated sequence polymorphisms. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 12839-12844.	3.3	118
18	Experimental Charge Density of Î±-Glycine at 23 K. Journal of Physical Chemistry A, 2000, 104, 1047-1054.	1.1	114

#	ARTICLE	IF	CITATIONS
19	Complement regulation at the molecular level: The structure of decay-accelerating factor. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 1279-1284.	3.3	112
20	Expression levels of MHC class I molecules are inversely correlated with promiscuity of peptide binding. ELife, 2015, 4, e05345.	2.8	107
21	An Atomic Resolution Model for Assembly, Architecture, and Function of the Dr Adhesins. Molecular Cell, 2004, 15, 647-657.	4.5	105
22	Interconversion of ATP Binding and Conformational Free Energies by Tryptophanyl-tRNA Synthetase: Structures of ATP Bound to Open and Closed, Pre-Transition-state Conformations. Journal of Molecular Biology, 2003, 325, 39-63.	2.0	84
23	Super-complexes of adhesion GPCRs and neural guidance receptors. Nature Communications, 2016, 7, 11184.	5.8	84
24	Charge density in crystalline citrinin from X-ray diffraction at 19â€šK. Canadian Journal of Chemistry, 1996, 74, 1145-1161.	0.6	82
25	A complex iron-calcium cofactor catalyzing phosphotransfer chemistry. Science, 2014, 345, 1170-1173.	6.0	80
26	Structural basis for cofactor-independent dioxygenation of <i>N</i>-heteroaromatic compounds at the Î±/Î²-hydrolase fold. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 657-662.	3.3	77
27	Structure of the heterodimeric core primase. Nature Structural and Molecular Biology, 2005, 12, 1137-1144.	3.6	73
28	A novel fold for the factor Hâ€š-binding protein BbCRASP-1 of Borrelia burgdorferi. Nature Structural and Molecular Biology, 2005, 12, 276-277.	3.6	72
29	Structural Basis of Latrophilin-FLRT Interaction. Structure, 2015, 23, 774-781.	1.6	67
30	Structures of mammalian ER Î±-glucosidase II capture the binding modes of broad-spectrum iminosugar antivirals. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E4630-8.	3.3	65
31	Modelling prior distributions of atoms for macromolecular refinement and completion. Acta Crystallographica Section D: Biological Crystallography, 2000, 56, 1316-1323.	2.5	60
32	Structural and Functional Characterization of a Novel T Cell Receptor Co-regulatory Protein Complex, CD97-CD55. Journal of Biological Chemistry, 2007, 282, 22023-22032.	1.6	60
33	Approximate anisotropic displacement parameters for H atoms in molecular crystals. Chemical Physics Letters, 2004, 386, 472-478.	1.2	58
34	Structure of Bacterial 3Î²/17Î²-Hydroxysteroid Dehydrogenase at 1.2 Å... Resolution:Â A Model for Multiple Steroid Recognitionâ€š. Biochemistry, 2002, 41, 14659-14668.	1.2	57
35	Factor I Autoantibodies in Patients with Atypical Hemolytic Uremic Syndrome. Clinical Journal of the American Society of Nephrology: CJASN, 2012, 7, 417-426.	2.2	56
36	High Resolution Studies of the Afa/Dr Adhesin DraE and Its Interaction with Chloramphenicol. Journal of Biological Chemistry, 2004, 279, 46851-46857.	1.6	55

#	ARTICLE	IF	CITATIONS
37	The Escherichia coli Cell Division Protein and Model Tat Substrate SufI (FtsP) Localizes to the Septal Ring and Has a Multicopper Oxidase-Like Structure. <i>Journal of Molecular Biology</i> , 2009, 386, 504-519.	2.0	54
38	The Structure of OMCI, a Novel Lipocalin Inhibitor of the Complement System. <i>Journal of Molecular Biology</i> , 2007, 369, 784-793.	2.0	50
39	Macrophage Scavenger Receptor A Mediates Adhesion to Apolipoproteins A-I and E. <i>Biochemistry</i> , 2009, 48, 11858-11871.	1.2	48
40	Interdomain conformational flexibility underpins the activity of UGGT, the eukaryotic glycoprotein secretion checkpoint. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 8544-8549.	3.3	48
41	Recovering experimental and theoretical electron densities in corundum using the multipolar model: IUCr Multipole Refinement Project. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2001, 57, 290-303.	0.3	46
42	Functional and structural characterization of a thermostable acetyl esterase from <i>Thermotoga maritima</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2012, 80, 1545-1559.	1.5	46
43	Mutational analyses of the BbCRASP-1 protein of <i>Borrelia burgdorferi</i> identify residues relevant for the architecture and binding of host complement regulators FHL-1 and factor H. <i>International Journal of Medical Microbiology</i> , 2009, 299, 255-268.	1.5	39
44	Mechanism for the Hydrolysis of a Sulfur-Sulfur Bond Based on the Crystal Structure of the Thiosulfohydrolase SoxB. <i>Journal of Biological Chemistry</i> , 2009, 284, 21707-21718.	1.6	37
45	<i>Drosophila</i> expresses a CD98 transporter with an evolutionarily conserved structure and amino acid-transport properties. <i>Biochemical Journal</i> , 2009, 420, 363-372.	1.7	37
46	Targeting Endoplasmic Reticulum α -Glucosidase I with a Single-Dose Iminosugar Treatment Protects against Lethal Influenza and Dengue Virus Infections. <i>Journal of Medicinal Chemistry</i> , 2020, 63, 4205-4214.	2.9	37
47	Crystal Structure and Functional Characterization of the Complement Regulator Mannose-binding Lectin (MBL)/Ficolin-associated Protein-1 (MAP-1). <i>Journal of Biological Chemistry</i> , 2012, 287, 32913-32921.	1.6	35
48	Structure-function mapping of BbCRASP-1, the key complement factor H and FHL-1 binding protein of <i>Borrelia burgdorferi</i> . <i>International Journal of Medical Microbiology</i> , 2006, 296, 177-184.	1.5	34
49	Bifunctional Lipocalin Ameliorates Murine Immune Complex-induced Acute Lung Injury. <i>Journal of Biological Chemistry</i> , 2013, 288, 18789-18802.	1.6	34
50	Structures of the <i>Shigella flexneri</i> Type 3 Secretion System Protein MxiC Reveal Conformational Variability Amongst Homologues. <i>Journal of Molecular Biology</i> , 2008, 377, 985-992.	2.0	32
51	Identification and characterization of a heterotrimeric archaeal DNA polymerase holoenzyme. <i>Nature Communications</i> , 2017, 8, 15075.	5.8	31
52	Structure of Human Complement C8, a Precursor to Membrane Attack. <i>Journal of Molecular Biology</i> , 2011, 405, 325-330.	2.0	30
53	Structural basis of pyrrole polymerization in human porphobilinogen deaminase. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2018, 1862, 1948-1955.	1.1	29
54	The simultaneous double Diels-Alder addition of 1,1-bis(3,5-dimethylfur-2-yl)ethane; toward a new, asymmetric synthesis of long-chain polypropionate fragments and analogues. <i>Tetrahedron Letters</i> , 1996, 37, 4149-4152.	0.7	28

#	ARTICLE	IF	CITATIONS
55	High-resolution experimental phases for tryptophanyl-tRNA synthetase (TrpRS) complexed with tryptophanyl-5â€²AMP. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 1595-1608.	2.5	28
56	Substituent Effect on the Competition between Hetero-Diels-Alder and Cheletropic Additions of Sulfur Dioxide to 1-Substituted Buta-1,3-dienes. <i>Helvetica Chimica Acta</i> , 2002, 85, 733.	1.0	28
57	The Structure of Echovirus Type 12 Bound to a Two-domain Fragment of Its Cellular Attachment Protein Decay-accelerating Factor (CD 55). <i>Journal of Biological Chemistry</i> , 2004, 279, 8325-8332.	1.6	27
58	Human complement factor I glycosylation: Structural and functional characterisation of the N-linked oligosaccharides. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2006, 1764, 1757-1766.	1.1	27
59	High-resolution structures of bacterially expressed soluble human CD59. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007, 63, 648-652.	0.7	25
60	Mechanism of Structural Tuning of the Hepatitis C Virus Human Cellular Receptor CD81 Large Extracellular Loop. <i>Structure</i> , 2017, 25, 53-65.	1.6	25
61	Expression, purification, crystallization and preliminary crystallographic analysis of MxiH, a subunit of the <i>Shigella flexneri</i> type III secretion system needle. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 302-305.	0.7	22
62	<i>Shigella flexneri</i> Spa15 Crystal Structure Verified in Solution by Double Electron Electron Resonance. <i>Journal of Molecular Biology</i> , 2011, 405, 427-435.	2.0	21
63	The Black cells phenotype is caused by a point mutation in the <i>Drosophila</i> pro-phenoloxidase 1 gene that triggers melanization and hematopoietic defects. <i>Developmental and Comparative Immunology</i> , 2015, 50, 166-174.	1.0	21
64	Isothiazoles. Part VI. Cycloaddition of azides to isothiazole dioxides: Synthesis of thiadiazabicyclo[3.1.0]hexene derivatives and their thermal rearrangement to thiazete dioxides, 1,2,6-thiadiazine dioxides and pyrazoles. <i>Tetrahedron</i> , 1996, 52, 7183-7200.	1.0	20
65	Identification and characterization of the â€˜missingâ€™ terminal enzyme for siroheme biosynthesis in <i>Î±-proteobacteria</i> . <i>Molecular Microbiology</i> , 2014, 92, 153-163.	1.2	20
66	X-ray absorption, refraction and resonant scattering tensors in selenated protein crystals: implications for data collection strategies in macromolecular crystallography. <i>Journal of Applied Crystallography</i> , 2005, 38, 168-182.	1.9	19
67	On the role of data quality in experimental charge-density studies. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2004, 60, 365-370.	0.3	18
68	Geometry and molecular parameters of 3,4-bis(dimethylamino)-3-cyclobutene-1,2-dione and its isomer bis(dimethylamino)squaraine. Combined study by IR spectroscopy, XRD and ab initio MO calculations. <i>Journal of the Chemical Society, Faraday Transactions</i> , 1996, 92, 3611.	1.7	17
69	Clamping, bending, and twisting inter-domain motions in the misfold-recognizing portion of UDP-glucose: Glycoprotein glucosyltransferase. <i>Structure</i> , 2021, 29, 357-370.e9.	1.6	15
70	Expression, purification, cocrystallization and preliminary crystallographic analysis of sucrose octasulfate/human complement regulator factor H SCRs 6â€“8. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007, 63, 480-483.	0.7	14
71	Tetartohedral twinning could happen to you too. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 418-424.	2.5	14
72	Structural basis of cholesterol binding by a novel clade of dendritic cell modulators from ticks. <i>Scientific Reports</i> , 2017, 7, 16057.	1.6	14

#	ARTICLE	IF	CITATIONS
73	Modulation of ERQC and ERAD: A Broad-Spectrum Spanner in the Works of Cancer Cells?. <i>Journal of Oncology</i> , 2019, 2019, 1-14.	0.6	14
74	Expression, limited proteolysis and preliminary crystallographic analysis of IpaD, a component of the <i>Shigella flexneri</i> type III secretion system. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 865-868.	0.7	12
75	Anharmonic motions versus dynamic disorder at the Mg ion from the charge densities in pyrope (Mg ₃ Al ₂ Si ₃ O ₁₂) crystals at 30 K: six of one, half a dozen of the other. <i>Acta Crystallographica Section B: Structural Science, Crystal Engineering and Materials</i> , 2017, 73, 722-736.	0.5	12
76	Target highlights from the first post-PSI CASP experiment (CASP12, May-August 2016). <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, 27-50.	1.5	11
77	Crystallization and preliminary crystallographic analysis of BbCRASP-1, a complement regulator-acquiring surface protein of <i>Borrelia burgdorferi</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 929-932.	2.5	9
78	Structural Insights into the Broad-Spectrum Antiviral Target Endoplasmic Reticulum Alpha-Glucosidase II. <i>Advances in Experimental Medicine and Biology</i> , 2018, 1062, 265-276.	0.8	8
79	Crystallization and preliminary X-ray diffraction analysis of three EGF domains of EMR2, a 7TM immune-system molecule. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 936-938.	2.5	7
80	Cooperative stabilisation of 14-3-3 ζ protein-protein interactions via covalent protein modification. <i>Chemical Science</i> , 2021, 12, 12985-12992.	3.7	7
81	Stereoselective conjugate addition of lithium and titanium enolates to \hat{I}^3 -alkoxy enones. <i>Tetrahedron</i> , 1996, 52, 3497-3508.	1.0	6
82	A structural study of the interaction between the Dr haemagglutinin DraE and derivatives of chloramphenicol. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2009, 65, 513-522.	2.5	6
83	Structures of the rat complement regulator CrrY. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 739-743.	0.7	6
84	Expression, purification, crystallization and preliminary crystallographic analysis of BipD, a component of the <i>Burkholderia pseudomallei</i> type III secretion system. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 861-864.	0.7	5
85	In Planta Preliminary Screening of ER Glycoprotein Folding Quality Control (ERQC) Modulators. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2135.	1.8	5
86	EFR-Mediated Innate Immune Response in <i>Arabidopsis thaliana</i> is a Useful Tool for Identification of Novel ERQC Modulators. <i>Genes</i> , 2019, 10, 15.	1.0	5
87	Anharmonic Thermal Motion Modelling in the Experimental XRD Charge Density Determination of 1-Methyluracil at T = 23 K. <i>Molecules</i> , 2021, 26, 3075.	1.7	5
88	With phases: how two wrongs can sometimes make a right. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2010, 66, 420-425.	2.5	4
89	Ten things I 'hate' about refinement. <i>Acta Crystallographica Section D: Structural Biology</i> , 2021, 77, 1497-1515.	1.1	4
90	Towards the crystal structure of intact Human Complement Factor I. <i>Molecular Immunology</i> , 2009, 46, 2864-2865.	1.0	3

#	ARTICLE	IF	CITATIONS
91	Partial catalytic Cys oxidation of human GAPDH to Cys-sulfonic acid.. Wellcome Open Research, 2020, 5, 114.	0.9	3
92	Partial catalytic Cys oxidation of human GAPDH. Wellcome Open Research, 2020, 5, 114.	0.9	3
93	In-house low-resolution X-ray crystallography. Acta Crystallographica Section D: Biological Crystallography, 2000, 56, 1304-1311.	2.5	2
94	Chicken TAP genes are polymorphic and co-evolve with the dominantly-expressed class I gene. Molecular Immunology, 2012, 51, 19-20.	1.0	2
95	Investigating the structure of the factor B vWF-A domain/CD55 proteinâ€“protein complex using DEER spectroscopy: successes and pitfalls. Molecular Physics, 2013, 111, 2865-2872.	0.8	2
96	Crystal structure of the 6-phosphogluconate dehydrogenase from Gluconobacter oxydans reveals tetrameric 6PGDHs as the crucial intermediate in the evolution of structure and cofactor preference in the 6PGDH family. Wellcome Open Research, 0, 6, 48.	0.9	2
97	Towards a structural basis for complement factor H linked age-related macular degeneration. Molecular Immunology, 2007, 44, 3930-3931.	1.0	1
98	Factor I autoantibodies are associated with atypical haemolytic uraemic syndrome. Molecular Immunology, 2010, 47, 2291-2292.	1.0	1
99	On the Charge Density Refinement of Odd-Order Multipoles Invariant under Crystal Point Group Symmetry. Symmetry, 2017, 9, 63.	1.1	1
100	Experimental Charge Density Analysis and Electrostatic Properties of Crystalline 1,3-Bis(Dimethylamino)Squaraine and Its Dihydrate from Low Temperature (T = 18 and 20 K) XRD Data. Crystals, 2020, 10, 894.	1.0	1
101	Maximum Entropy charge density studies: Bayesian viewpoint and test applications. , 2000, , 1-26.		1
102	Crystallographic studies of human complement factor I. Molecular Immunology, 2007, 44, 233-234.	1.0	0
103	The crystal structure of rat complement receptor 1-related protein Y (CrrY) helps dissecting decay-acceleration and fl-cofactor activities. Molecular Immunology, 2008, 45, 4096-4097.	1.0	0
104	Single-particle electron microscopy reconstruction of the structure of complement component 8 (C8) at 23Å... resolution. Molecular Immunology, 2008, 45, 4121.	1.0	0
105	From Structure to Function of a Complement Regulator. , 2005, , 213-231.		0
106	Structural basis for complement Factor I control and its disease-associated sequence polymorphisms. Acta Crystallographica Section A: Foundations and Advances, 2011, 67, C217-C218.	0.3	0
107	Structural comparison of the head-subdomain of human CD81 large extra-cellular loop. Acta Crystallographica Section A: Foundations and Advances, 2013, 69, s314-s314.	0.3	0
108	Clamping, Bending, and Twisting Inter-Domain Motions in the Misfold-Recognising Portion of UDP-Glucose: Glycoprotein Glucosyl-Transferase. SSRN Electronic Journal, 0, , .	0.4	0