

Pietro Roversi

List of Publications by Year in descending order

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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	Cooperative stabilisation of 14-3-3 β proteinâ€“protein interactions <i>via</i> covalent protein modification. <i>Chemical Science</i> , 2021, 12, 12985-12992.	3.7	7
2	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
3	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
4	Ten things I 'hate' about refinement. <i>Acta Crystallographica Section D: Structural Biology</i> , 2021, 77, 1497-1515.	1.1	4
5	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. <i>Crystals</i> , 2020, 10, 894.	1.0	1
6	Targeting Endoplasmic Reticulum Î±-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
7	Partial catalytic Cys oxidation of human GAPDH to Cys-sulfonic acid.. <i>Wellcome Open Research</i> , 2020, 5, 114.	0.9	3
8	Partial catalytic Cys oxidation of human GAPDH. <i>Wellcome Open Research</i> , 2020, 5, 114.	0.9	3
9	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
10	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
11	Target highlights from the first postâ€“PSI CASP experiment (CASP12, Mayâ€“August 2016). <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, 27-50.	1.5	11
12	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
13	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
14	Structural basis of pyrrole polymerization in human porphobilinogen deaminase. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2018, 1862, 1948-1955.	1.1	29
15	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
16	Identification and characterization of a heterotrimeric archaeal DNA polymerase holoenzyme. <i>Nature Communications</i> , 2017, 8, 15075.	5.8	31
17	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
18	Anharmonic motions<i>versus</i>dynamic disorder at the Mg ion from the charge densities in pyrope (Mg₃Al₂Si₃O₁₂) crystals at 30â€“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

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19	On the Charge Density Refinement of Odd-Order Multipoles Invariant under Crystal Point Group Symmetry. <i>Symmetry</i> , 2017, 9, 63.	1.1	1
20	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
21	Super-complexes of adhesion GPCRs and neural guidance receptors. <i>Nature Communications</i> , 2016, 7, 11184.	5.8	84
22	Structures of mammalian ER α -glucosidase II capture the binding modes of broad-spectrum iminosugar antivirals. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E4630-8.	3.3	65
23	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
24	Structural Basis of Latrophilin-FLRT Interaction. <i>Structure</i> , 2015, 23, 774-781.	1.6	67
25	Expression levels of MHC class I molecules are inversely correlated with promiscuity of peptide binding. <i>ELife</i> , 2015, 4, e05345.	2.8	107
26	Identification and characterization of the α -missing β terminal enzyme for siroheme biosynthesis in α -proteobacteria. <i>Molecular Microbiology</i> , 2014, 92, 153-163.	1.2	20
27	A complex iron-calcium cofactor catalyzing phosphotransfer chemistry. <i>Science</i> , 2014, 345, 1170-1173.	6.0	80
28	Architecture of the major component of the type III secretion system export apparatus. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 99-104.	3.6	200
29	Bifunctional Lipocalin Ameliorates Murine Immune Complex-induced Acute Lung Injury. <i>Journal of Biological Chemistry</i> , 2013, 288, 18789-18802.	1.6	34
30	Investigating the structure of the factor B vWF-A domain/CD55 protein α protein complex using DEER spectroscopy: successes and pitfalls. <i>Molecular Physics</i> , 2013, 111, 2865-2872.	0.8	2
31	Structural comparison of the head-subdomain of human CD81 large extra-cellular loop. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2013, 69, s314-s314.	0.3	0
32	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
33	Structure of the TatC core of the twin-arginine protein transport system. <i>Nature</i> , 2012, 492, 210-214.	13.7	164
34	Assembly and Regulation of the Membrane Attack Complex Based on Structures of C5b6 and sC5b9. <i>Cell Reports</i> , 2012, 1, 200-207.	2.9	161
35	Factor I Autoantibodies in Patients with Atypical Hemolytic Uremic Syndrome. <i>Clinical Journal of the American Society of Nephrology: CJASN</i> , 2012, 7, 417-426.	2.2	56
36	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

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37	Chicken TAP genes are polymorphic and co-evolve with the dominantly-expressed class I gene. <i>Molecular Immunology</i> , 2012, 51, 19-20.	1.0	2
38	Tetartohedral twinning could happen to you too. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 418-424.	2.5	14
39	Structure of Human Complement C8, a Precursor to Membrane Attack. <i>Journal of Molecular Biology</i> , 2011, 405, 325-330.	2.0	30
40	<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
41	Structures of the rat complement regulator CrrY. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 739-743.	0.7	6
42	Structural basis for complement factor I control and its disease-associated sequence polymorphisms. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 12839-12844.	3.3	118
43	Crystal structure of Toll-like receptor adaptor MAL/TIRAP reveals the molecular basis for signal transduction and disease protection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 14879-14884.	3.3	123
44	Structural basis for complement Factor I control and its disease-associated sequence polymorphisms. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2011, 67, C217-C218.	0.3	0
45	Factor I autoantibodies are associated with atypical haemolytic uraemic syndrome. <i>Molecular Immunology</i> , 2010, 47, 2291-2292.	1.0	1
46	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
47	Structural basis for cofactor-independent dioxygenation of <i>N</i> -heteroaromatic compounds at the β/β^2 -hydrolase fold. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 657-662.	3.3	77
48	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
49	Functional and structural characterization of the integrase from the prototype foamy virus. <i>Nucleic Acids Research</i> , 2009, 37, 243-255.	6.5	130
50	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
51	<i>Neisseria meningitidis</i> recruits factor H using protein mimicry of host carbohydrates. <i>Nature</i> , 2009, 458, 890-893.	13.7	287
52	Macrophage Scavenger Receptor A Mediates Adhesion to Apolipoproteins A-I and E. <i>Biochemistry</i> , 2009, 48, 11858-11871.	1.2	48
53	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
54	The <i>Escherichia coli</i> 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

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55	Towards the crystal structure of intact Human Complement Factor I. <i>Molecular Immunology</i> , 2009, 46, 2864-2865.	1.0	3
56	<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
57	A conserved face of the Jagged/Serrate DSL domain is involved in Notch trans-activation and cis-inhibition. <i>Nature Structural and Molecular Biology</i> , 2008, 15, 849-857.	3.6	222
58	Structure of and influence of a tick complement inhibitor on human complement component 5. <i>Nature Immunology</i> , 2008, 9, 753-760.	7.0	121
59	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
60	The crystal structure of rat complement receptor 1-related protein Y (CrrY) helps dissecting decay-acceleration and fl-cofactor activities. <i>Molecular Immunology</i> , 2008, 45, 4096-4097.	1.0	0
61	Single-particle electron microscopy reconstruction of the structure of complement component 8 (C8) at 23Å... resolution. <i>Molecular Immunology</i> , 2008, 45, 4121.	1.0	0
62	What's the point of the type III secretion system needle?. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 6507-6513.	3.3	125
63	Automated Structure Solution With autoSHARP. , 2007, 364, 215-230.		851
64	Self-chaperoning of the Type III Secretion System Needle Tip Proteins IpaD and BipD. <i>Journal of Biological Chemistry</i> , 2007, 282, 4035-4044.	1.6	129
65	Structural and Functional Characterization of a Novel T Cell Receptor Co-regulatory Protein Complex, CD97-CD55. <i>Journal of Biological Chemistry</i> , 2007, 282, 22023-22032.	1.6	60
66	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
67	Crystallographic studies of human complement factor I. <i>Molecular Immunology</i> , 2007, 44, 233-234.	1.0	0
68	Towards a structural basis for complement factor H linked age-related macular degeneration. <i>Molecular Immunology</i> , 2007, 44, 3930-3931.	1.0	1
69	Structural basis for complement factor H-linked age-related macular degeneration. <i>Journal of Experimental Medicine</i> , 2007, 204, 2277-2283.	4.2	168
70	Expression, purification, cocrystallization and preliminary crystallographic analysis of sucrose octasulfate/human complement regulator factor H SCRs 6-8. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007, 63, 480-483.	0.7	14
71	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
72	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

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73	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
74	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
75	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
76	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
77	Molecular model of a type III secretion system needle: Implications for host-cell sensing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 12529-12533.	3.3	149
78	Structure of the heterodimeric core primase. <i>Nature Structural and Molecular Biology</i> , 2005, 12, 1137-1144.	3.6	73
79	A novel fold for the factor H-binding protein BbCRASP-1 of <i>Borrelia burgdorferi</i> . <i>Nature Structural and Molecular Biology</i> , 2005, 12, 276-277.	3.6	72
80	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
81	From Structure to Function of a Complement Regulator. , 2005, , 213-231.		0
82	High Resolution Studies of the Afa/Dr Adhesin DraE and Its Interaction with Chloramphenicol. <i>Journal of Biological Chemistry</i> , 2004, 279, 46851-46857.	1.6	55
83	Complement regulation at the molecular level: The structure of decay-accelerating factor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 1279-1284.	3.3	112
84	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
85	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
86	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
87	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
88	Refinement of severely incomplete structures with maximum likelihood in BUSTER. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 2210-2221.	2.5	666
89	Approximate anisotropic displacement parameters for H atoms in molecular crystals. <i>Chemical Physics Letters</i> , 2004, 386, 472-478.	1.2	58
90	An Atomic Resolution Model for Assembly, Architecture, and Function of the Dr Adhesins. <i>Molecular Cell</i> , 2004, 15, 647-657.	4.5	105

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91	Antibody Multispecificity Mediated by Conformational Diversity. <i>Science</i> , 2003, 299, 1362-1367.	6.0	673
92	Interconversion of ATP Binding and Conformational Free Energies by Tryptophanyl-tRNA Synthetase: Structures of ATP Bound to Open and Closed, Pre-Transition-state Conformations. <i>Journal of Molecular Biology</i> , 2003, 325, 39-63.	2.0	84
93	Structure of Bacterial 3 β /17 β -Hydroxysteroid Dehydrogenase at 1.2 Å... Resolution: A Model for Multiple Steroid Recognition. <i>Biochemistry</i> , 2002, 41, 14659-14668.	1.2	57
94	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
95	The complex of Arl2-GTP and PDEdelta: from structure to function. <i>EMBO Journal</i> , 2002, 21, 2095-2106.	3.5	206
96	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
97	High-resolution experimental phases for tryptophanyl-tRNA synthetase (TrpRS) complexed with tryptophanyl-5 β -AMP. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 1595-1608.	2.5	28
98	Modelling prior distributions of atoms for macromolecular refinement and completion. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000, 56, 1316-1323.	2.5	60
99	In-house low-resolution X-ray crystallography. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000, 56, 1304-1311.	2.5	2
100	Experimental Charge Density of β -Glycine at 23 K. <i>Journal of Physical Chemistry A</i> , 2000, 104, 1047-1054.	1.1	114
101	Maximum Entropy charge density studies: Bayesian viewpoint and test applications. , 2000, , 1-26.		1
102	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
103	Charge density in crystalline citrinin from X-ray diffraction at 19 K. <i>Canadian Journal of Chemistry</i> , 1996, 74, 1145-1161.	0.6	82
104	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
105	Stereoselective conjugate addition of lithium and titanium enolates to β -alkoxy enones. <i>Tetrahedron</i> , 1996, 52, 3497-3508.	1.0	6
106	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
107	Crystal structure of the 6-phosphogluconate dehydrogenase from <i>Gluconobacter oxydans</i> reveals tetrameric 6PGDHs as the crucial intermediate in the evolution of structure and cofactor preference in the 6PGDH family. <i>Wellcome Open Research</i> , 0, 6, 48.	0.9	2
108	Clamping, Bending, and Twisting Inter-Domain Motions in the Misfold-Recognising Portion of UDP-Glucose: Glycoprotein Glucosyl-Transferase. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0