

Pierre Legrand

List of Publications by Year in descending order

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98
papers

5,855
citations

94433

37
h-index

76900

74
g-index

109
all docs

109
docs citations

109
times ranked

7664
citing authors

#	ARTICLE	IF	CITATIONS
1	Discovery and characterization of UipA, a uranium- and iron-binding PepSY protein involved in uranium tolerance by soil bacteria. ISME Journal, 2022, 16, 705-716.	9.8	13
2	The ionâ€œcoupling mechanism of human excitatory amino acid transporters. EMBO Journal, 2022, 41, e108341.	7.8	13
3	Atomic structure of Lanreotide nanotubes revealed by cryo-EM. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	18
4	Crystallographic snapshots of a B12-dependent radical SAM methyltransferase. Nature, 2022, 602, 336-342.	27.8	28
5	ComFC mediates transport and handling of single-stranded DNA during natural transformation. Nature Communications, 2022, 13, 1961.	12.8	5
6	MT9, a natural peptide from black mamba venom antagonizes the muscarinic type 2 receptor and reverses the M2R-agonist-induced relaxation in rat and human arteries. Biomedicine and Pharmacotherapy, 2022, 150, 113094.	5.6	3
7	The apo-form of the <i>Vibrio cholerae</i> replicative helicase DnaB is a labile and inactive planar trimer of dimers. FEBS Letters, 2022, , .	2.8	2
8	On Pyridopyrazinol Chemistry: Synthesis of Chemiluminescent Substances. Synthesis, 2021, 53, 2477-2484.	2.3	1
9	Optimal anchoring of a foldamer inhibitor of ASF1 histone chaperone through backbone plasticity. Science Advances, 2021, 7, .	10.3	11
10	How cyanophage S-2L rejects adenine and incorporates 2-aminoadenine to saturate hydrogen bonding in its DNA. Nature Communications, 2021, 12, 2420.	12.8	24
11	PROXIMA-1 beamline for macromolecular crystallography measurements at Synchrotron SOLEIL. Journal of Synchrotron Radiation, 2021, 28, 970-976.	2.4	12
12	Mechanism and dynamics of fatty acid photodecarboxylase. Science, 2021, 372, .	12.6	93
13	Study of the DnaB:DciA interplay reveals insights into the primary mode of loading of the bacterial replicative helicase. Nucleic Acids Research, 2021, 49, 6569-6586.	14.5	18
14	Molecular basis of the dual role of the Mlh1-Mlh3 endonuclease in MMR and in meiotic crossover formation. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	18
15	BRCA2 binding through a cryptic repeated motif to HSF2BP oligomers does not impact meiotic recombination. Nature Communications, 2021, 12, 4605.	12.8	8
16	Characterization of the first tetrameric transcription factor of the GntR superfamily with allosteric regulation from the bacterial pathogen <i>Agrobacterium fabrum</i> . Nucleic Acids Research, 2021, 49, 529-546.	14.5	15
17	Assembly of infectious Kaposi's sarcoma-associated herpesvirus progeny requires formation of a pORF19 pentamer. PLoS Biology, 2021, 19, e3001423.	5.6	8
18	A unique ferrous iron binding mode is associated with large conformational changes for the transport protein FpVC of <i>Pseudomonas aeruginosa</i> . FEBS Journal, 2020, 287, 295-309.	4.7	11

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19	An embedded lipid in the multidrug transporter LmrP suggests a mechanism for polyspecificity. <i>Nature Structural and Molecular Biology</i> , 2020, 27, 829-835.	8.2	57
20	Structural Studies of HNA Substrate Specificity in Mutants of an Archaeal DNA Polymerase Obtained by Directed Evolution. <i>Biomolecules</i> , 2020, 10, 1647.	4.0	7
21	Structural Insights into the Mechanism of the Radical SAM Carbide Synthase NifB, a Key Nitrogenase Cofactor Maturing Enzyme. <i>Journal of the American Chemical Society</i> , 2020, 142, 11006-11012.	13.7	25
22	Crystal structure of Mokola virus glycoprotein in its post-fusion conformation. <i>PLoS Pathogens</i> , 2020, 16, e1008383.	4.7	15
23	High-resolution snapshots of human N-myristoyltransferase in action illuminate a mechanism promoting N-terminal Lys and Gly myristoylation. <i>Nature Communications</i> , 2020, 11, 1132.	12.8	58
24	Import pathways of the mannitol-opines into the bacterial pathogen <i>Agrobacterium tumefaciens</i> : structural, affinity and <i>in vivo</i> approaches. <i>Biochemical Journal</i> , 2020, 477, 615-628.	3.7	0
25	Crystal structure of Mokola virus glycoprotein in its post-fusion conformation. , 2020, 16, e1008383.		0
26	Crystal structure of Mokola virus glycoprotein in its post-fusion conformation. , 2020, 16, e1008383.		0
27	Crystal structure of Mokola virus glycoprotein in its post-fusion conformation. , 2020, 16, e1008383.		0
28	Crystal structure of Mokola virus glycoprotein in its post-fusion conformation. , 2020, 16, e1008383.		0
29	<i>MXCuBE</i> : the dawn of <i>MXCuBE</i> Collaboration. <i>Journal of Synchrotron Radiation</i> , 2019, 26, 393-405.	2.4	30
30	Biophysical and structural characterization of a zinc-responsive repressor of the MarR superfamily. <i>PLoS ONE</i> , 2019, 14, e0210123.	2.5	6
31	Species-Specific Functional Regions of the Green Alga Gamete Fusion Protein HAP2 Revealed by Structural Studies. <i>Structure</i> , 2019, 27, 113-124.e4.	3.3	23
32	Structural basis for the recognition of LDL-receptor family members by VSV glycoprotein. <i>Nature Communications</i> , 2018, 9, 1029.	12.8	122
33	Structural Studies based on two Lysine Dioxygenases with Distinct Regioselectivity Brings Insights Into Enzyme Specificity within the Clavaminate Synthase-Like Family. <i>Scientific Reports</i> , 2018, 8, 16587.	3.3	17
34	XLF and APLF bind Ku80 at two remote sites to ensure DNA repair by non-homologous end joining. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 971-980.	8.2	78
35	Evolutionary Diversification of the HAP2 membrane insertion motifs to drive gamete fusion across eukaryotes. <i>PLoS Biology</i> , 2018, 16, e2006357.	5.6	51
36	The Crystal Structure of Gurmarin, a Sweet Taste Suppressing Protein: Identification of the Amino Acid Residues Essential for Inhibition. <i>Chemical Senses</i> , 2018, 43, 635-643.	2.0	12

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37	The crystal structure of the 5â€² functional domain of the transcription riboregulator 7SK. <i>Nucleic Acids Research</i> , 2017, 45, gkw1351.	14.5	25
38	Status of the crystallography beamlines at synchrotron SOLEIL. <i>European Physical Journal Plus</i> , 2017, 132, 1.	2.6	13
39	Structure and allosteric inhibition of excitatory amino acid transporter 1. <i>Nature</i> , 2017, 544, 446-451.	27.8	179
40	Type VI secretion TssK baseplate protein exhibits structural similarity with phage receptor-binding proteins and evolved to bind the membrane complex. <i>Nature Microbiology</i> , 2017, 2, 17103.	13.3	48
41	Nonredox thiolation in tRNA occurring via sulfur activation by a [4Fe-4S] cluster. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 7355-7360.	7.1	44
42	Crystal structure of the prefusion surface glycoprotein of the prototypic arenavirus LCMV. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 513-521.	8.2	65
43	Structure and specificity of the Type VI secretion system ClpV-TssC interaction in enteroaggregative <i>Escherichia coli</i> . <i>Scientific Reports</i> , 2016, 6, 34405.	3.3	31
44	The Atomic Structure of the Phage Tuc2009 Baseplate Tripod Suggests that Host Recognition Involves Two Different Carbohydrate Binding Modules. <i>MBio</i> , 2016, 7, e01781-15.	4.1	58
45	Priming and polymerization of a bacterial contractile tail structure. <i>Nature</i> , 2016, 531, 59-63.	27.8	127
46	Sqt1p is an eight-bladed WD40 protein. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2016, 72, 59-64.	0.8	2
47	S-SAD phasing of monoclinic histidine kinase from <i>Brucella abortus</i> combining data from multiple crystals and orientations: an example of data-collection strategy and a posteriori analysis of different data combinations. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 1433-1443.	2.5	12
48	Structural insight into how the human helicase subunit MCM2 may act as a histone chaperone together with ASF1 at the replication fork. <i>Nucleic Acids Research</i> , 2015, 43, 1905-1917.	14.5	108
49	Atomic view of the histidine environment stabilizing higher-pH conformations of pH-dependent proteins. <i>Nature Communications</i> , 2015, 6, 7771.	12.8	36
50	Natural Guided Genome Engineering Reveals Transcriptional Regulators Controlling Quorum-Sensing Signal Degradation. <i>PLoS ONE</i> , 2015, 10, e0141718.	2.5	11
51	Solving the RNA polymerase I structural puzzle. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 2570-2582.	2.5	23
52	RRP6 from <i>Trypanosoma brucei</i> : Crystal Structure of the Catalytic Domain, Association with EAP3 and Activity towards Structured and Non-Structured RNA Substrates. <i>PLoS ONE</i> , 2014, 9, e89138.	2.5	6
53	Backstage the RNA Polymerase I Structure: The Art of Crystallography. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2014, 70, C330-C330.	0.1	0
54	Crystal structure and functional mapping of human ASMT, the last enzyme of the melatonin synthesis pathway. <i>Journal of Pineal Research</i> , 2013, 54, 46-57.	7.4	51

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55	Structural insight into magnetochrome-mediated magnetite biomineralization. <i>Nature</i> , 2013, 502, 681-684.	27.8	119
56	Crystal structure of the 14-subunit RNA polymerase ϕ . <i>Nature</i> , 2013, 502, 644-649.	27.8	179
57	Structure of the MutL C-terminal domain reveals how Mlh1 contributes to Pms1 endonuclease site. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 461-468.	8.2	103
58	Pentameric ligand-gated ion channel ELIC is activated by GABA and modulated by benzodiazepines. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, E3028-34.	7.1	120
59	Dual functions of the Hsm3 protein in chaperoning and scaffolding regulatory particle subunits during the proteasome assembly. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, E1001-E1010.	7.1	54
60	Structure of the phage TP901-1 1.8 μ m baseplate suggests an alternative host adhesion mechanism. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 8954-8958.	7.1	121
61	Classical-style MAD phasing with wavelength interleaving and kappa goniometry on PROXIMA-1. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2012, 68, s18-s18.	0.3	0
62	Crystal structure of <i>Apis mellifera</i> OBP14, a C-minus odorant-binding protein, and its complexes with odorant molecules. <i>Insect Biochemistry and Molecular Biology</i> , 2012, 42, 41-50.	2.7	135
63	Energy resolution of the CdTe-XPAD detector: calibration and potential for Laue diffraction measurements on protein crystals. <i>Journal of Synchrotron Radiation</i> , 2012, 19, 323-331.	2.4	17
64	Workshop on simultaneous combination of spectroscopies with X-ray absorption, scattering and diffraction (Held on the 24th and 25th June 2010). <i>Phase Transitions</i> , 2011, 84, 673-674.	1.3	1
65	The PHD Finger of Human UHRF1 Reveals a New Subgroup of Unmethylated Histone H3 Tail Readers. <i>PLoS ONE</i> , 2011, 6, e27599.	2.5	36
66	Structure-function analysis of hRPC62 provides insights into RNA polymerase III transcription initiation. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 352-358.	8.2	43
67	Structural characterization of filaments formed by human Xrcc4/Cernunnos/XLF complex involved in nonhomologous DNA end-joining. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 12663-12668.	7.1	126
68	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
69	Structural studies of the catalytic core of the primate foamy virus (PFV-1) integrase. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 881-886.	0.7	3
70	Comparison of crystal structures of human type 3 17β -hydroxysteroid dehydrogenase reveals an α -induced-fit mechanism and a conserved basic motif involved in the binding of androgen. <i>Protein Science</i> , 2009, 14, 1485-1497.	7.6	21
71	Exploring TAR RNA aptamer loop-loop interaction by X-ray crystallography, UV spectroscopy and surface plasmon resonance. <i>Nucleic Acids Research</i> , 2008, 36, 7146-7156.	14.5	54
72	Mutation of ribosomal protein RPS24 in Diamond-Blackfan anemia results in a ribosome biogenesis disorder. <i>Human Molecular Genetics</i> , 2008, 17, 1253-1263.	2.9	100

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73	A beamline for anomalous diffraction at SOLEIL: Proxima 1. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2008, 64, C179-C179.	0.3	0
74	Molecular basis of Diamond Blackfan anemia: structure and function analysis of RPS19. <i>Nucleic Acids Research</i> , 2007, 35, 5913-5921.	14.5	56
75	Structural Characterization of the Human Androgen Receptor Ligand-binding Domain Complexed with EM5744, a Rationally Designed Steroidal Ligand Bearing a Bulky Chain Directed toward Helix 12. <i>Journal of Biological Chemistry</i> , 2007, 282, 30910-30919.	3.4	55
76	The structure of the CstF-77 homodimer provides insights into CstF assembly. <i>Nucleic Acids Research</i> , 2007, 35, 4515-4522.	14.5	42
77	Proxima 1, a New Beamline on the Third Generation SR Source SOLEIL Combining PX and Single-Crystal BioXAS. <i>AIP Conference Proceedings</i> , 2007, , .	0.4	5
78	Structure of the γ ,60/191 Subcomplex of Yeast Transcription Factor III _C : Insights into Preinitiation Complex Assembly. <i>Molecular Cell</i> , 2006, 24, 221-232.	9.7	32
79	Instrumentation for synchrotron-radiation macromolecular crystallography. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006, 62, 12-18.	2.5	7
80	Biochemical Characterization and Crystal Structure of Synechocystis Arogenate Dehydrogenase Provide Insights into Catalytic Reaction. <i>Structure</i> , 2006, 14, 767-776.	3.3	31
81	Crystallization of the pectate lyase Pell from <i>Erwinia chrysanthemi</i> and SAD phasing of a gold derivative. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 190-192.	2.5	3
82	A new highly integrated sample environment for protein crystallography. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 888-894.	2.5	20
83	Isolation and characterisation of mesenchymal stem cells from adult mouse bone marrow. <i>Experimental Cell Research</i> , 2004, 295, 395-406.	2.6	363
84	Loop Relaxation, A Mechanism that Explains the Reduced Specificity of Rabbit 20 α -Hydroxysteroid Dehydrogenase, A Member of the Aldo-Keto Reductase Superfamily. <i>Journal of Molecular Biology</i> , 2004, 339, 89-102.	4.2	35
85	Ni-Zn-[Fe ₄ S ₄] and Ni-Ni-[Fe ₄ S ₄] clusters in closed and open β subunits of acetyl-CoA synthase/carbon monoxide dehydrogenase. <i>Nature Structural and Molecular Biology</i> , 2003, 10, 271-279.	8.2	418
86	Human 20 α -Hydroxysteroid Dehydrogenase: Crystallographic and Site-directed Mutagenesis Studies Lead to the Identification of an Alternative Binding Site for C21-steroids. <i>Journal of Molecular Biology</i> , 2003, 331, 593-604.	4.2	71
87	Synergy between Extracellular Modules of Vascular Endothelial Cadherin Promotes Homotypic Hexameric Interactions. <i>Journal of Biological Chemistry</i> , 2002, 277, 12790-12801.	3.4	34
88	Expression, crystallization and preliminary X-ray analysis of human and rabbit 20 α -hydroxysteroid dehydrogenases in complex with NADP(H) and various steroid substrates. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 135-139.	2.5	14
89	Crystallization and 2.2 \AA resolution structure of R-phycoerythrin from <i>Gracilaria chilensis</i> : a case of perfect hemihedral twinning. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 52-60.	2.5	46
90	Self-assembly of the Vascular Endothelial Cadherin Ectodomain in a Ca ²⁺ -dependent Hexameric Structure. <i>Journal of Biological Chemistry</i> , 2001, 276, 3581-3588.	3.4	27

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91	Structure of the Human 3 β -Hydroxysteroid Dehydrogenase Type 3 in Complex with Testosterone and NADP at 1.25-Å... Resolution. <i>Journal of Biological Chemistry</i> , 2001, 276, 42091-42098.	3.4	53
92	<i>Desulfovibrio desulfuricans</i> iron hydrogenase: the structure shows unusual coordination to an active site Fe binuclear center. <i>Structure</i> , 1999, 7, 13-23.	3.3	1,320
93	Crystal structure of the oxidised and reduced acidic cytochrome c3 from <i>Desulfovibrio africanus</i> . <i>Journal of Molecular Biology</i> , 1999, 290, 881-902.	4.2	71
94	Role of Aspartate 70 and Tryptophan 82 in Binding of Succinylcholine to Human Butyrylcholinesterase. <i>Biochemistry</i> , 1997, 36, 2266-2277.	2.5	140
95	Oncogenic activation of RET by two distinct FMTC mutations affecting the tyrosine kinase domain. <i>Oncogene</i> , 1997, 15, 393-402.	5.9	99
96	MAINDEX manual indexation for area-detector crystallographic data. <i>Journal of Applied Crystallography</i> , 1997, 30, 206-206.	4.5	6
97	Protein crystallography with non-detergent sulfobetaines. <i>Journal of Crystal Growth</i> , 1996, 168, 150-154.	1.5	17
98	Species-Specific Functional Regions of the Green Alga Gamete Fusion Protein HAP2 Revealed by Structural Studies. <i>SSRN Electronic Journal</i> , 0, , .	0.4	1