

Gordon Leonard

List of Publications by Year in descending order

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104
papers

5,419
citations

61984

43
h-index

88630

70
g-index

106
all docs

106
docs citations

106
times ranked

6624
citing authors

#	ARTICLE	IF	CITATIONS
1	ID23-2: an automated and high-performance microfocus beamline for macromolecular crystallography at the ESRF. <i>Journal of Synchrotron Radiation</i> , 2022, 29, 581-590.	2.4	7
2	High-pressure crystallography shows noble gas intervention into protein-lipid interaction and suggests a model for anaesthetic action. <i>Communications Biology</i> , 2022, 5, 360.	4.4	4
3	Assembly of The Mitochondrial Complexâ€¦I Assembly Complex Suggests a Regulatory Role for DeFlavination. <i>Angewandte Chemie - International Edition</i> , 2021, 60, 4689-4697.	13.8	14
4	Molecular model of a sensor of two-component signaling system. <i>Scientific Reports</i> , 2021, 11, 10774.	3.3	14
5	Assembly of The Mitochondrial Complexâ€¦I Assembly Complex Suggests a Regulatory Role for DeFlavination. <i>Angewandte Chemie</i> , 2021, 133, 4739-4747.	2.0	0
6	ID30A-3 (MASSIF-3) â€œ a beamline for macromolecular crystallography at the ESRF with a small intense beam. <i>Journal of Synchrotron Radiation</i> , 2020, 27, 844-851.	2.4	23
7	Millisecond time-resolved serial oscillation crystallography of a blue-light photoreceptor at a synchrotron. <i>IUCr</i> , 2020, 7, 728-736.	2.2	12
8	<i>MXCuBE2</i>: the dawn of <i>MXCuBE</i> Collaboration. <i>Journal of Synchrotron Radiation</i> , 2019, 26, 393-405.	2.4	30
9	Structure Solution of the Fluorescent Protein Cerulean Using MeshAndCollect. <i>Journal of Visualized Experiments</i> , 2019, , .	0.3	1
10	CrystalDirect-To-Beam: Opening the shortest path from crystal to data. <i>AIP Conference Proceedings</i> , 2019, , .	0.4	1
11	Fully Autonomous Characterization and Data Collection from Crystals of Biological Macromolecules. <i>Journal of Visualized Experiments</i> , 2019, , .	0.3	2
12	Specific radiation damage is a lesser concern at room temperature. <i>IUCr</i> , 2019, 6, 665-680.	2.2	42
13	CM01: a facility for cryo-electron microscopy at the European Synchrotron. <i>Acta Crystallographica Section D: Structural Biology</i> , 2019, 75, 528-535.	2.3	83
14	The complex analysis of X-ray mesh scans for macromolecular crystallography. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 355-365.	2.3	15
15	Molecular comparison of Neanderthal and Modern Human adenylosuccinate lyase. <i>Scientific Reports</i> , 2018, 8, 18008.	3.3	6
16	ID30B â€œ a versatile beamline for macromolecular crystallography experiments at the ESRF. <i>Journal of Synchrotron Radiation</i> , 2018, 25, 1249-1260.	2.4	72
17	A new MR-SAD algorithm for the automatic building of protein models from low-resolution X-ray data and a poor starting model. <i>IUCr</i> , 2018, 5, 166-171.	2.2	33
18	MXCuBE3: A New Era of MX-Beamline Control Begins. <i>Synchrotron Radiation News</i> , 2017, 30, 22-27.	0.8	23

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19	Fast iodide-SAD phasing for high-throughput membrane protein structure determination. <i>Science Advances</i> , 2017, 3, e1602952.	10.3	38
20	Mechanism of transmembrane signaling by sensor histidine kinases. <i>Science</i> , 2017, 356, .	12.6	132
21	Hierarchical clustering for multiple-crystal macromolecular crystallography experiments: the <i>ccCluster</i> program. <i>Journal of Applied Crystallography</i> , 2017, 50, 1844-1851.	4.5	34
22	Gas-sensitive biological crystals processed in pressurized oxygen and krypton atmospheres: deciphering gas channels in proteins using a novel 'soak-and-freeze' methodology. <i>Journal of Applied Crystallography</i> , 2016, 49, 1478-1487.	4.5	25
23	Automated data collection based on RoboDiff at the ESRF beamline MASSIF-1. <i>AIP Conference Proceedings</i> , 2016, , .	0.4	0
24	The solution configurations of inactive and activated DntR have implications for the sliding dimer mechanism of LysR transcription factors. <i>Scientific Reports</i> , 2016, 6, 19988.	3.3	36
25	Facilitating best practices in collecting anomalous scattering data for <i>de novo</i> structure solution at the ESRF Structural Biology Beamlines. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016, 72, 413-420.	2.3	8
26	MASSIF-1: a beamline dedicated to the fully automatic characterization and data collection from crystals of biological macromolecules. <i>Journal of Synchrotron Radiation</i> , 2015, 22, 1540-1547.	2.4	133
27	<i>MeshAndCollect</i> : an automated multi-crystal data-collection workflow for synchrotron macromolecular crystallography beamlines. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 2328-2343.	2.5	108
28	<i>In crystallo</i> optical spectroscopy (<i>icOS</i>) as a complementary tool on the macromolecular crystallography beamlines of the ESRF. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 15-26.	2.5	63
29	Automatic processing of macromolecular crystallography X-ray diffraction data at the ESRF. <i>Journal of Applied Crystallography</i> , 2013, 46, 804-810.	4.5	107
30	How the ESRF helps industry and how they help the ESRF. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 1289-1296.	2.5	12
31	ID29: a high-intensity highly automated ESRF beamline for macromolecular crystallography experiments exploiting anomalous scattering. <i>Journal of Synchrotron Radiation</i> , 2012, 19, 455-461.	2.4	172
32	The structure of the <i>Helicobacter pylori</i> ferric uptake regulator Fur reveals three functional metal binding sites. <i>Molecular Microbiology</i> , 2011, 79, 1260-1275.	2.5	109
33	Crystal structures of DntR inducer binding domains in complex with salicylate offer insights into the activation of LysR-type transcriptional regulators. <i>Molecular Microbiology</i> , 2011, 81, 354-367.	2.5	43
34	Crystal structure of HP0721, a novel secreted protein from <i>Helicobacter pylori</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 1678-1681.	2.6	6
35	Diffraction cartography: applying microbeams to macromolecular crystallography sample evaluation and data collection. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2010, 66, 855-864.	2.5	93
36	<i>MxCuBE</i> : a synchrotron beamline control environment customized for macromolecular crystallography experiments. <i>Journal of Synchrotron Radiation</i> , 2010, 17, 700-707.	2.4	193

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37	Structural and Mutational Analyses of <i>Deinococcus radiodurans</i> UvrA2 Provide Insight into DNA Binding and Damage Recognition by UvrAs. <i>Structure</i> , 2009, 17, 547-558.	3.3	38
38	An inexpensive automatically operated device for the flash annealing of crystals of macromolecules. <i>Journal of Applied Crystallography</i> , 2009, 42, 125-128.	4.5	9
39	Online collection and analysis of X-ray fluorescence spectra on the macromolecular crystallography beamlines of the ESRF. <i>Journal of Applied Crystallography</i> , 2009, 42, 333-335.	4.5	24
40	Structures of <i>Staphylococcus aureus</i> D-Tagatose-6-phosphate Kinase Implicate Domain Motions in Specificity and Mechanism. <i>Journal of Biological Chemistry</i> , 2007, 282, 19948-19957.	3.4	32
41	Quickly Getting the Best Data from Your Macromolecular Crystals with a New Generation of Beamline Instruments. <i>AIP Conference Proceedings</i> , 2007, , .	0.4	15
42	In Vivo and in Vitro Investigation of Transcriptional Regulation by DntR. <i>Journal of Molecular Biology</i> , 2007, 372, 571-582.	4.2	29
43	Structure of the Pho85-Pho80 CDK-Cyclin Complex of the Phosphate-Responsive Signal Transduction Pathway. <i>Molecular Cell</i> , 2007, 28, 614-623.	9.7	47
44	Structure of the <i>Sulfolobus solfataricus</i> β -Glucosidase: Implications for Domain Conservation and Substrate Recognition in GH31. <i>Journal of Molecular Biology</i> , 2006, 358, 1106-1124.	4.2	126
45	The Crystal Structure of a Plant 3-Ketoacyl-CoA Thiolase Reveals the Potential for Redox Control of Peroxisomal Fatty Acid β -Oxidation. <i>Journal of Molecular Biology</i> , 2006, 359, 347-357.	4.2	22
46	The care and nurture of undulator data sets. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006, 62, 65-71.	2.5	13
47	Automation of sample mounting for macromolecular crystallography. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006, 62, 1251-1259.	2.5	99
48	High-throughput sample handling and data collection at synchrotrons: embedding the ESRF into the high-throughput gene-to-structure pipeline. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006, 62, 1162-1169.	2.5	58
49	Automation of macromolecular crystallography beamlines. <i>Progress in Biophysics and Molecular Biology</i> , 2005, 89, 124-152.	2.9	46
50	Automatic structure determination based on the single-wavelength anomalous diffraction technique away from an absorption edge. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 388-396.	2.5	8
51	Characterization of different crystal forms of the β -glucosidase MalA from <i>Sulfolobus solfataricus</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 1039-1042.	0.7	6
52	Crystal Structure of Maltooligosyltrehalose Trehalohydrolase from <i>Deinococcus radiodurans</i> in Complex with Disaccharides. <i>Journal of Molecular Biology</i> , 2005, 347, 949-963.	4.2	26
53	The Structure of the Organic Hydroperoxide Resistance Protein from <i>Deinococcus radiodurans</i> . <i>Journal of Biological Chemistry</i> , 2004, 279, 25830-25837.	3.4	36
54	Structural Basis of 5-Nitroimidazole Antibiotic Resistance. <i>Journal of Biological Chemistry</i> , 2004, 279, 55840-55849.	3.4	71

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55	Expression, purification, crystallization and preliminary crystal structure analysis of the Deinococcus radiodurans organic hydroperoxide-resistance protein. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 920-922.	2.5	2
56	Development of a Bacterial Biosensor for Nitrotoluenes: The Crystal Structure of the Transcriptional Regulator DntR. <i>Journal of Molecular Biology</i> , 2004, 340, 405-418.	4.2	80
57	The organization of divalent cations in the active site of cadmium <i>Escherichia coli</i> fructose-1,6-bisphosphate aldolase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 611-614.	2.5	8
58	Tryparedoxins from <i>Crithidia fasciculata</i> and <i>Trypanosoma brucei</i> . <i>Journal of Biological Chemistry</i> , 2003, 278, 25919-25925.	3.4	43
59	Biosynthesis of isoprenoids: Crystal structure of 4-diphosphocytidyl-2C-methyl-D-erythritol kinase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 9173-9178.	7.1	96
60	Structure of Tagatose-1,6-bisphosphate Aldolase. <i>Journal of Biological Chemistry</i> , 2002, 277, 22018-22024.	3.4	55
61	Variation on a Theme of SDR. <i>Structure</i> , 2002, 10, 773-786.	3.3	69
62	The 2.4 Å crystal structure of the penicillin-resistant penicillin-binding protein PBP5 _{fm} from <i>Enterococcus faecium</i> in complex with benzylpenicillin. <i>Cellular and Molecular Life Sciences</i> , 2002, 59, 1223-1232.	5.4	96
63	De novo phasing of two crystal forms of tryparedoxin II using the anomalous scattering from S atoms: a combination of small signal and medium resolution reveals this to be a general tool for solving protein crystal structures. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 21-28.	2.5	25
64	The crystal and molecular structures of diferric porcine and rabbit serum transferrins at resolutions of 2.15 and 2.60 Å, respectively. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 70-80.	2.5	86
65	Crystal structure of GerE, the ultimate transcriptional regulator of spore formation in <i>Bacillus subtilis</i> . <i>Journal of Molecular Biology</i> , 2001, 306, 759-771.	4.2	90
66	The C1 subunit of β -crustacyanin: the de novo phasing of the crystal structure of a 40 kDa homodimeric protein using the anomalous scattering from S atoms combined with direct methods. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 1230-1237.	2.5	23
67	Crystallization and preliminary X-ray diffraction studies of the peptide methionine sulfoxide reductase from <i>Escherichia coli</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000, 56, 1194-1197.	2.5	6
68	The purification, crystallization and preliminary structural characterization of glucose-1-phosphate thymidyltransferase (RmlA), the first enzyme of the dTDP-L-rhamnose synthesis pathway from <i>Pseudomonas aeruginosa</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000, 56, 1501-1504.	2.5	30
69	The high-resolution structure of the NADP(H)-binding component (dIII) of proton-translocating transhydrogenase from human heart mitochondria. <i>Structure</i> , 2000, 8, 1-12.	3.3	180
70	Domain swapping in the sporulation response regulator Spo0A. <i>Journal of Molecular Biology</i> , 2000, 297, 757-770.	4.2	67
71	The three-dimensional structure of a <i>Plasmodium falciparum</i> cyclophilin in complex with the potent anti-malarial cyclosporin A. <i>Journal of Molecular Biology</i> , 2000, 298, 123-133.	4.2	39
72	Structure of the AAA ATPase p97. <i>Molecular Cell</i> , 2000, 6, 1473-1484.	9.7	394

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73	The crystal structure of the RNA/DNA hybrid r(GAAGAGAAGC){middle dot}d(GCTTCTCTTC) shows significant differences to that found in solution. <i>Nucleic Acids Research</i> , 1999, 27, 555-561.	14.5	51
74	The High Resolution Crystal Structure of Recombinant <i>Crithidia fasciculata</i> Tryparedoxin-I. <i>Journal of Biological Chemistry</i> , 1999, 274, 25613-25622.	3.4	61
75	Initiating a crystallographic study of UDP-galactopyranose mutase from <i>Escherichia coli</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 399-402.	2.5	12
76	Two crystal forms of ModE, the molybdate-dependent transcriptional regulator from <i>Escherichia coli</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 542-543.	2.5	7
77	Overexpression, purification, crystallization and preliminary structural study of dTDP-6-deoxy-L-lyxo-4-hexulose reductase (RmlD), the fourth enzyme of the dTDP-L-rhamnose synthesis pathway, from <i>Salmonella enterica</i> serovar Typhimurium. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 2043-2046.	2.5	49
78	The 2 Å... structure of helix 6 of the human signal recognition particle RNA. <i>Structure</i> , 1999, 7, 1345-1352.	3.3	45
79	The high-resolution crystal structure of the molybdate-dependent transcriptional regulator (ModE) from <i>Escherichia coli</i> : a novel combination of domain folds. <i>EMBO Journal</i> , 1999, 18, 1435-1446.	7.8	74
80	Crystal Structure of Intact Elongation Factor EF-Tu from <i>Escherichia coli</i> in GDP Conformation at 2.05Å... Resolution. <i>Journal of Molecular Biology</i> , 1999, 285, 1245-1256.	4.2	128
81	The crystal structure of <i>Escherichia coli</i> class II fructose-1,6-bisphosphate aldolase in complex with phosphoglycolohydroxamate reveals details of mechanism and specificity 1 Edited by R. Huber. <i>Journal of Molecular Biology</i> , 1999, 287, 383-394.	4.2	117
82	Crystallization and preliminary X-ray diffraction studies of 6-phosphogluconate dehydrogenase from <i>Lactococcus lactis</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1998, 54, 1422-1424.	2.5	3
83	MAD Phasing Strategies Explored with a Brominated Oligonucleotide Crystal at 1.65Å... Resolution. <i>Journal of Synchrotron Radiation</i> , 1996, 3, 24-34.	2.4	18
84	The crystal structure of a class II fructose-1,6-bisphosphate aldolase shows a novel binuclear metal-binding active site embedded in a familiar fold. <i>Structure</i> , 1996, 4, 1303-1315.	3.3	112
85	The Crystal Structure Analysis of d(CGCGAASSCGCG) ₂ , a Synthetic DNA Dodecamer Duplex Containing Four 4'-Thio-2'-Deoxythymidine Nucleotides. <i>Nucleic Acids Research</i> , 1996, 24, 951-961.	14.5	27
86	Do C-H...O hydrogen bonds contribute to the stability of nucleic acid base pairs?. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1995, 51, 136-139.	2.5	72
87	Additional crystal forms of the <i>E. coli</i> class II fructose-1,6-bisphosphate aldolase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1995, 51, 833-834.	2.5	3
88	Self-association of a DNA loop creates a quadruplex: crystal structure of d(GCATGCT) at 1.8 Å resolution. <i>Structure</i> , 1995, 3, 335-340.	3.3	72
89	SR instrumentation for optimized anomalous scattering and high resolution structure studies of proteins and nucleic acids (invited). <i>Review of Scientific Instruments</i> , 1995, 66, 1287-1292.	1.3	12
90	Studies of the structure and stability of base pair mismatches, base pairs involving modified bases, and DNA-drug complexes. <i>Journal of Chemical Crystallography</i> , 1994, 24, 5-15.	1.1	1

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91	Crystal and molecular structure of r(CGCGAAUUAGCG): an RNA duplex containing two G(anti)·A(anti) base pairs. <i>Structure</i> , 1994, 2, 483-494.	3.3	76
92	Anthracycline·DNA interactions at unfavourable base-pair triplet-binding sites: structures of d(CGCCCG)/daunomycin and d(TGGCCA)/adriamycin complexes. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1993, 49, 458-467.	2.5	32
93	Crystal and Molecular Structure of d(CGTAGATCTACG) at 2.25 Å... Resolution. <i>Journal of Molecular Biology</i> , 1993, 234, 198-208.	4.2	47
94	The crystal structure of N4-methylcytosine-guanosine basepairs in the synthetic hexanucleotide d(CGCGm4CG). <i>Nucleic Acids Research</i> , 1993, 21, 5623-5629.	14.5	18
95	The conformational variability of an adenosine inosine base-pair in a synthetic DNA dodecamer. <i>Nucleic Acids Research</i> , 1992, 20, 4753-4759.	14.5	42
96	Studies on the molecular pharmacology of GR63178A. <i>Biochemical Pharmacology</i> , 1992, 44, 433-439.	4.4	1
97	Anthracycline binding to DNA. High-resolution structure of d(TGTACA) complexed with 4'-epiadriamycin. <i>FEBS Journal</i> , 1992, 204, 69-74.	0.2	32
98	High-resolution structure of a mutagenic lesion in DNA.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1990, 87, 9573-9576.	7.1	98
99	Structural and thermodynamic studies on the adenine.guanine mismatch in B-DNA. <i>Nucleic Acids Research</i> , 1990, 18, 5617-5623.	14.5	100
100	Influence of pH on the conformation and stability of mismatch base-pairs in DNA. <i>Journal of Molecular Biology</i> , 1990, 212, 437-440.	4.2	110
101	Refined crystal structure of an octanucleotide duplex with I.T. mismatched base pairs. <i>Nucleic Acids Research</i> , 1989, 17, 55-72.	14.5	52
102	Crystal structure and stability of a DNA duplex containing A(anti) · G(syn) base-pairs. <i>Journal of Molecular Biology</i> , 1989, 207, 455-457.	4.2	124
103	Structural and Spectroscopic Investigations of the 1:1 Complex between Europium Nitrate and a Tetraoxadiazia Macrocycle. <i>Helvetica Chimica Acta</i> , 1986, 69, 288-297.	1.6	33
104	The molecular structure of the diacetic acid adduct of guanidinium tetrabromochromate(II). <i>Journal of Crystallographic and Spectroscopic Research</i> , 1983, 13, 325-331.	0.2	1