

Alexander Wlodawer

List of Publications by Year in descending order

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127
papers

8,854
citations

50276

46
h-index

43889

91
g-index

131
all docs

131
docs citations

131
times ranked

7119
citing authors

#	ARTICLE	IF	CITATIONS
1	Structure-Based Inhibitors of HIV-1 Protease. <i>Annual Review of Biochemistry</i> , 1993, 62, 543-585.	11.1	854
2	INHIBITORS OF HIV-1 PROTEASE: A Major Success of Structure-Assisted Drug Design. <i>Annual Review of Biophysics and Biomolecular Structure</i> , 1998, 27, 249-284.	18.3	649
3	New protein fold revealed by a 2.3-Å... resolution crystal structure of nerve growth factor. <i>Nature</i> , 1991, 354, 411-414.	27.8	500
4	Structure of bovine pancreatic trypsin inhibitor. <i>Journal of Molecular Biology</i> , 1984, 180, 301-329.	4.2	478
5	Crystal structure of a retroviral protease proves relationship to aspartic protease family. <i>Nature</i> , 1989, 337, 576-579.	27.8	378
6	Structure at 2.5-Å resolution of chemically synthesized Human Immunodeficiency Virus Type 1 protease complexed with a hydroxyethylene-based inhibitor. <i>Biochemistry</i> , 1991, 30, 1600-1609.	2.5	242
7	Protein crystallography for non-crystallographers, or how to get the best (but not more) from published macromolecular structures. <i>FEBS Journal</i> , 2008, 275, 1-21.	4.7	231
8	Improved molecular replacement by density- and energy-guided protein structure optimization. <i>Nature</i> , 2011, 473, 540-543.	27.8	226
9	Crystal structure of interleukin-10 reveals the functional dimer with an unexpected topological similarity to interferon β . <i>Structure</i> , 1995, 3, 591-601.	3.3	219
10	Comparison of two highly refined structures of bovine pancreatic trypsin inhibitor. <i>Journal of Molecular Biology</i> , 1987, 193, 145-156.	4.2	217
11	The Catalytic Domain of Escherichia coli Lon Protease Has a Unique Fold and a Ser-Lys Dyad in the Active Site. <i>Journal of Biological Chemistry</i> , 2004, 279, 8140-8148.	3.4	167
12	Structural Basis for the Activity and Substrate Specificity of Erwinia chrysanthemi l-Asparaginase. <i>Biochemistry</i> , 2001, 40, 5655-5664.	2.5	160
13	Structural and biochemical studies of retroviral proteases. <i>BBA - Proteins and Proteomics</i> , 2000, 1477, 16-34.	2.1	151
14	Crystal structure of plant aspartic proteinase prophytepsin: inactivation and vacuolar targeting. <i>EMBO Journal</i> , 1999, 18, 3947-3955.	7.8	150
15	Domain-Swapped Structure of the Potent Antiviral Protein Griffithsin and Its Mode of Carbohydrate Binding. <i>Structure</i> , 2006, 14, 1127-1135.	3.3	149
16	Rational Approach to AIDS Drug Design Through Structural Biology. <i>Annual Review of Medicine</i> , 2002, 53, 595-614.	12.2	138
17	A small molecule compound with an indole moiety inhibits the main protease of SARS-CoV-2 and blocks virus replication. <i>Nature Communications</i> , 2021, 12, 668.	12.8	126
18	Structural and evolutionary relationships between retroviral and eukaryotic aspartic proteinases. <i>Biochemistry</i> , 1991, 30, 4663-4671.	2.5	113

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19	Crystal Structure and Amino Acid Sequence of Wolinella Succinogenesl-Asparaginase. FEBS Journal, 1996, 241, 201-207.	0.2	100
20	Nature's recipe for splitting inteins. Protein Engineering, Design and Selection, 2014, 27, 263-271.	2.1	96
21	Protein crystallography for aspiring crystallographers or how to avoid pitfalls and traps in macromolecular structure determination. FEBS Journal, 2013, 280, 5705-5736.	4.7	95
22	Crystal structure of human interleukin-10 at 1.6 Å... resolution and a model of a complex with its soluble receptor. Protein Science, 1996, 5, 1955-1962.	7.6	94
23	Classification of ATP-dependent proteases Lon and comparison of the active sites of their proteolytic domains. FEBS Journal, 2004, 271, 4865-4871.	0.2	88
24	A covalently bound catalytic intermediate in Escherichia coli asparaginase : Crystal structure of a Thr-89-Val mutant. FEBS Letters, 1996, 390, 211-216.	2.8	86
25	Monomerization of Viral Entry Inhibitor Griffithsin Elucidates the Relationship between Multivalent Binding to Carbohydrates and anti-HIV Activity. Structure, 2010, 18, 1104-1115.	3.3	85
26	Crystal structure of the AAA+ domain of E. coli Lon protease at 1.9 Å... resolution. Journal of Structural Biology, 2004, 146, 113-122.	2.8	84
27	Structural studies of algal lectins with anti-HIV activity.. Acta Biochimica Polonica, 2006, 53, 617-626.	0.5	84
28	A brief history of macromolecular crystallography, illustrated by a family tree and its obelisks. FEBS Journal, 2014, 281, 3985-4009.	4.7	83
29	Slicing a protease: Structural features of the ATP-dependent Lon proteases gleaned from investigations of isolated domains. Protein Science, 2006, 15, 1815-1828.	7.6	81
30	Structural Characterization of Pseudomonas 7A Glutaminase-Asparaginase. Biochemistry, 1994, 33, 10257-10265.	2.5	78
31	A left-handed crossover involved in amidohydrolase catalysis. FEBS Letters, 1993, 328, 275-279.	2.8	76
32	Crystal Structure of Human Interferon-1 in Complex with Its High-Affinity Receptor Interferon-1R1. Journal of Molecular Biology, 2010, 404, 650-664.	4.2	76
33	Crystal Structure of Interleukin-19 Defines a New Subfamily of Helical Cytokines. Journal of Biological Chemistry, 2003, 278, 3308-3313.	3.4	74
34	The future of crystallography in drug discovery. Expert Opinion on Drug Discovery, 2014, 9, 125-137.	5.0	70
35	Energy calculations and analysis of HIV-1 protease-inhibitor crystal structures. Protein Engineering, Design and Selection, 1994, 7, 309-316.	2.1	67
36	Structure of an inhibitor complex of the proteinase from feline immunodeficiency virus. Nature Structural and Molecular Biology, 1995, 2, 480-488.	8.2	66

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37	Transport and Activation of the Vacuolar Aspartic Proteinase Phytepsin in Barley (<i>Hordeum vulgare</i>) Tj ETQq1 1 0.784314 rgBT ₆₁ /Overlo	3.4	61
38	Stereochemical restraints revisited: how accurate are refinement targets and how much should protein structures be allowed to deviate from them?. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2007, 63, 611-620.	2.5	61
39	NMR and Crystal Structures of the <i>Pyrococcus horikoshii</i> RadA Intein Guide a Strategy for Engineering a Highly Efficient and Promiscuous Intein. <i>Journal of Molecular Biology</i> , 2012, 421, 85-99.	4.2	61
40	HIVdb: A Database of the Structures of Human Immunodeficiency Virus Protease. <i>Proteins: Structure, Function and Bioinformatics</i> , 2002, 49, 429-431.	2.6	60
41	Avoidable errors in deposited macromolecular structures: an impediment to efficient data mining. <i>IUCr</i> , 2014, 1, 179-193.	2.2	58
42	Crystallography and chemistry should always go together: a cautionary tale of protein complexes with cisplatin and carboplatin. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 1965-1979.	2.5	52
43	Database of three-dimensional structures of HIV proteinases. <i>Nature Structural and Molecular Biology</i> , 1997, 4, 8-8.	8.2	51
44	Crystal structure of the N-terminal domain of <i>E. coli</i> Lon protease. <i>Protein Science</i> , 2005, 14, 2895-2900.	7.6	49
45	Crystal Structures of the Histo-Aspartic Protease (HAP) from <i>Plasmodium falciparum</i> . <i>Journal of Molecular Biology</i> , 2009, 388, 520-540.	4.2	49
46	Unmet challenges of structural genomics. <i>Current Opinion in Structural Biology</i> , 2010, 20, 587-597.	5.7	49
47	Detect, correct, retract: How to manage incorrect structural models. <i>FEBS Journal</i> , 2018, 285, 444-466.	4.7	49
48	Structure of equine infectious anemia virus proteinase complexed with an inhibitor. <i>Protein Science</i> , 1996, 5, 1453-1465.	7.6	48
49	Crystal structure of human T cell leukemia virus protease, a novel target for anticancer drug design. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 18332-18337.	7.1	48
50	Structure-based engineering and comparison of novel split inteins for protein ligation. <i>Molecular BioSystems</i> , 2014, 10, 1023-1034.	2.9	48
51	Atomic resolution structure of <i>Erwinia chrysanthemi</i> L-asparaginase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 84-92.	2.5	47
52	High-Resolution Cryo-EM Maps and Models: A Crystallographer's Perspective. <i>Structure</i> , 2017, 25, 1589-1597.e1.	3.3	47
53	A close look onto structural models and primary ligands of metallo- β -lactamases. <i>Drug Resistance Updates</i> , 2018, 40, 1-12.	14.4	47
54	Atomic-resolution Crystal Structure of the Proteolytic Domain of <i>Archaeoglobus fulgidus</i> Lon Reveals the Conformational Variability in the Active Sites of Lon Proteases. <i>Journal of Molecular Biology</i> , 2005, 351, 144-157.	4.2	46

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55	Structural studies of algal lectins with anti-HIV activity. <i>Acta Biochimica Polonica</i> , 2006, 53, 617-26.	0.5	44
56	Practical experience with the use of halides for phasing macromolecular structures: a powerful tool for structural genomics. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 239-249.	2.5	42
57	Overexpression and purification of scytovirin, a potent, novel anti-HIV protein from the cultured cyanobacterium <i>Scytonema varium</i> . <i>Protein Expression and Purification</i> , 2006, 46, 233-239.	1.3	42
58	Structural and biochemical properties of L-asparaginase. <i>FEBS Journal</i> , 2021, 288, 4183-4209.	4.7	42
59	Do bacterial L-asparaginases utilize a catalytic triad Thr-Tyr-Glu?. <i>BBA - Proteins and Proteomics</i> , 2001, 1550, 117-128.	2.1	41
60	Structural studies of vacuolar plasmepsins. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2012, 1824, 207-223.	2.3	39
61	Crystal Structure of a Complex of the Intracellular Domain of Interferon λ Receptor 1 (IFNLR1) and the FERM/SH2 Domains of Human JAK1. <i>Journal of Molecular Biology</i> , 2016, 428, 4651-4668.	4.2	37
62	Stereochemistry and Validation of Macromolecular Structures. <i>Methods in Molecular Biology</i> , 2017, 1607, 595-610.	0.9	36
63	Mechanism of Catalysis by <i>scpK</i> -Asparaginase. <i>Biochemistry</i> , 2020, 59, 1927-1945.	2.5	36
64	Crystal structures of the free and inhibited forms of plasmepsin I (PMI) from <i>Plasmodium falciparum</i> . <i>Journal of Structural Biology</i> , 2011, 175, 73-84.	2.8	35
65	Ligand-centered assessment of SARS-CoV-2 drug target models in the Protein Data Bank. <i>FEBS Journal</i> , 2020, 287, 3703-3718.	4.7	35
66	Crystallographic studies of the complexes of antiviral protein griffithsin with glucose and N-acetylglucosamine. <i>Protein Science</i> , 2007, 16, 1485-1489.	7.6	34
67	Impact of synchrotron radiation on macromolecular crystallography: a personal view. <i>Journal of Synchrotron Radiation</i> , 2010, 17, 433-444.	2.4	34
68	Griffithsin tandemers: flexible and potent lectin inhibitors of the human immunodeficiency virus. <i>Retrovirology</i> , 2015, 12, 6.	2.0	34
69	Safeguarding Structural Data Repositories against Bad Apples. <i>Structure</i> , 2016, 24, 216-220.	3.3	34
70	Structure of the N-terminal fragment of <i>Escherichia coli</i> Lon protease. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2010, 66, 865-873.	2.5	33
71	Atomic-resolution crystal structure of the antiviral lectin scytovirin. <i>Protein Science</i> , 2007, 16, 2756-2760.	7.6	32
72	Correcting the record of structural publications requires joint effort of the community and journal editors. <i>FEBS Journal</i> , 2016, 283, 4452-4457.	4.7	31

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73	The expanding diversity of serine hydrolases. <i>Current Opinion in Structural Biology</i> , 2007, 17, 683-690.	5.7	30
74	Crystal Structures of a Plant Trypsin Inhibitor from <i>Enterolobium contortisiliquum</i> (EcTI) and of Its Complex with Bovine Trypsin. <i>PLoS ONE</i> , 2013, 8, e62252.	2.5	30
75	A model of the ternary complex of interleukin-10 with its soluble receptors. <i>BMC Structural Biology</i> , 2005, 5, 10.	2.3	27
76	Crystal structure of XMRV protease differs from the structures of other retropepsins. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 227-229.	8.2	27
77	Structures of two highly homologous bacterial L-asparaginases: a case of enantiomorphic space groups. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 369-377.	2.5	26
78	'Atomic resolution': a badly abused term in structural biology. <i>Acta Crystallographica Section D: Structural Biology</i> , 2017, 73, 379-380.	2.3	25
79	Pathological crystallography: case studies of several unusual macromolecular crystals. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 967-975.	2.5	24
80	Crystal Structures of Inhibitor Complexes of Human T-Cell Leukemia Virus (HTLV-1) Protease. <i>Journal of Molecular Biology</i> , 2010, 401, 626-641.	4.2	23
81	Progress in protein crystallography. <i>Protein and Peptide Letters</i> , 2016, 23, 201-210.	0.9	23
82	Crystallographic models of SARS-CoV-2 3CL ^{pro} : in-depth assessment of structure quality and validation. <i>IUCr</i> , 2021, 8, 238-256.	2.2	21
83	Geometric considerations support the double- ϵ displacement catalytic mechanism of L-asparaginase. <i>Protein Science</i> , 2019, 28, 1850-1864.	7.6	20
84	Limited proteolysis of <i>E. coli</i> ATP-dependent protease Lon - a unified view of the subunit architecture and characterization of isolated enzyme fragments.. <i>Acta Biochimica Polonica</i> , 2008, 55, 281-296.	0.5	20
85	Cryo-EM structure of substrate-free <i>E. coli</i> Lon protease provides insights into the dynamics of Lon machinery. <i>Current Research in Structural Biology</i> , 2019, 1, 13-20.	2.2	19
86	Complexes of Neutralizing and Non-Neutralizing Affinity Matured Fabs with a Mimetic of the Internal Trimeric Coiled-Coil of HIV-1 gp41. <i>PLoS ONE</i> , 2013, 8, e78187.	2.5	17
87	Topology of the disulfide bonds in the antiviral lectin scytovirin. <i>Protein Science</i> , 2010, 19, 1649-1661.	7.6	16
88	Structural Insights into the Activation and Inhibition of Histo-Aspartic Protease from <i>Plasmodium falciparum</i> . <i>Biochemistry</i> , 2011, 50, 8862-8879.	2.5	15
89	Structural Basis for the Persistence of Homing Endonucleases in Transcription Factor IIB Inteins. <i>Journal of Molecular Biology</i> , 2017, 429, 3942-3956.	4.2	15
90	New insights into structural and functional relationships between LonA proteases and ClpB chaperones. <i>FEBS Open Bio</i> , 2019, 9, 1536-1551.	2.3	15

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91	The crystal structure of the naturally split gp41 ¹ intein guides the engineering of orthogonal split inteins from cis-splicing inteins. FEBS Journal, 2020, 287, 1886-1898.	4.7	15
92	Covid-19.bioreproducibility.org: A web resource for SARS-CoV-2-related structural models. Protein Science, 2021, 30, 115-124.	7.6	15
93	Generalized enzymatic mechanism of catalysis by tetrameric L-asparaginases from mesophilic bacteria. Scientific Reports, 2020, 10, 17516.	3.3	14
94	Structure and the Mode of Activity of Lon Proteases from Diverse Organisms. Journal of Molecular Biology, 2022, 434, 167504.	4.2	14
95	Control of SARS-CoV-2 infection after Spike DNA or Spike DNA+Protein co-immunization in rhesus macaques. PLoS Pathogens, 2021, 17, e1009701.	4.7	12
96	Limited proteolysis of E. coli ATP-dependent protease Lon - a unified view of the subunit architecture and characterization of isolated enzyme fragments. Acta Biochimica Polonica, 2008, 55, 281-96.	0.5	12
97	Deciphering the mechanism of potent peptidomimetic inhibitors targeting plasmepsins – biochemical and structural insights. FEBS Journal, 2018, 285, 3077-3096.	4.7	11
98	Studies of two crystal forms of L-glutaminase-asparaginase from Acinetobacter glutaminasificans. Journal of Molecular Biology, 1975, 99, 295-299.	4.2	10
99	Opportunistic complexes of E. coli L-asparaginases with citrate anions. Scientific Reports, 2019, 9, 11070.	3.3	10
100	Structures of plasmepsin X from Plasmodium falciparum reveal a novel inactivation mechanism of the zymogen and molecular basis for binding of inhibitors in mature enzyme. Protein Science, 2022, 31, 882-899.	7.6	10
101	Structure of BbKI, a disulfide-free plasma kallikrein inhibitor. Acta Crystallographica Section F, Structural Biology Communications, 2015, 71, 1055-1062.	0.8	9
102	Structural and biochemical characterization of the inhibitor complexes of xenotropic murine leukemia virus-related virus protease. FEBS Journal, 2011, 278, 4413-4424.	4.7	8
103	Elucidation of the structure of retroviral proteases: a reminiscence. FEBS Journal, 2015, 282, 4059-4066.	4.7	8
104	Localization of ASV Integrase-DNA Contacts by Site-Directed Crosslinking and their Structural Analysis. PLoS ONE, 2011, 6, e27751.	2.5	8
105	Is the pseudo-dyad in retroviral proteinase monomers structural or evolutionary?. FEBS Letters, 1990, 260, 201-205.	2.8	7
106	Molecular replacement with pseudosymmetry and model dissimilarity: a case study. Acta Crystallographica Section D: Biological Crystallography, 2006, 62, 208-215.	2.5	7
107	Catalytic Pathways of Aspartic Peptidases. , 2013, , 19-26.		7
108	Lessons Learned Fighting HIV Can Be Applied to Anti-Cancer Drug Design. Cell Cycle, 2006, 5, 463-464.	2.6	6

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109	Enzymatic properties, evidence for in vivo expression, and intracellular localization of shewasin D, the pepsin homolog from <i>Shewanella denitrificans</i> . <i>Scientific Reports</i> , 2016, 6, 23869.	3.3	6
110	Group depositions to the Protein Data Bank need adequate presentation and different archiving protocol. <i>Protein Science</i> , 2022, 31, 784-786.	7.6	6
111	Structural Studies Reveal the Role of Helix 68 in the Elongation Step of Protein Biosynthesis. <i>MBio</i> , 2022, 13, e0030622.	4.1	6
112	Dynamic bulge nucleotides in the KSHV PAN ENE triple helix provide a unique binding platform for small molecule ligands. <i>Nucleic Acids Research</i> , 2021, 49, 13179-13193.	14.5	6
113	Purification, crystallization and preliminary crystallographic studies of the complex of interferon- β 1 with its receptor. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 61-63.	0.7	5
114	Structure of RC1339/APRc from <i>Rickettsia conorii</i> , a retropepsin-like aspartic protease. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 2109-2118.	2.5	5
115	Rapid response to emerging biomedical challenges and threats. <i>IUCr</i> , 2021, 8, 395-407.	2.2	5
116	Crystal structures of the complex of a kallikrein inhibitor from <i>Bauhinia bauhinioides</i> with trypsin and modeling of kallikrein complexes. <i>Acta Crystallographica Section D: Structural Biology</i> , 2019, 75, 56-69.	2.3	3
117	Activation mechanism of plasmepsins, pepsin-like aspartic proteases from <i>Plasmodium</i> , follows a unique trans-activation pathway. <i>FEBS Journal</i> , 2021, 288, 678-698.	4.7	3
118	Introduction: Celebrating the International Year of Crystallography. <i>FEBS Journal</i> , 2014, 281, 3983-3984.	4.7	2
119	Crystallographically correct but confusing presentation of structural models deposited in the Protein Data Bank. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 939-945.	2.3	2
120	The Convergence of the Hedgehog/Intein Fold in Different Protein Splicing Mechanisms. <i>International Journal of Molecular Sciences</i> , 2020, 21, 8367.	4.1	2
121	Protein crystallography: alive and well. <i>FEBS Journal</i> , 2021, 288, 5786-5787.	4.7	1
122	Structural studies of complexes of kallikrein 4 with wild-type and mutated forms of the Kunitz-type inhibitor BbKI. <i>Acta Crystallographica Section D: Structural Biology</i> , 2021, 77, 1084-1098.	2.3	1
123	Unexpected Specificity of a Trypsin-like Enzyme. <i>Structure</i> , 2018, 26, 530-531.	3.3	0
124	Correction to "Inhibitor Complexes of the <i>Pseudomonas</i> Serine-Carboxyl Proteinase". <i>Biochemistry</i> , 2018, 57, 6644-6644.	2.5	0
125	Celebrating the 75th birthday of Professor Wladek Minor, one of the most accomplished Polish-American structural biologists. <i>Acta Biochimica Polonica</i> , 2021, 68, 1-4.	0.5	0
126	Phytepsin. , 2013, , 118-124.		0

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127	Serendipity, politics, and crystal structures, or how I became a protein crystallographer. Postepy Biochemii, 2016, 62, 239-241.	0.2	0