

Alexander Wlodawer

List of Publications by Year in descending order

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127
papers

8,854
citations

57681

46
h-index

49824

91
g-index

131
all docs

131
docs citations

131
times ranked

7976
citing authors

#	ARTICLE	IF	CITATIONS
1	Group depositions to the Protein Data Bank need adequate presentation and different archiving protocol. <i>Protein Science</i> , 2022, 31, 784-786.	3.1	6
2	Structures of plasmepsin X from <i>Plasmodium falciparum</i> reveal a novel inactivation mechanism of the zymogen and molecular basis for binding of inhibitors in mature enzyme. <i>Protein Science</i> , 2022, 31, 882-899.	3.1	10
3	Structural Studies Reveal the Role of Helix 68 in the Elongation Step of Protein Biosynthesis. <i>MBio</i> , 2022, 13, e0030622.	1.8	6
4	Structure and the Mode of Activity of Lon Proteases from Diverse Organisms. <i>Journal of Molecular Biology</i> , 2022, 434, 167504.	2.0	14
5	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.	2.2	3
6	Covid-19.bioreproducibility.org: A web resource for SARS-CoV-2-related structural models. <i>Protein Science</i> , 2021, 30, 115-124.	3.1	15
7	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.	5.8	126
8	Crystallographic models of SARS-CoV-2 3CL ^{pro} : in-depth assessment of structure quality and validation. <i>IUCr</i> , 2021, 8, 238-256.	1.0	21
9	Rapid response to emerging biomedical challenges and threats. <i>IUCr</i> , 2021, 8, 395-407.	1.0	5
10	Protein crystallography: alive and well. <i>FEBS Journal</i> , 2021, 288, 5786-5787.	2.2	1
11	Structural and biochemical properties of L-asparaginase. <i>FEBS Journal</i> , 2021, 288, 4183-4209.	2.2	42
12	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.	1.1	1
13	Control of SARS-CoV-2 infection after Spike DNA or Spike DNA+Protein co-immunization in rhesus macaques. <i>PLoS Pathogens</i> , 2021, 17, e1009701.	2.1	12
14	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.	0.3	0
15	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.	6.5	6
16	The crystal structure of the naturally split gp41 ^{int} intein guides the engineering of orthogonal split inteins from cis-splicing inteins. <i>FEBS Journal</i> , 2020, 287, 1886-1898.	2.2	15
17	Generalized enzymatic mechanism of catalysis by tetrameric L-asparaginases from mesophilic bacteria. <i>Scientific Reports</i> , 2020, 10, 17516.	1.6	14
18	The Convergence of the Hedgehog/Intein Fold in Different Protein Splicing Mechanisms. <i>International Journal of Molecular Sciences</i> , 2020, 21, 8367.	1.8	2

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19	Ligand-centered assessment of SARS-CoV-2 drug target models in the Protein Data Bank. FEBS Journal, 2020, 287, 3703-3718.	2.2	35
20	Mechanism of Catalysis by <i>Asparaginase</i> . Biochemistry, 2020, 59, 1927-1945.	1.2	36
21	Geometric considerations support the double-displacement catalytic mechanism of <i>Asparaginase</i> . Protein Science, 2019, 28, 1850-1864.	3.1	20
22	Opportunistic complexes of <i>E. coli</i> L-asparaginases with citrate anions. Scientific Reports, 2019, 9, 11070.	1.6	10
23	New insights into structural and functional relationships between LonA proteases and ClpB chaperones. FEBS Open Bio, 2019, 9, 1536-1551.	1.0	15
24	Crystal structures of the complex of a kallikrein inhibitor from <i>Bauhinia bauhinioides</i> with trypsin and modeling of kallikrein complexes. Acta Crystallographica Section D: Structural Biology, 2019, 75, 56-69.	1.1	3
25	Cryo-EM structure of substrate-free <i>E. coli</i> Lon protease provides insights into the dynamics of Lon machinery. Current Research in Structural Biology, 2019, 1, 13-20.	1.1	19
26	Unexpected Specificity of a Trypsin-like Enzyme. Structure, 2018, 26, 530-531.	1.6	0
27	Detect, correct, retract: How to manage incorrect structural models. FEBS Journal, 2018, 285, 444-466.	2.2	49
28	Correction to "Inhibitor Complexes of the Pseudomonas Serine-Carboxyl Proteinase". Biochemistry, 2018, 57, 6644-6644.	1.2	0
29	Crystallographically correct but confusing presentation of structural models deposited in the Protein Data Bank. Acta Crystallographica Section D: Structural Biology, 2018, 74, 939-945.	1.1	2
30	A close look onto structural models and primary ligands of metallo- β -lactamases. Drug Resistance Updates, 2018, 40, 1-12.	6.5	47
31	Deciphering the mechanism of potent peptidomimetic inhibitors targeting plasmepsins – biochemical and structural insights. FEBS Journal, 2018, 285, 3077-3096.	2.2	11
32	Stereochemistry and Validation of Macromolecular Structures. Methods in Molecular Biology, 2017, 1607, 595-610.	0.4	36
33	'Atomic resolution': a badly abused term in structural biology. Acta Crystallographica Section D: Structural Biology, 2017, 73, 379-380.	1.1	25
34	Structural Basis for the Persistence of Homing Endonucleases in Transcription Factor IIB Inteins. Journal of Molecular Biology, 2017, 429, 3942-3956.	2.0	15
35	High-Resolution Cryo-EM Maps and Models: A Crystallographer's Perspective. Structure, 2017, 25, 1589-1597.e1.	1.6	47
36	Correcting the record of structural publications requires joint effort of the community and journal editors. FEBS Journal, 2016, 283, 4452-4457.	2.2	31

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37	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.	1.6	6
38	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.	2.0	37
39	Safeguarding Structural Data Repositories against Bad Apples. <i>Structure</i> , 2016, 24, 216-220.	1.6	34
40	Progress in protein crystallography. <i>Protein and Peptide Letters</i> , 2016, 23, 201-210.	0.4	23
41	Serendipity, politics, and crystal structures, or how I became a protein crystallographer. <i>Postepy Biochemii</i> , 2016, 62, 239-241.	0.5	0
42	Elucidation of the structure of retroviral proteases: a reminiscence. <i>FEBS Journal</i> , 2015, 282, 4059-4066.	2.2	8
43	Griffithsin tandemers: flexible and potent lectin inhibitors of the human immunodeficiency virus. <i>Retrovirology</i> , 2015, 12, 6.	0.9	34
44	Structure of BbKI, a disulfide-free plasma kallikrein inhibitor. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015, 71, 1055-1062.	0.4	9
45	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
46	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
47	Introduction: Celebrating the International Year of Crystallography. <i>FEBS Journal</i> , 2014, 281, 3983-3984.	2.2	2
48	The future of crystallography in drug discovery. <i>Expert Opinion on Drug Discovery</i> , 2014, 9, 125-137.	2.5	70
49	A brief history of macromolecular crystallography, illustrated by a family tree and its obel fruits. <i>FEBS Journal</i> , 2014, 281, 3985-4009.	2.2	83
50	Nature's recipe for splitting inteins. <i>Protein Engineering, Design and Selection</i> , 2014, 27, 263-271.	1.0	96
51	Structure-based engineering and comparison of novel split inteins for protein ligation. <i>Molecular BioSystems</i> , 2014, 10, 1023-1034.	2.9	48
52	Avoidable errors in deposited macromolecular structures: an impediment to efficient data mining. <i>IUCr</i> , 2014, 1, 179-193.	1.0	58
53	Protein crystallography for aspiring crystallographers or how to avoid pitfalls and traps in macromolecular structure determination. <i>FEBS Journal</i> , 2013, 280, 5705-5736.	2.2	95
54	Catalytic Pathways of Aspartic Peptidases. , 2013, , 19-26.		7

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55	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.	1.1	30
56	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.	1.1	17
57	Phytpsins. , 2013, , 118-124.		0
58	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.	2.0	61
59	Structural studies of vacuolar plasmepsins. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2012, 1824, 207-223.	1.1	39
60	Structural Insights into the Activation and Inhibition of Histo-Aspartic Protease from <i>Plasmodium falciparum</i> . <i>Biochemistry</i> , 2011, 50, 8862-8879.	1.2	15
61	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.	1.3	35
62	Structural and biochemical characterization of the inhibitor complexes of xenotropic murine leukemia virus-related virus protease. <i>FEBS Journal</i> , 2011, 278, 4413-4424.	2.2	8
63	Crystal structure of XMRV protease differs from the structures of other retropepsins. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 227-229.	3.6	27
64	Improved molecular replacement by density- and energy-guided protein structure optimization. <i>Nature</i> , 2011, 473, 540-543.	13.7	226
65	Localization of ASV Integrase-DNA Contacts by Site-Directed Crosslinking and their Structural Analysis. <i>PLoS ONE</i> , 2011, 6, e27751.	1.1	8
66	Unmet challenges of structural genomics. <i>Current Opinion in Structural Biology</i> , 2010, 20, 587-597.	2.6	49
67	Monomerization of Viral Entry Inhibitor Griffithsin Elucidates the Relationship between Multivalent Binding to Carbohydrates and anti-HIV Activity. <i>Structure</i> , 2010, 18, 1104-1115.	1.6	85
68	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
69	Impact of synchrotron radiation on macromolecular crystallography: a personal view. <i>Journal of Synchrotron Radiation</i> , 2010, 17, 433-444.	1.0	34
70	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
71	Topology of the disulfide bonds in the antiviral lectin scytovirin. <i>Protein Science</i> , 2010, 19, 1649-1661.	3.1	16
72	Crystal Structures of Inhibitor Complexes of Human T-Cell Leukemia Virus (HTLV-1) Protease. <i>Journal of Molecular Biology</i> , 2010, 401, 626-641.	2.0	23

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73	Crystal Structure of Human Interferon- β 1 in Complex with Its High-Affinity Receptor Interferon- β R1. <i>Journal of Molecular Biology</i> , 2010, 404, 650-664.	2.0	76
74	Crystal Structures of the Histo-Aspartic Protease (HAP) from <i>Plasmodium falciparum</i> . <i>Journal of Molecular Biology</i> , 2009, 388, 520-540.	2.0	49
75	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.	2.2	231
76	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.	0.3	20
77	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, 281-96.	0.3	12
78	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
79	The expanding diversity of serine hydrolases. <i>Current Opinion in Structural Biology</i> , 2007, 17, 683-690.	2.6	30
80	Crystallographic studies of the complexes of antiviral protein griffithsin with glucose and N-acetylglucosamine. <i>Protein Science</i> , 2007, 16, 1485-1489.	3.1	34
81	Atomic-resolution crystal structure of the antiviral lectin scytovirin. <i>Protein Science</i> , 2007, 16, 2756-2760.	3.1	32
82	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.	0.6	42
83	Molecular replacement with pseudosymmetry and model dissimilarity: a case study. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006, 62, 208-215.	2.5	7
84	Slicing a protease: Structural features of the ATP-dependent Lon proteases gleaned from investigations of isolated domains. <i>Protein Science</i> , 2006, 15, 1815-1828.	3.1	81
85	Domain-Swapped Structure of the Potent Antiviral Protein Griffithsin and Its Mode of Carbohydrate Binding. <i>Structure</i> , 2006, 14, 1127-1135.	1.6	149
86	Lessons Learned Fighting HIV Can Be Applied to Anti-Cancer Drug Design. <i>Cell Cycle</i> , 2006, 5, 463-464.	1.3	6
87	Structural studies of algal lectins with anti-HIV activity.. <i>Acta Biochimica Polonica</i> , 2006, 53, 617-626.	0.3	84
88	Structural studies of algal lectins with anti-HIV activity. <i>Acta Biochimica Polonica</i> , 2006, 53, 617-26.	0.3	44
89	Crystal structure of the N-terminal domain of <i>E. coli</i> Lon protease. <i>Protein Science</i> , 2005, 14, 2895-2900.	3.1	49
90	Pathological crystallography: case studies of several unusual macromolecular crystals. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 967-975.	2.5	24

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91	A model of the ternary complex of interleukin-10 with its soluble receptors. <i>BMC Structural Biology</i> , 2005, 5, 10.	2.3	27
92	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.	3.3	48
93	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.	2.0	46
94	The Catalytic Domain of <i>Escherichia coli</i> 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.	1.6	167
95	Classification of ATP-dependent proteases Lon and comparison of the active sites of their proteolytic domains. <i>FEBS Journal</i> , 2004, 271, 4865-4871.	0.2	88
96	Crystal structure of the AAA+ domain of <i>E. coli</i> Lon protease at 1.9Å... resolution. <i>Journal of Structural Biology</i> , 2004, 146, 113-122.	1.3	84
97	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
98	Crystal Structure of Interleukin-19 Defines a New Subfamily of Helical Cytokines. <i>Journal of Biological Chemistry</i> , 2003, 278, 3308-3313.	1.6	74
99	HIVdb: A Database of the Structures of Human Immunodeficiency Virus Protease. <i>Proteins: Structure, Function and Bioinformatics</i> , 2002, 49, 429-431.	1.5	60
100	Rational Approach to AIDS Drug Design Through Structural Biology. <i>Annual Review of Medicine</i> , 2002, 53, 595-614.	5.0	138
101	Structural Basis for the Activity and Substrate Specificity of <i>Erwinia chrysanthemi</i> L-Asparaginase. <i>Biochemistry</i> , 2001, 40, 5655-5664.	1.2	160
102	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
103	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
104	Do bacterial L-asparaginases utilize a catalytic triad Thr-Tyr-Glu?. <i>BBA - Proteins and Proteomics</i> , 2001, 1550, 117-128.	2.1	41
105	Structural and biochemical studies of retroviral proteases. <i>BBA - Proteins and Proteomics</i> , 2000, 1477, 16-34.	2.1	151
106	Crystal structure of plant aspartic proteinase prophytepsin: inactivation and vacuolar targeting. <i>EMBO Journal</i> , 1999, 18, 3947-3955.	3.5	150
107	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
108	Transport and Activation of the Vacuolar Aspartic Proteinase Phytepsin in Barley (<i>Hordeum vulgare</i>) <i>Trends in Biochemical Sciences</i> , 1998, 23, 10-16.	1.6	61

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109	Database of three-dimensional structures of HIV proteinases. <i>Nature Structural and Molecular Biology</i> , 1997, 4, 8-8.	3.6	51
110	A covalently bound catalytic intermediate in <i>Escherichia coli</i> asparaginase : Crystal structure of a Thr-89-Val mutant. <i>FEBS Letters</i> , 1996, 390, 211-216.	1.3	86
111	Crystal Structure and Amino Acid Sequence of <i>Wolinella Succinogenes</i> -Asparaginase. <i>FEBS Journal</i> , 1996, 241, 201-207.	0.2	100
112	Structure of equine infectious anemia virus proteinase complexed with an inhibitor. <i>Protein Science</i> , 1996, 5, 1453-1465.	3.1	48
113	Crystal structure of human interleukin-10 at 1.6 Å resolution and a model of a complex with its soluble receptor. <i>Protein Science</i> , 1996, 5, 1955-1962.	3.1	94
114	Crystal structure of interleukin-10 reveals the functional dimer with an unexpected topological similarity to interferon β. <i>Structure</i> , 1995, 3, 591-601.	1.6	219
115	Structure of an inhibitor complex of the proteinase from feline immunodeficiency virus. <i>Nature Structural and Molecular Biology</i> , 1995, 2, 480-488.	3.6	66
116	Energy calculations and analysis of HIV-1 protease-inhibitor crystal structures. <i>Protein Engineering, Design and Selection</i> , 1994, 7, 309-316.	1.0	67
117	Structural Characterization of <i>Pseudomonas</i> 7A Glutaminase-Asparaginase. <i>Biochemistry</i> , 1994, 33, 10257-10265.	1.2	78
118	A left-handed crossover involved in amidohydrolase catalysis. <i>FEBS Letters</i> , 1993, 328, 275-279.	1.3	76
119	Structure-Based Inhibitors of HIV-1 Protease. <i>Annual Review of Biochemistry</i> , 1993, 62, 543-585.	5.0	854
120	Structural and evolutionary relationships between retroviral and eukaryotic aspartic proteinases. <i>Biochemistry</i> , 1991, 30, 4663-4671.	1.2	113
121	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.	1.2	242
122	New protein fold revealed by a 2.3-Å resolution crystal structure of nerve growth factor. <i>Nature</i> , 1991, 354, 411-414.	13.7	500
123	Is the pseudo-dyad in retroviral proteinase monomers structural or evolutionary?. <i>FEBS Letters</i> , 1990, 260, 201-205.	1.3	7
124	Crystal structure of a retroviral protease proves relationship to aspartic protease family. <i>Nature</i> , 1989, 337, 576-579.	13.7	378
125	Comparison of two highly refined structures of bovine pancreatic trypsin inhibitor. <i>Journal of Molecular Biology</i> , 1987, 193, 145-156.	2.0	217
126	Structure of bovine pancreatic trypsin inhibitor. <i>Journal of Molecular Biology</i> , 1984, 180, 301-329.	2.0	478

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127	Studies of two crystal forms of l-glutaminase-asparaginase from <i>Acinetobacter glutaminasificans</i> . <i>Journal of Molecular Biology</i> , 1975, 99, 295-299.	2.0	10