

Albert M Berghuis

List of Publications by Year in descending order

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108
papers

6,024
citations

87888

38
h-index

76900

74
g-index

109
all docs

109
docs citations

109
times ranked

7799
citing authors

#	ARTICLE	IF	CITATIONS
1	De novo <i>TRPV4</i> Leu619Pro variant causes a new channelopathy characterised by giant cell lesions of the jaws and skull, skeletal abnormalities and polyneuropathy. <i>Journal of Medical Genetics</i> , 2022, 59, 305-312.	3.2	6
2	Structural and functional insights into esterase-mediated macrolide resistance. <i>Nature Communications</i> , 2021, 12, 1732.	12.8	21
3	Structural basis for plazomicin antibiotic action and resistance. <i>Communications Biology</i> , 2021, 4, 729.	4.4	13
4	Structural and phylogenetic analyses of resistance to next-generation aminoglycosides conferred by AAC(2) enzymes. <i>Scientific Reports</i> , 2021, 11, 11614.	3.3	9
5	Bisphosphoglycerate Mutase Deficiency Protects against Cerebral Malaria and Severe Malaria-Induced Anemia. <i>Cell Reports</i> , 2020, 32, 108170.	6.4	7
6	Histone H3.3G34-Mutant Interneuron Progenitors Co-opt PDGFRA for Gliomagenesis. <i>Cell</i> , 2020, 183, 1617-1633.e22.	28.9	93
7	Revisiting the Catalytic Cycle and Kinetic Mechanism of Aminoglycoside <i>O</i> -Nucleotidyltransferase(2): A Structural and Kinetic Study. <i>ACS Chemical Biology</i> , 2020, 15, 686-694.	3.4	0
8	ZBTB7B (ThPOK) Is Required for Pathogenesis of Cerebral Malaria and Protection against Pulmonary Tuberculosis. <i>Infection and Immunity</i> , 2020, 88, .	2.2	6
9	Phosphonate and Bisphosphonate Inhibitors of Farnesyl Pyrophosphate Synthases: A Structure-Guided Perspective. <i>Frontiers in Chemistry</i> , 2020, 8, 612728.	3.6	19
10	DGCR8 microprocessor defect characterizes familial multinodular goiter with schwannomatosis. <i>Journal of Clinical Investigation</i> , 2020, 130, 1479-1490.	8.2	31
11	Structure-Based Design of Dimeric Bisbenzimidazole Inhibitors to an Emergent Trimethoprim-Resistant Type II Dihydrofolate Reductase Guides the Design of Monomeric Analogues. <i>ACS Omega</i> , 2019, 4, 10056-10069.	3.5	7
12	Chirality-Driven Mode of Binding of $\hat{\pm}$ -Aminophosphonic Acid-Based Allosteric Inhibitors of the Human Farnesyl Pyrophosphate Synthase (hFPPS). <i>Journal of Medicinal Chemistry</i> , 2019, 62, 9691-9702.	6.4	10
13	The Structural Dynamics of Engineered $\hat{2}$ -Lactamases Vary Broadly on Three Timescales yet Sustain Native Function. <i>Scientific Reports</i> , 2019, 9, 6656.	3.3	19
14	A potential gain-of-function variant of SLC9A6 leads to endosomal alkalinization and neuronal atrophy associated with Christianson Syndrome. <i>Neurobiology of Disease</i> , 2019, 121, 187-204.	4.4	21
15	Plasticity of Aminoglycoside Binding to Antibiotic Kinase APH(2)-Ia. <i>Antimicrobial Agents and Chemotherapy</i> , 2018, 62, .	3.2	5
16	Look and Outlook on Enzyme-Mediated Macrolide Resistance. <i>Frontiers in Microbiology</i> , 2018, 9, 1942.	3.5	69
17	TRPV4 and KRAS and FGFR1 gain-of-function mutations drive giant cell lesions of the jaw. <i>Nature Communications</i> , 2018, 9, 4572.	12.8	58
18	Unraveling the Prenylation "Cancer Paradox in Multiple Myeloma with Novel Geranylgeranyl Pyrophosphate Synthase (GGPPS) Inhibitors. <i>Journal of Medicinal Chemistry</i> , 2018, 61, 6904-6917.	6.4	33

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19	Human farnesyl pyrophosphate synthase is allosterically inhibited by its own product. <i>Nature Communications</i> , 2017, 8, 14132.	12.8	32
20	Pharmacophore Mapping of Thienopyrimidine-Based Monophosphonate (ThP-MP) Inhibitors of the Human Farnesyl Pyrophosphate Synthase. <i>Journal of Medicinal Chemistry</i> , 2017, 60, 2119-2134.	6.4	21
21	Structural Basis for Kinase-Mediated Macrolide Antibiotic Resistance. <i>Structure</i> , 2017, 25, 750-761.e5.	3.3	23
22	Effect of solvent and protein dynamics in ligand recognition and inhibition of aminoglycoside adenylyltransferase 2â€³â€š. <i>Protein Science</i> , 2017, 26, 1852-1863.	7.6	2
23	Functionally Null <i><i>RAD51D</i></i> Missense Mutation Associates Strongly with Ovarian Carcinoma. <i>Cancer Research</i> , 2017, 77, 4517-4529.	0.9	34
24	Crystallographic and thermodynamic characterization of phenylaminopyridine bisphosphonates binding to human farnesyl pyrophosphate synthase. <i>PLoS ONE</i> , 2017, 12, e0186447.	2.5	5
25	Comprehensive characterization of ligandâ€š-induced plasticity changes in a dimeric enzyme. <i>FEBS Journal</i> , 2016, 283, 3029-3038.	4.7	4
26	Antibiotic Binding Drives Catalytic Activation of Aminoglycoside Kinase APH(2â€³)-Ia. <i>Structure</i> , 2016, 24, 935-945.	3.3	10
27	The role of conformational flexibility in Baeyer-Villiger monooxygenase catalysis and structure. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2016, 1864, 1641-1648.	2.3	21
28	An <i>Entamoeba histolytica</i> ADP-ribosyl transferase from the diphtheria toxin family modifies the bacterial elongation factor Tu. <i>Molecular and Biochemical Parasitology</i> , 2016, 207, 68-74.	1.1	1
29	Structural Analysis of the Tobramycin and Gentamicin Clinical Resistome Reveals Limitations for Next-generation Aminoglycoside Design. <i>ACS Chemical Biology</i> , 2016, 11, 1339-1346.	3.4	23
30	Germline and somatic FGFR1 abnormalities in dysembryoplastic neuroepithelial tumors. <i>Acta Neuropathologica</i> , 2016, 131, 847-863.	7.7	143
31	Drug-target networks in aminoglycoside resistance: hierarchy of priority in structural drug design. <i>MedChemComm</i> , 2016, 7, 103-113.	3.4	25
32	Derivatives of Mesoxalic Acid Block Translocation of HIV-1 Reverse Transcriptase. <i>Journal of Biological Chemistry</i> , 2015, 290, 1474-1484.	3.4	14
33	Probing the molecular and structural elements of ligands binding to the active site versus an allosteric pocket of the human farnesyl pyrophosphate synthase. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2015, 25, 1117-1123.	2.2	15
34	Inhibition of Outer Membrane Proteases of the Omptin Family by Aprotinin. <i>Infection and Immunity</i> , 2015, 83, 2300-2311.	2.2	22
35	Human isoprenoid synthase enzymes as therapeutic targets. <i>Frontiers in Chemistry</i> , 2014, 2, 50.	3.6	37
36	Lactone-Bound Structures of Cyclohexanone Monooxygenase Provide Insight into the Stereochemistry of Catalysis. <i>ACS Chemical Biology</i> , 2014, 9, 2843-2851.	3.4	39

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37	Structure of human farnesyl pyrophosphate synthase in complex with an aminopyridine bisphosphonate and two molecules of inorganic phosphate. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 299-304.	0.8	9
38	Overlapping and Distinct Roles of <i>Aspergillus fumigatus</i> UDP-glucose 4-Epimerases in Galactose Metabolism and the Synthesis of Galactose-containing Cell Wall Polysaccharides. <i>Journal of Biological Chemistry</i> , 2014, 289, 1243-1256.	3.4	102
39	Maintenance of Native-like Protein Dynamics May Not Be Required for Engineering Functional Proteins. <i>Chemistry and Biology</i> , 2014, 21, 1330-1340.	6.0	29
40	Substrate-dependent switching of the allosteric binding mechanism of a dimeric enzyme. <i>Nature Chemical Biology</i> , 2014, 10, 937-942.	8.0	23
41	Multistage Screening Reveals Chameleon Ligands of the Human Farnesyl Pyrophosphate Synthase: Implications to Drug Discovery for Neurodegenerative Diseases. <i>Journal of Medicinal Chemistry</i> , 2014, 57, 5764-5776.	6.4	29
42	Functional characterization of the human dendritic cell immunodeficiency associated with the IRF8K108E mutation. <i>Blood</i> , 2014, 124, 1894-1904.	1.4	65
43	Thienopyrimidine Bisphosphonate (ThPBP) Inhibitors of the Human Farnesyl Pyrophosphate Synthase: Optimization and Characterization of the Mode of Inhibition. <i>Journal of Medicinal Chemistry</i> , 2013, 56, 7939-7950.	6.4	43
44	A Recurrent PDGFRB Mutation Causes Familial Infantile Myofibromatosis. <i>American Journal of Human Genetics</i> , 2013, 92, 996-1000.	6.2	135
45	Identification of the Adenovirus E4orf4 Protein Binding Site on the B55Î± and Cdc55 Regulatory Subunits of PP2A: Implications for PP2A Function, Tumor Cell Killing and Viral Replication. <i>PLoS Pathogens</i> , 2013, 9, e1003742.	4.7	17
46	Structural Analysis of a Novel Cyclohexylamine Oxidase from <i>Brevibacterium oxydans</i> IH-35A. <i>PLoS ONE</i> , 2013, 8, e60072.	2.5	22
47	Prospects for circumventing aminoglycoside kinase mediated antibiotic resistance. <i>Frontiers in Cellular and Infection Microbiology</i> , 2013, 3, 22.	3.9	54
48	Structural Basis for Dual Nucleotide Selectivity of Aminoglycoside 2-Phosphotransferase IVa Provides Insight on Determinants of Nucleotide Specificity of Aminoglycoside Kinases. <i>Journal of Biological Chemistry</i> , 2012, 287, 13094-13102.	3.4	24
49	Small-Angle X-Ray Scattering Analysis of the Bifunctional Antibiotic Resistance Enzyme Aminoglycoside (6-AC) Acetyltransferase-Ie/Aminoglycoside (2-AC) Phosphotransferase-Ia Reveals a Rigid Solution Structure. <i>Antimicrobial Agents and Chemotherapy</i> , 2012, 56, 1899-1906.	3.2	23
50	Ternary complex structures of human farnesyl pyrophosphate synthase bound with a novel inhibitor and secondary ligands provide insights into the molecular details of the enzyme's active site closure. <i>BMC Structural Biology</i> , 2012, 12, 32.	2.3	21
51	The Substrate-Bound Crystal Structure of a Baeyer-Villiger Monooxygenase Exhibits a Criegee-like Conformation. <i>Journal of the American Chemical Society</i> , 2012, 134, 7788-7795.	13.7	81
52	Design and Synthesis of Active Site Inhibitors of the Human Farnesyl Pyrophosphate Synthase: Apoptosis and Inhibition of ERK Phosphorylation in Multiple Myeloma Cells. <i>Journal of Medicinal Chemistry</i> , 2012, 55, 3201-3215.	6.4	46
53	Crystal Structures of Antibiotic-Bound Complexes of Aminoglycoside 2-Phosphotransferase IVa Highlight the Diversity in Substrate Binding Modes among Aminoglycoside Kinases. <i>Biochemistry</i> , 2011, 50, 6237-6244.	2.5	19
54	IRF8 Mutations and Human Dendritic-Cell Immunodeficiency. <i>New England Journal of Medicine</i> , 2011, 365, 127-138.	27.0	564

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55	Competing allosteric mechanisms modulate substrate binding in a dimeric enzyme. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 288-294.	8.2	75
56	Novel crystallization conditions for tandem variant R67 DHFR yield a wild-type crystal structure. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 1316-1322.	0.7	8
57	Genetic Analysis of B55 $\hat{\pm}$ /Cdc55 Protein Phosphatase 2A Subunits: Association with the Adenovirus E4orf4 Protein. <i>Journal of Virology</i> , 2011, 85, 286-295.	3.4	13
58	Crystal Structures of Two Aminoglycoside Kinases Bound with a Eukaryotic Protein Kinase Inhibitor. <i>PLoS ONE</i> , 2011, 6, e19589.	2.5	23
59	Protein Tyrosine Phosphatases Are Regulated by Mononuclear Iron Dicitrate. <i>Journal of Biological Chemistry</i> , 2010, 285, 24620-24628.	3.4	25
60	Structure of the Antibiotic Resistance Factor Spectinomycin Phosphotransferase from <i>Legionella pneumophila</i> . <i>Journal of Biological Chemistry</i> , 2010, 285, 9545-9555.	3.4	36
61	Sustained Development in Baeyer-Villiger Biooxidation Technology. <i>ACS Symposium Series</i> , 2010, , 343-372.	0.5	6
62	Multiple Conformers in Active Site of Human Dihydrofolate Reductase F31R/Q35E Double Mutant Suggest Structural Basis for Methotrexate Resistance. <i>Journal of Biological Chemistry</i> , 2009, 284, 20079-20089.	3.4	33
63	Structural Basis of APH(3 $\hat{\epsilon}$)-IIla-Mediated Resistance to N1-Substituted Aminoglycoside Antibiotics. <i>Antimicrobial Agents and Chemotherapy</i> , 2009, 53, 3049-3055.	3.2	23
64	Crystal Structures of Cyclohexanone Monooxygenase Reveal Complex Domain Movements and a Sliding Cofactor. <i>Journal of the American Chemical Society</i> , 2009, 131, 8848-8854.	13.7	151
65	Expression and purification of recombinant M-Pol I from <i>Saccharomyces cerevisiae</i> with $\hat{\pm}$ -1,6 mannosylpolymerase activity. <i>Protein Expression and Purification</i> , 2009, 66, 1-6.	1.3	16
66	Preparation and Characterization of Bacterial Protein Complexes for Structural Analysis. <i>Advances in Protein Chemistry and Structural Biology</i> , 2009, 76, 1-42.	2.3	4
67	The type IA topoisomerase catalytic cycle: A normal mode analysis and molecular dynamics simulation. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 71, 1984-1994.	2.6	12
68	Flagellin Glycosylation in <i>Pseudomonas aeruginosa</i> PAK Requires the O-antigen Biosynthesis Enzyme WbpO. <i>Journal of Biological Chemistry</i> , 2008, 283, 3507-3518.	3.4	44
69	Structural basis for streptogramin B resistance in <i>Staphylococcus aureus</i> by virginiamycin B lyase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 10388-10393.	7.1	42
70	Structural Basis for Ubiquitin-Mediated Dimerization and Activation of the Ubiquitin Protein Ligase Cbl-b. <i>Molecular Cell</i> , 2007, 27, 474-485.	9.7	107
71	Synthesis and Structure $\hat{\sim}$ Activity Relationships of Truncated Bisubstrate Inhibitors of Aminoglycoside 6 $\hat{\epsilon}$ -N-Acetyltransferases. <i>Journal of Medicinal Chemistry</i> , 2006, 49, 5273-5281.	6.4	74
72	Identification and Characterization of a Protein-tyrosine Phosphatase in <i>Leishmania</i> . <i>Journal of Biological Chemistry</i> , 2006, 281, 36257-36268.	3.4	39

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73	Crystal structure of CTP:glycerol-3-phosphate cytidyltransferase from <i>Staphylococcus aureus</i> : Examination of structural basis for kinetic mechanism. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2006, 1764, 63-69.	2.3	16
74	Structural Studies of FlaA1 from <i>Helicobacter pylori</i> Reveal the Mechanism for Inverting 4,6-Dehydratase Activity. <i>Journal of Biological Chemistry</i> , 2006, 281, 24489-24495.	3.4	48
75	Towards a better understanding of the substrate specificity of the UDP-N-acetylglucosamine C4 epimerase WbpP. <i>Biochemical Journal</i> , 2005, 389, 173-180.	3.7	22
76	Regio- and Chemoselective 6'-N-Derivatization of Aminoglycosides: Bisubstrate Inhibitors as Probes To Study Aminoglycoside 6'-N-Acetyltransferases. <i>Angewandte Chemie - International Edition</i> , 2005, 44, 6859-6862.	13.8	54
77	Structures of aminoglycoside acetyltransferase AAC(6)-II in a novel crystal form: structural and normal-mode analyses. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 1273-1279.	2.5	23
78	Crystallization and preliminary crystallographic analysis of an aminoglycoside kinase from <i>Legionella pneumophila</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 606-608.	0.7	4
79	A Single Bifunctional UDP-GlcNAc/Glc 4-Epimerase Supports the Synthesis of Three Cell Surface Glycoconjugates in <i>Campylobacter jejuni</i> . <i>Journal of Biological Chemistry</i> , 2005, 280, 4792-4802.	3.4	117
80	Magnesium and Phosphate Ions Enable NAD Binding to Methylene tetrahydrofolate Dehydrogenase-Methenyltetrahydrofolate Cyclohydrolase. <i>Journal of Biological Chemistry</i> , 2005, 280, 34316-34323.	3.4	30
81	Crystal Structure of Homoserine Transacetylase from <i>Haemophilus influenzae</i> Reveals a New Family of β -Hydrolases. <i>Biochemistry</i> , 2005, 44, 15768-15773.	2.5	44
82	Crystal Structure of WbpP, a Genuine UDP-N-acetylglucosamine 4-Epimerase from <i>Pseudomonas aeruginosa</i> . <i>Journal of Biological Chemistry</i> , 2004, 279, 22635-22642.	3.4	80
83	Crystallization and preliminary crystallographic analysis of 3'-aminoglycoside kinase type IIIa complexed with a eukaryotic protein kinase inhibitor, CKI-7. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 1897-1899.	2.5	5
84	New phenolic inhibitors of yeast homoserine dehydrogenase. <i>Bioorganic and Medicinal Chemistry</i> , 2004, 12, 3825-3830.	3.0	24
85	Enzyme-Assisted Suicide. <i>Chemistry and Biology</i> , 2003, 10, 989-995.	6.0	28
86	X-ray structure of the AAC(6)-II antibiotic resistance enzyme at 1.8 Å resolution; examination of oligomeric arrangements in GNAT superfamily members. <i>Protein Science</i> , 2003, 12, 426-437.	7.6	78
87	Mechanism of Aminoglycoside Antibiotic Kinase APH(3)-IIIa: Role of the Nucleotide Positioning Loop. <i>Biochemistry</i> , 2002, 41, 7001-7007.	2.5	42
88	Protein kinase inhibitors and antibiotic resistance. , 2002, 93, 283-292.		23
89	Substrate promiscuity of an aminoglycoside antibiotic resistance enzyme via target mimicry. <i>EMBO Journal</i> , 2002, 21, 2323-2331.	7.8	132
90	Crystallization and preliminary X-ray diffraction studies of glycerol 3-phosphate cytidyltransferase from <i>Staphylococcus aureus</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 918-920.	2.5	3

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91	Resistance to aminoglycoside Antibiotics: Function meets structure. Focus on Biotechnology, 2001, , 85-98.	0.4	0
92	Crystal structures of homoserine dehydrogenase suggest a novel catalytic mechanism for oxidoreductases. Nature Structural Biology, 2000, 7, 238-244.	9.7	48
93	The COOH Terminus of Aminoglycoside Phosphotransferase (3â€²)-IIIa Is Critical for Antibiotic Recognition and Resistance. Journal of Biological Chemistry, 1999, 274, 30697-30706.	3.4	37
94	Crystal structure of an aminoglycoside 6â€²-N-acetyltransferase: defining the GCN5-related N-acetyltransferase superfamily fold. Structure, 1999, 7, 497-507.	3.3	137
95	Crystallization and preliminary X-ray diffraction studies of homoserine dehydrogenase from Saccharomyces cerevisiae. Acta Crystallographica Section D: Biological Crystallography, 1998, 54, 413-415.	2.5	3
96	Aminoglycoside Antibiotics. Advances in Experimental Medicine and Biology, 1998, , 27-69.	1.6	116
97	Structure of an Enzyme Required for Aminoglycoside Antibiotic Resistance Reveals Homology to Eukaryotic Protein Kinases. Cell, 1997, 89, 887-895.	28.9	236
98	Mechanistic and Structural Contributions of Critical Surface and Internal Residues to Cytochrome c Electron Transfer Reactivity. Biochemistry, 1996, 35, 10784-10792.	2.5	29
99	Structure of the GDPâ€³Pi complex of Gly203â†Ala Gî±1: a mimic of the ternary product complex of Gî±-catalyzed GTP hydrolysis. Structure, 1996, 4, 1277-1290.	3.3	67
100	The Role of a Conserved Water Molecule in the Redox-dependent Thermal Stability of Iso-1-cytochrome c. Journal of Biological Chemistry, 1996, 271, 29088-29093.	3.4	45
101	Structure of the first C2 domain of synaptotagmin I: A novel Ca ²⁺ /phospholipid-binding fold. Cell, 1995, 80, 929-938.	28.9	698
102	Mutation of Tyrosine-67 to Phenylalanine in Cytochrome c Significantly Alters the Local Heme Environment. Journal of Molecular Biology, 1994, 235, 1326-1341.	4.2	91
103	The Role of a Conserved Internal Water Molecule and Its Associated Hydrogen Bond Network in Cytochrome c. Journal of Molecular Biology, 1994, 236, 786-799.	4.2	119
104	Crystallization and Preliminary Crystallographic Studies of Gî±1 and Mutants of Gî±1 in the GTP and GDP-bound States. Journal of Molecular Biology, 1994, 238, 630-634.	4.2	50
105	Isolation, Crystallization and Preliminary Diffraction Analyses of Human Pancreatic Î±-Amylase. Journal of Molecular Biology, 1993, 230, 1084-1085.	4.2	9
106	Oxidation state-dependent conformational changes in cytochrome c. Journal of Molecular Biology, 1992, 223, 959-976.	4.2	391
107	Lactose binding to heat-labile enterotoxin revealed by X-ray crystallography. Nature, 1992, 355, 561-564.	27.8	223
108	Structural Aspects of Aminoglycoside-Modifying Enzymes. , 0, , 21-33.		5