Albert M Berghuis

List of Publications by Year in Descending Order

109 papers	5,036 citations	34 h-index	69 g-index
109 ext. papers	5,597 ext. citations	8.9 avg, IF	5.14 L-index

#	Paper	IF	Citations
109	Structural and functional insights into esterase-mediated macrolide resistance. *Nature Communications*, **2021**, 12, 1732	17.4	4
108	Structural basis for plazomicin antibiotic action and resistance. *Communications Biology*, **2021**, 4, 729	6.7	4
107	Structural and phylogenetic analyses of resistance to next-generation aminoglycosides conferred by AAC(2′)-enzymes. *Scientific Reports*, **2021**, 11, 11614	4.9	2
106	De novo Leu619Pro variant causes a new channelopathy characterised by giant cell lesions of the jaws and skull, skeletal abnormalities and polyneuropathy. *Journal of Medical Genetics*, **2021**,	5.8	1
105	Revisiting the Catalytic Cycle and Kinetic Mechanism of Aminoglycoside -Nucleotidyltransferase(2?): A Structural and Kinetic Study. *ACS Chemical Biology*, **2020**, 15, 686-694	4.9	
104	ZBTB7B (ThPOK) Is Required for Pathogenesis of Cerebral Malaria and Protection against Pulmonary Tuberculosis. *Infection and Immunity*, **2020**, 88,	3.7	2
103	DGCR8 microprocessor defect characterizes familial multinodular goiter with schwannomatosis. *Journal of Clinical Investigation*, **2020**, 130, 1479-1490	15.9	15
102	Bisphosphoglycerate Mutase Deficiency Protects against Cerebral Malaria and Severe Malaria-Induced Anemia. *Cell Reports*, **2020**, 32, 108170	10.6	1
101	Histone H3.3G34-Mutant Interneuron Progenitors Co-opt PDGFRA for Gliomagenesis. *Cell*, **2020**, 183, 1617-1633.e22	56.2	29
100	Phosphonate and Bisphosphonate Inhibitors of Farnesyl Pyrophosphate Synthases: A Structure-Guided Perspective. *Frontiers in Chemistry*, **2020**, 8, 612728	5	4
99	Chirality-Driven Mode of Binding of α-Aminophosphonic Acid-Based Allosteric Inhibitors of the Human Farnesyl Pyrophosphate Synthase (hFPPS). *Journal of Medicinal Chemistry*, **2019**, 62, 9691-9702	8.3	3
98	The Structural Dynamics of Engineered β-Lactamases Vary Broadly on Three Timescales yet Sustain Native Function. *Scientific Reports*, **2019**, 9, 6656	4.9	9
97	Structure-Based Design of Dimeric Bisbenzimidazole Inhibitors to an Emergent Trimethoprim-Resistant Type II Dihydrofolate Reductase Guides the Design of Monomeric Analogues. *ACS Omega*, **2019**, 4, 10056-10069	3.9	5
96	A potential gain-of-function variant of SLC9A6 leads to endosomal alkalinization and neuronal atrophy associated with Christianson Syndrome. *Neurobiology of Disease*, **2019**, 121, 187-204	7.5	11
95	Plasticity of Aminoglycoside Binding to Antibiotic Kinase APH(2?)-Ia. *Antimicrobial Agents and Chemotherapy*, **2018**, 62,	5.9	5
94	Unraveling the Prenylation-Cancer Paradox in Multiple Myeloma with Novel Geranylgeranyl Pyrophosphate Synthase (GGPPS) Inhibitors. *Journal of Medicinal Chemistry*, **2018**, 61, 6904-6917	8.3	22
93	Look and Outlook on Enzyme-Mediated Macrolide Resistance. *Frontiers in Microbiology*, **2018**, 9, 1942	5.7	33

92	TRPV4 and KRAS and FGFR1 gain-of-function mutations drive giant cell lesions of the jaw. *Nature Communications*, **2018**, 9, 4572	17.4	30
91	Human farnesyl pyrophosphate synthase is allosterically inhibited by its own product. *Nature Communications*, **2017**, 8, 14132	17.4	25
90	Pharmacophore Mapping of Thienopyrimidine-Based Monophosphonate (ThP-MP) Inhibitors of the Human Farnesyl Pyrophosphate Synthase. *Journal of Medicinal Chemistry*, **2017**, 60, 2119-2134	8.3	16
89	Structural Basis for Kinase-Mediated Macrolide Antibiotic Resistance. *Structure*, **2017**, 25, 750-761.e5	5.2	17
88	Crystallographic and thermodynamic characterization of phenylaminopyridine bisphosphonates binding to human farnesyl pyrophosphate synthase. *PLoS ONE*, **2017**, 12, e0186447	3.7	5
87	Effect of solvent and protein dynamics in ligand recognition and inhibition of aminoglycoside adenyltransferase 2?-Ia. *Protein Science*, **2017**, 26, 1852-1863	6.3	2
86	Functionally Null Missense Mutation Associates Strongly with Ovarian Carcinoma. *Cancer Research*, **2017**, 77, 4517-4529	10.1	18
85	The role of conformational flexibility in Baeyer-Villiger monooxygenase catalysis and structure. *Biochimica Et Biophysica Acta - Proteins and Proteomics*, **2016**, 1864, 1641-1648	4	20
84	An Entamoeba histolytica ADP-ribosyl transferase from the diphtheria toxin family modifies the bacterial elongation factor Tu. *Molecular and Biochemical Parasitology*, **2016**, 207, 68-74	1.9	1
83	Structural Analysis of the Tobramycin and Gentamicin Clinical Resistome Reveals Limitations for Next-generation Aminoglycoside Design. *ACS Chemical Biology*, **2016**, 11, 1339-46	4.9	18
82	Germline and somatic FGFR1 abnormalities in dysembryoplastic neuroepithelial tumors. *Acta Neuropathologica*, **2016**, 131, 847-63	14.3	105
81	Drug-target networks in aminoglycoside resistance: hierarchy of priority in structural drug design. *MedChemComm*, **2016**, 7, 103-113	5	21
80	Comprehensive characterization of ligand-induced plasticity changes in a dimeric enzyme. *FEBS Journal*, **2016**, 283, 3029-38	5.7	3
79	Antibiotic Binding Drives Catalytic Activation of Aminoglycoside Kinase APH(2?)-Ia. *Structure*, **2016**, 24, 935-45	5.2	8
78	Inhibition of outer membrane proteases of the omptin family by aprotinin. *Infection and Immunity*, **2015**, 83, 2300-11	3.7	17
77	Derivatives of mesoxalic acid block translocation of HIV-1 reverse transcriptase. *Journal of Biological Chemistry*, **2015**, 290, 1474-84	5.4	13
76	Probing the molecular and structural elements of ligands binding to the active site versus an allosteric pocket of the human farnesyl pyrophosphate synthase. *Bioorganic and Medicinal Chemistry Letters*, **2015**, 25, 1117-23	2.9	13
75	Overlapping and distinct roles of Aspergillus fumigatus UDP-glucose 4-epimerases in galactose metabolism and the synthesis of galactose-containing cell wall polysaccharides. *Journal of Biological Chemistry*, **2014**, 289, 1243-56	5.4	74

74	Maintenance of native-like protein dynamics may not be required for engineering functional proteins. *Chemistry and Biology*, **2014**, 21, 1330-1340		26
73	Substrate-dependent switching of the allosteric binding mechanism of a dimeric enzyme. *Nature Chemical Biology*, **2014**, 10, 937-42	11.7	17
72	Multistage screening reveals chameleon ligands of the human farnesyl pyrophosphate synthase: implications to drug discovery for neurodegenerative diseases. *Journal of Medicinal Chemistry*, **2014** , 57, 5764-76	8.3	25
71	Functional characterization of the human dendritic cell immunodeficiency associated with the IRF8(K108E) mutation. *Blood*, **2014**, 124, 1894-904	2.2	51
70	Human isoprenoid synthase enzymes as therapeutic targets. *Frontiers in Chemistry*, **2014**, 2, 50	5	32
69	Lactone-bound structures of cyclohexanone monooxygenase provide insight into the stereochemistry of catalysis. *ACS Chemical Biology*, **2014**, 9, 2843-51	4.9	34
68	Structure of human farnesyl pyrophosphate synthase in complex with an aminopyridine bisphosphonate and two molecules of inorganic phosphate. *Acta Crystallographica Section F, Structural Biology Communications*, **2014**, 70, 299-304	1.1	9
67	Thienopyrimidine bisphosphonate (ThPBP) inhibitors of the human farnesyl pyrophosphate synthase: optimization and characterization of the mode of inhibition. *Journal of Medicinal Chemistry*, **2013**, 56, 7939-50	8.3	39
66	A recurrent PDGFRB mutation causes familial infantile myofibromatosis. *American Journal of Human Genetics*, **2013**, 92, 996-1000	11	108
65	Identification of the adenovirus E4orf4 protein binding site on the B55□and Cdc55 regulatory subunits of PP2A: Implications for PP2A function, tumor cell killing and viral replication. *PLoS Pathogens*, **2013**, 9, e1003742	7.6	14
64	Structural analysis of a novel cyclohexylamine oxidase from Brevibacterium oxydans IH-35A. *PLoS ONE*, **2013**, 8, e60072	3.7	18
63	Prospects for circumventing aminoglycoside kinase mediated antibiotic resistance. *Frontiers in Cellular and Infection Microbiology*, **2013**, 3, 22	5.9	37
62	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□active site closure. *BMC Structural Biology*, **2012**, 12, 32	2.7	21
61	The substrate-bound crystal structure of a Baeyer-Villiger monooxygenase exhibits a Criegee-like conformation. *Journal of the American Chemical Society*, **2012**, 134, 7788-95	16.4	70
60	Design and synthesis of active site inhibitors of the human farnesyl pyrophosphate synthase: apoptosis and inhibition of ERK phosphorylation in multiple myeloma cells. *Journal of Medicinal Chemistry*, **2012**, 55, 3201-15	8.3	43
59	Structural basis for dual nucleotide selectivity of aminoglycoside 2□phosphotransferase IVa provides insight on determinants of nucleotide specificity of aminoglycoside kinases. *Journal of Biological Chemistry*, **2012**, 287, 13094-102	5.4	22
58	Small-angle X-ray scattering analysis of the bifunctional antibiotic resistance enzyme aminoglycoside (6□acetyltransferase-ie/aminoglycoside (2□phosphotransferase-ia reveals a rigid solution structure. *Antimicrobial Agents and Chemotherapy*, **2012**, 56, 1899-906	5.9	22
57	IRF8 mutations and human dendritic-cell immunodeficiency. *New England Journal of Medicine*, **2011**, 365, 127-38	59.2	469

56	Competing allosteric mechanisms modulate substrate binding in a dimeric enzyme. *Nature Structural and Molecular Biology*, **2011**, 18, 288-94	17.6	67
55	Novel crystallization conditions for tandem variant R67 DHFR yield a wild-type crystal structure. *Acta Crystallographica Section F: Structural Biology Communications*, **2011**, 67, 1316-22		8
54	Crystal structures of antibiotic-bound complexes of aminoglycoside 2″-phosphotransferase IVa highlight the diversity in substrate binding modes among aminoglycoside kinases. *Biochemistry*, **2011**, 50, 6237-44	3.2	19
53	Genetic analysis of B55alpha/Cdc55 protein phosphatase 2A subunits: association with the adenovirus E4orf4 protein. *Journal of Virology*, **2011**, 85, 286-95	6.6	11
52	Crystal structures of two aminoglycoside kinases bound with a eukaryotic protein kinase inhibitor. *PLoS ONE*, **2011**, 6, e19589	3.7	22
51	Structure of the antibiotic resistance factor spectinomycin phosphotransferase from Legionella pneumophila. *Journal of Biological Chemistry*, **2010**, 285, 9545-9555	5.4	31
50	Sustained Development in Baeyer-Villiger Biooxidation Technology. *ACS Symposium Series*, **2010**, 343-372	0.4	5
49	Protein tyrosine phosphatases are regulated by mononuclear iron dicitrate. *Journal of Biological Chemistry*, **2010**, 285, 24620-8	5.4	16
48	Multiple conformers in active site of human dihydrofolate reductase F31R/Q35E double mutant suggest structural basis for methotrexate resistance. *Journal of Biological Chemistry*, **2009**, 284, 20079-89	5.4	30
47	Structural basis of APH(3″)-IIIa-mediated resistance to N1-substituted aminoglycoside antibiotics. *Antimicrobial Agents and Chemotherapy*, **2009**, 53, 3049-55	5.9	22
46	Crystal structures of cyclohexanone monooxygenase reveal complex domain movements and a sliding cofactor. *Journal of the American Chemical Society*, **2009**, 131, 8848-54	16.4	135
45	Expression and purification of recombinant M-Pol I from Saccharomyces cerevisiae with alpha-1,6 mannosylpolymerase activity. *Protein Expression and Purification*, **2009**, 66, 1-6	2	14
44	Preparation and characterization of bacterial protein complexes for structural analysis. *Advances in Protein Chemistry and Structural Biology*, **2009**, 76, 1-42	5.3	4
43	Flagellin glycosylation in Pseudomonas aeruginosa PAK requires the O-antigen biosynthesis enzyme WbpO. *Journal of Biological Chemistry*, **2008**, 283, 3507-3518	5.4	35
42	The type IA topoisomerase catalytic cycle: A normal mode analysis and molecular dynamics simulation. *Proteins: Structure, Function and Bioinformatics*, **2008**, 71, 1984-94	4.2	11
41	Structural basis for streptogramin B resistance in Staphylococcus aureus by virginiamycin B lyase. *Proceedings of the National Academy of Sciences of the United States of America*, **2007**, 104, 10388-93	11.5	33
40	Structural basis for ubiquitin-mediated dimerization and activation of the ubiquitin protein ligase Cbl-b. *Molecular Cell*, **2007**, 27, 474-85	17.6	85
39	Structural studies of FlaA1 from Helicobacter pylori reveal the mechanism for inverting 4,6-dehydratase activity. *Journal of Biological Chemistry*, **2006**, 281, 24489-95	5.4	43

38	Synthesis and structure-activity relationships of truncated bisubstrate inhibitors of aminoglycoside 6Q-N-acetyltransferases. *Journal of Medicinal Chemistry*, **2006**, 49, 5273-81	8.3	66
37	Identification and characterization of a protein-tyrosine phosphatase in Leishmania: Involvement in virulence. *Journal of Biological Chemistry*, **2006**, 281, 36257-68	5.4	31
36	Crystal structure of CTP:glycerol-3-phosphate cytidylyltransferase from Staphylococcus aureus: examination of structural basis for kinetic mechanism. *Biochimica Et Biophysica Acta - Proteins and Proteomics*, **2006**, 1764, 63-9	4	16
35	Crystal structure of homoserine transacetylase from Haemophilus influenzae reveals a new family of alpha/beta-hydrolases. *Biochemistry*, **2005**, 44, 15768-73	3.2	39
34	Towards a better understanding of the substrate specificity of the UDP-N-acetylglucosamine C4 epimerase WbpP. *Biochemical Journal*, **2005**, 389, 173-80	3.8	20
33	Regio- and chemoselective 6Q-N-derivatization of aminoglycosides: bisubstrate inhibitors as probes to study aminoglycoside 6Q-N-acetyltransferases. *Angewandte Chemie - International Edition*, **2005**, 44, 6859-62	16.4	52
32	Regio- and Chemoselective 6?-N-Derivatization of Aminoglycosides: Bisubstrate Inhibitors as Probes To Study Aminoglycoside 6?-N-Acetyltransferases. *Angewandte Chemie*, **2005**, 117, 7019-7022	3.6	11
31	Structures of aminoglycoside acetyltransferase AAC(6Q)-Ii in a novel crystal form: structural and normal-mode analyses. *Acta Crystallographica Section D: Biological Crystallography*, **2005**, 61, 1273-9		22
30	Crystallization and preliminary crystallographic analysis of an aminoglycoside kinase from Legionella pneumophila. *Acta Crystallographica Section F: Structural Biology Communications*, **2005**, 61, 606-8		4
29	A single bifunctional UDP-GlcNAc/Glc 4-epimerase supports the synthesis of three cell surface glycoconjugates in Campylobacter jejuni. *Journal of Biological Chemistry*, **2005**, 280, 4792-802	5.4	100
28	Magnesium and phosphate ions enable NAD binding to methylenetetrahydrofolate dehydrogenase-methenyltetrahydrofolate cyclohydrolase. *Journal of Biological Chemistry*, **2005**, 280, 34316-23	5.4	20
27	Crystal structure of WbpP, a genuine UDP-N-acetylglucosamine 4-epimerase from Pseudomonas aeruginosa: substrate specificity in udp-hexose 4-epimerases. *Journal of Biological Chemistry*, **2004**, 279, 22635-42	5.4	67
26	Crystallization and preliminary crystallographic analysis of 3Q-aminoglycoside kinase type IIIa complexed with a eukaryotic protein kinase inhibitor, CKI-7. *Acta Crystallographica Section D: Biological Crystallography*, **2004**, 60, 1897-9		5
25	New phenolic inhibitors of yeast homoserine dehydrogenase. *Bioorganic and Medicinal Chemistry*, **2004**, 12, 3825-30	3.4	22
24	Enzyme-assisted suicide: molecular basis for the antifungal activity of 5-hydroxy-4-oxonorvaline by potent inhibition of homoserine dehydrogenase. *Chemistry and Biology*, **2003**, 10, 989-95		23
23	X-ray structure of the AAC(6Q)-Ii antibiotic resistance enzyme at 1.8 A resolution; examination of oligomeric arrangements in GNAT superfamily members. *Protein Science*, **2003**, 12, 426-37	6.3	75
22	Protein kinase inhibitors and antibiotic resistance **2002**, 93, 283-92		22
21	Substrate promiscuity of an aminoglycoside antibiotic resistance enzyme via target mimicry. *EMBO Journal*, **2002**, 21, 2323-31	13	118

20	Mechanism of aminoglycoside antibiotic kinase APH(3')-IIIa: role of the nucleotide positioning loop. *Biochemistry*, **2002**, 41, 7001-7	3.2	40
19	Crystallization and preliminary X-ray diffraction studies of glycerol 3-phosphate cytidylyltransferase from Staphylococcus aureus. *Acta Crystallographica Section D: Biological Crystallography*, **2001**, 57, 918-20		3
18	Resistance to aminoglycoside Antibiotics: Function meets structure. *Focus on Biotechnology*, **2001**, 85-98		
17	Crystal structures of homoserine dehydrogenase suggest a novel catalytic mechanism for oxidoreductases. *Nature Structural Biology*, **2000**, 7, 238-44		38
16	The COOH terminus of aminoglycoside phosphotransferase (3')-IIIa is critical for antibiotic recognition and resistance. *Journal of Biological Chemistry*, **1999**, 274, 30697-706	5.4	30
15	Crystal structure of an aminoglycoside 6'-N-acetyltransferase: defining the GCN5-related N-acetyltransferase superfamily fold. *Structure*, **1999**, 7, 497-507	5.2	127
14	Crystallization and preliminary X-ray diffraction studies of homoserine dehydrogenase from Saccharomyces cerevisiae. *Acta Crystallographica Section D: Biological Crystallography*, **1998**, 54, 413-5		2
13	Aminoglycoside Antibiotics. *Advances in Experimental Medicine and Biology*, **1998**, 27-69	3.6	111
12	Structure of an enzyme required for aminoglycoside antibiotic resistance reveals homology to eukaryotic protein kinases. *Cell*, **1997**, 89, 887-95	56.2	217
11	The role of a conserved water molecule in the redox-dependent thermal stability of iso-1-cytochrome c. *Journal of Biological Chemistry*, **1996**, 271, 29088-93	5.4	42
10	Mechanistic and structural contributions of critical surface and internal residues to cytochrome c electron transfer reactivity. *Biochemistry*, **1996**, 35, 10784-92	3.2	28
9	Structure of the GDP-Pi complex of Gly203-->Ala gialpha1: a mimic of the ternary product complex of galpha-catalyzed GTP hydrolysis. *Structure*, **1996**, 4, 1277-90	5.2	53
8	Structure of the first C2 domain of synaptotagmin I: a novel Ca2+/phospholipid-binding fold. *Cell*, **1995**, 80, 929-38	56.2	613
7	Mutation of tyrosine-67 to phenylalanine in cytochrome c significantly alters the local heme environment. *Journal of Molecular Biology*, **1994**, 235, 1326-41	6.5	83
6	The role of a conserved internal water molecule and its associated hydrogen bond network in cytochrome c. *Journal of Molecular Biology*, **1994**, 236, 786-99	6.5	110
5	Crystallization and preliminary crystallographic studies of Gi alpha 1 and mutants of Gi alpha 1 in the GTP and GDP-bound states. *Journal of Molecular Biology*, **1994**, 238, 630-4	6.5	45
4	Isolation, crystallization and preliminary diffraction analyses of human pancreatic alpha-amylase. *Journal of Molecular Biology*, **1993**, 230, 1084-5	6.5	9
3	Oxidation state-dependent conformational changes in cytochrome c. *Journal of Molecular Biology*, **1992**, 223, 959-76	6.5	364

2	Lactose binding to heat-labile enterotoxin revealed by X-ray crystallography. *Nature*, **1992**, 355, 561-4	50.4	201
1	Structural Aspects of Aminoglycoside-Modifying Enzymes21-33		3