

# Albert M Berghuis

## List of Publications by Citations

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papers

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34  
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69  
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109  
ext. papers

5,597  
ext. citations

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5.14  
L-index

#	Paper	IF	Citations
109	Structure of the first C2 domain of synaptotagmin I: a novel Ca <sup>2+</sup> /phospholipid-binding fold. <i>Cell</i> , <b>1995</b> , 80, 929-38	56.2	613
108	IRF8 mutations and human dendritic-cell immunodeficiency. <i>New England Journal of Medicine</i> , <b>2011</b> , 365, 127-38	59.2	469
107	Oxidation state-dependent conformational changes in cytochrome c. <i>Journal of Molecular Biology</i> , <b>1992</b> , 223, 959-76	6.5	364
106	Structure of an enzyme required for aminoglycoside antibiotic resistance reveals homology to eukaryotic protein kinases. <i>Cell</i> , <b>1997</b> , 89, 887-95	56.2	217
105	Lactose binding to heat-labile enterotoxin revealed by X-ray crystallography. <i>Nature</i> , <b>1992</b> , 355, 561-4	50.4	201
104	Crystal structures of cyclohexanone monooxygenase reveal complex domain movements and a sliding cofactor. <i>Journal of the American Chemical Society</i> , <b>2009</b> , 131, 8848-54	16.4	135
103	Crystal structure of an aminoglycoside 6QN-acetyltransferase: defining the GCN5-related N-acetyltransferase superfamily fold. <i>Structure</i> , <b>1999</b> , 7, 497-507	5.2	127
102	Substrate promiscuity of an aminoglycoside antibiotic resistance enzyme via target mimicry. <i>EMBO Journal</i> , <b>2002</b> , 21, 2323-31	13	118
101	Aminoglycoside Antibiotics. <i>Advances in Experimental Medicine and Biology</i> , <b>1998</b> , 27-69	3.6	111
100	The role of a conserved internal water molecule and its associated hydrogen bond network in cytochrome c. <i>Journal of Molecular Biology</i> , <b>1994</b> , 236, 786-99	6.5	110
99	A recurrent PDGFRB mutation causes familial infantile myofibromatosis. <i>American Journal of Human Genetics</i> , <b>2013</b> , 92, 996-1000	11	108
98	Germline and somatic FGFR1 abnormalities in dysembryoplastic neuroepithelial tumors. <i>Acta Neuropathologica</i> , <b>2016</b> , 131, 847-63	14.3	105
97	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> , <b>2005</b> , 280, 4792-802	5.4	100
96	Structural basis for ubiquitin-mediated dimerization and activation of the ubiquitin protein ligase Cbl-b. <i>Molecular Cell</i> , <b>2007</b> , 27, 474-85	17.6	85
95	Mutation of tyrosine-67 to phenylalanine in cytochrome c significantly alters the local heme environment. <i>Journal of Molecular Biology</i> , <b>1994</b> , 235, 1326-41	6.5	83
94	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> , <b>2003</b> , 12, 426-37	6.3	75
93	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> , <b>2014</b> , 289, 1243-56	5.4	74

92	The substrate-bound crystal structure of a Baeyer-Villiger monooxygenase exhibits a Criegee-like conformation. <i>Journal of the American Chemical Society</i> , <b>2012</b> , 134, 7788-95	16.4	70
91	Competing allosteric mechanisms modulate substrate binding in a dimeric enzyme. <i>Nature Structural and Molecular Biology</i> , <b>2011</b> , 18, 288-94	17.6	67
90	Crystal structure of WbpP, a genuine UDP-N-acetylglucosamine 4-epimerase from <i>Pseudomonas aeruginosa</i> : substrate specificity in udp-hexose 4-epimerases. <i>Journal of Biological Chemistry</i> , <b>2004</b> , 279, 22635-42	5.4	67
89	Synthesis and structure-activity relationships of truncated bisubstrate inhibitors of aminoglycoside 6Q-acetyltransferases. <i>Journal of Medicinal Chemistry</i> , <b>2006</b> , 49, 5273-81	8.3	66
88	Structure of the GDP-Pi complex of Gly203-->Ala galpha1: a mimic of the ternary product complex of galpha-catalyzed GTP hydrolysis. <i>Structure</i> , <b>1996</b> , 4, 1277-90	5.2	53
87	Regio- and chemoselective 6Q-derivatization of aminoglycosides: bisubstrate inhibitors as probes to study aminoglycoside 6Q-acetyltransferases. <i>Angewandte Chemie - International Edition</i> , <b>2005</b> , 44, 6859-62	16.4	52
86	Functional characterization of the human dendritic cell immunodeficiency associated with the IRF8(K108E) mutation. <i>Blood</i> , <b>2014</b> , 124, 1894-904	2.2	51
85	Crystallization and preliminary crystallographic studies of Gi alpha 1 and mutants of Gi alpha 1 in the GTP and GDP-bound states. <i>Journal of Molecular Biology</i> , <b>1994</b> , 238, 630-4	6.5	45
84	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> , <b>2012</b> , 55, 3201-15	8.3	43
83	Structural studies of FlaA1 from <i>Helicobacter pylori</i> reveal the mechanism for inverting 4,6-dehydratase activity. <i>Journal of Biological Chemistry</i> , <b>2006</b> , 281, 24489-95	5.4	43
82	The role of a conserved water molecule in the redox-dependent thermal stability of iso-1-cytochrome c. <i>Journal of Biological Chemistry</i> , <b>1996</b> , 271, 29088-93	5.4	42
81	Mechanism of aminoglycoside antibiotic kinase APH(3Q)IIIa: role of the nucleotide positioning loop. <i>Biochemistry</i> , <b>2002</b> , 41, 7001-7	3.2	40
80	Thienopyrimidine bisphosphonate (ThPBP) inhibitors of the human farnesyl pyrophosphate synthase: optimization and characterization of the mode of inhibition. <i>Journal of Medicinal Chemistry</i> , <b>2013</b> , 56, 7939-50	8.3	39
79	Crystal structure of homoserine transacetylase from <i>Haemophilus influenzae</i> reveals a new family of alpha/beta-hydrolases. <i>Biochemistry</i> , <b>2005</b> , 44, 15768-73	3.2	39
78	Crystal structures of homoserine dehydrogenase suggest a novel catalytic mechanism for oxidoreductases. <i>Nature Structural Biology</i> , <b>2000</b> , 7, 238-44		38
77	Prospects for circumventing aminoglycoside kinase mediated antibiotic resistance. <i>Frontiers in Cellular and Infection Microbiology</i> , <b>2013</b> , 3, 22	5.9	37
76	Flagellin glycosylation in <i>Pseudomonas aeruginosa</i> PAK requires the O-antigen biosynthesis enzyme WbpO. <i>Journal of Biological Chemistry</i> , <b>2008</b> , 283, 3507-3518	5.4	35
75	Lactone-bound structures of cyclohexanone monooxygenase provide insight into the stereochemistry of catalysis. <i>ACS Chemical Biology</i> , <b>2014</b> , 9, 2843-51	4.9	34

74	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> , <b>2007</b> , 104, 10388-93	11.5	33
73	Look and Outlook on Enzyme-Mediated Macrolide Resistance. <i>Frontiers in Microbiology</i> , <b>2018</b> , 9, 1942	5.7	33
72	Human isoprenoid synthase enzymes as therapeutic targets. <i>Frontiers in Chemistry</i> , <b>2014</b> , 2, 50	5	32
71	Structure of the antibiotic resistance factor spectinomycin phosphotransferase from <i>Legionella pneumophila</i> . <i>Journal of Biological Chemistry</i> , <b>2010</b> , 285, 9545-9555	5.4	31
70	Identification and characterization of a protein-tyrosine phosphatase in <i>Leishmania</i> : Involvement in virulence. <i>Journal of Biological Chemistry</i> , <b>2006</b> , 281, 36257-68	5.4	31
69	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> , <b>2009</b> , 284, 20079-85	5.4	30
68	The COOH terminus of aminoglycoside phosphotransferase (3Q11la) is critical for antibiotic recognition and resistance. <i>Journal of Biological Chemistry</i> , <b>1999</b> , 274, 30697-706	5.4	30
67	TRPV4 and KRAS and FGFR1 gain-of-function mutations drive giant cell lesions of the jaw. <i>Nature Communications</i> , <b>2018</b> , 9, 4572	17.4	30
66	Histone H3.3G34-Mutant Interneuron Progenitors Co-opt PDGFRA for Gliomagenesis. <i>Cell</i> , <b>2020</b> , 183, 1617-1633.e22	56.2	29
65	Mechanistic and structural contributions of critical surface and internal residues to cytochrome c electron transfer reactivity. <i>Biochemistry</i> , <b>1996</b> , 35, 10784-92	3.2	28
64	Maintenance of native-like protein dynamics may not be required for engineering functional proteins. <i>Chemistry and Biology</i> , <b>2014</b> , 21, 1330-1340		26
63	Human farnesyl pyrophosphate synthase is allosterically inhibited by its own product. <i>Nature Communications</i> , <b>2017</b> , 8, 14132	17.4	25
62	Multistage screening reveals chameleon ligands of the human farnesyl pyrophosphate synthase: implications to drug discovery for neurodegenerative diseases. <i>Journal of Medicinal Chemistry</i> , <b>2014</b> , 57, 5764-76	8.3	25
61	Enzyme-assisted suicide: molecular basis for the antifungal activity of 5-hydroxy-4-oxonorvaline by potent inhibition of homoserine dehydrogenase. <i>Chemistry and Biology</i> , <b>2003</b> , 10, 989-95		23
60	Unraveling the Prenylation-Cancer Paradox in Multiple Myeloma with Novel Geranylgeranyl Pyrophosphate Synthase (GGPPS) Inhibitors. <i>Journal of Medicinal Chemistry</i> , <b>2018</b> , 61, 6904-6917	8.3	22
59	Structural basis of APH(3Q11la)-mediated resistance to N1-substituted aminoglycoside antibiotics. <i>Antimicrobial Agents and Chemotherapy</i> , <b>2009</b> , 53, 3049-55	5.9	22
58	Structural basis for dual nucleotide selectivity of aminoglycoside 2Q phosphotransferase IVa provides insight on determinants of nucleotide specificity of aminoglycoside kinases. <i>Journal of Biological Chemistry</i> , <b>2012</b> , 287, 13094-102	5.4	22
57	Small-angle X-ray scattering analysis of the bifunctional antibiotic resistance enzyme aminoglycoside (6Q)acetyltransferase- <i>ie</i> /aminoglycoside (2Q)phosphotransferase- <i>ia</i> reveals a rigid solution structure. <i>Antimicrobial Agents and Chemotherapy</i> , <b>2012</b> , 56, 1899-906	5.9	22

56	New phenolic inhibitors of yeast homoserine dehydrogenase. <i>Bioorganic and Medicinal Chemistry</i> , <b>2004</b> , 12, 3825-30	3.4	22
55	Protein kinase inhibitors and antibiotic resistance <b>2002</b> , 93, 283-92		22
54	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> , <b>2005</b> , 61, 1273-9		22
53	Crystal structures of two aminoglycoside kinases bound with a eukaryotic protein kinase inhibitor. <i>PLoS ONE</i> , <b>2011</b> , 6, e19589	3.7	22
52	Drug-target networks in aminoglycoside resistance: hierarchy of priority in structural drug design. <i>MedChemComm</i> , <b>2016</b> , 7, 103-113	5	21
51	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> , <b>2012</b> , 12, 32	2.7	21
50	The role of conformational flexibility in Baeyer-Villiger monooxygenase catalysis and structure. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , <b>2016</b> , 1864, 1641-1648	4	20
49	Towards a better understanding of the substrate specificity of the UDP-N-acetylglucosamine C4 epimerase WbpP. <i>Biochemical Journal</i> , <b>2005</b> , 389, 173-80	3.8	20
48	Magnesium and phosphate ions enable NAD binding to methylenetetrahydrofolate dehydrogenase-methenyltetrahydrofolate cyclohydrolase. <i>Journal of Biological Chemistry</i> , <b>2005</b> , 280, 34316-23	5.4	20
47	Crystal structures of antibiotic-bound complexes of aminoglycoside 2-phosphotransferase IVa highlight the diversity in substrate binding modes among aminoglycoside kinases. <i>Biochemistry</i> , <b>2011</b> , 50, 6237-44	3.2	19
46	Structural Analysis of the Tobramycin and Gentamicin Clinical Resistome Reveals Limitations for Next-generation Aminoglycoside Design. <i>ACS Chemical Biology</i> , <b>2016</b> , 11, 1339-46	4.9	18
45	Functionally Null Missense Mutation Associates Strongly with Ovarian Carcinoma. <i>Cancer Research</i> , <b>2017</b> , 77, 4517-4529	10.1	18
44	Structural analysis of a novel cyclohexylamine oxidase from <i>Brevibacterium oxydans</i> IH-35A. <i>PLoS ONE</i> , <b>2013</b> , 8, e60072	3.7	18
43	Structural Basis for Kinase-Mediated Macrolide Antibiotic Resistance. <i>Structure</i> , <b>2017</b> , 25, 750-761.e5	5.2	17
42	Inhibition of outer membrane proteases of the ompT family by aprotinin. <i>Infection and Immunity</i> , <b>2015</b> , 83, 2300-11	3.7	17
41	Substrate-dependent switching of the allosteric binding mechanism of a dimeric enzyme. <i>Nature Chemical Biology</i> , <b>2014</b> , 10, 937-42	11.7	17
40	Pharmacophore Mapping of Thienopyrimidine-Based Monophosphonate (ThP-MP) Inhibitors of the Human Farnesyl Pyrophosphate Synthase. <i>Journal of Medicinal Chemistry</i> , <b>2017</b> , 60, 2119-2134	8.3	16
39	Protein tyrosine phosphatases are regulated by mononuclear iron dicitrate. <i>Journal of Biological Chemistry</i> , <b>2010</b> , 285, 24620-8	5.4	16

38	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> , <b>2006</b> , 1764, 63-9	4	16
37	DGCR8 microprocessor defect characterizes familial multinodular goiter with schwannomatosis. <i>Journal of Clinical Investigation</i> , <b>2020</b> , 130, 1479-1490	15.9	15
36	Identification of the adenovirus E4orf4 protein binding site on the B55 $\alpha$ and Cdc55 regulatory subunits of PP2A: Implications for PP2A function, tumor cell killing and viral replication. <i>PLoS Pathogens</i> , <b>2013</b> , 9, e1003742	7.6	14
35	Expression and purification of recombinant M-Pol I from <i>Saccharomyces cerevisiae</i> with alpha-1,6 mannosylpolymerase activity. <i>Protein Expression and Purification</i> , <b>2009</b> , 66, 1-6	2	14
34	Derivatives of mesoxalic acid block translocation of HIV-1 reverse transcriptase. <i>Journal of Biological Chemistry</i> , <b>2015</b> , 290, 1474-84	5.4	13
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> , <b>2015</b> , 25, 1117-23	2.9	13
32	Genetic analysis of B55 $\alpha$ /Cdc55 protein phosphatase 2A subunits: association with the adenovirus E4orf4 protein. <i>Journal of Virology</i> , <b>2011</b> , 85, 286-95	6.6	11
31	The type IA topoisomerase catalytic cycle: A normal mode analysis and molecular dynamics simulation. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2008</b> , 71, 1984-94	4.2	11
30	Regio- and Chemoselective 6'-N-Derivatization of Aminoglycosides: Bisubstrate Inhibitors as Probes To Study Aminoglycoside 6'-N-Acetyltransferases. <i>Angewandte Chemie</i> , <b>2005</b> , 117, 7019-7022	3.6	11
29	A potential gain-of-function variant of SLC9A6 leads to endosomal alkalinization and neuronal atrophy associated with Christianson Syndrome. <i>Neurobiology of Disease</i> , <b>2019</b> , 121, 187-204	7.5	11
28	The Structural Dynamics of Engineered $\beta$ -Lactamases Vary Broadly on Three Timescales yet Sustain Native Function. <i>Scientific Reports</i> , <b>2019</b> , 9, 6656	4.9	9
27	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> , <b>2014</b> , 70, 299-304	1.1	9
26	Isolation, crystallization and preliminary diffraction analyses of human pancreatic alpha-amylase. <i>Journal of Molecular Biology</i> , <b>1993</b> , 230, 1084-5	6.5	9
25	Novel crystallization conditions for tandem variant R67 DHFR yield a wild-type crystal structure. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , <b>2011</b> , 67, 1316-22		8
24	Antibiotic Binding Drives Catalytic Activation of Aminoglycoside Kinase APH(2?)-Ia. <i>Structure</i> , <b>2016</b> , 24, 935-45	5.2	8
23	Crystallographic and thermodynamic characterization of phenylaminopyridine bisphosphonates binding to human farnesyl pyrophosphate synthase. <i>PLoS ONE</i> , <b>2017</b> , 12, e0186447	3.7	5
22	Plasticity of Aminoglycoside Binding to Antibiotic Kinase APH(2?)-Ia. <i>Antimicrobial Agents and Chemotherapy</i> , <b>2018</b> , 62,	5.9	5
21	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> , <b>2019</b> , 4, 10056-10069	3.9	5

20	Sustained Development in Baeyer-Villiger Biooxidation Technology. <i>ACS Symposium Series</i> , <b>2010</b> , 343-370.4	5
19	Crystallization and preliminary crystallographic analysis of 3Qaminoglycoside kinase type IIIa complexed with a eukaryotic protein kinase inhibitor, CKI-7. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2004</b> , 60, 1897-9	5
18	Preparation and characterization of bacterial protein complexes for structural analysis. <i>Advances in Protein Chemistry and Structural Biology</i> , <b>2009</b> , 76, 1-42	5.3 4
17	Crystallization and preliminary crystallographic analysis of an aminoglycoside kinase from <i>Legionella pneumophila</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , <b>2005</b> , 61, 606-8	4
16	Structural and functional insights into esterase-mediated macrolide resistance. <i>Nature Communications</i> , <b>2021</b> , 12, 1732	17.4 4
15	Structural basis for plazomicin antibiotic action and resistance. <i>Communications Biology</i> , <b>2021</b> , 4, 729	6.7 4
14	Phosphonate and Bisphosphonate Inhibitors of Farnesyl Pyrophosphate Synthases: A Structure-Guided Perspective. <i>Frontiers in Chemistry</i> , <b>2020</b> , 8, 612728	5 4
13	Chirality-Driven Mode of Binding of E-Aminophosphonic Acid-Based Allosteric Inhibitors of the Human Farnesyl Pyrophosphate Synthase (hFPPS). <i>Journal of Medicinal Chemistry</i> , <b>2019</b> , 62, 9691-9702	8.3 3
12	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> , <b>2001</b> , 57, 918-20	3
11	Structural Aspects of Aminoglycoside-Modifying Enzymes21-33	3
10	Comprehensive characterization of ligand-induced plasticity changes in a dimeric enzyme. <i>FEBS Journal</i> , <b>2016</b> , 283, 3029-38	5.7 3
9	ZBTB7B (ThPOK) Is Required for Pathogenesis of Cerebral Malaria and Protection against Pulmonary Tuberculosis. <i>Infection and Immunity</i> , <b>2020</b> , 88,	3.7 2
8	Effect of solvent and protein dynamics in ligand recognition and inhibition of aminoglycoside adenylyltransferase 2?-Ia. <i>Protein Science</i> , <b>2017</b> , 26, 1852-1863	6.3 2
7	Crystallization and preliminary X-ray diffraction studies of homoserine dehydrogenase from <i>Saccharomyces cerevisiae</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>1998</b> , 54, 413-5	2
6	Structural and phylogenetic analyses of resistance to next-generation aminoglycosides conferred by AAC(2Q)enzymes. <i>Scientific Reports</i> , <b>2021</b> , 11, 11614	4.9 2
5	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> , <b>2016</b> , 207, 68-74	1.9 1
4	Bisphosphoglycerate Mutase Deficiency Protects against Cerebral Malaria and Severe Malaria-Induced Anemia. <i>Cell Reports</i> , <b>2020</b> , 32, 108170	10.6 1
3	De novo 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> , <b>2021</b> ,	5.8 1

- 2 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
- 1 Resistance to aminoglycoside Antibiotics: Function meets structure. *Focus on Biotechnology*, **2001**, 85-98