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List of Publications by Year in Descending Order

114 papers	7,046 citations	52 h-index	81 g-index
114 ext. papers	7,284 ext. citations	4.9 avg, IF	5.97 L-index

#	Paper	IF	Citations
114	Thiol-reactive drug substrates of human P-glycoprotein label the same sites to activate ATPase activity in membranes or dodecyl maltoside detergent micelles. *Biochemical and Biophysical Research Communications*, **2017**, 488, 573-577	3.4	4
113	Corrector VX-809 promotes interactions between cytoplasmic loop one and the first nucleotide-binding domain of CFTR. *Biochemical Pharmacology*, **2017**, 136, 24-31	6	31
112	Attachment of a Rmolecular springRrestores drug-stimulated ATPase activity to P-glycoprotein lacking both Q loop glutamines. *Biochemical and Biophysical Research Communications*, **2017**, 483, 366-370	3.4	12
111	A short cross-linker activates human P-glycoprotein missing a catalytic carboxylate. *Biochemical Pharmacology*, **2017**, 145, 27-33	6	2
110	P-glycoprotein ATPase activity requires lipids to activate a switch at the first transmission interface. *Biochemical and Biophysical Research Communications*, **2016**, 472, 379-83	3.4	18
109	Drugs Modulate Interactions between the First Nucleotide-Binding Domain and the Fourth Cytoplasmic Loop of Human P-Glycoprotein. *Biochemistry*, **2016**, 55, 2817-20	3.2	5
108	The Transmission Interfaces Contribute Asymmetrically to the Assembly and Activity of Human P-glycoprotein. *Journal of Biological Chemistry*, **2015**, 290, 16954-63	5.4	21
107	Mapping the Binding Site of the Inhibitor Tariquidar That Stabilizes the First Transmembrane Domain of P-glycoprotein. *Journal of Biological Chemistry*, **2015**, 290, 29389-401	5.4	32
106	Locking intracellular helices 2 and 3 together inactivates human P-glycoprotein. *Journal of Biological Chemistry*, **2014**, 289, 229-36	5.4	18
105	Cysteines introduced into extracellular loops 1 and 4 of human P-glycoprotein that are close only in the open conformation spontaneously form a disulfide bond that inhibits drug efflux and ATPase activity. *Journal of Biological Chemistry*, **2014**, 289, 24749-58	5.4	10
104	Tariquidar inhibits P-glycoprotein drug efflux but activates ATPase activity by blocking transition to an open conformation. *Biochemical Pharmacology*, **2014**, 92, 558-66	6	35
103	Identification of the distance between the homologous halves of P-glycoprotein that triggers the high/low ATPase activity switch. *Journal of Biological Chemistry*, **2014**, 289, 8484-92	5.4	19
102	The cystic fibrosis V232D mutation inhibits CFTR maturation by disrupting a hydrophobic pocket rather than formation of aberrant interhelical hydrogen bonds. *Biochemical Pharmacology*, **2014**, 88, 46-57	6	8
101	Corrector VX-809 stabilizes the first transmembrane domain of CFTR. *Biochemical Pharmacology*, **2013**, 86, 612-9	6	73
100	A salt bridge in intracellular loop 2 is essential for folding of human p-glycoprotein. *Biochemistry*, **2013**, 52, 3194-6	3.2	20
99	Niemann-Pick NPC1: sterols to the rescue and beyond. *Chemistry and Biology*, **2013**, 20, 297-8		3
98	Bithiazole correctors rescue CFTR mutants by two different mechanisms. *Biochemistry*, **2013**, 52, 5161-3	3.2	13

97	Drug rescue distinguishes between different structural models of human P-glycoprotein. *Biochemistry*, **2013**, 52, 7167-9	3.2	18
96	Human P-glycoprotein contains a greasy ball-and-socket joint at the second transmission interface. *Journal of Biological Chemistry*, **2013**, 288, 20326-33	5.4	36
95	Corrector-mediated rescue of misprocessed CFTR mutants can be reduced by the P-glycoprotein drug pump. *Biochemical Pharmacology*, **2012**, 83, 345-54	6	15
94	Thiorhodamines containing amide and thioamide functionality as inhibitors of the ATP-binding cassette drug transporter P-glycoprotein (ABCB1). *Bioorganic and Medicinal Chemistry*, **2012**, 20, 4290-302	3.4	8
93	Chalcogenopyrylium compounds as modulators of the ATP-binding cassette transporters P-glycoprotein (P-gp/ABCB1) and multidrug resistance protein 1 (MRP1/ABCC1). *Journal of Medicinal Chemistry*, **2012**, 55, 4683-99	8.3	38
92	The ATPase activity of the P-glycoprotein drug pump is highly activated when the N-terminal and central regions of the nucleotide-binding domains are linked closely together. *Journal of Biological Chemistry*, **2012**, 287, 26806-16	5.4	48
91	Predicting P-glycoprotein-mediated drug transport based on support vector machine and three-dimensional crystal structure of P-glycoprotein. *PLoS ONE*, **2011**, 6, e25815	3.7	89
90	The W232R suppressor mutation promotes maturation of a truncation mutant lacking both nucleotide-binding domains and restores interdomain assembly and activity of P-glycoprotein processing mutants. *Biochemistry*, **2011**, 50, 672-85	3.2	6
89	Benzbromarone stabilizes ΔF508 CFTR at the cell surface. *Biochemistry*, **2011**, 50, 4393-5	3.2	10
88	Repair of CFTR folding defects with correctors that function as pharmacological chaperones. *Methods in Molecular Biology*, **2011**, 741, 23-37	1.4	6
87	The V510D suppressor mutation stabilizes DeltaF508-CFTR at the cell surface. *Biochemistry*, **2010**, 49, 6352-7	3.2	48
86	Human P-glycoprotein is active when the two halves are clamped together in the closed conformation. *Biochemical and Biophysical Research Communications*, **2010**, 395, 436-40	3.4	52
85	Correctors enhance maturation of DeltaF508 CFTR by promoting interactions between the two halves of the molecule. *Biochemistry*, **2009**, 48, 9882-90	3.2	31
84	Rhodamine inhibitors of P-glycoprotein: an amide/thioamide "switch" for ATPase activity. *Journal of Medicinal Chemistry*, **2009**, 52, 3328-41	8.3	50
83	Identification of residues in the drug translocation pathway of the human multidrug resistance P-glycoprotein by arginine mutagenesis. *Journal of Biological Chemistry*, **2009**, 284, 24074-87	5.4	69
82	Mutational analysis of ABC proteins. *Archives of Biochemistry and Biophysics*, **2008**, 476, 51-64	4.1	69
81	Processing mutations disrupt interactions between the nucleotide binding and transmembrane domains of P-glycoprotein and the cystic fibrosis transmembrane conductance regulator (CFTR). *Journal of Biological Chemistry*, **2008**, 283, 28190-7	5.4	66
80	Arginines in the first transmembrane segment promote maturation of a P-glycoprotein processing mutant by hydrogen bond interactions with tyrosines in transmembrane segment 11. *Journal of Biological Chemistry*, **2008**, 283, 24860-70	5.4	24

79	Correctors promote folding of the CFTR in the endoplasmic reticulum. *Biochemical Journal*, **2008**, 413, 29-36	3.8	43
78	Correctors promote maturation of cystic fibrosis transmembrane conductance regulator (CFTR)-processing mutants by binding to the protein. *Journal of Biological Chemistry*, **2007**, 282, 33247-33251	5.4	106
77	Modulating the folding of P-glycoprotein and cystic fibrosis transmembrane conductance regulator truncation mutants with pharmacological chaperones. *Molecular Pharmacology*, **2007**, 71, 751-8	4.3	66
76	Chemical and pharmacological chaperones as new therapeutic agents. *Expert Reviews in Molecular Medicine*, **2007**, 9, 1-18	6.7	83
75	Additive effect of multiple pharmacological chaperones on maturation of CFTR processing mutants. *Biochemical Journal*, **2007**, 406, 257-63	3.8	53
74	Suppressor mutations in the transmembrane segments of P-glycoprotein promote maturation of processing mutants and disrupt a subset of drug-binding sites. *Journal of Biological Chemistry*, **2007**, 282, 32043-52	5.4	38
73	Nucleotide binding, ATP hydrolysis, and mutation of the catalytic carboxylates of human P-glycoprotein cause distinct conformational changes in the transmembrane segments. *Biochemistry*, **2007**, 46, 9328-36	3.2	23
72	Specific rescue of cystic fibrosis transmembrane conductance regulator processing mutants using pharmacological chaperones. *Molecular Pharmacology*, **2006**, 70, 297-302	4.3	85
71	Insertion of an arginine residue into the transmembrane segments corrects protein misfolding. *Journal of Biological Chemistry*, **2006**, 281, 29436-40	5.4	16
70	Transmembrane segment 1 of human P-glycoprotein contributes to the drug-binding pocket. *Biochemical Journal*, **2006**, 396, 537-45	3.8	76
69	Transmembrane segment 7 of human P-glycoprotein forms part of the drug-binding pocket. *Biochemical Journal*, **2006**, 399, 351-9	3.8	88
68	The chemical chaperone CFcor-325 repairs folding defects in the transmembrane domains of CFTR-processing mutants. *Biochemical Journal*, **2006**, 395, 537-42	3.8	40
67	Using a cysteine-less mutant to provide insight into the structure and mechanism of CFTR. *Journal of Physiology*, **2006**, 572, 312	3.9	7
66	Rescue of DeltaF508 and other misprocessed CFTR mutants by a novel quinazoline compound. *Molecular Pharmaceutics*, **2005**, 2, 407-13	5.6	67
65	Do drug substrates enter the common drug-binding pocket of P-glycoprotein through "gates"?. *Biochemical and Biophysical Research Communications*, **2005**, 329, 419-22	3.4	66
64	ATP hydrolysis promotes interactions between the extracellular ends of transmembrane segments 1 and 11 of human multidrug resistance P-glycoprotein. *Biochemistry*, **2005**, 44, 10250-8	3.2	40
63	Recent progress in understanding the mechanism of P-glycoprotein-mediated drug efflux. *Journal of Membrane Biology*, **2005**, 206, 173-85	2.3	162
62	Rescue of folding defects in ABC transporters using pharmacological chaperones. *Journal of Bioenergetics and Biomembranes*, **2005**, 37, 501-7	3.7	50

61	The dileucine motif at the COOH terminus of human multidrug resistance P-glycoprotein is important for folding but not activity. *Journal of Biological Chemistry*, **2005**, 280, 2522-8	5.4	21
60	Processing mutations located throughout the human multidrug resistance P-glycoprotein disrupt interactions between the nucleotide binding domains. *Journal of Biological Chemistry*, **2004**, 279, 38395-401	5.4	22
59	The DeltaF508 mutation disrupts packing of the transmembrane segments of the cystic fibrosis transmembrane conductance regulator. *Journal of Biological Chemistry*, **2004**, 279, 39620-7	5.4	76
58	Disulfiram metabolites permanently inactivate the human multidrug resistance P-glycoprotein. *Molecular Pharmaceutics*, **2004**, 1, 426-33	5.6	51
57	The drug-binding pocket of the human multidrug resistance P-glycoprotein is accessible to the aqueous medium. *Biochemistry*, **2004**, 43, 12081-9	3.2	50
56	Thapsigargin or curcumin does not promote maturation of processing mutants of the ABC transporters, CFTR, and P-glycoprotein. *Biochemical and Biophysical Research Communications*, **2004**, 325, 580-5	3.4	48
55	Val133 and Cys137 in transmembrane segment 2 are close to Arg935 and Gly939 in transmembrane segment 11 of human P-glycoprotein. *Journal of Biological Chemistry*, **2004**, 279, 18232-8	5.4	50
54	Disulfide cross-linking analysis shows that transmembrane segments 5 and 8 of human P-glycoprotein are close together on the cytoplasmic side of the membrane. *Journal of Biological Chemistry*, **2004**, 279, 7692-7	5.4	61
53	Drug binding in human P-glycoprotein causes conformational changes in both nucleotide-binding domains. *Journal of Biological Chemistry*, **2003**, 278, 1575-8	5.4	96
52	Methanethiosulfonate derivatives of rhodamine and verapamil activate human P-glycoprotein at different sites. *Journal of Biological Chemistry*, **2003**, 278, 50136-41	5.4	67
51	Simultaneous binding of two different drugs in the binding pocket of the human multidrug resistance P-glycoprotein. *Journal of Biological Chemistry*, **2003**, 278, 39706-10	5.4	146
50	Permanent activation of the human P-glycoprotein by covalent modification of a residue in the drug-binding site. *Journal of Biological Chemistry*, **2003**, 278, 20449-52	5.4	47
49	Application of chemical chaperones to the rescue of folding defects. *Methods in Molecular Biology*, **2003**, 232, 231-43	1.4	3
48	Substrate-induced conformational changes in the transmembrane segments of human P-glycoprotein. Direct evidence for the substrate-induced fit mechanism for drug binding. *Journal of Biological Chemistry*, **2003**, 278, 13603-6	5.4	139
47	Location of the rhodamine-binding site in the human multidrug resistance P-glycoprotein. *Journal of Biological Chemistry*, **2002**, 277, 44332-8	5.4	169
46	The "LSGGQ" motif in each nucleotide-binding domain of human P-glycoprotein is adjacent to the opposing walker A sequence. *Journal of Biological Chemistry*, **2002**, 277, 41303-6	5.4	120
45	Introduction of the most common cystic fibrosis mutation (Delta F508) into human P-glycoprotein disrupts packing of the transmembrane segments. *Journal of Biological Chemistry*, **2002**, 277, 27585-8	5.4	31
44	Vanadate trapping of nucleotide at the ATP-binding sites of human multidrug resistance P-glycoprotein exposes different residues to the drug-binding site. *Proceedings of the National Academy of Sciences of the United States of America*, **2002**, 99, 3511-6	11.5	76

43	Defining the drug-binding site in the human multidrug resistance P-glycoprotein using a methanethiosulfonate analog of verapamil, MTS-verapamil. *Journal of Biological Chemistry*, **2001**, 276, 14972-9	5.4	153
42	Cross-linking of human multidrug resistance P-glycoprotein by the substrate, tris-(2-maleimidoethyl)amine, is altered by ATP hydrolysis. Evidence for rotation of a transmembrane helix. *Journal of Biological Chemistry*, **2001**, 276, 31800-5	5.4	60
41	Determining the dimensions of the drug-binding domain of human P-glycoprotein using thiol cross-linking compounds as molecular rulers. *Journal of Biological Chemistry*, **2001**, 276, 36877-80	5.4	151
40	The packing of the transmembrane segments of human multidrug resistance P-glycoprotein is revealed by disulfide cross-linking analysis. *Journal of Biological Chemistry*, **2000**, 275, 5253-6	5.4	77
39	Identification of residues within the drug-binding domain of the human multidrug resistance P-glycoprotein by cysteine-scanning mutagenesis and reaction with dibromobimane. *Journal of Biological Chemistry*, **2000**, 275, 39272-8	5.4	106
38	Drug-stimulated ATPase activity of human P-glycoprotein is blocked by disulfide cross-linking between the nucleotide-binding sites. *Journal of Biological Chemistry*, **2000**, 275, 19435-8	5.4	52
37	The human multidrug resistance P-glycoprotein is inactive when its maturation is inhibited: potential for a role in cancer chemotherapy. *FASEB Journal*, **1999**, 13, 1724-32	0.9	80
36	The transmembrane domains of the human multidrug resistance P-glycoprotein are sufficient to mediate drug binding and trafficking to the cell surface. *Journal of Biological Chemistry*, **1999**, 274, 24759-65	5.4	110
35	Identification of residues in the drug-binding domain of human P-glycoprotein. Analysis of transmembrane segment 11 by cysteine-scanning mutagenesis and inhibition by dibromobimane. *Journal of Biological Chemistry*, **1999**, 274, 35388-92	5.4	95
34	Molecular dissection of the human multidrug resistance P-glycoprotein. *Biochemistry and Cell Biology*, **1999**, 77, 11-23	3.6	60
33	Determining the structure and mechanism of the human multidrug resistance P-glycoprotein using cysteine-scanning mutagenesis and thiol-modification techniques. *Biochimica Et Biophysica Acta - Biomembranes*, **1999**, 1461, 315-25	3.8	69
32	The glycosylation and orientation in the membrane of the third cytoplasmic loop of human P-glycoprotein is affected by mutations and substrates. *Biochemistry*, **1999**, 38, 5124-9	3.2	17
31	Nonylphenol ethoxylates, but not nonylphenol, are substrates of the human multidrug resistance P-glycoprotein. *Biochemical and Biophysical Research Communications*, **1998**, 247, 478-80	3.4	18
30	Quality control by proteases in the endoplasmic reticulum. Removal of a protease-sensitive site enhances expression of human P-glycoprotein. *Journal of Biological Chemistry*, **1998**, 273, 32373-6	5.4	45
29	Superfolding of the partially unfolded core-glycosylated intermediate of human P-glycoprotein into the mature enzyme is promoted by substrate-induced transmembrane domain interactions. *Journal of Biological Chemistry*, **1998**, 273, 14671-4	5.4	82
28	Mutational analysis of human P-glycoprotein. *Methods in Enzymology*, **1998**, 292, 480-92	1.7	16
27	Identification of residues in the drug-binding site of human P-glycoprotein using a thiol-reactive substrate. *Journal of Biological Chemistry*, **1997**, 272, 31945-8	5.4	117
26	Correction of defective protein kinesis of human P-glycoprotein mutants by substrates and modulators. *Journal of Biological Chemistry*, **1997**, 272, 709-12	5.4	192

25	Drug-stimulated ATPase activity of human P-glycoprotein requires movement between transmembrane segments 6 and 12. *Journal of Biological Chemistry*, **1997**, 272, 20986-9	5.4	84
24	Disease-associated mutations in cytoplasmic loops 1 and 2 of cystic fibrosis transmembrane conductance regulator impede processing or opening of the channel. *Biochemistry*, **1997**, 36, 11966-74	3.2	67
23	Cystic fibrosis: channel, catalytic, and folding properties of the CFTR protein. *Journal of Bioenergetics and Biomembranes*, **1997**, 29, 429-42	3.7	38
22	The minimum functional unit of human P-glycoprotein appears to be a monomer. *Journal of Biological Chemistry*, **1996**, 271, 27488-92	5.4	49
21	Inhibition of oxidative cross-linking between engineered cysteine residues at positions 332 in predicted transmembrane segments (TM) 6 and 975 in predicted TM12 of human P-glycoprotein by drug substrates. *Journal of Biological Chemistry*, **1996**, 271, 27482-7	5.4	69
20	Disease-associated mutations in the fourth cytoplasmic loop of cystic fibrosis transmembrane conductance regulator compromise biosynthetic processing and chloride channel activity. *Journal of Biological Chemistry*, **1996**, 271, 15139-45	5.4	93
19	Cytoplasmic loop three of cystic fibrosis transmembrane conductance regulator contributes to regulation of chloride channel activity. *Journal of Biological Chemistry*, **1996**, 271, 27493-9	5.4	80
18	Mutational analysis of the predicted first transmembrane segment of each homologous half of human P-glycoprotein suggests that they are symmetrically arranged in the membrane. *Journal of Biological Chemistry*, **1996**, 271, 15414-9	5.4	29
17	Expression of a functionally active human renal sodium-calcium exchanger lacking a signal sequence. *Journal of Biological Chemistry*, **1995**, 270, 19345-50	5.4	20
16	Membrane topology of a cysteine-less mutant of human P-glycoprotein. *Journal of Biological Chemistry*, **1995**, 270, 843-8	5.4	207
15	Covalent modification of human P-glycoprotein mutants containing a single cysteine in either nucleotide-binding fold abolishes drug-stimulated ATPase activity. *Journal of Biological Chemistry*, **1995**, 270, 22957-61	5.4	130
14	P-glycoprotein. Associations between domains and between domains and molecular chaperones. *Journal of Biological Chemistry*, **1995**, 270, 21839-44	5.4	103
13	Rapid purification of human P-glycoprotein mutants expressed transiently in HEK 293 cells by nickel-chelate chromatography and characterization of their drug-stimulated ATPase activities. *Journal of Biological Chemistry*, **1995**, 270, 21449-52	5.4	150
12	Mutations to amino acids located in predicted transmembrane segment 6 (TM6) modulate the activity and substrate specificity of human P-glycoprotein. *Biochemistry*, **1994**, 33, 14049-57	3.2	122
11	Deletion of NH2- and COOH-terminal sequences destroys function of the Ca2+ ATPase of rabbit fast-twitch skeletal muscle sarcoplasmic reticulum. *FEBS Letters*, **1993**, 336, 168-70	3.8	15
10	Expression and mutation of Ca2+ ATPases of the sarcoplasmic reticulum. *Cytoskeleton*, **1989**, 14, 26-34		17
9	Location of high affinity Ca2+-binding sites within the predicted transmembrane domain of the sarcoplasmic reticulum Ca2+-ATPase. *Nature*, **1989**, 339, 476-8	50.4	570
8	Expression of rubella virus cDNA coding for the structural proteins. *Gene*, **1988**, 65, 23-30	3.8	27

7	Nucleotide sequence and in vitro expression of rubella virus 24S subgenomic messenger RNA encoding the structural proteins E1, E2 and C. *Nucleic Acids Research*, **1987**, 15, 3041-57	20.1	95
6	Nucleotide sequence of the pntA and pntB genes encoding the pyridine nucleotide transhydrogenase of Escherichia coli. *FEBS Journal*, **1986**, 158, 647-53		91
5	Detection of antibodies to individual proteins of rubella virus. *Journal of Virological Methods*, **1986**, 13, 149-59	2.6	15
4	Structural analysis of a new GC-specific insertion element IS186. *FEBS Letters*, **1985**, 192, 47-52	3.8	21
3	Interaction of Escherichia coli F1-ATPase with dicyclohexylcarbodiimide-binding polypeptide. *Biochimica Et Biophysica Acta - Biomembranes*, **1983**, 733, 274-82	3.8	17
2	The DCCD-binding polypeptide is close to the F1 ATPase-binding site on the cytoplasmic surface of the cell membrane of Escherichia coli. *Biochemical and Biophysical Research Communications*, **1982**, 106, 400-6	3.4	23
1	The DCCD-binding polypeptide alone is insufficient for proton translocation through F0 in membranes of Escherichia coli. *Biochemical and Biophysical Research Communications*, **1981**, 103, 52-9	3.4	25