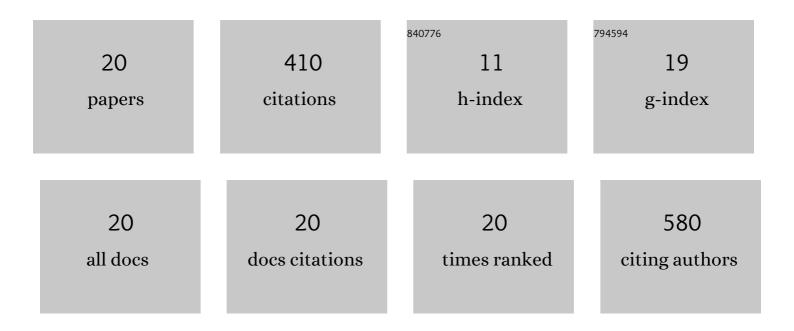
Yu Keung Mok

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Scaffold stability and P14' residue steric hindrance in the differential inhibition of FXIIa by <i>Aedes aegypti</i> trypsin inhibitor versus Infestin-4. Bioscience Reports, 2022, , .	2.4	0
2	Structure of Aedes aegypti carboxypeptidase B1 â€inhibitor complex uncover the disparity between mosquito and nonâ€mosquito insect carboxypeptidase inhibition mechanism. Protein Science, 2021, 30, 2445-2456.	7.6	4
3	Crystal structure of Aedes aegypti trypsin inhibitor in complex with μâ€plasmin reveals role for scaffold stability in Kazalâ€type serine protease inhibitor. Protein Science, 2021, , .	7.6	2
4	Exonic mutations associated with atopic dermatitis disrupt lymphoâ€epithelial Kazalâ€ŧype related inhibitor action and enhance its degradation. Allergy: European Journal of Allergy and Clinical Immunology, 2020, 75, 403-411.	5.7	8
5	Trxlp, a thioredoxin-like effector from Edwardsiella piscicida inhibits cellular redox signaling and nuclear translocation of NF-κB. International Journal of Biological Macromolecules, 2020, 148, 89-101.	7.5	2
6	Increased Mosquito Midgut Infection by Dengue Virus Recruitment of Plasmin Is Blocked by an Endogenous Kazal-type Inhibitor. IScience, 2019, 21, 564-576.	4.1	10
7	Homologous Lympho-Epithelial Kazal-type Inhibitor Domains Delay Blood Coagulation by Inhibiting Factor X and XI with Differential Specificity. Structure, 2018, 26, 1178-1186.e3.	3.3	6
8	Structural basis for the bacterial membrane insertion of dermcidin peptide, DCD-1L. Scientific Reports, 2017, 7, 13923.	3.3	9
9	Structure of AcrH–AopB Chaperone-Translocator Complex Reveals a Role for Membrane Hairpins in Type III Secretion System Translocon Assembly. Structure, 2015, 23, 2022-2031.	3.3	43
10	NMR Structure and IgE Epitopes of Blo t 21, a Major Dust Mite Allergen from Blomia tropicalis. Journal of Biological Chemistry, 2012, 287, 34776-34785.	3.4	29
11	Crystal Structure of Der f 7, a Dust Mite Allergen from Dermatophagoides farinae. PLoS ONE, 2012, 7, e44850.	2.5	23
12	Crystal Structure of the Heteromolecular Chaperone, AscE-AscG, from the Type III Secretion System in Aeromonas hydrophila. PLoS ONE, 2011, 6, e19208.	2.5	13
13	Cloning, expression, purification, crystallization and preliminary X-ray diffraction studies of a major group 7 allergen, Der f 7, from the dust mite <i>Dermatophagoides farinae</i> . Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 1612-1615.	0.7	2
14	Auto-FACE: An NMR Based Binding Site Mapping Program for Fast Chemical Exchange Protein-Ligand Systems. PLoS ONE, 2010, 5, e8943.	2.5	20
15	Structures of Two Major Allergens, Bla g 4 and Per a 4, from Cockroaches and Their IgE Binding Epitopes. Journal of Biological Chemistry, 2009, 284, 3148-3157.	3.4	39
16	Mapping of the chaperone AcrH binding regions of translocators AopB and AopD and characterization of oligomeric and metastable AcrHâ€AopBâ€AopD complexes in the type III secretion system of <i>Aeromonas hydrophila</i> . Protein Science, 2009, 18, 1724-1734.	7.6	15
17	Structure of AscE and induced burial regions in AscE and AscG upon formation of the chaperone needleâ€subunit complex of type III secretion system in <i>Aeromonas hydrophila</i> . Protein Science, 2008, 17, 1748-1760.	7.6	11
18	Nuclear Magnetic Resonance Structure and IgE Epitopes of Blo t 5, a Major Dust Mite Allergen. Journal of Immunology, 2008, 181, 2586-2596.	0.8	50

#	Article	IF	CITATIONS
19	Chelerythrine and Sanguinarine Dock at Distinct Sites on BclXL that are Not the Classic BH3 Binding Cleft. Journal of Molecular Biology, 2006, 364, 536-549.	4.2	58
20	Nuclear Magnetic Resonance Structure-Based Epitope Mapping and Modulation of Dust Mite Group 13 Allergen as a Hypoallergen. Journal of Immunology, 2006, 176, 4852-4860.	0.8	66