

# Kemin Tan

## List of Publications by Year in descending order

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63  
papers

3,557  
citations

147801

31  
h-index

138484

58  
g-index

63  
all docs

63  
docs citations

63  
times ranked

5329  
citing authors

#	ARTICLE	IF	CITATIONS
1	The Crystal Structure of a T Cell Receptor in Complex with Peptide and MHC Class II. <i>Science</i> , 1999, 286, 1913-1921.	12.6	376
2	Crystal structure of the TSP-1 type 1 repeats. <i>Journal of Cell Biology</i> , 2002, 159, 373-382.	5.2	249
3	Structure of a Heterophilic Adhesion Complex between the Human CD2 and CD58 (LFA-3) Counterreceptors. <i>Cell</i> , 1999, 97, 791-803.	28.9	216
4	<i>Bifidobacterium longum</i> subsp. <i>infantis</i> ATCC 15697 $\alpha$ -Fucosidases Are Active on Fucosylated Human Milk Oligosaccharides. <i>Applied and Environmental Microbiology</i> , 2012, 78, 795-803.	3.1	204
5	In situ proteolysis for protein crystallization and structure determination. <i>Nature Methods</i> , 2007, 4, 1019-1021.	19.0	197
6	Structure of the influenza virus A H5N1 nucleoprotein: implications for RNA binding, oligomerization, and vaccine design. <i>FASEB Journal</i> , 2008, 22, 3638-3647.	0.5	186
7	Masitinib is a broad coronavirus 3CL inhibitor that blocks replication of SARS-CoV-2. <i>Science</i> , 2021, 373, 931-936.	12.6	173
8	Crystal structure of murine sCEACAM1a[1,4]: a coronavirus receptor in the CEA family. <i>EMBO Journal</i> , 2002, 21, 2076-2086.	7.8	102
9	A conformational switch controls cell wall remodeling enzymes required for bacterial cell division. <i>Molecular Microbiology</i> , 2012, 85, 768-781.	2.5	98
10	Synthesis of a novel open-framework sulfide, CuGe <sub>2</sub> S <sub>5</sub> (C <sub>2</sub> H <sub>5</sub> ) <sub>4</sub> N, and its structure solution using synchrotron imaging plate data. <i>Journal of the American Chemical Society</i> , 1995, 117, 7039-7040.	13.7	96
11	The interaction of Thrombospondins with extracellular matrix proteins. <i>Journal of Cell Communication and Signaling</i> , 2009, 3, 177-187.	3.4	95
12	Large-scale evaluation of protein reductive methylation for improving protein crystallization. <i>Nature Methods</i> , 2008, 5, 853-854.	19.0	81
13	The Structures of the Thrombospondin-1 N-Terminal Domain and Its Complex with a Synthetic Pentameric Heparin. <i>Structure</i> , 2006, 14, 33-42.	3.3	80
14	Hydrothermal Growth of Single Crystals of TMA-CuGS-2, [C <sub>4</sub> H <sub>12</sub> N] <sub>6</sub> [(Cu <sub>0.44</sub> Ge <sub>0.56</sub> S <sub>2.23</sub> ) <sub>4</sub> (Ge <sub>4</sub> S <sub>8</sub> ) <sub>3</sub> ] and Their Characterization Using Synchrotron/Imaging Plate Data. <i>Chemistry of Materials</i> , 1996, 8, 448-453.	6.7	71
15	Functional Diversity of Haloacid Dehalogenase Superfamily Phosphatases from <i>Saccharomyces cerevisiae</i> . <i>Journal of Biological Chemistry</i> , 2015, 290, 18678-18698.	3.4	70
16	The structure of immunoglobulin superfamily domains 1 and 2 of MAdCAM-1 reveals novel features important for integrin recognition. <i>Structure</i> , 1998, 6, 793-801.	3.3	64
17	The crystal structure of the signature domain of cartilage oligomeric matrix protein: implications for collagen, glycosaminoglycan and integrin binding. <i>FASEB Journal</i> , 2009, 23, 2490-2501.	0.5	63
18	Novel Two-Dimensional Tin Sulfide Networks: Preparation and Structural Characterization of Sn <sub>4</sub> S <sub>9</sub> [(C <sub>3</sub> H <sub>7</sub> ) <sub>4</sub> N] <sub>2</sub> and Sn <sub>4</sub> S <sub>9</sub> [(C <sub>3</sub> H <sub>7</sub> ) <sub>4</sub> N] $\cdot$ [(CH <sub>3</sub> ) <sub>3</sub> NH]. <i>Journal of Solid State Chemistry</i> , 1995, 114, 506-511.	2.9	62

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19	Molecular Basis for Leukocyte Integrin $\alpha$ 5 $\beta$ 2 Adhesion to Epithelial (E)-Cadherin. <i>Journal of Experimental Medicine</i> , 2000, 191, 1555-1567.	8.5	56
20	Structural basis for suppression of hypernegative DNA supercoiling by <i>E. coli</i> topoisomerase I. <i>Nucleic Acids Research</i> , 2015, 43, 11031-11046.	14.5	52
21	Novel $\alpha$ -glucosidase from human gut microbiome: substrate specificities and their switch. <i>FASEB Journal</i> , 2010, 24, 3939-3949.	0.5	49
22	Room-temperature X-ray crystallography reveals the oxidation and reactivity of cysteine residues in SARS-CoV-2 3CL M <sup>pro</sup> : insights into enzyme mechanism and drug design. <i>IUCr</i> , 2020, 7, 1028-1035.	2.2	49
23	Structural Evolution from Tin Sulfide (Selenide) Layered Structures to Novel 3- and 4-Connected Tin Oxy-sulfides. <i>Journal of Solid State Chemistry</i> , 1995, 117, 219-228.	2.9	45
24	A Novel Antimony Sulfide Templated by Dimethylammonium: Its Synthesis and Structural Characterization Using Synchrotron/Imaging Plate Data. <i>Chemistry of Materials</i> , 1996, 8, 2510-2515.	6.7	40
25	Structure of Microporous QUI-MnGS-1 and in Situ Studies of Its Formation Using Time-Resolved Synchrotron X-ray Powder Diffraction. <i>Chemistry of Materials</i> , 1998, 10, 1453-1458.	6.7	40
26	Synthesis of a Novel Two-Dimensional Antimony Sulfide, [C <sub>4</sub> H <sub>10</sub> N] <sub>2</sub> [Sb <sub>8</sub> S <sub>13</sub> ]·0.15H <sub>2</sub> O, and Its Structure Solution Using Synchrotron/Imaging Plate Data. <i>Chemistry of Materials</i> , 1996, 8, 493-496.	6.7	39
27	Structural and Mutational Analyses of a CD8 $\alpha$ $\beta$ Heterodimer and Comparison with the CD8 $\alpha$ $\alpha$ Homodimer. <i>Immunity</i> , 2005, 23, 661-671.	14.3	39
28	Cleavable C-terminal His-tag vectors for structure determination. <i>Journal of Structural and Functional Genomics</i> , 2010, 11, 31-39.	1.2	38
29	Interaction of antidiabetic $\alpha$ -glucosidase inhibitors and gut bacteria $\alpha$ -glucosidase. <i>Protein Science</i> , 2018, 27, 1498-1508.	7.6	37
30	The Role of $\alpha$ and $\beta$ Chains in Ligand Recognition by $\alpha$ 7 Integrins. <i>Journal of Biological Chemistry</i> , 2000, 275, 25652-25664.	3.4	36
31	Insights from the Structure of Mycobacterium tuberculosis Topoisomerase I with a Novel Protein Fold. <i>Journal of Molecular Biology</i> , 2016, 428, 182-193.	4.2	36
32	Structures of open (R) and close (T) states of prephenate dehydratase (PDT) – Implication of allosteric regulation by l-phenylalanine. <i>Journal of Structural Biology</i> , 2008, 162, 94-107.	2.8	34
33	Heparin-induced cis- and trans-Dimerization Modes of the Thrombospondin-1 N-terminal Domain. <i>Journal of Biological Chemistry</i> , 2008, 283, 3932-3941.	3.4	33
34	N. meningitidis1681 is a member of the FinO family of RNA chaperones. <i>RNA Biology</i> , 2010, 7, 812-819.	3.1	28
35	Incorporation of isotopic, fluorescent, and heavy-atom-modified nucleotides into RNAs by position-selective labeling of RNA. <i>Nature Protocols</i> , 2018, 13, 987-1005.	12.0	27
36	Structure and function of human Naa60 (NatF), a Golgi-localized bi-functional acetyltransferase. <i>Scientific Reports</i> , 2016, 6, 31425.	3.3	25

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37	Pre-TCR cell receptors topologically sample self-ligands during thymocyte $\hat{I}^2$ -selection. <i>Science</i> , 2021, 371, 181-185.	12.6	25
38	Biochemical and Structural Studies of Uncharacterized Protein PA0743 from <i>Pseudomonas aeruginosa</i> Revealed NAD <sup>+</sup> -dependent L-Serine Dehydrogenase. <i>Journal of Biological Chemistry</i> , 2012, 287, 1874-1883.	3.4	23
39	Investigating mycobacterial topoisomerase I mechanism from the analysis of metal and DNA substrate interactions at the active site. <i>Nucleic Acids Research</i> , 2018, 46, 7296-7308.	14.5	23
40	The Crystal Structure of the Heparin-Binding Reelin-N Domain of F-Spondin. <i>Journal of Molecular Biology</i> , 2008, 381, 1213-1223.	4.2	21
41	Structural and functional characterization of solute binding proteins for aromatic compounds derived from lignin: <i>p</i> -Coumaric acid and related aromatic acids. <i>Proteins: Structure, Function and Bioinformatics</i> , 2013, 81, 1709-1726.	2.6	21
42	Mutational analysis of MADCAM-1/ $\hat{I}^4$ interactions reveals significant binding determinants in both the first and second immunoglobulin domains. <i>Cell Adhesion and Communication</i> , 1999, 7, 167-181.	1.7	20
43	GH1-family 6-P- $\hat{I}^2$ -glucosidases from human microbiome lactic acid bacteria. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 451-463.	2.5	19
44	Crystal Structures of SgcE6 and SgcC, the Two-Component Monooxygenase That Catalyzes Hydroxylation of a Carrier Protein-Tethered Substrate during the Biosynthesis of the Enediyne Antitumor Antibiotic C-1027 in <i>Streptomyces globisporus</i> . <i>Biochemistry</i> , 2016, 55, 5142-5154.	2.5	18
45	Structures of teixobactin-producing nonribosomal peptide synthetase condensation and adenylation domains. <i>Current Research in Structural Biology</i> , 2020, 2, 14-24.	2.2	18
46	Functional Profiling and Crystal Structures of Isothiocyanate Hydrolases Found in Gut-Associated and Plant-Pathogenic Bacteria. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	3.1	16
47	Structure and electrostatic property of cytoplasmic domain of ZntB transporter. <i>Protein Science</i> , 2009, 18, 2043-2052.	7.6	15
48	FMN riboswitch aptamer symmetry facilitates conformational switching through mutually exclusive coaxial stacking configurations. <i>Journal of Structural Biology: X</i> , 2020, 4, 100035.	1.3	15
49	The Mannitol Operon Repressor MtlR Belongs to a New Class of Transcription Regulators in Bacteria. <i>Journal of Biological Chemistry</i> , 2009, 284, 36670-36679.	3.4	14
50	CD8 $\hat{I}^2$ Has Two Distinct Binding Modes of Interaction with Peptide-Major Histocompatibility Complex Class I. <i>Journal of Biological Chemistry</i> , 2006, 281, 28090-28096.	3.4	13
51	EsxB, a secreted protein from <i>Bacillus anthracis</i> forms two distinct helical bundles. <i>Protein Science</i> , 2015, 24, 1389-1400.	7.6	12
52	Structural and functional characterization of three Type B and C chloramphenicol acetyltransferases from <i>Vibrio</i> species. <i>Protein Science</i> , 2020, 29, 695-710.	7.6	12
53	Mechanistic insights from structure of <i>Mycobacterium smegmatis</i> topoisomerase I with ssDNA bound to both N- and C-terminal domains. <i>Nucleic Acids Research</i> , 2020, 48, 4448-4462.	14.5	12
54	The crystal structures of the $\hat{I}^{\pm}$ -subunit of the $\hat{I}^{\pm 2}$ tetrameric Glycyl-tRNA synthetase. <i>Journal of Structural and Functional Genomics</i> , 2012, 13, 233-239.	1.2	11

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55	Sensor Domain of Histidine Kinase KinB of Pseudomonas. Journal of Biological Chemistry, 2014, 289, 12232-12244.	3.4	11
56	The structure of the Ca <sup>2+</sup> -binding, glycosylated F-spondin domain of F-spondin - A C2-domain variant in an extracellular matrix protein. BMC Structural Biology, 2011, 11, 22.	2.3	9
57	<i>In situ</i> X-ray data collection and structure phasing of protein crystals at Structural Biology Center 19-ID. Journal of Synchrotron Radiation, 2015, 22, 1386-1395.	2.4	8
58	Insights into PG-binding, conformational change, and dimerization of the OmpA C-terminal domains from Salmonella enterica serovar Typhimurium and Borrelia burgdorferi. Protein Science, 2017, 26, 1738-1748.	7.6	8
59	Structure of thrombospondin type 3 repeats in bacterial outer membrane protein A reveals its intra-repeat disulfide bond-dependent calcium-binding capability. Cell Calcium, 2017, 66, 78-89.	2.4	7
60	Structural analysis of free and liganded forms of the Fab fragment of a high-affinity anti-cocaine antibody, h2E2. Acta Crystallographica Section F, Structural Biology Communications, 2019, 75, 697-706.	0.8	7
61	Tying the knot in the tetrahydrofolate (THF) riboswitch: A molecular basis for gene regulation. Journal of Structural Biology, 2021, 213, 107703.	2.8	7
62	Sensor Domain of Histidine Kinase VxA of Vibrio cholerae: Hairpin-Swapped Dimer and Its Conformational Change. Journal of Bacteriology, 2021, 203, .	2.2	4
63	Structural and biochemical insights into CRISPR RNA processing by the Cas5c ribonuclease SMU1763 from Streptococcus mutans. Journal of Biological Chemistry, 2021, 297, 101251.	3.4	2