

# Sanguk Kim

## List of Publications by Year in descending order

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95  
papers

5,473  
citations

76326

40  
h-index

88630

70  
g-index

99  
all docs

99  
docs citations

99  
times ranked

8314  
citing authors

#	ARTICLE	IF	CITATIONS
1	Evolutionary rewiring of regulatory networks contributes to phenotypic differences between human and mouse orthologous genes. <i>Nucleic Acids Research</i> , 2022, 50, 1849-1863.	14.5	6
2	The implication of holochoyochrome c synthase mutation in Korean familial hypoplastic amelogenesis imperfecta. <i>Clinical Oral Investigations</i> , 2022, 26, 4487-4498.	3.0	1
3	Network-based machine learning approach to predict immunotherapy response in cancer patients. <i>Nature Communications</i> , 2022, 13, .	12.8	56
4	Phylogenetic analysis of <scp>ABCG</scp> subfamily proteins in plants: functional clustering and coevolution with <scp>ABCGs</scp> of pathogens. <i>Physiologia Plantarum</i> , 2021, 172, 1422-1438.	5.2	11
5	MON-2, a Golgi protein, mediates autophagy-dependent longevity in <i>Caenorhabditis elegans</i>. <i>Science Advances</i> , 2021, 7, eabj8156.	10.3	11
6	Network-based machine learning in colorectal and bladder organoid models predicts anti-cancer drug efficacy in patients. <i>Nature Communications</i> , 2020, 11, 5485.	12.8	94
7	Single-cell RNA sequencing identifies shared differentiation paths of mouse thymic innate T cells. <i>Nature Communications</i> , 2020, 11, 4367.	12.8	56
8	Creation of bladder assembloids mimicking tissue regeneration and cancer. <i>Nature</i> , 2020, 588, 664-669.	27.8	133
9	Capicua restricts cancer stem cell-like properties in breast cancer cells. <i>Oncogene</i> , 2020, 39, 3489-3506.	5.9	17
10	Domain-mediated interactions for protein subfamily identification. <i>Scientific Reports</i> , 2020, 10, 264.	3.3	2
11	Capicua suppresses colorectal cancer progression via repression of ETV4 expression. <i>Cancer Cell International</i> , 2020, 20, 42.	4.1	16
12	Tetrahydrobiopterin enhances mitochondrial biogenesis and cardiac contractility via stimulation of PGC1 $\pm$ signaling. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2019, 1865, 165524.	3.8	12
13	Variants at potential loci associated with Sjogren's syndrome in Koreans: A genetic association study. <i>Clinical Immunology</i> , 2019, 207, 79-86.	3.2	5
14	Link clustering explains non-central and contextually essential genes in protein interaction networks. <i>Scientific Reports</i> , 2019, 9, 11672.	3.3	2
15	Evolutionary coupling analysis identifies the impact of disease-associated variants at less-conserved sites. <i>Nucleic Acids Research</i> , 2019, 47, e94-e94.	14.5	11
16	Exomic and transcriptomic alterations of hereditary gingival fibromatosis. <i>Oral Diseases</i> , 2019, 25, 1374-1383.	3.0	6
17	KIN $\hat{4}$ /MAST kinase promotes PTEN $\hat{c}$ mediated longevity of <i>Caenorhabditis elegans</i> via binding through a PDZ domain. <i>Aging Cell</i> , 2019, 18, e12906.	6.7	10
18	Epigenetic regulation of mammalian Hedgehog signaling to the stroma determines the molecular subtype of bladder cancer. <i>ELife</i> , 2019, 8, .	6.0	19

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19	Capicua suppresses hepatocellular carcinoma progression by controlling the ETV4-MMP1 axis. <i>Hepatology</i> , 2018, 67, 2287-2301.	7.3	70
20	Divergence of Noncoding Regulatory Elements Explains Gene Phenotype Differences between Human and Mouse Orthologous Genes. <i>Molecular Biology and Evolution</i> , 2018, 35, 1653-1667.	8.9	12
21	March2 is required for head formation by mediating Dishevelled degradation in concert with Dapper1. <i>Development (Cambridge)</i> , 2018, 145, .	2.5	10
22	The mechanistic insight of a specific interaction between 15d-Prostaglandin-J2 and eIF4A suggests an evolutionary conserved role across species. <i>Biology Open</i> , 2018, 7, .	1.2	4
23	Energy metabolism and whole-exome sequencing-based analysis of Sasang constitution: a pilot study. <i>Integrative Medicine Research</i> , 2017, 6, 165-178.	1.8	4
24	Constitutive activation of T cells by $\beta$ 2-herpesviral GPCR through the interaction with cellular CXCR4. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2017, 1864, 1-11.	4.1	5
25	OASIS 2: online application for survival analysis 2 with features for the analysis of maximal lifespan and healthspan in aging research. <i>Oncotarget</i> , 2016, 7, 56147-56152.	1.8	330
26	Spread of Mutant Middle East Respiratory Syndrome Coronavirus with Reduced Affinity to Human CD26 during the South Korean Outbreak. <i>MBio</i> , 2016, 7, e00019.	4.1	76
27	Genetic Investigation of Bisphosphonate-Related Osteonecrosis of Jaw (BRONJ) via Whole Exome Sequencing and Bioinformatics. <i>PLoS ONE</i> , 2015, 10, e0118084.	2.5	17
28	Metazoans evolved by taking domains from soluble proteins to expand intercellular communication network. <i>Scientific Reports</i> , 2015, 5, 9576.	3.3	8
29	RNA helicase HEL-1 promotes longevity by specifically activating DAF-16/FOXO transcription factor signaling in <i>Caenorhabditis elegans</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E4246-55.	7.1	34
30	Network Modules of the Cross-Species Genotype-Phenotype Map Reflect the Clinical Severity of Human Diseases. <i>PLoS ONE</i> , 2015, 10, e0136300.	2.5	8
31	Computational Design of Binding Proteins to EGFR Domain II. <i>PLoS ONE</i> , 2014, 9, e92513.	2.5	9
32	Linear Motif-Mediated Interactions Have Contributed to the Evolution of Modularity in Complex Protein Interaction Networks. <i>PLoS Computational Biology</i> , 2014, 10, e1003881.	3.2	16
33	Feedback regulation via AMPK and HIF-1 mediates ROS-dependent longevity in <i>Caenorhabditis elegans</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E4458-67.	7.1	151
34	Pyrimidine inhibits nicotine-induced catecholamine secretion. <i>Neurochemistry International</i> , 2014, 74, 42-45.	3.8	4
35	Predictive combinatorial design of mRNA translation initiation regions for systematic optimization of gene expression levels. <i>Scientific Reports</i> , 2014, 4, 4515.	3.3	59
36	Investigation of Pathogenic Genes in Peri-Implantitis from Implant Clustering Failure Patients: A Whole-Exome Sequencing Pilot Study. <i>PLoS ONE</i> , 2014, 9, e99360.	2.5	20

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37	Predictive design of mRNA translation initiation region to control prokaryotic translation efficiency. <i>Metabolic Engineering</i> , 2013, 15, 67-74.	7.0	240
38	A novel role for Gadd45 $\pm$ in base excision repair: Modulation of APE1 activity by the direct interaction of Gadd45 $\pm$ with PCNA. <i>Biochemical and Biophysical Research Communications</i> , 2013, 434, 185-190.	2.1	13
39	Rampant Exchange of the Structure and Function of Extramembrane Domains between Membrane and Water Soluble Proteins. <i>PLoS Computational Biology</i> , 2013, 9, e1002997.	3.2	9
40	Protein design by fusion: implications for protein structure prediction and evolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 2451-2460.	2.5	3
41	Spatial and functional organization of mitochondrial protein network. <i>Scientific Reports</i> , 2013, 3, 1403.	3.3	14
42	Discovery of Cellular Proteins Required for the Early Steps of HCV Infection Using Integrative Genomics. <i>PLoS ONE</i> , 2013, 8, e60333.	2.5	17
43	Rational Engineering of Enzyme Allosteric Regulation through Sequence Evolution Analysis. <i>PLoS Computational Biology</i> , 2012, 8, e1002612.	3.2	71
44	Phenotypic Characterization of Peripheral T Cells and Their Dynamics in Scrub Typhus Patients. <i>PLoS Neglected Tropical Diseases</i> , 2012, 6, e1789.	3.0	44
45	Rewiring of PDZ Domain-Ligand Interaction Network Contributed to Eukaryotic Evolution. <i>PLoS Genetics</i> , 2012, 8, e1002510.	3.5	58
46	Evolutionary history of human disease genes reveals phenotypic connections and comorbidity among genetic diseases. <i>Scientific Reports</i> , 2012, 2, 757.	3.3	25
47	PDZ Domain-containing 1 (PDZK1) Protein Regulates Phospholipase C- $\beta$ 3 (PLC- $\beta$ 3)-specific Activation of Somatostatin by Forming a Ternary Complex with PLC- $\beta$ 3 and Somatostatin Receptors. <i>Journal of Biological Chemistry</i> , 2012, 287, 21012-21024.	3.4	27
48	Network rewiring is an important mechanism of gene essentiality change. <i>Scientific Reports</i> , 2012, 2, 900.	3.3	52
49	Structural differences between thermophilic and mesophilic membrane proteins. <i>Protein Science</i> , 2012, 21, 1746-1753.	7.6	45
50	The Protein Interaction Network of Extracellular Vesicles Derived from Human Colorectal Cancer Cells. <i>Journal of Proteome Research</i> , 2012, 11, 1144-1151.	3.7	66
51	Role of BI-1 (TEGT)-mediated ERK1/2 activation in mitochondria-mediated apoptosis and splenomegaly in BI-1 transgenic mice. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2012, 1823, 876-888.	4.1	23
52	Subtype-specific roles of phospholipase C- $\beta$ 2 via differential interactions with PDZ domain proteins. <i>Advances in Enzyme Regulation</i> , 2011, 51, 138-151.	2.6	29
53	A multifunctional core-shell nanoparticle for dendritic cell-based cancer immunotherapy. <i>Nature Nanotechnology</i> , 2011, 6, 675-682.	31.5	470
54	OASIS: Online Application for the Survival Analysis of Lifespan Assays Performed in Aging Research. <i>PLoS ONE</i> , 2011, 6, e23525.	2.5	259

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55	Protein localization as a principal feature of the etiology and comorbidity of genetic diseases. <i>Molecular Systems Biology</i> , 2011, 7, 494.	7.2	65
56	Both the Hydrophobicity and a Positively Charged Region Flanking the C-Terminal Region of the Transmembrane Domain of Signal-Anchored Proteins Play Critical Roles in Determining Their Targeting Specificity to the Endoplasmic Reticulum or Endosymbiotic Organelles in <i>Arabidopsis</i> Cells. <i>Plant Cell</i> , 2011, 23, 1588-1607.	6.6	63
57	Molecular Evolution of Protein Conformational Changes Revealed by a Network of Evolutionarily Coupled Residues. <i>Molecular Biology and Evolution</i> , 2011, 28, 2675-2685.	8.9	45
58	Network Clustering Revealed the Systemic Alterations of Mitochondrial Protein Expression. <i>PLoS Computational Biology</i> , 2011, 7, e1002093.	3.2	14
59	Global gene expression profile of <i>Orientia tsutsugamushi</i> . <i>Proteomics</i> , 2010, 10, 1699-1715.	2.2	26
60	Bax Inhibitor 1 Increases Cell Adhesion through Actin Polymerization: Involvement of Calcium and Actin Binding. <i>Molecular and Cellular Biology</i> , 2010, 30, 1800-1813.	2.3	29
61	ConPlex: a server for the evolutionary conservation analysis of protein complex structures. <i>Nucleic Acids Research</i> , 2010, 38, W450-W456.	14.5	9
62	Changes in Hepatic Gene Expression upon Oral Administration of Taurine-Conjugated Ursodeoxycholic Acid in ob/ob Mice. <i>PLoS ONE</i> , 2010, 5, e13858.	2.5	47
63	Integration of Evolutionary Features for the Identification of Functionally Important Residues in Major Facilitator Superfamily Transporters. <i>PLoS Computational Biology</i> , 2009, 5, e1000522.	3.2	16
64	Evolutionary conservation in multiple faces of protein interaction. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 77, 14-25.	2.6	60
65	Construction of Functional Interaction Networks through Consensus Localization Predictions of the Human Proteome. <i>Journal of Proteome Research</i> , 2009, 8, 3367-3376.	3.7	18
66	Bioinformatic approaches for the structure and function of membrane proteins. <i>BMB Reports</i> , 2009, 42, 697-704.	2.4	32
67	Common occurrence of internal repeat symmetry in membrane proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 71, 68-80.	2.6	28
68	Structure of the transmembrane region of the M2 protein H <sup>+</sup> channel. <i>Protein Science</i> , 2008, 10, 2241-2250.	7.6	221
69	<i>Arabidopsis</i> Nuclear-Encoded Plastid Transit Peptides Contain Multiple Sequence Subgroups with Distinctive Chloroplast-Targeting Sequence Motifs. <i>Plant Cell</i> , 2008, 20, 1603-1622.	6.6	117
70	Bax Inhibitor-1 Is a pH-dependent Regulator of Ca <sup>2+</sup> Channel Activity in the Endoplasmic Reticulum. <i>Journal of Biological Chemistry</i> , 2008, 283, 15946-15955.	3.4	101
71	Dimerization of the transmembrane domain of amyloid precursor proteins and familial Alzheimer's disease mutants. <i>BMC Neuroscience</i> , 2008, 9, 17.	1.9	73
72	Transmembrane Helix Uniformity Examined by Spectral Mapping of Torsion Angles. <i>Structure</i> , 2008, 16, 787-797.	3.3	77

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73	Functional analysis of dicer-2 missense mutations in the siRNA pathway of <i>Drosophila</i> . <i>Biochemical and Biophysical Research Communications</i> , 2008, 371, 525-530.	2.1	22
74	Expression of the Novel Wheat Gene TM20 Confers Enhanced Cadmium Tolerance to Bakers' Yeast. <i>Journal of Biological Chemistry</i> , 2008, 283, 15893-15902.	3.4	42
75	Genome-Based Construction of the Metabolic Pathways of <i>Orientia tsutsugamushi</i> and Comparative Analysis within the Rickettsiales Order. <i>Comparative and Functional Genomics</i> , 2008, 1-14.	2.0	42
76	Role of Amphipathic Helix of a Herpesviral Protein in Membrane Deformation and T Cell Receptor Downregulation. <i>PLoS Pathogens</i> , 2008, 4, e1000209.	4.7	24
77	Janus Model of The Na,K-ATPase $\beta$ -Subunit Transmembrane Domain: Distinct Faces Mediate $\beta$ Assembly and $\beta$ Homo-oligomerization. <i>Journal of Molecular Biology</i> , 2007, 365, 706-714.	4.2	46
78	Engineering a de novo internal disulfide bridge to improve the thermal stability of xylanase from <i>Bacillus stearothermophilus</i> No. 236. <i>Journal of Biotechnology</i> , 2007, 127, 300-309.	3.8	59
79	Transmembrane Domain of Myelin Protein Zero Can Form Dimers: Possible Implications for Myelin Construction. <i>Biochemistry</i> , 2007, 46, 12164-12173.	2.5	36
80	Association and functional relevance of E237G, a polymorphism of the high-affinity immunoglobulin E-receptor $\gamma$ chain gene, to airway hyper-responsiveness. <i>Clinical and Experimental Allergy</i> , 2007, 37, 592-598.	2.9	19
81	Self-association of the Transmembrane Domain of an Anthrax Toxin Receptor. <i>Journal of Molecular Biology</i> , 2006, 360, 145-156.	4.2	23
82	A limited universe of membrane protein families and folds. <i>Protein Science</i> , 2006, 15, 1723-1734.	7.6	77
83	Functional Characterization of Sequence Motifs in the Transit Peptide of Arabidopsis Small Subunit of Rubisco. <i>Plant Physiology</i> , 2006, 140, 466-483.	4.8	104
84	Pivotal role of the glycine-rich TM3 helix in gating the MscS mechanosensitive channel. <i>Nature Structural and Molecular Biology</i> , 2005, 12, 113-119.	8.2	125
85	Transmembrane glycine zippers: Physiological and pathological roles in membrane proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 14278-14283.	7.1	240
86	Transmembrane Domain Helix Packing Stabilizes Integrin $\beta$ 3 in the Low Affinity State. <i>Journal of Biological Chemistry</i> , 2005, 280, 7294-7300.	3.4	131
87	Membrane channel structure of <i>Helicobacter pylori</i> vacuolating toxin: Role of multiple GXXXG motifs in cylindrical channels. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 5988-5991.	7.1	77
88	The Affinity of GXXXG Motifs in Transmembrane Helix-Helix Interactions Is Modulated by Long-range Communication. <i>Journal of Biological Chemistry</i> , 2004, 279, 16591-16597.	3.4	103
89	2D solid state NMR spectral simulation of $^3\text{F}_2$ , $^3\text{F}_4$ , and $^3\text{F}_6$ -helices. <i>Journal of Magnetic Resonance</i> , 2004, 168, 187-193.	2.1	13
90	A Model of the Closed Form of the Nicotinic Acetylcholine Receptor M2 Channel Pore. <i>Biophysical Journal</i> , 2004, 87, 792-799.	0.5	20

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91	Snorkeling Preferences Foster an Amino Acid Composition Bias in Transmembrane Helices. <i>Journal of Molecular Biology</i> , 2004, 339, 471-479.	4.2	74
92	A Simple Method for Modeling Transmembrane Helix Oligomers. <i>Journal of Molecular Biology</i> , 2003, 329, 831-840.	4.2	73
93	Uniformity, Ideality, and Hydrogen Bonds in Transmembrane $\alpha$ -Helices. <i>Biophysical Journal</i> , 2002, 83, 2084-2095.	0.5	75
94	The Closed State of a H <sup>+</sup> Channel Helical Bundle Combining Precise Orientational and Distance Restraints from Solid State NMR. <i>Biochemistry</i> , 2002, 41, 13170-13177.	2.5	210
95	Complete Cross-Validation and R-Factor Calculation of a Solid-State NMR Derived Structure. <i>Journal of the American Chemical Society</i> , 2001, 123, 7292-7298.	13.7	25