

# Jie-Oh Lee

## List of Publications by Year in descending order

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64  
papers

12,870  
citations

94415

37  
h-index

123420

61  
g-index

64  
all docs

64  
docs citations

64  
times ranked

15259  
citing authors

#	ARTICLE	IF	CITATIONS
1	The structural basis of lipopolysaccharide recognition by the TLR4-MD-2 complex. <i>Nature</i> , 2009, 458, 1191-1195.	27.8	1,857
2	Crystal Structure of the TLR4-MD-2 Complex with Bound Endotoxin Antagonist Eritoran. <i>Cell</i> , 2007, 130, 906-917.	28.9	1,499
3	Crystal Structure of the TLR1-TLR2 Heterodimer Induced by Binding of a Tri-Acylated Lipopeptide. <i>Cell</i> , 2007, 130, 1071-1082.	28.9	1,154
4	Crystal Structure of the PTEN Tumor Suppressor. <i>Cell</i> , 1999, 99, 323-334.	28.9	974
5	Crystal structure of the A domain from the $\alpha$ subunit of integrin CR3 (CD11 b/CD18). <i>Cell</i> , 1995, 80, 631-638.	28.9	917
6	Recognition of lipopolysaccharide pattern by TLR4 complexes. <i>Experimental and Molecular Medicine</i> , 2013, 45, e66-e66.	7.7	816
7	Recognition of Lipopeptide Patterns by Toll-like Receptor 2-Toll-like Receptor 6 Heterodimer. <i>Immunity</i> , 2009, 31, 873-884.	14.3	641
8	Structures of the Toll-like Receptor Family and Its Ligand Complexes. <i>Immunity</i> , 2008, 29, 182-191.	14.3	470
9	Structural basis for inhibition of the cyclin-dependent kinase Cdk6 by the tumour suppressor p16INK4a. <i>Nature</i> , 1998, 395, 237-243.	27.8	468
10	Structure of the retinoblastoma tumour-suppressor pocket domain bound to a peptide from HPV E7. <i>Nature</i> , 1998, 391, 859-865.	27.8	430
11	Two conformations of the integrin A-domain (I-domain): a pathway for activation?. <i>Structure</i> , 1995, 3, 1333-1340.	3.3	396
12	Structural Biology of the Toll-Like Receptor Family. <i>Annual Review of Biochemistry</i> , 2011, 80, 917-941.	11.1	285
13	Reconstruction of LPS Transfer Cascade Reveals Structural Determinants within LBP, CD14, and TLR4-MD2 for Efficient LPS Recognition and Transfer. <i>Immunity</i> , 2017, 46, 38-50.	14.3	274
14	Structure of the catalytic domain of human phosphodiesterase 5 with bound drug molecules. <i>Nature</i> , 2003, 425, 98-102.	27.8	258
15	Crystal Structure of CD14 and Its Implications for Lipopolysaccharide Signaling. <i>Journal of Biological Chemistry</i> , 2005, 280, 11347-11351.	3.4	224
16	Role of the Tumor Suppressor RASSF1A in Mst1-Mediated Apoptosis. <i>Cancer Research</i> , 2006, 66, 2562-2569.	0.9	167
17	Sensing of microbial molecular patterns by Toll-like receptors. <i>Immunological Reviews</i> , 2012, 250, 216-229.	6.0	150
18	Structural insight into dimeric interaction of the SARAH domains from Mst1 and RASSF family proteins in the apoptosis pathway. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 9236-9241.	7.1	124

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19	The structural basis for the negative regulation of thioredoxin by thioredoxin-interacting protein. <i>Nature Communications</i> , 2014, 5, 2958.	12.8	114
20	Structural Diversity of the Hagfish Variable Lymphocyte Receptors. <i>Journal of Biological Chemistry</i> , 2007, 282, 6726-6732.	3.4	104
21	The Crystal Structure of Lipopolysaccharide Binding Protein Reveals the Location of a Frequent Mutation that Impairs Innate Immunity. <i>Immunity</i> , 2013, 39, 647-660.	14.3	102
22	Crystal structure of phosphodiesterase 4D and inhibitor complex1. <i>FEBS Letters</i> , 2002, 530, 53-58.	2.8	100
23	Structure of PP4397 Reveals the Molecular Basis for Different c-di-GMP Binding Modes by Pilz Domain Proteins. <i>Journal of Molecular Biology</i> , 2010, 398, 97-110.	4.2	94
24	Structural basis for LAR-RPTP/Slitrk complex-mediated synaptic adhesion. <i>Nature Communications</i> , 2014, 5, 5423.	12.8	94
25	Crystal structure of <i>Drosophila</i> angiotensin I-converting enzyme bound to captopril and lisinopril 1. <i>FEBS Letters</i> , 2003, 538, 65-70.	2.8	93
26	Crystal structure of the BAFF-BAFF-R complex and its implications for receptor activation. <i>Nature Structural and Molecular Biology</i> , 2003, 10, 342-348.	8.2	82
27	Structures of TLR-ligand complexes. <i>Current Opinion in Immunology</i> , 2008, 20, 414-419.	5.5	78
28	Crystallographic and Mutational Analysis of the CD40-CD154 Complex and Its Implications for Receptor Activation. <i>Journal of Biological Chemistry</i> , 2011, 286, 11226-11235.	3.4	78
29	Structural Studies of Potassium Transport Protein KtrA Regulator of Conductance of K <sup>+</sup> (RCK) C Domain in Complex with Cyclic Diadenosine Monophosphate (c-di-AMP). <i>Journal of Biological Chemistry</i> , 2015, 290, 16393-16402.	3.4	74
30	Crystal Structure of the Human N-Myc Downstream-regulated Gene 2 Protein Provides Insight into Its Role as a Tumor Suppressor. <i>Journal of Biological Chemistry</i> , 2011, 286, 12450-12460.	3.4	60
31	Higd-1a interacts with Opa1 and is required for the morphological and functional integrity of mitochondria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 13014-13019.	7.1	53
32	Activation of Ras Up-regulates Pro-apoptotic BNIP3 in Nitric Oxide-induced Cell Death. <i>Journal of Biological Chemistry</i> , 2006, 281, 33939-33948.	3.4	49
33	Cytosolic NADP <sup>+</sup> -dependent isocitrate dehydrogenase protects macrophages from LPS-induced nitric oxide and reactive oxygen species. <i>Biochemical and Biophysical Research Communications</i> , 2004, 317, 558-564.	2.1	48
34	Structural Insights into Modulation of Neurexin-Neuroigin Trans -synaptic Adhesion by MDGA1/Neuroigin-2 Complex. <i>Neuron</i> , 2017, 94, 1121-1131.e6.	8.1	48
35	Nitric oxide induces BNIP3 expression that causes cell death in macrophages. <i>Biochemical and Biophysical Research Communications</i> , 2004, 321, 298-305.	2.1	42
36	The survival effect of mitochondrial Higd-1a is associated with suppression of cytochrome C release and prevention of caspase activation. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2011, 1813, 2088-2098.	4.1	42

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37	Is TALL-1 a trimer or a virus-like cluster?. Nature, 2004, 427, 413-414.	27.8	37
38	Structural Insights into the Monosaccharide Specificity of Escherichia coli Rhamnose Mutarotase. Journal of Molecular Biology, 2005, 349, 153-162.	4.2	26
39	Construction of novel repeat proteins with rigid and predictable structures using a shared helix method. Scientific Reports, 2017, 7, 2595.	3.3	25
40	LAR-RPTP Clustering Is Modulated by Competitive Binding between Synaptic Adhesion Partners and Heparan Sulfate. Frontiers in Molecular Neuroscience, 2017, 10, 327.	2.9	25
41	Structural insights into the regulation of sialic acid catabolism by the <i>Vibrio vulnificus</i> transcriptional repressor NanR. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E2829-37.	7.1	22
42	Crystal structures of mono- and bi-specific diabodies and reduction of their structural flexibility by introduction of disulfide bridges at the Fv interface. Scientific Reports, 2016, 6, 34515.	3.3	19
43	Connecting two proteins using a fusion alpha helix stabilized by a chemical cross linker. Nature Communications, 2016, 7, 11031.	12.8	19
44	Application of hybrid LRR technique to protein crystallization. BMB Reports, 2008, 41, 353-357.	2.4	19
45	Toll-Like Receptor 4 Decoy, TOY, Attenuates Gram-Negative Bacterial Sepsis. PLoS ONE, 2009, 4, e7403.	2.5	18
46	The presence of monoglucosylated N196-glycan is important for the structural stability of storage protein, arylphorin. Biochemical Journal, 2009, 421, 87-96.	3.7	17
47	Structural diversity and flexibility of diabodies. Methods, 2019, 154, 136-142.	3.8	17
48	Interleukin-9 Inhibits Lung Metastasis of Melanoma through Stimulating Anti-Tumor M1 Macrophages. Molecules and Cells, 2020, 43, 479-490.	2.6	17
49	Application of antihelix antibodies in protein structure determination. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 17786-17791.	7.1	16
50	Structural insights into the elevator-like mechanism of the sodium/citrate symporter CitS. Scientific Reports, 2017, 7, 2548.	3.3	15
51	Structural Basis for the Conformational Integrity of the Arabidopsis thaliana HY5 Leucine Zipper Homodimer. Journal of Biological Chemistry, 2007, 282, 12989-13002.	3.4	14
52	Srs2 possesses a non-canonical PIP box in front of its SBM for precise recognition of SUMOylated PCNA. Journal of Molecular Cell Biology, 2012, 4, 258-261.	3.3	14
53	Insights into the regulation of human Rev1 for translesion synthesis polymerases revealed by the structural studies on its polymerase-interacting domain. Journal of Molecular Cell Biology, 2013, 5, 204-206.	3.3	14
54	Crosstalk between the Producers and Immune Targets of IL-9. Immune Network, 2020, 20, e45.	3.6	14

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55	A critical role for the histidine residues in the catalytic function of acyl-CoA:cholesterol acyltransferase catalysis: Evidence for catalytic difference between ACAT1 and ACAT2. <i>FEBS Letters</i> , 2006, 580, 2741-2749.	2.8	13
56	The application of helix fusion methods in structural biology. <i>Current Opinion in Structural Biology</i> , 2020, 60, 110-116.	5.7	13
57	Unique binding mode of Evogliptin with human dipeptidyl peptidase IV. <i>Biochemical and Biophysical Research Communications</i> , 2017, 494, 452-459.	2.1	11
58	Higd-1a regulates the proliferation of pancreatic cancer cells through a pERK/p27KIP1/pRB pathway. <i>Cancer Letters</i> , 2019, 461, 78-89.	7.2	10
59	Attachment of flagellin enhances the immunostimulatory activity of a hemagglutinin-ferritin nano-cage. <i>Nanomedicine: Nanotechnology, Biology, and Medicine</i> , 2019, 17, 223-235.	3.3	9
60	Regulation of CD40 reconstitution into a liposome using different ratios of solubilized LDAO to lipids. <i>Colloids and Surfaces B: Biointerfaces</i> , 2008, 62, 51-57.	5.0	5
61	Protective and Therapeutic Effects of an IL-15:IL-15R $\alpha$ -Secreting Cell-Based Cancer Vaccine Using a Baculovirus System. <i>Cancers</i> , 2021, 13, 4039.	3.7	2
62	Structural and biophysical properties of RIG-I bound to dsRNA with G-U wobble base pairs. <i>RNA Biology</i> , 2020, 17, 325-334.	3.1	0
63	Cryo-electron microscopy research at the institute of membrane proteins: current status and future prospects. <i>Biodesign</i> , 2020, 8, 87-92.	0.4	0
64	Structural features of a minimal intact methyltransferase of a type I restriction-modification system. <i>International Journal of Biological Macromolecules</i> , 2022, 208, 381-389.	7.5	0