

# Byung-Ha Oh

## List of Publications by Year in descending order

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85  
papers

8,761  
citations

36303

51  
h-index

54911

84  
g-index

86  
all docs

86  
docs citations

86  
times ranked

12361  
citing authors

#	ARTICLE	IF	CITATIONS
1	Autophagic and tumour suppressor activity of a novel Beclin1-binding protein UVRAG. <i>Nature Cell Biology</i> , 2006, 8, 688-698.	10.3	945
2	The <i>Drosophila</i> Amidase PGRP-LB Modulates the Immune Response to Bacterial Infection. <i>Immunity</i> , 2006, 24, 463-473.	14.3	423
3	Supramolecular assembly and acid resistance of <i>Helicobacter pylori</i> urease. <i>Nature Structural Biology</i> , 2001, 8, 505-509.	9.7	404
4	PGRP-LC and PGRP-LE have essential yet distinct functions in the <i>drosophila</i> immune response to monomeric DAP-type peptidoglycan. <i>Nature Immunology</i> , 2006, 7, 715-723.	14.5	345
5	Coordination of multiple dual oxidase-regulatory pathways in responses to commensal and infectious microbes in <i>drosophila</i> gut. <i>Nature Immunology</i> , 2009, 10, 949-957.	14.5	301
6	Crosstalk between the cGAS DNA Sensor and Beclin-1 Autophagy Protein Shapes Innate Antimicrobial Immune Responses. <i>Cell Host and Microbe</i> , 2014, 15, 228-238.	11.0	291
7	Evidence that inhibition of BAX activation by BCL-2 involves its tight and preferential interaction with the BH3 domain of BAX. <i>Cell Research</i> , 2011, 21, 627-641.	12.0	245
8	Crystal Structure of RNA Helicase from Genotype 1b Hepatitis C Virus. <i>Journal of Biological Chemistry</i> , 1998, 273, 15045-15052.	3.4	202
9	Crystal structure of peptidoglycan recognition protein LB from <i>Drosophila melanogaster</i> . <i>Nature Immunology</i> , 2003, 4, 787-793.	14.5	190
10	Structural and Biochemical Bases for the Inhibition of Autophagy and Apoptosis by Viral BCL-2 of Murine $\beta$ -Herpesvirus 68. <i>PLoS Pathogens</i> , 2008, 4, e25.	4.7	174
11	The Architecture of the Multisubunit TRAPP I Complex Suggests a Model for Vesicle Tethering. <i>Cell</i> , 2006, 127, 817-830.	28.9	166
12	2.8 Å... Resolution Crystal Structure of Human TRAIL, a Cytokine with Selective Antitumor Activity. <i>Immunity</i> , 1999, 11, 253-261.	14.3	158
13	DeSUMOylating isopeptidase: a second class of SUMO protease. <i>EMBO Reports</i> , 2012, 13, 339-346.	4.5	153
14	De novo design of modular and tunable protein biosensors. <i>Nature</i> , 2021, 591, 482-487.	27.8	153
15	Structure of Full-Length SMC and Rearrangements Required for Chromosome Organization. <i>Molecular Cell</i> , 2017, 67, 334-347.e5.	9.7	151
16	Structural Basis for Preferential Recognition of Diaminopimelic Acid-type Peptidoglycan by a Subset of Peptidoglycan Recognition Proteins. <i>Journal of Biological Chemistry</i> , 2006, 281, 8286-8295.	3.4	145
17	Structural Studies of a Bacterial Condensin Complex Reveal ATP-Dependent Disruption of Intersubunit Interactions. <i>Cell</i> , 2009, 136, 85-96.	28.9	145
18	Crystal Structure of a Maltogenic Amylase Provides Insights into a Catalytic Versatility. <i>Journal of Biological Chemistry</i> , 1999, 274, 26279-26286.	3.4	144

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19	Clustering of peptidoglycan recognition protein-SA is required for sensing lysine-type peptidoglycan in insects. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 6602-6607.	7.1	143
20	Cyclomaltodextrinase, Neopullulanase, and Maltogenic Amylase Are Nearly Indistinguishable from Each Other. <i>Journal of Biological Chemistry</i> , 2002, 277, 21891-21897.	3.4	139
21	Structural and functional insights into the B30.2/SPRY domain. <i>EMBO Journal</i> , 2006, 25, 1353-1363.	7.8	139
22	SMC condensin entraps chromosomal DNA by an ATP hydrolysis dependent loading mechanism in <i>Bacillus subtilis</i> . <i>ELife</i> , 2015, 4, .	6.0	130
23	Crystal structure of a clip-domain serine protease and functional roles of the clip domains. <i>EMBO Journal</i> , 2005, 24, 4404-4414.	7.8	129
24	Molecular Basis for SMC Rod Formation and Its Dissolution upon DNA Binding. <i>Molecular Cell</i> , 2015, 57, 290-303.	9.7	126
25	Crystal structures of a novel, thermostable phytase in partially and fully calcium-loaded states. <i>Nature Structural Biology</i> , 2000, 7, 147-153.	9.7	123
26	An asymmetric SMC-kinleisin bridge in prokaryotic condensin. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 371-379.	8.2	119
27	Crystal Structure of TRAIL-DR5 Complex Identifies a Critical Role of the Unique Frame Insertion in Conferring Recognition Specificity. <i>Journal of Biological Chemistry</i> , 2000, 275, 31171-31177.	3.4	114
28	Enzyme Mechanism and Catalytic Property of $\hat{I}^2$ Propeller Phytase. <i>Structure</i> , 2001, 9, 851-858.	3.3	113
29	Structural Basis for Protein Recognition by B30.2/SPRY Domains. <i>Molecular Cell</i> , 2006, 24, 967-976.	9.7	112
30	Molecular and enzymatic characterization of a maltogenic amylase that hydrolyzes and transglycosylates acarbose. <i>FEBS Journal</i> , 1998, 253, 251-262.	0.2	106
31	The TRAPP Complex: Insights into its Architecture and Function. <i>Traffic</i> , 2008, 9, 2032-2042.	2.7	106
32	Structure of malonamidase E2 reveals a novel Ser-cisSer-Lys catalytic triad in a new serine hydrolase fold that is prevalent in nature. <i>EMBO Journal</i> , 2002, 21, 2509-2516.	7.8	105
33	Structure-function studies of [2Fe-2S] ferredoxins. <i>Journal of Bioenergetics and Biomembranes</i> , 1994, 26, 67-88.	2.3	101
34	A computationally designed chimeric antigen receptor provides a small-molecule safety switch for T-cell therapy. <i>Nature Biotechnology</i> , 2020, 38, 426-432.	17.5	100
35	Optogenetic activation of intracellular antibodies for direct modulation of endogenous proteins. <i>Nature Methods</i> , 2019, 16, 1095-1100.	19.0	95
36	Structural Mechanism for Inactivation and Activation of CAD/DFP40 in the Apoptotic Pathway. <i>Molecular Cell</i> , 2004, 14, 531-539.	9.7	94

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37	Molecular basis for unidirectional scaffold switching of human Plk4 in centriole biogenesis. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 696-703.	8.2	94
38	VipD of <i>Legionella pneumophila</i> Targets Activated Rab5 and Rab22 to Interfere with Endosomal Trafficking in Macrophages. <i>PLoS Pathogens</i> , 2012, 8, e1003082.	4.7	89
39	Two-promoter vector is highly efficient for overproduction of protein complexes. <i>Protein Science</i> , 2004, 13, 1698-1703.	7.6	76
40	Crystal Structure of $\hat{1}$ "5-3-Ketosteroid Isomerase from <i>Pseudomonas testosteroni</i> in Complex with Equilenin Settles the Correct Hydrogen Bonding Scheme for Transition State Stabilization. <i>Journal of Biological Chemistry</i> , 1999, 274, 32863-32868.	3.4	74
41	Crystal Structure of SEDL and Its Implications for a Genetic Disease Spondyloepiphyseal Dysplasia Tarda. <i>Journal of Biological Chemistry</i> , 2002, 277, 49863-49869.	3.4	73
42	Kaposi's Sarcoma-Associated Herpesvirus K7 Modulates Rubicon-Mediated Inhibition of Autophagosome Maturation. <i>Journal of Virology</i> , 2013, 87, 12499-12503.	3.4	72
43	Resistance of mitochondrial DNA-deficient cells to TRAIL: role of Bax in TRAIL-induced apoptosis. <i>Oncogene</i> , 2002, 21, 3139-3148.	5.9	71
44	Structural insights into the dual nucleotide exchange and GDI displacement activity of SidM/DrrA. <i>EMBO Journal</i> , 2010, 29, 496-504.	7.8	66
45	5â€²-Triphosphate-RNA-independent activation of RIG-I via RNA aptamer with enhanced antiviral activity. <i>Nucleic Acids Research</i> , 2012, 40, 2724-2733.	14.5	62
46	Crystal Structure of the Csm1 Subunit of the Csm Complex and Its Single-Stranded DNA-Specific Nuclease Activity. <i>Structure</i> , 2015, 23, 782-790.	3.3	61
47	LIVRAG: A New Player in Autophagy and Tumor Cell Growth. <i>Autophagy</i> , 2007, 3, 69-71.	9.1	60
48	Crystal Structure of the Gtr1pGTP-Gtr2pGDP Protein Complex Reveals Large Structural Rearrangements Triggered by GTP-to-GDP Conversion. <i>Journal of Biological Chemistry</i> , 2012, 287, 29648-29653.	3.4	60
49	Architecture of the type IV coupling protein complex of <i>Legionella pneumophila</i> . <i>Nature Microbiology</i> , 2017, 2, 17114.	13.3	60
50	Macromolecular assembly of <i>Helicobacter pylori</i> urease investigated by mass spectrometry. <i>Journal of Mass Spectrometry</i> , 2003, 38, 315-320.	1.6	58
51	Crystal structure of bet3 reveals a novel mechanism for Golgi localization of tethering factor TRAPP. <i>Nature Structural and Molecular Biology</i> , 2005, 12, 38-45.	8.2	56
52	Characterization of a Novel Ser-cisSer-Lys Catalytic Triad in Comparison with the Classical Ser-His-Asp Triad. <i>Journal of Biological Chemistry</i> , 2003, 278, 24937-24943.	3.4	54
53	Characterization of a Thermostable Cyclodextrin Glucanotransferase Isolated from <i>Bacillus stearothermophilus</i> ET1â€¦. <i>Journal of Agricultural and Food Chemistry</i> , 1998, 46, 952-959.	5.2	43
54	Detection of Large pK Perturbations of an Inhibitor and a Catalytic Group at an Enzyme Active Site, a Mechanistic Basis for Catalytic Power of Many Enzymes. <i>Journal of Biological Chemistry</i> , 2000, 275, 41100-41106.	3.4	42

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55	Crystal structure of Hop2â€Mnd1 and mechanistic insights into its role in meiotic recombination. <i>Nucleic Acids Research</i> , 2015, 43, 3841-3856.	14.5	42
56	An insight into the mechanistic role of Beclin 1 and its inhibition by prosurvival Bcl-2 family proteins. <i>Autophagy</i> , 2008, 4, 519-520.	9.1	41
57	High-Resolution X-ray Crystallography Reveals Precise Binding Interactions between Human Nonpancreatic Secreted Phospholipase A2and a Highly Potent Inhibitor (FPL67047XX). <i>Journal of Medicinal Chemistry</i> , 1996, 39, 3878-3881.	6.4	40
58	Crystal structure and nucleic acidâ€binding activity of the CRISPRâ€associated protein Csx1 of <i>Pyrococcus furiosus</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2013, 81, 261-270.	2.6	40
59	High Resolution Crystal Structure of a Human Tumor Necrosis Factor-Î± Mutant with Low Systemic Toxicity. <i>Journal of Biological Chemistry</i> , 1998, 273, 2153-2160.	3.4	39
60	Regulation of <i>Drosophila</i> Vasa <i>In Vivo</i> through Paralogous Cullin-RING E3 Ligase Specificity Receptors. <i>Molecular and Cellular Biology</i> , 2010, 30, 1769-1782.	2.3	37
61	Folding of cohesinâ€™s coiled coil is important for Scc2/4-induced association with chromosomes. <i>ELife</i> , 2021, 10, .	6.0	37
62	Covalent binding of uracil DNA glycosylase UdgX to abasic DNA upon uracil excision. <i>Nature Chemical Biology</i> , 2019, 15, 607-614.	8.0	34
63	Phosphoinositides Differentially Regulate Protrudin Localization through the FYVE Domain. <i>Journal of Biological Chemistry</i> , 2012, 287, 41268-41276.	3.4	33
64	Autophagic UVRAG Promotes UV-Induced Photolesion Repair by Activation of the CRL4 DDB2 E3 Ligase. <i>Molecular Cell</i> , 2016, 62, 507-519.	9.7	33
65	Structural basis of intersubunit recognition in elongin BCâ€cullin 5â€SOCS box ubiquitinâ€protein ligase complexes. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 1587-1597.	2.5	32
66	Novel functions of viral anti-apoptotic factors. <i>Nature Reviews Microbiology</i> , 2015, 13, 7-12.	28.6	31
67	Association of Novel Domain in Active Site of Archaic Hyperthermophilic Maltogenic Amylase from <i>Staphylothermus marinus</i> . <i>Journal of Biological Chemistry</i> , 2012, 287, 7979-7989.	3.4	30
68	Structure/Function Analysis of the Periplasmic Histidine-binding Protein. <i>Journal of Biological Chemistry</i> , 1995, 270, 16097-16106.	3.4	29
69	Crystal structure of DeSlâ€1, a novel deSUMOylase belonging to a putative isopeptidase superfamily. <i>Proteins: Structure, Function and Bioinformatics</i> , 2012, 80, 2099-2104.	2.6	29
70	Identification, structural, and biochemical characterization of a group of large Csn2 proteins involved in CRISPRâ€mediated bacterial immunity. <i>Proteins: Structure, Function and Bioinformatics</i> , 2012, 80, 2573-2582.	2.6	29
71	Structural basis for effector protein recognition by the Dot/Icm Type IVB coupling protein complex. <i>Nature Communications</i> , 2020, 11, 2623.	12.8	29
72	Crystal structure of the MukB hinge domain with coiledâ€coil stretches and its functional implications. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 1483-1490.	2.6	28

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73	Biochemical and Crystallographic Studies Reveal a Specific Interaction Between TRAPP Subunits Trs33p and Bet3p. <i>Traffic</i> , 2005, 6, 1183-1195.	2.7	26
74	RNA activation-independent DNA targeting of the Type III CRISPR-Cas system by a Csm complex. <i>EMBO Reports</i> , 2017, 18, 826-840.	4.5	23
75	Crystal Structures of RbsD Leading to the Identification of Cytoplasmic Sugar-binding Proteins with a Novel Folding Architecture. <i>Journal of Biological Chemistry</i> , 2003, 278, 28173-28180.	3.4	20
76	Preliminary X-ray crystallographic analysis of a novel phytase from a <i>Bacillus amyloliquefaciens</i> strain. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 691-693.	2.5	19
77	Lpg0393 of <i>Legionella pneumophila</i> Is a Guanine-Nucleotide Exchange Factor for Rab5, Rab21 and Rab22. <i>PLoS ONE</i> , 2015, 10, e0118683.	2.5	16
78	Computational design of a neutralizing antibody with picomolar binding affinity for all concerning SARS-CoV-2 variants. <i>MAbs</i> , 2022, 14, 2021601.	5.2	11
79	Structural basis of inactivation of Ras and Rap1 small GTPases by Ras/Rap1-specific endopeptidase from the sepsis-causing pathogen <i>Vibrio vulnificus</i> . <i>Journal of Biological Chemistry</i> , 2018, 293, 18110-18122.	3.4	8
80	In vivo genome editing using the Cpf1 ortholog derived from <i>Eubacterium eligens</i> . <i>Scientific Reports</i> , 2019, 9, 13911.	3.3	6
81	Structural and functional characterization of a monoclonal antibody blocking TIGIT. <i>MAbs</i> , 2022, 14, 2013750.	5.2	6
82	Reversible modification of mitochondrial ADP/ATP translocases by paired <i>Legionella</i> effector proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	6
83	Identification of a Highly Conserved Hypothetical Protein TON_0340 as a Probable Manganese-Dependent Phosphatase. <i>PLoS ONE</i> , 2016, 11, e0167549.	2.5	1
84	Evidence for binary Smc complexes lacking kite subunits in archaea. <i>IUCr</i> , 2020, 7, 193-206.	2.2	1
85	Crystal structure of PYCH_01220 from <i>Pyrococcus yanosii</i> potentially involved in binding nucleic acid. <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 468-472.	2.6	0