

Gye Won Han

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

118 papers	14,328 citations	52 h-index	119 g-index
120 ext. papers	16,338 ext. citations	19 avg, IF	5.76 L-index

#	Paper	IF	Citations
118	Structural insights on ligand recognition at the human leukotriene B4 receptor 1. <i>Nature Communications</i> , 2021 , 12, 2971	17.4	4
117	Allosteric Coupling of Drug Binding and Intracellular Signaling in the A2A Adenosine Receptor 2021 , 184-196		
116	Structural basis of the activation of a metabotropic GABA receptor. <i>Nature</i> , 2020 , 584, 298-303	50.4	49
115	Full-length human GLP-1 receptor structure without orthosteric ligands. <i>Nature Communications</i> , 2020 , 11, 1272	17.4	42
114	Structural basis of ligand binding modes at the human formyl peptide receptor 2. <i>Nature Communications</i> , 2020 , 11, 1208	17.4	34
113	Harnessing the power of an X-ray laser for serial crystallography of membrane proteins crystallized in lipidic cubic phase. <i>IUCrJ</i> , 2020 , 7, 976-984	4.7	8
112	An orthogonal seryl-tRNA synthetase/tRNA pair for noncanonical amino acid mutagenesis in Escherichia coli. <i>Bioorganic and Medicinal Chemistry</i> , 2020 , 28, 115662	3.4	3
111	Determination of the melanocortin-4 receptor structure identifies Ca as a cofactor for ligand binding. <i>Science</i> , 2020 , 368, 428-433	33.3	46
110	A Single Reactive Noncanonical Amino Acid Is Able to Dramatically Stabilize Protein Structure. <i>ACS Chemical Biology</i> , 2019 , 14, 1150-1153	4.9	9
109	Structural basis of ligand recognition at the human MT melatonin receptor. <i>Nature</i> , 2019 , 569, 284-288	50.4	98
108	XFEL structures of the human MT melatonin receptor reveal the basis of subtype selectivity. <i>Nature</i> , 2019 , 569, 289-292	50.4	77
107	Structure-based mechanism of cysteinyl leukotriene receptor inhibition by antiasthmatic drugs. <i>Science Advances</i> , 2019 , 5, eaax2518	14.3	41
106	Toward G protein-coupled receptor structure-based drug design using X-ray lasers. <i>IUCrJ</i> , 2019 , 6, 1106-1119	11.9	28
105	Molecular Mechanism for Ligand Recognition and Subtype Selectivity of β -Adrenergic Receptor. <i>Cell Reports</i> , 2019 , 29, 2936-2943.e4	10.6	5
104	Elucidating the active μ -opioid receptor crystal structure with peptide and small-molecule agonists. <i>Science Advances</i> , 2019 , 5, eaax9115	14.3	38
103	Structural basis of ligand selectivity and disease mutations in cysteinyl leukotriene receptors. <i>Nature Communications</i> , 2019 , 10, 5573	17.4	31
102	Structural Basis of the Diversity of Adrenergic Receptors. <i>Cell Reports</i> , 2019 , 29, 2929-2935.e4	10.6	13

101	Crystal Structure of the Human Cannabinoid Receptor CB2. <i>Cell</i> , 2019 , 176, 459-467.e13	56.2	175
100	Crystal structure of misoprostol bound to the labor inducer prostaglandin E receptor. <i>Nature Chemical Biology</i> , 2019 , 15, 11-17	11.7	23
99	5-HT Receptor Structures Reveal the Structural Basis of GPCR Polypharmacology. <i>Cell</i> , 2018 , 172, 719-730.e14	36.1	123
98	Structural Connection between Activation Microswitch and Allosteric Sodium Site in GPCR Signaling. <i>Structure</i> , 2018 , 26, 259-269.e5	5.2	77
97	Allosteric Coupling of Drug Binding and Intracellular Signaling in the A Adenosine Receptor. <i>Cell</i> , 2018 , 172, 68-80.e12	56.2	119
96	Structure of the Nanobody-Stabilized Active State of the Kappa Opioid Receptor. <i>Cell</i> , 2018 , 172, 55-67.e15	36.1	205
95	Crystal structure of the Frizzled 4 receptor in a ligand-free state. <i>Nature</i> , 2018 , 560, 666-670	50.4	51
94	Advances in Structure Determination of G Protein-Coupled Receptors by SFX 2018 , 301-329		1
93	Structural basis for signal recognition and transduction by platelet-activating-factor receptor. <i>Nature Structural and Molecular Biology</i> , 2018 , 25, 488-495	17.6	37
92	Generation of an Orthogonal Protein-Protein Interface with a Noncanonical Amino Acid. <i>Journal of the American Chemical Society</i> , 2017 , 139, 5728-5731	16.4	13
91	Structure of the full-length glucagon class B G-protein-coupled receptor. <i>Nature</i> , 2017 , 546, 259-264	50.4	141
90	Human GLP-1 receptor transmembrane domain structure in complex with allosteric modulators. <i>Nature</i> , 2017 , 546, 312-315	50.4	143
89	Crystal structure of a multi-domain human smoothened receptor in complex with a super stabilizing ligand. <i>Nature Communications</i> , 2017 , 8, 15383	17.4	62
88	Structural Basis for Apelin Control of the Human Apelin Receptor. <i>Structure</i> , 2017 , 25, 858-866.e4	5.2	74
87	Structure of CC Chemokine Receptor 5 with a Potent Chemokine Antagonist Reveals Mechanisms of Chemokine Recognition and Molecular Mimicry by HIV. <i>Immunity</i> , 2017 , 46, 1005-1017.e5	32.3	106
86	Structural basis for selectivity and diversity in angiotensin II receptors. <i>Nature</i> , 2017 , 544, 327-332	50.4	128
85	Structural insights into the extracellular recognition of the human serotonin 2B receptor by an antibody. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, 8223-8228	11.5	43
84	Crystal structures of agonist-bound human cannabinoid receptor CB. <i>Nature</i> , 2017 , 547, 468-471	50.4	270

83	Structural insights into the molecular mechanisms of myasthenia gravis and their therapeutic implications. <i>ELife</i> , 2017 , 6,	8.9	10
82	Native phasing of x-ray free-electron laser data for a G protein-coupled receptor. <i>Science Advances</i> , 2016 , 2, e1600292	14.3	85
81	X-ray laser diffraction for structure determination of the rhodopsin-arrestin complex. <i>Scientific Data</i> , 2016 , 3, 160021	8.2	40
80	Crystal Structure of the Human Cannabinoid Receptor CB. <i>Cell</i> , 2016 , 167, 750-762.e14	56.2	323
79	Structure of CC chemokine receptor 2 with orthosteric and allosteric antagonists. <i>Nature</i> , 2016 , 540, 458-461	50.4	168
78	Structural biology. Crystal structure of the chemokine receptor CXCR4 in complex with a viral chemokine. <i>Science</i> , 2015 , 347, 1117-22	33.3	262
77	Crystal Structure of Antagonist Bound Human Lysophosphatidic Acid Receptor 1. <i>Cell</i> , 2015 , 161, 1633-43	56.2	129
76	Crystal structure of rhodopsin bound to arrestin by femtosecond X-ray laser. <i>Nature</i> , 2015 , 523, 561-7	50.4	572
75	Structure of the Angiotensin receptor revealed by serial femtosecond crystallography. <i>Cell</i> , 2015 , 161, 833-44	56.2	262
74	Two disparate ligand-binding sites in the human P2Y1 receptor. <i>Nature</i> , 2015 , 520, 317-21	50.4	239
73	The Importance of Ligand-Receptor Conformational Pairs in Stabilization: Spotlight on the N/OFQ G Protein-Coupled Receptor. <i>Structure</i> , 2015 , 23, 2291-2299	5.2	53
72	Structural Basis for Ligand Recognition and Functional Selectivity at Angiotensin Receptor. <i>Journal of Biological Chemistry</i> , 2015 , 290, 29127-39	5.4	111
71	Exploring the potential impact of an expanded genetic code on protein function. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, 6961-6	11.5	56
70	Transition states. Trapping a transition state in a computationally designed protein bottle. <i>Science</i> , 2015 , 347, 863-867	33.3	31
69	Structural basis for bifunctional peptide recognition at human Ebpioid receptor. <i>Nature Structural and Molecular Biology</i> , 2015 , 22, 265-8	17.6	133
68	Structure of a class C GPCR metabotropic glutamate receptor 1 bound to an allosteric modulator. <i>Science</i> , 2014 , 344, 58-64	33.3	406
67	Lipidic cubic phase injector facilitates membrane protein serial femtosecond crystallography. <i>Nature Communications</i> , 2014 , 5, 3309	17.4	416
66	Structure of the human P2Y12 receptor in complex with an antithrombotic drug. <i>Nature</i> , 2014 , 509, 115-8	50.4	272

65	Structural basis for Smoothed receptor modulation and chemoresistance to anticancer drugs. <i>Nature Communications</i> , 2014 , 5, 4355	17.4	175
64	Agonist-bound structure of the human P2Y12 receptor. <i>Nature</i> , 2014 , 509, 119-22	50.4	222
63	Structure of the human glucagon class B G-protein-coupled receptor. <i>Nature</i> , 2013 , 499, 444-9	50.4	312
62	The role of a sodium ion binding site in the allosteric modulation of the A(2A) adenosine G protein-coupled receptor. <i>Structure</i> , 2013 , 21, 2175-85	5.2	98
61	Serial femtosecond crystallography of G protein-coupled receptors. <i>Science</i> , 2013 , 342, 1521-4	33.3	367
60	Structure of the CCR5 chemokine receptor-HIV entry inhibitor maraviroc complex. <i>Science</i> , 2013 , 341, 1387-90	33.3	505
59	Structural features for functional selectivity at serotonin receptors. <i>Science</i> , 2013 , 340, 615-9	33.3	492
58	Structural basis for molecular recognition at serotonin receptors. <i>Science</i> , 2013 , 340, 610-4	33.3	370
57	Structure of the human smoothed receptor bound to an antitumour agent. <i>Nature</i> , 2013 , 497, 338-43	50.4	375
56	Crystal structure of a voltage-gated K ⁺ channel pore module in a closed state in lipid membranes.. <i>Journal of Biological Chemistry</i> , 2013 , 288, 3476	5.4	78
55	Crystal structure of a voltage-gated K ⁺ channel pore module in a closed state in lipid membranes. <i>Journal of Biological Chemistry</i> , 2012 , 287, 43063-70	5.4	19
54	Structural basis for allosteric regulation of GPCRs by sodium ions. <i>Science</i> , 2012 , 337, 232-6	33.3	714
53	Crystal structure of a lipid G protein-coupled receptor. <i>Science</i> , 2012 , 335, 851-5	33.3	538
52	Functional and structural characterization of a thermostable acetyl esterase from <i>Thermotoga maritima</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2012 , 80, 1545-59	4.2	36
51	Structure of the human Ebpioid receptor in complex with JD1c. <i>Nature</i> , 2012 , 485, 327-32	50.4	695
50	Structure of an agonist-bound human A2A adenosine receptor. <i>Science</i> , 2011 , 332, 322-7	33.3	706
49	Structure of the human histamine H1 receptor complex with doxepin. <i>Nature</i> , 2011 , 475, 65-70	50.4	630
48	Crystal structure of a metal-dependent phosphoesterase (YP_910028.1) from <i>Bifidobacterium adolescentis</i> : Computational prediction and experimental validation of phosphoesterase activity. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011 , 79, 2146-60	4.2	11

47	Crystal structure of soluble MD-1 and its interaction with lipid IVA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 10990-5	11.5	34
46	Structure of the human dopamine D3 receptor in complex with a D2/D3 selective antagonist. <i>Science</i> , 2010 , 330, 1091-5	33.3	93 ⁸
45	Bacterial pleckstrin homology domains: a prokaryotic origin for the PH domain. <i>Journal of Molecular Biology</i> , 2010 , 396, 31-46	6.5	25
44	Crystal structure of the first eubacterial Mre11 nuclease reveals novel features that may discriminate substrates during DNA repair. <i>Journal of Molecular Biology</i> , 2010 , 397, 647-63	6.5	37
43	The crystal structure of a bacterial Sufu-like protein defines a novel group of bacterial proteins that are similar to the N-terminal domain of human Sufu. <i>Protein Science</i> , 2010 , 19, 2131-40	6.3	12
42	Structural and functional characterizations of SsgB, a conserved activator of developmental cell division in morphologically complex actinomycetes. <i>Journal of Biological Chemistry</i> , 2009 , 284, 25268-79	5.4	17
41	Structural basis of murein peptide specificity of a gamma-D-glutamyl-L-diamino acid endopeptidase. <i>Structure</i> , 2009 , 17, 303-13	5.2	57
40	Crystal structure of a novel archaeal AAA+ ATPase SSO1545 from <i>Sulfolobus solfataricus</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2009 , 74, 1041-9	4.2	8
39	Crystal structure of the Fic (Filamentation induced by cAMP) family protein SO4266 (gi 24375750) from <i>Shewanella oneidensis</i> MR-1 at 1.6 Å resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009 , 75, 264-71	4.2	19
38	A structural basis for the regulatory inactivation of DnaA. <i>Journal of Molecular Biology</i> , 2009 , 385, 368-80	6.5	13
37	Crystal structure of histidine phosphotransfer protein ShpA, an essential regulator of stalk biogenesis in <i>Caulobacter crescentus</i> . <i>Journal of Molecular Biology</i> , 2009 , 390, 686-98	6.5	12
36	Crystal structure of AICAR transformylase IMP cyclohydrolase (TM1249) from <i>Thermotoga maritima</i> at 1.88 Å resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008 , 71, 1042-9	4.2	6
35	Crystal structure of an ADP-ribosylated protein with a cytidine deaminase-like fold, but unknown function (TM1506), from <i>Thermotoga maritima</i> at 2.70 Å resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008 , 71, 1546-52	4.2	6
34	Crystal structures of MW1337R and lin2004: representatives of a novel protein family that adopt a four-helical bundle fold. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008 , 71, 1589-96	4.2	3
33	Crystal structure of homoserine O-succinyltransferase from <i>Bacillus cereus</i> at 2.4 Å resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007 , 68, 999-1005	4.2	11
32	Crystal structure of NMA1982 from <i>Neisseria meningitidis</i> at 1.5 angstroms resolution provides a structural scaffold for nonclassical, eukaryotic-like phosphatases. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007 , 69, 415-21	4.2	7
31	Crystal structure of TM1030 from <i>Thermotoga maritima</i> at 2.3 Å resolution reveals molecular details of its transcription repressor function. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007 , 68, 418-24	4.2	5
30	Crystal structures of two novel dye-decolorizing peroxidases reveal a beta-barrel fold with a conserved heme-binding motif. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007 , 69, 223-33	4.2	68

29	Crystal structure of MtnX phosphatase from <i>Bacillus subtilis</i> at 2.0 angstroms resolution provides a structural basis for bipartite phosphomonoester hydrolysis of 2-hydroxy-3-keto-5-methylthiopentenyl-1-phosphate. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007 , 69, 433-9	4.2	6
28	Identification and structural characterization of heme binding in a novel dye-decolorizing peroxidase, TyrA. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007 , 69, 234-43	4.2	61
27	Structural and biophysical characterization of the EphB4*ephrinB2 protein-protein interaction and receptor specificity. <i>Journal of Biological Chemistry</i> , 2006 , 281, 28185-92	5.4	71
26	Crystal structure of phosphoribosylformylglycinamide synthase II (smPurL) from <i>Thermotoga maritima</i> at 2.15 Å resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006 , 63, 1106-11	4.2	7
25	Crystal structure of TM1367 from <i>Thermotoga maritima</i> at 1.90 Å resolution reveals an atypical member of the cyclophilin (peptidylprolyl isomerase) fold. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006 , 63, 1112-8	4.2	6
24	Crystal structure of acireductone dioxygenase (ARD) from <i>Mus musculus</i> at 2.06 angstrom resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006 , 64, 808-13	4.2	25
23	Crystal structure of the ApbE protein (TM1553) from <i>Thermotoga maritima</i> at 1.58 Å resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006 , 64, 1083-90	4.2	10
22	Crystal structure of an ORFan protein (TM1622) from <i>Thermotoga maritima</i> at 1.75 Å resolution reveals a fold similar to the Ran-binding protein Mog1p. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006 , 65, 777-82	4.2	7
21	Comparative structural analysis of a novel glutathioneS-transferase (ATU5508) from <i>Agrobacterium tumefaciens</i> at 2.0 Å resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006 , 65, 527-37	4.2	8
20	Crystal structure of virulence factor CJ0248 from <i>Campylobacter jejuni</i> at 2.25 Å resolution reveals a new fold. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006 , 62, 292-6	4.2	6
19	Structure-based chemical modification strategy for enzyme replacement treatment of phenylketonuria. <i>Molecular Genetics and Metabolism</i> , 2005 , 86, 134-40	3.7	54
18	Crystal structure of an alpha/beta serine hydrolase (YDR428C) from <i>Saccharomyces cerevisiae</i> at 1.85 Å resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005 , 58, 755-8	4.2	10
17	The structure of a eukaryotic nicotinic acid phosphoribosyltransferase reveals structural heterogeneity among type II PRTases. <i>Structure</i> , 2005 , 13, 1385-96	5.2	30
16	Crystal structure of an alanine-glyoxylate aminotransferase from <i>Anabaena</i> sp. at 1.70 Å resolution reveals a noncovalently linked PLP cofactor. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005 , 58, 971-5	4.2	11
15	Crystal structure of S-adenosylmethionine:tRNA ribosyltransferase-isomerase (QueA) from <i>Thermotoga maritima</i> at 2.0 Å resolution reveals a new fold. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005 , 59, 869-74	4.2	13
14	Crystal structure of an indigoidine synthase A (IndA)-like protein (TM1464) from <i>Thermotoga maritima</i> at 1.90 Å resolution reveals a new fold. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005 , 59, 864-8	4.2	12
13	Crystal structure of an Apo mRNA decapping enzyme (DcpS) from Mouse at 1.83 Å resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005 , 60, 797-802	4.2	10
12	Crystal structure of a putative modulator of DNA gyrase (pmbA) from <i>Thermotoga maritima</i> at 1.95 Å resolution reveals a new fold. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005 , 61, 444-8	4.2	8

11	Crystal structure of the global regulatory protein CsrA from <i>Pseudomonas putida</i> at 2.05 Å resolution reveals a new fold. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005 , 61, 449-53	4.2	45
10	Crystal structure of Hsp33 chaperone (TM1394) from <i>Thermotoga maritima</i> at 2.20 Å resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005 , 61, 669-73	4.2	13
9	Crystal structure of a conserved hypothetical protein (gi: 13879369) from Mouse at 1.90 Å resolution reveals a new fold. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005 , 61, 1132-6	4.2	9
8	An unusual sugar conformation in the structure of an RNA/DNA decamer of the polypurine tract may affect recognition by RNase H. <i>Journal of Molecular Biology</i> , 2003 , 334, 653-65	6.5	40
7	Crystal structure of an RNA/DNA hybrid reveals intermolecular intercalation: dimer formation by base-pair swapping. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003 , 100, 9214-9	11.5	16
6	Metal ions and phosphate binding in the H-N-H motif: crystal structures of the nuclease domain of ColE7/Im7 in complex with a phosphate ion and different divalent metal ions. <i>Protein Science</i> , 2002 , 11, 2947-57	6.3	45
5	Direct-methods determination of an RNA/DNA hybrid decamer at 1.15 Å resolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001 , 57, 213-8		6
4	Structural basis of non-specific lipid binding in maize lipid-transfer protein complexes revealed by high-resolution X-ray crystallography. <i>Journal of Molecular Biology</i> , 2001 , 308, 263-78	6.5	145
3	Lactate dehydrogenase from the hyperthermophilic archaeon <i>Methanococcus jannaschii</i> : overexpression, crystallization and preliminary X-ray analysis. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000 , 56, 81-3		2
2	Structure of a DNA analog of the primer for HIV-1 RT second strand synthesis. <i>Journal of Molecular Biology</i> , 1997 , 269, 811-26	6.5	48
1	Defining GC-specificity in the minor groove: side-by-side binding of the di-imidazole lexitropsin to C-A-T-G-G-C-C-A-T-G. <i>Structure</i> , 1997 , 5, 1033-46	5.2	98