

Ryuichi Kato

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8180244/publications.pdf>

Version: 2024-02-01

99
papers

4,631
citations

136740

32
h-index

106150

65
g-index

102
all docs

102
docs citations

102
times ranked

6083
citing authors

#	ARTICLE	IF	CITATIONS
1	Chemical and Chemo-Enzymatic Syntheses of Glycans Containing Ribitol Phosphate Scaffolding of Matriglycan. <i>ACS Chemical Biology</i> , 2022, 17, 1513-1523.	1.6	1
2	A fully automated crystallization apparatus for small protein quantities. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2021, 77, 29-36.	0.4	11
3	The structure of POMGNT2 provides new insights into the mechanism to determine the functional O- α -mannosylation site on β -mannidase. <i>Genes To Cells</i> , 2021, 26, 485-494.	0.5	5
4	Automation of Crystallization Screening at KEK. <i>Nihon Kessho Gakkaishi</i> , 2021, 63, 212-215.	0.0	0
5	How Does a Microbial Rhodopsin R \times R Realize Its Exceptionally High Thermostability with the Proton-Pumping Function Being Retained?. <i>Journal of Physical Chemistry B</i> , 2020, 124, 990-1000.	1.2	15
6	FAM3B/PANDER-Like Carbohydrate-Binding Domain in a Glycosyltransferase, POMGNT1. <i>Methods in Molecular Biology</i> , 2020, 2132, 609-619.	0.4	1
7	Crystal structures of fukutin-related protein (FKRP), a ribitol-phosphate transferase related to muscular dystrophy. <i>Nature Communications</i> , 2020, 11, 303.	5.8	21
8	Improvement of Production and Isolation of Human Neuraminidase-1 in Cellulose Crystals. <i>ACS Applied Bio Materials</i> , 2019, 2, 4941-4952.	2.3	5
9	<i>Structural Biology of Glycans</i> , 2019, , 35-63.		0
10	Carbohydrate Recognition Mechanism of the Mushroom Galectin ACG. <i>Trends in Glycoscience and Glycotechnology</i> , 2018, 30, SJ33-SJ46.	0.0	8
11	Carbohydrate Recognition Mechanism of the Mushroom Galectin ACG. <i>Trends in Glycoscience and Glycotechnology</i> , 2018, 30, SE75-SE88.	0.0	3
12	Role of the constant region domain in the structural diversity of human antibody light chains. <i>FASEB Journal</i> , 2017, 31, 1668-1677.	0.2	9
13	Phosphorylation of the mitochondrial autophagy receptor Nix enhances its interaction with LC3 proteins. <i>Scientific Reports</i> , 2017, 7, 1131.	1.6	203
14	Synthesis of seleno-fucose compounds and their application to the X-ray structural determination of carbohydrate-lectin complexes using single/multi-wavelength anomalous dispersion phasing. <i>Bioorganic and Medicinal Chemistry</i> , 2017, 25, 1132-1142.	1.4	13
15	X-ray structure of a protease-resistant mutant form of human galectin-9 having two carbohydrate recognition domains with a metal-binding site. <i>Biochemical and Biophysical Research Communications</i> , 2017, 490, 1287-1293.	1.0	5
16	Experimental phase determination with selenomethionine or mercury-derivatization in serial femtosecond crystallography. <i>IUCr</i> , 2017, 4, 639-647.	1.0	24
17	Classification and Comparison of Fucose-Binding Lectins Based on Their Structures. <i>Trends in Glycoscience and Glycotechnology</i> , 2016, 28, E25-E37.	0.0	3
18	In-situ data collection at the photon factory macromolecular crystallography beamlines. <i>AIP Conference Proceedings</i> , 2016, , .	0.3	1

#	ARTICLE	IF	CITATIONS
19	A novel method of preparing the monofrom structure of catalytic antibody light chain. FASEB Journal, 2016, 30, 895-908.	0.2	10
20	A conserved island of <sc>BAG</sc>6/Scythe is related to ubiquitin domains and participates in short hydrophobicity recognition. FEBS Journal, 2016, 283, 662-677.	2.2	23
21	Carbohydrate-binding domain of the POMGnT1 stem region modulates <i>O</i>-mannosylation sites of Î±-dystroglycan. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 9280-9285.	3.3	59
22	Six independent fucose-binding sites in the crystal structure of Aspergillus oryzae lectin. Biochemical and Biophysical Research Communications, 2016, 477, 477-482.	1.0	16
23	A novel mode of ubiquitin recognition by the ubiquitin-binding zinc finger domain of <sc>WRNIP</sc>1. FEBS Journal, 2016, 283, 2004-2017.	2.2	11
24	Selective Binding of AIRAPL Tandem UIMs to Lys48-Linked Tri-Ubiquitin Chains. Structure, 2016, 24, 412-422.	1.6	17
25	POMGNT1 Is Glycosylated by Mucin-Type &O&Glycans. Biological and Pharmaceutical Bulletin, 2015, 38, 1389-1394.	0.6	4
26	Structure of a BAG6 (Bcl-2-associated Athanogene 6)-Ubl4a (Ubiquitin-like Protein 4a) Complex Reveals a Novel Binding Interface That Functions in Tail-anchored Protein Biogenesis. Journal of Biological Chemistry, 2015, 290, 9387-9398.	1.6	29
27	X-Ray Crystallography of Sugar Related Proteins. , 2015, , 175-182.		0
28	Mechanism Underlying Î² Kinase Activation Mediated by the Linear Ubiquitin Chain Assembly Complex. Molecular and Cellular Biology, 2014, 34, 1322-1335.	1.1	107
29	Structural Basis of the Autophagy-Related LC3/Atg13 LIR Complex: Recognition and Interaction Mechanism. Structure, 2014, 22, 47-58.	1.6	93
30	Expanded potential of seleno-carbohydrates as a molecular tool for X-ray structural determination of a carbohydrate-protein complex with single/multi-wavelength anomalous dispersion phasing. Bioorganic and Medicinal Chemistry, 2014, 22, 2090-2101.	1.4	29
31	X-Ray Crystallography of Sugar Related Proteins. , 2014, , 1-8.		0
32	A New Structure Determination Method of Lectins Using a Selenium-Containing Sugar Ligand. Methods in Molecular Biology, 2014, 1200, 491-499.	0.4	0
33	Structural basis of preferential binding of fucose-containing saccharide by the Caenorhabditis elegans galectin LEC-6. Glycobiology, 2013, 23, 797-805.	1.3	11
34	Conformational change of a unique sequence in a fungal galectin from <i>Agroclybe cylindracea</i> controls glycan ligand-binding specificity. FEBS Letters, 2013, 587, 3620-3625.	1.3	18
35	Structural basis for phosphorylation-triggered autophagic clearance of <i>Salmonella</i>. Biochemical Journal, 2013, 454, 459-466.	1.7	92
36	Direct metal recognition by guanine nucleotide-exchange factor in the initial step of the exchange reaction. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 345-351.	2.5	2

#	ARTICLE	IF	CITATIONS
37	Structural Basis for Membrane Binding Specificity of the Bin/Amphiphysin/Rvs (BAR) Domain of Arfaptin-2 Determined by Arl1 GTPase. <i>Journal of Biological Chemistry</i> , 2012, 287, 25478-25489.	1.6	31
38	Structural basis for Arf6-MKLP1 complex formation on the Flemming body responsible for cytokinesis. <i>EMBO Journal</i> , 2012, 31, 2590-2603.	3.5	55
39	Structural Insights into the Phospholipid Binding Specificity of Human Evectin-2. <i>Nihon Kessho Gakkaishi</i> , 2012, 54, 101-106.	0.0	0
40	Structure of a compact conformation of linear diubiquitin. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 102-108.	2.5	29
41	Structural basis of the strict phospholipid binding specificity of the pleckstrin homology domain of human evectin-2. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 117-123.	2.5	15
42	Intracellular phosphatidylserine is essential for retrograde membrane traffic through endosomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 15846-15851.	3.3	163
43	Crystallization of small proteins assisted by green fluorescent protein. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2010, 66, 1059-1066.	2.5	31
44	Crystal Structures of the CERT START Domain with Inhibitors Provide Insights into the Mechanism of Ceramide Transfer. <i>Journal of Molecular Biology</i> , 2010, 396, 245-251.	2.0	69
45	Complexity in Influenza Virus Targeted Drug Design: Interaction with Human Sialidases. <i>Journal of Medicinal Chemistry</i> , 2010, 53, 2998-3002.	2.9	62
46	Specific Recognition of Linear Ubiquitin Chains by NEMO Is Important for NF- κ B Activation. <i>Cell</i> , 2009, 136, 1098-1109.	13.5	667
47	Purification, crystallization and preliminary X-ray crystallographic analysis of Rab27a GTPase in complex with exophilin4/Slp2-a effector. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008, 64, 599-601.	0.7	3
48	Miranda cargo-binding domain forms an elongated coiled-coil homodimer in solution: Implications for asymmetric cell division in <i>Drosophila</i> . <i>Protein Science</i> , 2008, 17, 908-917.	3.1	12
49	Nucleotide-Dependent Conformational Changes and Assembly of the AAA ATPase SKD1/VPS4B. <i>Traffic</i> , 2008, 9, 2180-2189.	1.3	29
50	1,2- α -Fucosyltransferase: A glycosyltransferase derived from an inverting α -glucosidase with an unusual reaction mechanism. <i>FEBS Letters</i> , 2008, 582, 3739-3743.	1.3	95
51	Elucidation of Rab27 Recruitment by Its Effectors: Structure of Rab27a Bound to Exophilin4/Slp2-a. <i>Structure</i> , 2008, 16, 1468-1477.	1.6	53
52	Structural Analysis of the Human Galectin-9 N-terminal Carbohydrate Recognition Domain Reveals Unexpected Properties that Differ from the Mouse Orthologue. <i>Journal of Molecular Biology</i> , 2008, 375, 119-135.	2.0	80
53	Structural basis for specific lipid recognition by CERT responsible for nonvesicular trafficking of ceramide. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 488-493.	3.3	202
54	Structural analysis of the recognition mechanism of poly-N-acetylglucosamine by the human galectin-9 N-terminal carbohydrate recognition domain. <i>Glycobiology</i> , 2008, 19, 112-117.	1.3	59

#	ARTICLE	IF	CITATIONS
55	1S6-4 Structure determination of a native protein crystal by S-SAD phasing with synchrotron radiation(1S6 Cutting edge of protein crystallography with synchrotron radiation,The 46th Annual) Tj ETQq1 1 0.784614 rgB0 /Overlo		
56	2P-031 Structure determination of a native protein crystal by S-SAD phasing with synchrotron radiation(The 46th Annual Meeting of the Biophysical Society of Japan). Seibutsu Butsuri, 2008, 48, S79.	0.0	0
57	Structural Basis of the Catalytic Reaction Mechanism of Novel 1,2- α -L-Fucosidase from Bifidobacterium bifidum. Journal of Biological Chemistry, 2007, 282, 18497-18509.	1.6	110
58	Structural Basis for Recognition of High Mannose Type Glycoproteins by Mammalian Transport Lectin VIP36. Journal of Biological Chemistry, 2007, 282, 28246-28255.	1.6	53
59	Design of Disulfide-linked Thioredoxin Dimers and Multimers Through Analysis of Crystal Contacts. Journal of Molecular Biology, 2007, 372, 1278-1292.	2.0	19
60	Structure of the small GTPase Rab27b shows an unexpected swapped dimer. Acta Crystallographica Section D: Biological Crystallography, 2007, 63, 769-779.	2.5	23
61	Molecular Basis for Autoregulatory Interaction Between GAE Domain and Hinge Region of GGA1. Traffic, 2007, 8, 904-913.	1.3	11
62	Development of an automated large-scale protein-crystallization and monitoring system for high-throughput protein-structure analyses. Acta Crystallographica Section D: Biological Crystallography, 2006, 62, 1058-1065.	2.5	62
63	Crystal structure of GlcAT-S, a human glucuronyltransferase, involved in the biosynthesis of the HNK-1 carbohydrate epitope. Proteins: Structure, Function and Bioinformatics, 2006, 65, 499-508.	1.5	20
64	Double-sided ubiquitin binding of Hrs-UIM in endosomal protein sorting. Nature Structural and Molecular Biology, 2006, 13, 272-277.	3.6	155
65	Structural basis of ubiquitin recognition by mammalian Eap45 GLUE domain. Nature Structural and Molecular Biology, 2006, 13, 1031-1032.	3.6	50
66	Structures of the Carbohydrate Recognition Domain of Ca ²⁺ -independent Cargo Receptors Emp46p and Emp47p. Journal of Biological Chemistry, 2006, 281, 10410-10419.	1.6	29
67	Crystal Structure of the Galectin-9 N-terminal Carbohydrate Recognition Domain from Mus musculus Reveals the Basic Mechanism of Carbohydrate Recognition*. Journal of Biological Chemistry, 2006, 281, 35884-35893.	1.6	75
68	Structural basis for Rab11-dependent membrane recruitment of a family of Rab11-interacting protein 3 (FIP3)/Arfophilin-1. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 15416-15421.	3.3	92
69	Molecular mechanism of ubiquitin recognition by GGA3 GAT domain. Genes To Cells, 2005, 10, 639-654.	0.5	37
70	Structure determination of GGA-GAE and β 1-ear in complex with peptides: crystallization of low-affinity complexes in membrane traffic. Acta Crystallographica Section D: Biological Crystallography, 2005, 61, 731-736.	2.5	6
71	Crystal Structure of the Human Cytosolic Sialidase Neu2. Journal of Biological Chemistry, 2005, 280, 469-475.	1.6	148
72	Structural basis for recognition of ubiquitinated cargo by Tom1-GAT domain. FEBS Letters, 2005, 579, 5385-5391.	1.3	34

#	ARTICLE	IF	CITATIONS
73	Structural Basis for Acceptor Substrate Recognition of a Human Glucuronyltransferase, GlcAT-P, an Enzyme Critical in the Biosynthesis of the Carbohydrate Epitope HNK-1. <i>Journal of Biological Chemistry</i> , 2004, 279, 22693-22703.	1.6	65
74	Molecular mechanism of membrane recruitment of GGA by ARF in lysosomal protein transport. <i>Nature Structural and Molecular Biology</i> , 2003, 10, 386-393.	3.6	122
75	Structural basis for recognition of acidic-cluster dileucine sequence by GGA1. <i>Nature</i> , 2002, 415, 937-941.	13.7	146
76	Structural basis for the accessory protein recruitment by the $\hat{1}^3$ -adaptin ear domain. <i>Nature Structural Biology</i> , 2002, 9, 527-31.	9.7	34
77	Direct observation of three conformations of MutS protein regulated by adenine nucleotides. <i>Journal of Molecular Biology</i> , 2001, 309, 227-238.	2.0	22
78	Interaction of UvrA and UvrB Proteins with a Fluorescent Single-stranded DNA. <i>Journal of Biological Chemistry</i> , 2000, 275, 13235-13242.	1.6	12
79	The RadA protein from a hyperthermophilic archaeon <i>Pyrobaculum islandicum</i> is a DNA-dependent ATPase that exhibits two disparate catalytic modes, with a transition temperature at 75°C. <i>FEBS Journal</i> , 2000, 267, 1125-1137.	0.2	25
80	Crystal structure of a repair enzyme of oxidatively damaged DNA, MutM (Fpg), from an extreme thermophile, <i>Thermus thermophilus</i> HB8. <i>EMBO Journal</i> , 2000, 19, 3857-3869.	3.5	141
81	DNA Binding and Protein-Protein Interaction Sites in MutS, a Mismatched DNA Recognition Protein from <i>Thermus thermophilus</i> HB8. <i>Journal of Biological Chemistry</i> , 2000, 275, 40703-40709.	1.6	13
82	Observation of RecA protein monomer by small angle X-ray scattering with synchrotron radiation. <i>FEBS Letters</i> , 2000, 482, 159-162.	1.3	1
83	Crystallization and preliminary X-ray diffraction studies of a DNA excision repair enzyme, UvrB, from <i>Thermus thermophilus</i> HB8. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 704-705.	2.5	5
84	Structure of <i>Thermus thermophilus</i> HB8 Aspartate Aminotransferase and Its Complex with Maleate. <i>Biochemistry</i> , 1999, 38, 2413-2424.	1.2	71
85	Crystal Structure of <i>Thermus thermophilus</i> HB8 UvrB Protein, a Key Enzyme of Nucleotide Excision Repair. <i>Journal of Biochemistry</i> , 1999, 126, 986-990.	0.9	69
86	Characterization of thermostable RecA protein and analysis of its interaction with single-stranded DNA. <i>FEBS Journal</i> , 1999, 259, 592-601.	0.2	10
87	Characterization of the Oligomeric States of RecA Protein: A Monomeric RecA Protein Can Form a Nucleoprotein Filament. <i>Biochemistry</i> , 1998, 37, 14788-14797.	1.2	19
88	Thermostable repair enzyme for oxidative DNA damage from extremely thermophilic bacterium, <i>Thermus thermophilus</i> HB8 [published erratum appears in <i>Nucleic Acids Res</i> 1998 Apr 1;26(7):following 1855]. <i>Nucleic Acids Research</i> , 1998, 26, 903-910.	6.5	24
89	The Novel Substrate Recognition Mechanism Utilized by Aspartate Aminotransferase of the Extreme Thermophile <i>Thermus thermophilus</i> HB8. <i>Journal of Biological Chemistry</i> , 1998, 273, 29554-29564.	1.6	33
90	Domain organization and functional analysis of <i>Thermus thermophilus</i> MutS protein [published erratum appears in <i>Nucleic Acids Res</i> 1998 Oct 15;26(20):following 4789]. <i>Nucleic Acids Research</i> , 1998, 26, 4153-4159.	6.5	17

#	ARTICLE	IF	CITATIONS
91	Domain Structure of <i>Thermus thermophilus</i> UvrB Protein. <i>Journal of Biological Chemistry</i> , 1997, 272, 22703-22713.	1.6	25
92	Cloning and characterization of the <i>uvrD</i> gene from an extremely thermophilic bacterium, <i>Thermus thermophilus</i> HB8. <i>Gene</i> , 1997, 199, 77-82.	1.0	11
93	Cloning, sequencing and expression of the <i>uvrA</i> gene from an extremely thermophilic bacterium, <i>Thermus thermophilus</i> HB8. <i>Gene</i> , 1996, 171, 103-106.	1.0	16
94	ATPase Activity of UvrB Protein from <i>Thermus thermophilus</i> HB8 and Its Interaction with DNA. <i>Journal of Biological Chemistry</i> , 1996, 271, 9612-9618.	1.6	23
95	An essential gene, <i>ESR1</i> , is required for mitotic growth, DNA repair and meiotic recombination <i>Saccharomyces cerevisiae</i> . <i>Nucleic Acids Research</i> , 1994, 22, 3104-3112.	6.5	223
96	Construction of Aminotransferase Chimeras and Analysis of Their Substrate Specificity ¹ . <i>Journal of Biochemistry</i> , 1994, 115, 568-577.	0.9	15
97	Interaction of <i>Escherichia coli</i> RecA Protein with ATP and Its Analogues ¹ . <i>Journal of Biochemistry</i> , 1994, 116, 960-966.	0.9	22
98	RecA Protein from an Extremely Thermophilic Bacterium, <i>Thermus thermophilus</i> HB8 ¹ . <i>Journal of Biochemistry</i> , 1993, 114, 926-929.	0.9	33
99	Structural Diversity Problems and the Solving Method for Antibody Light Chains. , 0, , .		3