Koichi Kato

List of Publications by Year
in descending order

329 papers	11,244 citations	31976 53 h-index	51608 86 g-index
346 all docs	346 docs citations	346 times ranked	10476 citing authors

#	Article	IF	Citations
1	Comparison of the methods for profiling glycoprotein glycansâ€"HUPO Human Disease Glycomics/Proteome Initiative multi-institutional study. Glycobiology, 2007, 17, 411-422.	2.5	382
2	Structural Comparison of Fucosylated and Nonfucosylated Fc Fragments of Human Immunoglobulin G1. Journal of Molecular Biology, 2007, 368, 767-779.	4.2	273
3	Structural basis for recognition of the nonclassical MHC molecule HLA-G by the leukocyte Ig-like receptor B2 (LILRB2/LIR2/ILT4/CD85d). Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 16412-16417.	7.1	238
4	Parkin binds the Rpn10 subunit of 26S proteasomes through its ubiquitinâ€like domain. EMBO Reports, 2003, 4, 301-306.	4.5	233
5	Structural basis for improved efficacy of therapeutic antibodies on defucosylation of their Fc glycans. Genes To Cells, 2011, 16, 1071-1080.	1.2	213
6	Defining the Glycan Destruction Signal for Endoplasmic Reticulum-Associated Degradation. Molecular Cell, 2008, 32, 870-877.	9.7	211
7	Protein encapsulation within synthetic molecular hosts. Nature Communications, 2012, 3, 1093.	12.8	208
8	AÎ² polymerization through interaction with membrane gangliosides. Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids, 2010, 1801, 868-877.	2.4	202
9	Glycoform-dependent conformational alteration of the Fc region of human immunoglobulin G1 as revealed by NMR spectroscopy. Biochimica Et Biophysica Acta - General Subjects, 2006, 1760, 693-700.	2.4	180
10	Human OS-9, a Lectin Required for Glycoprotein Endoplasmic Reticulum-associated Degradation, Recognizes Mannose-trimmed N-Glycans. Journal of Biological Chemistry, 2009, 284, 17061-17068.	3.4	170
11	Comparison of Methods for Profiling O-Glycosylation. Molecular and Cellular Proteomics, 2010, 9, 719-727.	3.8	136
12	Synthesis of Monoglucosylated High-Mannose-Type Dodecasaccharide, a Putative Ligand for Molecular Chaperone, Calnexin, and Calreticurin. Journal of the American Chemical Society, 2003, 125, 3402-3403.	13.7	135
13	Dissecting Î²-ring assembly pathway of the mammalian 20S proteasome. EMBO Journal, 2008, 27, 2204-2213.	7.8	134
14	Molecular Basis of Sugar Recognition by the Human L-type Lectins ERGIC-53, VIPL, and VIP36. Journal of Biological Chemistry, 2008, 283, 1857-1861.	3.4	131
15	Ero1-Î± and PDIs constitute a hierarchical electron transfer network of endoplasmic reticulum oxidoreductases. Journal of Cell Biology, 2013, 202, 861-874.	5.2	131
16	EDEM2 initiates mammalian glycoprotein ERAD by catalyzing the first mannose trimming step. Journal of Cell Biology, 2014, 206, 347-356.	5.2	131
17	Edible bird's nest extract inhibits influenza virus infection. Antiviral Research, 2006, 70, 140-146.	4.1	130
18	EDEM1 accelerates the trimming of Â1,2-linked mannose on the C branch of N-glycans. Glycobiology, 2010, 20, 567-575.	2.5	115

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19	Hydrogen Bonding Makes a Difference in the Rhodium-Catalyzed Enantioselective Hydrogenation Using Monodentate Phosphoramidites. Journal of the American Chemical Society, 2006, 128, 14212-14213.	13.7	113
20	Rapid Protein Anchoring into the Membranes of Mammalian Cells Using Oleyl Chain and Poly(ethylene) Tj ETQq0 0 0 rgBT /Overlock 10 T	2.6	109
21	Structural and molecular basis for hyperspecificity of RNA aptamer to human immunoglobulin G. Rna, 2008, 14, 1154-1163.	3.5	108
22	14-3-3Î· is a novel regulator of parkin ubiquitin ligase. EMBO Journal, 2006, 25, 211-221.	7.8	107
23	Differential N-Glycan Patterns of Secreted and Intracellular IgG Produced in Trichoplusia ni Cells. Journal of Biological Chemistry, 1997, 272, 9062-9070.	3.4	106
24	Direct interactions between NEDD8 and ubiquitin E2 conjugating enzymes upregulate cullin-based E3 ligase activity. Nature Structural and Molecular Biology, 2007, 14, 167-168.	8.2	105
25	Crystal structure of a chaperone complex that contributes to the assembly of yeast 20S proteasomes. Nature Structural and Molecular Biology, 2008, 15, 228-236.	8.2	101
26	The N-linked oligosaccharide at FcÂRIIIa Asn-45: an inhibitory element for high FcÂRIIIa binding affinity to IgG glycoforms lacking core fucosylation. Glycobiology, 2008, 19, 126-134.	2.5	97
27	Crystal Structure of UbcH5bâ^¼Ubiquitin Intermediate: Insight into the Formation of the Self-Assembled E2â^¼Ub Conjugates. Structure, 2010, 18, 138-147.	3.3	90
28	The quail and chicken intestine have sialyl-galactose sugar chains responsible for the binding of influenza A viruses to human type receptors. Glycobiology, 2007, 17, 713-724.	2.5	88
29	NIST Interlaboratory Study on Glycosylation Analysis of Monoclonal Antibodies: Comparison of Results from Diverse Analytical Methods. Molecular and Cellular Proteomics, 2020, 19, 11-30.	3.8	87
30	Up-and-down topological mode of amyloid Î²-peptide lying on hydrophilic/hydrophobic interface of ganglioside clusters. Glycoconjugate Journal, 2009, 26, 999-1006.	2.7	85
31	Model for the complex between protein G and an antibody Fc fragment in solution. Structure, 1995, 3, 79-85.	3.3	82
32	Structural basis of sugar-recognizing ubiquitin ligase. Nature Structural and Molecular Biology, 2004, 11, 365-370.	8.2	82
33	O-GlcNAc on NOTCH1 EGF repeats regulates ligand-induced Notch signaling and vascular development in mammals. ELife, 2017, 6, .	6.0	82
34	GALXY(Glycoanalysis by the Three Axes of MS and Chromatography): a Web Application that Assists Structural Analyses of N-Glycans. Trends in Glycoscience and Glycotechnology, 2003, 15, 235-251.	0.1	82
35	Sugar-binding Properties of VIP36, an Intracellular Animal Lectin Operating as a Cargo Receptor. Journal of Biological Chemistry, 2005, 280, 37178-37182.	3.4	80
36	Structural basis of the interaction between IgG and fcÎ³ receptors. Journal of Molecular Biology, 2000, 295, 213-224.	4.2	76

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37	Pairing of oligosaccharides in the Fc region of immunoglobulin G. FEBS Letters, 2000, 473, 349-357.	2.8	76
38	Proteolytic fragmentation with high specificity of mouse immunoglobulin G mapping of proteolytic cleavage sites in the hinge region. Journal of Immunological Methods, 1995, 181, 259-267.	1.4	73
39	Folding a De Novo Designed Peptide into an Î±-Helix through Hydrophobic Binding by a Bowl-Shaped Host. Angewandte Chemie - International Edition, 2006, 45, 241-244.	13.8	70
40	NMR Study of the Interaction between the B Domain of Staphylococcal Protein A and the Fc Portion of Immunoglobulin G. Biochemistry, 1998, 37, 129-136.	2.5	69
41	The role of MRH domain-containing lectins in ERAD. Glycobiology, 2010, 20, 651-660.	2.5	69
42	The Unfolded Protein Response Transducer ATF6 Represents a Novel Transmembrane-type Endoplasmic Reticulum-associated Degradation Substrate Requiring Both Mannose Trimming and SEL1L Protein. Journal of Biological Chemistry, 2013, 288, 31517-31527.	3.4	68
43	Enabling adoption of 2D-NMR for the higher order structure assessment of monoclonal antibody therapeutics. MAbs, 2019, 11, 94-105.	5.2	67
44	Development of structural analysis of sulfated N-glycans by multidimensional high performance liquid chromatography mapping methods. Glycobiology, 2005, 15, 1051-1060.	2.5	64
45	Complete assignment of the methionyl carbonyl carbon resonances in switch variant anti-dansyl antibodies labeled with [1-13C]methionine. Biochemistry, 1991, 30, 270-278.	2.5	61
46	Dynamics of the carbohydrate chains attached to the Fc portion of immunoglobulin G as studied by NMR spectroscopy assisted by selective 13C labeling of the glycans. Journal of Biomolecular NMR, 1998, 12, 385-394.	2.8	61
47	NMR characterization of the interactions between lysoâ€GM1 aqueous micelles and amyloid Î². FEBS Letters, 2010, 584, 831-836.	2.8	61
48	Molecular and structural basis for N-glycan-dependent determination of glycoprotein fates in cells. Biochimica Et Biophysica Acta - General Subjects, 2012, 1820, 1327-1337.	2.4	60
49	Exploration of Conformational Spaces of Highâ€Mannoseâ€Type Oligosaccharides by an NMRâ€Validated Simulation. Angewandte Chemie - International Edition, 2014, 53, 10941-10944.	13.8	60
50	Complete and Rapid Peptide and Glycopeptide Mapping of Mouse Monoclonal Antibody by LC/MS/MS Using Ion Trap Mass Spectrometry. Analytical Chemistry, 1998, 70, 2718-2725.	6.5	59
51	HNK-1 Epitope-carrying Tenascin-C Spliced Variant Regulates the Proliferation of Mouse Embryonic Neural Stem Cells. Journal of Biological Chemistry, 2010, 285, 37293-37301.	3.4	58
52	Redox-Dependent Domain Rearrangement of Protein Disulfide Isomerase Coupled with Exposure of Its Substrate-Binding Hydrophobic Surface. Journal of Molecular Biology, 2010, 396, 361-374.	4.2	58
53	Conformational effects of N-glycan core fucosylation of immunoglobulin G Fc region on its interaction with FcÎ³ receptor IIIa. Scientific Reports, 2017, 7, 13780.	3.3	57
54	Solution structure and dynamics of Ufm1, a ubiquitin-fold modifier 1. Biochemical and Biophysical Research Communications, 2006, 343, 21-26.	2.1	55

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55	Structural basis for amyloidogenic peptide recognition by sorLA. Nature Structural and Molecular Biology, 2015, 22, 199-206.	8.2	55
56	Paramagnetic Lanthanide Tagging for NMR Conformational Analyses of Nâ€Linked Oligosaccharides. Chemistry - A European Journal, 2011, 17, 9280-9282.	3.3	54
57	Lewis X-carrying N-Glycans Regulate the Proliferation of Mouse Embryonic Neural Stem Cells via the Notch Signaling Pathway. Journal of Biological Chemistry, 2012, 287, 24356-24364.	3.4	54
58	Carbon-13 NMR study of switch variant anti-dansyl antibodies: antigen binding and domain-domain interactions. Biochemistry, 1991, 30, 6604-6610.	2.5	53
59	Structural views of glycoprotein-fate determination in cells. Glycobiology, 2007, 17, 1031-1044.	2.5	53
60	Stable-isotope-assisted NMR approaches to glycoproteins using immunoglobulin G as a model system. Progress in Nuclear Magnetic Resonance Spectroscopy, 2010, 56, 346-359.	7.5	53
61	A nonâ€canonical UBAâ€“UBL interaction forms the linearâ€ubiquitinâ€chain assembly complex. EMBO Reports, 2012, 13, 462-468.	4.5	52
62	Conformational Dynamics of Wild-type Lys-48-linked Diubiquitin in Solution. Journal of Biological Chemistry, 2011, 286, 37496-37502.	3.4	51
63	Recombinant curculin heterodimer exhibits taste-modifying and sweet-tasting activities. FEBS Letters, 2004, 573, 135-138.	2.8	50
64	Sugar-binding activity of the MRH domain in the ER Â-glucosidase II Â subunit is important for efficient glucose trimming. Glycobiology, 2009, 19, 1127-1135.	2.5	50
65	N-Glycans from Porcine Trachea and Lung: Predominant NeuAcÎ±2-6Gal Could Be a Selective Pressure for Influenza Variants in Favor of Human-Type Receptor. PLoS ONE, 2011, 6, e16302.	2.5	50
66	Dynamical Structure of the Hinge Region of Immunoglobulin G as Studied by 13C Nuclear Magnetic Resonance Spectroscopy. Journal of Molecular Biology, 1994, 236, 300-309.	4.2	49
67	Spectroscopic Characterization of Intermolecular Interaction of AmyloidÎ²Promoted on GM1 Micelles. International Journal of Alzheimer's Disease, 2011, 2011, 1-8.	2.0	49
68	Lanthanide-assisted NMR evaluation of a dynamic ensemble of oligosaccharide conformations. Chemical Communications, 2012, 48, 4752.	4.1	49
69	The expression of sialylated high-antennary N-glycans in edible birdâ€™s nest. Carbohydrate Research, 2008, 343, 1373-1377.	2.3	47
70	Structural basis for the cooperative interplay between the two causative gene products of combined factor V and factor VIII deficiency. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 4034-4039.	7.1	46
71	Analysis of N-glycans in embryonated chicken egg chorioallantoic and amniotic cells responsible for binding and adaptation of human and avian influenza viruses. Glycoconjugate Journal, 2009, 26, 433-443.	2.7	44
72	Alterations in receptor-binding properties of swine influenza viruses of the H1 subtype after isolation in embryonated chicken eggs. Journal of General Virology, 2010, 91, 938-948.	2.9	43

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73	Structural and Molecular Basis of Carbohydrate-Protein Interaction Systems as Potential Therapeutic Targets. Current Pharmaceutical Design, 2011, 17, 1672-1684.	1.9	43
74	Nrf2 activation attenuates genetic endoplasmic reticulum stress induced by a mutation in the phosphomannomutase 2 gene in zebrafish. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 2758-2763.	7.1	43
75	N-Glycan structures of squid rhodopsin. Existence of the alpha1-3 and alpha1-6 difucosylated innermost GlcNAc residue in a molluscan glycoprotein. FEBS Journal, 2003, 270, 2627-2632.	0.2	42
76	Peptide Recognition: Encapsulation and Î±-Helical Folding of a Nine-Residue Peptide within a Hydrophobic Dimeric Capsule of a Bowl-Shaped Host. Chemistry - A European Journal, 2006, 12, 3211-3217.	3.3	42
77	Application of Paramagnetic NMR-Validated Molecular Dynamics Simulation to the Analysis of a Conformational Ensemble of a Branched Oligosaccharide. Molecules, 2012, 17, 6658-6671.	3.8	41
78	920ÂMHz ultra-high field NMR approaches to structural glycobiology. Biochimica Et Biophysica Acta - General Subjects, 2008, 1780, 619-625.	2.4	40
79	Parallel-Stacked Aromatic Hosts for Orienting Small Molecules in a Magnetic Field: Induced Residual Dipolar Coupling by Encapsulation. Journal of the American Chemical Society, 2010, 132, 3670-3671.	13.7	40
80	Inhibition of Î±â€synuclein fibril assembly by small molecules: Analysis using epitopeâ€specific antibodies. FEBS Letters, 2009, 583, 787-791.	2.8	39
81	Forcible destruction of severely misfolded mammalian glycoproteins by the non-glycoprotein ERAD pathway. Journal of Cell Biology, 2015, 211, 775-784.	5.2	39
82	Gentamicin binds to the lectin site of calreticulin and inhibits its chaperone activity. Biochemical and Biophysical Research Communications, 2004, 323, 281-287.	2.1	38
83	Solution structures and behavior oftrans-RuH(Î·1-BH4) (binap)(1,2-diamine) complexes. Magnetic Resonance in Chemistry, 2006, 44, 66-75.	1.9	38
84	A Selfâ€Assembled Spherical Complex Displaying a Gangliosidic Glycan Cluster Capable of Interacting with Amyloidogenic Proteins. Angewandte Chemie - International Edition, 2015, 54, 8435-8439.	13.8	38
85	Backbone 1H, 13C, and 15N resonance assignments of the Fc fragment of human immunoglobulin G glycoprotein. Biomolecular NMR Assignments, 2015, 9, 257-260.	0.8	38
86	Paramagnetic NMR probes for characterization of the dynamic conformations and interactions of oligosaccharides. Glycoconjugate Journal, 2015, 32, 505-513.	2.7	38
87	Stable isotope labeling approaches for NMR characterization of glycoproteins using eukaryotic expression systems. Journal of Biomolecular NMR, 2018, 71, 193-202.	2.8	38
88	Desiccation-induced fibrous condensation of CAHS protein from an anhydrobiotic tardigrade. Scientific Reports, 2021, 11, 21328.	3.3	38
89	Molecular mechanism of ubiquitin recognition by GGA3 GAT domain. Genes To Cells, 2005, 10, 639-654.	1.2	37
90	Application of Metabolic 13C Labeling in Conjunction with High-Field Nuclear Magnetic Resonance Spectroscopy for Comparative Conformational Analysis of High Mannose-Type Oligosaccharides. Biomolecules, 2013, 3, 108-123.	4.0	37

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91	Emerging Structural Insights into Glycoprotein Quality Control Coupled with N-Glycan Processing in the Endoplasmic Reticulum. Molecules, 2015, 20, 2475-2491.	3.8	37
92	13 C NMR study of the mode of interaction in solution of the B fragment of staphylococcal protein A and the Fc fragments of mouse immunoglobulin G. FEBS Letters, 1993, 328, 49-54.	2.8	36
93	Ultra-high field NMR studies of antibody binding and site-specific phosphorylation of Î±-synuclein. Biochemical and Biophysical Research Communications, 2007, 363, 795-799.	2.1	36
94	Chiral Î·⁶â€Arene/Nâ€Tosylethylenediamineâ€“Ruthenium(II) Complexes: Solution Behavior and Catalytic Activity for Asymmetric Hydrogenation. Chemistry - an Asian Journal, 2010, 5, 806-816.	3.3	36
95	Overexpression of a homogeneous oligosaccharide with 13C labeling by genetically engineered yeast strain. Journal of Biomolecular NMR, 2011, 50, 397-401.	2.8	36
96	Visualisation of a flexible modular structure of the ER folding-sensor enzyme UGGT. Scientific Reports, 2017, 7, 12142.	3.3	36
97	Effects of a Hydrophilic/Hydrophobic Interface on Amyloid-Î² Peptides Studied by Molecular Dynamics Simulations and NMR Experiments. Journal of Physical Chemistry B, 2019, 123, 160-169.	2.6	36
98	Impaired O-Linked N-Acetylglucosaminylation in the Endoplasmic Reticulum by Mutated Epidermal Growth Factor (EGF) Domain-specific O-Linked N-Acetylglucosamine Transferase Found in Adams-Oliver Syndrome. Journal of Biological Chemistry, 2015, 290, 2137-2149.	3.4	35
99	Ganglioside-Mediated Assembly of Amyloid Î²-Protein: Roles in Alzheimer's Disease. Progress in Molecular Biology and Translational Science, 2018, 156, 413-434.	1.7	35
100	The Fab portion of immunoglobulin G contributes to its binding to FcÎ³ receptor III. Scientific Reports, 2019, 9, 11957.	3.3	35
101	Application of 13C Nuclear Magnetic Resonance Spectroscopy to Molecular Structural Analyses of Antibody Molecules1. Journal of Biochemistry, 1989, 105, 867-869.	1.7	34
102	NMR analysis of the interaction between protein L and Ig light chains. Journal of Molecular Biology, 1997, 270, 8-13.	4.2	34
103	Structural basis for recognition of ubiquitinated cargo by Tom1-GAT domain. FEBS Letters, 2005, 579, 5385-5391.	2.8	34
104	Structural and functional mosaic nature of MHC class I molecules in their peptide-free form. Molecular Immunology, 2013, 55, 393-399.	2.2	34
105	New NMR Tools for Characterizing the Dynamic Conformations and Interactions of Oligosaccharides. Chemistry Letters, 2013, 42, 1455-1462.	1.3	34
106	Structural insight into substrate recognition by the endoplasmic reticulum folding-sensor enzyme: crystal structure of third thioredoxin-like domain of UDP-glucose:glycoprotein glucosyltransferase. Scientific Reports, 2014, 4, 7322.	3.3	34
107	Interaction of N-linked glycans, having multivalent GlcNAc termini, with GM3 ganglioside. Glycoconjugate Journal, 2006, 23, 639-649.	2.7	33
108	Endoplasmic reticulum lectin <scp>XTP</scp>3â€B inhibits endoplasmic reticulumâ€associated degradation of a misfolded Î±1â€antitrypsin variant. FEBS Journal, 2013, 280, 1563-1575.	4.7	33

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109	AGO61-dependent GlcNAc modification primes the formation of functional glycans on Î±-dystroglycan. Scientific Reports, 2013, 3, 3288.	3.3	32
110	New insight into the dynamical system of Î±B-crystallin oligomers. Scientific Reports, 2016, 6, 29208.	3.3	32
111	Evolutionally Conserved Intermediates Between Ubiquitin and NEDD8. Journal of Molecular Biology, 2006, 363, 395-404.	4.2	31
112	Curculin Exhibits Sweet-tasting and Taste-modifying Activities through Its Distinct Molecular Surfaces. Journal of Biological Chemistry, 2007, 282, 33252-33256.	3.4	31
113	Structural Basis for Disparate Sugar-Binding Specificities in the Homologous Cargo Receptors ERGIC-53 and VIP36. PLoS ONE, 2014, 9, e87963.	2.5	31
114	Structural basis for two-step glucose trimming by glucosidase II involved in ER glycoprotein quality control. Scientific Reports, 2016, 6, 20575.	3.3	31
115	Nâ€glycan structures of human alveoli provide insight into influenza A virus infection and pathogenesis. FEBS Journal, 2018, 285, 1611-1634.	4.7	31
116	EDEM2 stably disulfide-bonded to TXNDC11 catalyzes the first mannose trimming step in mammalian glycoprotein ERAD. ELife, 2020, 9, .	6.0	31
117	Redox-Dependent Domain Rearrangement of Protein Disulfide Isomerase from a Thermophilic Fungus. Biochemistry, 2010, 49, 6953-6962.	2.5	30
118	Structural Basis for Specific Recognition of Rpt1p, an ATPase Subunit of 26 S Proteasome, by Proteasome-dedicated Chaperone Hsm3p. Journal of Biological Chemistry, 2012, 287, 12172-12182.	3.4	30
119	Multinuclear NMR study of the structure of Fv fragment of anti-dansyl mouse IgG2a antibody. Biochemistry, 1991, 30, 6611-6619.	2.5	29
120	Probing the Interaction between a High-Affinity Single-Chain Fv and a Pyrimidine (6-4) Pyrimidone Photodimer by Site-Directed Mutagenesis. Biochemistry, 1999, 38, 532-539.	2.5	29
121	Comparison of the N-linked glycosylation of human Î²1,3-N-acetylglucosaminyltransferase 2 expressed in insect cells and silkworm larvae. Journal of Biotechnology, 2009, 143, 27-33.	3.8	29
122	Glycomic Analyses of Glycoproteins in Bile and Serum during Rat Hepatocarcinogenesis. Journal of Proteome Research, 2010, 9, 4888-4896.	3.7	29
123	Ganglioside-embedding small bicelles for probing membrane-landing processes of intrinsically disordered proteins. Chemical Communications, 2013, 49, 1235.	4.1	29
124	Dynamic Views of the Fc Region of Immunoglobulin G Provided by Experimental and Computational Observations. Antibodies, 2019, 8, 39.	2.5	29
125	[15] Nuclear magnetic resonance study of antibodies: A multinuclear approach. Methods in Enzymology, 1994, 239, 440-464.	1.0	28
126	Structure of the putative 32â€ƒkDa myrosinaseâ€binding protein from Arabidopsis (At3g16450.1) determined by SAILâ€NMR. FEBS Journal, 2008, 275, 5873-5884.	4.7	28

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127	Specificities and Rates of Binding of Anti-(6-4) Photoproduct Antibody Fragments to Synthetic Thymine Photoproducts. Journal of Biochemistry, 1998, 123, 182-188.	1.7	27
128	Structural basis of redox-dependent substrate binding of protein disulfide isomerase. Scientific Reports, 2015, 5, 13909.	3.3	27
129	Probing Dynamics and Conformational Change of the GroEL-GroES Complex by 13C NMR Spectroscopy. Journal of Biochemistry, 2006, 140, 591-598.	1.7	26
130	Human IgG1 expression in silkworm larval hemolymph using BmNPV bacmids and its N-linked glycan structure. Journal of Biotechnology, 2009, 139, 108-114.	3.8	26
131	Dynamics and Interactions of Glycoconjugates Probed by Stable-Isotope-Assisted NMR Spectroscopy. Methods in Enzymology, 2010, 478, 305-322.	1.0	26
132	Solution Structure of the Q41N Variant of Ubiquitin as a Model for the Alternatively Folded N₂ State of Ubiquitin. Biochemistry, 2013, 52, 1874-1885.	2.5	26
133	Conformational Analysis of a Highâ€Mannoseâ€Type Oligosaccharide Displaying Glucosyl Determinant Recognised by Molecular Chaperones Using NMRâ€Validated Molecular Dynamics Simulation. ChemBioChem, 2017, 18, 396-401.	2.6	26
134	Solution NMR views of dynamical ordering of biomacromolecules. Biochimica Et Biophysica Acta - General Subjects, 2018, 1862, 287-306.	2.4	26
135	Terminal Spin Labeling of a High-mannose-type Oligosaccharide for Quantitative NMR Analysis of Its Dynamic Conformation. Chemistry Letters, 2013, 42, 544-546.	1.3	25
136	Pba3â€“Pba4 heterodimer acts as a molecular matchmaker in proteasome Î±-ring formation. Biochemical and Biophysical Research Communications, 2014, 450, 1110-1114.	2.1	25
137	Importance of the Side Chain at Position 296 of Antibody Fc in Interactions with FcÎ³RIIIa and Other FcÎ³ Receptors. PLoS ONE, 2015, 10, e0140120.	2.5	25
138	Direct Mapping of Additional Modifications on Phosphorylated O-glycans of Î±-Dystroglycan by Mass Spectrometry Analysis in Conjunction with Knocking Out of Causative Genes for Dystroglycanopathy. Molecular and Cellular Proteomics, 2016, 15, 3424-3434.	3.8	25
139	Comparison of analytical methods for profiling N- and O-linked glycans from cultured cell lines. Glycoconjugate Journal, 2016, 33, 405-415.	2.7	25
140	A conformational change in the Fc precludes the binding of two FcÎ³ receptor molecules to one IgG. Trends in Immunology, 2000, 21, 310-312.	7.5	24
141	Lysosome-associated membrane protein 1 is a major SSEA-1-carrier protein in mouse neural stem cells. Glycobiology, 2010, 20, 976-981.	2.5	24
142	Spatial arrangement and functional role of Î± subunits of proteasome activator PA28 in hetero-oligomeric form. Biochemical and Biophysical Research Communications, 2013, 432, 141-145.	2.1	24
143	Structural characterization of the circadian clock protein complex composed of KaiB and KaiC by inverse contrast-matching small-angle neutron scattering. Scientific Reports, 2016, 6, 35567.	3.3	24
144	13C-NMR quantification of proton exchange at LewisX hydroxyl groups in water. Chemical Communications, 2011, 47, 10800.	4.1	23

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145	Structural Basis for Proteasome Formation Controlled by an Assembly Chaperone Nas2. Structure, 2014, 22, 731-743.	3.3	23
146	Recent advances in glycoprotein production for structural biology: toward tailored design of glycoforms. Current Opinion in Structural Biology, 2014, 26, 44-53.	5.7	23
147	Disassembly of the self-assembled, double-ring structure of proteasome Î±7 homo-tetradecamer by Î±6. Scientific Reports, 2015, 5, 18167.	3.3	23
148	N-glycan structures of murine hippocampus serine protease, neuropsin, produced in Trichoplusia ni cells. Glycoconjugate Journal, 1999, 16, 405-414.	2.7	22
149	N-glycosylation profile of recombinant human soluble FcÂ receptor III. Glycobiology, 2002, 12, 507-515.	2.5	22
150	Fbs1 protects the malfolded glycoproteins from the attack of peptide:N-glycanase. Biochemical and Biophysical Research Communications, 2007, 362, 712-716.	2.1	22
151	Characterization of Inhibitor-Bound Î±-Synuclein Dimer: Role of Î±-Synuclein N-Terminal Region in Dimerization and Inhibitor Binding. Journal of Molecular Biology, 2010, 395, 445-456.	4.2	22
152	Structural and dynamic views of GM1 ganglioside. Glycoconjugate Journal, 2015, 32, 105-112.	2.7	22
153	A13C NMR study of the hinge region of a mouse monoclonal antibody. Journal of Biomolecular NMR, 1991, 1, 379-390.	2.8	21
154	Crystal structure of cyclic Lys48-linked tetraubiquitin. Biochemical and Biophysical Research Communications, 2010, 400, 329-333.	2.1	21
155	NMR characterization of the interaction of GroEL with amyloid Î² as a model ligand. FEBS Letters, 2013, 587, 1605-1609.	2.8	21
156	Site-specific N-glycosylation analysis of soluble FcÎ³ receptor IIIb in human serum. Scientific Reports, 2018, 8, 2719.	3.3	21
157	Newly developed Laboratory-based Size exclusion chromatography Small-angle x-ray scattering System (La-SSS). Scientific Reports, 2019, 9, 12610.	3.3	21
158	Temperature-dependent isologous Fabâ€“Fab interaction that mediates cryocrystallization of a monoclonal immunoglobulin G. Molecular Immunology, 2004, 41, 1211-1215.	2.2	20
159	Deletion of 3 residues from the C-terminus of MCFD2 affects binding to ERGIC-53 and causes combined factor V and factor VIII deficiency. Blood, 2008, 111, 1299-1301.	1.4	20
160	Câ€terminal regionâ€dependent change of antibodyâ€binding to the Eighth Reelin repeat reflects the signaling activity of Reelin. Journal of Neuroscience Research, 2009, 87, 3043-3053.	2.9	20
161	Crystal Structure of Yeast Rpn14, a Chaperone of the 19 S Regulatory Particle of the Proteasome. Journal of Biological Chemistry, 2010, 285, 15159-15166.	3.4	20
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