

Rodolfo Ghirlando

List of Publications by Year in descending order

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162
papers

11,305
citations

19657

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36028

97
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165
all docs

165
docs citations

165
times ranked

14230
citing authors

#	ARTICLE	IF	CITATIONS
1	Bivalent recognition of fatty acyl-CoA by a human integral membrane palmitoyltransferase. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	15
2	Modulation of the monomer-dimer equilibrium and catalytic activity of SARS-CoV-2 main protease by a transition-state analog inhibitor. Communications Biology, 2022, 5, 160.	4.4	20
3	The dimerization interface of initiator RctB governs chaperone and enhancer dependence of <i>Vibrio cholerae</i> chromosome 2 replication. Nucleic Acids Research, 2022, 50, 4529-4544.	14.5	2
4	Distinct Structures and Dynamics of Chromatosomes with Different Human Linker Histone Isoforms. Molecular Cell, 2021, 81, 166-182.e6.	9.7	74
5	Structure elucidation of the elusive Enzyme I monomer reveals the molecular mechanisms linking oligomerization and enzymatic activity. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	12
6	Quantitative NMR Study of Insulin-Degrading Enzyme Using Amyloid- β^2 and HIV-1 p6 Elucidates Its Chaperone Activity. Biochemistry, 2021, 60, 2519-2523.	2.5	8
7	HIV-1 matrix-tRNA complex structure reveals basis for host control of Gag localization. Cell Host and Microbe, 2021, 29, 1421-1436.e7.	11.0	22
8	Structures of <i>IS</i> <i>C</i> <i>th4</i> transpososomes reveal the role of asymmetry in copy-out/paste-in <i>DNA</i> transposition. EMBO Journal, 2021, 40, e105666.	7.8	16
9	Transient lipid-bound states of spike protein heptad repeats provide insights into SARS-CoV-2 membrane fusion. Science Advances, 2021, 7, eabk2226.	10.3	28
10	Proline-rich domain of human ALIX contains multiple TSG101-UEV interaction sites and forms phosphorylation-mediated reversible amyloids. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 24274-24284.	7.1	21
11	Allosteric control of hemoglobin S fiber formation by oxygen and its relation to the pathophysiology of sickle cell disease. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 15018-15027.	7.1	26
12	Hybrid Thermophilic/Mesophilic Enzymes Reveal a Role for Conformational Disorder in Regulation of Bacterial Enzyme I. Journal of Molecular Biology, 2020, 432, 4481-4498.	4.2	17
13	Biochemical and structural analyses reveal that the tumor suppressor neurofibromin (NF1) forms a high-affinity dimer. Journal of Biological Chemistry, 2020, 295, 1105-1119.	3.4	25
14	Abrogation of prenucleation, transient oligomerization of the Huntingtin exon 1 protein by human profilin I. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 5844-5852.	7.1	20
15	Biochemical and structural analyses reveal that the tumor suppressor neurofibromin (NF1) forms a high-affinity dimer. Journal of Biological Chemistry, 2020, 295, 1105-1119.	3.4	25
16	Application of millisecond time-resolved solid state NMR to the kinetics and mechanism of melittin self-assembly. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 16717-16722.	7.1	42
17	The iron-regulated vacuolar <i>Legionella pneumophila</i> MavN protein is a transition-metal transporter. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 17775-17785.	7.1	21
18	Bacillus anthracis Virulence Regulator AtxA Binds Specifically to the <i>pagA</i> Promoter Region. Journal of Bacteriology, 2019, 201, .	2.2	17

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19	KRAS Prenylation Is Required for Bivalent Binding with Calmodulin in a Nucleotide-Independent Manner. <i>Biophysical Journal</i> , 2019, 116, 1049-1063.	0.5	41
20	Molecular architecture of a cylindrical self-assembly at human centrosomes. <i>Nature Communications</i> , 2019, 10, 1151.	12.8	34
21	Bismaleimide cross-linked anthrax toxin forms functional octamers with high specificity in tumor targeting. <i>Protein Science</i> , 2019, 28, 1059-1070.	7.6	1
22	Probing initial transient oligomerization events facilitating Huntingtin fibril nucleation at atomic resolution by relaxation-based NMR. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 3562-3571.	7.1	61
23	Cryo-EM structure of substrate-free E.Âcoli Lon protease provides insights into the dynamics of Lon machinery. <i>Current Research in Structural Biology</i> , 2019, 1, 13-20.	2.2	19
24	Probing transient excited states of the bacterial cell division regulator MinE by relaxation dispersion NMR spectroscopy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 25446-25455.	7.1	16
25	Tilted, Uninterrupted, Monomeric HIV-1 gp41 Transmembrane Helix from Residual Dipolar Couplings. <i>Journal of the American Chemical Society</i> , 2018, 140, 34-37.	13.7	39
26	Structural mechanisms of centromeric nucleosome recognition by the kinetochore protein CENP-N. <i>Science</i> , 2018, 359, 339-343.	12.6	98
27	The oligomerization state of bacterial enzyme I (EI) determines EI's allosteric stimulation or competitive inhibition by Î±-ketoglutarate. <i>Journal of Biological Chemistry</i> , 2018, 293, 2631-2639.	3.4	13
28	Probing the mechanism of inhibition of amyloid-Î²(1â€“42)-induced neurotoxicity by the chaperonin GroEL. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E11924-E11932.	7.1	29
29	Revisit of Reconstituted 30-nm Nucleosome Arrays Reveals an Ensemble of Dynamic Structures. <i>Journal of Molecular Biology</i> , 2018, 430, 3093-3110.	4.2	42
30	Chemical and Biophysical Approaches for Complete Characterization of Lectinâ€“Carbohydrate Interactions. <i>Methods in Enzymology</i> , 2018, 598, 3-35.	1.0	1
31	Cryo-EM structures and atomic model of the HIV-1 strand transfer complex intasome. <i>Science</i> , 2017, 355, 89-92.	12.6	166
32	Confinement and Stabilization of Fyn SH3 Folding Intermediate Mimetics within the Cavity of the Chaperonin GroEL Demonstrated by Relaxation-Based NMR. <i>Biochemistry</i> , 2017, 56, 903-906.	2.5	25
33	Nanodisc characterization by analytical ultracentrifugation. <i>Nanotechnology Reviews</i> , 2017, 6, 3-14.	5.8	9
34	The DnaK Chaperone Uses Different Mechanisms To Promote and Inhibit Replication of <i>Vibrio cholerae</i> Chromosome 2. <i>MBio</i> , 2017, 8, .	4.1	16
35	Sirt1 carboxyl-domain is an ATP-repressible domain that is transferrable to other proteins. <i>Nature Communications</i> , 2017, 8, 15560.	12.8	24
36	Molecular basis of CENP-C association with the CENP-A nucleosome at yeast centromeres. <i>Genes and Development</i> , 2017, 31, 1958-1972.	5.9	45

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37	Structural Basis for Substrate Recognition by the Ankyrin Repeat Domain of Human DHHC17 Palmitoyltransferase. <i>Structure</i> , 2017, 25, 1337-1347.e6.	3.3	55
38	Enrichment and characterization of ferritin for nanomaterial applications. <i>Nanotechnology</i> , 2016, 27, 045102.	2.6	11
39	CTCF: making the right connections. <i>Genes and Development</i> , 2016, 30, 881-891.	5.9	258
40	Binding Site Geometry and Subdomain Valency Control Effects of Neutralizing Lectins on HIV-1 Viral Particles. <i>ACS Infectious Diseases</i> , 2016, 2, 882-891.	3.8	20
41	Quantitative Resolution of Monomer-Dimer Populations by Inversion Modulated DEER EPR Spectroscopy. <i>ChemPhysChem</i> , 2016, 17, 2987-2991.	2.1	16
42	A Small Number of Residues Can Determine if Linker Histones Are Bound On or Off Dyad in the Chromatosome. <i>Journal of Molecular Biology</i> , 2016, 428, 3948-3959.	4.2	47
43	Structural basis of recognition of farnesylated and methylated KRAS4b by PDE1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E6766-E6775.	7.1	145
44	AND™ logic gates at work: Crystal structure of Rad53 bound to Dbf4 and Cdc7. <i>Scientific Reports</i> , 2016, 6, 34237.	3.3	17
45	Transient HIV-1 Gag-protease interactions revealed by paramagnetic NMR suggest origins of compensatory drug resistance mutations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 12456-12461.	7.1	25
46	Insights into the Conformation of the Membrane Proximal Regions Critical to the Trimerization of the HIV-1 gp41 Ectodomain Bound to Dodecyl Phosphocholine Micelles. <i>PLoS ONE</i> , 2016, 11, e0160597.	2.5	13
47	Farnesylated and methylated KRAS4b: high yield production of protein suitable for biophysical studies of prenylated protein-lipid interactions. <i>Scientific Reports</i> , 2015, 5, 15916.	3.3	65
48	Hfq in <i>Bacillus anthracis</i> : Role of protein sequence variation in the structure and function of proteins in the Hfq family. <i>Protein Science</i> , 2015, 24, 1808-1819.	7.6	14
49	Complete dissociation of the HIV-1 gp41 ectodomain and membrane proximal regions upon phospholipid binding. <i>Journal of Biomolecular NMR</i> , 2015, 61, 235-248.	2.8	15
50	Conformation and dynamics of the Gag polyprotein of the human immunodeficiency virus 1 studied by NMR spectroscopy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 3374-3379.	7.1	48
51	G Protein-Coupled Receptor Kinase 2 (GRK2) and 5 (GRK5) Exhibit Selective Phosphorylation of the Neurotensin Receptor <i>in Vitro</i> . <i>Biochemistry</i> , 2015, 54, 4320-4329.	2.5	40
52	Successive Stages of Amyloid- β^2 Self-Assembly Characterized by Solid-State Nuclear Magnetic Resonance with Dynamic Nuclear Polarization. <i>Journal of the American Chemical Society</i> , 2015, 137, 8294-8307.	13.7	103
53	Structural Mechanisms of Nucleosome Recognition by Linker Histones. <i>Molecular Cell</i> , 2015, 59, 628-638.	9.7	191
54	Variable-Field Analytical Ultracentrifugation: I. Time-Optimized Sedimentation Equilibrium. <i>Biophysical Journal</i> , 2015, 109, 827-837.	0.5	12

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55	A Multilaboratory Comparison of Calibration Accuracy and the Performance of External References in Analytical Ultracentrifugation. <i>PLoS ONE</i> , 2015, 10, e0126420.	2.5	71
56	Initiator protein dimerization plays a key role in replication control of <i>Vibrio cholerae</i> chromosome 2. <i>Nucleic Acids Research</i> , 2014, 42, 10538-10549.	14.5	15
57	Improved measurement of the rotor temperature in analytical ultracentrifugation. <i>Analytical Biochemistry</i> , 2014, 451, 69-75.	2.4	20
58	The Catalytic Subunit of the SWR1 Remodeler Is a Histone Chaperone for the H2A.Z-H2B Dimer. <i>Molecular Cell</i> , 2014, 53, 498-505.	9.7	71
59	Measurement of the temperature of the resting rotor in analytical ultracentrifugation. <i>Analytical Biochemistry</i> , 2014, 458, 37-39.	2.4	14
60	Investigation of the Structure and Dynamics of the Capsidâ€œSpacer Peptideâ€œ...1â€œNucleocapsid Fragment of the HIVâ€œ1 Gag Polyprotein by Solution NMR Spectroscopy. <i>Angewandte Chemie - International Edition</i> , 2014, 53, 1025-1028.	13.8	20
61	Physical chemistry of nucleic acids and their complexes. <i>Biopolymers</i> , 2013, 99, 910-915.	2.4	5
62	Structure and Dynamics of Full-Length HIV-1 Capsid Protein in Solution. <i>Journal of the American Chemical Society</i> , 2013, 135, 16133-16147.	13.7	114
63	Chromatin structure outside and inside the nucleus. <i>Biopolymers</i> , 2013, 99, 225-232.	2.4	20
64	Improving the thermal, radial, and temporal accuracy of the analytical ultracentrifuge through external references. <i>Analytical Biochemistry</i> , 2013, 440, 81-95.	2.4	60
65	Identification of Functionally Conserved Regions in the Structure of the Chaperone/CenH3/H4 Complex. <i>Journal of Molecular Biology</i> , 2013, 425, 536-545.	4.2	8
66	Recorded scan times can limit the accuracy of sedimentation coefficients in analytical ultracentrifugation. <i>Analytical Biochemistry</i> , 2013, 437, 104-108.	2.4	102
67	Overview of Current Methods in Sedimentation Velocity and Sedimentation Equilibrium Analytical Ultracentrifugation. <i>Current Protocols in Protein Science</i> , 2013, 71, Unit20.12.	2.8	154
68	Structural Basis for Enzyme I Inhibition by $\hat{1}\pm$ -Ketoglutarate. <i>ACS Chemical Biology</i> , 2013, 8, 1232-1240.	3.4	26
69	Crystal structure of the DdrB/ssDNA complex from <i>Deinococcus radiodurans</i> reveals a DNA binding surface involving higher-order oligomeric states. <i>Nucleic Acids Research</i> , 2013, 41, 9934-9944.	14.5	10
70	A Conserved Mechanism for Centromeric Nucleosome Recognition by Centromere Protein CENP-C. <i>Science</i> , 2013, 340, 1110-1113.	12.6	290
71	Engineering Anthrax Toxin Variants That Exclusively Form Octamers and Their Application to Targeting Tumors. <i>Journal of Biological Chemistry</i> , 2013, 288, 9058-9065.	3.4	35
72	Complexes of Neutralizing and Non-Neutralizing Affinity Matured Fabs with a Mimetic of the Internal Trimeric Coiled-Coil of HIV-1 gp41. <i>PLoS ONE</i> , 2013, 8, e78187.	2.5	17

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73	Polymerization and nucleic acid-binding properties of human L1 ORF1 protein. <i>Nucleic Acids Research</i> , 2012, 40, 813-827.	14.5	52
74	The processing of repetitive extragenic palindromes: the structure of a repetitive extragenic palindrome bound to its associated nuclease. <i>Nucleic Acids Research</i> , 2012, 40, 9964-9979.	14.5	36
75	Assembly and Architecture of Biogenesis of Lysosome-related Organelles Complex-1 (BLOC-1). <i>Journal of Biological Chemistry</i> , 2012, 287, 5882-5890.	3.4	55
76	The dynamin-like GTPase Sey1p mediates homotypic ER fusion in <i>S. cerevisiae</i> . <i>Journal of Cell Biology</i> , 2012, 197, 209-217.	5.2	104
77	Modulation of the Interaction between Neurotensin Receptor NTS1 and Gq Protein by Lipid. <i>Journal of Molecular Biology</i> , 2012, 417, 95-111.	4.2	113
78	Histone H4 K16Q Mutation, an Acetylation Mimic, Causes Structural Disorder of Its N-Terminal Basic Patch in the Nucleosome. <i>Journal of Molecular Biology</i> , 2012, 421, 30-37.	4.2	73
79	Chromatin domains, insulators, and the regulation of gene expression. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2012, 1819, 644-651.	1.9	115
80	Characterization and Carbohydrate Specificity of Pradimicin S. <i>Journal of the American Chemical Society</i> , 2012, 134, 12346-12349.	13.7	19
81	Crystal Structure of the Minimalist Max-E47 Protein Chimera. <i>PLoS ONE</i> , 2012, 7, e32136.	2.5	12
82	Combined Use of Residual Dipolar Couplings and Solution X-ray Scattering To Rapidly Probe Rigid-Body Conformational Transitions in a Non-phosphorylatable Active-Site Mutant of the 128 kDa Enzyme I Dimer. <i>Journal of the American Chemical Society</i> , 2011, 133, 424-427.	13.7	37
83	Atomic-resolution dynamics on the surface of amyloid- β protofibrils probed by solution NMR. <i>Nature</i> , 2011, 480, 268-272.	27.8	374
84	The Role of MukE in Assembling a Functional MukBEF Complex. <i>Journal of Molecular Biology</i> , 2011, 412, 578-590.	4.2	20
85	The analysis of macromolecular interactions by sedimentation equilibrium. <i>Methods</i> , 2011, 54, 145-156.	3.8	38
86	Structural basis for recognition of centromere histone variant CenH3 by the chaperone Scm3. <i>Nature</i> , 2011, 472, 234-237.	27.8	119
87	Solution Structure of the Monovalent Lectin Microvirin in Complex with Man α 1(1 \rightarrow 2)Man Provides a Basis for Anti-HIV Activity with Low Toxicity. <i>Journal of Biological Chemistry</i> , 2011, 286, 20788-20796.	3.4	67
88	Accounting for Solvent Signal Offsets in the Analysis of Interferometric Sedimentation Velocity Data. <i>Macromolecular Bioscience</i> , 2010, 10, 736-745.	4.1	26
89	Macromol. Biosci. 7/2010. <i>Macromolecular Bioscience</i> , 2010, 10, .	4.1	0
90	Acyldepsipeptide Antibiotics Induce the Formation of a Structured Axial Channel in ClpP: A Model for the ClpX/ClpA-Bound State of ClpP. <i>Chemistry and Biology</i> , 2010, 17, 959-969.	6.0	168

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91	Oligomerization state and supramolecular structure of the HIV-1 Vpu protein transmembrane segment in phospholipid bilayers. <i>Protein Science</i> , 2010, 19, 1877-1896.	7.6	60
92	ATP control of dynamic P1 ParA-DNA interactions: a key role for the nucleoid in plasmid partition. <i>Molecular Microbiology</i> , 2010, 78, 78-91.	2.5	156
93	Maintenance of a constitutive heterochromatin domain in vertebrates by a Dicer-dependent mechanism. <i>Nature Cell Biology</i> , 2010, 12, 94-99.	10.3	51
94	Assembly of the Biogenesis of Lysosome-related Organelles Complex-3 (BLOC-3) and Its Interaction with Rab9. <i>Journal of Biological Chemistry</i> , 2010, 285, 7794-7804.	3.4	90
95	Solution Structure of the 128 kDa Enzyme I Dimer from <i>Escherichia coli</i> and Its 146 kDa Complex with HPr Using Residual Dipolar Couplings and Small- and Wide-Angle X-ray Scattering. <i>Journal of the American Chemical Society</i> , 2010, 132, 13026-13045.	13.7	118
96	Sin Resolvase Catalytic Activity and Oligomerization State are Tightly Coupled. <i>Journal of Molecular Biology</i> , 2010, 404, 16-33.	4.2	16
97	Functional and structural characterization of a dense core secretory granule sorting domain from the PC1/3 protease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 7408-7413.	7.1	39
98	Mechanistic insights into active site-associated polyubiquitination by the ubiquitin-conjugating enzyme Ube2g2. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 3722-3727.	7.1	84
99	Lipid-regulated sterol transfer between closely apposed membranes by oxysterol-binding protein homologues. <i>Journal of Cell Biology</i> , 2009, 187, 889-903.	5.2	196
100	Hybrid Structural Model of the Complete Human ESCRT-0 Complex. <i>Structure</i> , 2009, 17, 406-416.	3.3	56
101	Characterization of the N-Terminal Tail Domain of Histone H3 in Condensed Nucleosome Arrays by Hydrogen Exchange and NMR. <i>Journal of the American Chemical Society</i> , 2009, 131, 15104-15105.	13.7	38
102	Biochemical and structural characterization of innate immunity kinase complex proteins. <i>FASEB Journal</i> , 2009, 23, 707.1.	0.5	0
103	Specific recognition of RNA/DNA hybrid and enhancement of human RNase H1 activity by HBD. <i>EMBO Journal</i> , 2008, 27, 1172-1181.	7.8	91
104	The mode of Hedgehog binding to Ihog homologues is not conserved across different phyla. <i>Nature</i> , 2008, 455, 979-983.	27.8	141
105	Sedimentation Studies on Human Amylin Fail to Detect Low-Molecular-Weight Oligomers. <i>Biophysical Journal</i> , 2008, 94, L45-L47.	0.5	39
106	Visualization of Transient Ultra-Weak Protein Self-Association in Solution Using Paramagnetic Relaxation Enhancement. <i>Journal of the American Chemical Society</i> , 2008, 130, 4048-4056.	13.7	80
107	Hydrodynamic Studies on Defined Heterochromatin Fragments Support a 30-nm Fiber Having Six Nucleosomes per Turn. <i>Journal of Molecular Biology</i> , 2008, 376, 1417-1425.	4.2	70
108	The High-Resolution NMR Structure of the Early Folding Intermediate of the <i>Thermus thermophilus</i> Ribonuclease H. <i>Journal of Molecular Biology</i> , 2008, 384, 531-539.	4.2	19

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109	The TLR3 signaling complex forms by cooperative receptor dimerization. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 258-263.	7.1	255
110	Midbody Targeting of the ESCRT Machinery by a Noncanonical Coiled Coil in CEP55. Science, 2008, 322, 576-580.	12.6	228
111	Interaction of yeast RNA-binding proteins Nrd1 and Nab3 with RNA polymerase II terminator elements. Rna, 2007, 13, 361-373.	3.5	114
112	Solution NMR Structure of the Barrier-to-Autointegration Factor-Emerin Complex. Journal of Biological Chemistry, 2007, 282, 14525-14535.	3.4	75
113	MukE and MukF Form Two Distinct High Affinity Complexes. Journal of Biological Chemistry, 2007, 282, 14373-14378.	3.4	8
114	Desiccation and Zinc Binding Induce Transition of Tomato Abscisic Acid Stress Ripening 1, a Water Stress- and Salt Stress-Regulated Plant-Specific Protein, from Unfolded to Folded State. Plant Physiology, 2007, 143, 617-628.	4.8	94
115	The Inner Cavity of Escherichia coli DegP Protein Is Not Essential for Molecular Chaperone and Proteolytic Activity. Journal of Bacteriology, 2007, 189, 706-716.	2.2	43
116	Role of the PDZ Domains in Escherichia coli DegP Protein. Journal of Bacteriology, 2007, 189, 3176-3186.	2.2	74
117	Molecular Architecture and Functional Model of the Complete Yeast ESCRT-I Heterotetramer. Cell, 2007, 129, 485-498.	28.9	150
118	The Vps27/Hse1 Complex Is a GAT Domain-Based Scaffold for Ubiquitin-Dependent Sorting. Developmental Cell, 2007, 12, 973-986.	7.0	67
119	Structure of Human RNase H1 Complexed with an RNA/DNA Hybrid: Insight into HIV Reverse Transcription. Molecular Cell, 2007, 28, 264-276.	9.7	282
120	RAD51AP1 Is a Structure-Specific DNA Binding Protein that Stimulates Joint Molecule Formation during RAD51-Mediated Homologous Recombination. Molecular Cell, 2007, 28, 468-481.	9.7	105
121	Sae2 Is an Endonuclease that Processes Hairpin DNA Cooperatively with the Mre11/Rad50/Xrs2 Complex. Molecular Cell, 2007, 28, 638-651.	9.7	253
122	Structure of colicin I receptor bound to the R-domain of colicin Ia: implications for protein import. EMBO Journal, 2007, 26, 2594-2604.	7.8	91
123	Molecular Activities of Meiosis-specific Proteins Hop2, Mnd1, and the Hop2-Mnd1 Complex. Journal of Biological Chemistry, 2006, 281, 18426-18434.	3.4	65
124	Structural and Functional Organization of the ESCRT-I Trafficking Complex. Cell, 2006, 125, 113-126.	28.9	105
125	Structure of a heparin-dependent complex of Hedgehog and Ihog. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 17208-17213.	7.1	82
126	Efficient secretion of a folded protein domain by a monomeric bacterial autotransporter. Molecular Microbiology, 2005, 58, 945-958.	2.5	100

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127	Molecular architecture of a eukaryotic DNA transposase. <i>Nature Structural and Molecular Biology</i> , 2005, 12, 715-721.	8.2	111
128	Structural basis for DNA bridging by barrier-to-autointegration factor. <i>Nature Structural and Molecular Biology</i> , 2005, 12, 935-936.	8.2	101
129	Crystal structure of a SeqA ϵ N filament: implications for DNA replication and chromosome organization. <i>EMBO Journal</i> , 2005, 24, 1502-1511.	7.8	48
130	Solution Structure of Enzyme II AChitobiose from the N,N ϵ ² -Diacetylchitobiose Branch of the <i>Escherichia coli</i> Phosphotransferase System. <i>Journal of Biological Chemistry</i> , 2005, 280, 11770-11780.	3.4	9
131	Active Site Sharing and Subterminal Hairpin Recognition in a New Class of DNA Transposases. <i>Molecular Cell</i> , 2005, 20, 143-154.	9.7	66
132	MutH Complexed with Hemi- and Unmethylated DNAs: Coupling Base Recognition and DNA Cleavage. <i>Molecular Cell</i> , 2005, 20, 155-166.	9.7	76
133	Structure of the MutL C-terminal domain: a model of intact MutL and its roles in mismatch repair. <i>EMBO Journal</i> , 2004, 23, 4134-4145.	7.8	163
134	Physical Properties of a Genomic Condensed Chromatin Fragment. <i>Journal of Molecular Biology</i> , 2004, 336, 597-605.	4.2	38
135	New Carbohydrate Specificity and HIV-1 Fusion Blocking Activity of the Cyanobacterial Protein MVL: NMR, ITC and Sedimentation Equilibrium Studies. <i>Journal of Molecular Biology</i> , 2004, 339, 901-914.	4.2	56
136	Structural Basis for Dimerization of the Grb10 Src Homology 2 Domain. <i>Journal of Biological Chemistry</i> , 2003, 278, 13257-13264.	3.4	56
137	Tetramerization and DNA Ligase IV Interaction of the DNA Double-strand Break Repair Protein XRCC4 are Mutually Exclusive. <i>Journal of Molecular Biology</i> , 2003, 334, 215-228.	4.2	67
138	Mechanism of Ubiquitin Recognition by the CUE Domain of Vps9p. <i>Cell</i> , 2003, 113, 609-620.	28.9	215
139	Structural Basis for Recruitment of the Adaptor Protein APS to the Activated Insulin Receptor. <i>Molecular Cell</i> , 2003, 12, 1379-1389.	9.7	113
140	Regulation of Mre11/Rad50 by Nbs1. <i>Journal of Biological Chemistry</i> , 2003, 278, 45171-45181.	3.4	81
141	Determinants of GATA-1 Binding to DNA. <i>Journal of Biological Chemistry</i> , 2003, 278, 45620-45628.	3.4	27
142	Design of a Novel Peptide Inhibitor of HIV Fusion That Disrupts the Internal Trimeric Coiled-coil of gp41. <i>Journal of Biological Chemistry</i> , 2002, 277, 14238-14245.	3.4	125
143	Insights into negative modulation of <i>E. coli</i> replication initiation from the structure of SeqA ϵ hemimethylated DNA complex. <i>Nature Structural Biology</i> , 2002, 9, 839-43.	9.7	29
144	Crystal Structure of the 14-3-3 η :Serotonin N-Acetyltransferase Complex. <i>Cell</i> , 2001, 105, 257-267.	28.9	372

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145	Role of Oligosaccharide Residues of IgG1-Fc in Fc γ RIIb Binding. <i>Journal of Biological Chemistry</i> , 2001, 276, 45539-45547.	3.4	223
146	Regulation of IgE Production Requires Oligomerization of CD23. <i>Journal of Immunology</i> , 2001, 167, 3139-3145.	0.8	38
147	Folded Monomer of HIV-1 Protease. <i>Journal of Biological Chemistry</i> , 2001, 276, 49110-49116.	3.4	85
148	GATA Zinc Finger Interactions Modulate DNA Binding and Transactivation. <i>Journal of Biological Chemistry</i> , 2000, 275, 28157-28166.	3.4	91
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