

Elena Orlova

List of Publications by Year in descending order

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112
papers

10,080
citations

50566

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98
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120
all docs

120
docs citations

120
times ranked

10735
citing authors

#	ARTICLE	IF	CITATIONS
1	Cryo-EM structure of a type IV secretion system. <i>Nature</i> , 2022, 607, 191-196.	13.7	56
2	Unwinding of a DNA replication fork by a hexameric viral helicase. <i>Nature Communications</i> , 2021, 12, 5535.	5.8	8
3	Cryo-EM Structures of Two Bacteriophage Portal Proteins Provide Insights for Antimicrobial Phage Engineering. <i>Viruses</i> , 2021, 13, 2532.	1.5	1
4	The structural basis for Z ¹ -antitrypsin polymerization in the liver. <i>Science Advances</i> , 2020, 6, .	4.7	26
5	Lysis Performance of Bacteriophages with Different Plaque Sizes and Comparison of Lysis Kinetics After Simultaneous and Sequential Phage Addition. <i>Phage</i> , 2020, 1, 149-157.	0.8	0
6	Structural transitions during the scaffolding-driven assembly of a viral capsid. <i>Nature Communications</i> , 2019, 10, 4840.	5.8	21
7	Unravelling Ribosome Function Through Structural Studies. <i>Sub-Cellular Biochemistry</i> , 2019, 93, 53-81.	1.0	6
8	The absence or presence of a lytic coliphage affects the response of <i>Escherichia coli</i> to heat, chlorine, or UV exposure. <i>Folia Microbiologica</i> , 2018, 63, 599-606.	1.1	2
9	Structures of biomolecular complexes by combination of NMR and cryoEM methods. <i>Current Opinion in Structural Biology</i> , 2017, 43, 104-113.	2.6	32
10	Use of chimeric type IV secretion systems to define contributions of outer membrane subassemblies for contact-dependent translocation. <i>Molecular Microbiology</i> , 2017, 105, 273-293.	1.2	49
11	The ribosome and its role in protein folding: looking through a magnifying glass. <i>Acta Crystallographica Section D: Structural Biology</i> , 2017, 73, 509-521.	1.1	32
12	Structure of a VirD4 coupling protein bound to a VirB type IV secretion machinery. <i>EMBO Journal</i> , 2017, 36, 3080-3095.	3.5	79
13	Structural Analysis of Protein Complexes by Cryo Electron Microscopy. <i>Methods in Molecular Biology</i> , 2017, 1615, 377-413.	0.4	15
14	Structural Study of Heterogeneous Biological Samples by Cryoelectron Microscopy and Image Processing. <i>BioMed Research International</i> , 2017, 2017, 1-23.	0.9	17
15	Two p53 tetramers bind one consensus DNA response element. <i>Nucleic Acids Research</i> , 2016, 44, 6185-6199.	6.5	28
16	Bacteriophage SPP1 Tail Tube Protein Self-assembles into β^2 -Structure-rich Tubes. <i>Journal of Biological Chemistry</i> , 2015, 290, 3836-3849.	1.6	24
17	DNA Induces Conformational Changes in a Recombinant Human Minichromosome Maintenance Complex. <i>Journal of Biological Chemistry</i> , 2015, 290, 7973-7979.	1.6	8
18	Structural basis for DNA strand separation by a hexameric replicative helicase. <i>Nucleic Acids Research</i> , 2015, 43, 8551-8563.	6.5	9

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19	Structural rearrangements in the phage head-to-tail interface during assembly and infection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 7009-7014.	3.3	53
20	A molecular syringe that kills cells. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 357-359.	3.6	2
21	Novel Inter-Subunit Contacts in Barley Stripe Mosaic Virus Revealed by Cryo-Electron Microscopy. <i>Structure</i> , 2015, 23, 1815-1826.	1.6	28
22	Nanoscale stiffness topography reveals structure and mechanics of the transport barrier in intact nuclear pore complexes. <i>Nature Nanotechnology</i> , 2015, 10, 60-64.	15.6	57
23	Structural studies of T4S systems by electron microscopy. <i>AIMS Biophysics</i> , 2015, 2, 184-199.	0.3	1
24	Structural organisation of the type IV secretion systems. <i>Current Opinion in Microbiology</i> , 2014, 17, 24-31.	2.3	25
25	Structure of a type IV secretion system. <i>Nature</i> , 2014, 508, 550-553.	13.7	280
26	Structure of a bacterial type IV secretion core complex at subnanometre resolution. <i>EMBO Journal</i> , 2013, 32, 1195-1204.	3.5	85
27	Atomic structure and hierarchical assembly of a cross- β^2 amyloid fibril. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 5468-5473.	3.3	479
28	Capsid Structure and Its Stability at the Late Stages of Bacteriophage SPP1 Assembly. <i>Journal of Virology</i> , 2012, 86, 6768-6777.	1.5	46
29	Structure of the VirB4 ATPase, alone and bound to the core complex of a type IV secretion system. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 11348-11353.	3.3	86
30	Direct three-dimensional visualization of membrane disruption by amyloid fibrils. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 20455-20460.	3.3	162
31	Genome Gating in Tailed Bacteriophage Capsids. <i>Advances in Experimental Medicine and Biology</i> , 2012, 726, 585-600.	0.8	39
32	Quaternary structure of the specific p53-DNA complex reveals the mechanism of p53 mutant dominance. <i>Nucleic Acids Research</i> , 2011, 39, 8960-8971.	6.5	43
33	Structural Analysis of Macromolecular Assemblies by Electron Microscopy. <i>Chemical Reviews</i> , 2011, 111, 7710-7748.	23.0	146
34	The structural basis for membrane binding and pore formation by lymphocyte perforin. <i>Nature</i> , 2010, 468, 447-451.	13.7	364
35	Structure of the hDmc1-ssDNA Filament Reveals the Principles of Its Architecture. <i>PLoS ONE</i> , 2010, 5, e8586.	1.1	20
36	Methods for Three-Dimensional Reconstruction of Heterogeneous Assemblies. <i>Methods in Enzymology</i> , 2010, 482, 321-341.	0.4	38

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37	4.6Å... Cryo-EM reconstruction of tobacco mosaic virus from images recorded at 300keV on a 4kÅ—4k CCD camera. <i>Journal of Structural Biology</i> , 2010, 171, 303-308.	1.3	61
38	Structure of bacteriophage SPP1 head-to-tail connection reveals mechanism for viral DNA gating. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 8507-8512.	3.3	107
39	Structural biology of the p53 tumour suppressor. <i>Current Opinion in Structural Biology</i> , 2009, 19, 197-202.	2.6	56
40	How viruses infect bacteria?. <i>EMBO Journal</i> , 2009, 28, 797-798.	3.5	10
41	Globular Tetramers of Î²2-Microglobulin Assemble into Elaborate Amyloid Fibrils. <i>Journal of Molecular Biology</i> , 2009, 389, 48-57.	2.0	73
42	Structure of a Type IV Secretion System Core Complex. <i>Science</i> , 2009, 323, 266-268.	6.0	277
43	Detection and separation of heterogeneity in molecular complexes by statistical analysis of their two-dimensional projections. <i>Journal of Structural Biology</i> , 2008, 162, 108-120.	1.3	75
44	Structural Analysis of the Saf Pilus by Electron Microscopy and Image Processing. <i>Journal of Molecular Biology</i> , 2008, 379, 174-187.	2.0	31
45	Topologies of a Substrate Protein Bound to the Chaperonin GroEL. <i>Molecular Cell</i> , 2007, 26, 415-426.	4.5	96
46	Structural framework for DNA translocation via the viral portal protein. <i>EMBO Journal</i> , 2007, 26, 1984-1994.	3.5	207
47	Structure of bacteriophage SPP1 tail reveals trigger for DNA ejection. <i>EMBO Journal</i> , 2007, 26, 3720-3728.	3.5	120
48	Hexameric ring structure of human MCM10 DNA replication factor. <i>EMBO Reports</i> , 2007, 8, 925-930.	2.0	35
49	Elongated Oligomers Assemble into Mammalian PrP Amyloid Fibrils. <i>Journal of Molecular Biology</i> , 2006, 357, 975-985.	2.0	61
50	The structure of p53 tumour suppressor protein reveals the basis for its functional plasticity. <i>EMBO Journal</i> , 2006, 25, 5191-5200.	3.5	113
51	An Expanded and Flexible Form of the Vacuolar ATPase Membrane Sector. <i>Structure</i> , 2006, 14, 1149-1156.	1.6	26
52	Multiple Distinct Assemblies Reveal Conformational Flexibility in the Small Heat Shock Protein Hsp26. <i>Structure</i> , 2006, 14, 1197-1204.	1.6	87
53	Lensin Is a Survivor of an Ancient Family of Class I Glutamine Synthetases Re-engineered by Evolution for a Role in the Vertebrate Lens. <i>Structure</i> , 2006, 14, 1823-1834.	1.6	33
54	Removal of Divalent Cations Induces Structural Transitions in Red Clover Necrotic Mosaic Virus , Revealing a Potential Mechanism for RNA Release. <i>Journal of Virology</i> , 2006, 80, 10395-10406.	1.5	106

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55	Dodecameric Structure of the Small Heat Shock Protein Acr1 from <i>Mycobacterium tuberculosis</i> . <i>Journal of Biological Chemistry</i> , 2005, 280, 33419-33425.	1.6	91
56	Structural Basis of Pore Formation by the Bacterial Toxin Pneumolysin. <i>Cell</i> , 2005, 121, 247-256.	13.5	369
57	Molecular structure of human geminin. <i>Nature Structural and Molecular Biology</i> , 2004, 11, 1021-1022.	3.6	34
58	Structure determination of macromolecular assemblies by single-particle analysis of cryo-electron micrographs. <i>Current Opinion in Structural Biology</i> , 2004, 14, 584-590.	2.6	48
59	Recognition and Separation of Single Particles with Size Variation by Statistical Analysis of their Images. <i>Journal of Molecular Biology</i> , 2004, 336, 453-460.	2.0	61
60	The Structure of Red Clover Necrotic Mosaic Dianthovirus at 10 Å... Resolution. <i>Microscopy and Microanalysis</i> , 2004, 10, 1486-1487.	0.2	0
61	Structure of a viral DNA gatekeeper at 10 Å resolution by cryo-electron microscopy. <i>EMBO Journal</i> , 2003, 22, 1255-1262.	3.5	124
62	Dynamic force microscopy imaging of native membranes. <i>Ultramicroscopy</i> , 2003, 97, 229-237.	0.8	62
63	Structure of the <i>Escherichia coli</i> ribosomal termination complex with release factor 2. <i>Nature</i> , 2003, 421, 90-94.	13.7	191
64	Structure of Triglyceride-Rich Human Low-Density Lipoproteins According to Cryoelectron Microscopy. <i>Biochemistry</i> , 2003, 42, 14988-14993.	1.2	30
65	Voltage-gated K ⁺ Channel from Mammalian Brain: 3D Structure at 18 Å... of the Complete (α ₁) ₄ (β ₂) ₄ Complex. <i>Journal of Molecular Biology</i> , 2003, 326, 1005-1012.	2.0	39
66	Quaternary Structure of the European Spiny Lobster (<i>Palinurus elephas</i>) 1 Å—6-mer Hemocyanin from cryoEM and Amino Acid Sequence Data. <i>Journal of Molecular Biology</i> , 2003, 325, 99-109.	2.0	24
67	Mutant α-Latrotoxin (LTXN4C) Does Not Form Pores and Causes Secretion by Receptor Stimulation. <i>Journal of Biological Chemistry</i> , 2003, 278, 31058-31066.	1.6	40
68	Determination of <i>Escherichia coli</i> RNA Polymerase Structure by Single Particle Cryoelectron Microscopy. <i>Methods in Enzymology</i> , 2003, 370, 24-42.	0.4	4
69	Structural organisation of the head-to-tail interface of a bacterial virus 1 Edited by T. Richmond. <i>Journal of Molecular Biology</i> , 2001, 310, 1027-1037.	2.0	88
70	Localisation of the PsbH subunit in photosystem II: a new approach using labelling of his-tags with a Ni ²⁺ -NTA gold cluster and single particle analysis. <i>Journal of Molecular Biology</i> , 2001, 312, 371-379.	2.0	66
71	α-Latrotoxin, Acting via Two Ca ²⁺ -dependent Pathways, Triggers Exocytosis of Two Pools of Synaptic Vesicles. <i>Journal of Biological Chemistry</i> , 2001, 276, 44695-44703.	1.6	79
72	Single-particle electron cryo-microscopy: towards atomic resolution. <i>Quarterly Reviews of Biophysics</i> , 2000, 33, 307-369.	2.4	535

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73	Structural analysis of non-crystalline macromolecules: the ribosome. Acta Crystallographica Section D: Biological Crystallography, 2000, 56, 1253-1258.	2.5	11
74	3D map of the plant photosystem II supercomplex obtained by cryoelectron microscopy and single particle analysis. Nature Structural Biology, 2000, 7, 44-47.	9.7	172
75	Structure of alpha-latrotoxin oligomers reveals that divalent cation-dependent tetramers form membrane pores. Nature Structural Biology, 2000, 7, 48-53.	9.7	128
76	Escherichia coli RNA polymerase core and holoenzyme structures. EMBO Journal, 2000, 19, 6833-6844.	3.5	35
77	Tetramerisation of α -latrotoxin by divalent cations is responsible for toxin-induced non-vesicular release and contributes to the Ca^{2+} -dependent vesicular exocytosis from synaptosomes. Biochimie, 2000, 82, 453-468.	1.3	41
78	Structure of the AAA ATPase p97. Molecular Cell, 2000, 6, 1473-1484.	4.5	394
79	Three-dimensional structure of low density lipoproteins by electron cryomicroscopy. Proceedings of the National Academy of Sciences of the United States of America, 1999, 96, 8420-8425.	3.3	126
80	Structure of the 13-fold symmetric portal protein of bacteriophage SPP1. Nature Structural Biology, 1999, 6, 842-846.	9.7	62
81	Cryo-electron microscopy structure of an SH3 amyloid fibril and model of the molecular packing. EMBO Journal, 1999, 18, 815-821.	3.5	487
82	The Escherichia coli large ribosomal subunit at 7.5 Å... resolution. Structure, 1999, 7, 1575-1583.	1.6	127
83	The Skeletal Muscle Calcium-Release Channel Visualised By Electron Cryomicroscopy and Angular Reconstitution. , 1998, , 23-46.		2
84	Structure of keyhole limpet hemocyanin type 1 (KLH1) at 15 Å... resolution by electron cryomicroscopy and angular reconstitution â€ 1 â€ This article is dedicated to the memory of Anneke van Heel. 1 Edited by M.F. Moody. Journal of Molecular Biology, 1997, 271, 417-437.	2.0	202
85	Arrangement of tRNAs in Pre- and Posttranslocational Ribosomes Revealed by Electron Cryomicroscopy. Cell, 1997, 88, 19-28.	13.5	247
86	A New Generation of the IMAGIC Image Processing System. Journal of Structural Biology, 1996, 116, 17-24.	1.3	1,182
87	Intrinsic versus imposed curvature in cyclical oligomers: the portal protein of bacteriophage SPP1.. EMBO Journal, 1996, 15, 4785-4788.	3.5	20
88	Two structural configurations of the skeletal muscle calcium release channel. Nature Structural and Molecular Biology, 1996, 3, 547-552.	3.6	161
89	Intrinsic versus imposed curvature in cyclical oligomers: the portal protein of bacteriophage SPP1. EMBO Journal, 1996, 15, 4785-8.	3.5	2
90	The 70S Escherichia coli ribosome at 23 Å resolution: fitting the ribosomal RNA. Structure, 1995, 3, 815-821.	1.6	237

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91	Electron cryomicroscopy and angular reconstitution used to visualize the skeletal muscle calcium release channel. <i>Nature Structural Biology</i> , 1995, 2, 18-24.	9.7	185
92	The SPP1 connection. <i>FEMS Microbiology Reviews</i> , 1995, 17, 47-56.	3.9	20
93	Structure of <i>Lumbricus terrestris</i> Hemoglobin at 30 Å... Resolution Determined Using Angular Reconstitution. <i>Journal of Structural Biology</i> , 1995, 114, 28-40.	1.3	119
94	Three-Dimensional Structure of Keyhole Limpet Hemocyanin by Cryoelectron Microscopy and Angular Reconstitution. <i>Journal of Structural Biology</i> , 1995, 115, 226-232.	1.3	20
95	3-D structure of single macromolecules at 15Å... resolution by cryo-microscopy and angular reconstitution. <i>Proceedings Annual Meeting Electron Microscopy Society of America</i> , 1995, 53, 838-839.	0.0	0
96	Correlation functions revisited. <i>Ultramicroscopy</i> , 1992, 46, 307-316.	0.8	91
97	HREM of epitaxial layers in the InAs/GaAs system. <i>Ultramicroscopy</i> , 1991, 35, 11-18.	0.8	9
98	Correlation Averaging and Filtering of Electron Micrographs. , 1991, , 327-332.		0
99	Structure of the ATP-synthase studied by electron microscopy and image processing. <i>FEBS Letters</i> , 1989, 244, 279-282.	1.3	23
100	Electron microscopy of multiple forms of glutamine synthetase from bacteroids and the cytosol of yellow lupin root nodules. <i>BBA - Proteins and Proteomics</i> , 1987, 913, 368-376.	2.1	9
101	Quaternary structure of the liver microsomal cytochrome P-450. <i>FEBS Letters</i> , 1986, 205, 35-40.	1.3	39
102	Electron microscopy of the nitrogenase molecule from <i>azotobacter vinelandii</i> . <i>Journal of Inorganic Biochemistry</i> , 1986, 27, 141-146.	1.5	2
103	Electron microscopy of the Mo-Fe-protein from <i>Azotobacter vinelandii</i> nitrogenase. <i>FEBS Journal</i> , 1985, 149, 389-392.	0.2	10
104	Fine structure of the 30 S ribosomal subunit. <i>FEBS Letters</i> , 1985, 186, 21-25.	1.3	2
105	Electron microscopy of beef heart mitochondrial F1 -ATPase. <i>FEBS Letters</i> , 1984, 167, 285-290.	1.3	30
106	Computer averaging of 50 S ribosomal subunit electron micrographs. <i>Journal of Molecular Biology</i> , 1983, 169, 345-350.	2.0	10
107	On the fine structure of rat liver ribosome small subunits. <i>Molecular Biology Reports</i> , 1982, 8, 185-189.	1.0	6
108	Strand-like structures and their three-dimensional organization in the large subunit of the <i>Escherichia coli</i> ribosome. <i>Molecular Biology Reports</i> , 1982, 8, 191-197.	1.0	9

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109	On the negative staining of the protein crystal structure. <i>Ultramicroscopy</i> , 1981, 7, 131-137.	0.8	17
110	Bacteriophages: Their Structural Organisation and Function. , 0, , .		6
111	The SPP1 connection. , 0, .		1
112	Visualization of the Translational Elongation Cycle by Cryo-Electron Microscopy. , 0, , 35-44.		1