Reidun Twarock

List of Publications by Year
in descending order

86	2,393	172207	233125
papers	citations	29 h-index	45 g-index

92	92	92	1484
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	An age-structured model of hepatitis B viral infection highlights the potential of different therapeutic strategies. Scientific Reports, 2022, 12, 1252.	1.6	9
2	Programmable polymorphism of a virus-like particle. Communications Materials, 2022, 3, 7.	2.9	22
3	Dysregulation of Hepatitis B Virus Nucleocapsid Assembly in vitro by RNA-binding Small Ligands. Journal of Molecular Biology, 2022, 434, 167557.	2.0	6
4	Dataset of high-throughput ligand screening against the RNA Packaging Signals regulating Hepatitis B Virus nucleocapsid formation. Data in Brief, 2022, 42, 108206.	0.5	0
5	Local rules for the self-assembly of a non-quasi-equivalent viral capsid. Physical Review E, 2022, 105, .	0.8	3
6	Mathematical Modeling of Virus Architecture. , 2021, , 248-256.		0
7	Genome Packaging. , 2021, , 488-494.		0
8	Evolution of a virus-like architecture and packaging mechanism in a repurposed bacterial protein. Science, 2021, 372, 1220-1224.	6.0	53
9	Percolation Theory Reveals Biophysical Properties of Virus-like Particles. ACS Nano, 2021, 15, 12988-12995.	7.3	10
10	Comparing antiviral strategies against COVID-19 via multiscale within-host modelling. Royal Society Open Science, 2021, 8, 210082.	1.1	17
11	The impact of local assembly rules on RNA packaging in a T = 1 satellite plant virus. PLoS Computational Biology, 2021, 17, e1009306.	1.5	4
12	An Intracellular Model of Hepatitis B Viral Infection: An In Silico Platform for Comparing Therapeutic Strategies. Viruses, 2021, 13, 11.	1.5	13
13	In vitro functional analysis of gRNA sites regulating assembly of hepatitis B virus. Communications Biology, 2021, 4, 1407.	2.0	6
14	Therapeutic interfering particles exploiting viral replication and assembly mechanisms show promising performance: a modelling study. Scientific Reports, 2021, 11, 23847.	1.6	1
15	Intra- and intermolecular atomic-scale interactions in the receptor binding domain of SARS-CoV-2 spike protein: implication for ACE2 receptor binding. Physical Chemistry Chemical Physics, 2020, 22, 18272-18283.	1.3	53
16	Viral Genome Conformations and Contacts across Different Lifecycle Stages. Proceedings (mdpi), 2020, 50, .	0.2	0
17	Surface stresses in complex viral capsids and non-quasi-equivalent viral architectures. Journal of the Royal Society Interface, 2020, 17, 20200455.	1.5	2
18	A multiscale model of virus pandemic: Heterogeneous interactive entities in a globally connected world. Mathematical Models and Methods in Applied Sciences, 2020, 30, 1591-1651.	1.7	105

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19	Conservation of Genetically-Embedded Virus Assembly Instructions: A Novel Route to Antiviral Therapy. Proceedings (mdpi), 2020, 50, 87.	0.2	0
20	Assembly of infectious enteroviruses depends on multiple, conserved genomic RNA-coat protein contacts. PLoS Pathogens, 2020, 16, e1009146.	2.1	31
21	Structural characterization of genomic RNA-coat protein contacts in single-stranded RNA viruses by high-resolution cryo-EM. Access Microbiology, 2020, 2, .	0.2	0
22	Mathematical Virology. Inference, 2020, 5, .	0.0	0
23	A coarse-grained model of the expansion of the human rhinovirus 2 capsid reveals insights in genome release. Journal of the Royal Society Interface, 2019, 16, 20190044.	1.5	4
24	Structural puzzles in virology solved with an overarching icosahedral design principle. Nature Communications, 2019, 10, 4414.	5.8	66
25	RNA-Mediated Virus Assembly: Mechanisms and Consequences for Viral Evolution and Therapy. Annual Review of Biophysics, 2019, 48, 495-514.	4.5	54
26	Dynamic network approach for the modelling of genomic sub-complexes in multi-segmented viruses. Nucleic Acids Research, 2018, 46, 12087-12098.	6.5	11
27	A modelling paradigm for RNA virus assembly. Current Opinion in Virology, 2018, 31, 74-81.	2.6	62
28	Hamiltonian path analysis of viral genomes. Nature Communications, 2018, 9, 2021.	5.8	30
29	HBV RNA pre-genome encodes specific motifs that mediate interactions with the viral core protein that promote nucleocapsid assembly. Nature Microbiology, 2017, 2, 17098.	5.9	69
30	Impact of Hydrogen Bonding in the Binding Site between Capsid Protein and MS2 Bacteriophage ssRNA. Journal of Physical Chemistry B, 2017, 121, 6321-6330.	1.2	30
31	Genomic RNA folding mediates assembly of human parechovirus. Nature Communications, 2017, 8, 5.	5.8	67
32	Rewriting natureâ€™s assembly manual for a ssRNA virus. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 12255-12260.	3.3	47
33	RNA Virus Evolution via a Quasispecies-Based Model Reveals a Drug Target with a High Barrier to Resistance. Viruses, 2017, 9, 347.	1.5	20
34	A group theoretical approach to structural transitions of icosahedral quasicrystals and point arrays. Journal of Physics A: Mathematical and Theoretical, 2016, 49, 175203.	0.7	8
35	Direct Evidence for Packaging Signal-Mediated Assembly of Bacteriophage MS2. Journal of Molecular Biology, 2016, 428, 431-448.	2.0	80
36	Bacteriophage MS2 genomic RNA encodes an assembly instruction manual for its capsid. Bacteriophage, 2016, 6, e1157666.	1.9	38

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37	Principles Governing the Self-Assembly of Coiled-Coil Protein Nanoparticles. Biophysical Journal, 2016, 110, 646-660.	0.2	31
38	Orbits of crystallographic embedding of non-crystallographic groups and applications to virology. Acta Crystallographica Section A: Foundations and Advances, 2015, 71, 569-582.	0.0	4
39	Revealing the density of encoded functions in a viral RNA. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 2227-2232.	3.3	64
40	Asymmetric Genome Organization in an RNA Virus Revealed via Graph-Theoretical Analysis of Tomographic Data. PLoS Computational Biology, 2015, 11, e1004146.	1.5	12
41	On the subgroup structure of the hyperoctahedral group in six dimensions. Acta Crystallographica Section A: Foundations and Advances, 2014, 70, 417-428.	0.0	6
42	Solving a Levinthal's paradox for virus assembly identifies a unique antiviral strategy. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 5361-5366.	3.3	102
43	Viruses and fullerenes â€“ symmetry as a common thread?. Acta Crystallographica Section A: Foundations and Advances, 2014, 70, 162-167.	0.0	21
44	The Role of Symmetry in Conformational Changes of Viral Capsids: A Mathematical Approach. Natural Computing Series, 2014, , 217-240.	2.2	2
45	Packaging signals in single-stranded RNA viruses: natureâ€™s alternative to a purely electrostatic assembly mechanism. Journal of Biological Physics, 2013, 39, 277-287.	0.7	86
46	Packaging Signals in Two Single-Stranded RNA Viruses Imply a Conserved Assembly Mechanism and Geometry of the Packaged Genome. Journal of Molecular Biology, 2013, 425, 3235-3249.	2.0	80
47	On the interaction mechanisms of a p53 peptide and nutlin with the MDM2 and MDMX proteins: A Brownian dynamics study. Cell Cycle, 2013, 12, 394-404.	1.3	38
48	A new paradigm for the roles of the genome in ssRNA viruses. Future Virology, 2013, 8, 531-543.	0.9	18
49	Affine extensions of non-crystallographic Coxeter groups induced by projection. Journal of Mathematical Physics, 2013, 54, 093508.	0.5	16
50	Mechanical and Assembly Units of Viral Capsids Identified via Quasi-Rigid Domain Decomposition. PLoS Computational Biology, 2013, 9, e1003331.	1.5	35
51	Structural constraints on the three-dimensional geometry of simple viruses: case studies of a new predictive tool. Acta Crystallographica Section A: Foundations and Advances, 2013, 69, 140-150.	0.3	25
52	Nonicosahedral pathways for capsid expansion. Physical Review E, 2013, 88, 032710.	0.8	8
53	Building a viral capsid in the presence of genomic RNA. Physical Review E, 2013, 87, 022717.	0.8	45
54	A MATHEMATICAL APPROACH TO STRUCTURAL TRANSITIONS IN VIRAL CAPSIDS. International Journal of Modern Physics Conference Series, 2012, 09, 11-23.	0.7	0

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55	Novel Kacâ€“Moody-type affine extensions of non-crystallographic Coxeter groups. Journal of Physics A: Mathematical and Theoretical, 2012, 45, 285202.	0.7	17
56	Characterization of the Ligand Receptor Encounter Complex and Its Potential for in Silico Kinetics-Based Drug Development. Journal of Chemical Theory and Computation, 2012, 8, 314-321.	2.3	15
57	Peptide Inhibitors of Viral Assembly: A Novel Route to Broad-Spectrum Antivirals. Journal of Chemical Information and Modeling, 2012, 52, 770-776.	2.5	17
58	Structure and RNA Recognition in Recombinant STNV Capsids. Biophysical Journal, 2012, 102, 641a.	0.2	0
59	Structural transformations in quasicrystals induced by higher dimensional lattice transitions. Proceedings of the Royal Society A: Mathematical, Physical and Engineering Sciences, 2012, 468, 1452-1471.	1.0	7
60	A crystallographic approach to structural transitions in icosahedral viruses. Journal of Mathematical Biology, 2012, 64, 745-773.	0.8	18
61	On the Origin of Order in the Genome Organization of ssRNA Viruses. Biophysical Journal, 2011, 101, 774-780.	0.2	12
62	Simple Rules for Efficient Assembly Predict the Layout of a Packaged Viral RNA. Journal of Molecular Biology, 2011, 408, 399-407.	2.0	59
63	Degenerate RNA Packaging Signals in the Genome of Satellite Tobacco Necrosis Virus: Implications for the Assembly of a T= 1 Capsid. Journal of Molecular Biology, 2011, 413, 51-65.	2.0	65
64	The physics of virus assembly. Physical Biology, 2010, 7, 040301.	0.8	1
65	All-atom normal-mode analysis reveals an RNA-induced allostery in a bacteriophage coat protein. Physical Review E, 2010, 81, 031908.	0.8	27
66	The Impact of Viral RNA on the Association Rates of Capsid Protein Assembly: Bacteriophage MS2 as a Case Study. Journal of Molecular Biology, 2010, 400, 935-947.	2.0	23
67	The Impact of Viral RNA on Assembly Pathway Selection. Journal of Molecular Biology, 2010, 401, 298-308.	2.0	64
68	Beyond Quasi-Equivalence: New Insights Into Viral Architecture via Affine Extended Symmetry Groups. , 2010, , 59-83.		5
69	Emerging Topics in Physical Virology. , 2010, , .		15
70	Affine extensions of the icosahedral group with applications to the three-dimensional organisation of simple viruses. Journal of Mathematical Biology, 2009, 59, 287-313.	0.8	46
71	DNA Cages with Icosahedral Symmetry inÂBionanotechnology. Natural Computing Series, 2009, , 141-158.	2.2	1
72	Blueprints for viral capsids in the family of Polyomaviridae. Journal of Theoretical Biology, 2008, 253, 808-816.	0.8	24

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73	The Three-dimensional Structure of Genomic RNA in Bacteriophage MS2: Implications for Assembly. Journal of Molecular Biology, 2008, 375, 824-836.	2.0	105
74	Polyomaviridae Assembly Polymorphism from an Energy Landscape Perspective. Computational and Mathematical Methods in Medicine, 2008, 9, 245-256.	0.7	2
75	New Insights into Viral Architecture via Affine Extended Symmetry Groups. Computational and Mathematical Methods in Medicine, 2008, 9, 221-229.	0.7	10
76	Mathematical virology: a novel approach to the structure and assembly of viruses. Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences, 2006, 364, 3357-3373.	1.6	60
77	Master equation approach to the assembly of viral capsids. Journal of Theoretical Biology, 2006, 242, 713-721.	0.8	55
78	Classification of capped tubular viral particles in the family of Papovaviridae. Journal of Physics Condensed Matter, 2006, 18, S375-S387.	0.7	7
79	Mathematical models for tubular structures in the family of. Bulletin of Mathematical Biology, 2005, 67, 973-987.	0.9	18
80	Mathematical Virology. Journal of Theoretical Medicine, 2005, 6, 67-68.	0.5	1
81	Assembly models forPapovaviridaebased on tiling theory. Physical Biology, 2005, 2, 175-188.	0.8	25
82	A tiling approach to virus capsid assembly explaining a structural puzzle in virology. Journal of Theoretical Biology, 2004, 226, 477-482.	0.8	120
83	Quadratic algebras in traffic flow models. Reports on Mathematical Physics, 2003, 51, 381-389.	0.4	1
84	Affine extension of noncrystallographic Coxeter groups and quasicrystals. Journal of Physics A, 2002, 35, 1551-1574.	1.6	33
85	Quasicrystal Lie algebras. Physics Letters, Section A: General, Atomic and Solid State Physics, 1998, 246, 209-213.	0.9	16
86	Representations of Uh(su(N))derived from quantum flag manifolds. Journal of Mathematical Physics, 1997, 38, 1161-1182.	0.5	3