Gennady A Bocharov

List of Publications by Year
in descending order

113 papers	2,962 citations	186209 28 h-index	189801 50 g-index
124 all docs	124 docs citations	124 times ranked	2774 citing authors

#	Article	IF	Citations
1	Multiply infected spleen cells in HIV patients. Nature, 2002, 418, 144-144.	13.7	381
2	Numerical modelling in biosciences using delay differential equations. Journal of Computational and Applied Mathematics, 2000, 125, 183-199.	1.1	262
3	Mathematical Model of Antiviral Immune Response III. Influenza A Virus Infection. Journal of Theoretical Biology, 1994, 167, 323-360.	0.8	141
4	Mathematical modelling of infectious diseases. British Medical Bulletin, 2009, 92, 33-42.	2.7	131
5	Underwhelming the Immune Response: Effect of Slow Virus Growth on CD8 + -T-Lymphocyte Responses. Journal of Virology, 2004, 78, 2247-2254.	1.5	99
6	Topological Small-World Organization of the Fibroblastic Reticular Cell Network Determines Lymph Node Functionality. PLoS Biology, 2016, 14, e1002515.	2.6	96
7	Modelling the Dynamics of LCMV Infection in Mice: Conventional and Exhaustive CTL Responses. Journal of Theoretical Biology, 1998, 192, 283-308.	0.8	78
8	Direct quantitation of rapid elimination of viral antigen-positive lymphocytes by antiviral CD8+ T cellsin vivo. European Journal of Immunology, 2000, 30, 1356-1363.	1.6	78
9	Structured Population Models, Conservation Laws, and Delay Equations. Journal of Differential Equations, 2000, 168, 212-237.	1.1	62
10	Estimation of Cell Proliferation Dynamics Using CFSE Data. Bulletin of Mathematical Biology, 2011, 73, 116-150.	0.9	62
11	Numerical modelling of label-structured cell population growth using CFSE distribution data. Theoretical Biology and Medical Modelling, 2007, 4, 26.	2.1	54
12	Determining control parameters for dendritic cell-cytotoxic T lymphocyte interaction. European Journal of Immunology, 2004, 34, 2407-2418.	1.6	51
13	A genetic-algorithm approach to simulating human immunodeficiency virus evolution reveals the strong impact of multiply infected cells and recombination. Journal of General Virology, 2005, 86, 3109-3118.	1.3	50
14	The Impact of Variation in the Number of CD8+T-Cell Precursors on the Outcome of Virus Infection. Cellular Immunology, 1998, 189, 67-73.	1.4	46
15	Rival approaches to mathematical modelling in immunology. Journal of Computational and Applied Mathematics, 2007, 205, 669-686.	1.1	46
16	Feedback regulation of proliferation vs. differentiation rates explains the dependence of CD4 T-cell expansion on precursor number. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 3318-3323.	3.3	44
17	Human Immunodeficiency Virus Infection : from Biological Observations to Mechanistic Mathematical Modelling. Mathematical Modelling of Natural Phenomena, 2012, 7, 78-104.	0.9	43
18	Mathematical Immunology of Virus Infections. , 2018, , .		42

#	ARTICLE	IF	CITATIONS
19	Spatiotemporal Dynamics of Virus Infection Spreading in Tissues. PLoS ONE, 2016, 11, e0168576.	1.1	39
20	A new model for the estimation of cell proliferation dynamics using CFSE data. Journal of Immunological Methods, 2011, 373, 143-160.	0.6	38
21	Computational analysis of CFSE proliferation assay. Journal of Mathematical Biology, 2006, 54, 57-89.	0.8	37
22	Computational approaches to parameter estimation and model selection in immunology. Journal of Computational and Applied Mathematics, 2005, 184, 50-76.	1.1	36
23	Antigen-stimulated CD4 T-cell expansion is inversely and log-linearly related to precursor number. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 3312-3317.	3.3	35
24	Computational Approach to 3D Modeling of the Lymph Node Geometry. Computation, 2015, 3, 222-234.	1.0	35
25	Topological Structure and Robustness of the Lymph Node Conduit System. Cell Reports, 2020, 30, 893-904.e6.	2.9	35
26	Asymmetry of Cell Division in CFSE-Based Lymphocyte Proliferation Analysis. Frontiers in Immunology, 2013, 4, 264.	2.2	34
27	Developing Computational Geometry and Network Graph Models of Human Lymphatic System. Computation, 2018, 6, 1.	1.0	33
28	Distributed parameter identification for a label-structured cell population dynamics model using CFSE histogram time-series data. Journal of Mathematical Biology, 2009, 59, 581-603.	0.8	32
29	A global "imaging" view on systems approaches in immunology. European Journal of Immunology, 2012, 42, 3116-3125.	1.6	32
30	Low level viral persistence after infection with LCMV: a quantitative insight through numerical bifurcation analysis. Mathematical Biosciences, 2001, 173, 1-23.	0.9	30
31	Hybrid approach to model the spatial regulation of T cell responses. BMC Immunology, 2017, 18, 29.	0.9	29
32	Integrative Computational Modeling of the Lymph Node Stromal Cell Landscape. Frontiers in Immunology, 2018, 9, 2428.	2.2	27
33	'Rinse and Replace': Boosting T Cell Turnover To Reduce HIV-1 Reservoirs. Trends in Immunology, 2020, 41, 466-480.	2.9	26
34	A Systems Immunology Approach to Plasmacytoid Dendritic Cell Function in Cytopathic Virus Infections. PLoS Pathogens, 2010, 6, e1001017.	2.1	25
35	RNAtips: analysis of temperature-induced changes of RNA secondary structure. Nucleic Acids Research, 2013, 41, W486-W491.	6.5	25
36	Mathematical model of the Tat-Rev regulation of HIV-1 replication in an activated cell predicts the existence of oscillatory dynamics in the synthesis of viral components. BMC Genomics, 2014, 15, S1.	1.2	25

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37	Computational modelling with functional differential equations: Identification, selection, and sensitivity. Applied Numerical Mathematics, 2005, 53, 107-129.	1.2	24
38	Fitness Ranking of Individual Mutants Drives Patterns of Epistatic Interactions in HIV-1. PLoS ONE, 2011, 6, e18375.	1.1	22
39	Reaction-Diffusion Modelling of Interferon Distribution in Secondary Lymphoid Organs. Mathematical Modelling of Natural Phenomena, 2011, 6, 13-26.	0.9	21
40	Mathematical models for CFSE labelled lymphocyte dynamics: asymmetry and time-lag in division. Journal of Mathematical Biology, 2014, 69, 1547-1583.	0.8	21
41	Systems analysis reveals complex biological processes during virus infection fate decisions. Genome Research, 2019, 29, 907-919.	2.4	21
42	Modelling the dynamics of virus infection and immune response in space and time. International Journal of Parallel, Emergent and Distributed Systems, 2019, 34, 341-355.	0.7	21
43	Modelling the Dynamics of LCMV Infection in Mice: II. Compartmental Structure and Immunopathology. Journal of Theoretical Biology, 2003, 221, 349-378.	0.8	20
44	Stochastic modeling of the impact of random forcing on persistent hepatitis B virus infection. Mathematics and Computers in Simulation, 2014, 96, 54-65.	2.4	19
45	Adjoint equations and analysis of complex systems: Application to virus infection modelling. Journal of Computational and Applied Mathematics, 2005, 184, 177-204.	1.1	18
46	Understanding Experimental LCMV Infection of Mice: The Role of Mathematical Models. Journal of Immunology Research, 2015, 2015, 1-10.	0.9	18
47	Modeling of the HIV-1 Life Cycle in Productively Infected Cells to Predict Novel Therapeutic Targets. Pathogens, 2020, 9, 255.	1.2	18
48	Data-driven modelling of the FRC network for studying the fluid flow in the conduit system. Engineering Applications of Artificial Intelligence, 2017, 62, 341-349.	4.3	17
49	Towards a Multiscale Model of Acute HIV Infection. Computation, 2017, 5, 6.	1.0	17
50	Dendritic Cell Homeostasis in the Regulation of Self-Reactivity. Current Pharmaceutical Design, 2003, 9, 221-231.	0.9	17
51	Intracellular Life Cycle Kinetics of SARS-CoV-2 Predicted Using Mathematical Modelling. Viruses, 2021, 13, 1735.	1.5	15
52	Pathogenesis and Treatment of HIV Infection: The Cellular, the Immune System and the Neuroendocrine Systems Perspective. International Reviews of Immunology, 2013, 32, 282-306.	1.5	14
53	Interplay between reaction and diffusion processes in governing the dynamics of virus infections. Journal of Theoretical Biology, 2018, 457, 221-236.	0.8	14
54	Numerical bifurcation analysis of immunological models with time delays. Journal of Computational and Applied Mathematics, 2005, 184, 165-176.	1.1	13

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55	Maintenance of HIV-Specific Central and Effector Memory CD4 and CD8 T Cells Requires Antigen Persistence. AIDS Research and Human Retroviruses, 2007, 23, 549-553.	0.5	12
56	Predicting the dynamics of antiviral cytotoxic T-cell memory in response to different stimuli: Cell population structure and protective function. Immunology and Cell Biology, 2001, 79, 74-86.	1.0	11
57	Graph Theory for Modeling and Analysis of the Human Lymphatic System. Mathematics, 2020, 8, 2236.	1.1	11
58	Markov Chain-Based Stochastic Modelling of HIV-1 Life Cycle in a CD4 T Cell. Mathematics, 2021, 9, 2025.	1.1	11
59	Editorial: Mathematical Modeling of the Immune System in Homeostasis, Infection and Disease. Frontiers in Immunology, 2019, 10, 2944.	2.2	11
60	Critical Issues in Modelling Lymph Node Physiology. Computation, 2017, 5, 3.	1.0	10
61	Tensor based approach to the numerical treatment of the parameter estimation problems in mathematical immunology. Journal of Inverse and Ill-Posed Problems, 2018, 26, 51-66.	0.5	10
62	Prediction of PD-L1 inhibition effects for HIV-infected individuals. PLoS Computational Biology, 2019, 15, e1007401.	1.5	10
63	Nonlocal Reaction–Diffusion Model of Viral Evolution: Emergence of Virus Strains. Mathematics, 2020, 8, 117.	1.1	10
64	Understanding Complex Regulatory Systems: Integrating Molecular Biology and Systems Analysis. Transfusion Medicine and Hemotherapy, 2005, 32, 304-321.	0.7	9
65	Modelling Stochastic and Deterministic Behaviours in Virus Infection Dynamics. Mathematical Modelling of Natural Phenomena, 2017, 12, 63-77.	0.9	9
66	Modelling lymph flow in the lymphatic system: from 0D to 1D spatial resolution. Mathematical Modelling of Natural Phenomena, 2018, 13, 45.	0.9	8
67	Bistability analysis of virus infection models with time delays. Discrete and Continuous Dynamical Systems - Series S, 2020, 13, 2385-2401.	0.6	8
68	Mathematical Modeling of Lymph Node Drainage Function by Neural Network. Mathematics, 2021, 9, 3093.	1.1	8
69	An extremal shift method for control of HIV infection dynamics. Russian Journal of Numerical Analysis and Mathematical Modelling, 2015, 30, .	0.2	7
70	Graph Theory-Based Analysis of the Lymph Node Fibroblastic Reticular Cell Network. Methods in Molecular Biology, 2017, 1591, 43-57.	0.4	7
71	Spatial Lymphocyte Dynamics in Lymph Nodes Predicts the Cytotoxic T Cell Frequency Needed for HIV Infection Control. Frontiers in Immunology, 2019, 10, 1213.	2.2	7
72	Linking Cell Dynamics With Gene Coexpression Networks to Characterize Key Events in Chronic Virus Infections. Frontiers in Immunology, 2019, 10, 1002.	2.2	7

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73	Viral Infection Dynamics Model Based on a Markov Process with Time Delay between Cell Infection and Progeny Production. Mathematics, 2020, 8, 1207.	1.1	7
74	Genotype-dependent virus distribution and competition of virus strains. Mathematics and Mechanics of Complex Systems, 2020, 8, 101-126.	0.5	7
75	Examining the cooperativity mode of antibody and CD8+ T cell immune responses for vaccinology. Trends in Immunology, 2021, 42, 852-855.	2.9	7
76	Delay reaction-diffusion equation for infection dynamics. Discrete and Continuous Dynamical Systems - Series B, 2019, 24, 2073-2091.	0.5	7
77	Some aspects of causal & neutral equations used in modelling. Journal of Computational and Applied Mathematics, 2009, 229, 335-349.	1.1	6
78	Maximum response perturbation-based control of virus infection model with time-delays. Russian Journal of Numerical Analysis and Mathematical Modelling, 2017, 32, .	0.2	6
79	Numbers Game and Immune Geography as Determinants of Coronavirus Pathogenicity. Frontiers in Cellular and Infection Microbiology, 2020, 10, 559209.	1.8	6
80	A Mathematical Approach for Optimizing Dendritic Cell-Based Immunotherapy. , 2005, 109, 019-034.		5
81	Reaction–Diffusion Equations in Immunology. Computational Mathematics and Mathematical Physics, 2018, 58, 1967-1976.	0.2	5
82	Optimal Disturbances of Bistable Time-Delay Systems Modeling Virus Infections. Doklady Mathematics, 2018, 98, 313-316.	0.1	5
83	Existence and Dynamics of Strains in a Nonlocal Reaction-Diffusion Model of Viral Evolution. SIAM Journal on Applied Mathematics, 2021, 81, 107-128.	0.8	5
84	Methods of Potential Theory in a Filtration Problem for a Viscous Fluid. Differential Equations, 2019, 55, 1182-1197.	0.1	4
85	Mathematical modelling of the within-host HIV quasispecies dynamics in response to antiviral treatment. Russian Journal of Numerical Analysis and Mathematical Modelling, 2015, 30, .	0.2	3
86	Spatially resolved modelling of immune responses following a multiscale approach: from computational implementation to quantitative predictions. Russian Journal of Numerical Analysis and Mathematical Modelling, 2019, 34, 253-260.	0.2	3
87	A Mathematical Model of HIF-1 Regulated Cellular Energy Metabolism. Vietnam Journal of Mathematics, 2021, 49, 119-141.	0.4	3
88	Mathematical immunology: from phenomenological to multiphysics modelling. Russian Journal of Numerical Analysis and Mathematical Modelling, 2020, 35, 203-213.	0.2	3
89	Sensitivity of SARS-CoV-2 Life Cycle to IFN Effects and ACE2 Binding Unveiled with a Stochastic Model. Viruses, 2022, 14, 403.	1.5	3
90	Simulation of the interferon-mediated protective field in lymphoid organs with their spatial and functional organization taken into consideration. Doklady Biological Sciences, 2011, 439, 194-6.	0.2	2

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91	Critical Issues in the Numerical Treatment of the Parameter Estimation Problems in Immunology. Journal of Computational Mathematics, 2012, 30, 59-79.	0.2	2
92	A drug pharmacodynamics and pharmacokinetics based approach towards stabilization of HIV infection dynamics. Russian Journal of Numerical Analysis and Mathematical Modelling, 2015, 30, .	0.2	2
93	Multi-scale and Integrative Modelling Approaches. , 2018, , 221-242.		2
94	Mathematical Modeling of the Intracellular Regulation of Immune Processes. Molecular Biology, 2019, 53, 718-731.	0.4	2
95	Numerical steady state analysis of the Marchukâ€"Petrov model of antiviral immune response. Russian Journal of Numerical Analysis and Mathematical Modelling, 2020, 35, 95-110.	0.2	2
96	Space and Genotype-Dependent Virus Distribution during Infection Progression. Mathematics, 2022, 10, 96.	1.1	2
97	Preface. Distributed Parameter Systems in Immunology. Mathematical Modelling of Natural Phenomena, 2012, 7, 1-3.	0.9	1
98	Mathematics of Pharmacokinetics and Pharmacodynamics: Diversity of Topics, Models and Methods. Mathematical Modelling of Natural Phenomena, 2016, 11, 1-8.	0.9	1
99	Modelling the structural organization of lymph nodes. , 2017, , .		1
100	Parameter Estimation and Model Selection. , 2018, , 35-95.		1
101	Principles of Virusâ€"Host Interaction. , 2018, , 1-14.		1
102	Modelling the FRC network of lymph node. , 2015, , .		0
103	Basic Principles of Building aÂMathematical Model of Immune Response. , 2018, , 15-34.		0
104	Spatial Modelling Using Reactionâ€"Diffusion Systems. , 2018, , 195-219.		0
105	Application of the Global Optimization Methods for Solving the Parameter Estimation Problem in Mathematical Immunology. Lecture Notes in Computer Science, 2020, , 203-209.	1.0	0
106	Corrigendum to: Mathematical immunology: from phenomenological to multiphysics modelling. Russian Journal of Numerical Analysis and Mathematical Modelling, 2021, 36, 55-55.	0.2	0
107	Research Priorities for HIV/M. tuberculosis Co-Infection. The Open Infectious Diseases Journal, 2011, 5, 14-20.	0.6	0
108	On the Potential for Multiscale Oscillatory Behavior in HIV. , 2017, , 897-924.		0

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109	Modelling of Experimental Infections. , 2018, , 97-152.		0
110	Modelling of Human Infections. , 2018, , 153-194.		0
111	Hybrid models in biomedical applications. Computer Research and Modeling, 2019, 11, 287-309.	0.2	0
112	From the guest editors: "Delay Differential Equations: Theory, Applications and New Trends". Discrete and Continuous Dynamical Systems - Series S, 2020, 13, i-iv.	0.6	0
113	Frontiers in mathematical modelling of the lipid metabolism under normal conditions and its alterations in heart diseases. Russian Journal of Numerical Analysis and Mathematical Modelling, 2021, 36, 255-266.	0.2	0