# Gennady A Bocharov

List of Publications by Year
in descending order



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|---|---|---|---|
| 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 | 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 |
| 2 | Space and Genotype-Dependent Virus Distribution during Infection Progression. Mathematics, 2022, 10, 96. | 1.1 | 2 |
| 3 | A Mathematical Model of HIF-1 Regulated Cellular Energy Metabolism. Vietnam Journal of Mathematics, 2021, 49, 119-141. | 0.4 | 3 |
| 4 | Corrigendum to: Mathematical immunology: from phenomenological to multiphysics modelling. Russian Journal of Numerical Analysis and Mathematical Modelling, 2021, 36, 55-55. | 0.2 | 0 |
| 5 | Markov Chain-Based Stochastic Modelling of HIV-1 Life Cycle in a CD4 T Cell. Mathematics, 2021, 9, 2025. | 1.1 | 11 |
| 6 | Intracellular Life Cycle Kinetics of SARS-CoV-2 Predicted Using Mathematical Modelling. Viruses, 2021, 13, 1735. | 1.5 | 15 |
| 7 | Examining the cooperativity mode of antibody and CD8+ T cell immune responses for vaccinology. Trends in Immunology, 2021, 42, 852-855. | 2.9 | 7 |
| 8 | 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 |
| 9 | 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 |
| 10 | Mathematical Modeling of Lymph Node Drainage Function by Neural Network. Mathematics, 2021, 9, 3093. | 1.1 | 8 |
| 11 | 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 |
| 12 | Graph Theory for Modeling and Analysis of the Human Lymphatic System. Mathematics, 2020, 8, 2236. | 1.1 | 11 |
| 13 | â€˜Rinse and Replaceâ€™: Boosting T Cell Turnover To Reduce HIV-1 Reservoirs. Trends in Immunology, 2020, 41, 466-480. | 2.9 | 26 |
| 14 | Genotype-dependent virus distribution and competition of virus strains. Mathematics and Mechanics of Complex Systems, 2020, 8, 101-126. | 0.5 | 7 |
| 15 | 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 |
| 16 | Topological Structure and Robustness of the Lymph Node Conduit System. Cell Reports, 2020, 30, 893-904.e6. | 2.9 | 35 |
| 17 | Modeling of the HIV-1 Life Cycle in Productively Infected Cells to Predict Novel Therapeutic Targets. Pathogens, 2020, 9, 255. | 1.2 | 18 |
| 18 | Numbers Game and Immune Geography as Determinants of Coronavirus Pathogenicity. Frontiers in Cellular and Infection Microbiology, 2020, 10, 559209. | 1.8 | 6 |

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|---|---|---|---|
| 19 | Nonlocal Reactionâ€"Diffusion Model of Viral Evolution: Emergence of Virus Strains. Mathematics, 2020, 8, 117. | 1.1 | 10 |
| 20 | 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 |
| 21 | Mathematical immunology: from phenomenological to multiphysics modelling. Russian Journal of Numerical Analysis and Mathematical Modelling, 2020, 35, 203-213. | 0.2 | 3 |
| 22 | Bistability analysis of virus infection models with time delays. Discrete and Continuous Dynamical Systems - Series S, 2020, 13, 2385-2401. | 0.6 | 8 |
| 23 | 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 |
| 24 | Prediction of PD-L1 inhibition effects for HIV-infected individuals. PLoS Computational Biology, 2019, 15, e1007401. | 1.5 | 10 |
| 25 | Mathematical Modeling of the Intracellular Regulation of Immune Processes. Molecular Biology, 2019, 53, 718-731. | 0.4 | 2 |
| 26 | 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 |
| 27 | Linking Cell Dynamics With Gene Coexpression Networks to Characterize Key Events in Chronic Virus Infections. Frontiers in Immunology, 2019, 10, 1002. | 2.2 | 7 |
| 28 | Systems analysis reveals complex biological processes during virus infection fate decisions. Genome Research, 2019, 29, 907-919. | 2.4 | 21 |
| 29 | 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 |
| 30 | Methods of Potential Theory in a Filtration Problem for a Viscous Fluid. Differential Equations, 2019, 55, 1182-1197. | 0.1 | 4 |
| 31 | 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 |
| 32 | Editorial: Mathematical Modeling of the Immune System in Homeostasis, Infection and Disease. Frontiers in Immunology, 2019, 10, 2944. | 2.2 | 11 |
| 33 | Delay reaction-diffusion equation for infection dynamics. Discrete and Continuous Dynamical Systems - Series B, 2019, 24, 2073-2091. | 0.5 | 7 |
| 34 | Hybrid models in biomedical applications. Computer Research and Modeling, 2019, 11, 287-309. | 0.2 | 0 |
| 35 | 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 |
| 36 | Reactionâ€"Diffusion Equations in Immunology. Computational Mathematics and Mathematical Physics, 2018, 58, 1967-1976. | 0.2 | 5 |

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|---|---|---|---|
| 37 | Integrative Computational Modeling of the Lymph Node Stromal Cell Landscape. Frontiers in Immunology, 2018, 9, 2428. | 2.2 | 27 |
| 38 | Optimal Disturbances of Bistable Time-Delay Systems Modeling Virus Infections. Doklady Mathematics, 2018, 98, 313-316. | 0.1 | 5 |
| 39 | Modelling lymph flow in the lymphatic system: from 0D to 1D spatial resolution. Mathematical Modelling of Natural Phenomena, 2018, 13, 45. | 0.9 | 8 |
| 40 | Interplay between reaction and diffusion processes in governing the dynamics of virus infections. Journal of Theoretical Biology, 2018, 457, 221-236. | 0.8 | 14 |
| 41 | Basic Principles of Building aÂMathematical Model of Immune Response. , 2018, , 15-34. | | 0 |
| 42 | Multi-scale and Integrative Modelling Approaches. , 2018, , 221-242. | | 2 |
| 43 | Parameter Estimation and Model Selection. , 2018, , 35-95. | | 1 |
| 44 | Developing Computational Geometry and Network Graph Models of Human Lymphatic System. Computation, 2018, 6, 1. | 1.0 | 33 |
| 45 | Mathematical Immunology of Virus Infections. , 2018, , . | | 42 |
| 46 | Spatial Modelling Using Reactionâ€"Diffusion Systems. , 2018, , 195-219. | | 0 |
| 47 | Modelling of Experimental Infections. , 2018, , 97-152. | | 0 |
| 48 | Modelling of Human Infections. , 2018, , 153-194. | | 0 |
| 49 | Principles of Virusâ€"Host Interaction. , 2018, , 1-14. | | 1 |
| 50 | Graph Theory-Based Analysis of the Lymph Node Fibroblastic Reticular Cell Network. Methods in Molecular Biology, 2017, 1591, 43-57. | 0.4 | 7 |
| 51 | Modelling Stochastic and Deterministic Behaviours in Virus Infection Dynamics. Mathematical Modelling of Natural Phenomena, 2017, 12, 63-77. | 0.9 | 9 |
| 52 | 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 |
| 53 | Modelling the structural organization of lymph nodes. , 2017, , . | | 1 |
| 54 | Hybrid approach to model the spatial regulation of T cell responses. BMC Immunology, 2017, 18, 29. | 0.9 | 29 |

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| 55 | 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 |
| 56 | Critical Issues in Modelling Lymph Node Physiology. Computation, 2017, 5, 3. | 1.0 | 10 |
| 57 | Towards a Multiscale Model of Acute HIV Infection. Computation, 2017, 5, 6. | 1.0 | 17 |
| 58 | On the Potential for Multiscale Oscillatory Behavior in HIV. , 2017, , 897-924. | | 0 |
| 59 | Topological Small-World Organization of the Fibroblastic Reticular Cell Network Determines Lymph Node Functionality. PLoS Biology, 2016, 14, e1002515. | 2.6 | 96 |
| 60 | Spatiotemporal Dynamics of Virus Infection Spreading in Tissues. PLoS ONE, 2016, 11, e0168576. | 1.1 | 39 |
| 61 | Mathematics of Pharmacokinetics and Pharmacodynamics: Diversity of Topics, Models and Methods. Mathematical Modelling of Natural Phenomena, 2016, 11, 1-8. | 0.9 | 1 |
| 62 | 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 |
| 63 | Modelling the FRC network of lymph node. , 2015, , . | | 0 |
| 64 | Computational Approach to 3D Modeling of the Lymph Node Geometry. Computation, 2015, 3, 222-234. | 1.0 | 35 |
| 65 | Understanding Experimental LCMV Infection of Mice: The Role of Mathematical Models. Journal of Immunology Research, 2015, 2015, 1-10. | 0.9 | 18 |
| 66 | An extremal shift method for control of HIV infection dynamics. Russian Journal of Numerical Analysis and Mathematical Modelling, 2015, 30, . | 0.2 | 7 |
| 67 | 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 |
| 68 | Mathematical models for CFSE labelled lymphocyte dynamics: asymmetry and time-lag in division. Journal of Mathematical Biology, 2014, 69, 1547-1583. | 0.8 | 21 |
| 69 | 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 |
| 70 | 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 |
| 71 | 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 |
| 72 | Asymmetry of Cell Division in CFSE-Based Lymphocyte Proliferation Analysis. Frontiers in Immunology, 2013, 4, 264. | 2.2 | 34 |

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| 73 | RNAtips: analysis of temperature-induced changes of RNA secondary structure. Nucleic Acids Research, 2013, 41, W486-W491. | 6.5 | 25 |
| 74 | Critical Issues in the Numerical Treatment of the Parameter Estimation Problems in Immunology. Journal of Computational Mathematics, 2012, 30, 59-79. | 0.2 | 2 |
| 75 | Preface. Distributed Parameter Systems in Immunology. Mathematical Modelling of Natural Phenomena, 2012, 7, 1-3. | 0.9 | 1 |
| 76 | A global â€œimagingâ€™â€™ view on systems approaches in immunology. European Journal of Immunology, 2012, 42, 3116-3125. | 1.6 | 32 |
| 77 | Human Immunodeficiency Virus Infection : from Biological Observations to Mechanistic Mathematical Modelling. Mathematical Modelling of Natural Phenomena, 2012, 7, 78-104. | 0.9 | 43 |
| 78 | 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 |
| 79 | A new model for the estimation of cell proliferation dynamics using CFSE data. Journal of Immunological Methods, 2011, 373, 143-160. | 0.6 | 38 |
| 80 | Estimation of Cell Proliferation Dynamics Using CFSE Data. Bulletin of Mathematical Biology, 2011, 73, 116-150. | 0.9 | 62 |
| 81 | 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 |
| 82 | Reaction-Diffusion Modelling of Interferon Distribution in Secondary Lymphoid Organs. Mathematical Modelling of Natural Phenomena, 2011, 6, 13-26. | 0.9 | 21 |
| 83 | 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 |
| 84 | Fitness Ranking of Individual Mutants Drives Patterns of Epistatic Interactions in HIV-1. PLoS ONE, 2011, 6, e18375. | 1.1 | 22 |
| 85 | Research Priorities for HIV/M. tuberculosis Co-Infection. The Open Infectious Diseases Journal, 2011, 5, 14-20. | 0.6 | 0 |
| 86 | A Systems Immunology Approach to Plasmacytoid Dendritic Cell Function in Cytopathic Virus Infections. PLoS Pathogens, 2010, 6, e1001017. | 2.1 | 25 |
| 87 | Mathematical modelling of infectious diseases. British Medical Bulletin, 2009, 92, 33-42. | 2.7 | 131 |
| 88 | 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 |
| 89 | Some aspects of causal & neutral equations used in modelling. Journal of Computational and Applied Mathematics, 2009, 229, 335-349. | 1.1 | 6 |
| 90 | 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 |

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| 91 | Rival approaches to mathematical modelling in immunology. Journal of Computational and Applied Mathematics, 2007, 205, 669-686. | 1.1 | 46 |
| 92 | Numerical modelling of label-structured cell population growth using CFSE distribution data. Theoretical Biology and Medical Modelling, 2007, 4, 26. | 2.1 | 54 |
| 93 | Computational analysis of CFSE proliferation assay. Journal of Mathematical Biology, 2006, 54, 57-89. | 0.8 | 37 |
| 94 | A Mathematical Approach for Optimizing Dendritic Cell-Based Immunotherapy. , 2005, 109, 019-034. | | 5 |
| 95 | Understanding Complex Regulatory Systems: Integrating Molecular Biology and Systems Analysis. Transfusion Medicine and Hemotherapy, 2005, 32, 304-321. | 0.7 | 9 |
| 96 | Computational modelling with functional differential equations: Identification, selection, and sensitivity. Applied Numerical Mathematics, 2005, 53, 107-129. | 1.2 | 24 |
| 97 | Numerical bifurcation analysis of immunological models with time delays. Journal of Computational and Applied Mathematics, 2005, 184, 165-176. | 1.1 | 13 |
| 98 | 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 |
| 99 | Computational approaches to parameter estimation and model selection in immunology. Journal of Computational and Applied Mathematics, 2005, 184, 50-76. | 1.1 | 36 |
| 100 | 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 |
| 101 | Underwhelming the Immune Response: Effect of Slow Virus Growth on CD8 + -T-Lymphocyte Responses. Journal of Virology, 2004, 78, 2247-2254. | 1.5 | 99 |
| 102 | Determining control parameters for dendritic cell-cytotoxic T lymphocyte interaction. European Journal of Immunology, 2004, 34, 2407-2418. | 1.6 | 51 |
| 103 | Modelling the Dynamics of LCMV Infection in Mice: II. Compartmental Structure and Immunopathology. Journal of Theoretical Biology, 2003, 221, 349-378. | 0.8 | 20 |
| 104 | Dendritic Cell Homeostasis in the Regulation of Self-Reactivity. Current Pharmaceutical Design, 2003, 9, 221-231. | 0.9 | 17 |
| 105 | Multiply infected spleen cells in HIV patients. Nature, 2002, 418, 144-144. | 13.7 | 381 |
| 106 | Low level viral persistence after infection with LCMV: a quantitative insight through numerical bifurcation analysis. Mathematical Biosciences, 2001, 173, 1-23. | 0.9 | 30 |
| 107 | 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 |
| 108 | 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 |

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| 109 | Structured Population Models, Conservation Laws, and Delay Equations. Journal of Differential Equations, 2000, 168, 212-237. | 1.1 | 62 |
| 110 | Numerical modelling in biosciences using delay differential equations. Journal of Computational and Applied Mathematics, 2000, 125, 183-199. | 1.1 | 262 |
| 111 | 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 |
| 112 | Modelling the Dynamics of LCMV Infection in Mice: Conventional and Exhaustive CTL Responses. Journal of Theoretical Biology, 1998, 192, 283-308. | 0.8 | 78 |
| 113 | Mathematical Model of Antiviral Immune Response III. Influenza A Virus Infection. Journal of Theoretical Biology, 1994, 167, 323-360. | 0.8 | 141 |