

Сведения об официальном оппоненте

Фамилия Имя Отчество (полностью)	Галзитская Оксана Валериановна	
Ученая степень и наименование отрасли наук, научных специальностей, по которым защищена диссертация	Степень Доктор физико-математических наук	Наименование 03.00.02 - Биофизика
Полное наименование организации - основное место работы, должность	Федеральное государственное бюджетное учреждение науки Институт белка Российской академии наук	Руководитель группы биоинформатики
Список основных публикаций оппонента по теме диссертации в рецензируемых научных изданиях за посл. 5 лет (не более 15)	<ol style="list-style-type: none"> 1. Lobanov, M.Y.; Galzitskaya, O.V. How Common Is Disorder? Occurrence of Disordered Residues in Four Domains of Life. <i>Int. J. Mol. Sci.</i> 2015, <i>16</i>, 19490-19507. 2. Pereyaslavets LB, Sokolovsky IV, Galzitskaya OV. FoldNucleus: web server for the prediction of RNA and protein folding nuclei from their 3D structures. <i>Bioinformatics</i>. 2015 Jun 22. pii: btv369. [Epub ahead of print] PubMed PMID: 26104744. 3. Galzitskaya OV. Repeats are one of the main characteristics of RNA-binding proteins with prion-like domains. <i>Mol Biosyst</i>. 2015 Jul 14;11(8):2210-8. 4. Dovidchenko NV, Galzitskaya OV. Computational Approaches to Identification of Aggregation Sites and the Mechanism of Amyloid Growth. <i>Adv Exp Med Biol</i>. 2015; 855:213-39. 5. Pereyaslavets L.B., Glyakina A.V., Dovidchenko N.V., Sokolovskiy I.V., and Galzitskaya O.V. (2015) What handedness and angles between helices has the studied three-helical protein domain? <i>Bioinformatics</i>, Mar 15;31(6):963-5. 6. Galzitskaya OV, Lobanov MY. Phyloproteomic Analysis of 11780 Six-Residue-Long Motifs Occurrences. <i>Biomed Res Int</i>. 2015;2015:208346. 7. Glyakina A.V., Likhachev IV, Balabaev N.K., Galzitskaya O.V., Mechanical stability analysis of the protein L immunoglobulin-binding domain by full 	

- alanine screening using molecular dynamics simulations. *Biotechnol J.* 2015 Mar;10(3):386-94.
8. Leonova EI, Galzitskaya OV. Cell communication using intrinsically disordered proteins: what can syndecans say? *J Biomol Struct Dyn.* 2015 May;33(5):1037-50.
 9. Mikhail Yu. Lobanov, Igor V. Sokolovskiy, Oxana V. Galzitskaya HRap: Database of occurrence of HomoRepeats and Patterns in proteomes. *Nucleic Acids Research, Nucleic Acids Res.* 2014 Jan;42(Database issue):D273-8.
 10. Selivanova OM, Suvorina MY, Dovidchenko NV, Eliseeva IA, Surin AK, Finkelstein AV, Schmatchenko VV, Galzitskaya OV. How to Determine the Size of Folding Nuclei of Protofibrils from the Concentration Dependence of the Rate and Lag-Time of Aggregation. II. Experimental Application for Insulin and LysPro Insulin: Aggregation Morphology, Kinetics, and Sizes of Nuclei. *J Phys Chem B.* 2014 Feb 6;118(5):1198-206.
 11. Dovidchenko N.V., Finkelstein A.V., Galzitskaya, O.V. How to determine the size of folding nuclei of protofibrils from the concentration dependence of the rate and lag-time of aggregation. I. Modeling the amyloid protofibril formation // *The Journal of Physical Chemistry.* 2014 Feb 6;118(5):1189-97.
 12. Glyakina AV, Likhachev IV, Balabaev NK, Galzitskaya OV. Right- and left-handed three-helix proteins: II. Similarity and Differences in Mechanical Unfolding of Proteins. *Proteins.* 2014, 82:90–102.
 13. Lobanov M.Yu., Suvorina M.Yu., Dovidchenko N.V., Sokolovskiy I.V., Surin A. K. and Galzitskaya O. V. A novel web server predicts amino acid residue protection against hydrogen-deuterium exchange. *Bioinformatics,* 2013, 29(11), 1375-1381.
 14. Е. И. Леонова, М.В. Баранов, О.В. Галзитская Формирование пространственной структуры молекул РНК. *Молекулярная биология,* 46, 37-51.
 15. Л.Б. Переяславец, М.В. Баранов, Е.И. Леонова, О.В. Галзитская Предсказание ядер сворачивания в молекулах тРНК. *Биохимия.* 2011, 76 (2), 299-308.