

Сведения об официальном оппоненте

Фамилия Имя Отчество (полностью)	Раменский Василий Евгеньевич	
Ученая степень и наименование отрасли наук, научных специальностей, по которым защищена диссертация	Степень Кандидат физико-математических наук	Наименование 03.00.03 – Молекулярная биология
Полное наименование организации - основное место работы, должность	Федеральное государственное бюджетное учреждение «Национальный медицинский исследовательский центр профилактической медицины» Министерства здравоохранения Российской Федерации	Руководитель Лаборатории геномной и медицинской 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"> <li>1. Lioznova AV, Khamis AM, Artemov AV, Besedina E, <u>Ramensky V</u>, Bajic VB, Kulakovskiy IV, Medvedeva YA. CpG traffic lights are markers of regulatory regions in human genome. BMC Genomics. 2019; 20:102.</li> <li>2. Wang S, Mandell JD, Kumar Y, ..., <u>Ramensky V</u>, et al (152 co-authors). De Novo Sequence and Copy Number Variants Are Strongly Associated with Tourette Disorder and Implicate Cell Polarity in Pathogenesis. Cell Rep. 24:3441-3454.e12.</li> <li>3. Brainstorm Consortium, ... , <u>Ramensky V</u>, et al. Analysis of shared heritability in common disorders of the brain. Science. 2018; 360.</li> <li>4. Mooney, J.A., Huber, C.D., Service, S., Sul, J.H., Marsden, C.D., Zhang, Z., Sabatti, C., Ruiz-Linares, A., Bedoya, G., Costa Rica/Colombia Consortium for Genetic Investigation of Bipolar Endophenotypes, et al. Understanding the Hidden Complexity of Latin American Population Isolates. Am. J. Hum. Genet. 2018; 103: 707–726.</li> <li>5. Ganna, A., Satterstrom, F.K., Zekavat, S.M., Das, I., Kurki, M.I., Churchhouse, C., Alfoldi, J., Martin, A.R., Havulinna, A.S., Byrnes, A., et al. Quantifying the Impact of Rare and Ultra-rare Coding Variation across the Phenotypic Spectrum. Am. J. Hum. Genet. 2018; 102: 1204–1211.</li> </ol>	

6. Jasinska AJ, Zelaya I, Service SK, Peterson CB, Cantor RM, Choi O-W, Young JD, Eskin E, Fairbanks LA, Fears S, Furterer AE, Huang YS, Ramensky V, et al. Genetic variation and gene expression across multiple tissues and developmental stages in a nonhuman primate. *Nature Genetics*. 2017; 49: 1714–1721.
7. Svardal H, Jasinska AJ, Apetrei C, Coppola G, Huang Y, Schmitt CA, Jacquelin B, Ramensky V, et al. Ancient hybridization and strong adaptation to viruses across African vervet monkey populations. *Nature Genetics*. 2017; 49: 1705–1713.
8. Gress A, Ramensky V, Kalinina OV. Spatial distribution of disease-associated variants in three-dimensional structures of protein complexes. *Oncogenesis*. 2017; 6: e380.
9. Huang AY, Yu D, Davis LK, Sul JH, Tsetsos F, Ramensky V, et al. Rare copy number variants in NRXN1 and CNTN6 increase risk for Tourette syndrome. *Neuron*. 2017; 94: 1101–1111.e7.
10. Willsey AJ, Fernandez TV, Yu D, King RA, Dietrich A, Xing J, ..., Ramensky V, et al (125 co-authors). De novo coding variants are strongly associated with Tourette disorder. *Neuron*. 2017; 94: 486-499.e9.
11. Gress A, Ramensky V, Büch J, Keller A, Kalinina OV. StructMAN: annotation of single-nucleotide polymorphisms in the structural context. *Nucl Acids Res*. 2016; 44: W463–W468.
12. Wesley C, Warren, Jasinska AJ, García-Pérez R, Svardal H, Tomlinson C, Rocchi M, Archidiacono N, Capozzi O, Minx P, Montague MJ, Kyung K, Hillier LW, Kremitzki M, Graves T, Chiang C, Hughes J, Tran N, Huang Y, Ramensky V, et al. The genome of the vervet (*Chlorocebus aethiops sabaeus*). *Genome Res*. 2015; 25: 1921-1933.
13. Huang YS, Ramensky V, Service SK, Jasinska AJ, Jung Y, Choi O-W, et al. Sequencing strategies and characterization of 721 vervet monkey genomes for future genetic analyses of medically relevant traits. *BMC Biology*. 2015; 13: 41.
14. Service, S.K., Teslovich, T.M., Fuchsberger, C., Ramensky, V., Yajnik, P., Koboldt, D.C., Larson, D.E., Zhang, Q., Lin, L., Welch, R., et al. Re-sequencing Expands Our Understanding of the Phenotypic Impact of Variants at GWAS Loci. *PLoS Genet* 2014; 10: e100414.