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работников организации по теме диссертации за последние 5 лет (не более 15)	<ol style="list-style-type: none"> 1. Pronina IV, Loginov VI, Burdenny AM, Fridman MV, Kazubskaya TP, Dmitriev AA, et al. Expression and DNA methylation alterations of seven cancer-associated 3p genes and their predicted regulator miRNAs (miR-129-2, miR-9-1) in breast and ovarian cancers. <i>Gene</i>. 2016;576: 483–491. 2. Hill SM, Heiser LM, Cokelaer T, Unger M, Nesser NK, Carlin DE, et al. Inferring causal molecular networks: empirical assessment through a community-based effort. <i>Nature methods</i>. 2016;13: 310–318. 3. Fertig EJ, Ozawa H, Thakar M, Howard JD, Kagohara LT, Krigsfeld G, et al. CoGAPS matrix factorization algorithm identifies transcriptional changes in AP-2alpha target genes in feedback from therapeutic inhibition of the EGFR network. <i>Oncotarget</i>. 2016;7: 73845–73864. 4. Vorontsov IE, Khimulya G, Lukianova EN, Nikolaeva DD, Eliseeva IA, Kulakovskiy IV, et al. Negative selection maintains transcription factor binding motifs in human cancer. <i>BMC Genomics</i>. 2016;17: 395. 5. Kulakovskiy IV, Vorontsov IE, Yevshin IS, Soboleva AV, Kasianov AS, Ashoor H, et al. HOCOMOCO: expansion and enhancement of the collection of transcription factor binding sites models. <i>Nucl Acids Res</i>. 2016;44: D116–

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