

МАТЕРИАЛЫ
КОНГРЕССА

CONGRESS
PROCEEDINGS

2017
**BIO
TECH**
WORLD

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TOM 1 / PART 1

IX МЕЖДУНАРОДНЫЙ КОНГРЕСС

**БИОТЕХНОЛОГИЯ:
СОСТОЯНИЕ
И ПЕРСПЕКТИВЫ
РАЗВИТИЯ**

20-22 ФЕВРАЛЯ 2017
МОСКВА, ГОСТИНЫЙ ДВОР,
ИЛЬИНКА, 4

IX INTERNATIONAL CONGRESS

**BIOTECHNOLOGY:
STATE OF THE ART
AND PERSPECTIVES**

20-22 FEBRUARY, 2017
ILYNKA 4, GOSTINY DVOR,
MOSCOW

IGF1	miR-11-27078-5p (9)	4042 ÷ 4058	-108	89	23
IGF1	miR-3-5147-5p (9)	4042 ÷ 4058	-100	90	22
OLR1	miR-11-27078-5p (2)	1054 ÷ 1056	-108	89	23
OLR1	miR-3-5147-5p (2)	1054 ÷ 1056	-100	90	22
SP1	miR-10-29282-3p (8)	4147 ÷ 4161	-104	89	23
SP1	miR-15-36862-3p (7)	4147 ÷ 4159	-108	89	23
SCAP	miR-19-33623-3p (2)	102 ÷ 105	-132 ÷ -134	89 ÷ 90	24
SCAP	mir-1-2121-3p (5)	99 ÷ 106	-140 ÷ -142	89 ÷ 92	25
SCAP	miR-19-21199-3p (6)	102 ÷ 111	-138 ÷ -151	88 ÷ 96	25
SCAP	miR-1-155-3p (5)	102 ÷ 114	-125 ÷ -132	91 ÷ 95	22
ADRB1	mir-1-2121-3p (5)	946 ÷ 959	-138 ÷ -155	88 ÷ 99	25
ADRB1	miR-19-21199-3p (5)	951 ÷ 961	-138 ÷ -151	88 ÷ 96	25
ADRB1	miR-1-155-3p (2)	961 ÷ 967	-127 ÷ -136	92 ÷ 98	22
PDE4D	mir-1-2121-3p (4)	404 ÷ 411	-138 ÷ -142	88 ÷ 91	25
PDE4D	miR-19-21199-3p (6)	337 ÷ 412	-138 ÷ -144	88 ÷ 92	25
PDE4D	miR-1-155-3p (4)	344 ÷ 413	-125 ÷ -129	91 ÷ 94	22

Примечание. В скобках указано число сайтов связывания.

Литература:

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2. Londin E. et al. Analysis of 13 cell types reveals evidence for the expression of numerous novel primate- and tissue-specific microRNAs// PNAS. 2015. E1106-E1115.

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miRNA INTERACTION WITH mRNA OF GENES WHICH EXPRESSION IS CHANGED AT MYOCARDIAL INFARCTION

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It was determined binding sites characteristics of miR-11-27078-5p, miR-3-5147-5p, miR-10-29282-3p, miR-15-36862-3p, miR-1-2121-3p, miR-19-21199-3p, miR-1-155-3p, miR-19-33623-3p that have binding sites in mRNA of CDKN2B, IGF1, OLR1, SP1, SCAP, ADRB1, PDE4D genes which expression is changed at myocardial infarction.

Key words: miRNA, mRNA, gene, myocardial infarction, diagnostics

miRNAs are one of the possible factors of myocardial infarction development act as genes expression regulators. The main problem of miRNA binding sites prediction is imperfection of appropriate programs. We've developed MirTarget program [1] that is able to determine the following features of binding miRNAs: the start of the initiation of miRNAs binding to mRNAs; the localization of miRNAs binding sites in the 5'UTRs, CDSs and 3'UTRs of the mRNAs; the free energy of hybridization ΔG (kJ/mole); the ratio $\Delta G/\Delta G_m$ (%), which was determined for each site (ΔG_m equals the free energy of miRNA binding with its perfect complementary nucleotide sequence); the schemes of nucleotide interactions between miRNAs and mRNAs.

We defined miRNAs from 3701 ones [2] that have two and more binding sites in mRNAs of target-genes.