

Mikhail G Dozmorov

List of Publications by Year in descending order

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Version: 2024-02-01

125
papers

4,917
citations

109321

35
h-index

118850

62
g-index

144
all docs

144
docs citations

144
times ranked

9228
citing authors

#	ARTICLE	IF	CITATIONS
1	Variants at multiple loci implicated in both innate and adaptive immune responses are associated with Sjögren's syndrome. <i>Nature Genetics</i> , 2013, 45, 1284-1292.	21.4	427
2	Genome-wide DNA methylation study suggests epigenetic accessibility and transcriptional poising of interferon-regulated genes in naïve CD4+ T cells from lupus patients. <i>Journal of Autoimmunity</i> , 2013, 43, 78-84.	6.5	294
3	Genome-wide DNA methylation patterns in CD4+ T cells from patients with systemic lupus erythematosus. <i>Epigenetics</i> , 2011, 6, 593-601.	2.7	224
4	High-density genotyping of immune-related loci identifies new SLE risk variants in individuals with Asian ancestry. <i>Nature Genetics</i> , 2016, 48, 323-330.	21.4	219
5	PDGFR β signaling drives adipose tissue fibrosis by targeting progenitor cell plasticity. <i>Genes and Development</i> , 2015, 29, 1106-1119.	5.9	131
6	Preexisting Commensal Dysbiosis Is a Host-Intrinsic Regulator of Tissue Inflammation and Tumor Cell Dissemination in Hormone Receptor-Positive Breast Cancer. <i>Cancer Research</i> , 2019, 79, 3662-3675.	0.9	118
7	Analysis of The Cancer Genome Atlas sequencing data reveals novel properties of the human papillomavirus 16 genome in head and neck squamous cell carcinoma. <i>Oncotarget</i> , 2017, 8, 17684-17699.	1.8	113
8	High density methylation QTL analysis in human blood via next-generation sequencing of the methylated genomic DNA fraction. <i>Genome Biology</i> , 2015, 16, 291.	8.8	112
9	HiCompare: an R-package for joint normalization and comparison of Hi-C datasets. <i>BMC Bioinformatics</i> , 2018, 19, 279.	2.6	110
10	Abnormal Expression of Differentiation Related Proteins and Proteoglycan Core Proteins in the Urothelium of Patients With Interstitial Cystitis. <i>Journal of Urology</i> , 2008, 179, 764-769.	0.4	106
11	Exploitation of the Apoptosis-Primed State of MYCN-Amplified Neuroblastoma to Develop a Potent and Specific Targeted Therapy Combination. <i>Cancer Cell</i> , 2016, 29, 159-172.	16.8	104
12	Epigenetic Reprogramming in Naive CD4+ T Cells Favoring T Cell Activation and Non-Th1 Effector T Cell Immune Response as an Early Event in Lupus Flares. <i>Arthritis and Rheumatology</i> , 2016, 68, 2200-2209.	5.6	88
13	Unique patterns of molecular profiling between human prostate cancer LNCaP and PC3 cells. <i>Prostate</i> , 2009, 69, 1077-1090.	2.3	82
14	Epithelial-to-Mesenchymal Transition Antagonizes Response to Targeted Therapies in Lung Cancer by Suppressing BIM. <i>Clinical Cancer Research</i> , 2018, 24, 197-208.	7.0	74
15	Systematic classification of non-coding RNAs by epigenomic similarity. <i>BMC Bioinformatics</i> , 2013, 14, S2.	2.6	73
16	MYCN-Amplified Neuroblastoma Is Addicted to Iron and Vulnerable to Inhibition of the System Xc-/Glutathione Axis. <i>Cancer Research</i> , 2021, 81, 1896-1908.	0.9	73
17	Targeted inhibition of histone H3K27 demethylation is effective in high-risk neuroblastoma. <i>Science Translational Medicine</i> , 2018, 10, .	12.4	70
18	multiHiCompare: joint normalization and comparative analysis of complex Hi-C experiments. <i>Bioinformatics</i> , 2019, 35, 2916-2923.	4.1	70

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19	IGFBP-3/IGFBP-3 Receptor System as an Anti-Tumor and Anti-Metastatic Signaling in Cancer. <i>Cells</i> , 2020, 9, 1261.	4.1	68
20	Sexually divergent DNA methylation patterns with hippocampal aging. <i>Aging Cell</i> , 2017, 16, 1342-1352.	6.7	67
21	The role of epigenomics in personalized medicine. <i>Expert Review of Precision Medicine and Drug Development</i> , 2017, 2, 33-45.	0.7	61
22	Polycomb repressive complex 2 epigenomic signature defines age-associated hypermethylation and gene expression changes. <i>Epigenetics</i> , 2015, 10, 484-495.	2.7	60
23	Activation of the JAK/STAT pathway in Behcet's disease. <i>Genes and Immunity</i> , 2015, 16, 170-175.	4.1	59
24	Syndecan-1 facilitates breast cancer metastasis to the brain. <i>Breast Cancer Research and Treatment</i> , 2019, 178, 35-49.	2.5	57
25	Functional characterization of the MECP2/IRAK1 lupus risk haplotype in human T cells and a human MECP2 transgenic mouse. <i>Journal of Autoimmunity</i> , 2013, 41, 168-174.	6.5	55
26	The cell cycle regulatory DREAM complex is disrupted by high expression of oncogenic B-Myb. <i>Oncogene</i> , 2019, 38, 1080-1092.	5.9	54
27	Transcriptional Classification and Functional Characterization of Human Airway Macrophage and Dendritic Cell Subsets. <i>Journal of Immunology</i> , 2017, 198, 1183-1201.	0.8	53
28	Elevated AKR1C3 expression promotes prostate cancer cell survival and prostate cell-mediated endothelial cell tube formation: implications for prostate cancer progression. <i>BMC Cancer</i> , 2010, 10, 672.	2.6	52
29	Angiopoietin pathway gene expression associated with poor breast cancer survival. <i>Breast Cancer Research and Treatment</i> , 2017, 162, 191-198.	2.5	51
30	Age-associated DNA methylation changes in naive CD4 ⁺ T cells suggest an evolving autoimmune epigenotype in aging T cells. <i>Epigenomics</i> , 2017, 9, 429-445.	2.1	47
31	GenomeRunner web server: regulatory similarity and differences define the functional impact of SNP sets. <i>Bioinformatics</i> , 2016, 32, 2256-2263.	4.1	46
32	Differentially expressed gene networks in cultured smooth muscle cells from normal and neuropathic bladder. <i>Journal of Smooth Muscle Research</i> , 2007, 43, 55-72.	1.2	45
33	Epigenomic elements enriched in the promoters of autoimmunity susceptibility genes. <i>Epigenetics</i> , 2014, 9, 276-285.	2.7	42
34	GenomeRunner: automating genome exploration. <i>Bioinformatics</i> , 2012, 28, 419-420.	4.1	41
35	A Whole Methylome CpG-SNP Association Study of Psychosis in Blood and Brain Tissue. <i>Schizophrenia Bulletin</i> , 2016, 42, 1018-1026.	4.3	41
36	Disruption of the MBD2-NuRD complex but not MBD3-NuRD induces high level HbF expression in human adult erythroid cells. <i>Haematologica</i> , 2019, 104, 2361-2371.	3.5	41

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37	Hypomethylation coordinates antagonistically with hypermethylation in cancer development: a case study of leukemia. <i>Human Genomics</i> , 2016, 10, 18.	2.9	40
38	Identification of breast cancer associated variants that modulate transcription factor binding. <i>PLoS Genetics</i> , 2017, 13, e1006761.	3.5	37
39	TADCompare: An R Package for Differential and Temporal Analysis of Topologically Associated Domains. <i>Frontiers in Genetics</i> , 2020, 11, 158.	2.3	37
40	Establishing an analytic pipeline for genome-wide DNA methylation. <i>Clinical Epigenetics</i> , 2016, 8, 45.	4.1	36
41	Separation of breast cancer and organ microenvironment transcriptomes in metastases. <i>Breast Cancer Research</i> , 2019, 21, 36.	5.0	36
42	A novel role of astrocyte elevated gene-1 (AEG-1) in regulating nonalcoholic steatohepatitis (NASH). <i>Hepatology</i> , 2017, 66, 466-480.	7.3	35
43	Persistent LTP without triggered protein synthesis. <i>Neuroscience Research</i> , 2009, 63, 59-65.	1.9	33
44	Fine mapping and conditional analysis identify a new mutation in the autoimmunity susceptibility gene BLK that leads to reduced half-life of the BLK protein. <i>Annals of the Rheumatic Diseases</i> , 2012, 71, 1219-1226.	0.9	33
45	Staphylococcal Nuclease and Tudor Domain Containing 1 (SND1 Protein) Promotes Hepatocarcinogenesis by Inhibiting Monoglyceride Lipase (MGLL). <i>Journal of Biological Chemistry</i> , 2016, 291, 10736-10746.	3.4	33
46	OKN-007 Increases temozolomide (TMZ) Sensitivity and Suppresses TMZ-Resistant Glioblastoma (GBM) Tumor Growth. <i>Translational Oncology</i> , 2019, 12, 320-335.	3.7	33
47	Epigenomic annotation-based interpretation of genomic data: from enrichment analysis to machine learning. <i>Bioinformatics</i> , 2017, 33, 3323-3330.	4.1	32
48	DYRK1A regulates the recruitment of 53BP1 to the sites of DNA damage in part through interaction with RNF169. <i>Cell Cycle</i> , 2019, 18, 531-551.	2.6	32
49	HDAC2-dependent Antipsychotic-like Effects of Chronic Treatment with the HDAC Inhibitor SAHA in Mice. <i>Neuroscience</i> , 2018, 388, 102-117.	2.3	31
50	B-Cell and Monocyte Contribution to Systemic Lupus Erythematosus Identified by Cell-Type-Specific Differential Expression Analysis in RNA-Seq Data. <i>Bioinformatics and Biology Insights</i> , 2015, 9s3, BBI.S29470.	2.0	30
51	Human effector B lymphocytes express ARID3a and secrete interferon alpha. <i>Journal of Autoimmunity</i> , 2016, 75, 130-140.	6.5	30
52	Associations between maternal cytokine levels during gestation and measures of child cognitive abilities and executive functioning. <i>Brain, Behavior, and Immunity</i> , 2018, 70, 390-397.	4.1	30
53	Gut microbiota manipulation during the prepubertal period shapes behavioral abnormalities in a mouse neurodevelopmental disorder model. <i>Scientific Reports</i> , 2020, 10, 4697.	3.3	29
54	Effects of DNA Methylation on Progression to Interstitial Fibrosis and Tubular Atrophy in Renal Allograft Biopsies: A Multi-Omics Approach. <i>American Journal of Transplantation</i> , 2017, 17, 3060-3075.	4.7	28

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55	Characterizing the efficacy of cancer therapeutics in patient-derived xenograft models of metastatic breast cancer. <i>Breast Cancer Research and Treatment</i> , 2018, 170, 221-234.	2.5	28
56	Regulatory T Cells Support Breast Cancer Progression by Opposing IFN- γ -Dependent Functional Reprogramming of Myeloid Cells. <i>Cell Reports</i> , 2020, 33, 108482.	6.4	28
57	Gene expression profiling of human alveolar macrophages infected by <i>B. anthracis</i> spores demonstrates TNF- α and NF- κ B are key components of the innate immune response to the pathogen. <i>BMC Infectious Diseases</i> , 2009, 9, 152.	2.9	27
58	Differential effects of selective frankincense (Ru Xiang) essential oil versus non-selective sandalwood (Tan Xiang) essential oil on cultured bladder cancer cells: a microarray and bioinformatics study. <i>Chinese Medicine</i> , 2014, 9, 18.	4.0	27
59	Predicting gene ontology from a global meta-analysis of 1-color microarray experiments. <i>BMC Bioinformatics</i> , 2011, 12, S14.	2.6	26
60	DNA methylation and histone acetylation changes to cytochrome P450 2E1 regulation in normal aging and impact on rates of drug metabolism in the liver. <i>GeroScience</i> , 2020, 42, 819-832.	4.6	26
61	Analysis of the interaction of extracellular matrix and phenotype of bladder cancer cells. <i>BMC Cancer</i> , 2006, 6, 12.	2.6	25
62	The curcuminoid CLEFMA selectively induces cell death in H441 lung adenocarcinoma cells via oxidative stress. <i>Investigational New Drugs</i> , 2012, 30, 558-567.	2.6	24
63	SpectralTAD: an R package for defining a hierarchy of topologically associated domains using spectral clustering. <i>BMC Bioinformatics</i> , 2020, 21, 319.	2.6	24
64	Bile acids as global regulators of hepatic nutrient metabolism. <i>Liver Research</i> , 2017, 1, 10-16.	1.4	23
65	Coamplification of miR-4728 protects HER2-amplified breast cancers from targeted therapy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E2594-E2603.	7.1	23
66	Sjögren's Syndrome Minor Salivary Gland CD4+ Memory T Cells Associate with Glandular Disease Features and Have a Germinal Center T Follicular Helper Transcriptional Profile. <i>Journal of Clinical Medicine</i> , 2020, 9, 2164.	2.4	23
67	Astrocyte Elevated Gene-1 Regulates Macrophage Activation in Hepatocellular Carcinogenesis. <i>Cancer Research</i> , 2018, 78, 6436-6446.	0.9	22
68	Adolescent stress sensitizes the adult neuroimmune transcriptome and leads to sex-specific microglial and behavioral phenotypes. <i>Neuropsychopharmacology</i> , 2021, 46, 949-958.	5.4	22
69	Characterization of NMDA induced depression in rat hippocampus: involvement of AMPA and NMDA receptors. <i>Neuroscience Letters</i> , 2004, 357, 87-90.	2.1	20
70	Detrimental effects of duplicate reads and low complexity regions on RNA- and ChIP-seq data. <i>BMC Bioinformatics</i> , 2015, 16, S10.	2.6	19
71	Disease classification: from phenotypic similarity to integrative genomics and beyond. <i>Briefings in Bioinformatics</i> , 2019, 20, 1769-1780.	6.5	19
72	Review of multi-omics data resources and integrative analysis for human brain disorders. <i>Briefings in Functional Genomics</i> , 2021, 20, 223-234.	2.7	19

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73	Distinct hepatic immunological patterns are associated with the progression or inhibition of hepatocellular carcinoma. <i>Cell Reports</i> , 2022, 38, 110454.	6.4	19
74	mirCoX: a database of miRNA-mRNA expression correlations derived from RNA-seq meta-analysis. <i>BMC Bioinformatics</i> , 2013, 14, S17.	2.6	18
75	Fucosyltransferase VII improves the function of selectin ligands on cord blood hematopoietic stem cells. <i>Glycobiology</i> , 2013, 23, 1184-1191.	2.5	18
76	Concomitant PPAR α and FXR Activation as a Putative Mechanism of NASH Improvement after Gastric Bypass Surgery: a GEO Datasets Analysis. <i>Journal of Gastrointestinal Surgery</i> , 2019, 23, 51-57.	1.7	18
77	Contribution of AMPA and NMDA receptors to early and late phases of LTP in hippocampal slices. <i>Neuroscience Research</i> , 2006, 55, 182-188.	1.9	17
78	GitHub Statistics as a Measure of the Impact of Open-Source Bioinformatics Software. <i>Frontiers in Bioengineering and Biotechnology</i> , 2018, 6, 198.	4.1	16
79	From microarray to biology: an integrated experimental, statistical and in silico analysis of how the extracellular matrix modulates the phenotype of cancer cells. <i>BMC Bioinformatics</i> , 2008, 9, S4.	2.6	15
80	A Comprehensive and Universal Method for Assessing the Performance of Differential Gene Expression Analyses. <i>PLoS ONE</i> , 2010, 5, e12657.	2.5	15
81	DNA Methylation in Babies Born to Nonsmoking Mothers Exposed to Secondhand Smoke during Pregnancy: An Epigenome-Wide Association Study. <i>Environmental Health Perspectives</i> , 2021, 129, 57010.	6.0	15
82	Suppression and Activation of the Malignant Phenotype by Extracellular Matrix in Xenograft Models of Bladder Cancer: A Model for Tumor Cell "Dormancy". <i>PLoS ONE</i> , 2013, 8, e64181.	2.5	15
83	High-throughput processing and normalization of one-color microarrays for transcriptional meta-analyses. <i>BMC Bioinformatics</i> , 2011, 12, S2.	2.6	13
84	Longitudinal studies can identify distinct inflammatory cytokines associated with the inhibition or progression of liver cancer. <i>Liver International</i> , 2020, 40, 468-472.	3.9	13
85	Epigenomic functional characterization of genetic susceptibility variants in systemic vasculitis. <i>Journal of Autoimmunity</i> , 2016, 67, 76-81.	6.5	12
86	Trans-Ethnic Mapping of BANK1 Identifies Two Independent SLE-Risk Linkage Groups Enriched for Co-Transcriptional Splicing Marks. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2331.	4.1	12
87	Assessing the Role of Long Noncoding RNA in Nucleus Accumbens in Subjects With Alcohol Dependence. <i>Alcoholism: Clinical and Experimental Research</i> , 2020, 44, 2468-2480.	2.4	12
88	Improving sensitivity of linear regression-based cell type-specific differential expression deconvolution with per-gene vs. global significance threshold. <i>BMC Bioinformatics</i> , 2016, 17, 334.	2.6	11
89	Targeting transcription of MCL-1 sensitizes HER2-amplified breast cancers to HER2 inhibitors. <i>Cell Death and Disease</i> , 2021, 12, 179.	6.3	11
90	RIG-I Signaling via MAVS Is Dispensable for Survival in Lethal Influenza Infection <i>In Vivo</i> . <i>Mediators of Inflammation</i> , 2018, 2018, 1-14.	3.0	10

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91	Catastrophic ATP loss underlies a metabolic combination therapy tailored for MYCN-amplified neuroblastoma. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	10
92	Venetoclax-based Rational Combinations are Effective in Models of MYCN-amplified Neuroblastoma. Molecular Cancer Therapeutics, 2021, 20, 1400-1411.	4.1	10
93	Systems biology approach for mapping the response of human urothelial cells to infection by Enterococcus faecalis. BMC Bioinformatics, 2007, 8, S2.	2.6	9
94	Expression and methylation data from SLE patient and healthy control blood samples subdivided with respect to ARID3a levels. Data in Brief, 2016, 9, 213-219.	1.0	9
95	Exploitation of Sulfated Glycosaminoglycan Status for Precision Medicine of Triplatin in Triple-Negative Breast Cancer. Molecular Cancer Therapeutics, 2022, 21, 271-281.	4.1	9
96	Active decay of composite excitatory postsynaptic potentials in hippocampal slices from young rats. Brain Research, 2003, 973, 44-55.	2.2	8
97	Proteome-level display by 2-dimensional chromatography of extracellular matrix-dependent modulation of the phenotype of bladder cancer cells. Proteome Science, 2006, 4, 13.	1.7	8
98	The Coherence Problem: Finding Meaning in GWAS Complexity. Behavior Genetics, 2019, 49, 187-195.	2.1	8
99	Pharmaceutical Interference of the EWS-FLI1-driven Transcriptome By Cotargeting H3K27ac and RNA Polymerase Activity in Ewing Sarcoma. Molecular Cancer Therapeutics, 2021, 20, 1868-1879.	4.1	8
100	Identification of nuclear export inhibitor-based combination therapies in preclinical models of triple-negative breast cancer. Translational Oncology, 2021, 14, 101235.	3.7	7
101	R Tutorial: Detection of Differentially Interacting Chromatin Regions From Multiple Hi-C Datasets. Current Protocols in Bioinformatics, 2019, 66, e76.	25.8	6
102	Oncogenic B-Myb Is Associated With Deregulation of the DREAM-Mediated Cell Cycle Gene Expression Program in High Grade Serous Ovarian Carcinoma Clinical Tumor Samples. Frontiers in Oncology, 2021, 11, 637193.	2.8	6
103	Chromatin conformation capture (Hi-C) sequencing of patient-derived xenografts: analysis guidelines. GigaScience, 2021, 10, .	6.4	6
104	Unmasking BCL-2 Addiction in Synovial Sarcoma by Overcoming Low NOXA. Cancers, 2021, 13, 2310.	3.7	6
105	Current Developments in Machine Learning Techniques in Biological Data Mining. Bioinformatics and Biology Insights, 2017, 11, 117793221668754.	2.0	6
106	System Level Changes in Gene Expression in Maturing Bladder Mucosa. Journal of Urology, 2011, 185, 1952-1958.	0.4	5
107	Anthrax Edema and Lethal Toxins Differentially Target Human Lung and Blood Phagocytes. Toxins, 2020, 12, 464.	3.4	5
108	Histone acetylation at the sulfotransferase 1a1 gene is associated with its hepatic expression in normal aging. Pharmacogenetics and Genomics, 2021, 31, 207-214.	1.5	5

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109	Overexpression of ERAP2N in Human Trophoblast Cells Promotes Cell Death. <i>International Journal of Molecular Sciences</i> , 2021, 22, 8585.	4.1	5
110	Restoring the DREAM Complex Inhibits the Proliferation of High-Risk HPV Positive Human Cells. <i>Cancers</i> , 2021, 13, 489.	3.7	5
111	MYCN upregulates the transsulfuration pathway to suppress the ferroptotic vulnerability in MYCN-amplified neuroblastoma. <i>Cell Stress</i> , 2022, 6, 21-29.	3.2	5
112	Slowly developing depression of N-methyl-D-aspartate receptor mediated responses in young rat hippocampi. <i>BMC Neuroscience</i> , 2004, 5, 26.	1.9	4
113	Dissecting the Balance Between Metabolic and Oncogenic Functions of Astrocyte- α 1/Metadherin. <i>Hepatology Communications</i> , 2022, 6, 561-575.	4.3	4
114	preciseTAD: a transfer learning framework for 3D domain boundary prediction at base-pair resolution. <i>Bioinformatics</i> , 2022, 38, 621-630.	4.1	4
115	5 α -androstane-3 β ,17 β -diol selectively activates the canonical PI3K/AKT pathway: a bioinformatics-based evidence for androgen-activated cytoplasmic signaling. <i>Genomic Medicine</i> , 2007, 1, 139-146.	0.3	3
116	Gloomy Prospects and Roller Coasters: Finding Coherence in Genome-Wide Association Studies. <i>Philosophy of Science</i> , 2020, 87, 1084-1095.	1.0	3
117	Comparing fluctuations of synaptic responses mediated via AMPA and NMDA receptor channels—implications for synaptic plasticity. <i>BioSystems</i> , 2001, 62, 45-56.	2.0	2
118	Gene expression profiling of primary human type I alveolar epithelial cells exposed to <i>Bacillus anthracis</i> spores reveals induction of neutrophil and monocyte chemokines. <i>Microbial Pathogenesis</i> , 2018, 121, 9-21.	2.9	2
119	Evaluation of combined BCL-2/MCL-1 inhibition as a therapeutic approach for synovial sarcoma.. <i>Journal of Clinical Oncology</i> , 2020, 38, e23561-e23561.	1.6	2
120	A method for estimating coherence of molecular mechanisms in major human disease and traits. <i>BMC Bioinformatics</i> , 2020, 21, 473.	2.6	1
121	Reforming disease classification system—are we there yet?. <i>Annals of Translational Medicine</i> , 2018, 6, S30-S30.	1.7	1
122	PATH-61. IMMUNOHISTOCHEMICAL PHENOTYPING AND SURVIVAL ANALYSIS OF WHO GRADE II-IV GLIOMAS. <i>Neuro-Oncology</i> , 2019, 21, vi157-vi157.	1.2	0
123	From Microarray to Biology. <i>Systems Biology</i> , 2010, , 85-107.	0.1	0
124	Abstract 1473: Are the genomic gene expression profiles maintained between the original donor and patient-derived xenograft tumors. , 2015, , .		0
125	Risk stratification of gastrointestinal stromal tumors by CtBP2 and CD44 analysis.. <i>Journal of Clinical Oncology</i> , 2018, 36, 48-48.	1.6	0