

Luda Diatchenko

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

118 papers	10,195 citations	47 h-index	100 g-index
127 ext. papers	11,926 ext. citations	8.6 avg, IF	5.54 L-index

#	Paper	IF	Citations
118	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002 , 99, 16899-903	11.5	1457
117	Genetic basis for individual variations in pain perception and the development of a chronic pain condition. <i>Human Molecular Genetics</i> , 2005 , 14, 135-43	5.6	980
116	GTP cyclohydrolase and tetrahydrobiopterin regulate pain sensitivity and persistence. <i>Nature Medicine</i> , 2006 , 12, 1269-77	50.5	435
115	N6-methyladenosine alters RNA structure to regulate binding of a low-complexity protein. <i>Nucleic Acids Research</i> , 2017 , 45, 6051-6063	20.1	339
114	Suppression subtractive hybridization: a versatile method for identifying differentially expressed genes. <i>Methods in Enzymology</i> , 1999 , 303, 349-80	1.7	300
113	Idiopathic pain disorders--pathways of vulnerability. <i>Pain</i> , 2006 , 123, 226-230	8	283
112	Catechol-O-methyltransferase gene polymorphisms are associated with multiple pain-evoking stimuli. <i>Pain</i> , 2006 , 125, 216-224	8	275
111	Genetically determined P2X7 receptor pore formation regulates variability in chronic pain sensitivity. <i>Nature Medicine</i> , 2012 , 18, 595-9	50.5	265
110	Caveolin-1 is down-regulated in human ovarian carcinoma and acts as a candidate tumor suppressor gene. <i>American Journal of Pathology</i> , 2001 , 159, 1635-43	5.8	234
109	Pain perception is altered by a nucleotide polymorphism in SCN9A. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 5148-53	11.5	230
108	Equalizing cDNA subtraction based on selective suppression of polymerase chain reaction: cloning of Jurkat cell transcripts induced by phytohemagglutinin and phorbol 12-myristate 13-acetate. <i>Analytical Biochemistry</i> , 1996 , 240, 90-7	3.1	223
107	A genome-wide Drosophila screen for heat nociception identifies <i>TRPA</i> as an evolutionarily conserved pain gene. <i>Cell</i> , 2010 , 143, 628-38	56.2	217
106	Psychological factors associated with development of TMD: the OPPERA prospective cohort study. <i>Journal of Pain</i> , 2013 , 14, T75-90	5.2	212
105	Catechol-O-methyltransferase inhibition increases pain sensitivity through activation of both beta2- and beta3-adrenergic receptors. <i>Pain</i> , 2007 , 128, 199-208	8	207
104	Orofacial pain prospective evaluation and risk assessment study--the OPPERA study. <i>Journal of Pain</i> , 2011 , 12, T4-11.e1-2	5.2	190
103	Multiple chronic pain states are associated with a common amino acid-changing allele in KCNS1. <i>Brain</i> , 2010 , 133, 2519-27	11.2	187
102	Gene expression analysis of purified hematopoietic stem cells and committed progenitors. <i>Blood</i> , 2003 , 102, 94-101	2.2	177

101	Genetic architecture of human pain perception. <i>Trends in Genetics</i> , 2007 , 23, 605-13	8.5	161
100	The phenotypic and genetic signatures of common musculoskeletal pain conditions. <i>Nature Reviews Rheumatology</i> , 2013 , 9, 340-50	8.1	152
99	Beta2 adrenergic receptor activation stimulates pro-inflammatory cytokine production in macrophages via PKA- and NF-kappaB-independent mechanisms. <i>Cellular Signalling</i> , 2007 , 19, 251-60	4.9	152
98	Expansion of the human mu-opioid receptor gene architecture: novel functional variants. <i>Human Molecular Genetics</i> , 2009 , 18, 1037-51	5.6	137
97	Potential genetic risk factors for chronic TMD: genetic associations from the OPPERA case control study. <i>Journal of Pain</i> , 2011 , 12, T92-101	5.2	135
96	Stress-induced secretion of growth inhibitors: a novel tumor suppressor function of p53. <i>Oncogene</i> , 1998 , 17, 1089-96	9.2	130
95	Summary of findings from the OPPERA prospective cohort study of incidence of first-onset temporomandibular disorder: implications and future directions. <i>Journal of Pain</i> , 2013 , 14, T116-24	5.2	128
94	N(6)-Methyladenosine Modification in a Long Noncoding RNA Hairpin Predisposes Its Conformation to Protein Binding. <i>Journal of Molecular Biology</i> , 2016 , 428, 822-833	6.5	122
93	Low back pain. <i>Nature Reviews Disease Primers</i> , 2018 , 4, 52	51.1	118
92	Signs and symptoms of first-onset TMD and sociodemographic predictors of its development: the OPPERA prospective cohort study. <i>Journal of Pain</i> , 2013 , 14, T20-32.e1-3	5.2	114
91	Quantitative H2S-mediated protein sulfhydrylation reveals metabolic reprogramming during the integrated stress response. <i>ELife</i> , 2015 , 4, e10067	8.9	113
90	Clinical orofacial characteristics associated with risk of first-onset TMD: the OPPERA prospective cohort study. <i>Journal of Pain</i> , 2013 , 14, T33-50	5.2	102
89	Study methods, recruitment, sociodemographic findings, and demographic representativeness in the OPPERA study. <i>Journal of Pain</i> , 2011 , 12, T12-26	5.2	100
88	Cytokine biomarkers and chronic pain: association of genes, transcription, and circulating proteins with temporomandibular disorders and widespread palpation tenderness. <i>Pain</i> , 2011 , 152, 2802-2812	8	86
87	Potential autonomic risk factors for chronic TMD: descriptive data and empirically identified domains from the OPPERA case-control study. <i>Journal of Pain</i> , 2011 , 12, T75-91	5.2	84
86	miR-183 cluster scales mechanical pain sensitivity by regulating basal and neuropathic pain genes. <i>Science</i> , 2017 , 356, 1168-1171	33.3	80
85	Catechol O-methyltransferase haplotype predicts immediate musculoskeletal neck pain and psychological symptoms after motor vehicle collision. <i>Journal of Pain</i> , 2011 , 12, 101-7	5.2	72
84	Pain modality- and sex-specific effects of COMT genetic functional variants. <i>Pain</i> , 2013 , 154, 1368-76	8	69

83	Large candidate gene association study reveals genetic risk factors and therapeutic targets for fibromyalgia. <i>Arthritis and Rheumatism</i> , 2012 , 64, 584-93		67
82	Homogeneous reporter system enables quantitative functional assessment of multiple transcription factors. <i>Nature Methods</i> , 2008 , 5, 253-60	21.6	66
81	Identification of clusters of individuals relevant to temporomandibular disorders and other chronic pain conditions: the OPPERA study. <i>Pain</i> , 2016 , 157, 1266-1278	8	62
80	Multivariable modeling of phenotypic risk factors for first-onset TMD: the OPPERA prospective cohort study. <i>Journal of Pain</i> , 2013 , 14, T102-15	5.2	58
79	Neuropathic pain phenotyping by international consensus (NeuroPPIC) for genetic studies: a NeuPSIG systematic review, Delphi survey, and expert panel recommendations. <i>Pain</i> , 2015 , 156, 2337-2353	8	54
78	Epiregulin and EGFR interactions are involved in pain processing. <i>Journal of Clinical Investigation</i> , 2017 , 127, 3353-3366	15.9	54
77	Structure and regulation of the mouse <i>ing1</i> gene. Three alternative transcripts encode two phd finger proteins that have opposite effects on p53 function. <i>Journal of Biological Chemistry</i> , 1999 , 274, 32172-81	5.4	53
76	Use of SMART-generated cDNA for gene expression studies in multiple human tumors. <i>BioTechniques</i> , 2001 , 30, 158-63	2.5	52
75	Summary of findings from the OPPERA baseline case-control study: implications and future directions. <i>Journal of Pain</i> , 2011 , 12, T102-7	5.2	51
74	A novel alternatively spliced isoform of the mu-opioid receptor: functional antagonism. <i>Molecular Pain</i> , 2010 , 6, 33	3.4	51
73	Orthodontic Treatment, Genetic Factors and Risk of Temporomandibular Disorder. <i>Seminars in Orthodontics</i> , 2008 , 14, 146-156	1.2	51
72	Study protocol, sample characteristics, and loss to follow-up: the OPPERA prospective cohort study. <i>Journal of Pain</i> , 2013 , 14, T2-19	5.2	47
71	Relationship between temporomandibular disorders, widespread palpation tenderness, and multiple pain conditions: a case-control study. <i>Journal of Pain</i> , 2012 , 13, 1016-27	5.2	47
70	Epistasis between polymorphisms in COMT, ESR1, and GCH1 influences COMT enzyme activity and pain. <i>Pain</i> , 2014 , 155, 2390-9	8	45
69	The nicotinic β subunit gene determines variability in chronic pain sensitivity via cross-inhibition of P2X2/3 receptors. <i>Science Translational Medicine</i> , 2015 , 7, 287ra72	17.5	44
68	Human Genetic Variability Contributes to Postoperative Morphine Consumption. <i>Journal of Pain</i> , 2016 , 17, 628-36	5.2	44
67	Multisystem dysregulation in painful temporomandibular disorders. <i>Journal of Pain</i> , 2013 , 14, 983-96	5.2	43
66	Disruptive mRNA folding increases translational efficiency of catechol-O-methyltransferase variant. <i>Nucleic Acids Research</i> , 2011 , 39, 6201-12	20.1	42

65	Low enzymatic activity haplotypes of the human catechol-O-methyltransferase gene: enrichment for marker SNPs. <i>PLoS ONE</i> , 2009 , 4, e5237	3.7	38
64	Genetic studies of human neuropathic pain conditions: a review. <i>Pain</i> , 2018 , 159, 583-594	8	38
63	Human pain genetics database: a resource dedicated to human pain genetics research. <i>Pain</i> , 2018 , 159, 749-763	8	37
62	Construction of cDNA libraries from small amounts of total RNA using the suppression PCR effect. <i>Biochemical and Biophysical Research Communications</i> , 1997 , 230, 285-8	3.4	37
61	Identification of novel mediators of NF-kappaB through genome-wide survey of monocyte adherence-induced genes. <i>Journal of Leukocyte Biology</i> , 2005 , 78, 1366-77	6.5	37
60	Single cell transcriptomics of primate sensory neurons identifies cell types associated with chronic pain. <i>Nature Communications</i> , 2021 , 12, 1510	17.4	35
59	Cartilage-binding antibodies induce pain through immune complex-mediated activation of neurons. <i>Journal of Experimental Medicine</i> , 2019 , 216, 1904-1924	16.6	34
58	Effect of Human Genetic Variability on Gene Expression in Dorsal Root Ganglia and Association with Pain Phenotypes. <i>Cell Reports</i> , 2017 , 19, 1940-1952	10.6	34
57	T-Cell Mediation of Pregnancy Analgesia Affecting Chronic Pain in Mice. <i>Journal of Neuroscience</i> , 2017 , 37, 9819-9827	6.6	33
56	Subgrouping of low back pain patients for targeting treatments: evidence from genetic, psychological, and activity-related behavioral approaches. <i>Clinical Journal of Pain</i> , 2015 , 31, 123-32	3.5	31
55	Genetic pathway analysis reveals a major role for extracellular matrix organization in inflammatory and neuropathic pain. <i>Pain</i> , 2019 , 160, 932-944	8	31
54	Modification of COMT-dependent pain sensitivity by psychological stress and sex. <i>Pain</i> , 2016 , 157, 858-867		29
53	Excess risk of temporomandibular disorder associated with cigarette smoking in young adults. <i>Journal of Pain</i> , 2012 , 13, 21-31	5.2	28
52	Facial pain with localized and widespread manifestations: separate pathways of vulnerability. <i>Pain</i> , 2013 , 154, 2335-2343	8	27
51	Signaling pathways mediating beta3-adrenergic receptor-induced production of interleukin-6 in adipocytes. <i>Molecular Immunology</i> , 2009 , 46, 2256-66	4.3	27
50	Complex multilocus effects of catechol-O-methyltransferase haplotypes predict pain and pain interference 6 weeks after motor vehicle collision. <i>NeuroMolecular Medicine</i> , 2014 , 16, 83-93	4.6	26
49	Genome-wide association reveals contribution of MRAS to painful temporomandibular disorder in males. <i>Pain</i> , 2019 , 160, 579-591	8	26
48	Structural and functional interactions between six-transmembrane Epioid receptors and α -adrenoreceptors modulate opioid signaling. <i>Scientific Reports</i> , 2015 , 5, 18198	4.9	25

47	Disentangling the genetics of lean mass. <i>American Journal of Clinical Nutrition</i> , 2019 , 109, 276-287	7	24
46	Carbonic anhydrase-8 regulates inflammatory pain by inhibiting the ITPR1-cytosolic free calcium pathway. <i>PLoS ONE</i> , 2015 , 10, e0118273	3.7	24
45	μ Opioid receptor 6-transmembrane isoform: A potential therapeutic target for new effective opioids. <i>Progress in Neuro-Psychopharmacology and Biological Psychiatry</i> , 2015 , 62, 61-7	5.5	23
44	Structural basis for μ Opioid receptor binding and activation. <i>Structure</i> , 2011 , 19, 1683-90	5.2	23
43	Structural mechanism of S-adenosyl methionine binding to catechol O-methyltransferase. <i>PLoS ONE</i> , 2011 , 6, e24287	3.7	23
42	Differences in the Antinociceptive Effects and Binding Properties of Propranolol and Bupranolol Enantiomers. <i>Journal of Pain</i> , 2015 , 16, 1321-1333	5.2	21
41	COMT gene locus: new functional variants. <i>Pain</i> , 2015 , 156, 2072-2083	8	20
40	Responses to Drs. Kim and Dionne regarding comments on Diatchenko, et al. Catechol-O-methyltransferase gene polymorphisms are associated with multiple pain-evoking stimuli. <i>Pain</i> 2006; 125: 216-24. <i>Pain</i> , 2007 , 129, 366-370	8	17
39	Gene expression profiling in RAS oncogene-transformed cell lines and in solid tumors using subtractive suppression hybridization and cDNA arrays. <i>Advances in Enzyme Regulation</i> , 2002 , 42, 63-82		17
38	Construction of a global pain systems network highlights phospholipid signaling as a regulator of heat nociception. <i>PLoS Genetics</i> , 2012 , 8, e1003071	6	15
37	Agonist-dependence of functional properties for common nonsynonymous variants of human transient receptor potential vanilloid 1. <i>Pain</i> , 2016 , 157, 1515-1524	8	14
36	Alternative Splicing of the Delta-Opioid Receptor Gene Suggests Existence of New Functional Isoforms. <i>Molecular Neurobiology</i> , 2019 , 56, 2855-2869	6.2	13
35	Differential Regulation of 6- and 7-Transmembrane Helix Variants of μ Opioid Receptor in Response to Morphine Stimulation. <i>PLoS ONE</i> , 2015 , 10, e0142826	3.7	13
34	Genome-wide association meta-analyses to identify common genetic variants associated with hallux valgus in Caucasian and African Americans. <i>Journal of Medical Genetics</i> , 2015 , 52, 762-9	5.8	13
33	Elucidation of mu-Opioid Gene Structure: How Genetics Can Help Predict Responses to Opioids. <i>European Journal of Pain Supplements</i> , 2011 , 5, 433-438		13
32	Dual allosteric modulation of opioid antinociceptive potency by α A-adrenoceptors. <i>Neuropharmacology</i> , 2015 , 99, 285-300	5.5	12
31	Premorbid and concurrent predictors of TMD onset and persistence. <i>European Journal of Pain</i> , 2020 , 24, 145-158	3.7	12
30	NK cell recruitment limits tissue damage during an enteric helminth infection. <i>Mucosal Immunology</i> , 2020 , 13, 357-370	9.2	11

29	CACNG2 polymorphisms associate with chronic pain after mastectomy. <i>Pain</i> , 2019 , 160, 561-568	8	11
28	Genetic variant rs3750625 in the 3'UTR of ADRA2A affects stress-dependent acute pain severity after trauma and alters a microRNA-34a regulatory site. <i>Pain</i> , 2017 , 158, 230-239	8	10
27	The dichotomous role of epiregulin in pain. <i>Pain</i> , 2020 , 161, 1052-1064	8	7
26	A functional polymorphism in the ATP-Binding Cassette B1 transporter predicts pharmacologic response to combination of nortriptyline and morphine in neuropathic pain patients. <i>Pain</i> , 2020 , 161, 619-629	8	7
25	Sex- and age-specific genetic analysis of chronic back pain. <i>Pain</i> , 2021 , 162, 1176-1187	8	6
24	Car8 dorsal root ganglion expression and genetic regulation of analgesic responses are associated with a cis-eQTL in mice. <i>Mammalian Genome</i> , 2017 , 28, 407-415	3.2	5
23	A functional substitution in the L-aromatic amino acid decarboxylase enzyme worsens somatic symptoms via a serotonergic pathway. <i>Annals of Neurology</i> , 2019 , 86, 168-180	9.4	5
22	The geriatric pain experience in mice: intact cutaneous thresholds but altered responses to tonic and chronic pain. <i>Neurobiology of Aging</i> , 2020 , 89, 1-11	5.6	5
21	Molecular genetic mechanisms of allelic specific regulation of murine Comt expression. <i>Pain</i> , 2015 , 156, 1965-1977	8	5
20	Single-cell RNA sequencing reveals time- and sex-specific responses of mouse spinal cord microglia to peripheral nerve injury and links ApoE to chronic pain.. <i>Nature Communications</i> , 2022 , 13, 843	17.4	5
19	Stabilization of μ opioid receptor facilitates its cellular translocation and signaling. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019 , 87, 878-884	4.2	4
18	A genetic polymorphism that is associated with mitochondrial energy metabolism increases risk of fibromyalgia. <i>Pain</i> , 2020 , 161, 2860-2871	8	4
17	A study in scarlet: MC1R as the main predictor of red hair and exemplar of the flip-flop effect. <i>Human Molecular Genetics</i> , 2019 , 28, 2093-2106	5.6	4
16	Human carbonic anhydrase-8 AAV8 gene therapy inhibits nerve growth factor signaling producing prolonged analgesia and anti-hyperalgesia in mice. <i>Gene Therapy</i> , 2018 , 25, 297-311	4	4
15	Profound analgesia is associated with a truncated peptide resulting from tissue specific alternative splicing of DRG CA8-204 regulated by an exon-level cis-eQTL. <i>PLoS Genetics</i> , 2019 , 15, e1008226	6	3
14	Single cell transcriptomics of primate sensory neurons identifies cell types associated with human chronic pain		3
13	Post-concussion symptoms and chronic pain after mild traumatic brain injury are modulated by multiple locus effect in the gene through the expression of antisense: A pilot prospective control study.. <i>Canadian Journal of Pain</i> , 2017 , 1, 112-126	1.5	2
12	Phenotypic profile clustering pragmatically identifies diagnostically and mechanistically informative subgroups of chronic pain patients. <i>Pain</i> , 2021 , 162, 1528-1538	8	2

11	Genome-wide analysis identifies significant contribution of brain-expressed genes in chronic, but not acute, back pain		2
10	Identification and characterization of novel candidate compounds targeting 6- and 7-transmembrane μ opioid receptor isoforms. <i>British Journal of Pharmacology</i> , 2021 , 178, 2709-2726	8.6	2
9	Reversion mutation of cDNA CA8-204 minigene construct produces a truncated functional peptide that regulates calcium release in vitro and produces profound analgesia in vivo. <i>Mammalian Genome</i> , 2020 , 31, 287-294	3.2	1
8	Detangling red hair from pain: phenotype-specific contributions from different genetic variants in melanocortin-1 receptor. <i>Pain</i> , 2020 , 161, 938-948	8	1
7	Alternative Splicing of Opioid Receptor Genes Shows a Conserved Pattern for 6TM Receptor Variants. <i>Cellular and Molecular Neurobiology</i> , 2021 , 41, 1039-1055	4.6	1
6	Acute inflammatory response via neutrophil activation protects against the development of chronic pain.. <i>Science Translational Medicine</i> , 2022 , 14, eabj9954	17.5	1
5	The more you test, the more you find: The smallest P-values become increasingly enriched with real findings as more tests are conducted. <i>Genetic Epidemiology</i> , 2017 , 41, 726-743	2.6	0
4	Mast cell stabilizer ketotifen fumarate reverses inflammatory but not neuropathic-induced mechanical pain in mice. <i>Pain Reports</i> , 2021 , 6, e902	3.5	0
3	Identifying genetic determinants of inflammatory pain in mice using a large-scale gene-targeted screen.. <i>Pain</i> , 2022 , 163, 1139-1157	8	0
2	The human pain genetics database: an interview with Luda Diatchenko. <i>Pain Management</i> , 2018 , 8, 259-263		
1	Modeling Secondary Phenotypes Conditional on Genotypes in Case-Control Studies. <i>Stats</i> , 2022 , 5, 203-214		