

# Luda Diatchenko

## List of Publications by Year in descending order

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122  
papers

13,314  
citations

30070

54  
h-index

22832

112  
g-index

127  
all docs

127  
docs citations

127  
times ranked

14411  
citing authors

#	ARTICLE	IF	CITATIONS
1	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 16899-16903.	7.1	1,610
2	Genetic basis for individual variations in pain perception and the development of a chronic pain condition. Human Molecular Genetics, 2005, 14, 135-143.	2.9	1,134
3	N 6-methyladenosine alters RNA structure to regulate binding of a low-complexity protein. Nucleic Acids Research, 2017, 45, 6051-6063.	14.5	586
4	GTP cyclohydrolase and tetrahydrobiopterin regulate pain sensitivity and persistence. Nature Medicine, 2006, 12, 1269-1277.	30.7	504
5	[20] Suppression subtractive hybridization: A versatile method for identifying differentially expressed genes. Methods in Enzymology, 1999, 303, 349-380.	1.0	349
6	Genetically determined P2X7 receptor pore formation regulates variability in chronic pain sensitivity. Nature Medicine, 2012, 18, 595-599.	30.7	335
7	Idiopathic pain disorders – Pathways of vulnerability. Pain, 2006, 123, 226-230.	4.2	328
8	Psychological Factors Associated With Development of TMD: The OPPERA Prospective Cohort Study. Journal of Pain, 2013, 14, T75-T90.	1.4	321
9	Catechol- O -methyltransferase gene polymorphisms are associated with multiple pain-evoking stimuli. Pain, 2006, 125, 216-224.	4.2	320
10	A Genome-wide Drosophila Screen for Heat Nociception Identifies $\hat{\pm}2\hat{\pm}3$ as an Evolutionarily Conserved Pain Gene. Cell, 2010, 143, 628-638.	28.9	283
11	Pain perception is altered by a nucleotide polymorphism in <i>SCN9A</i> . Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 5148-5153.	7.1	279
12	Orofacial Pain Prospective Evaluation and Risk Assessment Study – The OPPERA Study. Journal of Pain, 2011, 12, T4-T11.e2.	1.4	275
13	Low back pain. Nature Reviews Disease Primers, 2018, 4, 52.	30.5	262
14	Caveolin-1 Is Down-Regulated in Human Ovarian Carcinoma and Acts as a Candidate Tumor Suppressor Gene. American Journal of Pathology, 2001, 159, 1635-1643.	3.8	260
15	Catechol- O -methyltransferase inhibition increases pain sensitivity through activation of both $\hat{\pm}2$ - and $\hat{\pm}3$ -adrenergic receptors. Pain, 2007, 128, 199-208.	4.2	243
16	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. Analytical Biochemistry, 1996, 240, 90-97.	2.4	239
17	Multiple chronic pain states are associated with a common amino acid –changing allele in KCNS1. Brain, 2010, 133, 2519-2527.	7.6	224
18	The phenotypic and genetic signatures of common musculoskeletal pain conditions. Nature Reviews Rheumatology, 2013, 9, 340-350.	8.0	215

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19	Genetic architecture of human pain perception. <i>Trends in Genetics</i> , 2007, 23, 605-613.	6.7	207
20	Gene expression analysis of purified hematopoietic stem cells and committed progenitors. <i>Blood</i> , 2003, 102, 94-101.	1.4	191
21	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-T124.	1.4	189
22	$\beta$ 2 adrenergic receptor activation stimulates pro-inflammatory cytokine production in macrophages via PKA- and NF- $\kappa$ B-independent mechanisms. <i>Cellular Signalling</i> , 2007, 19, 251-260.	3.6	178
23	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-T32.e3.	1.4	176
24	N6-Methyladenosine Modification in a Long Noncoding RNA Hairpin Predisposes Its Conformation to Protein Binding. <i>Journal of Molecular Biology</i> , 2016, 428, 822-833.	4.2	164
25	Potential Genetic Risk Factors for Chronic TMD: Genetic Associations from the OPPERA Case Control Study. <i>Journal of Pain</i> , 2011, 12, T92-T101.	1.4	157
26	Quantitative H2S-mediated protein sulfhydration reveals metabolic reprogramming during the integrated stress response. <i>ELife</i> , 2015, 4, e10067.	6.0	154
27	Expansion of the human $\mu$ -opioid receptor gene architecture: novel functional variants. <i>Human Molecular Genetics</i> , 2009, 18, 1037-1051.	2.9	150
28	Clinical Orofacial Characteristics Associated With Risk of First-Onset TMD: The OPPERA Prospective Cohort Study. <i>Journal of Pain</i> , 2013, 14, T33-T50.	1.4	142
29	Stress-induced secretion of growth inhibitors: a novel tumor suppressor function of p53. <i>Oncogene</i> , 1998, 17, 1089-1096.	5.9	140
30	Study Methods, Recruitment, Sociodemographic Findings, and Demographic Representativeness in the OPPERA Study. <i>Journal of Pain</i> , 2011, 12, T12-T26.	1.4	130
31	miR-183 cluster scales mechanical pain sensitivity by regulating basal and neuropathic pain genes. <i>Science</i> , 2017, 356, 1168-1171.	12.6	124
32	Single cell transcriptomics of primate sensory neurons identifies cell types associated with chronic pain. <i>Nature Communications</i> , 2021, 12, 1510.	12.8	121
33	Acute inflammatory response via neutrophil activation protects against the development of chronic pain. <i>Science Translational Medicine</i> , 2022, 14, eabj9954.	12.4	115
34	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.	4.2	108
35	Identification of clusters of individuals relevant to temporomandibular disorders and other chronic pain conditions. <i>Pain</i> , 2016, 157, 1266-1278.	4.2	104
36	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-T91.	1.4	96

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37	Neuropathic pain phenotyping by international consensus (NeuroPPIC) for genetic studies. <i>Pain</i> , 2015, 156, 2337-2353.	4.2	86
38	Epiregulin and EGFR interactions are involved in pain processing. <i>Journal of Clinical Investigation</i> , 2017, 127, 3353-3366.	8.2	85
39	Catechol O-Methyltransferase Haplotype Predicts Immediate Musculoskeletal Neck Pain and Psychological Symptoms After Motor Vehicle Collision. <i>Journal of Pain</i> , 2011, 12, 101-107.	1.4	83
40	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.	6.4	83
41	Pain modality- and sex-specific effects of COMT genetic functional variants. <i>Pain</i> , 2013, 154, 1368-1376.	4.2	81
42	Homogeneous reporter system enables quantitative functional assessment of multiple transcription factors. <i>Nature Methods</i> , 2008, 5, 253-260.	19.0	80
43	Human pain genetics database: a resource dedicated to human pain genetics research. <i>Pain</i> , 2018, 159, 749-763.	4.2	80
44	Multivariable Modeling of Phenotypic Risk Factors for First-Onset TMD: The OPPERA Prospective Cohort Study. <i>Journal of Pain</i> , 2013, 14, T102-T115.	1.4	79
45	Large candidate gene association study reveals genetic risk factors and therapeutic targets for fibromyalgia. <i>Arthritis and Rheumatism</i> , 2012, 64, 584-593.	6.7	78
46	Cartilage-binding antibodies induce pain through immune complex-mediated activation of neurons. <i>Journal of Experimental Medicine</i> , 2019, 216, 1904-1924.	8.5	71
47	Summary of Findings from the OPPERA Baseline Case-Control Study: Implications and Future Directions. <i>Journal of Pain</i> , 2011, 12, T102-T107.	1.4	64
48	Genetic studies of human neuropathic pain conditions: a review. <i>Pain</i> , 2018, 159, 583-594.	4.2	64
49	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.	12.8	62
50	Structure and Regulation of the Mouse <i>ing1</i> Gene. <i>Journal of Biological Chemistry</i> , 1999, 274, 32172-32181.	3.4	60
51	Study Protocol, Sample Characteristics, and Loss to Follow-Up: The OPPERA Prospective Cohort Study. <i>Journal of Pain</i> , 2013, 14, T2-T19.	1.4	59
52	Epistasis between polymorphisms in COMT, ESR1, and GCH1 influences COMT enzyme activity and pain. <i>Pain</i> , 2014, 155, 2390-2399.	4.2	59
53	The nicotinic $\alpha 6$ subunit gene determines variability in chronic pain sensitivity via cross-inhibition of P2X2/3 receptors. <i>Science Translational Medicine</i> , 2015, 7, 287ra72.	12.4	59
54	Use of SMARTer-Generated cDNA for Gene Expression Studies in Multiple Human Tumors. <i>BioTechniques</i> , 2001, 30, 158-163.	1.8	58

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55	Relationship Between Temporomandibular Disorders, Widespread Palpation Tenderness, and Multiple Pain Conditions: A Case-Control Study. <i>Journal of Pain</i> , 2012, 13, 1016-1027.	1.4	57
56	Human Genetic Variability Contributes to Postoperative Morphine Consumption. <i>Journal of Pain</i> , 2016, 17, 628-636.	1.4	57
57	A Novel Alternatively Spliced Isoform of the Mu-Opioid Receptor: Functional Antagonism. <i>Molecular Pain</i> , 2010, 6, 1744-8069-6-33.	2.1	56
58	Orthodontic Treatment, Genetic Factors, and Risk of Temporomandibular Disorder. <i>Seminars in Orthodontics</i> , 2008, 14, 146-156.	1.4	54
59	Genetic pathway analysis reveals a major role for extracellular matrix organization in inflammatory and neuropathic pain. <i>Pain</i> , 2019, 160, 932-944.	4.2	53
60	Microglia-mediated degradation of perineuronal nets promotes pain. <i>Science</i> , 2022, 377, 80-86.	12.6	52
61	Disruptive mRNA folding increases translational efficiency of catechol-O-methyltransferase variant. <i>Nucleic Acids Research</i> , 2011, 39, 6201-6212.	14.5	51
62	Multisystem Dysregulation in Painful Temporomandibular Disorders. <i>Journal of Pain</i> , 2013, 14, 983-996.	1.4	51
63	Modification of COMT-dependent pain sensitivity by psychological stress and sex. <i>Pain</i> , 2016, 157, 858-867.	4.2	49
64	Low Enzymatic Activity Haplotypes of the Human Catechol-O-Methyltransferase Gene: Enrichment for Marker SNPs. <i>PLoS ONE</i> , 2009, 4, e5237.	2.5	46
65	T-Cell Mediation of Pregnancy Analgesia Affecting Chronic Pain in Mice. <i>Journal of Neuroscience</i> , 2017, 37, 9819-9827.	3.6	46
66	Construction of cDNA Libraries from Small Amounts of Total RNA Using the Suppression PCR Effect. <i>Biochemical and Biophysical Research Communications</i> , 1997, 230, 285-288.	2.1	44
67	Identification of novel mediators of NF- $\kappa$ B through genome-wide survey of monocyte adherence-induced genes. <i>Journal of Leukocyte Biology</i> , 2005, 78, 1366-1377.	3.3	43
68	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.	3.4	39
69	Disentangling the genetics of lean mass. <i>American Journal of Clinical Nutrition</i> , 2019, 109, 276-287.	4.7	38
70	Excess Risk of Temporomandibular Disorder Associated With Cigarette Smoking in Young Adults. <i>Journal of Pain</i> , 2012, 13, 21-31.	1.4	37
71	Genome-wide association reveals contribution of MRAS to painful temporomandibular disorder in males. <i>Pain</i> , 2019, 160, 579-591.	4.2	37
72	Subgrouping of Low Back Pain Patients for Targeting Treatments. <i>Clinical Journal of Pain</i> , 2015, 31, 123-132.	1.9	36

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73	Structural and functional interactions between six-transmembrane $\mu$ -opioid receptors and $\beta$ -adrenoreceptors modulate opioid signaling. <i>Scientific Reports</i> , 2016, 5, 18198.	3.3	34
74	Signaling pathways mediating $\beta$ -adrenergic receptor-induced production of interleukin-6 in adipocytes. <i>Molecular Immunology</i> , 2009, 46, 2256-2266.	2.2	32
75	Facial pain with localized and widespread manifestations: Separate pathways of vulnerability. <i>Pain</i> , 2013, 154, 2335-2343.	4.2	31
76	Structural Mechanism of S-Adenosyl Methionine Binding to Catechol O-Methyltransferase. <i>PLoS ONE</i> , 2011, 6, e24287.	2.5	31
77	Structural Basis for $\mu$ -Opioid Receptor Binding and Activation. <i>Structure</i> , 2011, 19, 1683-1690.	3.3	30
78	Carbonic Anhydrase-8 Regulates Inflammatory Pain by Inhibiting the ITPR1-Cytosolic Free Calcium Pathway. <i>PLoS ONE</i> , 2015, 10, e0118273.	2.5	30
79	COMT gene locus. <i>Pain</i> , 2015, 156, 2072-2083.	4.2	28
80	Differences in the Antinociceptive Effects and Binding Properties of Propranolol and Bupranolol Enantiomers. <i>Journal of Pain</i> , 2015, 16, 1321-1333.	1.4	27
81	$\mu$ -Opioid receptor 6-transmembrane isoform: A potential therapeutic target for new effective opioids. <i>Progress in Neuro-Psychopharmacology and Biological Psychiatry</i> , 2015, 62, 61-67.	4.8	26
82	Premorbid and concurrent predictors of TMD onset and persistence. <i>European Journal of Pain</i> , 2020, 24, 145-158.	2.8	26
83	Long-term male-specific chronic pain via telomere- and p53-mediated spinal cord cellular senescence. <i>Journal of Clinical Investigation</i> , 2022, 132, .	8.2	25
84	Construction of a Global Pain Systems Network Highlights Phospholipid Signaling as a Regulator of Heat Nociception. <i>PLoS Genetics</i> , 2012, 8, e1003071.	3.5	23
85	CACNG2 polymorphisms associate with chronic pain after mastectomy. <i>Pain</i> , 2019, 160, 561-568.	4.2	22
86	Sex- and age-specific genetic analysis of chronic back pain. <i>Pain</i> , 2021, 162, 1176-1187.	4.2	21
87	Alternative Splicing of the Delta-Opioid Receptor Gene Suggests Existence of New Functional Isoforms. <i>Molecular Neurobiology</i> , 2019, 56, 2855-2869.	4.0	20
88	NK cell recruitment limits tissue damage during an enteric helminth infection. <i>Mucosal Immunology</i> , 2020, 13, 357-370.	6.0	20
89	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.	2.6	19
90	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.	4.2	19

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91	Phenotypic profile clustering pragmatically identifies diagnostically and mechanistically informative subgroups of chronic pain patients. <i>Pain</i> , 2021, 162, 1528-1538.	4.2	19
92	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, 762-769.	3.2	18
93	Agonist-dependence of functional properties for common nonsynonymous variants of human transient receptor potential vanilloid 1. <i>Pain</i> , 2016, 157, 1515-1524.	4.2	17
94	A genetic polymorphism that is associated with mitochondrial energy metabolism increases risk of fibromyalgia. <i>Pain</i> , 2020, 161, 2860-2871.	4.2	17
95	The dichotomous role of epiregulin in pain. <i>Pain</i> , 2020, 161, 1052-1064.	4.2	17
96	Elucidation of mu-opioid gene structure: How genetics can help predict therapeutic response to opioids. <i>European Journal of Pain Supplements</i> , 2011, 5, 433-438.	0.0	16
97	Dual allosteric modulation of opioid antinociceptive potency by $\hat{1}\pm 2A$ -adrenoceptors. <i>Neuropharmacology</i> , 2015, 99, 285-300.	4.1	16
98	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.	3.1	16
99	Differential Regulation of 6- and 7-Transmembrane Helix Variants of $\hat{1}\frac{3}{4}$ -Opioid Receptor in Response to Morphine Stimulation. <i>PLoS ONE</i> , 2015, 10, e0142826.	2.5	14
100	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.	4.2	13
101	Genetic variant rs3750625 in the 3 $\hat{1}$ 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.	4.2	12
102	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.	2.9	11
103	Detangling red hair from pain: phenotype-specific contributions from different genetic variants in melanocortin-1 receptor. <i>Pain</i> , 2020, 161, 938-948.	4.2	11
104	A functional substitution in the L $\hat{1}$ aromatic amino acid decarboxylase enzyme worsens somatic symptoms via a serotonergic pathway. <i>Annals of Neurology</i> , 2019, 86, 168-180.	5.3	9
105	Relax, you won't feel the pain. <i>Nature Neuroscience</i> , 2011, 14, 1496-1497.	14.8	8
106	Molecular genetic mechanisms of allelic specific regulation of murine Comt expression. <i>Pain</i> , 2015, 156, 1965-1977.	4.2	8
107	Letting the Gene out of the Bottle. <i>Anesthesiology</i> , 2014, 121, 678-680.	2.5	8
108	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.	2.2	7

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109	Mast cell stabilizer ketotifen fumarate reverses inflammatory but not neuropathic-induced mechanical pain in mice. <i>Pain Reports</i> , 2021, 6, e902.	2.7	7
110	Sodium-calcium exchanger-3 regulates pain "wind-up". From human psychophysics to spinal mechanisms. <i>Neuron</i> , 2022, 110, 2571-2587.e13.	8.1	7
111	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.	4.5	6
112	Stabilization of $\mu$ -opioid receptor facilitates its cellular translocation and signaling. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019, 87, 878-884.	2.6	6
113	Alternative Splicing of Opioid Receptor Genes Shows a Conserved Pattern for 6TM Receptor Variants. <i>Cellular and Molecular Neurobiology</i> , 2021, 41, 1039-1055.	3.3	5
114	Multi-ethnic GWAS and meta-analysis of sleep quality identify MPP6 as a novel gene that functions in sleep center neurons. <i>Sleep</i> , 2021, 44, .	1.1	5
115	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.	3.5	4
116	Identification and characterization of novel candidate compounds targeting $\delta$ - and $\zeta$ -transmembrane $\mu$ -opioid receptor isoforms. <i>British Journal of Pharmacology</i> , 2021, 178, 2709-2726.	5.4	4
117	Identifying genetic determinants of inflammatory pain in mice using a large-scale gene-targeted screen. <i>Pain</i> , 2022, 163, 1139-1157.	4.2	4
118	The more you test, the more you find: The smallest <i>p</i> -values become increasingly enriched with real findings as more tests are conducted. <i>Genetic Epidemiology</i> , 2017, 41, 726-743.	1.3	3
119	Post-concussion symptoms and chronic pain after mild traumatic brain injury are modulated by multiple locus effect in the <i>BDNF</i> gene through the expression of antisense: A pilot prospective control study. <i>Canadian Journal of Pain</i> , 2017, 1, 112-126.	1.7	2
120	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.	2.2	1
121	The human pain genetics database: an interview with Luda Diatchenko. <i>Pain Management</i> , 2018, 8, 259-261.	1.5	0
122	Modeling Secondary Phenotypes Conditional on Genotypes in Case-Control Studies. <i>Stats</i> , 2022, 5, 203-214.	0.9	0