

# Torben A Kruse

## List of Publications by Year in descending order

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86  
papers

4,078  
citations

172457

29  
h-index

128289

60  
g-index

90  
all docs

90  
docs citations

90  
times ranked

8662  
citing authors

#	ARTICLE	IF	CITATIONS
1	Multiple independent variants at the TERT locus are associated with telomere length and risks of breast and ovarian cancer. <i>Nature Genetics</i> , 2013, 45, 371-384.	21.4	493
2	Association of Type and Location of <i>BRCA1</i> and <i>BRCA2</i> Mutations With Risk of Breast and Ovarian Cancer. <i>JAMA - Journal of the American Medical Association</i> , 2015, 313, 1347.	7.4	390
3	Identification of 12 new susceptibility loci for different histotypes of epithelial ovarian cancer. <i>Nature Genetics</i> , 2017, 49, 680-691.	21.4	356
4	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. <i>Nature Genetics</i> , 2017, 49, 1767-1778.	21.4	289
5	Mutational spectrum in a worldwide study of 29,700 families with <i>BRCA1</i> or <i>BRCA2</i> mutations. <i>Human Mutation</i> , 2018, 39, 593-620.	2.5	224
6	Identification of six new susceptibility loci for invasive epithelial ovarian cancer. <i>Nature Genetics</i> , 2015, 47, 164-171.	21.4	221
7	Prediction of Breast and Prostate Cancer Risks in Male <i>BRCA1</i> and <i>BRCA2</i> Mutation Carriers Using Polygenic Risk Scores. <i>Journal of Clinical Oncology</i> , 2017, 35, 2240-2250.	1.6	152
8	Evaluation of Nine Somatic Variant Callers for Detection of Somatic Mutations in Exome and Targeted Deep Sequencing Data. <i>PLoS ONE</i> , 2016, 11, e0151664.	2.5	144
9	Large scale multifactorial likelihood quantitative analysis of <i>BRCA1</i> and <i>BRCA2</i> variants: An ENIGMA resource to support clinical variant classification. <i>Human Mutation</i> , 2019, 40, 1557-1578.	2.5	102
10	Classifications within Molecular Subtypes Enables Identification of <i>BRCA1/BRCA2</i> Mutation Carriers by RNA Tumor Profiling. <i>PLoS ONE</i> , 2013, 8, e64268.	2.5	89
11	Polygenic risk scores and breast and epithelial ovarian cancer risks for carriers of <i>BRCA1</i> and <i>BRCA2</i> pathogenic variants. <i>Genetics in Medicine</i> , 2020, 22, 1653-1666.	2.4	82
12	Familial Isolated Hyperparathyroidism as a Variant of Multiple Endocrine Neoplasia Type 1 in a Large Danish Pedigree1. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2000, 85, 165-167.	3.6	74
13	Hereditary Breast Cancer: Clinical, Pathological and Molecular Characteristics. <i>Breast Cancer: Basic and Clinical Research</i> , 2014, 8, BCBCR.S18715.	1.1	71
14	Ruxolitinib and interferon- $\gamma$ 2 combination therapy for patients with polycythemia vera or myelofibrosis: a phase II study. <i>Haematologica</i> , 2020, 105, 2262-2272.	3.5	67
15	Molecular signature of different lesion types in the brain white matter of patients with progressive multiple sclerosis. <i>Acta Neuropathologica Communications</i> , 2019, 7, 205.	5.2	61
16	Allergic rhinitis “a total genome-scan for susceptibility genes suggests a locus on chromosome 4q24-q27. <i>European Journal of Human Genetics</i> , 2001, 9, 945-952.	2.8	59
17	Whole Blood Transcriptional Profiling Reveals Deregulation of Oxidative and Antioxidative Defence Genes in Myelofibrosis and Related Neoplasms. Potential Implications of Downregulation of Nrf2 for Genomic Instability and Disease Progression. <i>PLoS ONE</i> , 2014, 9, e112786.	2.5	59
18	A new locus for Seckel syndrome on chromosome 18p11.31-q11.2. <i>European Journal of Human Genetics</i> , 2001, 9, 753-757.	2.8	54

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19	Mathematical modelling as a proof of concept for MPNs as a human inflammation model for cancer development. <i>PLoS ONE</i> , 2017, 12, e0183620.	2.5	51
20	The <i>BRCA1</i> c. 5096G>A p.Arg1699Gln (R1699Q) intermediate risk variant: breast and ovarian cancer risk estimation and recommendations for clinical management from the ENIGMA consortium. <i>Journal of Medical Genetics</i> , 2018, 55, 15-20.	3.2	50
21	Long non-coding RNA expression profiles predict metastasis in lymph node-negative breast cancer independently of traditional prognostic markers. <i>Breast Cancer Research</i> , 2015, 17, 55.	5.0	49
22	DNA Glycosylases Involved in Base Excision Repair May Be Associated with Cancer Risk in <i>BRCA1</i> and <i>BRCA2</i> Mutation Carriers. <i>PLoS Genetics</i> , 2014, 10, e1004256.	3.5	47
23	Molecular Concordance Between Primary Breast Cancer and Matched Metastases. <i>Breast Journal</i> , 2016, 22, 420-430.	1.0	44
24	Clonal expansion and linear genome evolution through breast cancer progression from pre-invasive stages to asynchronous metastasis. <i>Oncotarget</i> , 2015, 6, 5634-5649.	1.8	42
25	Association of Genomic Domains in <i>BRCA1</i> and <i>BRCA2</i> with Prostate Cancer Risk and Aggressiveness. <i>Cancer Research</i> , 2020, 80, 624-638.	0.9	39
26	Differential Dynamics of <i>CALR</i> Mutant Allele Burden in Myeloproliferative Neoplasms during Interferon Alfa Treatment. <i>PLoS ONE</i> , 2016, 11, e0165336.	2.5	38
27	Safety and efficacy of combination therapy of interferon- $\alpha$ 2 and ruxolitinib in polycythemia vera and myelofibrosis. <i>Cancer Medicine</i> , 2018, 7, 3571-3581.	2.8	38
28	Search for a shared segment on chromosome 10q26 in patients with bipolar affective disorder or schizophrenia from the Faroe Islands. <i>American Journal of Medical Genetics Part A</i> , 2002, 114, 196-204.	2.4	34
29	Assessing Associations between the <i>AURKA-HMMR-TPX2-TUBG1</i> Functional Module and Breast Cancer Risk in <i>BRCA1/2</i> Mutation Carriers. <i>PLoS ONE</i> , 2015, 10, e0120020.	2.5	34
30	Human longevity and variation in DNA damage response and repair: study of the contribution of sub-processes using competitive gene-set analysis. <i>European Journal of Human Genetics</i> , 2014, 22, 1131-1136.	2.8	31
31	Myelin-specific <i>T</i> cells induce interleukin-1 $\beta$ expression in lesion-reactive microglial-like cells in zones of axonal degeneration. <i>Glia</i> , 2016, 64, 407-424.	4.9	28
32	The microRNA-132/212 family fine-tunes multiple targets in Angiotensin II signalling in cardiac fibroblasts. <i>JRAAS - Journal of the Renin-Angiotensin-Aldosterone System</i> , 2015, 16, 1288-1297.	1.7	27
33	An original phylogenetic approach identified mitochondrial haplogroup T1a1 as inversely associated with breast cancer risk in <i>BRCA2</i> mutation carriers. <i>Breast Cancer Research</i> , 2015, 17, 61.	5.0	26
34	Genomic profiling of a randomized trial of interferon- $\alpha$ vs hydroxyurea in MPN reveals mutation-specific responses. <i>Blood Advances</i> , 2022, 6, 2107-2119.	5.2	26
35	The subclonal structure and genomic evolution of oral squamous cell carcinoma revealed by ultra-deep sequencing. <i>Oncotarget</i> , 2017, 8, 16571-16580.	1.8	25
36	Genomic Analyses of Breast Cancer Progression Reveal Distinct Routes of Metastasis Emergence. <i>Scientific Reports</i> , 2017, 7, 43813.	3.3	24

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37	Identification of metastasis driver genes by massive parallel sequencing of successive steps of breast cancer progression. <i>PLoS ONE</i> , 2018, 13, e0189887.	2.5	24
38	Association of miR-548c-5p, miR-7-5p, miR-210-3p, miR-128-3p with recurrence in systemically untreated breast cancer. <i>Oncotarget</i> , 2018, 9, 9030-9042.	1.8	22
39	CFP suppresses breast cancer cell growth by TES-mediated upregulation of the transcription factor DDIT3. <i>Oncogene</i> , 2019, 38, 4560-4573.	5.9	22
40	Subtypes in BRCA-mutated breast cancer. <i>Human Pathology</i> , 2019, 84, 192-201.	2.0	22
41	Microarray-Based RNA Profiling of Breast Cancer: Batch Effect Removal Improves Cross-Platform Consistency. <i>BioMed Research International</i> , 2014, 2014, 1-11.	1.9	21
42	Use of next generation sequencing in head and neck squamous cell carcinomas: A review. <i>Oral Oncology</i> , 2014, 50, 1035-1040.	1.5	21
43	Effect of thrombopoietin receptor agonists on markers of coagulation and P-selectin in patients with immune thrombocytopenia. <i>Platelets</i> , 2019, 30, 206-212.	2.3	21
44	Breast and Prostate Cancer Risks for Male <i>BRCA1</i> and <i>BRCA2</i> Pathogenic Variant Carriers Using Polygenic Risk Scores. <i>Journal of the National Cancer Institute</i> , 2022, 114, 109-122.	6.3	19
45	RNA profiling reveals familial aggregation of molecular subtypes in non- <i>BRCA1/2</i> breast cancer families. <i>BMC Medical Genomics</i> , 2014, 7, 9.	1.5	18
46	The impact of interferon-alpha2 on HLA genes in patients with polycythemia vera and related neoplasms. <i>Leukemia and Lymphoma</i> , 2017, 58, 1914-1921.	1.3	17
47	Investigating a case of possible field cancerization in oral squamous cell carcinoma by the use of next-generation sequencing. <i>Oral Oncology</i> , 2017, 68, 74-80.	1.5	15
48	Sorted peripheral blood cells identify <i>CALR</i> mutations in B- and T-lymphocytes. <i>Leukemia and Lymphoma</i> , 2018, 59, 973-977.	1.3	15
49	Tumor-specific genetic aberrations in cell-free DNA of gastroesophageal cancer patients. <i>Journal of Gastroenterology</i> , 2019, 54, 108-121.	5.1	14
50	Long-Term Efficacy and Safety of Recombinant Interferon Alpha-2 Vs. Hydroxyurea in Polycythemia Vera: Preliminary Results from the Three-Year Analysis of the Daliah Trial - a Randomized Controlled Phase III Clinical Trial. <i>Blood</i> , 2018, 132, 580-580.	1.4	14
51	Safety and Efficacy of Combination Therapy of Interferon-Alpha2 + JAK1-2 Inhibitor in the Philadelphia-Negative Chronic Myeloproliferative Neoplasms. Preliminary Results from the Danish Combi-Trial - an Open Label, Single Arm, Non-Randomized Multicenter Phase II Study. <i>Blood</i> , 2015, 126, 824-824.	1.4	14
52	Transcriptional Profiling of Whole Blood Identifies a Unique 5-Gene Signature for Myelofibrosis and Imminent Myelofibrosis Transformation. <i>PLoS ONE</i> , 2014, 9, e85567.	2.5	13
53	Epithelial ovarian cancer and the use of circulating tumor DNA: A systematic review. <i>Gynecologic Oncology</i> , 2021, 161, 884-895.	1.4	12
54	Spotting and validation of a genome wide oligonucleotide chip with duplicate measurement of each gene. <i>Biochemical and Biophysical Research Communications</i> , 2006, 344, 1111-1120.	2.1	11

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55	Tumour-infiltrating CD4-, CD8- and FOXP3-positive immune cells as predictive markers of mortality in BRCA1- and BRCA2-associated breast cancer. <i>British Journal of Cancer</i> , 2021, 125, 1388-1398.	6.4	11
56	Whole Blood Gene Expression Profiling in patients undergoing colon cancer surgery identifies differential expression of genes involved in immune surveillance, inflammation and carcinogenesis. <i>Surgical Oncology</i> , 2018, 27, 208-215.	1.6	10
57	High Expression of Carcinoembryonic Antigen-Related Cell Adhesion Molecule(CEACAM) 6 In Primary Myelofibrosis. <i>Blood</i> , 2010, 116, 4116-4116.	1.4	10
58	Myeloproliferative Neoplasms in Danish Twins. <i>Acta Haematologica</i> , 2018, 139, 195-198.	1.4	8
59	Heterogeneity and tumor evolution reflected in liquid biopsy in metastatic breast cancer patients: a review. <i>Cancer and Metastasis Reviews</i> , 2022, 41, 433-446.	5.9	8
60	Feature Selection for Predicting Tumor Metastases in Microarray Experiments using Paired Design. <i>Cancer Informatics</i> , 2007, 3, 117693510700300.	1.9	7
61	The gene expression and immunohistochemical time-course of diphenylcyclopropenone-induced contact allergy in healthy humans following repeated epicutaneous challenges. <i>Experimental Dermatology</i> , 2017, 26, 926-933.	2.9	7
62	Molecular characterization of sorted malignant B cells from patients clinically identified with mantle cell lymphoma. <i>Experimental Hematology</i> , 2020, 84, 7-18.e12.	0.4	7
63	Significantly Upregulated Thrombo-Inflammatory Genes Are Normoregulated or Significantly Downregulated during Treatment with Interferon-Alpha2 in Patients with Philadelphia-Negative Chronic Myeloproliferative Neoplasms. <i>Blood</i> , 2019, 134, 2978-2978.	1.4	6
64	A 7-Genes Signature Depicts the Biochemical Profile of Early Prefibrotic Myelofibrosis. <i>PLoS ONE</i> , 2016, 11, e0161570.	2.5	6
65	Increased oxidative stress with substantial dysregulation of genes related to oxidative stress and DNA repair after laparoscopic colon cancer surgery. <i>Surgical Oncology</i> , 2020, 35, 71-78.	1.6	5
66	Increased Expression of Proteasome-Related Genes In Patients with Primary Myelofibrosis. <i>Blood</i> , 2010, 116, 4117-4117.	1.4	5
67	Interferon-alfa2 Treatment of Patients with Polycythemia Vera and Related Neoplasms Impacts Deregulation of Oxidative Stress Genes and Antioxidative Defence Mechanisms. Potential Implications of IFN-Alpha Induced Changes in TP53, NRF2 and CXCR4 for Genomic Instability and CD34+ Mobilisation. <i>Blood</i> , 2018, 132, 4326-4326.	1.4	3
68	Interferon-alfa2 Treatment of Patients with Polycythemia Vera and Related Neoplasms Influences Deregulated Inflammation and Immune Genes in Polycythemia Vera and Allied Neoplasms. <i>Blood</i> , 2018, 132, 5490-5490.	1.4	3
69	The Optimal Sequencing Depth of Tumor Biopsies for Identifying Clonal Cell Populations. <i>Journal of Molecular Diagnostics</i> , 2019, 21, 790-795.	2.8	2
70	Extracellular Matrix-Related Genes Are Deregulated in Peripheral Blood from Patients with Myelofibrosis and Related Neoplasms. <i>Blood</i> , 2018, 132, 5491-5491.	1.4	2
71	Search for a shared segment on chromosome 10q26 in patients with bipolar affective disorder or schizophrenia from the Faroe Islands. <i>American Journal of Medical Genetics Part A</i> , 2002, 114, 196-204.	2.4	1
72	The Impact of Interferon on Interferon-Related Genes in Polycythemia Vera and Allied Neoplasms. <i>Blood</i> , 2018, 132, 4328-4328.	1.4	1

#	ARTICLE	IF	CITATIONS
73	Genomic Profiling of a Phase III Clinical Trial of Interferon Versus Hydroxyurea in MPN Patients Reveals Mutation-Specific and Treatment-Specific Patterns of Response. <i>Blood</i> , 2019, 134, 4202-4202.	1.4	1
74	Increased Gene Expression of Histone Deacetylases In Patients with Philadelphia-Negative Chronic Myeloproliferative Neoplasms. <i>Blood</i> , 2010, 116, 4119-4119.	1.4	1
75	Whole Blood Transcriptional Profiling Reveals Highly Deregulated Atherosclerosis Genes in Myeloproliferative Cancer. <i>Blood</i> , 2018, 132, 3071-3071.	1.4	1
76	Highly Deregulated Fibulins in Patients with Philadelphia-Negative Chronic Myeloproliferative Neoplasms. <i>Blood</i> , 2019, 134, 5396-5396.	1.4	1
77	Latent growth curve modeling of incomplete timecourse data in microarray gene expression studies. , 2012, , .		0
78	OTEH-4. Deeper insight into intratumoral heterogeneity by MRI and PET-guided stereotactic biopsies from glioblastoma patients. <i>Neuro-Oncology Advances</i> , 2021, 3, ii11-ii11.	0.7	0
79	Comparison of the Metastasis Predictive Potential of mRNA and Long Non-Coding RNA Profiling in Systemically Untreated Breast Cancer. <i>Cancers</i> , 2021, 13, 4907.	3.7	0
80	Enhanced Gene Expression of EZH2 In Patients with Primary Myelofibrosis. <i>Blood</i> , 2010, 116, 4118-4118.	1.4	0
81	Gene Expression Profiling with Principal Component Analysis Depicts the Biological Continuum From Essential Thrombocythemia Over Polycythemia Vera to Myelofibrosis. <i>Blood</i> , 2010, 116, 4115-4115.	1.4	0
82	The Impact of Interferon-alpha2 on HLA-Genes in Patients with Polycythemia Vera and Related Neoplasms. <i>Blood</i> , 2015, 126, 4097-4097.	1.4	0
83	Genetic Evidence for Involvement of Human Endogenous Retrovirus Herv-Fc1 in the Pathogenesis of MPNs. <i>Blood</i> , 2018, 132, 5488-5488.	1.4	0
84	The Impact of the Mutational Landscape upon the Molecular Responses to Interferon-Alfa2 in Calr-Mutated MPN Patients. <i>Blood</i> , 2018, 132, 4327-4327.	1.4	0
85	The Impact of Somatic Mutations upon the Response to Combination Therapy with Ruxolitinib and Interferon in MPN Patients. <i>Blood</i> , 2021, 138, 3589-3589.	1.4	0
86	Abstract P5-07-07: Mapping clonal evolution and tumor heterogeneity by whole exome sequencing of tissue and plasma circulating tumor DNA in metastatic breast cancer. <i>Cancer Research</i> , 2022, 82, P5-07-07-P5-07-07.	0.9	0