Martin Dugas

List of Publications by Year
in descending order

247	7,816	87888 38	66911 78
papers	citations	h-index	g-index
270	270	270	12624
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Landscape of genetic lesions in 944 patients with myelodysplastic syndromes. Leukemia, 2014, 28, 241-247.	7.2	1,291
2	Inhibition of the LSD1 (KDM1A) demethylase reactivates the all-trans-retinoic acid differentiation pathway in acute myeloid leukemia. Nature Medicine, 2012, 18, 605-611.	30.7	584
3	Benchmarking atlas-level data integration in single-cell genomics. Nature Methods, 2022, 19, 41-50.	19.0	403
4	Inherited and Somatic Defects in DDX41 in Myeloid Neoplasms. Cancer Cell, 2015, 27, 658-670.	16.8	341
5	Electronic health records: new opportunities for clinical research. Journal of Internal Medicine, 2013, 274, 547-560.	6.0	234
6	Loss of the histone methyltransferase EZH2 induces resistance to multiple drugs in acute myeloid leukemia. Nature Medicine, 2017, 23, 69-78.	30.7	192
7	Evaluating Variant Calling Tools for Non-Matched Next-Generation Sequencing Data. Scientific Reports, 2017, 7, 43169.	3.3	185
8	European academy of dermatology and venereology European prurigo project: expert consensus on the definition, classification and terminology of chronic prurigo. Journal of the European Academy of Dermatology and Venereology, 2018, 32, 1059-1065.	2.4	150
9	Using electronic health records for clinical research: The case of the EHR4CR project. Journal of Biomedical Informatics, 2015, 53, 162-173.	4.3	142
10	AML1-ETO requires enhanced C/D box snoRNA/RNP formation to induce self-renewal and leukaemia. Nature Cell Biology, 2017, 19, 844-855.	10.3	132
11	Clonal evolution in myelodysplastic syndromes. Nature Communications, 2017, 8, 15099.	12.8	118
12	Infection Exposure Is a Causal Factor in B-cell Precursor Acute Lymphoblastic Leukemia as a Result of *Pax5*-Inherited Susceptibility. Cancer Discovery, 2015, 5, 1328-1343.	9.4	117
13	Pediatric acute lymphoblastic leukemia (ALL) gene expression signatures classify an independent cohort of adult ALL patients. Leukemia, 2004, 18, 63-71.	7.2	105
14	Effects of computerized decision support system implementations on patient outcomes in inpatient care: a systematic review. Journal of the American Medical Informatics Association: JAMIA, 2018, 25, 593-602.	4.4	98
15	The Interlaboratory RObustness of Next-generation sequencing (IRON) study: a deep sequencing investigation of TET2, CBL and KRAS mutations by an international consortium involving 10 laboratories. Leukemia, 2011, 25, 1840-1848.	7.2	96
16	Success criteria for electronic medical record implementations in low-resource settings: a systematic review. Journal of the American Medical Informatics Association: JAMIA, 2015, 22, 479-488.	4.4	96
17	Genomic landscape of liposarcoma. Oncotarget, 2015, 6, 42429-42444.	1.8	94
18	Genomic organization and evolution of double minutes/homogeneously staining regions with *MYC* amplification in human cancer. Nucleic Acids Research, 2014, 42, 9131-9145.	14.5	91

#	Article	IF	Citations
19	Impact of Molecular Genetics on Outcome in Myelofibrosis Patients after Allogeneic Stem Cell Transplantation. Biology of Blood and Marrow Transplantation, 2017, 23, 1095-1101.	2.0	89
20	RSVSim: an R/Bioconductor package for the simulation of structural variations. Bioinformatics, 2013, 29, 1679-1681.	4.1	87
21	Evaluation of data completeness in the electronic health record for the purpose of patient recruitment into clinical trials: a retrospective analysis of element presence. BMC Medical Informatics and Decision Making, 2013, 13, 37.	3.0	77
22	Infection Exposure Promotes *ETV6-RUNX1* Precursor B-cell Leukemia via Impaired H3K4 Demethylases. Cancer Research, 2017, 77, 4365-4377.	0.9	76
23	Epigenetic dysregulation of $K_{Ca}3.1$ channels induces poor prognosis in lung cancer. International Journal of Cancer, 2015, 137, 1306-1317.	5.1	75
24	Deep Sequencing in Conjunction with Expression and Functional Analyses Reveals Activation of FGFR1 in Ewing Sarcoma. Clinical Cancer Research, 2015, 21, 4935-4946.	7.0	68
25	Bi-allelic Mutations in M1AP Are a Frequent Cause of Meiotic Arrest and Severely Impaired Spermatogenesis Leading to Male Infertility. American Journal of Human Genetics, 2020, 107, 342-351.	6.2	68
26	Qualitative and quantitative evaluation of EHR-integrated mobile patient questionnaires regarding usability and cost-efficiency. International Journal of Medical Informatics, 2012, 81, 303-313.	3.3	64
27	DNA methylation changes are a late event in acute promyelocytic leukemia and coincide with loss of transcription factor binding. Blood, 2013, 121, 178-187.	1.4	61
28	Humanistic burden of chronic pruritus in patients with inflammatory dermatoses: Results of the European Academy of Dermatology and Venereology Network on Assessment of Severity and Burden of Pruritus (PruNet) cross-sectional trial. Journal of the American Academy of Dermatology, 2018, 79, 457-463.e5.	1.2	58
29	Routine data from hospital information systems can support patient recruitment for clinical studies. Clinical Trials, 2010, 7, 183-189.	1.6	56
30	A proof of concept phase I/II pilot trial of LSD1 inhibition by tranylcypromine combined with ATRA in refractory/relapsed AML patients not eligible for intensive therapy. Leukemia, 2021, 35, 701-711.	7.2	56
31	Site-specific methylation of 18S ribosomal RNA by SNORD42A is required for acute myeloid leukemia cell proliferation. Blood, 2020, 135, 2059-2070.	1.4	52
32	Genetic characterization of acquired aplastic anemia by targeted sequencing. Haematologica, 2014, 99, e165-e167.	3.5	51
33	Portal of medical data models: information infrastructure for medical research and healthcare. Database: the Journal of Biological Databases and Curation, 2016, 2016, bav121.	3.0	50
34	Azacitidine in combination with intensive induction chemotherapy in older patients with acute myeloid leukemia: The AML-AZA trial of the study alliance leukemia. Leukemia, 2016, 30, 555-561.	7.2	47
35	Leukemia Gene Atlas – A Public Platform for Integrative Exploration of Genome-Wide Molecular Data. PLoS ONE, 2012, 7, e39148.	2.5	47
36	Chronic nodular prurigo: clinical profile and burden. A European cross‐sectional study. Journal of the European Academy of Dermatology and Venereology, 2020, 34, 2373-2383.	2.4	44

#	Article	IF	Citations
37	Immunophenotyping in pemphigus reveals a TH17/TFH17 cellâ€"dominated immune response promoting desmoglein1/3-specific autoantibody production. Journal of Allergy and Clinical Immunology, 2021, 147, 2358-2369.	2.9	44
38	Less severe course of COVID-19 is associated with elevated levels of antibodies against seasonal human coronaviruses OC43 and HKU1 (HCoV OC43, HCoV HKU1). International Journal of Infectious Diseases, 2021, 105, 304-306.	3.3	42
39	European <scp>EADV</scp> network on assessment of severity and burden of Pruritus (PruNet): first meeting on outcome tools. Journal of the European Academy of Dermatology and Venereology, 2016, 30, 1144-1147.	2.4	41
40	Safeguard function of PU.1 shapes the inflammatory epigenome of neutrophils. Nature Immunology, 2019, 20, 546-558.	14.5	40
41	Mapping Turnaround Times (TAT) to a Generic Timeline: A Systematic Review of TAT Definitions in Clinical Domains. BMC Medical Informatics and Decision Making, 2011, 11, 34.	3.0	39
42	Increased DNA methylation of Dnmt3b targets impairs leukemogenesis. Blood, 2016, 127, 1575-1586.	1.4	38
43	Crossâ€European validation of the ItchyQoL in pruritic dermatoses. Journal of the European Academy of Dermatology and Venereology, 2019, 33, 391-397.	2.4	38
44	A European inventory of common electronic health record data elements for clinical trial feasibility. Trials, 2014, 15, 18.	1.6	37
45	Loss of Pax5 Exploits Sca1-BCR-ABLp190 Susceptibility to Confer the Metabolic Shift Essential for pB-ALL. Cancer Research, 2018, 78, 2669-2679.	0.9	37
46	Lack of antibodies against seasonal coronavirus OC43 nucleocapsid protein identifies patients at risk of critical COVID-19. Journal of Clinical Virology, 2021, 139, 104847.	3.1	37
47	Comparison of Electronic Health Record System Functionalities to support the patient recruitment process in clinical trials. International Journal of Medical Informatics, 2014, 83, 860-868.	3.3	36
48	Persistent symptoms and lab abnormalities in patients who recovered from COVID-19. Scientific Reports, 2021, 11, 12775.	3.3	36
49	Workflow to improve patient recruitment for clinical trials within hospital information systems â€" a case-study. Trials, 2008, 9, 2.	1.6	34
50	AML1/ETO induces self-renewal in hematopoietic progenitor cells via the Groucho-related amino-terminal AES protein. Blood, 2011, 117, 4328-4337.	1.4	34
51	Next-generation-sequencing of recurrent childhood high hyperdiploid acute lymphoblastic leukemia reveals mutations typically associated with high risk patients. Leukemia Research, 2015, 39, 990-1001.	0.8	32
52	Lmo2 expression defines tumor cell identity during Tâ€cell leukemogenesis. EMBO Journal, 2018, 37, .	7.8	32
53	Comprehensive germline-genomic and clinical profiling in 160 unselected children and adolescents with cancer. European Journal of Human Genetics, 2021, 29, 1301-1311.	2.8	32
54	Integrative analysis of histone ChIP-seq and transcription data using Bayesian mixture models. Bioinformatics, 2014, 30, 1154-1162.	4.1	31

#	Article	IF	Citations
55	ODMedit: uniform semantic annotation for data integration in medicine based on a public metadata repository. BMC Medical Research Methodology, 2016, 16, 65.	3.1	31
56	Common data elements for secondary use of electronic health record data for clinical trial execution and serious adverse event reporting. BMC Medical Research Methodology, 2016, 16, 159.	3.1	31
57	Integrative genomic analysis of pediatric T-cell lymphoblastic lymphoma reveals candidates of clinical significance. Blood, 2021, 137, 2347-2359.	1.4	31
58	Design and multicentric Implementation of a generic Software Architecture for Patient Recruitment Systems re-using existing HIS tools and Routine Patient Data. Applied Clinical Informatics, 2014, 05, 264-283.	1.7	30
59	Genetic predisposition in children with cancer â€" affected families' acceptance of Trio-WES. European Journal of Pediatrics, 2018, 177, 53-60.	2.7	30
60	Chronic pruritus: evaluation of patient needs and treatment goals with a special regard to differences according to pruritus classification and sex. British Journal of Dermatology, 2017, 176, 363-370.	1.5	29
61	Clinical relevance of molecular characteristics in Burkitt lymphoma differs according to age. Nature Communications, 2022, 13, .	12.8	28
62	Piloting the EHR4CR Feasibility Platform across Europe. Methods of Information in Medicine, 2014, 53, 264-268.	1.2	27
63	LOINC(R) Codes for Hospital Information Systems Documents: A Case Study. Journal of the American Medical Informatics Association: JAMIA, 2009, 16, 400-403.	4.4	26
64	Multilingual Medical Data Models in ODM Format. Applied Clinical Informatics, 2012, 03, 276-289.	1.7	26
65	appreci8: a pipeline for precise variant calling integrating 8 tools. Bioinformatics, 2018, 34, 4205-4212.	4.1	26
66	The burden in chronic prurigo: patients with chronic prurigo suffer more than patients with chronic pruritus on nonâ€'lesional skin. Journal of the European Academy of Dermatology and Venereology, 2021, 35, 738-743.	2.4	25
67	Connecting healthcare and clinical research: Workflow optimizations through seamless integration of EHR, pseudonymization services and EDC systems. International Journal of Medical Informatics, 2018, 119, 103-108.	3.3	24
68	Macrophage-tumor cell interaction promotes ATRT progression and chemoresistance. Acta Neuropathologica, 2020, 139, 913-936.	7.7	24
69	Does single-source create an added value? Evaluating the impact of introducing x4T into the clinical routine on workflow modifications, data quality and costâ€"benefit. International Journal of Medical Informatics, 2014, 83, 915-928.	3.3	23
70	The need for harmonized structured documentation and chances of secondary use â€" Results of a systematic analysis with automated form comparison for prostate and breast cancer. Journal of Biomedical Informatics, 2014, 51, 86-99.	4.3	23
71	The sperm epigenome does not display recurrent epimutations in patients with severely impaired spermatogenesis. Clinical Epigenetics, 2020, 12, 61.	4.1	23
72	Identification of the Adapter Molecule MTSS1 as a Potential Oncogene-Specific Tumor Suppressor in Acute Myeloid Leukemia. PLoS ONE, 2015, 10, e0125783.	2.5	23

#	Article	IF	Citations
73	Basic4Cseq: an R/Bioconductor package for analyzing 4C-seq data. Bioinformatics, 2014, 30, 3268-3269.	4.1	21
74	A Smart Device System to Identify New Phenotypical Characteristics in Movement Disorders. Frontiers in Neurology, 2019, 10, 48.	2.4	21
75	Infectious stimuli promote malignant B-cell acute lymphoblastic leukemia in the absence of AID. Nature Communications, 2019, 10, 5563.	12.8	21
76	Frequency Analysis of Medical Concepts in Clinical Trials and their Coverage in MeSH and SNOMED-CT. Methods of Information in Medicine, 2015, 54, 83-92.	1.2	20
77	BRCC3 mutations in myeloid neoplasms. Haematologica, 2015, 100, 1051-7.	3.5	20
78	Infection as a cause of childhood leukemia: virus detection employing whole genome sequencing. Haematologica, 2017, 102, e179-e183.	3.5	20
79	MYST2 acetyltransferase expression and Histone H4 Lysine acetylation are suppressed in AML. Experimental Hematology, 2015, 43, 794-802.e4.	0.4	19
80	Memorandum â€œOpen Metadataâ€. Methods of Information in Medicine, 2015, 54, 376-378.	1.2	18
81	Myeloid leukemia with transdifferentiation plasticity developing from Tâ€cell progenitors. EMBO Journal, 2016, 35, 2399-2416.	7.8	17
82	Pruritus Intensity Scales across Europe: a prospective validation study. Journal of the European Academy of Dermatology and Venereology, 2021, 35, 1176-1185.	2.4	17
83	Automated UMLS-Based Comparison of Medical Forms. PLoS ONE, 2013, 8, e67883.	2.5	17
84	Understanding the Nature of Metadata: Systematic Review. Journal of Medical Internet Research, 2022, 24, e25440.	4.3	17
85	Low SMC1A protein expression predicts poor survival in acute myeloid leukemia. Oncology Reports, 2010, 24, 47-56.	2.6	16
86	CIS-based registration of quality of life in a single source approach. BMC Medical Informatics and Decision Making, 2011, 11, 26.	3.0	16
87	Reconstructing clonal evolution in relapsed and non-relapsed Burkitt lymphoma. Leukemia, 2021, 35, 639-643.	7.2	16
88	Defective Interfering Genomes and the Full-Length Viral Genome Trigger RIG-I After Infection With Vesicular Stomatitis Virus in a Replication Dependent Manner. Frontiers in Immunology, 2021, 12, 595390.	4.8	16
89	Interoperability in clinical research: from metadata registries to semantically annotated CDISC ODM. Studies in Health Technology and Informatics, 2012, 180, 564-8.	0.3	16
90	Estimation of Patient Accrual Rates in Clinical Trials Based on Routine Data from Hospital Information Systems. Methods of Information in Medicine, 2009, 48, 263-266.	1.2	15

#	Article	IF	Citations
91	HIS-based Kaplan-Meier plots - a single source approach for documenting and reusing routine survival information. BMC Medical Informatics and Decision Making, 2011, 11, 11.	3.0	15
92	Missing Semantic Annotation in Databases. Methods of Information in Medicine, 2014, 53, 516-517.	1.2	15
93	Mr Lewis on the Webï¿½?ï¿½how to convert learning resources for Intranet technology. Medical Education, 1999, 33, 42-46.	2.1	14
94	Landscape Of Genetic Lesions In 944 Patients With Myelodysplastic Syndromes. Blood, 2013, 122, 521-521.	1.4	14
95	Somatic Structural Variations in Pediatric High Hyperdiploid Acute Lymphoblastic Leukemia Revealed by Paired-End Parallel Sequencing. Blood, 2011, 118, 401-401.	1.4	14
96	Single source information systems to connect patient care and clinical research. Studies in Health Technology and Informatics, 2009, 150, 61-5.	0.3	14
97	Concept and implementation of a computer-based reminder system to increase completeness in clinical documentation. International Journal of Medical Informatics, 2011, 80, 351-358.	3.3	13
98	CDEGenerator: an online platform to learn from existing data models to build model registries. Clinical Epidemiology, 2018, Volume 10, 961-970.	3.0	13
99	The Male Fertility Gene Atlas: a web tool for collecting and integrating OMICS data in the context of male infertility. Human Reproduction, 2020, 35, 1983-1990.	0.9	13
100	Complexity of biomedical data models in cardiology: the Intranet-based AF registry. Computer Methods and Programs in Biomedicine, 2002, 68, 49-61.	4.7	12
101	Temporal autoregulation during human PU.1 locus SubTAD formation. Blood, 2018, 132, 2643-2655.	1.4	12
102	Association of contact to small children with a mild course of COVID-19. International Journal of Infectious Diseases, 2020, 100, 314-315.	3.3	12
103	Whole-genome methylation analysis of testicular germ cells from cryptozoospermic men points to recurrent and functionally relevant DNA methylation changes. Clinical Epigenetics, 2021, 13, 160.	4.1	12
104	Does the <i>FSHB</i> c.â€211G>T polymorphism impact Sertoli cell number and the spermatogenic potential in infertile patients?. Andrology, 2020, 8, 1030-1037.	3.5	11
105	EMR-integrated minimal core dataset for routine health care and multiple research settings: A case study for neuroinflammatory demyelinating diseases. PLoS ONE, 2019, 14, e0223886.	2.5	10
106	Genetic alterations in human papillomavirus-associated oropharyngeal squamous cell carcinoma of patients with treatment failure. Oral Oncology, 2019, 93, 59-65.	1.5	10
107	Conceptual Design, Implementation, and Evaluation of Generic and Standard-Compliant Data Transfer into Electronic Health Records. Applied Clinical Informatics, 2020, 11, 374-386.	1.7	10
108	Differential transcript usage analysis of bulk and single-cell RNA-seq data with DTUrtle. Bioinformatics, 2021, 37, 3781-3787.	4.1	10

#	Article	IF	Citations
109	InterCellar enables interactive analysis and exploration of cell–cell communication in single-cell transcriptomic data. Communications Biology, 2022, 5, 21.	4.4	10
110	ODMSummary: A Tool for Automatic Structured Comparison of Multiple Medical Forms Based on Semantic Annotation with the Unified Medical Language System. PLoS ONE, 2016, 11, e0164569.	2.5	9
111	Leveraging the EHR4CR platform to support patient inclusion in academic studies: challenges and lessons learned. BMC Medical Research Methodology, 2017, 17, 36.	3.1	9
112	Electronic Collection of Multilingual Patient-Reported Outcomes across Europe. Methods of Information in Medicine, 2018, 57, e107-e114.	1.2	9
113	Mutation patterns in recurrent and/or metastatic oropharyngeal squamous cell carcinomas in relation to human papillomavirus status. Cancer Medicine, 2021, 10, 1347-1356.	2.8	9
114	Calcitonin receptor-like (CALCRL) is a marker of stemness and an independent predictor of outcome in pediatric AML. Blood Advances, 2021, 5, 4413-4421.	5.2	9
115	Core Data Elements in Acute Myeloid Leukemia: A Unified Medical Language System–Based Semantic Analysis and Experts' Review. JMIR Medical Informatics, 2019, 7, e13554.	2.6	9
116	Final Induction Therapy Results of an Open Label Phase II Study Using Inotuzumab Ozogamicin for Induction Therapy, Followed By a Conventional Chemotherapy Based Consolidation and Maintenance Therapy in Patients Aged 56 Years and Older with Acute B-Lymphoblastic Leukemia (INITIAL-1 trial). Blood, 2021, 138, 2300-2300.	1.4	9
117	Single-cell transcriptomics identifies potential cells of origin of MYC rhabdoid tumors. Nature Communications, 2022, 13, 1544.	12.8	9
118	Benchmarking of hospital information systems: Monitoring of discharge letters and scheduling can reveal heterogeneities and time trends. BMC Medical Informatics and Decision Making, 2008, 8, 15.	3.0	8
119	A Generic Method to Monitor Completeness and Speed of Medical Documentation Processes. Methods of Information in Medicine, 2012, 51, 252-257.	1.2	8
120	Using Electronic Health Records to Support Clinical Trials: A Report on Stakeholder Engagement for EHR4CR. BioMed Research International, 2015, 2015, 1-8.	1.9	8
121	Germline POT1 Deregulation Can Predispose to Myeloid Malignancies in Childhood. International Journal of Molecular Sciences, 2021, 22, 11572.	4.1	8
122	Design and implementation of a common drug information database for a university hospital. International Journal of Clinical Pharmacy, 2003, 25, 156-161.	1.4	7
123	Clinical Research Informatics: Recent Advances and Future Directions. Yearbook of Medical Informatics, 2015, 24, 174-177.	1.0	7
124	VIPER: a web application for rapid expert review of variant calls. Bioinformatics, 2018, 34, 1928-1929.	4.1	7
125	Integrated Data Management for Clinical Studies: Automatic Transformation of Data Models with Semantic Annotations for Principal Investigators, Data Managers and Statisticians. PLoS ONE, 2014, 9, e90492.	2.5	7
126	GLM-based optimization of NGS data analysis: A case study of Roche 454, Ion Torrent PGM and Illumina NextSeq sequencing data. PLoS ONE, 2017, 12, e0171983.	2.5	7

#	Article	IF	Citations
127	Common Data Elements for Acute Coronary Syndrome: Analysis Based on the Unified Medical Language System. JMIR Medical Informatics, 2019, 7, e14107.	2.6	7
128	Converting ODM Metadata to FHIR Questionnaire Resources. Studies in Health Technology and Informatics, 2016, 228, 456-60.	0.3	7
129	ELaPro, a LOINC-mapped core dataset for top laboratory procedures of eligibility screening for clinical trials. BMC Medical Research Methodology, 2022, 22, 141.	3.1	7
130	An intranet-based system for quality assurance in surgery. Journal of Medical Systems, 1999, 23, 13-19.	3.6	6
131	Interactive decision support in hepatic surgery. BMC Medical Informatics and Decision Making, 2002, 2, 5.	3.0	6
132	Concept and implementation of a single source information system in nuclear medicine for myocardial scintigraphy (SPECT-CT data). Applied Clinical Informatics, 2010, 01, 50-67.	1.7	6
133	ODM2CDA and CDA2ODM: Tools to convert documentation forms between EDC and EHR systems. BMC Medical Informatics and Decision Making, 2015, 15, 40.	3.0	6
134	Design of case report forms based on a public metadata registry: re-use of data elements to improve compatibility of data. Trials, 2016, 17, 566.	1.6	6
135	ODM Data Analysis—A tool for the automatic validation, monitoring and generation of generic descriptive statistics of patient data. PLoS ONE, 2018, 13, e0199242.	2.5	6
136	Benchmarking of 4C-seq pipelines based on real and simulated data. Bioinformatics, 2019, 35, 4938-4945.	4.1	6
137	Comparison of Open-access Databases for Clinical Variant Interpretation in Cancer: A Case Study of MDS/AML. Cancer Genomics and Proteomics, 2021, 18, 157-166.	2.0	6
138	Annotating Medical Forms Using UMLS. Lecture Notes in Computer Science, 2015, , 55-69.	1.3	6
139	The Interlaboratory Robustness of Next-Generation Sequencing (IRON) Study Phase II: Deep-Sequencing Analyses of Hematological Malignancies Performed by an International Network Involving 26 Laboratories. Blood, 2012, 120, 1399-1399.	1.4	6
140	Compatible Data Models at Design Stage of Medical Information Systems: Leveraging Related Data Elements from the MDM Portal. Studies in Health Technology and Informatics, 2019, 264, 113-117.	0.3	6
141	Repeated Digitized Assessment of Risk and Symptom Profiles During Inpatient Treatment of Affective Disorder: Observational Study. JMIR Mental Health, 2020, 7, e24066.	3.3	6
142	Machine learning based prediction models in male reproductive health: Development of a proof-of-concept model for Klinefelter Syndrome in azoospermic patients. Andrology, 2022, 10, 534-544.	3.5	6
143	Impact of integrating clinical and genetic information. In Silico Biology, 2002, 2, 383-91.	0.9	6
144	Divergent Effects of EZH1 and EZH2 Protein Expression on the Prognosis of Patients with T-Cell Lymphomas. Biomedicines, 2021, 9, 1842.	3.2	6

#	Article	IF	Citations
145	The Smart Device System for Movement Disorders: Preliminary Evaluation of Diagnostic Accuracy in a Prospective Study. Studies in Health Technology and Informatics, 2020, 270, 889-893.	0.3	6
146	XML-based visualization of design and completeness in medical databases. Informatics for Health and Social Care, 2001, 26, 237-250.	1.0	5
147	CopyDetective: Detection threshold–aware copy number variant calling in whole-exome sequencing data. GigaScience, 2020, 9, .	6.4	5
148	Serum concentrations of dihydrotestosterone are associated with symptoms of hypogonadism in biochemically eugonadal men. Journal of Endocrinological Investigation, 2021, 44, 2465-2474.	3.3	5
149	Online Information Infrastructure Increases Inter-Rater Reliability of Medical Coders: A Quasi-Experimental Study (Preprint). Journal of Medical Internet Research, 2018, 20, e274.	4.3	5
150	Standardized Cardiovascular Quality Assurance Forms with Multilingual Support, UMLS Coding and Medical Concept Analyses. Studies in Health Technology and Informatics, 2015, 216, 837-41.	0.3	5
151	An intranet database for a university hospital drug information center. American Journal of Health-System Pharmacy, 2001, 58, 799-802.	1.0	4
152	Efficiency and effectiveness evaluation of an automated multi-country patient count cohort system. BMC Medical Research Methodology, 2015, 15, 44.	3.1	4
153	Sharing clinical trial data. Lancet, The, 2016, 387, 2287.	13.7	4
154	AMLVaran: a software approach to implement variant analysis of targeted NGS sequencing data in an oncological care setting. BMC Medical Genomics, 2020, 13, 17.	1.5	4
155	FhirExtinguisher: A FHIR Resource Flattening Tool Using FHIRPath. Studies in Health Technology and Informatics, 2021, 281, 1112-1113.	0.3	4
156	Pragmatic MDR: a metadata repository with bottom-up standardization of medical metadata through reuse. BMC Medical Informatics and Decision Making, 2021, 21, 160.	3.0	4
157	Design and Implementation of an Informatics Infrastructure for Standardized Data Acquisition, Transfer, Storage, and Export in Psychiatric Clinical Routine: Feasibility Study. JMIR Mental Health, 2021, 8, e26681.	3.3	4
158	SimFFPE and FilterFFPE: improving structural variant calling in FFPE samples. GigaScience, 2021, 10, .	6.4	4
159	A GWAS in Idiopathic/Unexplained Infertile Men Detects a Genomic Region Determining Follicle-Stimulating Hormone Levels. Journal of Clinical Endocrinology and Metabolism, 2022, 107, 2350-2361.	3.6	4
160	HIS-based support of follow-up documentation – concept and implementation for clinical studies. Applied Clinical Informatics, 2011, 02, 1-17.	1.7	3
161	Characterization of Image Transfer Patterns in a Regional Trauma Network. Journal of Medical Systems, 2014, 38, 137.	3.6	3
162	S2O – A software tool for integrating research data from general purpose statistic software into electronic data capture systems. BMC Medical Informatics and Decision Making, 2017, 17, 3.	3.0	3

#	Article	IF	Citations
163	Feasibility, Safety and Effects of a One-Week, Ski-Based Exercise Intervention in Brain Tumor Patients and Their Relatives: A Pilot Study. Journal of Clinical Medicine, 2020, 9, 1006.	2.4	3
164	An Open-Source, Standard-Compliant, and Mobile Electronic Data Capture System for Medical Research (OpenEDC): Design and Evaluation Study. JMIR Medical Informatics, 2021, 9, e29176.	2.6	3
165	A Topical Collection on ICT for Health Science Research â€" EFMI Special Topic Conference. Journal of Medical Systems, 2021, 45, 70.	3.6	3
166	Why we need a large-scale open metadata initiative in health informatics - a vision paper on open data models for clinical phenotypes. Studies in Health Technology and Informatics, 2013, 192, 899-902.	0.3	3
167	Protocol feasibility workflow using an automated multi-country patient cohort system. Studies in Health Technology and Informatics, 2014, 205, 985-9.	0.3	3
168	Standardized quality assurance forms for organ transplantations with multilingual support, open access and UMLS coding. Studies in Health Technology and Informatics, 2015, 212, 15-22.	0.3	3
169	Key Data Elements in Myeloid Leukemia. Studies in Health Technology and Informatics, 2016, 228, 282-6.	0.3	3
170	Implementation of an ODM and HL7 Compliant Electronic Patient-Reported Outcome System. Studies in Health Technology and Informatics, 2016, 228, 421-5.	0.3	3
171	Automatic Conversion of Metadata from the Study of Health in Pomerania to ODM. Studies in Health Technology and Informatics, 2017, 236, 88-96.	0.3	3
172	The Portal of Medical Data Models: Where Have We Been and Where Are We Going?. Studies in Health Technology and Informatics, 2017, 245, 858-862.	0.3	3
173	Interoperability Improvement of Mobile Patient Survey (MoPat) Implementing Fast Health Interoperability Resources (FHIR). Studies in Health Technology and Informatics, 2019, 258, 141-145.	0.3	3
174	StudyPortal â€" Geovisualization of Study Research Networks. Journal of Medical Systems, 2020, 44, 22.	3.6	2
175	Comparing SDTM and FHIRÂ® for Real World Data from Electronic Health Records for Clinical Trial Submissions. Studies in Health Technology and Informatics, 2021, 281, 585-589.	0.3	2
176	Transcriptional Profiling Identifies Genes Differentially Regulated by the BCR/ABL Fusion Oncogene.. Blood, 2004, 104, 1537-1537.	1.4	2
177	Individual Gene Expression Profiling of Bone Marrow CD34 Cells in Acquired Severe Aplastic Anemia (aSAA) in Children.. Blood, 2006, 108, 978-978.	1.4	2
178	An intranet-based information system for nurses. M D Computing, 1998, 15, 158-61.	0.1	2
179	A generic concept for large-scale microarray analysis dedicated to medical diagnostics. Methods of Information in Medicine, 2006, 45, 146-52.	1.2	2
180	Web-based multi-site feasibility questionnaire tool. Studies in Health Technology and Informatics, 2015, 212, 88-93.	0.3	2

#	Article	IF	Citations
181	A Web Service to Suggest Semantic Codes Based on the MDM-Portal. Studies in Health Technology and Informatics, 2018, 253, 35-39.	0.3	2
182	Design of a targeted next‐generation DNA sequencing panel for pediatric T‐cell lymphoblastic lymphoma to unravel biology and optimize treatment. Genes Chromosomes and Cancer, 2022, 61, 459-470.	2.8	2
183	Curcumin as an Epigenetic Therapeutic Agent in Myelodysplastic Syndromes (MDS). International Journal of Molecular Sciences, 2022, 23, 411.	4.1	2
184	Smarcb1 Loss Results in a Deregulation of esBAF Binding and Impacts the Expression of Neurodevelopmental Genes. Cells, 2022, 11, 1354.	4.1	2
185	Noncancer-related Secondary Findings in a Cohort of 231 Children With Cancer and Their Parents. Journal of Pediatric Hematology/Oncology, 2022, Publish Ahead of Print, .	0.6	2
186	Recurrent Germline Variant in RAD21 Predisposes Children to Lymphoblastic Leukemia or Lymphoma. International Journal of Molecular Sciences, 2022, 23, 5174.	4.1	2
187	Clonal Evolution at First Sight: A Combined Visualization of Diverse Diagnostic Methods Improves Understanding of Leukemic Progression. Frontiers in Oncology, 0, 12, .	2.8	2
188	Time for open access to all medical documentation forms. BMJ, The, 2013, 347, f5824-f5824.	6.0	1
189	Multicenter Next-Generation Sequencing Studies between Theory and Practice. Journal of Molecular Diagnostics, 2021, 23, 347-357.	2.8	1
190	Numerous Genomic Abnormalities in AML with Normal Karyotype.. Blood, 2007, 110, 1811-1811.	1.4	1
191	Combined Analysis of Valproic Acid Induced MicroRNA and Gene Expression Changes in Acute Myeloid Leukemia.. Blood, 2007, 110, 869-869.	1.4	1
192	Robust and Sensitive Detection of Insertions, Deletions and Point Mutations In CEBPA, a GC-Rich Content Gene, Using 454 Next-Generation Deep-Sequencing (NGS).. Blood, 2010, 116, 1657-1657.	1.4	1
193	Chromothripsis-Mediated Structural Variations and Clonal Evolution In Recurrent Childhood High Hyperdiploid Acute Lymphoblastic Leukemia. Blood, 2013, 122, 233-233.	1.4	1
194	Two Novel Distinct Subtypes of Myeloid Neoplasms Molecularly Associated with Histone H3K36 Methylations. Blood, 2015, 126, 2841-2841.	1.4	1
195	Targeted Next-Generation Sequencing and Genome-Wide High-Resolution Copy Number DNA Arrays Allow the Identification of Five Novel RUNX1 Fusions In Hematological Malignancies.. Blood, 2010, 116, 1193-1193.	1.4	1
196	Validation of the Qualms Questionnaire to Assess Health-Related Quality of Life in European and Israeli Patients with Myelodysplastic Syndromes: Results from the MDS-Right Project. Blood, 2021, 138, 1982-1982.	1.4	1
197	MedIDok--an Intranet tool for XML-based data modelling in medicine. Studies in Health Technology and Informatics, 2000, 77, 983-7.	0.3	1
198	Analysis of eligibility criteria from ClinicalTrials.gov. Studies in Health Technology and Informatics, 2014, 205, 853-7.	0.3	1

#	Article	IF	Citations
199	Standardized mappings--a framework to combine different semantic mappers into a standardized web-API. Studies in Health Technology and Informatics, 2015, 212, 23-6.	0.3	1
200	Clinical Trial Feasibility Study Questionnaire Analysis. Studies in Health Technology and Informatics, 2015, 216, 1029.	0.3	1
201	Automated Transformation of CDISC ODM to OpenClinica. Studies in Health Technology and Informatics, 2017, 243, 95-99.	0.3	1
202	What Information Does Your EHR Contain? Automatic Generation of a Clinical Metadata Warehouse (CMDW) to Support Identification and Data Access Within Distributed Clinical Research Networks. Studies in Health Technology and Informatics, 2017, 245, 313-317.	0.3	1
203	Medical Effect of Venous Thromboembolism Prophylaxis Systems and Common Input Categories: Preliminary Findings from a Systematic Review. Studies in Health Technology and Informatics, 2017, 245, 1175-1179.	0.3	1
204	Standardising the Development of ODM Converters: The ODMToolBox. Studies in Health Technology and Informatics, 2018, 247, 231-235.	0.3	1
205	Evaluation of openEHR Repositories Regarding Standard Compliance. Studies in Health Technology and Informatics, 2020, 270, 592-596.	0.3	1
206	CityPlot: Colored ER Diagrams to Visualize Structure and Contents of Databases. Datenbank-Spektrum, 2012, 12, 215-218.	1.3	0
207	BBCAnalyzer: a visual approach to facilitate variant calling. BMC Bioinformatics, 2017, 18, 133.	2.6	0
208	Common Data Elements for Meaningful Stroke Documentation in Routine Care and Clinical Research: Retrospective Data Analysis. JMIR Medical Informatics, 2021, 9, e27396.	2.6	0
209	Portal of Medical Data Models: Stakeholder Feedback and Requirements. Studies in Health Technology and Informatics, 2021, 281, 488-489.	0.3	0
210	A Seamless Pseudonymization and Randomization Workflow for REDCap. Studies in Health Technology and Informatics, 2021, 281, 952-956.	0.3	0
211	Patient Empowerment Through Digital Voice Pens: A Feasibility Study. Studies in Health Technology and Informatics, 2021, 278, 29-34.	0.3	0
212	MainzelHandler: A Library for a Simple Integration and Usage of the Mainzelliste. Studies in Health Technology and Informatics, 2021, 281, 233-237.	0.3	0
213	ODM Clinical Data Generator: Syntactically Correct Clinical Data Based on Metadata Definition. Studies in Health Technology and Informatics, 2021, 278, 35-40.	0.3	0
214	O-089 A Genome Wide Association Study in men with unexplained infertility identifies nine SNPs at the FSHB locus to be associated with Follicle Stimulating Hormone level. Human Reproduction, 2021, 36, .	0.9	0
215	Arginine (R) at Position 595 in FLT3 Is Critical for Transforming Potential of FLT3-Length Mutations.. Blood, 2005, 106, 1598-1598.	1.4	0
216	Global Identification of Genomic Structural Variants In Childhood ETV6/RUNX1 (TEL/AML1) Acute Lymphoblastic Leukemias by Mate-Pair Massively Parallel Sequencing.. Blood, 2010, 116, 3364-3364.	1.4	0

#	Article	IF	Citations
217	Dominant-Negative Impact of PAX5/TEL on Downstream Targets of PAX5 and Essential Pre-B Cell Receptor Genes. Blood, 2010, 116, 3231-3231.	1.4	0
218	The Interlaboratory RObustness of Next-Generation Sequencing (IRON) Study: Deep-Sequencing Investigating TET2, CBL, and KRAS Mutations In 4464 Amplicons by An International Group Involving 8 Laboratories.. Blood, 2010, 116, 1665-1665.	1.4	0
219	Targeted Next-Generation Sequencing (NGS) Enables a Broad Screening of 95 Molecular Mutations In a One-Step Approach and Detects Recurrent Mutations In AML with a Normal Karyotype In MYH11 and NOTCH1. Blood, 2010, 116, 175-175.	1.4	0
220	ChIP-on-Chip Analysis Identified HLXB9 as a Transcription Factor In Hematopoietic Cells and Alters the Expression of Genes Involved In Cell-Adhesion. Blood, 2010, 116, 2486-2486.	1.4	0
221	Whole Genome Amplification with Subsequent High Throughput Sequencing Allows Comprehensive Genome-Wide Analysis of Single Leukemic Cells. Blood, 2011, 118, 1437-1437.	1.4	0
222	Identification of the PML-RARÎ± Associated DNA Methylome Using Reduced Representation Bisulfite Sequencing in Primary Patient Samples. Blood, 2011, 118, 2436-2436.	1.4	0
223	A Specific DNA Methylation Pattern Is Associated with Delayed Leukemogenesis and Altered Response to Chemotherapeutic Treatment in an Inducible DNMT3b Expressing Mouse Model. Blood, 2012, 120, 398-398.	1.4	0
224	Novel Genomic Structural Variations in Relapsed Childhood ETV6/RUNX1 (TEL/AML1) Acute Lymphoblastic Leukemias Identified by Next Generation Sequencing. Blood, 2012, 120, 518-518.	1.4	0
225	Genetic Characterization Of Aplastic Anemia Patients By Targeted Sequencing. Blood, 2013, 122, 2470-2470.	1.4	0
226	Identification Of Leukemia Suppressive Genes By Inducible Overexpression Of The DNA Methyltransferase DNMT3B During Leukemogenesis In Mice. Blood, 2013, 122, 2493-2493.	1.4	0
227	The Clinical and Prognostic Influence Of Mutations In The Cohesin Complex In Acute Myeloid Leukemia. Blood, 2013, 122, 1314-1314.	1.4	0
228	A New ETV6-RUNX1 In Vivo Model Produces a Phenocopy of the Human Pb-ALL. Blood, 2015, 126, 3658-3658.	1.4	0
229	Medizininformatik. , 2017, , 81-223.		0
230	Data Structures in Medicineâ€"On the Road to Data Standards. , 2019, , 263-270.		0
231	ATRT-13. DIFFERENT CELLS OF ORIGIN PAVE THE WAY FOR MOLECULAR HETEROGENEITY IN RHABDOID TUMORS. Neuro-Oncology, 2020, 22, iii278-iii278.	1.2	0
232	ATRT-14. MACROPHAGE-TUMOR CELL INTERACTION PROMOTES ATRT PROGRESSION AND CHEMORESISTANCE. Neuro-Oncology, 2020, 22, iii278-iii278.	1.2	0
233	Bioinformatics for medical diagnostics: assessment of microarray data in the context of clinical databases. AMIA ... Annual Symposium proceedings, 2003, , 210-4.	0.2	0
234	Recurrent Germline Variant in the Cohesin Complex Gene *RAD21* Predisposes Children to Lymphoblastic Leukemia and Lymphoma. Blood, 2021, 138, 3358-3358.	1.4	0

#	Article	IF	Citations
235	Novel Germline *POT1* Variant Predisposes to Childhood Acute Myeloid Leukemia. Blood, 2021, 138, 3449-3449.	1.4	0
236	XML-based visual data mining in medicine. Studies in Health Technology and Informatics, 2001, 84, 1324-8.	0.3	0
237	Towards a trial-ready mobile patient questionnaire system. Studies in Health Technology and Informatics, 2014, 205, 768-72.	0.3	0
238	Operational Data Model Conversion to ResearchKit. Studies in Health Technology and Informatics, 2017, 245, 225-229.	0.3	0
239	A Secure Architecture to Provide a Medical Emergency Dataset for Patients in Germany and Abroad. Studies in Health Technology and Informatics, 2017, 245, 230-234.	0.3	0
240	Compatibility Between Metadata Standards: Import Pipeline of CDISC ODM to the Samply.MDR. Studies in Health Technology and Informatics, 2018, 247, 221-225.	0.3	0
241	Conducting a Multilingual Study Researching Traumatised Refugees Utilizing a Patient-Reported Outcome System. Studies in Health Technology and Informatics, 2018, 253, 109-113.	0.3	0
242	Reviving 30 Year Old Technology: Lessons Learned from Transferring Patient Data Using Data Matrix Codes. Studies in Health Technology and Informatics, 2019, 258, 90-94.	0.3	0
243	StudyPortal - A Novel Method to Visualize Study Research Networks. Studies in Health Technology and Informatics, 2019, 258, 163.	0.3	0
244	Portal of Medical Data Models: Status 2018. Studies in Health Technology and Informatics, 2019, 258, 239-240.	0.3	0
245	Electronic Image Documentation of Patient Reported Outcomes Using Mobile Technologies. Studies in Health Technology and Informatics, 2019, 264, 1779-1780.	0.3	0
246	ATRT-15. Primordial germ cells identified as one potential cell of origin of MYC rhabdoid tumors. Neuro-Oncology, 2022, 24, i6-i6.	1.2	0
247	ODM-DQA-Reporter: A Generic Approach to Assess and Monitor Basic Data Quality of Medical Research Data in Operational Data Model (ODM) Format. Studies in Health Technology and Informatics, 2022, , .	0.3	0