Ken Chen

List of Publications by Citations

156 papers	28,419 citations	55 h-index	168 g-index
175 ext. papers	35,330 ext. citations	16.2 avg, IF	5.79 L-index

#	Paper	IF	Citations
156	Genomic and epigenomic landscapes of adult de novo acute myeloid leukemia. *New England Journal of Medicine*, **2013**, 368, 2059-74	59.2	3137
155	Somatic mutations affect key pathways in lung adenocarcinoma. *Nature*, **2008**, 455, 1069-75	50.4	2280
154	Recurring mutations found by sequencing an acute myeloid leukemia genome. *New England Journal of Medicine*, **2009**, 361, 1058-66	59.2	1765
153	The Immune Landscape of Cancer. *Immunity*, **2018**, 48, 812-830.e14	32.3	1754
152	Clonal evolution in relapsed acute myeloid leukaemia revealed by whole-genome sequencing. *Nature*, **2012**, 481, 506-10	50.4	1511
151	An integrated map of structural variation in 2,504 human genomes. *Nature*, **2015**, 526, 75-81	50.4	1368
150	The origin and evolution of mutations in acute myeloid leukemia. *Cell*, **2012**, 150, 264-78	56.2	1143
149	DNA sequencing of a cytogenetically normal acute myeloid leukaemia genome. *Nature*, **2008**, 456, 66-72	50.4	1064
148	BreakDancer: an algorithm for high-resolution mapping of genomic structural variation. *Nature Methods*, **2009**, 6, 677-81	21.6	1062
147	Genome remodelling in a basal-like breast cancer metastasis and xenograft. *Nature*, **2010**, 464, 999-1005	50.4	935
146	VarScan: variant detection in massively parallel sequencing of individual and pooled samples. *Bioinformatics*, **2009**, 25, 2283-5	7.2	890
145	Genomic landscape of non-small cell lung cancer in smokers and never-smokers. *Cell*, **2012**, 150, 1121-34	56.2	860
144	Comprehensive Characterization of Cancer Driver Genes and Mutations. *Cell*, **2018**, 173, 371-385.e18	56.2	854
143	Mapping copy number variation by population-scale genome sequencing. *Nature*, **2011**, 470, 59-65	50.4	833
142	Whole-genome analysis informs breast cancer response to aromatase inhibition. *Nature*, **2012**, 486, 353-60	50.4	793
141	Clonal evolution in breast cancer revealed by single nucleus genome sequencing. *Nature*, **2014**, 512, 155-60	50.4	730
140	Clonal architecture of secondary acute myeloid leukemia. *New England Journal of Medicine*, **2012**, 366, 1090-8	59.2	582

139	SomaticSniper: identification of somatic point mutations in whole genome sequencing data. *Bioinformatics*, **2012**, 28, 311-7	7.2	425
138	CREST maps somatic structural variation in cancer genomes with base-pair resolution. *Nature Methods*, **2011**, 8, 652-4	21.6	396
137	Multi-platform discovery of haplotype-resolved structural variation in human genomes. *Nature Communications*, **2019**, 10, 1784	17.4	346
136	Pathogenic Germline Variants in 10,389 Adult Cancers. *Cell*, **2018**, 173, 355-370.e14	56.2	342
135	Driver Fusions and Their Implications in the Development and Treatment of Human Cancers. *Cell Reports*, **2018**, 23, 227-238.e3	10.6	235
134	Use of whole-genome sequencing to diagnose a cryptic fusion oncogene. *JAMA - Journal of the American Medical Association*, **2011**, 305, 1577-84	27.4	199
133	Ph-like acute lymphoblastic leukemia: a high-risk subtype in adults. *Blood*, **2017**, 129, 572-581	2.2	191
132	Comprehensive analysis of chromothripsis in 2,658 human cancers using whole-genome sequencing. *Nature Genetics*, **2020**, 52, 331-341	36.3	168
131	Background mutations in parental cells account for most of the genetic heterogeneity of induced pluripotent stem cells. *Cell Stem Cell*, **2012**, 10, 570-82	18	165
130	A decision support framework for genomically informed investigational cancer therapy. *Journal of the National Cancer Institute*, **2015**, 107,	9.7	135
129	Computational analysis and prediction of the binding motif and protein interacting partners of the Abl SH3 domain. *PLoS Computational Biology*, **2006**, 2, e1	5	129
128	Characterization of twenty-five ovarian tumour cell lines that phenocopy primary tumours. *Nature Communications*, **2015**, 6, 7419	17.4	125
127	Identification of a novel TP53 cancer susceptibility mutation through whole-genome sequencing of a patient with therapy-related AML. *JAMA - Journal of the American Medical Association*, **2011**, 305, 1568-76	27.4	125
126	Pan-cancer analysis of whole genomes identifies driver rearrangements promoted by LINE-1 retrotransposition. *Nature Genetics*, **2020**, 52, 306-319	36.3	122
125	Systematic Analysis of Splice-Site-Creating Mutations in Cancer. *Cell Reports*, **2018**, 23, 270-281.e3	10.6	121
124	Systematic Functional Annotation of Somatic Mutations in Cancer. *Cancer Cell*, **2018**, 33, 450-462.e10	24.3	114
123	Monovar: single-nucleotide variant detection in single cells. *Nature Methods*, **2016**, 13, 505-7	21.6	101
122	Identification of Variant-Specific Functions of PIK3CA by Rapid Phenotyping of Rare Mutations. *Cancer Research*, **2015**, 75, 5341-54	10.1	99

121	A robust benchmark for detection of germline large deletions and insertions. *Nature Biotechnology*, **2020**, 38, 1347-1355	44.5	98
120	Sequential Therapy with PARP and WEE1 Inhibitors Minimizes Toxicity while Maintaining Efficacy. *Cancer Cell*, **2019**, 35, 851-867.e7	24.3	94
119	BreakDancer: Identification of Genomic Structural Variation from Paired-End Read Mapping. *Current Protocols in Bioinformatics*, **2014**, 45, 15.6.1-11	24.2	89
118	Novel algorithmic approach predicts tumor mutation load and correlates with immunotherapy clinical outcomes using a defined gene mutation set. *BMC Medicine*, **2016**, 14, 168	11.4	87
117	SiFit: inferring tumor trees from single-cell sequencing data under finite-sites models. *Genome Biology*, **2017**, 18, 178	18.3	83
116	Sequencing a mouse acute promyelocytic leukemia genome reveals genetic events relevant for disease progression. *Journal of Clinical Investigation*, **2011**, 121, 1445-55	15.9	82
115	Clinical actionability enhanced through deep targeted sequencing of solid tumors. *Clinical Chemistry*, **2015**, 61, 544-53	5.5	76
114	CanDrA: cancer-specific driver missense mutation annotation with optimized features. *PLoS ONE*, **2013**, 8, e77945	3.7	76
113	Genetic Biomarkers Of Sensitivity and Resistance to Venetoclax Monotherapy in Patients With Relapsed Acute Myeloid Leukemia. *American Journal of Hematology*, **2018**, 93, E202	7.1	73
112	TIGRA: a targeted iterative graph routing assembler for breakpoint assembly. *Genome Research*, **2014**, 24, 310-7	9.7	69
111	Gene mutations in primary tumors and corresponding patient-derived xenografts derived from non-small cell lung cancer. *Cancer Letters*, **2015**, 357, 179-185	9.9	68
110	novoBreak: local assembly for breakpoint detection in cancer genomes. *Nature Methods*, **2017**, 14, 65-67	21.6	67
109	PolyScan: an automatic indel and SNP detection approach to the analysis of human resequencing data. *Genome Research*, **2007**, 17, 659-66	9.7	66
108	Prediction of binding affinities between the human amphiphysin-1 SH3 domain and its peptide ligands using homology modeling, molecular dynamics and molecular field analysis. *Journal of Proteome Research*, **2006**, 5, 32-43	5.6	65
107	Targeting a cytokine checkpoint enhances the fitness of armored cord blood CAR-NK cells. *Blood*, **2021**, 137, 624-636	2.2	60
106	Genome Modeling System: A Knowledge Management Platform for Genomics. *PLoS Computational Biology*, **2015**, 11, e1004274	5	59
105	Analysis of deletion breakpoints from 1,092 humans reveals details of mutation mechanisms. *Nature Communications*, **2015**, 6, 7256	17.4	56
104	RET fusion as a novel driver of medullary thyroid carcinoma. *Journal of Clinical Endocrinology and Metabolism*, **2015**, 100, 788-93	5.6	55

103	An Organismal CNV Mutator Phenotype Restricted to Early Human Development. *Cell*, **2017**, 168, 830-842.e7	56.2	53
102	BreakFusion: targeted assembly-based identification of gene fusions in whole transcriptome paired-end sequencing data. *Bioinformatics*, **2012**, 28, 1923-4	7.2	52
101	A survey of intragenic breakpoints in glioblastoma identifies a distinct subset associated with poor survival. *Genes and Development*, **2013**, 27, 1462-72	12.6	50
100	CMDS: a population-based method for identifying recurrent DNA copy number aberrations in cancer from high-resolution data. *Bioinformatics*, **2010**, 26, 464-9	7.2	49
99	Sarcomatoid Renal Cell Carcinoma Has a Distinct Molecular Pathogenesis, Driver Mutation Profile, and Transcriptional Landscape. *Clinical Cancer Research*, **2017**, 23, 6686-6696	12.9	48
98	Functional annotation of rare gene aberration drivers of pancreatic cancer. *Nature Communications*, **2016**, 7, 10500	17.4	47
97	Delineating copy number and clonal substructure in human tumors from single-cell transcriptomes. *Nature Biotechnology*, **2021**, 39, 599-608	44.5	47
96	Catalytic mTOR inhibitors can overcome intrinsic and acquired resistance to allosteric mTOR inhibitors. *Oncotarget*, **2014**, 5, 8544-57	3.3	46
95	Divergent viral presentation among human tumors and adjacent normal tissues. *Scientific Reports*, **2016**, 6, 28294	4.9	44
94	Single-nuclei RNA-seq on human retinal tissue provides improved transcriptome profiling. *Nature Communications*, **2019**, 10, 5743	17.4	44
93	TransVar: a multilevel variant annotator for precision genomics. *Nature Methods*, **2015**, 12, 1002-3	21.6	40
92	SiCloneFit: Bayesian inference of population structure, genotype, and phylogeny of tumor clones from single-cell genome sequencing data. *Genome Research*, **2019**, 29, 1847-1859	9.7	40
91	Relative Abundance of SARS-CoV-2 Entry Genes in the Enterocytes of the Lower Gastrointestinal Tract. *Genes*, **2020**, 11,	4.2	39
90	Ability to Generate Patient-Derived Breast Cancer Xenografts Is Enhanced in Chemoresistant Disease and Predicts Poor Patient Outcomes. *PLoS ONE*, **2015**, 10, e0136851	3.7	39
89	MET amplification in metastatic colorectal cancer: an acquired response to EGFR inhibition, not a de novo phenomenon. *Oncotarget*, **2016**, 7, 54627-54631	3.3	39
88	Massively parallel sequencing approaches for characterization of structural variation. *Methods in Molecular Biology*, **2012**, 838, 369-84	1.4	38
87	An expanded universe of cancer targets. *Cell*, **2021**, 184, 1142-1155	56.2	38
86	Comprehensive Genomic Profiling of Metastatic Squamous Cell Carcinoma of the Anal Canal. *Molecular Cancer Research*, **2017**, 15, 1542-1550	6.6	36

85	Implementation of biomarker-driven cancer therapy: existing tools and remaining gaps. *Discovery Medicine*, **2014**, 17, 101-14	2.5	35
84	The degree of intratumor mutational heterogeneity varies by primary tumor sub-site. *Oncotarget*, **2016**, 7, 27185-98	3.3	34
83	A robust benchmark for germline structural variant detection		34
82	Megabase Length Hypermutation Accompanies Human Structural Variation at 17p11.2. *Cell*, **2019**, 176, 1310-1324.e10	56.2	34
81	A Population of Heterogeneous Breast Cancer Patient-Derived Xenografts Demonstrate Broad Activity of PARP Inhibitor in BRCA1/2 Wild-Type Tumors. *Clinical Cancer Research*, **2017**, 23, 6468-6477	12.9	31
80	Bias from removing read duplication in ultra-deep sequencing experiments. *Bioinformatics*, **2014**, 30, 1073-1080	7.2	30
79	Single-cell dissection of intratumoral heterogeneity and lineage diversity in metastatic gastric adenocarcinoma. *Nature Medicine*, **2021**, 27, 141-151	50.5	30
78	Combining accurate tumor genome simulation with crowdsourcing to benchmark somatic structural variant detection. *Genome Biology*, **2018**, 19, 188	18.3	29
77	Functional consequence of the MET-T1010I polymorphism in breast cancer. *Oncotarget*, **2015**, 6, 2604-14	3.3	27
76	Multi-platform discovery of haplotype-resolved structural variation in human genomes		26
75	Distinct Biological Types of Ocular Adnexal Sebaceous Carcinoma: HPV-Driven and Virus-Negative Tumors Arise through Nonoverlapping Molecular-Genetic Alterations. *Clinical Cancer Research*, **2019**, 25, 1280-1290	12.9	24
74	Simultaneous recognition of words and prosody in the Boston University Radio Speech Corpus. *Speech Communication*, **2005**, 46, 418-439	2.8	23
73	Survival Outcomes by Mutation Status in Metastatic Breast Cancer. *JCO Precision Oncology*, **2018**, 2018,	3.6	23
72	Hotspot mutations delineating diverse mutational signatures and biological utilities across cancer types. *BMC Genomics*, **2016**, 17 Suppl 2, 394	4.5	21
71	HySA: a Hybrid Structural variant Assembly approach using next-generation and single-molecule sequencing technologies. *Genome Research*, **2017**, 27, 793-800	9.7	20
70	Targeted next generation sequencing of well-differentiated/dedifferentiated liposarcoma reveals novel gene amplifications and mutations. *Oncotarget*, **2018**, 9, 19891-19899	3.3	19
69	In vivo screening identifies GATAD2B as a metastasis driver in KRAS-driven lung cancer. *Nature Communications*, **2018**, 9, 2732	17.4	18
68	BreakTrans: uncovering the genomic architecture of gene fusions. *Genome Biology*, **2013**, 14, R87	18.3	18

67	Targeting the integrin/TGF- axis improves natural killer cell function against glioblastoma stem cells. *Journal of Clinical Investigation*, **2021**, 131,	15.9	17
66	Elevated Endogenous SDHA Drives Pathological Metabolism in Highly Metastatic Uveal Melanoma **2019**, 60, 4187-4195		15
65	Use of Targeted Next-Generation Sequencing to Identify Activating Hot Spot Mutations in Cherry Angiomas. *JAMA Dermatology*, **2019**, 155, 211-215	5.1	15
64	GenomeVIP: a cloud platform for genomic variant discovery and interpretation. *Genome Research*, **2017**, 27, 1450-1459	9.7	14
63	Untying the gordion knot of targeting MET in cancer. *Cancer Treatment Reviews*, **2018**, 66, 95-103	14.4	14
62	Hybrid oncocytic/chromophobe renal tumors are molecularly distinct from oncocytoma and chromophobe renal cell carcinoma. *Modern Pathology*, **2019**, 32, 1698-1707	9.8	14
61	Validation of Amplification as a Predictive Biomarker for Anti-Epidermal Growth Factor Receptor Antibody Therapy in Metastatic Colorectal Cancer.. *JCO Precision Oncology*, **2019**, 3, 1-13	3.6	14
60	SCMarker: Ab initio marker selection for single cell transcriptome profiling. *PLoS Computational Biology*, **2019**, 15, e1007445	5	13
59	Dynamic clonal remodelling in breast cancer metastases is associated with subtype conversion. *European Journal of Cancer*, **2019**, 120, 54-64	7.5	13
58	Adaptive responses in a PARP inhibitor window of opportunity trial illustrate limited functional interlesional heterogeneity and potential combination therapy options. *Oncotarget*, **2019**, 10, 3533-3546	3.3	12
57	A feasibility study of returning clinically actionable somatic genomic alterations identified in a research laboratory. *Oncotarget*, **2017**, 8, 41806-41814	3.3	12
56	A novel immature natural killer cell subpopulation predicts relapse after cord blood transplantation. *Blood Advances*, **2019**, 3, 4117-4130	7.8	12
55	Computational approaches for inferring tumor evolution from single-cell genomic data. *Current Opinion in Systems Biology*, **2018**, 7, 16-25	3.2	12
54	Genotyping tumor clones from single-cell data. *Nature Methods*, **2016**, 13, 555-6	21.6	11
53	An automatic prosody labeling system using ANN-based syntactic-prosodic model and GMM-based acoustic-prosodic model		11
52	Pan-cancer analysis of whole genomes reveals driver rearrangements promoted by LINE-1 retrotransposition in human tumours		10
51	Retrospective evaluation of whole exome and genome mutation calls in 746 cancer samples. *Nature Communications*, **2020**, 11, 4748	17.4	10
50	ClinSeK: a targeted variant characterization framework for clinical sequencing. *Genome Medicine*, **2015**, 7, 34	14.4	9

49	Cancer driver mutation prediction through Bayesian integration of multi-omic data. *PLoS ONE*, **2018**, 13, e0196939	3.7	8
48	Genomic analysis of exceptional responder to regorafenib in treatment-refractory metastatic rectal cancer: a case report and review of the literature. *Oncotarget*, **2017**, 8, 57882-57888	3.3	8
47	Generation of glucocorticoid-resistant SARS-CoV-2 T cells for adoptive cell therapy. *Cell Reports*, **2021**, 36, 109432	10.6	8
46	Variants with a low allele frequency detected in genomic DNA affect the accuracy of mutation detection in cell-free DNA by next-generation sequencing. *Cancer*, **2018**, 124, 1061-1069	6.4	8
45	Hypervirulent group A Streptococcus emergence in an acaspular background is associated with marked remodeling of the bacterial cell surface. *PLoS ONE*, **2018**, 13, e0207897	3.7	8
44	Oxidative Phosphorylation Is a Metabolic Vulnerability in Chemotherapy-Resistant Triple-Negative Breast Cancer. *Cancer Research*, **2021**, 81, 5572-5581	10.1	8
43	Prospective Clinical Sequencing of Adult Glioma. *Molecular Cancer Therapeutics*, **2019**, 18, 991-1000	6.1	7
42	Towards accurate characterization of clonal heterogeneity based on structural variation. *BMC Bioinformatics*, **2014**, 15, 299	3.6	7
41	Combining AFM13, a Bispecific CD30/CD16 Antibody, with Cytokine-Activated Blood and Cord Blood-Derived NK Cells Facilitates CAR-like Responses Against CD30 Malignancies. *Clinical Cancer Research*, **2021**, 27, 3744-3756	12.9	7
40	Ploidy-Seq: inferring mutational chronology by sequencing polyploid tumor subpopulations. *Genome Medicine*, **2015**, 7, 6	14.4	6
39	Latent periodic process inference from single-cell RNA-seq data. *Nature Communications*, **2020**, 11, 1441	17.4	6
38	Single-cell RNA-seq analysis reveals compartment-specific heterogeneity and plasticity of microglia. *IScience*, **2021**, 24, 102186	6.1	6
37	GMP-Compliant Universal Antigen Presenting Cells (uAPC) Promote the Metabolic Fitness and Antitumor Activity of Armored Cord Blood CAR-NK Cells. *Frontiers in Immunology*, **2021**, 12, 626098	8.4	6
36	BreakPoint Surveyor: a pipeline for structural variant visualization. *Bioinformatics*, **2017**, 33, 3121-3122	7.2	5
35	Comparison of different functional prediction scores using a gene-based permutation model for identifying cancer driver genes. *BMC Medical Genomics*, **2019**, 12, 22	3.7	4
34	Integrated transcriptomic-genomic tool Texomer profiles cancer tissues. *Nature Methods*, **2019**, 16, 401-404	26.6	4
33	SiCloneFit: Bayesian inference of population structure, genotype,and phylogeny of tumor clones from single-cell genome sequencing data		4
32	Single-cell manifold-preserving feature selection for detecting rare cell populations. *Nature Computational Science*, **2021**, 1, 374-384		4

31	Computational Prediction of Genetic Drivers in Cancer **2016**, 1-16		4
30	Expanded analysis of secondary germline findings from matched tumor/normal sequencing identifies additional clinically significant mutations. *JCO Precision Oncology*, **2019**, 3,	3.6	4
29	Structural Variant Breakpoint Detection with novoBreak. *Methods in Molecular Biology*, **2018**, 1833, 129-141	1.4	3
28	Whole Genome Sequencing in Cancer Clinics. *EBioMedicine*, **2015**, 2, 15-6	8.8	3
27	Inhibition of the v integrin-TGF- axis improves natural killer cell function against glioblastoma stem cells		3
26	Metabolic Reprogramming of GMP Grade Cord Tissue Derived Mesenchymal Stem Cells Enhances Their Suppressive Potential in GVHD. *Frontiers in Immunology*, **2021**, 12, 631353	8.4	3
25	MEDALT: single-cell copy number lineage tracing enabling gene discovery. *Genome Biology*, **2021**, 22, 70	18.3	3
24	Clinical and Molecular Characterization of Mutations as Predictive Biomarkers of Response to Immune Checkpoint Inhibitors in Advanced Cancers.. *JCO Precision Oncology*, **2022**, 6, e2100267	3.6	2
23	Genomic alterations driving breast cancer (BC) metastases and their relationship with the subtype switch in the GEICAM ConvertHER study.. *Journal of Clinical Oncology*, **2017**, 35, 1017-1017	2.2	2
22	Stratified Test Alleviates Batch Effects in Single-Cell Data. *Lecture Notes in Computer Science*, **2020**, 167-177	0.7	2
21	Sensei: How many samples to tell evolution in single-cell studies?		2
20	Ab initio spillover compensation in mass cytometry data. *Cytometry Part A: the Journal of the International Society for Analytical Cytology*, **2021**, 99, 899-909	4.6	2
19	Spatially interacting phosphorylation sites and mutations in cancer. *Nature Communications*, **2021**, 12, 2313	17.4	2
18	Spatial drivers and pre-cancer populations collaborate with the microenvironment in untreated and chemo-resistant pancreatic cancer		2
17	Bi-order multimodal integration of single-cell data.. *Genome Biology*, **2022**, 23, 112	18.3	2
16	Active Disclosure of Secondary Germline Findings to Deceased Research ParticipantsTPersonal Representatives: Process and Outcomes. *JCO Precision Oncology*, **2017**, 1,	3.6	1
15	Targeting Polo-like Kinase 4 Triggers Polyploidy and Apoptotic Cell Death in TP53-Mutant Acute Myeloid Leukemia. *Blood*, **2021**, 138, 1167-1167	2.2	1
14	Sensei: how many samples to tell a change in cell type abundance?. *BMC Bioinformatics*, **2022**, 23, 2	3.6	1

13	Combining accurate tumour genome simulation with crowd-sourcing to benchmark somatic structural variant detection		1
12	HySA: A Hybrid Structural variant Assembly approach using next generation and single-molecule sequencing technologies		1
11	SiFit: A Method for Inferring Tumor Trees from Single-Cell Sequencing Data under Finite-site Models		1
10	Genomic, Transcriptomic, and Proteomic Profiling of Metastatic Breast Cancer. *Clinical Cancer Research*, **2021**, 27, 3243-3252	12.9	1
9	Extended live-cell barcoding approach for multiplexed mass cytometry. *Scientific Reports*, **2021**, 11, 12388	4.9	1
8	Spatially resolved transcriptomics of high-grade serous ovarian carcinoma.. *IScience*, **2022**, 25, 103923	6.1	1
7	Comments on the model parameters in "SiFit: inferring tumor trees from single-cell sequencing data under finite-sites models". *Genome Biology*, **2019**, 20, 95	18.3	0
6	Metachronous Medulloblastoma in a Child With Successfully Treated Neuroblastoma: Case Report and Novel Findings of DNA Sequencing. *Journal of the National Comprehensive Cancer Network: JNCCN*, **2018**, 16, 683-691	7.3	0
5	Response to Hypomethylating Agents in Myelodysplastic Syndrome Is Associated With Emergence of Novel TCR Clonotypes. *Frontiers in Immunology*, **2021**, 12, 659625	8.4	0
4	Uncoupling of gene expression from copy number presents therapeutic opportunities in aneuploid cancers. *Cell Reports Medicine*, **2021**, 2, 100349	18	0
3	Stratified Test Accurately Identifies Differentially Expressed Genes Under Batch Effects in Single-Cell Data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, **2021**, 18, 2072-2079	3	0
2	Decoupling Lineage-Associated Genes in Acute Myeloid Leukemia Reveals Inflammatory and Metabolic Signatures Associated With Outcomes. *Frontiers in Oncology*, **2021**, 11, 705627	5.3	0
1	Whole genome sequencing to characterize luminal-type breast cancer.. *Journal of Clinical Oncology*, **2012**, 30, 503-503	2.2	