Peter J Campbell

List of Publications by Year
in descending order

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164 papers	79,256 citations	2565 99 h-index	6024 165 g-index
208 all docs	208 docs citations	208 times ranked	81804 citing authors

#	Article	IF	Citations
1	Life histories of myeloproliferative neoplasms inferred from phylogenies. Nature, 2022, 602, 162-168.	13.7	140
2	The eternal quest for self-improvement of somatic cells. Cell Genomics, 2022, 2, 100094.	3.0	0
3	Bayesian networks elucidate complex genomic landscapes in cancer. Communications Biology, 2022, 5, 306.	2.0	5
4	Somatic mutation rates scale with lifespan across mammals. Nature, 2022, 604, 517-524.	13.7	211
5	Mutational landscape of normal epithelial cells in Lynch Syndrome patients. Nature Communications, 2022, 13, 2710.	5.8	19
6	The longitudinal dynamics and natural history of clonal haematopoiesis. Nature, 2022, 606, 335-342.	13.7	136
7	Clonal dynamics of haematopoiesis across the human lifespan. Nature, 2022, 606, 343-350.	13.7	160
8	Acetyl-CoA metabolism drives epigenome change and contributes to carcinogenesis risk in fatty liver disease. Genome Medicine, 2022, 14, .	3.6	12
9	Estimation of tumor cell total mRNA expression in 15 cancer types predicts disease progression. Nature Biotechnology, 2022, 40, 1624-1633.	9.4	31
10	Inherited MUTYH mutations cause elevated somatic mutation rates and distinctive mutational signatures in normal human cells. Nature Communications, 2022, 13, .	5.8	30
11	Interrogating breast cancer heterogeneity using single and pooled circulating tumor cell analysis. Npj Breast Cancer, 2022, 8, .	2.3	8
12	Reliable detection of somatic mutations in solid tissues by laser-capture microdissection and low-input DNA sequencing. Nature Protocols, 2021, 16, 841-871.	5.5	82
13	Chromothripsis drives the evolution of gene amplification in cancer. Nature, 2021, 591, 137-141.	13.7	228
14	Development, maturation, and maintenance of human prostate inferred from somatic mutations. Cell Stem Cell, 2021, 28, 1262-1274.e5.	5.2	29
15	Whole-genome sequencing reveals progressive versus stable myeloma precursor conditions as two distinct entities. Nature Communications, 2021, 12, 1861.	5.8	68
16	Inherent mosaicism and extensive mutation of human placentas. Nature, 2021, 592, 80-85.	13.7	126
17	Somatic mutation landscapes at single-molecule resolution. Nature, 2021, 593, 405-410.	13.7	254
18	Protection of the C. elegans germ cell genome depends on diverse DNA repair pathways during normal proliferation. PLoS ONE, 2021, 16, e0250291.	1.1	18

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19	Characterizing genetic intra-tumor heterogeneity across 2,658 human cancer genomes. Cell, 2021, 184, 2239-2254.e39.	13.5	260
20	Lineage tracing of human development through somatic mutations. Nature, 2021, 595, 85-90.	13.7	79
21	Extensive phylogenies of human development inferred from somatic mutations. Nature, 2021, 597, 387-392.	13.7	87
22	The mutational landscape of human somatic and germline cells. Nature, 2021, 597, 381-386.	13.7	180
23	Increased somatic mutation burdens in normal human cells due to defective DNA polymerases. Nature Genetics, 2021, 53, 1434-1442.	9.4	85
24	<i>CDKN2A</i> deletion is a frequent event associated with poor outcome in patients with peripheral T-cell lymphoma not otherwise specified (PTCL-NOS). Haematologica, 2021, 106, 2918-2926.	1.7	18
25	Convergent somatic mutations in metabolism genes in chronic liver disease. Nature, 2021, 598, 473-478.	13.7	87
26	C. elegans genome-wide analysis reveals DNA repair pathways that act cooperatively to preserve genome integrity upon ionizing radiation. PLoS ONE, 2021, 16, e0258269.	1.1	0
27	Aberrant integration of Hepatitis B virus DNA promotes major restructuring of human hepatocellular carcinoma genome architecture. Nature Communications, 2021, 12, 6910.	5.8	27
28	The mutational signature profile of known and suspected human carcinogens in mice. Nature Genetics, 2020, 52, 1189-1197.	9.4	84
29	Framework for quality assessment of whole genome cancer sequences. Nature Communications, 2020, 11, 5040.	5.8	5
30	Somatic mutation distributions in cancer genomes vary with three-dimensional chromatin structure. Nature Genetics, 2020, 52, 1178-1188.	9.4	79
31	Somatic Evolution in Non-neoplastic IBD-Affected Colon. Cell, 2020, 182, 672-684.e11.	13.5	122
32	Tissue-Biased Expansion of DNMT3A-Mutant Clones in a Mosaic Individual Is Associated with Conserved Epigenetic Erosion. Cell Stem Cell, 2020, 27, 326-335.e4.	5.2	25
33	Immune Surveillance in Clinical Regression of Preinvasive Squamous Cell Lung Cancer. Cancer Discovery, 2020, 10, 1489-1499.	7.7	60
34	APOBEC3-dependent kataegis and TREX1-driven chromothripsis during telomere crisis. Nature Genetics, 2020, 52, 884-890.	9.4	106
35	Pervasive chromosomal instability and karyotype order in tumour evolution. Nature, 2020, 587, 126-132.	13.7	221
36	Multi-site clonality analysis uncovers pervasive heterogeneity across melanoma metastases. Nature Communications, 2020, 11, 4306.	5.8	26

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37	Revealing the Impact of Structural Variants in Multiple Myeloma. Blood Cancer Discovery, 2020, 1, 258-273.	2.6	81
38	IgCaller for reconstructing immunoglobulin gene rearrangements and oncogenic translocations from whole-genome sequencing in lymphoid neoplasms. Nature Communications, 2020, 11, 3390.	5.8	24
39	Transcription phenotypes of pancreatic cancer are driven by genomic events during tumor evolution. Nature Genetics, 2020, 52, 231-240.	9.4	365
40	Tobacco smoking and somatic mutations in human bronchial epithelium. Nature, 2020, 578, 266-272.	13.7	336
41	Patterns of somatic structural variation in human cancer genomes. Nature, 2020, 578, 112-121.	13.7	560
42	Analyses of non-coding somatic drivers in 2,658Âcancer whole genomes. Nature, 2020, 578, 102-111.	13.7	424
43	Pan-cancer analysis of whole genomes identifies driver rearrangements promoted by LINE-1 retrotransposition. Nature Genetics, 2020, 52, 306-319.	9.4	275
44	Disruption of chromatin folding domains by somatic genomic rearrangements in human cancer. Nature Genetics, 2020, 52, 294-305.	9.4	180
45	Comprehensive analysis of chromothripsis in 2,658 human cancers using whole-genome sequencing. Nature Genetics, 2020, 52, 331-341.	9.4	431
46	Mutational signatures are jointly shaped by DNA damage and repair. Nature Communications, 2020, 11, 2169.	5.8	137
47	Timing the initiation of multiple myeloma. Nature Communications, 2020, 11, 1917.	5.8	99
48	The mutational landscape of normal human endometrial epithelium. Nature, 2020, 580, 640-646.	13.7	338
49	Comprehensive molecular characterization of mitochondrial genomes in human cancers. Nature Genetics, 2020, 52, 342-352.	9.4	256
50	Extensive heterogeneity in somatic mutation and selection in the human bladder. Science, 2020, 370, 75-82.	6.0	195
51	A practical guide for mutational signature analysis in hematological malignancies. Nature Communications, 2019, 10, 2969.	5.8	145
52	Genomic landscape and chronological reconstruction of driver events in multiple myeloma. Nature Communications, 2019, 10, 3835.	5.8	183
53	Deciphering the genomic, epigenomic, and transcriptomic landscapes of pre-invasive lung cancer lesions. Nature Medicine, 2019, 25, 517-525.	15.2	178
54	Undifferentiated Sarcomas Develop through Distinct Evolutionary Pathways. Cancer Cell, 2019, 35, 441-456.e8.	7.7	82

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55	Characterizing Mutational Signatures in Human Cancer Cell Lines Reveals Episodic APOBEC Mutagenesis. Cell, 2019, 176, 1282-1294.e20.	13.5	298
56	Chromosome segregation errors generate a diverse spectrum of simple and complex genomic rearrangements. Nature Genetics, 2019, 51, 705-715.	9.4	145
57	Embryonal precursors of Wilms tumor. Science, 2019, 366, 1247-1251.	6.0	101
58	Somatic mutations and clonal dynamics in healthy and cirrhotic human liver. Nature, 2019, 574, 538-542.	13.7	251
59	The landscape of somatic mutation in normal colorectal epithelial cells. Nature, 2019, 574, 532-537.	13.7	468
60	Genome Sequencing during a Patientâ€™s Journey through Cancer. New England Journal of Medicine, 2019, 381, 2145-2156.	13.9	50
61	COSMIC: the Catalogue Of Somatic Mutations In Cancer. Nucleic Acids Research, 2019, 47, D941-D947.	6.5	3,196
62	Recurrent histone mutations in Tâ€cell acute lymphoblastic leukaemia. British Journal of Haematology, 2019, 184, 676-679.	1.2	7
63	Mutational signatures of DNA mismatch repair deficiency in C. elegans and human cancers. Genome Research, 2018, 28, 666-675.	2.4	112
64	Intra-tumour diversification in colorectal cancer at the single-cell level. Nature, 2018, 556, 457-462.	13.7	406
65	Timing the Landmark Events in the Evolution of Clear Cell Renal Cell Cancer: TRACERx Renal. Cell, 2018, 173, 611-623.e17.	13.5	398
66	Deterministic Evolutionary Trajectories Influence Primary Tumor Growth: TRACERx Renal. Cell, 2018, 173, 595-610.e11.	13.5	472
67	A Distinct Class of Genome Rearrangements Driven by Heterologous Recombination. Molecular Cell, 2018, 69, 292-305.e6.	4.5	33
68	SvABA: genome-wide detection of structural variants and indels by local assembly. Genome Research, 2018, 28, 581-591.	2.4	288
69	Hydroxycarbamide Plus Aspirin Versus Aspirin Alone in Patients With Essential Thrombocythemia Age 40 to 59 Years Without High-Risk Features. Journal of Clinical Oncology, 2018, 36, 3361-3369.	0.8	54
70	Classification and Personalized Prognosis in Myeloproliferative Neoplasms. New England Journal of Medicine, 2018, 379, 1416-1430.	13.9	442
71	Integrative Molecular Characterization of Malignant Pleural Mesothelioma. Cancer Discovery, 2018, 8, 1548-1565.	7.7	422
72	Somatic mutant clones colonize the human esophagus with age. Science, 2018, 362, 911-917.	6.0	805

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73	Population dynamics of normal human blood inferred from somatic mutations. Nature, 2018, 561, 473-478.	13.7	427
74	Rearrangement bursts generate canonical gene fusions in bone and soft tissue tumors. Science, 2018, 361, .	6.0	121
75	Analysis of the genomic landscape of multiple myeloma highlights novel prognostic markers and disease subgroups. Leukemia, 2018, 32, 2604-2616.	3.3	137
76	Prediction of acute myeloid leukaemia risk in healthy individuals. Nature, 2018, 559, 400-404.	13.7	617
77	Genomic patterns of progression in smoldering multiple myeloma. Nature Communications, 2018, 9, 3363.	5.8	163
78	Recurrent intragenic rearrangements of EGFR and BRAF in soft tissue tumors of infants. Nature Communications, 2018, 9, 2378.	5.8	72
79	A somatic-mutational process recurrently duplicates germline susceptibility loci and tissue-specific super-enhancers in breast cancers. Nature Genetics, 2017, 49, 341-348.	9.4	75
80	COSMIC: somatic cancer genetics at high-resolution. Nucleic Acids Research, 2017, 45, D777-D783.	6.5	1,692
81	Precision oncology for acute myeloid leukemia using a knowledge bank approach. Nature Genetics, 2017, 49, 332-340.	9.4	229
82	HRDetect is a predictor of BRCA1 and BRCA2 deficiency based on mutational signatures. Nature Medicine, 2017, 23, 517-525.	15.2	769
83	Somatic mutations reveal asymmetric cellular dynamics in the early human embryo. Nature, 2017, 543, 714-718.	13.7	229
84	Pan-cancer analysis of homozygous deletions in primary tumours uncovers rare tumour suppressors. Nature Communications, 2017, 8, 1221.	5.8	75
85	The driver landscape of sporadic chordoma. Nature Communications, 2017, 8, 890.	5.8	115
86	Universal Patterns of Selection in Cancer and Somatic Tissues. Cell, 2017, 171, 1029-1041.e21.	13.5	1,085
87	Integrative Genomics Identifies the Molecular Basis of Resistance to Azacitidine Therapy in Myelodysplastic Syndromes. Cell Reports, 2017, 20, 572-585.	2.9	99
88	Genomic Evolution of Breast Cancer Metastasis and Relapse. Cancer Cell, 2017, 32, 169-184.e7.	7.7	534
89	Cliques and Schisms of Cancer Genes. Cancer Cell, 2017, 32, 129-130.	7.7	6
90	The Human Cell Atlas. ELife, 2017, 6, .	2.8	1,547

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91	cgpCaVEManWrapper: Simple Execution of CaVEMan in Order to Detect Somatic Single Nucleotide Variants in NGS Data. Current Protocols in Bioinformatics, 2016, 56, 15.10.1-15.10.18.	25.8	155
92	ascatNgs: Identifying Somatically Acquired Copyâ€Number Alterations from Wholeâ€Genome Sequencing Data. Current Protocols in Bioinformatics, 2016, 56, 15.9.1-15.9.17.	25.8	111
93	Landscape of somatic mutations in 560 breast cancer whole-genome sequences. Nature, 2016, 534, 47-54.	13.7	1,760
94	A renewed model of pancreatic cancer evolution based on genomic rearrangement patterns. Nature, 2016, 538, 378-382.	13.7	418
95	Direct Transcriptional Consequences of Somatic Mutation in Breast Cancer. Cell Reports, 2016, 16, 2032-2046.	2.9	36
96	The topography of mutational processes in breast cancer genomes. Nature Communications, 2016, 7, 11383.	5.8	235
97	Mutational signatures of ionizing radiation in second malignancies. Nature Communications, 2016, 7, 12605.	5.8	214
98	Mutational signatures associated with tobacco smoking in human cancer. Science, 2016, 354, 618-622.	6.0	842
99	Genomic Classification and Prognosis in Acute Myeloid Leukemia. New England Journal of Medicine, 2016, 374, 2209-2221.	13.9	3,067
100	Constrained positive selection on cancer mutations in normal skin. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E1128-9.	3.3	23
101	DNMT3A mutations occur early or late in patients with myeloproliferative neoplasms and mutation order influences phenotype. Haematologica, 2015, 100, e438-e442.	1.7	105
102	cgpPindel: Identifying Somatically Acquired Insertion and Deletion Events from Paired End Sequencing. Current Protocols in Bioinformatics, 2015, 52, 15.7.1-15.7.12.	25.8	104
103	VAGrENT: Variation Annotation Generator. Current Protocols in Bioinformatics, 2015, 52, 15.8.1-15.8.11.	25.8	15
104	High burden and pervasive positive selection of somatic mutations in normal human skin. Science, 2015, 348, 880-886.	6.0	1,431
105	A comprehensive assessment of somatic mutation detection in cancer using whole-genome sequencing. Nature Communications, 2015, 6, 10001.	5.8	266
106	Chromothripsis and Kataegis Induced by Telomere Crisis. Cell, 2015, 163, 1641-1654.	13.5	541
107	Effect of Mutation Order on Myeloproliferative Neoplasms. New England Journal of Medicine, 2015, 372, 601-612.	13.9	467
108	Combined hereditary and somatic mutations of replication error repair genes result in rapid onset of ultra-hypermutated cancers. Nature Genetics, 2015, 47, 257-262.	9.4	306

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109	Subclonal diversification of primary breast cancer revealed by multiregion sequencing. Nature Medicine, 2015, 21, 751-759.	15.2	711
110	Frequent somatic transfer of mitochondrial DNA into the nuclear genome of human cancer cells. Genome Research, 2015, 25, 814-824.	2.4	69
111	Analysis of the genetic phylogeny of multifocal prostate cancer identifies multiple independent clonal expansions in neoplastic and morphologically normal prostate tissue. Nature Genetics, 2015, 47, 367-372.	9.4	380
112	The evolutionary history of lethal metastatic prostate cancer. Nature, 2015, 520, 353-357.	13.7	1,185
113	Somatic mutation in cancer and normal cells. Science, 2015, 349, 1483-1489.	6.0	996
114	COSMIC: exploring the world's knowledge of somatic mutations in human cancer. Nucleic Acids Research, 2015, 43, D805-D811.	6.5	2,096
115	Clock-like mutational processes in human somatic cells. Nature Genetics, 2015, 47, 1402-1407.	9.4	837
116	Origins and functional consequences of somatic mitochondrial DNA mutations in human cancer. ELife, 2014, 3, .	2.8	318
117	Processed pseudogenes acquired somatically during cancer development. Nature Communications, 2014, 5, 3644.	5.8	86
118	C. elegans whole-genome sequencing reveals mutational signatures related to carcinogens and DNA repair deficiency. Genome Research, 2014, 24, 1624-1636.	2.4	164
119	Subclonal variant calling with multiple samples and prior knowledge. Bioinformatics, 2014, 30, 1198-1204.	1.8	122
120	Constitutional and somatic rearrangement of chromosome 21 in acute lymphoblastic leukaemia. Nature, 2014, 508, 98-102.	13.7	261
121	Heterogeneity of genomic evolution and mutational profiles in multiple myeloma. Nature Communications, 2014, 5, 2997.	5.8	741
122	RAG-mediated recombination is the predominant driver of oncogenic rearrangement in ETV6-RUNX1 acute lymphoblastic leukemia. Nature Genetics, 2014, 46, 116-125.	9.4	313
123	Inactivating CUX1 mutations promote tumorigenesis. Nature Genetics, 2014, 46, 33-38.	9.4	111
124	Genomic catastrophes frequently arise in esophageal adenocarcinoma and drive tumorigenesis. Nature Communications, 2014, 5, 5224.	5.8	236
125	Extensive transduction of nonrepetitive DNA mediated by L1 retrotransposition in cancer genomes. Science, 2014, 345, 1251343.	6.0	348
126	Spatial and temporal diversity in genomic instability processes defines lung cancer evolution. Science, 2014, 346, 251-256.	6.0	962

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127	Genome sequencing of normal cells reveals developmental lineages and mutational processes. Nature, 2014, 513, 422-425.	13.7	315
128	Differential and limited expression of mutant alleles in multiple myeloma. Blood, 2014, 124, 3110-3117.	0.6	54
129	Signatures of mutational processes in human cancer. Nature, 2013, 500, 415-421.	13.7	8,060
130	Deciphering Signatures of Mutational Processes Operative in Human Cancer. Cell Reports, 2013, 3, 246-259.	2.9	1,087
131	Clinical and biological implications of driver mutations in myelodysplastic syndromes. Blood, 2013, 122, 3616-3627.	0.6	1,562
132	Criteria for Inference of Chromothripsis in Cancer Genomes. Cell, 2013, 152, 1226-1236.	13.5	457
133	The Genomic Landscape of Myeloproliferative Neoplasms: Somatic Calr Mutations in the Majority of JAK2-Wildtype Patients. Blood, 2013, 122, LBA-2-LBA-2.	0.6	1
134	Next-generation sequencing in breast cancer. Current Opinion in Oncology, 2012, 24, 597-604.	1.1	76
135	Estimation of rearrangement phylogeny for cancer genomes. Genome Research, 2012, 22, 346-361.	2.4	108
136	JAK2V617F homozygosity arises commonly and recurrently in PV and ET, but PV is characterized by expansion of a dominant homozygous subclone. Blood, 2012, 120, 2704-2707.	0.6	94
137	Telomeres and Cancer: From Crisis to Stability to Crisis to Stability. Cell, 2012, 148, 633-635.	13.5	25
138	Evolution of the cancer genome. Nature Reviews Genetics, 2012, 13, 795-806.	7.7	532
139	Circulating DNA and Next-Generation Sequencing. Recent Results in Cancer Research, 2012, 195, 143-149.	1.8	11
140	The landscape of cancer genes and mutational processes in breast cancer. Nature, 2012, 486, 400-404.	13.7	1,535
141	Mutational Processes Molding the Genomes of 21 Breast Cancers. Cell, 2012, 149, 979-993.	13.5	1,673
142	The Life History of 21 Breast Cancers. Cell, 2012, 149, 994-1007.	13.5	1,249
143	Tandem duplication of chromosomal segments is common in ovarian and breast cancer genomes. Journal of Pathology, 2012, 227, 446-455.	2.1	81
144	Whole-genome sequencing identifies recurrent mutations in chronic lymphocytic leukaemia. Nature, 2011, 475, 101-105.	13.7	1,364

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145	Massive Genomic Rearrangement Acquired in a Single Catastrophic Event during Cancer Development. Cell, 2011, 144, 27-40.	13.5	2,020
146	Response: essential thrombocythemia: seeing the wood for the trees. Blood, 2011, 118, 1180-1181.	0.6	0
147	Exome sequencing identifies frequent mutation of the SWI/SNF complex gene PBRM1 in renal carcinoma. Nature, 2011, 469, 539-542.	13.7	1,127
148	Use of cancerâ€specific genomic rearrangements to quantify disease burden in plasma from patients with solid tumors. Genes Chromosomes and Cancer, 2010, 49, 1062-1069.	1.5	172
149	A small-cell lung cancer genome with complex signatures of tobacco exposure. Nature, 2010, 463, 184-190.	13.7	972
150	A comprehensive catalogue of somatic mutations from a human cancer genome. Nature, 2010, 463, 191-196.	13.7	1,519
151	Systematic sequencing of renal carcinoma reveals inactivation of histone modifying genes. Nature, 2010, 463, 360-363.	13.7	1,062
152	The patterns and dynamics of genomic instability in metastatic pancreatic cancer. Nature, 2010, 467, 1109-1113.	13.7	1,200
153	The JAK2 46/1 haplotype predisposes to MPL-mutated myeloproliferative neoplasms. Blood, 2010, 115, 4517-4523.	0.6	93
154	Reticulin Accumulation in Essential Thrombocythemia: Prognostic Significance and Relationship to Therapy. Journal of Clinical Oncology, 2009, 27, 2991-2999.	0.8	116
155	The cancer genome. Nature, 2009, 458, 719-724.	13.7	2,904
156	Complex landscapes of somatic rearrangement in human breast cancer genomes. Nature, 2009, 462, 1005-1010.	13.7	776
157	Somatic and germline genetics at the JAK2 locus. Nature Genetics, 2009, 41, 385-386.	9.4	52
158	Identification of somatically acquired rearrangements in cancer using genome-wide massively parallel paired-end sequencing. Nature Genetics, 2008, 40, 722-729.	9.4	736
159	Subclonal phylogenetic structures in cancer revealed by ultra-deep sequencing. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 13081-13086.	3.3	320
160	Architectures of somatic genomic rearrangement in human cancer amplicons at sequence-level resolution. Genome Research, 2007, 17, 1296-1303.	2.4	180
161	Patterns of somatic mutation in human cancer genomes. Nature, 2007, 446, 153-158.	13.7	2,802
162	Chromosomally unstable mouse tumours have genomic alterations similar to diverse human cancers. Nature, 2007, 447, 966-971.	13.7	355

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163	The Myeloproliferative Disorders. New England Journal of Medicine, 2006, 355, 2452-2466.	13.9	619
164	Management of Polycythemia Vera and Essential Thrombocythemia. Hematology American Society of Hematology Education Program, 2005, 2005, 201-208.	0.9	45