

David Reich

List of Publications by Year in descending order

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Version: 2024-02-01

154
papers

55,299
citations

8181

76
h-index

6654

156
g-index

187
all docs

187
docs citations

187
times ranked

44614
citing authors

#	ARTICLE	IF	CITATIONS
1	A high-resolution picture of kinship practices in an Early Neolithic tomb. <i>Nature</i> , 2022, 601, 584-587.	27.8	65
2	Large-scale migration into Britain during the Middle to Late Bronze Age. <i>Nature</i> , 2022, 601, 588-594.	27.8	86
3	Ancient DNA and deep population structure in sub-Saharan African foragers. <i>Nature</i> , 2022, 603, 290-296.	27.8	51
4	A unified genealogy of modern and ancient genomes. <i>Science</i> , 2022, 375, eabi8264.	12.6	59
5	Indian genetic heritage in Southeast Asian populations. <i>PLoS Genetics</i> , 2022, 18, e1010036.	3.5	19
6	South-to-north migration preceded the advent of intensive farming in the Maya region. <i>Nature Communications</i> , 2022, 13, 1530.	12.8	21
7	An integrative skeletal and paleogenomic analysis of stature variation suggests relatively reduced health for early European farmers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2106743119.	7.1	21
8	Ancient genomes reveal origin and rapid trans-Eurasian migration of 7th century Avar elites. <i>Cell</i> , 2022, 185, 1402-1413.e21.	28.9	26
9	Stone Age <i>Yersinia pestis</i> genomes shed light on the early evolution, diversity, and ecology of plague. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2116722119.	7.1	31
10	Ancient DNA reveals five streams of migration into Micronesia and matrilocality in early Pacific seafarers. <i>Science</i> , 2022, 377, 72-79.	12.6	13
11	A genetic history of the pre-contact Caribbean. <i>Nature</i> , 2021, 590, 103-110.	27.8	67
12	Assessing the performance of qpAdm: a statistical tool for studying population admixture. <i>Genetics</i> , 2021, 217, .	2.9	84
13	A minimally destructive protocol for DNA extraction from ancient teeth. <i>Genome Research</i> , 2021, 31, 472-483.	5.5	31
14	Genomic insights into the formation of human populations in East Asia. <i>Nature</i> , 2021, 591, 413-419.	27.8	216
15	Genome-wide analysis of nearly all the victims of a 6200 year old massacre. <i>PLoS ONE</i> , 2021, 16, e0247332.	2.5	11
16	Genetic landscape of Gullah African Americans. <i>American Journal of Physical Anthropology</i> , 2021, 175, 905-919.	2.1	9
17	Ancient mitochondrial genomes from the Argentinian Pampas inform the early peopling of the Southern Cone of South America. <i>IScience</i> , 2021, 24, 102553.	4.1	11
18	Dynamic changes in genomic and social structures in third millennium BCE central Europe. <i>Science Advances</i> , 2021, 7, .	10.3	46

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19	The return of the Beaker folk? Rethinking migration and population change in British prehistory. <i>Antiquity</i> , 2021, 95, 1464-1477.	1.0	14
20	Combining ancient DNA and radiocarbon dating data to increase chronological accuracy. <i>Journal of Archaeological Science</i> , 2021, 133, 105452.	2.4	7
21	Dairying enabled Early Bronze Age Yamnaya steppe expansions. <i>Nature</i> , 2021, 598, 629-633.	27.8	47
22	Mitochondrial genome diversity on the Central Siberian Plateau with particular reference to the prehistory of northernmost Eurasia. <i>PLoS ONE</i> , 2021, 16, e0244228.	2.5	4
23	Ethics of DNA research on human remains: five globally applicable guidelines. <i>Nature</i> , 2021, 599, 41-46.	27.8	49
24	Genomic transformation and social organization during the Copper Age–Bronze Age transition in southern Iberia. <i>Science Advances</i> , 2021, 7, eabi7038.	10.3	39
25	Social stratification without genetic differentiation at the site of Kulubnarti in Christian Period Nubia. <i>Nature Communications</i> , 2021, 12, 7283.	12.8	13
26	No statistical evidence for an effect of CCR5-Δ32 on lifespan in the UK Biobank cohort. <i>Nature Medicine</i> , 2020, 26, 178-180.	30.7	16
27	Two genetic variants explain the association of European ancestry with multiple sclerosis risk in African-Americans. <i>Scientific Reports</i> , 2020, 10, 16902.	3.3	10
28	Ancient genomes in South Patagonia reveal population movements associated with technological shifts and geography. <i>Nature Communications</i> , 2020, 11, 3868.	12.8	28
29	ContamLD: estimation of ancient nuclear DNA contamination using breakdown of linkage disequilibrium. <i>Genome Biology</i> , 2020, 21, 199.	8.8	29
30	Three Phases of Ancient Migration Shaped the Ancestry of Human Populations in Vanuatu. <i>Current Biology</i> , 2020, 30, 4846-4856.e6.	3.9	27
31	Increased rate of close-kin unions in the central Andes in the half millennium before European contact. <i>Current Biology</i> , 2020, 30, R980-R981.	3.9	9
32	Ancient DNA reveals monozygotic newborn twins from the Upper Palaeolithic. <i>Communications Biology</i> , 2020, 3, 650.	4.4	25
33	A Paleogenomic Reconstruction of the Deep Population History of the Andes. <i>Cell</i> , 2020, 181, 1131-1145.e21.	28.9	69
34	Ancient DNA indicates human population shifts and admixture in northern and southern China. <i>Science</i> , 2020, 369, 282-288.	12.6	214
35	Natural hybridization reveals incompatible alleles that cause melanoma in swordtail fish. <i>Science</i> , 2020, 368, 731-736.	12.6	86
36	The Genomic History of the Bronze Age Southern Levant. <i>Cell</i> , 2020, 181, 1146-1157.e11.	28.9	51

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37	Insights into human genetic variation and population history from 929 diverse genomes. <i>Science</i> , 2020, 367, .	12.6	534
38	Differential DNA methylation of vocal and facial anatomy genes in modern humans. <i>Nature Communications</i> , 2020, 11, 1189.	12.8	69
39	Human auditory ossicles as an alternative optimal source of ancient DNA. <i>Genome Research</i> , 2020, 30, 427-436.	5.5	37
40	Genetic history from the Middle Neolithic to present on the Mediterranean island of Sardinia. <i>Nature Communications</i> , 2020, 11, 939.	12.8	96
41	The spread of steppe and Iranian-related ancestry in the islands of the western Mediterranean. <i>Nature Ecology and Evolution</i> , 2020, 4, 334-345.	7.8	95
42	Ancient West African foragers in the context of African population history. <i>Nature</i> , 2020, 577, 665-670.	27.8	86
43	Kinship and social organization in Copper Age Europe. A cross-disciplinary analysis of archaeology, DNA, isotopes, and anthropology from two Bell Beaker cemeteries. <i>PLoS ONE</i> , 2020, 15, e0241278.	2.5	35
44	Ancient DNA from the skeletons of Roopkund Lake reveals Mediterranean migrants in India. <i>Nature Communications</i> , 2019, 10, 3670.	12.8	19
45	An Ancient Harappan Genome Lacks Ancestry from Steppe Pastoralists or Iranian Farmers. <i>Cell</i> , 2019, 179, 729-735.e10.	28.9	62
46	The formation of human populations in South and Central Asia. <i>Science</i> , 2019, 365, .	12.6	383
47	Ancient DNA reveals a multistep spread of the first herders into sub-Saharan Africa. <i>Science</i> , 2019, 365, .	12.6	96
48	Palaeo-Eskimo genetic ancestry and the peopling of Chukotka and North America. <i>Nature</i> , 2019, 570, 236-240.	27.8	118
49	Polygenic adaptation on height is overestimated due to uncorrected stratification in genome-wide association studies. <i>ELife</i> , 2019, 8, .	6.0	276
50	Ancient genomes indicate population replacement in Early Neolithic Britain. <i>Nature Ecology and Evolution</i> , 2019, 3, 765-771.	7.8	156
51	The genetic history of admixture across inner Eurasia. <i>Nature Ecology and Evolution</i> , 2019, 3, 966-976.	7.8	135
52	African evolutionary history inferred from whole genome sequence data of 44 indigenous African populations. <i>Genome Biology</i> , 2019, 20, 82.	8.8	84
53	Revisiting ancient DNA insights into the human history of the Pacific Islands. <i>Archaeology in Oceania</i> , 2019, 54, 53-56.	0.7	3
54	The genomic history of the Iberian Peninsula over the past 8000 years. <i>Science</i> , 2019, 363, 1230-1234.	12.6	340

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55	The Promise of Paleogenomics Beyond Our Own Species. <i>Trends in Genetics</i> , 2019, 35, 319-329.	6.7	55
56	An ancient DNA Pacific journey: a case study of collaboration between archaeologists and geneticists. <i>World Archaeology</i> , 2019, 51, 620-639.	1.1	7
57	Ancient human genome-wide data from a 3000-year interval in the Caucasus corresponds with eco-geographic regions. <i>Nature Communications</i> , 2019, 10, 590.	12.8	113
58	Interactions between earliest Linearbandkeramik farmers and central European hunter gatherers at the dawn of European Neolithization. <i>Scientific Reports</i> , 2019, 9, 19544.	3.3	35
59	The Beaker phenomenon and the genomic transformation of northwest Europe. <i>Nature</i> , 2018, 555, 190-196.	27.8	503
60	The genomic history of southeastern Europe. <i>Nature</i> , 2018, 555, 197-203.	27.8	479
61	A comprehensive genomic history of extinct and living elephants. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E2566-E2574.	7.1	142
62	Population Turnover in Remote Oceania Shortly after Initial Settlement. <i>Current Biology</i> , 2018, 28, 1157-1165.e7.	3.9	91
63	The genetic prehistory of the Baltic Sea region. <i>Nature Communications</i> , 2018, 9, 442.	12.8	151
64	Evaluating the contribution of rare variants to type 2 diabetes and related traits using pedigrees. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 379-384.	7.1	28
65	No evidence for unknown archaic ancestry in South Asia. <i>Nature Genetics</i> , 2018, 50, 632-633.	21.4	7
66	Arrival routes of first Americans uncertain. <i>Science</i> , 2018, 359, 1224-1225.	12.6	42
67	Reconstructing the genetic history of late Neanderthals. <i>Nature</i> , 2018, 555, 652-656.	27.8	197
68	Discussion: Are the Origins of Indo-European Languages Explained by the Migration of the Yamnaya Culture to the West?. <i>European Journal of Archaeology</i> , 2018, 21, 3-17.	0.5	17
69	Reconstructing the Deep Population History of Central and South America. <i>Cell</i> , 2018, 175, 1185-1197.e22.	28.9	259
70	Reconciling material cultures in archaeology with genetic data: The nomenclature of clusters emerging from archaeogenomic analysis. <i>Scientific Reports</i> , 2018, 8, 13003.	3.3	69
71	Ancient genomes document multiple waves of migration in Southeast Asian prehistory. <i>Science</i> , 2018, 361, 92-95.	12.6	250
72	Biological Sexing of a 4000-Year-Old Egyptian Mummy Head to Assess the Potential of Nuclear DNA Recovery from the Most Damaged and Limited Forensic Specimens. <i>Genes</i> , 2018, 9, 135.	2.4	39

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73	Current evidence allows multiple models for the peopling of the Americas. <i>Science Advances</i> , 2018, 4, eaat5473.	10.3	114
74	Ancient DNA from Chalcolithic Israel reveals the role of population mixture in cultural transformation. <i>Nature Communications</i> , 2018, 9, 3336.	12.8	71
75	A working model of the deep relationships of diverse modern human genetic lineages outside of Africa. <i>Molecular Biology and Evolution</i> , 2017, 34, msw293.	8.9	55
76	Archaeogenomic evidence reveals prehistoric matrilineal dynasty. <i>Nature Communications</i> , 2017, 8, 14115.	12.8	210
77	Direct dating of human skeletal material from Ganj Dareh, Early Neolithic of the Iranian Zagros. <i>Journal of Archaeological Science: Reports</i> , 2017, 12, 165-172.	0.5	4
78	Ancestry and demography and descendants of Iron Age nomads of the Eurasian Steppe. <i>Nature Communications</i> , 2017, 8, 14615.	12.8	96
79	Failure to replicate a genetic signal for sex bias in the steppe migration into central Europe. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E3873-E3874.	7.1	18
80	A high-coverage Neandertal genome from Vindija Cave in Croatia. <i>Science</i> , 2017, 358, 655-658.	12.6	501
81	Reconstructing Prehistoric African Population Structure. <i>Cell</i> , 2017, 171, 59-71.e21.	28.9	308
82	A Late Bronze Age II clay coffin from Tel Shaddud in the Central Jezreel Valley, Israel: context and historical implications. <i>Levant</i> , 2017, 49, 105-135.	0.9	21
83	A multi-stage genome-wide association study of uterine fibroids in African Americans. <i>Human Genetics</i> , 2017, 136, 1363-1373.	3.8	39
84	Interpreting short tandem repeat variations in humans using mutational constraint. <i>Nature Genetics</i> , 2017, 49, 1495-1501.	21.4	78
85	The promise of discovering population-specific disease-associated genes in South Asia. <i>Nature Genetics</i> , 2017, 49, 1403-1407.	21.4	129
86	Genetic origins of the Minoans and Mycenaeans. <i>Nature</i> , 2017, 548, 214-218.	27.8	203
87	Genome diversity in the Neolithic Globular Amphorae culture and the spread of Indo-European languages. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2017, 284, 20171540.	2.6	24
88	Parallel palaeogenomic transects reveal complex genetic history of early European farmers. <i>Nature</i> , 2017, 551, 368-372.	27.8	306
89	Palaeogenomes of Eurasian straight-tusked elephants challenge the current view of elephant evolution. <i>ELife</i> , 2017, 6, .	6.0	50
90	Differences in the rare variant spectrum among human populations. <i>PLoS Genetics</i> , 2017, 13, e1006581.	3.5	88

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91	Mitochondrial DNA analysis of eneolithic trypillians from Ukraine reveals neolithic farming genetic roots. PLoS ONE, 2017, 12, e0172952.	2.5	19
92	The genetic history of Ice Age Europe. Nature, 2016, 534, 200-205.	27.8	729
93	A genetic method for dating ancient genomes provides a direct estimate of human generation interval in the last 45,000 years. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 5652-5657.	7.1	141
94	Genomic insights into the peopling of the Southwest Pacific. Nature, 2016, 538, 510-513.	27.8	262
95	A genomic view of the peopling of the Americas. Current Opinion in Genetics and Development, 2016, 41, 27-35.	3.3	103
96	The Simons Genome Diversity Project: 300 genomes from 142 diverse populations. Nature, 2016, 538, 201-206.	27.8	1,216
97	Genomic insights into the origin of farming in the ancient Near East. Nature, 2016, 536, 419-424.	27.8	733
98	Ancient mitochondrial DNA provides high-resolution time scale of the peopling of the Americas. Science Advances, 2016, 2, e1501385.	10.3	306
99	The contribution of rare variation to prostate cancer heritability. Nature Genetics, 2016, 48, 30-35.	21.4	139
100	The Combined Landscape of Denisovan and Neanderthal Ancestry in Present-Day Humans. Current Biology, 2016, 26, 1241-1247.	3.9	377
101	The Kalash Genetic Isolate? The Evidence for Recent Admixture. American Journal of Human Genetics, 2016, 98, 396-397.	6.2	6
102	Whole-exome sequencing of over 4100 men of African ancestry and prostate cancer risk. Human Molecular Genetics, 2016, 25, 371-381.	2.9	26
103	African Ancestry Analysis and Admixture Genetic Mapping for Proliferative Diabetic Retinopathy in African Americans. , 2015, 56, 3999.		10
104	Dominance of Deleterious Alleles Controls the Response to a Population Bottleneck. PLoS Genetics, 2015, 11, e1005436.	3.5	78
105	Calibrating the Human Mutation Rate via Ancestral Recombination Density in Diploid Genomes. PLoS Genetics, 2015, 11, e1005550.	3.5	49
106	Extreme selective sweeps independently targeted the X chromosomes of the great apes. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 6413-6418.	7.1	75
107	The Genetic Ancestry of African Americans, Latinos, and European Americans across the United States. American Journal of Human Genetics, 2015, 96, 37-53.	6.2	516
108	No evidence that selection has been less effective at removing deleterious mutations in Europeans than in Africans. Nature Genetics, 2015, 47, 126-131.	21.4	182

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109	Massive migration from the steppe was a source for Indo-European languages in Europe. <i>Nature</i> , 2015, 522, 207-211.	27.8	1,435
110	Global diversity, population stratification, and selection of human copy-number variation. <i>Science</i> , 2015, 349, aab3761.	12.6	293
111	Genetic evidence for two founding populations of the Americas. <i>Nature</i> , 2015, 525, 104-108.	27.8	348
112	An early modern human from Romania with a recent Neanderthal ancestor. <i>Nature</i> , 2015, 524, 216-219.	27.8	633
113	Complete Genomes Reveal Signatures of Demographic and Genetic Declines in the Woolly Mammoth. <i>Current Biology</i> , 2015, 25, 1395-1400.	3.9	263
114	Genome-wide patterns of selection in 230 ancient Eurasians. <i>Nature</i> , 2015, 528, 499-503.	27.8	1,160
115	Partial uracilâ€“DNAâ€“glycosylase treatment for screening of ancient DNA. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015, 370, 20130624.	4.0	381
116	A Re-Appraisal of the Early Andean Human Remains from Lauricocha in Peru. <i>PLoS ONE</i> , 2015, 10, e0127141.	2.5	41
117	Non-crossover gene conversions show strong GC bias and unexpected clustering in humans. <i>ELife</i> , 2015, 4, .	6.0	95
118	Reconstructing Austronesian population history in Island Southeast Asia. <i>Nature Communications</i> , 2014, 5, 4689.	12.8	158
119	The complete genome sequence of a Neanderthal from the Altai Mountains. <i>Nature</i> , 2014, 505, 43-49.	27.8	1,830
120	The genomic landscape of Neanderthal ancestry in present-day humans. <i>Nature</i> , 2014, 507, 354-357.	27.8	877
121	Ancient west Eurasian ancestry in southern and eastern Africa. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 2632-2637.	7.1	246
122	Leveraging population admixture to characterize the heritability of complex traits. <i>Nature Genetics</i> , 2014, 46, 1356-1362.	21.4	69
123	Genome sequence of a 45,000-year-old modern human from western Siberia. <i>Nature</i> , 2014, 514, 445-449.	27.8	856
124	Toward a new history and geography of human genes informed by ancient DNA. <i>Trends in Genetics</i> , 2014, 30, 377-389.	6.7	227
125	Gibbon genome and the fast karyotype evolution of small apes. <i>Nature</i> , 2014, 513, 195-201.	27.8	320
126	Ancient human genomes suggest three ancestral populations for present-day Europeans. <i>Nature</i> , 2014, 513, 409-413.	27.8	1,179

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127	Genome-wide Scan of 29,141 African Americans Finds No Evidence of Directional Selection since Admixture. <i>American Journal of Human Genetics</i> , 2014, 95, 437-444.	6.2	69
128	Genetic Evidence for Recent Population Mixture in India. <i>American Journal of Human Genetics</i> , 2013, 93, 422-438.	6.2	234
129	Ancient DNA Reveals Key Stages in the Formation of Central European Mitochondrial Genetic Diversity. <i>Science</i> , 2013, 342, 257-261.	12.6	293
130	A Revised Timescale for Human Evolution Based on Ancient Mitochondrial Genomes. <i>Current Biology</i> , 2013, 23, 553-559.	3.9	540
131	Inferring Admixture Histories of Human Populations Using Linkage Disequilibrium. <i>Genetics</i> , 2013, 193, 1233-1254.	2.9	445
132	Efficient Moment-Based Inference of Admixture Parameters and Sources of Gene Flow. <i>Molecular Biology and Evolution</i> , 2013, 30, 1788-1802.	8.9	121
133	The genetic prehistory of southern Africa. <i>Nature Communications</i> , 2012, 3, 1143.	12.8	271
134	Ancient Admixture in Human History. <i>Genetics</i> , 2012, 192, 1065-1093.	2.9	2,012
135	A High-Coverage Genome Sequence from an Archaic Denisovan Individual. <i>Science</i> , 2012, 338, 222-226.	12.6	1,695
136	Cost-effective, high-throughput DNA sequencing libraries for multiplexed target capture. <i>Genome Research</i> , 2012, 22, 939-946.	5.5	976
137	Reconstructing Native American population history. <i>Nature</i> , 2012, 488, 370-374.	27.8	699
138	Testing for Ancient Admixture between Closely Related Populations. <i>Molecular Biology and Evolution</i> , 2011, 28, 2239-2252.	8.9	1,078
139	Denisova Admixture and the First Modern Human Dispersals into Southeast Asia and Oceania. <i>American Journal of Human Genetics</i> , 2011, 89, 516-528.	6.2	525
140	The landscape of recombination in African Americans. <i>Nature</i> , 2011, 476, 170-175.	27.8	319
141	The History of African Gene Flow into Southern Europeans, Levantines, and Jews. <i>PLoS Genetics</i> , 2011, 7, e1001373.	3.5	224
142	A Draft Sequence of the Neandertal Genome. <i>Science</i> , 2010, 328, 710-722.	12.6	3,588
143	Genetic history of an archaic hominin group from Denisova Cave in Siberia. <i>Nature</i> , 2010, 468, 1053-1060.	27.8	1,537
144	Reduced Neutrophil Count in People of African Descent Is Due To a Regulatory Variant in the Duffy Antigen Receptor for Chemokines Gene. <i>PLoS Genetics</i> , 2009, 5, e1000360.	3.5	335

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145	Reconstructing Indian population history. <i>Nature</i> , 2009, 461, 489-494.	27.8	1,442
146	Admixture Mapping of an Allele Affecting Interleukin 6 Soluble Receptor and Interleukin 6 Levels. <i>American Journal of Human Genetics</i> , 2007, 80, 716-726.	6.2	160
147	Measurement of the human allele frequency spectrum demonstrates greater genetic drift in East Asians than in Europeans. <i>Nature Genetics</i> , 2007, 39, 1251-1255.	21.4	249
148	Principal components analysis corrects for stratification in genome-wide association studies. <i>Nature Genetics</i> , 2006, 38, 904-909.	21.4	8,889
149	Population Structure and Eigenanalysis. <i>PLoS Genetics</i> , 2006, 2, e190.	3.5	4,163
150	A whole-genome admixture scan finds a candidate locus for multiple sclerosis susceptibility. <i>Nature Genetics</i> , 2005, 37, 1113-1118.	21.4	243
151	Will admixture mapping work to find disease genes?. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2005, 360, 1605-1607.	4.0	78
152	A High-Density Admixture Scan in 1,670 African Americans with Hypertension. <i>PLoS Genetics</i> , 2005, preprint, e196.	3.5	0
153	Methods for High-Density Admixture Mapping of Disease Genes. <i>American Journal of Human Genetics</i> , 2004, 74, 979-1000.	6.2	437
154	Ancestry and demography and descendants of Iron Age nomads of the Eurasian Steppe. , 0, .		1