Todd Edwards

List of Publications by Year
in descending order

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Version: 2024-02-01

134	10,672	53751 45	42364 92
papers	citations	h-index	g-index

153	153	153	18681
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Genetic overlap analysis of endometriosis and asthma identifies shared loci implicating sex hormones and thyroid signalling pathways. Human Reproduction, 2022, 37, 366-383.	0.4	19
2	Effect of CYP3A5 and CYP3A4 Genetic Variants on Fentanyl Pharmacokinetics in a Pediatric Population. Clinical Pharmacology and Therapeutics, 2022, 111, 896-908.	2.3	6
3	Impact of obesity on post-operative arrhythmias after congenital heart surgery in children and young adults. Cardiology in the Young, 2022, 32, 1820-1825.	0.4	2
4	Integrating gene expression and clinical data to identify drug repurposing candidates for hyperlipidemia and hypertension. Nature Communications, 2022, 13, 46.	5.8	19
5	Population pharmacokinetic analysis of dexmedetomidine in children using realâ€world data from electronic health records and remnant specimens. British Journal of Clinical Pharmacology, 2022, 88, 2885-2898.	1.1	7
6	Uterine fibroid polygenic risk score (PRS) associates and predicts risk for uterine fibroid. Human Genetics, 2022, 141, 1739-1748.	1.8	4
7	Diastolic Blood Pressure Alleles Improve Congenital Heart Defect Repair Outcomes. Circulation Research, 2022, 130, 1030-1037.	2.0	2
8	Blood Pressure Polygenic Scores Are Associated With Apparent Treatment-Resistant Hypertension. Circulation Genomic and Precision Medicine, 2022, , 101161CIRCGEN121003554.	1.6	2
9	Using Mendelian randomisation to identify opportunities for type 2 diabetes prevention by repurposing medications used for lipid management. EBioMedicine, 2022, 80, 104038.	2.7	7
10	A multiancestry genome-wide association study of unexplained chronic ALT elevation as a proxy for nonalcoholic fatty liver disease with histological and radiological validation. Nature Genetics, 2022, 54, 761-771.	9.4	68
11	Large-Scale Multi-Omics Studies Provide New Insights into Blood Pressure Regulation. International Journal of Molecular Sciences, 2022, 23, 7557.	1.8	10
12	Insights From a Large-Scale Whole-Genome Sequencing Study of Systolic Blood Pressure, Diastolic Blood Pressure, and Hypertension. Hypertension, 2022, 79, 1656-1667.	1.3	12
13	Cross-Cancer Genome-Wide Association Study of Endometrial Cancer and Epithelial Ovarian Cancer Identifies Genetic Risk Regions Associated with Risk of Both Cancers. Cancer Epidemiology Biomarkers and Prevention, 2021, 30, 217-228.	1.1	12
14	Blunted PTH response to vitamin D insufficiency/deficiency and colorectal neoplasia risk. Clinical Nutrition, 2021, 40, 3305-3313.	2.3	3
15	Genetic analysis of endometriosis and depression identifies shared loci and implicates causal links with gastric mucosa abnormality. Human Genetics, 2021, 140, 529-552.	1.8	36
16	Exome-wide evaluation of rare coding variants using electronic health records identifies new geneâ€“phenotype associations. Nature Medicine, 2021, 27, 66-72.	15.2	44
17	Relationship Between Blood Pressure and Incident Cardiovascular Disease: Linear and Nonlinear Mendelian Randomization Analyses. Hypertension, 2021, 77, 2004-2013.	1.3	55
18	Association Between Genetic Variation in Blood Pressure and Increased Lifetime Risk of Peripheral Artery Disease. Arteriosclerosis, Thrombosis, and Vascular Biology, 2021, 41, 2027-2034.	1.1	24

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19	Abstract LB011: Meta-analysis in more than 80,000 men of African ancestry identified nine novel variants associated with prostate cancer. , 2021, , .		0
20	Genetic analyses of gynecological disease identify genetic relationships between uterine fibroids and endometrial cancer, and a novel endometrial cancer genetic risk region at the WNT4 1p36.12 locus. Human Genetics, 2021, 140, 1353-1365.	1.8	18
21	Evidence that geographic variation in genetic ancestry associates with uterine fibroids. Human Genetics, 2021, 140, 1433-1440.	1.8	9
22	Association of Apparent Treatment-Resistant Hypertension With Differential Risk of End-Stage Kidney Disease Across Racial Groups in the Million Veteran Program. Hypertension, 2021, 78, 376-386.	1.3	2
23	Mapping the genetic architecture of human traits to cell types in the kidney identifies mechanisms of disease and potential treatments. Nature Genetics, 2021, 53, 1322-1333.	9.4	87
24	Associations of biogeographic ancestry with hypertension traits. Journal of Hypertension, 2021, 39, 633-642.	0.3	1
25	PheMap: a multi-resource knowledge base for high-throughput phenotyping within electronic health records. Journal of the American Medical Informatics Association: JAMIA, 2020, 27, 1675-1687.	2.2	28
26	Genetic Architecture of Abdominal Aortic Aneurysm in the Million Veteran Program. Circulation, 2020, 142, 1633-1646.	1.6	78
27	Discovery of rare variants associated with blood pressure regulation through meta-analysis of 1.3 million individuals. Nature Genetics, 2020, 52, 1314-1332.	9.4	91
28	Equity in Health: Consideration of Race and Ethnicity in Precision Medicine. Trends in Genetics, 2020, 36, 807-809.	2.9	14
29	4577 Resistant hypertension potentiates the risk of End-Stage Kidney Disease among African-Americans independent of APOL1 genotype in the Million Veteran Program. Journal of Clinical and Translational Science, 2020, 4, 36-36.	0.3	0
30	The polygenic architecture of left ventricular mass mirrors the clinical epidemiology. Scientific Reports, 2020, 10, 7561.	1.6	13
31	Discovery of 318 new risk loci for type 2 diabetes and related vascular outcomes among 1.4 million participants in a multi-ancestry meta-analysis. Nature Genetics, 2020, 52, 680-691.	9.4	445
32	Mendelian Randomization of Circulating Polyunsaturated Fatty Acids and Colorectal Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2020, 29, 860-870.	1.1	26
33	Information Loss in Harmonizing Granular Race and Ethnicity Data: Descriptive Study of Standards. Journal of Medical Internet Research, 2020, 22, e14591.	2.1	4
34	Sex specific associations in genome wide association analysis of renal cell carcinoma. European Journal of Human Genetics, 2019, 27, 1589-1598.	1.4	27
35	Genome-wide association and epidemiological analyses reveal common genetic origins between uterine leiomyomata and endometriosis. Nature Communications, 2019, 10, 4857.	5.8	90
36	Mapping eGFR loci to the renal transcriptome and phenome in the VA Million Veteran Program. Nature Communications, 2019, 10, 3842.	5.8	90

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37	Genome-wide association meta-analyses and fine-mapping elucidate pathways influencing albuminuria. Nature Communications, 2019, 10, 4130.	5.8	133
38	Estimating Uterine Fibroid SNP-Based Heritability in European American Women with Imaging-Confirmed Fibroids. Human Heredity, 2019, 84, 73-81.	0.4	5
39	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. Nature Genetics, 2019, 51, 1459-1474.	9.4	251
40	Calcium: magnesium intake ratio and colorectal carcinogenesis, results from the prostate, lung, colorectal, and ovarian cancer screening trial. British Journal of Cancer, 2019, 121, 796-804.	2.9	19
41	Genome-Wide Association Study of Apparent Treatment-Resistant Hypertension in the CHARGE Consortium: The CHARGE Pharmacogenetics Working Group. American Journal of Hypertension, 2019, 32, 1146-1153.	1.0	17
42	Association of Thyroid Function Genetic Predictors With Atrial Fibrillation. JAMA Cardiology, 2019, 4, 136.	3.0	23
43	A catalog of genetic loci associated with kidney function from analyses of a million individuals. Nature Genetics, 2019, 51, 957-972.	9.4	549
44	A Trans-Ethnic Genome-Wide Association Study of Uterine Fibroids. Frontiers in Genetics, 2019, 10, 511.	1.1	32
45	Evaluation of vitamin D biosynthesis and pathway target genes reveals UGT2A1/2 and EGFR polymorphisms associated with epithelial ovarian cancer in African American Women. Cancer Medicine, 2019, 8, 2503-2513.	1.3	6
46	Heritability and genome-wide association study of benign prostatic hyperplasia (BPH) in the eMERGE network. Scientific Reports, 2019, 9, 6077.	1.6	21
47	The influence of obesity-related factors in the etiology of renal cell carcinomaâ€"A mendelian randomization study. PLoS Medicine, 2019, 16, e1002724.	3.9	59
48	Trans-ethnic association study of blood pressure determinants in over 750,000 individuals. Nature Genetics, 2019, 51, 51-62.	9.4	328
49	Incidence and effect of early postoperative ventricular arrhythmias after congenital heart surgery. Heart Rhythm, 2019, 16, 710-716.	0.3	11
50	Combined linkage and association analysis identifies rare and low frequency variants for blood pressure at 1q31. European Journal of Human Genetics, 2019, 27, 269-277.	1.4	5
51	Gene-based evaluation of low-frequency variation and genetically-predicted gene expression impacting risk of keloid formation. Annals of Human Genetics, 2018, 82, 206-215.	0.3	15
52	Analysis of clinical and candidate genetic risk factors for postoperative atrial tachycardia after congenital heart surgery in infants. American Heart Journal, 2018, 202, 1-4.	1.2	5
53	LPA Variants Are Associated With Residual Cardiovascular Risk in Patients Receiving Statins. Circulation, 2018, 138, 1839-1849.	1.6	64
54	Phenotype risk scores identify patients with unrecognized Mendelian disease patterns. Science, 2018, 359, 1233-1239.	6.0	164

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55	Interethnic analyses of blood pressure loci in populations of East Asian and European descent. Nature Communications, 2018, 9, 5052.	5.8	75
56	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. Nature Genetics, 2018, 50, 1412-1425.	9.4	924
57	A study paradigm integrating prospective epidemiologic cohorts and electronic health records to identify disease biomarkers. Nature Communications, 2018, 9, 3522.	5.8	13
58	Transethnic and race-stratified genome-wide association study of fibroid characteristics in African American and European American women. Fertility and Sterility, 2018, 110, 737-745.e34.	0.5	12
59	Prognostic value of D-dimer and markers of coagulation for stratification of abdominal aortic aneurysm growth. Blood Advances, 2018, 2, 3088-3096.	2.5	20
60	Exploring the phenotypic consequences of tissue specific gene expression variation inferred from GWAS summary statistics. Nature Communications, 2018, 9, 1825.	5.8	748
61	Evaluating risk factors for differences in fibroid size and number using a large electronic health record population. Maturitas, 2018, 114, 9-13.	1.0	8
62	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. Nature Genetics, 2018, 50, 26-41.	9.4	286
63	Rare and low-frequency coding variants alter human adult height. Nature, 2017, 542, 186-190.	13.7	544
64	Genetic and familial predisposition to rotator cuff disease: a systematic review. Journal of Shoulder and Elbow Surgery, 2017, 26, 1103-1112.	1.2	38
65	Obesity and pelvic organ prolapse: a systematic review and meta-analysis of observational studies. American Journal of Obstetrics and Gynecology, 2017, 217, 11-26.e3.	0.7	81
66	Investigating the Genetic Architecture of the PR Interval Using Clinical Phenotypes. Circulation: Cardiovascular Genetics, 2017, 10, .	5.1	8
67	Genetic variation in SLC7A2 interacts with calcium and magnesium intakes in modulating the risk of colorectal polyps. Journal of Nutritional Biochemistry, 2017, 47, 35-40.	1.9	8
68	Genome-wide association study identifies multiple risk loci for renal cell carcinoma. Nature Communications, 2017, 8, 15724.	5.8	106
69	Meta-analysis identifies five novel loci associated with endometriosis highlighting key genes involved in hormone metabolism. Nature Communications, 2017, 8, 15539.	5.8	230
70	Interactions between calcium intake and polymorphisms in genes essential for calcium reabsorption and risk of colorectal neoplasia in a twoâ€phase study. Molecular Carcinogenesis, 2017, 56, 2258-2266.	1.3	7
71	Identification of 12 new susceptibility loci for different histotypes of epithelial ovarian cancer. Nature Genetics, 2017, 49, 680-691.	9.4	356
72	New Blood Pressureâ€“Associated Loci Identified in Meta-Analyses of 475â€‰000 Individuals. Circulation: Cardiovascular Genetics, 2017, 10, .	5.1	48

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73	Population Stratification in Genetic Association Studies. Current Protocols in Human Genetics, 2017, 95, 1.22.1-1.22.23.	3.5	108
74	A multi-stage genome-wide association study of uterine fibroids in African Americans. Human Genetics, 2017, 136, 1363-1373.	1.8	39
75	Analysis of potential protein-modifying variants in 9000 endometriosis patients and 150000 controls of European ancestry. Scientific Reports, 2017, 7, 11380.	1.6	16
76	Nonsteroidal Anti-inflammatory Drug Interaction with Prostacyclin Synthase Protects from Miscarriage. Scientific Reports, 2017, 7, 9874.	1.6	1
77	Admixture mapping of uterine fibroid size and number in African American women. Fertility and Sterility, 2017, 108, 1034-1042.e26.	0.5	11
78	Evaluating the role of race and medication in protection of uterine fibroids by type 2 diabetes exposure. BMC Women's Health, 2017, 17, 28.	0.8	7
79	Association of gene coding variation and resting metabolic rate in a multi-ethnic sample of children and adults. BMC Obesity, 2017, 4, 12.	3.1	6
80	Evaluating electronic health record data sources and algorithmic approaches to identify hypertensive individuals. Journal of the American Medical Informatics Association: JAMIA, 2017, 24, 162-171.	2.2	74
81	Admixture mapping of pelvic organ prolapse in African Americans from the Womenâ€™s Health Initiative Hormone Therapy trial. PLoS ONE, 2017, 12, e0178839.	1.1	4
82	Evidence of selection as a cause for racial disparities in fibroproliferative disease. PLoS ONE, 2017, 12, e0182791.	1.1	17
83	Rare variants in fox-1 homolog A (RBFOX1) are associated with lower blood pressure. PLoS Genetics, 2017, 13, e1006678.	1.5	18
84	Single-trait and multi-trait genome-wide association analyses identify novel loci for blood pressure in African-ancestry populations. PLoS Genetics, 2017, 13, e1006728.	1.5	88
85	African genetic ancestry interacts with body mass index to modify risk for uterine fibroids. PLoS Genetics, 2017, 13, e1006871.	1.5	25
86	Calcium/magnesium intake ratio, but not magnesium intake, interacts with genetic polymorphism in relation to colorectal neoplasia in a two-phase study. Molecular Carcinogenesis, 2016, 55, 1449-1457.	1.3	14
87	Exome Genotyping Identifies Pleiotropic Variants Associated with Red Blood Cell Traits. American Journal of Human Genetics, 2016, 99, 8-21.	2.6	60
88	Renal cell cancer histological subtype distribution differs by race and sex. BJU International, 2016, 117, 260-265.	1.3	115
89	Mapping adipose and muscle tissue expression quantitative trait loci in African Americans to identify genes for type 2 diabetes and obesity. Human Genetics, 2016, 135, 869-880.	1.8	44
90	A genome-wide association study meta-analysis of clinical fracture in 10,012 African American women. Bone Reports, 2016, 5, 233-242.	0.2	20

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91	Meta-analysis identifies common and rare variants influencing blood pressure and overlapping with metabolic trait loci. Nature Genetics, 2016, 48, 1162-1170.	9.4	223
92	Genome-Wide Meta-Analyses of Breast, Ovarian, and Prostate Cancer Association Studies Identify Multiple New Susceptibility Loci Shared by at Least Two Cancer Types. Cancer Discovery, 2016, 6, 1052-1067.	7.7	157
93	Defining a Contemporary Ischemic Heart Disease Genetic Risk Profile Using Historical Data. Circulation: Cardiovascular Genetics, 2016, 9, 521-530.	5.1	7
94	Platelet-Related Variants Identified by Exomechip Meta-analysis in 157,293 Individuals. American Journal of Human Genetics, 2016, 99, 40-55.	2.6	82
95	Large-Scale Exome-wide Association Analysis Identifies Loci for White Blood Cell Traits and Pleiotropy with Immune-Mediated Diseases. American Journal of Human Genetics, 2016, 99, 22-39.	2.6	50
96	Trans-ethnic Meta-analysis and Functional Annotation Illuminates theÂGenetic Architecture of Fasting Glucose and Insulin. American Journal of Human Genetics, 2016, 99, 56-75.	2.6	55
97	Testing the role of predicted gene knockouts in human anthropometric trait variation. Human Molecular Genetics, 2016, 25, 2082-2092.	1.4	10
98	Genetic Determinants of Pelvic Organ Prolapse among African American and Hispanic Women in the Womenâ€™s Health Initiative. PLoS ONE, 2015, 10, e0141647.	1.1	17
99	Meta-analysis of Correlated Traits via Summary Statistics from GWASs with an Application in Hypertension. American Journal of Human Genetics, 2015, 96, 21-36.	2.6	321
100	Common Genetic Variants and Response to Atrial Fibrillation Ablation. Circulation: Arrhythmia and Electrophysiology, 2015, 8, 296-302.	2.1	98
101	Smoking, sex, risk factors and abdominal aortic aneurysms: a prospective study of 18â€…782 persons aged above 65 years in the Southern Community Cohort Study. Journal of Epidemiology and Community Health, 2015, 69, 481-488.	2.0	78
102	Contribution of common non-synonymous variants in PCSK1 to body mass index variation and risk of obesity: a systematic review and meta-analysis with evidence from up to 331 175 individuals. Human Molecular Genetics, 2015, 24, 3582-3594.	1.4	53
103	Trans-ancestry genome-wide association study identifies 12 genetic loci influencing blood pressure and implicates a role for DNA methylation. Nature Genetics, 2015, 47, 1282-1293.	9.4	294
104	Genetic Determinants of Metabolism and Benign Prostate Enlargement: Associations with Prostate Volume. PLoS ONE, 2015, 10, e0132028.	1.1	13
105	Endogenous Production of Long-Chain Polyunsaturated Fatty Acids and Metabolic Disease Risk. Current Cardiovascular Risk Reports, 2014, 8, 1.	0.8	31
106	Phenome-wide association studies demonstrating pleiotropy of genetic variants within FTO with and without adjustment for body mass index. Frontiers in Genetics, 2014, 5, 250.	1.1	66
107	Admixture mapping identifies a locus at 15q21.2â€“22.3 associated with keloid formation in African Americans. Human Genetics, 2014, 133, 1513-1523.	1.8	47
108	Enhancing Uterine Fibroid Research Through Utilization of Biorepositories Linked to Electronic Medical Record Data. Journal of Women's Health, 2014, 23, 1027-1032.	1.5	20

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109	Calcium Intake and Ion Transporter Genetic Polymorphisms Interact in Human Colorectal Neoplasia Risk in a 2-Phase Study. Journal of Nutrition, 2014, 144, 1734-1741.	1.3	9
110	Genetic epidemiology of pelvic organ prolapse: a systematic review. American Journal of Obstetrics and Gynecology, 2014, 211, 326-335.	0.7	62
111	Variants in BET1L and TNRC6B associate with increasing fibroid volume and fibroid type among European Americans. Human Genetics, 2013, 132, 1361-1369.	1.8	28
112	Gene-environment interactions and obesity traits among postmenopausal African-American and Hispanic women in the Womenâ€™s Health Initiative SHARe Study. Human Genetics, 2013, 132, 323-336.	1.8	41
113	Genome-wide Association Analysis of Blood-Pressure Traits in African-Ancestry Individuals Reveals Common Associated Genes in African and Non-African Populations. American Journal of Human Genetics, 2013, 93, 545-554.	2.6	189
114	BET1L and TNRC6B associate with uterine fibroid risk among European Americans. Human Genetics, 2013, 132, 943-953.	1.8	33
115	A meta-analysis identifies new loci associated with body mass index in individuals of African ancestry. Nature Genetics, 2013, 45, 690-696.	9.4	232
116	Identification of Genetic Susceptibility Loci for Colorectal Tumors in a Genome-Wide Meta-analysis. Gastroenterology, 2013, 144, 799-807.e24.	0.6	292
117	Pleiotropy between Genetic Markers of Obesity and Risk of Prostate Cancer. Cancer Epidemiology Biomarkers and Prevention, 2013, 22, 1538-1546.	1.1	3
118	Genome-Wide Association Study Meta-Analysis Reveals Transethnic Replication of Mean Arterial and Pulse Pressure Loci. Hypertension, 2013, 62, 853-859.	1.3	63
119	Genome-Wide Association Study Identifies Possible Genetic Risk Factors for Colorectal Adenomas. Cancer Epidemiology Biomarkers and Prevention, 2013, 22, 1219-1226.	1.1	11
120	A Study of Prostaglandin Pathway Genes and Interactions with Current Nonsteroidal Anti-inflammatory Drug Use in Colorectal Adenoma. Cancer Prevention Research, 2012, 5, 855-863.	0.7	14
121	Association of genetic variants for colorectal cancer differs by subtypes of polyps in the colorectum. Carcinogenesis, 2012, 33, 2417-2423.	1.3	23
122	HTR1B, ADIPOR1, PPARGC1A, and CYP19A1 and Obesity in a Cohort of Caucasians and African Americans: An Evaluation of Gene-Environment Interactions and Candidate Genes. American Journal of Epidemiology, 2012, 175, 11-21.	1.6	42
123	Methods for Detecting and Correcting for Population Stratification. Current Protocols in Human Genetics, 2012, 73, Unit 1.22.1-14.	3.5	10
124	Optimized Selection of Unrelated Subjects for Wholeâ€Genome Sequencing Studies of Rare Highâ€Penetrance Alleles. Genetic Epidemiology, 2012, 36, 472-479.	0.6	1
125	Genome-Wide Association Studies in Disease Risk Calculation: The Role of Bioinformatics in Patient Care. , 2012, , 103-129.		0
126	Vitamin D Receptor Gene as a Candidate Gene for Parkinson Disease. Annals of Human Genetics, 2011, 75, 201-210.	0.3	95

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127	Enriching targeted sequencing experiments for rare disease alleles. Bioinformatics, 2011, 27, 2112-2118.	1.8	8
128	A crossâ€validation procedure for general pedigrees and matched odds ratio fitness metric implemented for the multifactor dimensionality reduction pedigree disequilibrium test. Genetic Epidemiology, 2010, 34, 194-199.	0.6	7
129	A rare novel deletion of the tyrosine hydroxylase gene in Parkinson disease. Human Mutation, 2010, 31, E1767-E1771.	1.1	29
130	Genomeâ€Wide Association Study Confirms SNPs in SNCA and the MAPT Region as Common Risk Factors for Parkinson Disease. Annals of Human Genetics, 2010, 74, 97-109.	0.3	417
131	A General Framework for Formal Tests of Interaction after Exhaustive Search Methods with Applications to MDR and MDR-PDT. PLoS ONE, 2010, 5, e9363.	1.1	13
132	Exploring the Performance of Multifactor Dimensionality Reduction in Large Scale SNP Studies and in the Presence of Genetic Heterogeneity among Epistatic Disease Models. Human Heredity, 2009, 67, 183-192.	0.4	32
133	An association analysis of Alzheimer disease candidate genes detects an ancestral risk haplotype clade in ACE and putative multilocus association between ACE, A2M, and LRRTM3. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2009, 150B, 721-735.	1.1	34
134	Interaction between interleukin 3 and dystrobrevin-binding protein 1 in schizophrenia. Schizophrenia Research, 2008, 106, 208-217.	1.1	19