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DOI: 10.1038/nature21039 Nature, 2017, 542, 186-190.

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497	The impact of rare and low-frequency genetic variants in common disease. 2017 , 18, 77		174
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495	The Rotterdam Study: 2018 update on objectives, design and main results. 2017 , 32, 807-850		296
494	CNV-association meta-analysis in 191,161 European adults reveals new loci associated with anthropometric traits. 2017 , 8, 744		37
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491	Genetics of hypertension: an assessment of progress in the spontaneously hypertensive rat. 2017 , 49, 601-617		36
490	Genome-wide compound heterozygote analysis highlights alleles associated with adult height in Europeans. 2017 , 136, 1407-1417		12
489	Association analyses based on false discovery rate implicate new loci for coronary artery disease. 2017 , 49, 1385-1391		361
488	Response to Commentaries. 2017 , 46, 1625-1629		2
487	Detecting gene subnetworks under selection in biological pathways. 2017 , 45, e149		35
486	Rare genetic variants in CX3CR1 and their contribution to the increased risk of schizophrenia and autism spectrum disorders. 2017 , 7, e1184		35
485	One level up: abnormal proteolytic regulation of IGF activity plays a role in human pathophysiology. 2017 , 9, 1338-1345		40

484 Evolution of Complex Traits in Human Populations. **2017**, 165-186

483	Imaging IGF-I uptake in growth plate cartilage using in vivo multiphoton microscopy. 2017 , 123, 1101-1109	3
482	Integrating Clinical and Multiple Omics Data for Prognostic Assessment across Human Cancers. 2017 , 7, 16954	56
481	Beyond disease susceptibility-Leveraging genome-wide association studies for new insights into complex disease biology. 2017 , 90, 329-334	3
480	Give GWAS a Chance. 2017 , 66, 2741-2742	6
479	Modeling human disease in rodents by CRISPR/Cas9 genome editing. 2017 , 28, 291-301	44
478	The role of human host genetics in tuberculosis resistance. 2017 , 11, 721-737	14
477	10 Years of GWAS Discovery: Biology, Function, and Translation. 2017 , 101, 5-22	1651
476	Genome-wide association analysis identifies a GLUL haplotype for familial hepatitis B virus-related hepatocellular carcinoma. 2017 , 123, 3966-3976	13
475	Polygenicity and Epistasis Underlie Fitness-Proximal Traits in the Multiparental Experimental Evolution (CeMEE) Panel. 2017 , 207, 1663-1685	32
474	Rare coding variants pinpoint genes that control human hematological traits. 2017, 13, e1006925	28
473	Contribution of rare and low-frequency whole-genome sequence variants to complex traits variation in dairy cattle. 2017 , 49, 60	6
472	From forensic epigenetics to forensic epigenomics: broadening DNA investigative intelligence. 2017 , 18, 238	39
47 ¹	[Common and rare variants, polygenic traits and missing heritability]. 2017, 33, 674-676	O
470	The Genetics of Facial Morphology. 2017 , 1-9	1
469	Genetics of biologically based psychological differences. 2018 , 373,	15
468	Genome-wide association studies in Crohn's disease: Past, present and future. 2018 , 7, e1001	45
467	Analysis of predicted loss-of-function variants in UK Biobank identifies variants protective for disease. 2018 , 9, 1613	55

466	Signatures of negative selection in the genetic architecture of human complex traits. 2018 , 50, 746-753	178
465	Neutral Theory: From Complex Population History to Natural Selection and Sociocultural Phenomena in Human Populations. 2018 , 35, 1304-1307	
464	A genetic approach to evaluation of short stature of undetermined cause. 2018 , 6, 564-574	28
463	Genome-Wide Association Mapping of Complex Traits in Rice. 2018 , 497-510	2
462	What Happened to the IGF Binding Proteins?. 2018 , 159, 570-578	20
461	IHH Gene Mutations Causing Short Stature With Nonspecific Skeletal Abnormalities and Response to Growth Hormone Therapy. 2018 , 103, 604-614	36
460	Full genetic analysis for genome-wide association study of Fangji: a powerful approach for effectively dissecting the molecular architecture of personalized traditional Chinese medicine. 2018 , 39, 906-911	5
459	Reference quality assembly of the 3.5-Gb genome of from a single linked-read library. 2018 , 5, 4	75
458	IGF-binding proteins. 2018 , 61, T11-T28	100
457	Growth and growth disorders in 2017: Genetic and epigenetic regulation of childhood growth. 2018 , 14, 70-72	О
456	Genetic short stature. 2018 , 38, 29-33	22
455	Pan-genome analysis highlights the extent of genomic variation in cultivated and wild rice. 2018 , 50, 278-284	277
454	De novo mutations implicate novel genes in systemic lupus erythematosus. 2018 , 27, 421-429	29
453	Phenotype risk scores identify patients with unrecognized Mendelian disease patterns. 2018 , 359, 1233-1239	101
452	Functional annotation of genomic variants in studies of late-onset Alzheimer's disease. 2018 , 34, 2724-2731	13
451	Multiple genetic variations confer risks for obesity and type 2 diabetes mellitus in arab descendants from UAE. 2018 , 42, 1345-1353	17
450	Precision medicine screening using whole-genome sequencing and advanced imaging to identify disease risk in adults. 2018 , 115, 3686-3691	55
449	Psychiatric Genomics: An Update and an Agenda. 2018 , 175, 15-27	328

(2018-2018)

448	Clinical relevance of systematic phenotyping and exome sequencing in patients with short stature. 2018 , 20, 630-638	68
447	Cholangiocytes in the pathogenesis of primary sclerosing cholangitis and development of cholangiocarcinoma. 2018 , 1864, 1390-1400	31
446	The Influence of Big (Clinical) Data and Genomics on Precision Medicine and Drug Development. 2018 , 103, 409-418	26
445	New genetic tools in the diagnosis of growth defects. 2018 , 38, 24-28	3
444	Genome-wide and Phenome-wide Approaches to Understand Variable Drug Actions in Electronic Health Records. 2018 , 11, 112-122	24
443	Genetic architecture: the shape of the genetic contribution to human traits and disease. 2018 , 19, 110-124	219
442	The SNP rs4252548 (R112H) which is associated with reduced human height compromises the stability of IL-11. 2018 , 1865, 496-506	13
441	Drug development in the era of precision medicine. 2018 , 17, 183-196	176
440	Genetik der allgemeinen kognitiven FBigkeit. 2018 , 30, 306-317	
439	Polygenic adaptation and convergent evolution on growth and cardiac genetic pathways in African and Asian rainforest hunter-gatherers. 2018 , 115, E11256-E11263	21
438	Imputation-Aware Tag SNP Selection To Improve Power for Large-Scale, Multi-ethnic Association Studies. 2018 , 8, 3255-3267	17
437	Population structure in genetic studies: Confounding factors and mixed models. 2018, 14, e1007309	62
436	Samasy: an automated system for sample selection and robotic transfer. 2018 , 65, 357-360	2
435	PAPPA2 as a Therapeutic Modulator of IGF-I Bioavailability: and Evidence. 2018 , 2, 646-656	14
434	Functional architecture of low-frequency variants highlights strength of negative selection across coding and non-coding annotations. 2018 , 50, 1600-1607	72
433	Adjustment for covariates using summary statistics of genome-wide association studies. 2018 , 42, 812-825	3
432	Genetics of blood lipids among ~300,000 multi-ethnic participants of the Million Veteran Program. 2018 , 50, 1514-1523	260
431	Large-scale whole-exome sequencing association studies identify rare functional variants influencing serum urate levels. 2018 , 9, 4228	31

430	Low-Frequency and Rare-Coding Variation Contributes to Multiple Sclerosis Risk. 2018, 175, 1679-1687.e7	72
429	Meta-analysis of Icelandic and UK data sets identifies missense variants in SMO, IL11, COL11A1 and 13 more new loci associated with osteoarthritis. 2018 , 50, 1681-1687	67
428	A large-scale integrative analysis of GWAS and common meQTLs across whole life course identifies genes, pathways and tissue/cell types for three major psychiatric disorders. 2018 , 95, 347-352	16
427	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. 2018 , 50, 1412-1425	386
426	Accurate Genomic Prediction of Human Height. 2018 , 210, 477-497	67
425	Insights and Implications of Genome-Wide Association Studies of Height. 2018 , 103, 3155-3168	16
424	Relevance of polymorphisms in MC4R and BDNF in short normal stature. 2018 , 18, 278	2
423	Towards broadening Forensic DNA Phenotyping beyond pigmentation: Improving the prediction of head hair shape from DNA. 2018 , 37, 241-251	24
422	The insulin-like growth factor 2 gene and locus in nonmammalian vertebrates: Organizational simplicity with duplication but limited divergence in fish. 2018 , 293, 15912-15932	15
421	New developments in the genetic diagnosis of short stature. 2018 , 30, 541-547	19
420	Quantifying the Impact of Rare and Ultra-rare Coding Variation across the Phenotypic Spectrum. 2018 , 102, 1204-1211	59
419	PAPP-A and cancer. 2018 , 61, T1-T10	22
418	The Genetic Background of Neonatal Disease. 2018 , 113, 400-405	4
417	Exploring the role of low-frequency and rare exonic variants in alcohol and tobacco use. 2018 , 188, 94-101	7
416	Efficient pathway enrichment and network analysis of GWAS summary data using GSA-SNP2. 2018 , 46, e60	36
415	Similarity and variation in the insulin-like growth factor 2 - H19 locus in primates. 2018 , 50, 425-439	6
414	Genome data uncover four synergistic key regulators for extremely small body size in horses. 2018 , 19, 492	13
413	Identification of 613 new loci associated with heel bone mineral density and a polygenic risk score for bone mineral density, osteoporosis and fracture. 2018 , 13, e0200785	74

412	Insulin- like Growth Factor-Binding Protein Action in Bone Tissue: A Key Role for Pregnancy-Associated Plasma Protein-A. 2018 , 9, 31	10
411	First High-Density Linkage Map and Single Nucleotide Polymorphisms Significantly Associated With Traits of Economic Importance in Yellowtail Kingfish. 2018 , 9, 127	16
410	Evaluation and application of summary statistic imputation to discover new height-associated loci. 2018 , 14, e1007371	22
409	Gene Variants and Diabetic Kidney Disease in MODY. 2018 , 13, 1162-1171	16
408	Proper conditional analysis in the presence of missing data: Application to large scale meta-analysis of tobacco use phenotypes. 2018 , 14, e1007452	11
407	Elongation of the Long Bones in Humans by the Growth Plates. 2018 , 89, 13-23	1
406	Identification of nine new susceptibility loci for endometrial cancer. 2018 , 9, 3166	7º
405	Analysis of Epistasis in Natural Traits Using Model Organisms. 2018 , 34, 883-898	9
404	A subregion-based burden test for simultaneous identification of susceptibility loci and subregions within. 2018 , 42, 673-683	3
403	IGFBP-4 and PAPP-A in normal physiology and disease. 2018 , 41, 7-22	27
402	Genetic causes of proportionate short stature. 2018 , 32, 499-522	18
401	Does Malnutrition Have a Genetic Component?. 2018 , 19, 247-262	8
400	Common Disease Is More Complex Than Implied by the Core Gene Omnigenic Model. 2018 , 173, 1573-1580	151
399	Disease Heritability Studies Harness the Healthcare System to Achieve Massive Scale. 2018 , 173, 1568-1570	2
398	ADAMTS proteins in human disorders. 2018 , 71-72, 225-239	94
397	A transcriptome-wide association study of 229,000 women identifies new candidate susceptibility genes for breast cancer. 2018 , 50, 968-978	101
396	Rediscovering the value of families for psychiatric genetics research. 2019 , 24, 523-535	30
395	Potential benefits and harms of NADPH oxidase type 4 in the kidneys and cardiovascular system. 2019 , 34, 567-576	24

394	Gene hunting with hidden Markov model knockoffs. 2019 , 106, 1-18	39
393	Analysis of the genetic basis of height in large Jewish nuclear families. 2019 , 15, e1008082	1
392	Temperature and insulin signaling regulate body size in Hydra by the Wnt and TGF-beta pathways. 2019 , 10, 3257	16
391	Mendelian randomization integrating GWAS and eQTL data reveals genetic determinants of complex and clinical traits. 2019 , 10, 3300	78
390	Exome sequencing of Finnish isolates enhances rare-variant association power. <i>Nature</i> , 2019 , 572, 323-3 28 .4	69
389	A frequent variant in the Japanese population determines quasi-Mendelian inheritance of rare retinal ciliopathy. 2019 , 10, 2884	15
388	The insulin-like growth factor 2 gene in mammals: Organizational complexity within a conserved locus. 2019 , 14, e0219155	9
387	Cohort Profile: The National Longitudinal Study of Adolescent to Adult Health (Add Health). 2019 , 48, 1415-1415k	106
386	Genetic contributions to variation in human stature in prehistoric Europe. 2019 , 116, 21484-21492	34
385	Genome-Wide Association Studies. 2019 ,	O
384	Genomic interrogation of familial short stature contributes to the discovery of the pathophysiological mechanisms and pharmaceutical drug repositioning. 2019 , 26, 91	1
383	Estimation of DNA contamination and its sources in genotyped samples. 2019 , 43, 980-995	3
383	Estimation of DNA contamination and its sources in genotyped samples. 2019 , 43, 980-995 Sequencing Analysis at 8p23 Identifies Multiple Rare Variants in DLC1 Associated with Sleep-Related Oxyhemoglobin Saturation Level. 2019 , 105, 1057-1068	3
	Sequencing Analysis at 8p23 Identifies Multiple Rare Variants in DLC1 Associated with	
382	Sequencing Analysis at 8p23 Identifies Multiple Rare Variants in DLC1 Associated with Sleep-Related Oxyhemoglobin Saturation Level. 2019 , 105, 1057-1068	
382 381	Sequencing Analysis at 8p23 Identifies Multiple Rare Variants in DLC1 Associated with Sleep-Related Oxyhemoglobin Saturation Level. 2019 , 105, 1057-1068 Efficient Mining of Variants From Trios for Ventricular Septal Defect Association Study. 2019 , 10, 670	4
382 381 380	Sequencing Analysis at 8p23 Identifies Multiple Rare Variants in DLC1 Associated with Sleep-Related Oxyhemoglobin Saturation Level. 2019, 105, 1057-1068 Efficient Mining of Variants From Trios for Ventricular Septal Defect Association Study. 2019, 10, 670 Assessment of network module identification across complex diseases. 2019, 16, 843-852	91

376	Genetics of Growth Disorders-Which Patients Require Genetic Testing?. 2019 , 10, 602	16
375	Adiposity and attained height in adolescents: a longitudinal analysis from the LabMed Physical Activity Study. 2019 , 32, 1131-1137	1
374	Associations of short stature and components of height with incidence of type 2 diabetes: mediating effects of cardiometabolic risk factors. 2019 , 62, 2211-2221	25
373	Epigenetic disturbances in obesity and diabetes: Epidemiological and functional insights. 2019 , 27S, S33-S41	20
372	PAPP-A and the IGF system in atherosclerosis: what's up, what's down?. 2019 , 317, H1039-H1049	7
371	A common variant of the pregnancy-associated plasma protein-A (PAPPA) gene encodes a protein with reduced proteolytic activity towards IGF-binding proteins. 2019 , 9, 13231	5
370	Characterizing rare and low-frequency height-associated variants in the Japanese population. 2019 , 10, 4393	51
369	The Challenge of Defining and Investigating the Causes of Idiopathic Short Stature and Finding an Effective Therapy. 2019 , 92, 71-83	22
368	Deconstructing the sources of genotype-phenotype associations in humans. 2019 , 365, 1396-1400	68
367	Genome-wide association study on antipsychotic-induced weight gain in Europeans and African-Americans. 2019 , 212, 204-212	5
366	Association mapping in plants in the post-GWAS genomics era. 2019 , 104, 75-154	49
366 365	Association mapping in plants in the post-GWAS genomics era. 2019 , 104, 75-154 Validation of Genome-Wide Polygenic Risk Scores for Coronary Artery Disease in French Canadians. 2019 , 12, e002481	49 33
	Validation of Genome-Wide Polygenic Risk Scores for Coronary Artery Disease in French Canadians.	
365	Validation of Genome-Wide Polygenic Risk Scores for Coronary Artery Disease in French Canadians. 2019 , 12, e002481	33
365 364	Validation of Genome-Wide Polygenic Risk Scores for Coronary Artery Disease in French Canadians. 2019 , 12, e002481 Advances in genetics of migraine. 2019 , 20, 72	33 56
365 364 363	Validation of Genome-Wide Polygenic Risk Scores for Coronary Artery Disease in French Canadians. 2019, 12, e002481 Advances in genetics of migraine. 2019, 20, 72 Update on the predictability of tall stature from DNA markers in Europeans. 2019, 42, 8-13	335610
365 364 363 362	Validation of Genome-Wide Polygenic Risk Scores for Coronary Artery Disease in French Canadians. 2019, 12, e002481 Advances in genetics of migraine. 2019, 20, 72 Update on the predictability of tall stature from DNA markers in Europeans. 2019, 42, 8-13 Exome-Derived Adiponectin-Associated Variants Implicate Obesity and Lipid Biology. 2019, 105, 15-28 A local score approach improves GWAS resolution and detects minor QTL: application to Medicago	33561012

358	RAD-sequencing for estimating genomic relatedness matrix-based heritability in the wild: A case study in roe deer. 2019 , 19, 1205-1217	8
357	Weighting sequence variants based on their annotation increases the power of genome-wide association studies in dairy cattle. 2019 , 51, 20	6
356	Functional rare and low frequency variants in BLK and BANK1 contribute to human lupus. 2019 , 10, 2201	43
355	Genetic Testing for the Child With Short Stature-Has the Time Come To Change Our Diagnostic Paradigm?. 2019 , 104, 2766-2769	14
354	Genetic regulation of linear growth. 2019 , 24, 2-14	4
353	GWAS of bone size yields twelve loci that also affect height, BMD, osteoarthritis or fractures. 2019 , 10, 2054	36
352	Mutations in PIK3C2A cause syndromic short stature, skeletal abnormalities, and cataracts associated with ciliary dysfunction. 2019 , 15, e1008088	27
351	Pleiotropy and Specificity: Insights from the Interleukin 6 Family of Cytokines. 2019 , 50, 812-831	182
350	The genetics of depression: successful genome-wide association studies introduce new challenges. 2019 , 9, 114	49
349	Statistical power in genome-wide association studies and quantitative trait locus mapping. 2019 , 123, 287-306	26
348	Pervasive function and evidence for selection across standing genetic variation in S. cerevisiae. 2019 , 10, 1222	6
347	Circulating Adipokine VASPIN Is Associated with Serum Lipid Profiles in Humans. 2019 , 54, 203-210	5
346	Defining the Genetic, Genomic, Cellular, and Diagnostic Architectures of Psychiatric Disorders. 2019 , 177, 162-183	166
345	Genomic basis of delayed reward discounting. 2019 , 162, 157-161	6
344	The Monocarboxylate Transporter SLC16A6 Regulates Adult Length in Zebrafish and Is Associated With Height in Humans. 2018 , 9, 1936	3
343	Genetic causes of isolated short stature. 2019 , 63, 70-78	17
342	ACAT: A Fast and Powerful p Value Combination Method for Rare-Variant Analysis in Sequencing Studies. 2019 , 104, 410-421	66
341	Predicting adult height from DNA variants in a European-Asian admixed population. 2019 , 133, 1667-1679	5

340	Genetic Polymorphisms Associated with Idiopathic Short Stature and First-Year Response to Growth Hormone Treatment. 2019 , 91, 164-174	2
339	Roadmap for a precision-medicine initiative in the Nordic region. 2019 , 51, 924-930	12
338	Mendelian randomisation analyses find pulmonary factors mediate the effect of height on coronary artery disease. 2019 , 2, 119	18
337	Meta-analysis of genome-wide association studies provides insights into genetic control of tomato flavor. 2019 , 10, 1534	48
336	Multigene Sequencing Analysis of Children Born Small for Gestational Age With Isolated Short Stature. 2019 , 104, 2023-2030	30
335	Evolutionary conserved networks of human height identify multiple Mendelian causes of short stature. 2019 , 27, 1061-1071	7
334	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. 2019 , 51, 452-469	44
333	Advances in identifying coding variants of common complex diseases. 2019 , 2, 153-158	
332	DNA Sequence Variations Contribute to Variability in Fitness and Trainability. 2019 , 51, 1781-1785	13
331	Improved power and precision with whole genome sequencing data in genome-wide association studies of inflammatory biomarkers. 2019 , 9, 16844	20
330	Sex-dependent and sex-independent regulatory systems of size variation in natural populations. 2019 , 15, e9012	3
329	The insulin-like growth factor-1 system in the adult mammalian brain and its implications in central maternal adaptation. 2019 , 52, 181-194	5
328	Growth hormone therapy in children; research and practice - A review. 2019 , 44, 20-32	29
327	Unravelling the genetic loci for growth and carcass traits in Chinese Bamaxiang pigs based on a 1.4 million SNP array. 2019 , 136, 3-14	18
326	Activating mutations of the gp130/JAK/STAT pathway in human diseases. 2019 , 116, 283-309	12
325	Deleterious Mutation Burden and Its Association with Complex Traits in Sorghum (). 2019 , 211, 1075-1087	27
324	Functionally oriented analysis of cardiometabolic traits in a trans-ethnic sample. 2019 , 28, 1212-1224	5
323	Exome Chip Meta-analysis Fine Maps Causal Variants and Elucidates the Genetic Architecture of Rare Coding Variants in Smoking and Alcohol Use. 2019 , 85, 946-955	35

322	Combined linkage and association analysis identifies rare and low frequency variants for blood pressure at 1q31. 2019 , 27, 269-277	3
321	Exploring rare and low-frequency variants in the Saguenay-Lac-Saint-Jean population identified genes associated with asthma and allergy traits. 2019 , 27, 90-101	5
320	RNA sequencing of bipolar disorder lymphoblastoid cell lines implicates the neurotrophic factor HRP-3 in lithium's clinical efficacy. 2019 , 20, 449-461	8
319	Mutations in MERTK are not associated with age-related macular degeneration. 2019 , 39, 63-67	1
318	Missing heritability of complex diseases: case solved?. 2020 , 139, 103-113	44
317	Longitudinal associations between body composition and regional fat distribution and later attained height at school entry among preschool children predisposed to overweight. 2020 , 74, 465-471	O
316	Advances in genome-wide association studies of complex traits in rice. 2020 , 133, 1415-1425	23
315	Genetic determinants of bone mass and osteoporotic fracture. 2020 , 1615-1630	1
314	Forensic inference of biogeographical ancestry from genotype: The Genetic Ancestry Lab. 2020, 2,	1
313	Genetic disorders caused by mutations in the parathyroid hormone/parathyroid hormonefielated peptide receptor, its ligands, and downstream effector molecules. 2020 , 1379-1404	
312	Shortened Fingers and Toes: GNAS Abnormalities are Not the Only Cause. 2020 , 128, 681-686	
311	Fine-mapping and QTL tissue-sharing information improves the reliability of causal gene identification. 2020 , 44, 854	9
310	Practicing precision medicine with intelligently integrative clinical and multi-omics data analysis. 2020 , 14, 35	25
309	Population-specific and trans-ancestry genome-wide analyses identify distinct and shared genetic risk loci for coronary artery disease. 2020 , 52, 1169-1177	51
308	Discovery of rare variants associated with blood pressure regulation through meta-analysis of 1.3 million individuals. 2020 , 52, 1314-1332	26
307	General Introduction. 2020 , 1-10	
306	Structural Understanding of Interleukin 6 Family Cytokine Signaling and Targeted Therapies: Focus on Interleukin 11. 2020 , 11, 1424	18
305	Protein-Protein Interactions Mediated by Intrinsically Disordered Protein Regions Are Enriched in Missense Mutations. 2020 , 10,	7

304	Short Stature is Progressive in Patients with Heterozygous NPR2 Mutations. 2020, 105,	8
303	Disorders caused by genetic defects associated with GH-dependent genes: PAPPA2 defects. 2020 , 518, 110967	4
302	The genetic architecture of appendicular lean mass characterized by association analysis in the UK Biobank study. 2020 , 3, 608	7
301	Disorders of IGFs and IGF-1R signaling pathways. 2020 , 518, 111035	25
300	Pan-genomic open reading frames: A potential supplement of single nucleotide polymorphisms in estimation of heritability and genomic prediction. 2020 , 16, e1008995	1
299	Trans-ethnic and Ancestry-Specific Blood-Cell Genetics in 746,667 Individuals from 5 Global Populations. 2020 , 182, 1198-1213.e14	88
298	Novel Mutations and Genes That Impact on Growth in Short Stature of Undefined Aetiology: The EPIGROW Study. 2020 , 4, bvaa105	1
297	What Has a Century of Quantitative Genetics Taught Us About Nature's Genetic Tool Kit?. 2020 , 54, 439-464	5
296	Functional Characterization Reveals the Significance of Rare Coding Variations in Human Organic Anion Transporting Polypeptide 2B1 (21). 2020 , 17, 3966-3978	6
295	A patient-based model of RNA mis-splicing uncovers treatment targets in Parkinson's disease. 2020 , 12,	10
294	Genetic Studies of Leptin Concentrations Implicate Leptin in the Regulation of Early Adiposity. 2020 , 69, 2806-2818	10
293	Expression of acid-labile subunit (ALS) in developing and adult zebrafish and its role in dorso-ventral patterning during development. 2020 , 299, 113591	1
292	Sex-Specific Control of Muscle Mass: Elevated IGFBP Proteolysis and Reductions of IGF-1 Levels Are Associated with Substantial Loss of Carcass Weight in Male DU6PxIGFBP-2 Transgenic Mice. 2020 , 9,	
291	The Trait Approach. 2020 , 31-43	
290	Accuracy in Person Perception. 2020 , 44-55	
289	Models of Personality Structure. 2020 , 115-128	
288	The Five-Factor Model of Personality: Consensus and Controversy. 2020 , 129-141	1
287	Temperament and Brain Networks of Attention. 2020 , 155-168	1

286	Personality in Nonhuman Animals. 2020 , 235-246	
285	Genetics of Personality. 2020 , 247-258	
284	ApproachAvoidance Theories of Personality. 2020 , 259-272	1
283	Cognitive Processes and Models. 2020 , 295-315	
282	Basic Needs, Goals and Motivation. 2020 , 330-338	
281	Personality and the Self. 2020 , 339-351	4
280	Social Relations and Social Support. 2020 , 386-399	
279	Personality and Politics. 2020 , 413-424	
278	Personality at Work. 2020 , 427-438	1
277	Educational Psychology. 2020 , 439-450	O
276	Personality in Clinical Psychology. 2020 , 451-462	
275	Addendum: Statistical Analyses and Computer Programming in Personality. 2020 , 495-534	
274	Conceptual and Historical Perspectives. 2020 , 13-30	2
273	Personality and the Unconscious. 2020 , 69-80	
272	Personality and Emotion. 2020 , 81-100	3
271	Personality Assessment Methods. 2020 , 103-114	

(2020-2020)

268 Personality Traits and Mental Disorders. **2020**, 183-192

267	Attachment Theory. 2020 , 208-220	
266	Evolutionary Personality Psychology. 2020 , 223-234	3
265	Personality Neuroscience. 2020 , 273-292	3
264	Self-Regulation and Control in Personality Functioning. 2020 , 316-329	
263	Traits and Dynamic Processes. 2020 , 352-363	
262	Anxiety, Depression and Cognitive Dysfunction. 2020, 364-374	
261	Personality in Cross-Cultural Perspective. 2020 , 400-412	O
260	Personality, Preferences and Socioeconomic Behavior. 2020 , 477-494	2
259	Index. 2020 , 535-552	
258	States and Situations, Traits and Environments. 2020 , 56-68	O
257	Narrative Identity in the Social World. 2020 , 377-385	
256	Personality and Crime. 2020 , 463-476	
255	Models of Physical Health and Personality. 2020 , 193-207	1
254	Insights into the Genetic Underpinnings of Endocrine Traits from Large-Scale Genome-Wide Association Studies. 2020 , 49, 725-739	1
253	Preface. 2020 , xv-xvi	
252	Scalable generalized linear mixed model for region-based association tests in large biobanks and cohorts. 2020 , 52, 634-639	41
251	Statistical Data Analysis in the Era of Big Data. 2020 , 92, 831-841	3

250	A positively selected FBN1 missense variant reduces height in Peruvian individuals. <i>Nature</i> , 2020 , 582, 234-239	50.4	15
249	Identifying novel associations in GWAS by hierarchical Bayesian latent variable detection of differentially misclassified phenotypes. 2020 , 21, 178		3
248	Genetic causes of growth disorders. 2020 , 14, 7-14		1
247	The challenge of predicting human pigmentation traits in degraded bone samples with the MPS-based HIrisPlex-S system. 2020 , 47, 102301		10
246	Exome Sequencing Identifies Genes and Gene Sets Contributing to Severe Childhood Obesity, Linking PHIP Variants to Repressed POMC Transcription. 2020 , 31, 1107-1119.e12		16
245	Protein QTL analysis of IGF-I and its binding proteins provides insights into growth biology. 2020 , 29, 2625-2636		1
244	Estimation of non-null SNP effect size distributions enables the detection of enriched genes underlying complex traits. 2020 , 16, e1008855		3
243	Common polymorphisms in MC4R and FTO genes are associated with BMI and metabolic indicators in Mexican children: Differences by sex and genetic ancestry. 2020 , 754, 144840		5
242	A missense variant in CREBRF is associated with taller stature in Samoans. 2020 , 32, e23414		8
241	Precision medicine - networks to the rescue. 2020 , 63, 177-189		17
240	Genome-wide association meta-analysis of corneal curvature identifies novel loci and shared genetic influences across axial length and refractive error. 2020 , 3, 133		9
239	Genetic Architecture Associated With Familial Short Stature. 2020 , 105,		9
238	Revisiting the Population Genetics of Human Height. 2020 , 4, bvaa025		3
237	Update on NAFLD genetics: From new variants to the clinic. 2020 , 72, 1196-1209		85
236	Overlap of Peak Growth Activity and Peak IGF-1 to IGFBP Ratio: Delayed Increase of IGFBPs versus IGF-1 in Serum as a Mechanism to Speed up and down Postnatal Weight Gain in Mice. 2020 , 9,		4
235	Loss-of-Function Variants in Patients With Severe Hypertriglyceridemia. 2020 , 40, 1935-1941		9
234	Microevolutionary Dynamics of Chicken Genomes under Divergent Selection for Adiposity. 2020 , 23, 101193		1
233	Pregnancy-associated plasma proteins and Stanniocalcin-2 - Novel players controlling IGF-I physiology. 2020 , 53-54, 101330		4

232	Applications of Functional Genomics for Drug Discovery. 2020 , 25, 823-842	3
231	Genomics-assisted breeding in minor and pseudo-cereals. 2020 , 70, 19-31	18
230	Intolerance of loud sounds in childhood: Is there an intergenerational association with grandmaternal smoking in pregnancy?. 2020 , 15, e0229323	4
229	Contribution of common and rare variants to bipolar disorder susceptibility in extended pedigrees from population isolates. 2020 , 10, 74	8
228	Genetically Determined Height and Risk of Non-hodgkin Lymphoma. 2019 , 9, 1539	1
227	Identification of small and large genomic candidate variants in bovine pulmonary hypoplasia and anasarca syndrome. 2020 , 51, 382-390	11
226	Beyond large-effect loci: large-scale GWAS reveals a mixed large-effect and polygenic architecture for age at maturity of Atlantic salmon. 2020 , 52, 9	27
225	Osteoporosis- and obesity-risk interrelationships: an epigenetic analysis of GWAS-derived SNPs at the developmental gene. 2020 , 15, 728-749	4
224	Next-generation drug repurposing using human genetics and network biology. 2020, 51, 78-92	35
223	Genome-wide rare variant analysis for thousands of phenotypes in over 70,000 exomes from two cohorts. 2020 , 11, 542	47
222	The contribution of rare genetic variants to the pathogenesis of polycystic ovary syndrome. 2020 , 12, 26-32	10
221	Rare genetic variants in systemic autoimmunity. 2020 , 98, 490-499	2
220	New Insights Into Physiological and Pathophysiological Functions of Stanniocalcin 2. 2020 , 11, 172	9
219	Genetic Regulation of Adult Stature in Humans. 2020 , 105,	1
218	Clinical and Molecular Description of 16 Families With Heterozygous IHH Variants. 2020 , 105,	3
217	Morphological Characters Can Strongly Influence Early Animal Relationships Inferred from Phylogenomic Data Sets. 2021 , 70, 360-375	6
216	Growth plate gene involment and isolated short stature. 2021 , 71, 28-34	3
215	The impact of correlations between pigmentation phenotypes and underlying genotypes on genetic prediction of pigmentation traits. 2021 , 50, 102395	1

214	Causal Inference Methods to Integrate Omics and Complex Traits. 2021, 11,	4
213	Exploiting the GTEx resources to decipher the mechanisms at GWAS loci. 2021 , 22, 49	38
212	Genetic Epidemiology of Complex Phenotypes. 2021 , 2249, 335-367	2
211	Reduced Fragmentation of IGFBP-2 and IGFBP-3 as a Potential Mechanism for Decreased Ratio of IGF-II to IGFBPs in Cerebrospinal Fluid in Response to Repeated Intrathecal Administration of Triamcinolone Acetonide in Patients With Multiple Sclerosis. 2020 , 11, 565557	Ο
210	Disorders of Childhood Growth. 2021 , 299-356	1
209	The current and future state of sports genomics. 2021 , 217-233	
208	Queering Evolution: The Socio-political Entanglements of Natural and Cultural Evolutionary Mechanisms. 2021 , 95-121	1
207	Impact of low-frequency coding variants on human facial shape. 2021 , 11, 748	1
206	Idfix: identifying accidental sample mix-ups in biobanks using polygenic scores.	
205	The long-term effects of genomic selection: Response to selection, additive genetic variance and genetic architecture.	1
204	Nicotinic regulation of local and long-range input balance drives top-down attentional circuit maturation. 2021 , 7,	1
203	Genomics-driven drug discovery based on disease-susceptibility genes. 2021 , 41, 8	1
202	Can Genetic Testing Predict Talent? A Case Study of 5 Elite Athletes. 2020 , 16, 429-434	4
201	The Meaning of "Cause" in Genetics. 2021 , 11,	4
200	Growth failure: 'idiopathic' only after a detailed diagnostic evaluation. 2021, 10, R125-R138	6
199	Genetics of Obesity: What We Have Learned Over Decades of Research. 2021 , 29, 802-820	13
198	Advancing drug discovery using the power of the human genome. 2021 , 254, 418-429	1
197	Geographic variation in the polygenic score of height in Japan. 2021 , 140, 1097-1108	2

196	Identifying therapeutic drug targets using bidirectional effect genes. 2021, 12, 2224	3
195	Discovery and fine-mapping of height loci via high-density imputation of GWASs in individuals of African ancestry. 2021 , 108, 564-582	7
194	Transhumanist Genetic Enhancement: Creation of a 'New Man' Through Technological Innovation. 2021 , 27, 105-126	
193	FAN1 nuclease activity affects CAG expansion and age at onset of Huntington disease.	O
192	Calcium State-Dependent Regulation of Epithelial Cell Quiescence by Stanniocalcin 1a. 2021 , 9, 662915	
191	Variation in upstream open reading frames contributes to allelic diversity in protein abundance.	
190	Dissecting the loci underlying maturation timing in Atlantic salmon using haplotype and multi-SNP based association methods.	1
189	Ancestral diversity improves discovery and fine-mapping of genetic loci for anthropometric traits - the Hispanic/Latino Anthropometry Consortium.	
188	The genetic architecture and population genomic signatures of glyphosate resistance in Amaranthus tuberculatus. 2021 , 30, 5373-5389	6
187	Snow White and the Seven Dwarfs: a fairytale for endocrinologists. 2021 , 10, R189-R199	
186	Stability of Polygenic Scores Across Discovery Genome-Wide Association Studies.	2
185	Contributions of PTSD polygenic risk and environmental stress to suicidality in preadolescents.	1
184	Interleukin 11 (IL-11): Role(s) in Breast Cancer Bone Metastases. 2021 , 9,	2
183	Longitudinal Associations between Intake of Fruit and Vegetables and Height Attainment from Preschool to School Entry. 2021 , 18,	O
182	Systematic single-variant and gene-based association testing of 3,700 phenotypes in 281,850 UK Biobank exomes.	6
181	Clinical relevance of targeted exome sequencing in patients with rare syndromic short stature. 2021 , 16, 297	O
180	Can biomarkers be used to improve diagnosis and prediction of metabolic syndrome in childhood cancer survivors? A systematic review. 2021 , 22, e13312	2
179	Increased burden of rare variants in genes of the endosomal Toll-like receptor pathway in patients with systemic lupus erythematosus. 2021 , 30, 1756-1763	1

178	Searching for improvements in predicting human eye colour from DNA. 2021, 135, 2175-2187	O
177	Whole-exome imputation within UK Biobank powers rare coding variant association and fine-mapping analyses. 2021 , 53, 1260-1269	7
176	Longer or shorter spines: Reciprocal trait evolution in stickleback via triallelic regulatory changes in. 2021 , 118,	1
175	Posthumanism: Creation of 'New Men' Through Technological Innovation. 2021 , 27, 197-218	
174	The cytokine interleukin-11 crucially links bone formation, remodeling and resorption. 2021 , 60, 18-27	6
173	Genome-wide meta-analysis and omics integration identifies novel genes associated with diabetic kidney disease.	O
172	Evaluation of height as a disease risk factor through a phenome-wide association study of genetically-predicted height.	0
171	Partitioning gene-level contributions to complex-trait heritability by allele frequency identifies disease-relevant genes.	1
170	A genome-wide association analysis for body weight at 35 days measured on 137,343 broiler chickens. 2021 , 53, 70	0
169	Trans-ancestry genome-wide analysis of atrial fibrillation provides new insights into disease biology and enables polygenic prediction of cardioembolic risk.	
168	Role of K and Ca-Permeable Channels in Osteoblast Functions. 2021 , 22,	2
167	Common, low-frequency, rare, and ultra-rare coding variants contribute to COVID-19 severity.	
166	Advances and challenges in quantitative delineation of the genetic architecture of complex traits 2021 , 9, 168-184	
165	Physiological regulation of bone length and skeletal proportion in mammals. 2021 , 106, 389-395	1
164	The Cambridge Handbook of Personality Psychology. 2020 ,	5
163	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. 2018 , 50, 26-41	186
162	Imputation aware tag SNP selection to improve power for multi-ethnic association studies.	1
161	Psychiatric Genomics: An Update and an Agenda.	3

160	Widespread signatures of negative selection in the genetic architecture of human complex traits.	7
159	Exome chip meta-analysis elucidates the genetic architecture of rare coding variants in smoking and drinking behavior.	1
158	Accurate Genomic Prediction Of Human Height.	4
157	Genetic analysis of over one million people identifies 535 novel loci for blood pressure.	4
156	Trans-ethnic and ancestry-specific blood-cell genetics in 746,667 individuals from 5 global populations.	О
155	Identifying therapeutic drug targets for rare and common forms of short stature.	1
154	The genetic architecture and genomic context of glyphosate resistance in Amaranthus tuberculatus.	1
153	The mixed genetic origin of the first farmers of Europe.	1
152	Open Community Challenge Reveals Molecular Network Modules with Key Roles in Diseases.	10
151	Protein-Coding Variants Implicate Novel Genes Related to Lipid Homeostasis Contributing to Body Fat Distribution.	1
150	Leveraging mutational burden for complex trait prediction in sorghum.	3
149	Genomic underpinnings of lifespan allow prediction and reveal basis in modern risks.	1
148	Mendelian Randomization integrating GWAS and eQTL data reveals genetic determinants of complex and clinical traits.	4
147	Mutations In PIK3C2A Cause Syndromic Short Stature, Skeletal Abnormalities, and Cataracts Associated With Ciliary Dysfunction.	1
146	Validation of genome-wide polygenic risk scores for coronary artery disease in French Canadians.	1
145	A positively selected, common, missense variant in FBN1 confers a 2.2 centimeter reduction of height in the Peruvian population.	3
144	Scalable generalized linear mixed model for region-based association tests in large biobanks and cohorts.	7
143	Estimation of Non-null SNP Effect Size Distributions Enables the Detection of Enriched Genes Underlying Complex Traits.	О

142	Rare variants contribute disproportionately to quantitative trait variation in yeast.	2
141	A Fast and Scalable Framework for Large-scale and Ultrahigh-dimensional Sparse Regression with Application to the UK Biobank.	5
140	Exautomate: A user-friendly tool for region-based rare variant association analysis (RVAA).	1
139	Genetic contributions to variation in human stature in prehistoric Europe.	2
138	Genome-wide rare variant analysis for thousands of phenotypes in 54,000 exomes.	3
137	Tissue-Specific Alteration of Metabolic Pathways Influences Glycemic Regulation.	4
136	Exploiting the GTEx resources to decipher the mechanisms at GWAS loci.	21
135	Genomic architecture of artificially and sexually selected traits in a wild cervid.	2
134	Selective trade-offs maintain alleles underpinning complex trait variation in plants. 2018, 361, 475-478	58
133	Regulation of plasma von Willebrand factor. 2018 , 7, 96	8
133	Regulation of plasma von Willebrand factor. 2018, 7, 96 A fast and scalable framework for large-scale and ultrahigh-dimensional sparse regression with application to the UK Biobank. 2020, 16, e1009141	22
	A fast and scalable framework for large-scale and ultrahigh-dimensional sparse regression with	22
132	A fast and scalable framework for large-scale and ultrahigh-dimensional sparse regression with application to the UK Biobank. 2020 , 16, e1009141	22
132 131	A fast and scalable framework for large-scale and ultrahigh-dimensional sparse regression with application to the UK Biobank. 2020 , 16, e1009141 Age-related changes in microbial composition and function in cynomolgus macaques. 2019 , 11, 12080-12096	10
132 131 130	A fast and scalable framework for large-scale and ultrahigh-dimensional sparse regression with application to the UK Biobank. 2020, 16, e1009141 Age-related changes in microbial composition and function in cynomolgus macaques. 2019, 11, 12080-12096 Nouveaux usages de IADN en matile pliale': promesses, savoirs et pratiques. 2019, 83-93 Novel Modulators of the Growth Hormone - Insulin-Like Growth Factor Axis: Pregnancy-Associated	10
132 131 130	A fast and scalable framework for large-scale and ultrahigh-dimensional sparse regression with application to the UK Biobank. 2020, 16, e1009141 Age-related changes in microbial composition and function in cynomolgus macaques. 2019, 11, 12080-12096 Nouveaux usages de IADN en matifie pfiale? promesses, savoirs et pratiques. 2019, 83-93 Novel Modulators of the Growth Hormone - Insulin-Like Growth Factor Axis: Pregnancy-Associated Plasma Protein-A2 and Stanniocalcin-2. 2017, 9, 1-8 Genomics of 1 million parent lifespans implicates novel pathways and common diseases and	22 10 1
132 131 130 129	A fast and scalable framework for large-scale and ultrahigh-dimensional sparse regression with application to the UK Biobank. 2020, 16, e1009141 Age-related changes in microbial composition and function in cynomolgus macaques. 2019, 11, 12080-12096 Nouveaux usages de IADN en matifie pfiale: promesses, savoirs et pratiques. 2019, 83-93 Novel Modulators of the Growth Hormone - Insulin-Like Growth Factor Axis: Pregnancy-Associated Plasma Protein-A2 and Stanniocalcin-2. 2017, 9, 1-8 Genomics of 1 million parent lifespans implicates novel pathways and common diseases and distinguishes survival chances. 2019, 8,	22 10 1 14 82

124	Searching for solutions to the missing heritability problem. 2019 , 8,	5
123	Determinants of Stunting in Children Aged 6-59 Months in Glagah Sub-District, Indonesia. 2021 , 9, 239	
122	Influences of rare copy number variation on human complex traits.	О
121	Allen Orr and the genetics of adaptation. 2021 , 75, 2624-2640	2
120	Polygenicity and epistasis underlie fitness-proximal traits in the Caenorhabditis elegans multiparental experimental evolution (CeMEE) panel.	0
119	Causal analyses, statistical efficiency and phenotypic precision through Recall-by-Genotype study design.	2
118	Detecting gene subnetworks under selection in biological pathways.	
117	De novo mutations implicate novel genes with burden of rare variants in Systemic Lupus Erythematosus.	
116	Reference Quality Assembly of the 3.5 Gb genome of Capsicum annuum from a Single Linked-Read Library.	2
115	Quantifying the impact of rare and ultra-rare coding variation across the phenotypic spectrum.	1
114	Cytokine Polymorphisms, Immunosenescence, and Neurodegeneration. 2018, 1-34	
113	Low Pass Genomes of 141,431 Chinese Reveal Patterns of Viral Infection, Novel Phenotypic Associations, and the Genetic History of China.	1
112	A frequent variant in the Japanese population determines quasi-Mendelian inheritance of rare retinal ciliopathy.	2
111	Low frequency and rare coding variation contributes to multiple sclerosis risk.	
110	Analysis of the genetic basis of height in large Jewish nuclear families.	0
109	Polygenic adaptation and convergent evolution across both growth and cardiac genetic pathways in African and Asian rainforest hunter-gatherers.	
108	Low-frequency variant functional architectures reveal strength of negative selection across coding and non-coding annotations.	1
107	Trans-ethnic polygenic analysis supports genetic overlaps of lumbar disc degeneration with height, body mass index, and bone mineral density.	O

106	ACAT: A Fast and Powerful P-value Combination Method for Rare-variant Analysis in Sequencing Studies.	0
105	The role of glycaemic, lipid, blood pressure and obesity risk factors as mediators of the effect of height on Coronary Artery Disease and Type 2 Diabetes Mellitus: A Mendelian Randomisation Study.	
104	RAD-sequencing for estimating GRM-based heritability in the wild: a case study in roe deer.	
103	A Framework with Randomized Encoding for a Fast Privacy Preserving Calculation of Non-linear Kernels for Machine Learning Applications in Precision Medicine. 2019 , 493-511	
102	Phenotype. 2019 , 1-5	
101	The Future of and Beyond GWAS. 2019 , 193-209	
100	Cytokine Polymorphisms, Immunosenescence, and Neurodegeneration. 2019 , 1057-1090	
99	Pleiotropic effects for Parkin and LRRK2 in leprosy type-1 reactions and Parkinson disease. 2019 ,	
98	Socioeconomic and Genomic Roots of Verbal Ability.	
97	Sp1 contributes to overexpression of stanniocalcin 2 through regulation of promoter activity in colon adenocarcinoma. 2019 , 25, 2776-2787	5
96	Osteoporosis- and obesity-risk interrelationships: An epigenetic analysis of GWAS-derived SNPs at the developmental geneTBX15.	
95	Stanniocalcin 1a is a Ca2+-regulated switch controlling epithelial cell quiescence-proliferation balance and Ca2+ uptake.	
94	Contributions of PTSD polygenic risk and environmental stress to suicidality in preadolescents. 2021 , 15, 100411	2
93	Perspectives on studying molecular adaptations of amphibians in the genomic era. 2020 , 41, 351-364	2
92	Harveian Oration 2019: Prediction and prevention in the genomic era. 2020 , 20, 8-20	
91	Rare Genetic Variants Underlie Outlying levels of DNA Methylation and Gene-Expression.	O
90	Fine-mapping and QTL tissue-sharing information improve causal gene identification and transcriptome prediction performance.	2
89	Deciphering the Genetic Architecture of Plant Virus Resistance by GWAS, State of the Art and Potential Advances. 2021 , 10,	Ο

88	MC3R links nutritional state to childhood growth and the timing of puberty. <i>Nature</i> , 2021 , 599, 436-441 $_{50.4}$	9
87	Predicting skeletal stature using ancient DNA.	2
86	Impact of low-frequency coding variants on human facial shape.	
85	Pathway Analysis within Multiple Human Ancestries Reveals Novel Signals for Epistasis in Complex Traits.	О
84	A weighted empirical Bayes risk prediction model using multiple traits. 2020 , 19,	
83	Growth change in Polish women: Reduction of the secular trends?. 2020 , 15, e0242074	2
82	Whole-exome imputation within UK Biobank powers rare coding variant association and fine-mapping analyses.	О
81	Encyclopedia of Gerontology and Population Aging. 2021 , 3811-3815	
80	Clinical profiles and genetic spectra of 814 Chinese children with short stature. 2021 ,	3
79	Idfix: identifying accidental sample mix-ups in biobanks using polygenic scores. 2021 ,	
78	Bench Research Informed by GWAS Results. 2021 , 10,	0
78 77		o 5
,	Bench Research Informed by GWAS Results. 2021 , 10,	
77	Bench Research Informed by GWAS Results. 2021, 10, The sequences of 150,119 genomes in the UK biobank. A Saturated Map of Common Genetic Variants Associated with Human Height from 5.4 Million	5
77 76	Bench Research Informed by GWAS Results. 2021, 10, The sequences of 150,119 genomes in the UK biobank. A Saturated Map of Common Genetic Variants Associated with Human Height from 5.4 Million Individuals of Diverse Ancestries. Altered IGF-I activity and accelerated bone elongation in growth plates precedes excess weight	5
77 76 75	Bench Research Informed by GWAS Results. 2021, 10, The sequences of 150,119 genomes in the UK biobank. A Saturated Map of Common Genetic Variants Associated with Human Height from 5.4 Million Individuals of Diverse Ancestries. Altered IGF-I activity and accelerated bone elongation in growth plates precedes excess weight gain in a mouse model of juvenile obesity 2022,	5 O
77 76 75 74	Bench Research Informed by GWAS Results. 2021, 10, The sequences of 150,119 genomes in the UK biobank. A Saturated Map of Common Genetic Variants Associated with Human Height from 5.4 Million Individuals of Diverse Ancestries. Altered IGF-I activity and accelerated bone elongation in growth plates precedes excess weight gain in a mouse model of juvenile obesity 2022, Stability of polygenic scores across discovery genome-wide association studies 2022, 3, 100091	5 O

70	Common, low-frequency, rare, and ultra-rare coding variants contribute to COVID-19 severity. 2021 , 141, 147	3
69	P2RY8 variants in lupus patients uncover a role for the receptor in immunological tolerance. 2022 , 219,	4
68	Gene Region Association Analysis of Longitudinal Quantitative Traits Based on a Function-On-Function Regression Model 2022 , 13, 781740	O
67	Exploring the genetic causes of isolated short stature. What has happened to idiopathic short stature?. 2022 , 28, 28/8S27-28/8S32	
66	Large-scale association study on daily weight gain in pigs reveals overlap of genetic factors for growth in humans 2022 , 23, 133	O
65	Analysis of rare genetic variation underlying cardiometabolic diseases and traits among 200,000 individuals in the UK Biobank 2022 ,	4
64	The long-term effects of genomic selection: 1. Response to selection, additive genetic variance, and genetic architecture 2022 , 54, 19	1
63	Meta-analysis fine-mapping is often miscalibrated at single-variant resolution.	1
62	Estimating genetic variance contributed by a quantitative trait locus: A random model approach 2022 , 18, e1009923	
61	Ancestral diversity improves discovery and fine-mapping of genetic loci for anthropometric traits-The Hispanic/Latino Anthropometry Consortium 2022 , 3, 100099	O
60	Exome sequencing of individuals with Huntington's disease implicates FAN1 nuclease activity in slowing CAG expansion and disease onset 2022 ,	3
59	Partitioning gene-level contributions to complex-trait heritability by allele frequency identifies disease-relevant genes 2022 ,	
58	SUMMIT: An integrative approach for better transcriptomic data imputation improves causal gene identification.	
57	Mendelian randomization analyses reveal mediating factors of the causal effect of height on coronary artery disease.	
56	Pregnancy-Associated Plasma Protein (PAPP)-A2 in Physiology and Disease 2021 , 10,	1
55	The Waring Worlds of H. G. Wells: The Entangled Histories of Education, Sociobiology, Post-genomics, and Science Fiction. 2022 , 53-71	
54	Variation in upstream open reading frames contributes to allelic diversity in maize protein abundance 2022 , 119, e2112516119	1
53	Cerebral Polymorphisms for Lateralisation: Modelling the Genetic and Phenotypic Architectures of Multiple Functional Modules. 2022 , 14, 814	1

52 Forensic DNA phenotyping: Inferring phenotypic traits from crime scene DNA.. **2022**, 88, 102351

51	Data_Sheet_1.zip. 2018 ,	
50	Table_1.xlsx. 2019 ,	
49	Data_Sheet_1.docx. 2020 ,	
48	The Effects of Nutrition on Linear Growth 2022 , 14,	1
47	Stanniocalcin 2 (STC2): a universal tumour biomarker and a potential therapeutical target 2022 , 41, 161	1
46	The genomic origins of the world's first farmers 2022,	1
45	Importance of Including Non-European Populations in Large Human Genetic Studies to Enhance Precision Medicine 2022 ,	2
44	Increased activity of the metalloproteinase PAPP-A promotes diabetes-induced glomerular hypertrophy 2022 , 155218	1
43	Incorporating Genetic Determinants of Prostate-Specific Antigen Levels Improves Prostate Cancer Screening.	0
42	Host genetic basis of COVID-19: from methodologies to genes.	1
41	Mapping the Mountains of Giants: Anthropometric Data from the Western Balkans Reveal a Nucleus of Extraordinary Physical Stature in Europe. 2022 , 11, 786	0
40	A multi-population phenome-wide association study of genetically-predicted height in the Million Veteran Program. 2022 , 18, e1010193	0
39	Genome-wide meta-analysis and omics integration identifies novel genes associated with diabetic kidney disease.	1
38	An association study of ABCG2 rs2231142 on the concentrations of allopurinol and its metabolites.	1
37	Applications of artificial intelligence multiomics in precision oncology.	O
36	The sequences of 150,119 genomes in the UK Biobank. <i>Nature</i> , 2022 , 607, 732-740	50.4 6
35	Pappalysins and Stanniocalcins and Their Relationship With the Peripheral IGF Axis in Newborns and During Development.	0

34	Systematic single-variant and gene-based association testing of thousands of phenotypes in 394,841 UK Biobank exomes. 2022 , 100168	0
33	DNA: current developments and perspectives. 2022 , 109-141	
32	Deleterious Mutations and the Rare Allele Burden on Rice Gene Expression. 2022, 39,	1
31	Genome-Wide Association Mapping and Genomic Selection Approaches for Stress Resilience in Rice. 2022 , 45-94	O
30	Twin studies in social science. 2022 , 261-276	O
29	A saturated map of common genetic variants associated with human height. 2022 , 610, 704-712	2
28	Structure of the proteolytic enzyme PAPP-A with the endogenous inhibitor stanniocalcin-2 reveals its inhibitory mechanism. 2022 , 13,	1
27	Influences of rare copy-number variation on human complex traits. 2022 , 185, 4233-4248.e27	O
26	SUMMIT: An integrative approach for better transcriptomic data imputation improves causal gene identification. 2022 , 13,	O
25	Identification of Diagnostic Variants in FGFR2 and NPR2 Genes in a Chinese Family Affected by Crouzon Syndrome and Acromesomelic Dysplasia, Type Maroteaux.	O
24	Meta-analysis fine-mapping is often miscalibrated at single-variant resolution. 2022, 100210	O
23	Adult Height, 22q11.2 Deletion Extent, and Short Stature in 22q11.2 Deletion Syndrome. 2022 , 13, 2038	O
22	Genetics for the pediatric endocrinologists 12 Primordial short stature in children and adolescents. 2, 68-77	O
21	Diagnostic yield of a multigene sequencing approach in children classified as idiopathic short stature. 2022 , 11,	O
20	Examination of runs of homozygosity in relation to height in an endogamous Namibian population.	0
19	Whole-exome sequence analysis of anthropometric traits illustrates challenges in identifying effects of rare genetic variants. 2023 , 4, 100163	O
18	Structural insights into the covalent regulation of PAPP-A activity by proMBP and STC2. 2022, 8,	O
17	Region-related patterns of the main physical development indicators observed in northerners in the ontogenetic aspect. 2022 , 7, 173-181	0

CITATION REPORT

16	Idiopathic Short Stature: What to Expect from Genomic Investigations. 2023, 4, 1-17	О
15	Using inbreeding to test the contribution of non-additive genetic effects to additive genetic variance: a case study inDrosophila serrata.	1
14	The Stanniocalcin-PAPP-A-IGFBP-IGF Axis.	O
13	Behavioural genetics methods. 2023 , 3,	1
12	Females present higher dose-adjusted drug concentrations of metoprolol and allopurinol/oxypurinol than males.	0
11	Rare variant analyses in large-scale cohorts identified SLC13A1 associated with chronic pain. 2023 , Publish Ahead of Print,	O
10	Stature estimation in Ancient Greece: population-specific equations and secular trends from 9000 BC to 900 AD. 2023 , 15,	0
9	Modern Humans Disperse From Africa. 2022 , 581-623	O
8	Genome-wide association study reveals BET1L associated with survival time in the 137,693 Japanese individuals. 2023 , 6,	O
7	SUMMIT-FA: A new resource for improved transcriptome imputation using functional annotations.	О
6	Host genetics and COVID-19 severity: increasing the accuracy of latest severity scores by Boolean quantum features.	О
5	Rare genetic variants underlie outlying levels of DNA methylation and gene-expression.	O
4	The long-term effects of genomic selection: 2. Changes in allele frequencies of causal loci and new mutations.	0
3	Adult Body Height Is Associated with the Risk of Type 2 but Not Type 1 Diabetes Mellitus: A Retrospective Cohort Study of 783,029 Individuals in Germany. 2023 , 12, 2199	O
2	Using inbreeding to test the contribution of non-additive genetic effects to additive genetic variance: a case study in Drosophila serrata. 2023 , 290,	0
1	Gradualism, natural selection, and the randomness of mutation fi sher, Kimura, and Orr, connecting the dots. 2023 , 38,	O