## Allen Ancient DNA Resource (AADR): Downloadable genotypes of present-day and ancient data

\*\*\* V62.0: Data release: Sep 12 2024 \*\*\*

On this page you can download a merged dataset consisting of genotypes for thousands of ancient and present-day individuals at up to 1.23 million positions in the genome (in hg19 coordinates).  
  
The aim of Allen Ancient DNA Resource (AADR) is to provide a uniformly curated dataset that can be useful for scientists interested in carrying out analyses of population history and natural selection.  
  
The genotypes in the AADR are not always a perfect match to those from the associated published papers. This is because to make it easier to coanalyze datasets we have started from bam or fastq files, trimmed the ends of sequences to reduce errors due to ancient DNA damage in a way that is largely uniform across datasets, which may be slightly different from that used in the individual publications, and determined genotypes anew by sampling a random sequence to cover each position.   
  
Researchers who wish to use this compilation as the basis of their publications should cite this source and release version (i.e.. "https://dataverse.harvard.edu/dataverse/reich\_lab", version 62.0), while also citing the individual papers that report the data for each of the individuals they analyze (all references for the source data are listed below).   
Going forward, we expect to be updating this resource more regularly to keep it maximally usefult to the community. Please let us know if you have recommendations of identify errors or others issues.  
  
We thank the Paul G. Allen Foundation, the John Templeton Foundation, a grant from the U.S. National Institutes of Health, and the Howard Hughes Medical Institute, for providing the resources needed to create and update this dataset.  
  
**Updated in this release:**  
• substantial additional samples,  
• runs of homozygosity are reported for segments >4cM and >20cM, as well as contamination estimates [HuangRingbauer2022].   
  
All data released here:  
(a) have already been published (some by our group and some by other groups - see full list of references below),  
(b) have permissions appropriate for fully public data release,  
(c) have data reported for 1,233,013 sites in the genome (or 584,131 sites for modern individuals genotyped on the Affymetrix Human Origins array). For most individuals, genetic data are represented by randomly sampled sequences at positions covered by at least one sequence.

**Description of data:**

There are two datasets:

*"1240K" : Ancient and present-day individuals (from either shotgun sequencing data or in-solution target capture, with a range of coverages) at 1,233,013 sites,*

*"1240K+HO": Data from the above set merged with present-day individuals typed on the Human Origins array with 584,131 sites.*

Each dataset consists of four files, in [eigenstrat](https://reich.hms.harvard.edu/software/InputFileFormats) format. For details, please see: [eigensoft](https://github.com/DReichLab/EIG/tree/master/EIGENSTRAT):  
  
*.anno*: Rich meta-information for each individual. For convenience, this is provided in two formats (i) xlsx, OR (ii) tab delimited text (tsv). Both are encoded in utf-8 format.  
*.ind* : Three columns: Genetic ID, sex determination, and group label (population).  
*.snp* : Information on each analyzed SNP position (SNP id, physical/genetic location and reference/variant alleles, where the reference allele matches hg19).  
*.geno*: Genotypes (see footnote 2 below).   
  
  
**Version v62.0**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| *Description* | *.anno* | *.ind* | *.snp* | *.geno* | *Current version* | *Previous version (v54.1p1)* |
| *1240k* | xlsx (4.5 Mb), or tsv (7.9 Mb) | 800Kb | 75Mb | 5.1Gb | *17629 unique individuals (13571 ancient, 4058 present-day)1* | *16389 unique individuals (9990 ancient, 6399 present-day)1* |
| *1240K+HO* | xlsx (5.2 Mb), or txt (9.5 Mb) | 953Kb | 36Mb | 3.0Gb | *21945 unique individuals (13571 ancient, 8374 present-day)1* | *20503 unique individuals (9990 ancient, 10513 present-day)1* |

*1: (a) includes one ancestral reference, and three present-day references: human, chimp, gorilla, (b) the number of ancient individuals is slightly different as very low coverage samples for each SNP set are removed, (c) the number of modern samples has dropped to an update in our 1kg samples, where previously we use the low coverage phase 3 dataset releasing both pseudo-haploid calls directly from alignment files as well as imputed diploid calls; we have now switched to the newer high coverage sequencing and only use the diploid calls released by the 1kg consortium, at these SNP sites.*   
*2: genotypes are in a binary form using the 'packedancestrymap' format described in in* [*eigensoft*](https://github.com/DReichLab/EIG/tree/master/EIGENSTRAT)*; this may be converted to a (large) text file (i.e. 'eigenstrat' format, using the software 'convertf').*  
*3: md5sums are available. These may be used to verify that files which are downloaded match this distribution, using the linux command: 'md5sum < file >'.*  
  
**Please note**: The unique individual identifier is given in the 'Master ID' field. Multiple representatives of the same individual are thus indicated by a duplicated master ID. Some individuals are represented more than once to reflect different versions of processing or different publications. This may happen for example, when increased coverage has been generated after an initial publication. For many analyses it may be necessary to select only one version: for example the single sample masterID=Loschbour is represented by three Genetic IDs, 'Loschbour\_snpAD.DG', 'Loschbour\_published.DG', and I0001.AG. It would be incorrect to consider these as three separate samples from the same population. If it is not important which version is used, we suggest choosing the master ID which has the highest number of SNPs hit on autosomal targets.   
  
In addition, mitogenomes for samples generated at the Reich Lab (filtered for coverage) are available.  
  
We continue to be grateful if/when users of this dataset could alert us to any errors they detect and help us to fill in missing data. This could include: (1) errors or missing information for location, latitude, longitude, archaeological context, date, and group label, (2) concerns about Y chromosome or mitochondrial DNA haplogroup determinations, and (3) evidence for other problems in the data or annotations for individuals. Please write to [Swapan 'Shop' Mallick](mailto:shop@genetics.med.harvard.edu) and [David Reich](mailto:reich@genetics.med.harvard.edu) with any suggestions. We would also be grateful if members of the community could suggest additional content that would be helpful to add to this page to make it maximally useful. Finally, please let us know if there are any published ancient or modern DNA datasets that are not included in this compendium and that should be. The following datasets are already processed for inclusion in the next release which will be v63. However, if you write to us to let us know of any missing datasets not on this list we will make a special effort to include them.   
  
**Terminology and abbreviations used:**  
*HG=hunter-gatherer, N=Neolithic, C=Chalcolithic/CopperAge, BA=BronzeAge, IA=IronAge  
E=Early, M=Middle, L=Late, A=Antiquity  
SG=samples with whole genome shotgun sequence data, randomly drawing a single read to represent each position in the genome  
DG=samples shotgun sequenced with high enough coverage to call diploid genotypes, allowing for heterozygous calls  
snpAD.DG=samples shotgun sequenced with diploid calls made using snpAD [PrüferBioinformatics2018]  
SDG=Sanger dipoid genotypes  
WGC=Whole genome capture  
WGA=Whole genome amplified  
AG=Agilent sequencing  
TW=Twist sequencing (see note below)*  
*Individuals marked as 'Ignore\_' or 'outlier' have been identified as ones which may be filtered out from primary analyses for various reasons, such as being outliers from their main clusters or close relatives of others from the same group.*   
  
**UDG treatments:**  
Various UDG protocols are available to researchers, indicated in field 'Library type'.   
• UDG-minus means that no UDG treatment is used. The typical deamination profile that results is then high towards the ends of the molecules and drops off slowly as one moves 5-10 bases towards the centre of the molecule; deamination still occurs throughout the molecule.   
• UDG-plus means that UDG is used. With this, molecules are cleaved where a uracil exists prior to sequencing. This means that deamination (generally) does not exist (there are some situations where UDG treatment fails, for example at methylated sites).   
• UDG-half is a specialised form of UDG treatment, where uracils are not completely removed, and left at the first one or two bases. The profile of deamination is then very high at the first base, drops fast and by the third base is very low. This continues throughout the molecule, until one or two bases at the other end. This is useful in that molecules which are clearly ancient from the deamination signature may be identified (using tools such as MapDamage, or pmdtools), but the number of bases which are 'damaged' and typically have to be removed prior to analysis is low - just one or two bases, whereas with UDG-minus, typically, five or even ten bases should be removed. Given how short ancient DNA molecules can be compared with modern DNA, because of degradation, losing five or ten bases can be a considerable loss of data for some samples (in the dataset provided here, we almost always ignore data derives from sites 1-2 nucleotides from either end for UDG-half, and 5-10 nucleotides from either end for UDG-minus).   
• mixed treatments, eg:UDG-plus,half: For each sample, a number of libraries may be constructed, and of course different UDG treatments can be used for different libraries. The different libraries are useful because they capture different molecules and thus increase data quality for the individual. When these libraries are combined into a single bam (or aligned dataset) for an individual sample, these can be annotated according to the separate treatments, eg: "plus,half".   
  
**Notes:**  
• "Twist" sequencing is a significant update in our protocol for capture and data for all newer samples are captured this way, as described in [RohlandMallickGenomeResearch2022]. These samples are indicated in the genetic ids with "TW", in contrast to our older Agilent sequencing, marked "AG". One significant advantage is that twist capture reduces bias when co-analysed with shotgun data,  
• the pseudo-haploid calling procedure has been updated to objectively determine thresholding parameters based on error rates (technical note to follow),  
• 13442 poor performing SNPs were dropped from the Human Origins array, compared with previous releases.

**Previous versions:**  
[V54.1.p1](https://reichdata.hms.harvard.edu/pub/datasets/amh_repo/curated_releases/index_v54.1.p1.html): released Mar 6 2023   
[V54.1](https://reichdata.hms.harvard.edu/pub/datasets/amh_repo/curated_releases/index_v54.1.html): released Nov 22 2022   
[V52.2](https://reichdata.hms.harvard.edu/pub/datasets/amh_repo/curated_releases/index_v52.2.html): released Aug 22 2022   
[V50.0.p1](https://reichdata.hms.harvard.edu/pub/datasets/amh_repo/curated_releases/index_v50.0.p1.html): released Aug 1 2022   
[V50.0](https://reichdata.hms.harvard.edu/pub/datasets/amh_repo/curated_releases/index_v50.0.html): released Oct 2021   
[V44.3](https://reichdata.hms.harvard.edu/pub/datasets/amh_repo/curated_releases/index_v44.3.html): released Jan 2021   
[V42.4](https://reichdata.hms.harvard.edu/pub/datasets/amh_repo/curated_releases/index_v42.4.html): released Mar 2020   
[V37.2](https://reichdata.hms.harvard.edu/pub/datasets/amh_repo/curated_releases/index_v37.2.html): released Feb 2019

### References:

[1KGPhase3]:   
**A global reference for human genetic variation.** 1000 Genomes Project Consortium, Auton A, Brooks LD, Durbin RM, Garrison EP, Kang HM, Korbel JO, Marchini JL, McCarthy S, McVean GA, Abecasis GR. Nature. 2015 Oct 1;526(7571):68-74. doi: 10.1038/nature15393. PMID: 26432245. <http://www.internationalgenome.org/data/> .   
  
[AgranatTamirWaldmanCell2020]:  
**The Genomic History of the Bronze Age Southern Levant.** Agranat-Tamir L, Waldman S, Martin MAS, Gokhman D, Mishol N, Eshel T, Cheronet O, Rohland N, Mallick S, Adamski N, Lawson AM, Mah M, Michel M, Oppenheimer J, Stewardson K, Candilio F, Keating D, Gamarra B, Tzur S, Novak M, Kalisher R, Bechar S, Eshed V, Kennett DJ, Faerman M, Yahalom-Mack N, Monge JM, Govrin Y, Erel Y, Yakir B, Pinhasi R, Carmi S, Finkelstein I, Carmel L, Reich D.Cell. 2020 May 28;181(5):1146-1157.e11. doi: 10.1016/j.cell.2020.04.024. PMID: 32470400.   
  
[AllentoftNature2015]:  
**Population genomics of Bronze Age Eurasia.** Allentoft ME, Sikora M, Sjögren KG, Rasmussen S, Rasmussen M, Stenderup J, Damgaard PB, Schroeder H, Ahlström T, Vinner L, Malaspinas AS, Margaryan A, Higham T, Chivall D, Lynnerup N, Harvig L, Baron J, Della Casa P, Dąbrowski P, Duffy PR, Ebel AV, Epimakhov A, Frei K, Furmanek M, Gralak T, Gromov A, Gronkiewicz S, Grupe G, Hajdu T, Jarysz R, Khartanovich V, Khokhlov A, Kiss V, Kolář J, Kriiska A, Lasak I, Longhi C, McGlynn G, Merkevicius A, Merkyte I, Metspalu M, Mkrtchyan R, Moiseyev V, Paja L, Pálfi G, Pokutta D, Pospieszny Ł, Price TD, Saag L, Sablin M, Shishlina N, Smrčka V, Soenov VI, Szeverényi V, Tóth G, Trifanova SV, Varul L, Vicze M, Yepiskoposyan L, Zhitenev V, Orlando L, Sicheritz-Pontén T, Brunak S, Nielsen R, Kristiansen K, Willerslev E. Nature. 2015 Jun 11;522(7555):167-72. doi: 10.1038/nature14507.  
  
[AllentoftNature2024]:  
**100 ancient genomes show repeated population turnovers in Neolithic Denmark.** Allentoft ME, Sikora M, Fischer A, Sjögren KG, Ingason A, Macleod R, Rosengren A, Schulz Paulsson B, Jørkov MLS, Novosolov M, Stenderup J, Price TD, Fischer Mortensen M, Nielsen AB, Ulfeldt Hede M, Sørensen L, Nielsen PO, Rasmussen P, Jensen TZT, Refoyo-Martínez A, Irving-Pease EK, Barrie W, Pearson A, Sousa da Mota B, Demeter F, Henriksen RA, Vimala T, McColl H, Vaughn A, Vinner L, Renaud G, Stern A, Johannsen NN, Ramsøe AD, Schork AJ, Ruter A, Gotfredsen AB, Henning Nielsen B, Brinch Petersen E, Kannegaard E, Hansen J, Buck Pedersen K, Pedersen L, Klassen L, Meldgaard M, Johansen M, Uldum OC, Lotz P, Lysdahl P, Bangsgaard P, Petersen PV, Maring R, Iversen R, Wåhlin S, Anker Sørensen S, Andersen SH, Jørgensen T, Lynnerup N, Lawson DJ, Rasmussen S, Korneliussen TS, Kjær KH, Durbin R, Nielsen R, Delaneau O, Werge T, Kristiansen K, Willerslev E. Nature. 2024 Jan;625(7994):329-337. doi: 10.1038/s41586-023-06862-3. Epub 2024 Jan 10. PMID: 38200294; PMCID: PMC10781617.

[AllentoftSikoraNature2024]:  
**Population genomics of post-glacial western Eurasia.** Allentoft ME, Sikora M, Refoyo-Martínez A, Irving-Pease EK, Fischer A, Barrie W, Ingason A, Stenderup J, Sjögren KG, Pearson A, Sousa da Mota B, Schulz Paulsson B, Halgren A, Macleod R, Jørkov MLS, Demeter F, Sørensen L, Nielsen PO, Henriksen RA, Vimala T, McColl H, Margaryan A, Ilardo M, Vaughn A, Fischer Mortensen M, Nielsen AB, Ulfeldt Hede M, Johannsen NN, Rasmussen P, Vinner L, Renaud G, Stern A, Jensen TZT, Scorrano G, Schroeder H, Lysdahl P, Ramsøe AD, Skorobogatov A, Schork AJ, Rosengren A, Ruter A, Outram A, Timoshenko AA, Buzhilova A, Coppa A, Zubova A, Silva AM, Hansen AJ, Gromov A, Logvin A, Gotfredsen AB, Henning Nielsen B, González-Rabanal B, Lalueza-Fox C, McKenzie CJ, Gaunitz C, Blasco C, Liesau C, Martinez-Labarga C, Pozdnyakov DV, Cuenca-Solana D, Lordkipanidze DO, En'shin D, Salazar-García DC, Price TD, Borić D, Kostyleva E, Veselovskaya EV, Usmanova ER, Cappellini E, Brinch Petersen E, Kannegaard E, Radina F, Eylem Yediay F, Duday H, Gutiérrez-Zugasti I, Merts I, Potekhina I, Shevnina I, Altinkaya I, Guilaine J, Hansen J, Aura Tortosa JE, Zilhão J, Vega J, Buck Pedersen K, Tunia K, Zhao L, Mylnikova LN, Larsson L, Metz L, Yepiskoposyan L, Pedersen L, Sarti L, Orlando L, Slimak L, Klassen L, Blank M, González-Morales M, Silvestrini M, Vretemark M, Nesterova MS, Rykun M, Rolfo MF, Szmyt M, Przybyła M, Calattini M, Sablin M, Dobisíková M, Meldgaard M, Johansen M, Berezina N, Card N, Saveliev NA, Poshekhonova O, Rickards O, Lozovskaya OV, Gábor O, Uldum OC, Aurino P, Kosintsev P, Courtaud P, Ríos P, Mortensen P, Lotz P, Persson P, Bangsgaard P, de Barros Damgaard P, Vang Petersen P, Martinez PP, Włodarczak P, Smolyaninov RV, Maring R, Menduiña R, Badalyan R, Iversen R, Turin R, Vasilyev S, Wåhlin S, Borutskaya S, Skochina S, Sørensen SA, Andersen SH, Jørgensen T, Serikov YB, Molodin VI, Smrcka V, Merts V, Appadurai V, Moiseyev V, Magnusson Y, Kjær KH, Lynnerup N, Lawson DJ, Sudmant PH, Rasmussen S, Korneliussen TS, Durbin R, Nielsen R, Delaneau O, Werge T, Racimo F, Kristiansen K, Willerslev E. Nature. 2024 Jan;625(7994):301-311. doi: 10.1038/s41586-023-06865-0. Epub 2024 Jan 10. Erratum in: Nature. 2024 Feb;626(7997):E3. doi: 10.1038/s41586-024-07044-5. PMID: 38200295; PMCID: PMC10781627. <br[altınışıkscienceadvances2022]:>  
Altınışık NE, Kazancı DD, Aydoğan A, Gemici HC, Erdal ÖD, Sarıaltun S, Vural KB, Koptekin D, Gürün K, Sağj.cub.2022.04.069. Epub 2022 May 18. PMID: 35588742; PMCID: PMC9245899.  
  
[ArmitAntiquity2023]:  
**Kinship practices in Early Iron Age southeast Europe: genetic and isotopic analysis of burials from the Dolge njive barrow cemetery, Dolenjska, Slovenia.** Armit, I., Fischer, C.-E. M. C., Koon, H., Nicholls, R., Olalde, I., Rohland, N., Buckberry, J., Montgomery, J., Mason, P., Črešnar, M., Buster, L. S., & Reich, D. (2023). Antiquity, 97(392), 403-418. https://doi.org/10.15184/aqy.2023.2  
  
[BarbieriMolBiolEvol2019]:  
**The Current Genomic Landscape of Western South America: Andes, Amazonia, and Pacific Coast.** Barbieri C, Barquera R, Arias L, Sandoval JR, Acosta O, Zurita C, Aguilar-Campos A, Tito-Álvarez AM, Serrano-Osuna R, Gray RD, Mafessoni F, Heggarty P, Shimizu KK, Fujita R, Stoneking M, Pugach I, Fehren-Schmitz L. Mol Biol Evol. 2019 Dec 1;36(12):2698-2713. doi: 10.1093/molbev/msz174. PMID: 31350885; PMCID: PMC6878948.  
  
[BarqueraKrauseCurrBio2020]:  
**Origin and Health Status of First-Generation Africans from Early Colonial Mexico.** Barquera R, Lamnidis TC, Lankapalli AK, Kocher A, Hernández-Zaragoza DI, Nelson EA, Zamora-Herrera AC, Ramallo P, Bernal-Felipe N, Immel A, Bos K, Acuña-Alonzo V, Barbieri C, Roberts P, Herbig A, Kühnert D, Márquez-Morfín L, Krause J. Curr Biol. 2020 Jun 8;30(11):2078-2091.e11. doi: 10.1016/j.cub.2020.04.002. Epub 2020 Apr 30. PMID: 32359431.  
  
[BarqueraKrauseNature2024]:  
**Ancient genomes reveal insights into ritual life at Chichén Itzá.** Barquera R, Del Castillo-Chávez O, Nägele K, Pérez-Ramallo P, Hernández-Zaragoza DI, Szolek A, Rohrlach AB, Librado P, Childebayeva A, Bianco RA, Penman BS, Acuña-Alonzo V, Lucas M, Lara-Riegos JC, Moo-Mezeta ME, Torres-Romero JC, Roberts P, Kohlbacher O, Warinner C, Krause J. Nature. 2024 Jun;630(8018):912-919. doi: 10.1038/s41586-024-07509-7. Epub 2024 Jun 12. PMID: 38867041; PMCID: PMC11208145.  
  
[BeggKrauseCurrBio2023]:  
**Genomic analyses of hair from Ludwig van Beethoven.** Begg TJA, Schmidt A, Kocher A, Larmuseau MHD, Runfeldt G, Maier PA, Wilson JD, Barquera R, Maj C, Szolek A, Sager M, Clayton S, Peltzer A, Hui R, Ronge J, Reiter E, Freund C, Burri M, Aron F, Tiliakou A, Osborn J, Behar DM, Boecker M, Brandt G, Cleynen I, Strassburg C, Prüfer K, Kühnert D, Meredith WR, Nöthen MM, Attenborough RD, Kivisild T, Krause J. Curr Biol. 2023 Apr 24;33(8):1431-1447.e22. doi: 10.1016/j.cub.2023.02.041. Epub 2023 Mar 22. PMID: 36958333.  
  
[BennettNatEcoEvo2023]:  
**Genome sequences of 36,000- to 37,000-year-old modern humans at Buran-Kaya III in Crimea.** Bennett EA, Parasayan O, Prat S, Péan S, Crépin L, Yanevich A, Grange T, Geigl EM. Nat Ecol Evol. 2023 Dec;7(12):2160-2172. doi: 10.1038/s41559-023-02211-9. Epub 2023 Oct 23. Erratum in: Nat Ecol Evol. 2024 Mar;8(3):589. doi: 10.1038/s41559-024-02332-9. PMID: 37872416.  
  
[BergstromScience2020]:  
**Insights into human genetic variation and population history from 929 diverse genomes.** Bergström A, McCarthy SA, Hui R, Almarri MA, Ayub Q, Danecek P, Chen Y, Felkel S, Hallast P, Kamm J, Blanché H, Deleuze JF, Cann H, Mallick S, Reich D, Sandhu MS, Skoglund P, Scally A, Xue Y, Durbin R, Tyler-Smith C. Science. 2020 Mar 20;367(6484):eaay5012. doi: 10.1126/science.aay5012. PMID: 32193295; PMCID: PMC7115999.  
  
[BagnascoStoddartSciReps2024]:  
**Bioarchaeology aids the cultural understanding of six characters in search of their agency (Tarquinia, ninth-seventh century BC, central Italy).** Bagnasco G, Marzullo M, Cattaneo C, Biehler-Gomez L, Mazzarelli D, Ricciardi V, Müller W, Coppa A, McLaughlin R, Motta L, Prato O, Schmidt F, Gaveriaux F, Marras GB, Millet MA, Madgwick R, Ballantyne R, Makarewicz CA, Trentacoste A, Reimer P, Mattiangeli V, Bradley DG, Malone C, Esposito C, Breslin EM, Stoddart S. Sci Rep. 2024 May 28;14(1):11895. doi: 10.1038/s41598-024-61052-z. PMID: 38806487; PMCID: PMC11133411.  
  
[BiaginiEJHG2019]:  
**People from Ibiza: an unexpected isolate in the Western Mediterranean.** Biagini SA, Solé-Morata N, Matisoo-Smith E, Zalloua P, Comas D, Calafell F. People from Ibiza: an unexpected isolate in the Western Mediterranean. Eur J Hum Genet. 2019 Jun;27(6):941-951. doi: 10.1038/s41431-019-0361-1. Epub 2019 Feb 14. PMID: 30765884; PMCID: PMC6777470.  
  
[BlocherPNAS2023]:  
**Descent, marriage, and residence practices of a 3,800-year-old pastoral community in Central Eurasia.** Blöcher J, Brami M, Feinauer IS, Stolarczyk E, Diekmann Y, Vetterdietz L, Karapetian M, Winkelbach L, Kokot V, Vallini L, Stobbe A, Haak W, Papageorgopoulou C, Krause R, Sharapova S, Burger J. Proc Natl Acad Sci U S A. 2023 Sep 5;120(36):e2303574120. doi: 10.1073/pnas.2303574120. Epub 2023 Aug 21. PMID: 37603728; PMCID: PMC10483636.  
  
[BongersPNAS2020]:  
**Integration of ancient DNA with transdisciplinary dataset finds strong support for Inca resettlement in the south Peruvian coast.** Bongers JL, Nakatsuka N, O'Shea C, Harper TK, Tantaleán H, Stanish C, Fehren-Schmitz L. Proc Natl Acad Sci U S A. 2020 Aug 4;117(31):18359-18368. doi: 10.1073/pnas.2005965117. Epub 2020 Jul 13. PMID: 32661160; PMCID: PMC7414190.  
  
[BortoliniBenazziCurBio2021]:  
**Early Alpine occupation backdates westward human migration in Late Glacial Europe.** Bortolini E, Pagani L, Oxilia G, Posth C, Fontana F, Badino F, Saupe T, Montinaro F, Margaritora D, Romandini M, Lugli F, Papini A, Boggioni M, Perrini N, Oxilia A, Cigliano RA, Barcelona R, Visentin D, Fasser N, Arrighi S, Figus C, Marciani G, Silvestrini S, Bernardini F, Menghi Sartorio JC, Fiorenza L, Cecchi JM, Tuniz C, Kivisild T, Gianfrancesco F, Peresani M, Scheib CL, Talamo S, D'Esposito M, Benazzi S. Early Alpine occupation backdates westward human migration in Late Glacial Europe. Curr Biol. 2021 Jun 7;31(11):2484-2493.e7. doi: 10.1016/j.cub.2021.03.078. Epub 2021 Apr 21. PMID: 33887180.  
  
[BraceCurrBio2022]:  
D**Genomes from a medieval mass burial show Ashkenazi-associated hereditary diseases pre-date the 12th century.** Brace S, Diekmann Y, Booth T, Macleod R, Timpson A, Stephen W, Emery G, Cabot S, Thomas MG, Barnes I. Curr Biol. 2022 Oct 24;32(20):4350-4359.e6. doi: 10.1016/j.cub.2022.08.036. Epub 2022 Aug 30. PMID: 36044903; PMCID: PMC10499757.  
  
[BraceDiekmannNatureEcologyEvolution2019]:  
**Ancient genomes indicate population replacement in Early Neolithic Britain.** Brace S, Diekmann Y, Booth TJ, van Dorp L, Faltyskova Z, Rohland N, Mallick S, Olalde I, Ferry M, Michel M, Oppenheimer J, Broomandkhoshbacht N, Stewardson K, Martiniano R, Walsh S, Kayser M, Charlton S, Hellenthal G, Armit I, Schulting R, Craig OE, Sheridan A, Parker Pearson M, Stringer C, Reich D, Thomas MG, Barnes I. Nat Ecol Evol. 2019 May;3(5):765-771. doi: 10.1038/s41559-019-0871-9. Epub 2019 Apr 15. Erratum in: Nat Ecol Evol. 2019 Jun;3(6):986-987. doi: 10.1038/s41559-019-0912-4. PMID: 30988490; PMCID: PMC6520225.

[BrielleFleisherWynneJonesNature2023]:  
**Entwined African and Asian genetic roots of medieval peoples of the Swahili coast.** Brielle ES, Fleisher J, Wynne-Jones S, Sirak K, Broomandkhoshbacht N, Callan K, Curtis E, Iliev L, Lawson AM, Oppenheimer J, Qiu L, Stewardson K, Workman JN, Zalzala F, Ayodo G, Gidna AO, Kabiru A, Kwekason A, Mabulla AZP, Manthi FK, Ndiema E, Ogola C, Sawchuk E, Al-Gazali L, Ali BR, Ben-Salem S, Letellier T, Pierron D, Radimilahy C, Rakotoarisoa JA, Raaum RL, Culleton BJ, Mallick S, Rohland N, Patterson N, Mwenje MA, Ahmed KB, Mohamed MM, Williams SR, Monge J, Kusimba S, Prendergast ME, Reich D, Kusimba CM. Nature. 2023 Mar;615(7954):866-873. doi: 10.1038/s41586-023-05754-w. Epub 2023 Mar 29. PMID: 36991187; PMCID: PMC10060156.  
  
[BroushakiScience2016]:  
**Early Neolithic genomes from the eastern Fertile Crescent.** Broushaki F, Thomas MG, Link V, López S, van Dorp L, Kirsanow K, Hofmanová Z, Diekmann Y, Cassidy LM, Díez-Del-Molino D, Kousathanas A, Sell C, Robson HK, Martiniano R, Blöcher J, Scheu A, Kreutzer S, Bollongino R, Bobo D, Davudi H, Munoz O, Currat M, Abdi K, Biglari F, Craig OE, Bradley DG, Shennan S, Veeramah K, Mashkour M, Wegmann D, Hellenthal G, Burger J. Science. 2016 Jul 29;353(6298):499-503. doi: 10.1126/science.aaf7943. Epub 2016 Jul 14. PubMed PMID: 27417496; PubMed Central PMCID: PMC5113750.  
  
[BrunelPNAS2020]:  
**Ancient genomes from present-day France unveil 7,000 years of its demographic history.** Brunel S, Bennett EA, Cardin L, Garraud D, Barrand Emam H, Beylier A, Boulestin B, Chenal F, Ciesielski E, Convertini F, Dedet B, Desbrosse-Degobertiere S, Desenne S, Dubouloz J, Duday H, Escalon G, Fabre V, Gailledrat E, Gandelin M, Gleize Y, Goepfert S, Guilaine J, Hachem L, Ilett M, Lambach F, Maziere F, Perrin B, Plouin S, Pinard E, Praud I, Richard I, Riquier V, Roure R, Sendra B, Thevenet C, Thiol S, Vauquelin E, Vergnaud L, Grange T, Geigl EM, Pruvost M. Proc Natl Acad Sci U S A. 2020 Jun 9;117(23):12791-12798. doi: 10.1073/pnas.1918034117. Epub 2020 May 26. PMID: 32457149; PMCID: PMC7293694.  
  
[CapodiferroAchilliCell2021]:  
**Archaeogenomic distinctiveness of the Isthmo-Colombian area.** Capodiferro MR, Aram B, Raveane A, Rambaldi Migliore N, Colombo G, Ongaro L, Rivera J, Mendizábal T, Hernández-Mora I, Tribaldos M, Perego UA, Li H, Scheib CL, Modi A, Gòmez-Carballa A, Grugni V, Lombardo G, Hellenthal G, Pascale JM, Bertolini F, Grieco GS, Cereda C, Lari M, Caramelli D, Pagani L, Metspalu M, Friedrich R, Knipper C, Olivieri A, Salas A, Cooke R, Montinaro F, Motta J, Torroni A, Martín JG, Semino O, Malhi RS, Achilli A. Archaeogenomic distinctiveness of the Isthmo-Colombian area. Cell. 2021 Apr 1;184(7):1706-1723.e24. doi: 10.1016/j.cell.2021.02.040. Epub 2021 Mar 23. PMID: 33761327; PMCID: PMC8024902.  
  
[Byrska-BishopCell2022]:  
**High-coverage whole-genome sequencing of the expanded 1000 Genomes Project cohort including 602 trios.** Byrska-Bishop M, Evani US, Zhao X, Basile AO, Abel HJ, Regier AA, Corvelo A, Clarke WE, Musunuri R, Nagulapalli K, Fairley S, Runnels A, Winterkorn L, Lowy E; Human Genome Structural Variation Consortium; Paul Flicek, Germer S, Brand H, Hall IM, Talkowski ME, Narzisi G, Zody MC. Cell. 2022 Sep 1;185(18):3426-3440.e19. doi: 10.1016/j.cell.2022.08.004. PMID: 36055201; PMCID: PMC9439720.  
  
[CarlhoffBrummNature2021]:  
**Genome of a middle Holocene hunter-gatherer from Wallacea.** Carlhoff S, Duli A, Nägele K, Nur M, Skov L, Sumantri I, Oktaviana AA, Hakim B, Burhan B, Syahdar FA, McGahan DP, Bulbeck D, Perston YL, Newman K, Saiful AM, Ririmasse M, Chia S, Hasanuddin, Pulubuhu DAT, Suryatman, Supriadi, Jeong C, Peter BM, Prüfer K, Powell A, Krause J, Posth C, Brumm A. Nature. 2021 Aug;596(7873):543-547. doi: 10.1038/s41586-021-03823-6. Epub 2021 Aug 25. PMID: 34433944; PMCID: PMC8387238.  
  
[CarlhoffKrauseNatComm2023]:  
**Genomic portrait and relatedness patterns of the Iron Age Log Coffin culture in northwestern Thailand.** Carlhoff S, Kutanan W, Rohrlach AB, Posth C, Stoneking M, Nägele K, Shoocongdej R, Krause J. Nat Commun. 2023 Dec 22;14(1):8527. doi: 10.1038/s41467-023-44328-2. PMID: 38135688; PMCID: PMC10746721.  
  
[CassidyPNAS2016]:  
**Neolithic and Bronze Age migration to Ireland and establishment of the insular Atlantic genome.** Cassidy LM, Martiniano R, Murphy EM, Teasdale MD, Mallory J, Hartwell B, Bradley DG. Proc Natl Acad Sci U S A. 2016 Jan 12;113(2):368-73. doi: 10.1073/pnas.1518445113. Epub 2015 Dec 28.  
  
[CassidyNature2020]:  
**A dynastic elite in monumental Neolithic society.** Cassidy LM, Maoldúin RÓ, Kador T, Lynch A, Jones C, Woodman PC, Murphy E, Ramsey G, Dowd M, Noonan A, Campbell C, Jones ER, Mattiangeli V, Bradley DG. Nature. 2020 Jun;582(7812):384-388. doi: 10.1038/s41586-020-2378-6. Epub 2020 Jun 17. PMID: 32555485.  
  
[ChangmaiScientificReports2022]:  
**Ancient DNA from Protohistoric Period Cambodia indicates that South Asians admixed with local populations as early as 1st-3rd centuries CE.** Changmai P, Pinhasi R, Pietrusewsky M, Stark MT, Ikehara-Quebral RM, Reich D, Flegontov P. Sci Rep. 2022 Dec 29;12(1):22507. doi: 10.1038/s41598-022-26799-3. PMID: 36581666; PMCID: PMC9800559.  
  
[ChangmaiPLoSGenetics2022]:  
**Indian genetic heritage in Southeast Asian populations.** Changmai P, Jaisamut K, Kampuansai J, Kutanan W, Altınışık NE, Flegontova O, Inta A, Yüncü E, Boonthai W, Pamjav H, Reich D, Flegontov P. PLoS Genet. 2022 Feb 17;18(2):e1010036. doi: 10.1371/journal.pgen.1010036. PMID: 35176016; PMCID: PMC8853555.  
  
[ChildebayevaHaakMolBioEvo2022]:  
**Population Genetics and Signatures of Selection in Early Neolithic European Farmers.** Childebayeva A, Rohrlach AB, Barquera R, Rivollat M, Aron F, Szolek A, Kohlbacher O, Nicklisch N, Alt KW, Gronenborn D, Meller H, Friederich S, Prüfer K, Deguilloux MF, Krause J, Haak W. Population Genetics and Signatures of Selection in Early Neolithic European Farmers. Mol Biol Evol. 2022 Jun 2;39(6):msac108. doi: 10.1093/molbev/msac108. PMID: 35578825; PMCID: PMC9171004.  
  
[ChylenshiNatureComm2023]:  
**Patrilocality and hunter-gatherer-related ancestry of populations in East-Central Europe during the Middle Bronze Age.** Chyleński M, Makarowicz P, Juras A, Krzewińska M, Pospieszny Ł, Ehler E, Breszka A, Górski J, Taras H, Szczepanek A, Polańska M, Włodarczak P, Lasota-Kuś A, Wójcik I, Romaniszyn J, Szmyt M, Kośko A, Ignaczak M, Sadowski S, Matoga A, Grossman A, Ilchyshyn V, Yahodinska MO, Romańska A, Tunia K, Przybyła M, Grygiel R, Szostek K, Dabert M, Götherström A, Jakobsson M, Malmström H. Nat Commun. 2023 Aug 1;14(1):4395. doi: 10.1038/s41467-023-40072-9. PMID: 37528090; PMCID: PMC10393988.  
  
[ClementeCell2021]:  
**The genomic history of the Aegean palatial civilizations.** Clemente F, Unterländer M, Dolgova O, Amorim CEG, Coroado-Santos F, Neuenschwander S, Ganiatsou E, Cruz Dávalos DI, Anchieri L, Michaud F, Winkelbach L, Blöcher J, Arizmendi Cárdenas YO, Sousa da Mota B, Kalliga E, Souleles A, Kontopoulos I, Karamitrou-Mentessidi G, Philaniotou O, Sampson A, Theodorou D, Tsipopoulou M, Akamatis I, Halstead P, Kotsakis K, Urem-Kotsou D, Panagiotopoulos D, Ziota C, Triantaphyllou S, Delaneau O, Jensen JD, Moreno-Mayar JV, Burger J, Sousa VC, Lao O, Malaspinas AS, Papageorgopoulou C. The genomic history of the Aegean palatial civilizations. Cell. 2021 May 13;184(10):2565-2586.e21. doi: 10.1016/j.cell.2021.03.039. Epub 2021 Apr 29. PMID: 33930288; PMCID: PMC8127963.  
  
[CookeNakagomeSciAdv2021]:  
**Ancient genomics reveals tripartite origins of Japanese populations.** Cooke NP, Mattiangeli V, Cassidy LM, Okazaki K, Stokes CA, Onbe S, Hatakeyama S, Machida K, Kasai K, Tomioka N, Matsumoto A, Ito M, Kojima Y, Bradley DG, Gakuhari T, Nakagome S. Sci Adv. 2021 Sep 17;7(38):eabh2419. doi: 10.1126/sciadv.abh2419. Epub 2021 Sep 17. PMID: 34533991; PMCID: PMC8448447.  
  
[CoutinhoJakobssonAJPA2020]:  
**The Neolithic Pitted Ware culture foragers were culturally but not genetically influenced by the Battle Axe culture herders.** Coutinho A, Günther T, Munters AR, Svensson EM, Götherström A, Storå J, Malmström H, Jakobsson M. The Neolithic Pitted Ware culture foragers were culturally but not genetically influenced by the Battle Axe culture herders. Am J Phys Anthropol. 2020 Aug;172(4):638-649. doi: 10.1002/ajpa.24079. Epub 2020 Jun 4. PMID: 32497286.

[DamgaardNature2018]:  
**137 ancient human genomes from across the Eurasian steppes.** Damgaard PB, Marchi N, Rasmussen S, Peyrot M, Renaud G, Korneliussen T, Moreno-Mayar JV, Pedersen MW, Goldberg A, Usmanova E, Baimukhanov N, Loman V, Hedeager L, Pedersen AG, Nielsen K, Afanasiev G, Akmatov K, Aldashev A, Alpaslan A, Baimbetov G, Bazaliiskii VI, Beisenov A, Boldbaatar B, Boldgiv B, Dorzhu C, Ellingvag S, Erdenebaatar D, Dajani R, Dmitriev E, Evdokimov V, Frei KM, Gromov A, Goryachev A, Hakonarson H, Hegay T, Khachatryan Z, Khaskhanov R, Kitov E, Kolbina A, Kubatbek T, Kukushkin A, Kukushkin I, Lau N, Margaryan A, Merkyte I, Mertz IV, Mertz VK, Mijiddorj E, Moiyesev V, Mukhtarova G, Nurmukhanbetov B, Orozbekova Z, Panyushkina I, Pieta K, Smrčka V, Shevnina I, Logvin A, Sjögren KG, Štolcová T, Taravella AM, Tashbaeva K, Tkachev A, Tulegenov T, Voyakin D, Yepiskoposyan L, Undrakhbold S, Varfolomeev V, Weber A, Wilson Sayres MA, Kradin N, Allentoft ME, Orlando L, Nielsen R, Sikora M, Heyer E, Kristiansen K, Willerslev E. Nature. 2018 May;557(7705):369-374. doi: 10.1038/s41586-018-0094-2. Epub 2018 May 9.  
  
[DamgaardScience2018]:  
**The first horse herders and the impact of early Bronze Age steppe expansions into Asia.** de Barros Damgaard P, Martiniano R, Kamm J, Moreno-Mayar JV, Kroonen G, Peyrot M, Barjamovic G, Rasmussen S, Zacho C, Baimukhanov N, Zaibert V, Merz V, Biddanda A, Merz I, Loman V, Evdokimov V, Usmanova E, Hemphill B, Seguin-Orlando A, Yediay FE, Ullah I, Sjögren KG, Iversen KH, Choin J, de la Fuente C, Ilardo M, Schroeder H, Moiseyev V, Gromov A, Polyakov A, Omura S, Senyurt SY, Ahmad H, McKenzie C, Margaryan A, Hameed A, Samad A, Gul N, Khokhar MH, Goriunova OI, Bazaliiskii VI, Novembre J, Weber AW, Orlando L, Allentoft ME, Nielsen R, Kristiansen K, Sikora M, Outram AK, Durbin R, Willerslev E. Science. 2018 Jun 29;360(6396). pii: eaar7711. doi: 10.1126/science.aar7711. Epub 2018 May 9. PubMed PMID: 29743352.  
  
[DeAngelisRickardsGenes2022]  
**First Glimpse into the Genomic Characterization of People from the Imperial Roman Community of Casal Bertone (Rome, First–Third Centuries AD).** De Angelis F, Romboni M, Veltre V, Catalano P, Martínez-Labarga C, Gazzaniga V, Rickards O. First Glimpse into the Genomic Characterization of People from the Imperial Roman Community of Casal Bertone (Rome, First-Third Centuries AD). Genes (Basel). 2022 Jan 13;13(1):136. doi: 10.3390/genes13010136. PMID: 35052476; PMCID: PMC8774527.  
  
[DuliasPNAS2022]  
**Ancient DNA at the edge of the world: Continental immigration and the persistence of Neolithic male lineages in Bronze Age Orkney.** Dulias K, Foody MGB, Justeau P, Silva M, Martiniano R, Oteo-García G, Fichera A, Rodrigues S, Gandini F, Meynert A, Donnelly K, Aitman TJ; Scottish Genomes Partnership, Chamberlain A, Lelong O, Kozikowski G, Powlesland D, Waddington C, Mattiangeli V, Bradley DG, Bryk J, Soares P, Wilson JF, Wilson G, Moore H, Pala M, Edwards CJ, Richards MB. Ancient DNA at the edge of the world: Continental immigration and the persistence of Neolithic male lineages in Bronze Age Orkney. Proc Natl Acad Sci U S A. 2022 Feb 22;119(8):e2108001119. doi: 10.1073/pnas.2108001119. PMID: 35131896; PMCID: PMC8872714.  
  
[EbenesersdottirScience2018]  
**Ancient genomes from Iceland reveal the making of a human population.** Ebenesersdóttir SS, Sandoval-Velasco M, Gunnarsdóttir ED, Jagadeesan A, Guòmundsdóttir VB, Thordardóttir VB, Thordardóttir MS, Moore KHS, Siguròsson Á, Magnúsdóttir DN, Jónsson H, Snorradóttir S, Hovig E, Møller P, Kockum I, Olsson T, Alfredsson L, Hansen TF, Werge T, Cavalleri GL, Gilbert E, Lalueza-Fox C, Walser JW 3rd, Kristjánsdóttir S, Gopalakrishnan S, Árnadóttir L, Magnússon ÓP, Gilbert MTP, Stefánsson K, Helgason A. Science. 2018 Jun 1;360(6392):1028-1032. doi: 10.1126/science.aar2625. PMID: 29853688.  
  
[EgfjordAllentoftPLOS2021]:  
**Genomic Steppe ancestry in skeletons from the Neolithic Single Grave Culture in Denmark.** Egfjord AF, Margaryan A, Fischer A, Sjögren KG, Price TD, Johannsen NN, Nielsen PO, Sørensen L, Willerslev E, Iversen R, Sikora M, Kristiansen K, Allentoft ME. Genomic Steppe ancestry in skeletons from the Neolithic Single Grave Culture in Denmark. PLoS One. 2021 Jan 14;16(1):e0244872. doi: 10.1371/journal.pone.0244872. PMID: 33444387; PMCID: PMC7808695.

[FanGenomeBiology2019]:  
**African evolutionary history inferred from whole genome sequence data of 44 indigenous African populations.** Fan S, Kelly DE, Beltrame MH, Hansen MEB, Mallick S, Ranciaro A, Hirbo J, Thompson S, Beggs W, Nyambo T, Omar SA, Meskel DW, Belay G, Froment A, Patterson N, Reich D, Tishkoff SA. Genome Biol. 2019 Apr 26;20(1):82. doi: 10.1186/s13059-019-1679-2. Erratum in: Genome Biol. 2019 Oct 9;20(1):204. doi: 10.1186/s13059-019-1821-1. PMID: 31023338; PMCID: PMC6485071.  
  
[FeldmanNatureCommunications2019]:  
**Late Pleistocene human genome suggests a local origin for the first farmers of central Anatolia.** Feldman M, Fernández-Domínguez E, Reynolds L, Baird D, Pearson J, Hershkovitz I, May H, Goring-Morris N, Benz M, Gresky J, Bianco RA, Fairbairn A, Mustafaolu G, Stockhammer PW, Posth C, Haak W, Jeong C, Krause J. Nat Commun. 2019 Mar 19;10(1):1218. doi: 10.1038/s41467-019-09209-7. PMID: 30890703.  
  
[FeldmanScienceAdvances2019]:  
**Ancient DNA sheds light on the genetic origins of early Iron Age Philistines.** Feldman M, Master DM, Bianco RA, Burri M, Stockhammer PW, Mittnik A, Aja AJ, Jeong C, Krause J. Sci Adv. 2019 Jul 3;5(7):eaax0061. doi: 10.1126/sciadv.aax0061. eCollection 2019 Jul. PMID: 31281897.  
  
[FerrazNatEcoEvo2023]:  
**Genomic history of coastal societies from eastern South America.** Ferraz T, Suarez Villagran X, Nägele K, Radzevičiūtė R, Barbosa Lemes R, Salazar-García DC, Wesolowski V, Lopes Alves M, Bastos M, Rapp Py-Daniel A, Pinto Lima H, Mendes Cardoso J, Estevam R, Liryo A, Guimarães GM, Figuti L, Eggers S, Plens CR, Azevedo Erler DM, Valadares Costa HA, da Silva Erler I, Koole E, Henriques G, Solari A, Martin G, Serafim Monteiro da Silva SF, Kipnis R, Müller LM, Ferreira M, Carvalho Resende J, Chim E, da Silva CA, Borella AC, Tomé T, Müller Plumm Gomes L, Barros Fonseca D, Santos da Rosa C, de Moura Saldanha JD, Costa Leite L, Cunha CMS, Viana SA, Ozorio Almeida F, Klokler D, Fernandes HLA, Talamo S, DeBlasis P, Mendonça de Souza S, de Paula Moraes C, Elias Oliveira R, Hünemeier T, Strauss A, Posth C. Nat Ecol Evol. 2023 Aug;7(8):1315-1330. doi: 10.1038/s41559-023-02114-9. Epub 2023 Jul 31. PMID: 37524799; PMCID: PMC10406606.  
  
[FernandesNatureEcologyEvolution2020]:  
**The spread of steppe and Iranian-related ancestry in the islands of the western Mediterranean.** Fernandes DM, Mittnik A, Olalde I, Lazaridis I, Cheronet O, Rohland N, Mallick S, Bernardos R, Broomandkhoshbacht N, Carlsson J, Culleton BJ, Ferry M, Gamarra B, Lari M, Mah M, Michel M, Modi A, Novak M, Oppenheimer J, Sirak KA, Stewardson K, Mandl K, Schattke C, Özdoğan KT, Lucci M, Gasperetti G, Candilio F, Salis G, Vai S, Camarós E, Calò C, Catalano G, Cueto M, Forgia V, Lozano M, Marini E, Micheletti M, Miccichè RM, Palombo MR, Ramis D, Schimmenti V, Sureda P, Teira L, Teschler-Nicola M, Kennett DJ, Lalueza-Fox C, Patterson N, Sineo L, Coppa A, Caramelli D, Pinhasi R, Reich D. Nat Ecol Evol. 2020 Mar;4(3):334-345. doi: 10.1038/s41559-020-1102-0. Epub 2020 Feb 24. Erratum in: Nat Ecol Evol. 2020 May;4(5):764. PMID: 32094539; PMCID: PMC7080320.  
  
[FernandesSirakNature2020]:  
**A genetic history of the pre-contact Caribbean.** Fernandes DM, Sirak KA, Ringbauer H, Sedig J, Rohland N, Cheronet O, Mah M, Mallick S, Olalde I, Culleton BJ, Adamski N, Bernardos R, Bravo G, Broomandkhoshbacht N, Callan K, Candilio F, Demetz L, Carlson KSD, Eccles L, Freilich S, George RJ, Lawson AM, Mandl K, Marzaioli F, McCool WC, Oppenheimer J, Özdogan KT, Schattke C, Schmidt R, Stewardson K, Terrasi F, Zalzala F, Antúnez CA, Canosa EV, Colten R, Cucina A, Genchi F, Kraan C, La Pastina F, Lucci M, Maggiolo MV, Marcheco-Teruel B, Maria CT, Martínez C, París I, Pateman M, Simms TM, Sivoli CG, Vilar M, Kennett DJ, Keegan WF, Coppa A, Lipson M, Pinhasi R, Reich D. Nature. 2020 Dec 23. doi: 10.1038/s41586-020-03053-2. Epub ahead of print. PMID: 33361817.  
  
[FischerCell2022]:  
**Origin and mobility of Iron Age Gaulish groups in present-day France revealed through archaeogenomics.** Fischer CE, Pemonge MH, Ducoussau I, Arzelier A, Rivollat M, Santos F, Barrand Emam H, Bertaud A, Beylier A, Ciesielski E, Dedet B, Desenne S, Duday H, Chenal F, Gailledrat E, Goepfert S, Gorgé O, Gorgues A, Kuhnle G, Lambach F, Lefort A, Mauduit A, Maziere F, Oudry S, Paresys C, Pinard E, Plouin S, Richard I, Roth-Zehner M, Roure R, Thevenet C, Thomas Y, Rottier S, Deguilloux MF, Pruvost M. iScience. 2022 Mar 16;25(4):104094. doi: 10.1016/j.isci.2022.104094. PMID: 35402880; PMCID: PMC8983337.  
  
[FowlerOlaldeNature2021]:  
**A high-resolution picture of kinship practices in an Early Neolithic tomb.** Fowler C, Olalde I, Cummings V, Armit I, Büster L, Cuthbert S, Rohland N, Cheronet O, Pinhasi R, Reich D. Nature. 2022 Jan;601(7894):584-587. doi: 10.1038/s41586-021-04241-4. Epub 2021 Dec 22. PMID: 34937939; PMCID: PMC8896835.  
  
[FreilichPinhasiScientificReports2021]:  
**Reconstructing genetic histories and social organisation in Neolithic and Bronze Age Croatia. .** Freilich S, Ringbauer H, Los D, Novak M, Pavičić DT, Schiffels S, Pinhasi R. Sci Rep. 2021 Aug 18;11(1):16729. doi: 10.1038/s41598-021-94932-9. PMID: 34408163; PMCID: PMC8373892.  
  
[delaFuentePNAS2018]:  
**Genomic insights into the origin and diversification of late maritime hunter-gatherers from the Chilean Patagonia.** De la Fuente C, Ávila-Arcos MC, Galimany J, Carpenter ML, Homburger JR, Blanco A, Contreras P, Cruz Dávalos D, Reyes O, San Roman M, Moreno-Estrada A, Campos PF, Eng C, Huntsman S, Burchard EG, Malaspinas AS, Bustamante CD, Willerslev E, Llop E, Verdugo RA, Moraga M. Proc Natl Acad Sci U S A. 2018 Apr 24;115(17):E4006-E4012. doi: 10.1073/pnas.1715688115. Epub 2018 Apr 9. PubMed PMID: 29632188; PubMed Central PMCID: PMC5924884.  
  
[FernandesScientificReports2018]:  
**A genomic Neolithic time transect of hunter-farmer admixture in central Poland.** Fernandes DM, Strapagiel D, Borówka P, Marciniak B, Żądzińska E, Sirak K, Siska V, Grygiel R, Carlsson J, Manica A, Lorkiewicz W, Pinhasi R. Sci Rep. 2018 Oct 5;8(1):14879. doi: 10.1038/s41598-018-33067-w.  
  
[FlegontovNature2019]:  
**Palaeo-Eskimo genetic ancestry and the peopling of Chukotka and North America.** Flegontov P, Altinisik NE, Changmai P, Rohland N, Mallick S, Adamski N, Bolnick DA, Broomandkhoshbacht N, Candilio F, Culleton BJ, Flegontova O, Friesen TM, Jeong C, Harper TK, Keating D, Kennett DJ, Kim AM, Lamnidis TC, Lawson AM, Olalde I, Oppenheimer J, Potter BA, Raff J, Sattler RA, Skoglund P, Stewardson K, Vajda EJ, Vasilyev S, Veselovskaya E, Hayes MG, O'Rourke DH, Krause J, Pinhasi R, Reich D, Schiffels S. Nature. 2019 Jun;570(7760):236-240. doi: 10.1038/s41586-019-1251-y. Epub 2019 Jun 5. PMID: 31168094.  
  
[FregelPNAS2018]:  
**Ancient genomes from North Africa evidence prehistoric migrations to the Maghreb from both the Levant and Europe.** Fregel R, Méndez FL, Bokbot Y, Martín-Socas D, Camalich-Massieu MD, Santana J, Morales J, Ávila-Arcos MC, Underhill PA, Shapiro B, Wojcik G, Rasmussen M, Soares AER, Kapp J, Sockell A, Rodríguez-Santos FJ, Mikdad A, Trujillo-Mederos A, Bustamante CD. Proc Natl Acad Sci U S A. 2018 Jun 26;115(26):6774-6779. doi: 10.1073/pnas.1800851115. Epub 2018 Jun 12. Erratum in: Proc Natl Acad Sci U S A. 2018 Jul 24;115(30):E7231. PubMed PMID: 29895688; PubMed Central PMCID: PMC6042094.  
  
[FuNature2014]:  
**Genome sequence of a 45,000-year-old modern human from western Siberia.** Fu Q, Li H, Moorjani P, Jay F, Slepchenko SM, Bondarev AA, Johnson PL, Aximu-Petri A, Prüfer K, de Filippo C, Meyer M, Zwyns N, Salazar-García DC, Kuzmin YV, Keates SG, Kosintsev PA, Razhev DI, Richards MP, Peristov NV, Lachmann M, Douka K, Higham TF, Slatkin M, Hublin JJ, Reich D, Kelso J, Viola TB, Pääbo S. Nature. 2014 Oct 23;514(7523):445-9. doi: 10.1038/nature13810.   
  
[FuNature2015]:  
**An early modern human from Romania with a recent Neanderthal ancestor.** Fu Q, Hajdinjak M, Moldovan OT, Constantin S, Mallick S, Skoglund P, Patterson N, Rohland N, Lazaridis I, Nickel B, Viola B, Prüfer K, Meyer M, Kelso J, Reich D, Pääbo S. Nature. 2015 Aug 13;524(7564):216-9. doi: 10.1038/nature14558. Epub 2015 Jun 22.

[FuNature2016]:  
**The genetic history of Ice Age Europe.** Fu Q, Posth C, Hajdinjak M, Petr M, Mallick S, Fernandes D, Furtwängler A, Haak W, Meyer M, Mittnik A, Nickel B, Peltzer A, Rohland N, Slon V, Talamo S, Lazaridis I, Lipson M, Mathieson I, Schiffels S, Skoglund P, Derevianko AP, Drozdov N, Slavinsky V, Tsybankov A, Cremonesi RG, Mallegni F, Gély B, Vacca E, Morales MR, Straus LG, Neugebauer-Maresch C, Teschler-Nicola M, Constantin S, Moldovan OT, Benazzi S, Peresani M, Coppola D, Lari M, Ricci S, Ronchitelli A, Valentin F, Thevenet C, Wehrberger K, Grigorescu D, Rougier H, Crevecoeur I, Flas D, Semal P, Mannino MA, Cupillard C, Bocherens H, Conard NJ, Harvati K, Moiseyev V, Drucker DG, Svoboda J, Richards MP, Caramelli D, Pinhasi R, Kelso J, Patterson N, Krause J, Pääbo S, Reich D. Nature. 2016 Jun 9;534(7606):200-5. doi: 10.1038/nature17993. Epub 2016 May 2.   
  
[FurtwanglerNatureCommunications2020]:  
**Comparison of target enrichment strategies for ancient pathogen DNA.** Furtwängler A, Neukamm J, Böhme L, Reiter E, Vollstedt M, Arora N, Singh P, Cole ST, Knauf S, Calvignac-Spencer S, Krause-Kyora B, Krause J, Schuenemann VJ, Herbig A. Biotechniques. 2020 Dec;69(6):455-459. doi: 10.2144/btn-2020-0100. Epub 2020 Nov 2. PMID: 33135465.  
  
[GambaNatureCommunications2014]:  
**Genome flux and stasis in a five millennium transect of European prehistory.** Gamba C, Jones ER, Teasdale MD, McLaughlin RL, Gonzalez-Fortes G, Mattiangeli V, Domboróczki L, Kővári I, Pap I, Anders A, Whittle A, Dani J, Raczky P, Higham TF, Hofreiter M, Bradley DG, Pinhasi R. Nat Commun. 2014 Oct 21;5:5257. doi: 10.1038/ncomms6257. PubMed PMID: 25334030; PubMed Central PMCID: PMC4218962.  
  
[GelabertBioRxiv2023]:  
**Social and genetic diversity among the first farmers of Central Europe.** Pere Gelabert, Penny Bickle, Daniela Hofmann, Maria Teschler-Nicola, Alexandra Anders, Xin Huang, Iñigo Olalde, Romain Fournier, Harald Ringbauer, Ali Akbari, Olivia Cheronet, Iosif Lazaridis, Nasreen Broomandkhoshbacht, Daniel M. Fernandes, Katharina Buttinger, Kim Callan, Francesca Candilio, Guillermo Bravo, Elizabeth Curtis, Matthew Ferry, Denise Keating, Suzanne Freilich, Aisling Kearns, Éadaoin Harney, Ann Marie Lawson, Kirsten Mandl, Megan Michel, Victoria Oberreiter, Jonas Oppenheimer, Susanna Sawyer, Constanze Schattke, Kadir Toykan Ozdogan, Michelle Hämmerle, Lijun Qiu, Noah Workman, Fatma Zalzala, Swapan Mallick, Matthew Mah, Adam Micco, Franz Pieler, Juraj Pavuk, Catalin Lazar, Tibor Paluch, Maja Krznarić Škrivanko, Mario Šlaus, Željka Bedić, Friederike Novotny, László D. Szabó, Orsolya Cserpák-Laczi, Tamara Hága, Zsigmond Hajdú, Pavel Mirea, Emese Gyöngyvér Nagy, Zsuzsanna M. Virág, Attila M. Horváth, László András Horváth, Katalin T. Biró, László Domboróczki, Tamás Szeniczey, János Jakucs, Márta Szelekovszky, Farkas Zoltán, Sándor Sztáncsuj, Krisztián Tóth, Piroska Csengeri, Ildikó Pap, Róbert Patay, Anđelka Putica, Branislav Vasov, Bálint Havasi, Katalin Sebők, Pál Raczky, Gabriella Lovász, Zdeněk Tvrdý, Nadin Rohland, Mario Novak, Matej Ruttkay, Dusan Boric, János Dani, Martin Kuhlwilm, Pier Francesco Palamara, Tamás Hajdu, Ron Pinhasi, David Reich bioRxiv 2023.07.07.548126; doi: https://doi.org/10.1101/2023.07.07.548126  
  
[GelabertCurrBio2022]:  
**Northeastern Asian and Jomon-related genetic structure in the Three Kingdoms period of Gimhae, Korea.** Gelabert P, Blazyte A, Chang Y, Fernandes DM, Jeon S, Hong JG, Yoon J, Ko Y, Oberreiter V, Cheronet O, Özdoğan KT, Sawyer S, Yang S, Greytak EM, Choi H, Kim J, Kim JI, Jeong C, Bae K, Bhak J, Pinhasi R. Northeastern Asian and Jomon-related genetic structure in the Three Kingdoms period of Gimhae, Korea. Curr Biol. 2022 Aug 8;32(15):3232-3244.e6. doi: 10.1016/j.cub.2022.06.004. Epub 2022 Jun 21. PMID: 35732180.  
  
[GelabertSciRep2022]:  
**Genomes from Verteba cave suggest diversity within the Trypillians in Ukraine.** Gelabert P, Schmidt RW, Fernandes DM, Karsten JK, Harper TK, Madden GD, Ledogar SH, Sokhatsky M, Oota H, Kennett DJ, Pinhasi R. Genomes from Verteba cave suggest diversity within the Trypillians in Ukraine. Sci Rep. 2022 May 4;12(1):7242. doi: 10.1038/s41598-022-11117-8. PMID: 35508651; PMCID: PMC9068698.  
  
[GerberbioRxiv2024]:  
**Ancient genomes reveal Avar-Hungarian transformations in the 9th-10th centuries CE Carpathian Basin.** Dániel Gerber, Veronika Csáky, Bea Szeifert, Noémi Borbély, Kristóf Jakab, György Mező, Zsolt Petkes, Frigyes Szücsi, Sándor Évinger, Csilla Líbor, Piroska Rácz, Krisztián Kiss, Balázs Gusztáv Mende, Béla Miklós Szőke, Anna Szécsényi-Nagy  
bioRxiv 2024.05.29.596386; doi: https://doi.org/10.1101/2024.05.29.596386   
  
[GnecchiRusconeCell2022]:  
**Ancient genomes reveal origin and rapid trans-Eurasian migration of 7th century Avar elites** Gnecchi-Ruscone GA, Szécsényi-Nagy A, Koncz I, Csiky G, Rácz Z, Rohrlach AB, Brandt G, Rohland N, Csáky V, Cheronet O, Szeifert B, Rácz TÁ, Benedek A, Bernert Z, Berta N, Czifra S, Dani J, Farkas Z, Hága T, Hajdu T, Jászberényi M, Kisjuhász V, Kolozsi B, Major P, Marcsik A, Kovacsóczy BN, Balogh C, Lezsák GM, Ódor JG, Szelekovszky M, Szeniczey T, Tárnoki J, Tóth Z, Tutkovics EK, Mende BG, Geary P, Pohl W, Vida T, Pinhasi R, Reich D, Hofmanová Z, Jeong C, Krause J. Ancient genomes reveal origin and rapid trans-Eurasian migration of 7th century Avar elites. Cell. 2022 Apr 14;185(8):1402-1413.e21. doi: 10.1016/j.cell.2022.03.007. Epub 2022 Apr 1. PMID: 35366416; PMCID: PMC9042794.   
  
[GnecchiRusconeNature2024]:  
**Network of large pedigrees reveals social practices of Avar communities.** Gnecchi-Ruscone GA, Rácz Z, Samu L, Szeniczey T, Faragó N, Knipper C, Friedrich R, Zlámalová D, Traverso L, Liccardo S, Wabnitz S, Popli D, Wang K, Radzeviciute R, Gulyás B, Koncz I, Balogh C, Lezsák GM, Mácsai V, Bunbury MME, Spekker O, le Roux P, Szécsényi-Nagy A, Mende BG, Colleran H, Hajdu T, Geary P, Pohl W, Vida T, Krause J, Hofmanová Z. Nature. 2024 May;629(8011):376-383. doi: 10.1038/s41586-024-07312-4. Epub 2024 Apr 24. PMID: 38658749; PMCID: PMC11078744.

[GnecchiRusconeScienceAdvances2021]:  
**Ancient genomic time transect from the Central Asian Steppe unravels the history of the Scythians.** Gnecchi-Ruscone GA, Khussainova E, Kahbatkyzy N, Musralina L, Spyrou MA, Bianco RA, Radzeviciute R, Martins NFG, Freund C, Iksan O, Garshin A, Zhaniyazov Z, Bekmanov B, Kitov E, Samashev Z, Beisenov A, Berezina N, Berezin Y, Bíró AZ, Évinger S, Bissembaev A, Akhatov G, Mamedov A, Onggaruly A, Voyakin D, Chotbayev A, Kariyev Y, Buzhilova A, Djansugurova L, Jeong C, Krause J. Ancient genomic time transect from the Central Asian Steppe unravels the history of the Scythians. Sci Adv. 2021 Mar 26;7(13):eabe4414. doi: 10.1126/sciadv.abe4414. PMID: 33771866; PMCID: PMC7997506.

[GokhmanNatureCommunications2020]:  
**Differential DNA methylation of vocal and facial anatomy genes in modern humans.** Gokhman D, Nissim-Rafinia M, Agranat-Tamir L, Housman G, García-Pérez R, Lizano E, Cheronet O, Mallick S, Nieves-Colón MA, Li H, Alpaslan-Roodenberg S, Novak M, Gu H, Osinski JM, Ferrando-Bernal M, Gelabert P, Lipende I, Mjungu D, Kondova I, Bontrop R, Kullmer O, Weber G, Shahar T, Dvir-Ginzberg M, Faerman M, Quillen EE, Meissner A, Lahav Y, Kandel L, Liebergall M, Prada ME, Vidal JM, Gronostajski RM, Stone AC, Yakir B, Lalueza-Fox C, Pinhasi R, Reich D, Marques-Bonet T, Meshorer E, Carmel L. Nat Commun. 2020 Mar 4;11(1):1189. doi: 10.1038/s41467-020-15020-6. PMID: 32132541; PMCID: PMC7055320.  
  
[GonzalesFortesCurrentBiology2017]:  
**Paleogenomic Evidence for Multi-generational Mixing between Neolithic Farmers and Mesolithic Hunter-Gatherers in the Lower Danube Basin.** González-Fortes G, Jones ER, Lightfoot E, Bonsall C, Lazar C, Grandal-d'Anglade A, Garralda MD, Drak L, Siska V, Simalcsik A, Boroneanţ A, Vidal Romaní JR, Vaqueiro Rodríguez M, Arias P, Pinhasi R, Manica A, Hofreiter M. Paleogenomic Evidence for Multi-generational Mixing between Neolithic Farmers and Mesolithic Hunter-Gatherers in the Lower Danube Basin. Curr Biol. 2017 Jun 19;27(12):1801-1810.e10. doi: 10.1016/j.cub.2017.05.023. Epub 2017 May 25. PubMed PMID: 28552360; PubMed Central PMCID: PMC5483232.  
  
[GonzalesFortesProcRoyalSocB2019]:  
**A western route of prehistoric human migration from Africa into the Iberian Peninsula.** González-Fortes G, Tassi F, Trucchi E, Henneberger K, Paijmans JLA, Díez-Del-Molino D, Schroeder H, Susca RR, Barroso-Ruíz C, Bermudez FJ, Barroso-Medina C, Bettencourt AMS, Sampaio HA, Grandal-d'Anglade A, Salas A, de Lombera-Hermida A, Fabregas Valcarce R, Vaquero M, Alonso S, Lozano M, Rodríguez-Alvarez XP, Fernández-Rodríguez C, Manica A, Hofreiter M, Barbujani G. Proc Biol Sci. 2019 Jan 30;286(1895):20182288. doi: 10.1098/rspb.2018.2288. PMID: 30963949.  
  
[GretzingerNature2022]:  
**The Anglo-Saxon migration and the formation of the early English gene pool.** Gretzinger J, Sayer D, Justeau P, Altena E, Pala M, Dulias K, Edwards CJ, Jodoin S, Lacher L, Sabin S, Vågene ÅJ, Haak W, Ebenesersdóttir SS, Moore KHS, Radzeviciute R, Schmidt K, Brace S, Bager MA, Patterson N, Papac L, Broomandkhoshbacht N, Callan K, Harney É, Iliev L, Lawson AM, Michel M, Stewardson K, Zalzala F, Rohland N, Kappelhoff-Beckmann S, Both F, Winger D, Neumann D, Saalow L, Krabath S, Beckett S, Van Twest M, Faulkner N, Read C, Barton T, Caruth J, Hines J, Krause-Kyora B, Warnke U, Schuenemann VJ, Barnes I, Dahlström H, Clausen JJ, Richardson A, Popescu E, Dodwell N, Ladd S, Phillips T, Mortimer R, Sayer F, Swales D, Stewart A, Powlesland D, Kenyon R, Ladle L, Peek C, Grefen-Peters S, Ponce P, Daniels R, Spall C, Woolcock J, Jones AM, Roberts AV, Symmons R, Rawden AC, Cooper A, Bos KI, Booth T, Schroeder H, Thomas MG, Helgason A, Richards MB, Reich D, Krause J, Schiffels S. The Anglo-Saxon migration and the formation of the early English gene pool. Nature. 2022 Oct;610(7930):112-119. doi: 10.1038/s41586-022-05247-2. Epub 2022 Sep 21. Erratum in: Nature. 2022 Nov;611(7934):E3. PMID: 36131019; PMCID: PMC9534755.   
  
[GretzingerNature2024]:  
**Evidence for dynastic succession among early Celtic elites in Central Europe.** Gretzinger J, Schmitt F, Mötsch A, Carlhoff S, Lamnidis TC, Huang Y, Ringbauer H, Knipper C, Francken M, Mandt F, Hansen L, Freund C, Posth C, Rathmann H, Harvati K, Wieland G, Granehäll L, Maixner F, Zink A, Schier W, Krausse D, Krause J, Schiffels S. Nat Hum Behav. 2024 Aug;8(8):1467-1480. doi: 10.1038/s41562-024-01888-7. Epub 2024 Jun 3. PMID: 38831077; PMCID: PMC11343710.  
  
[Guarino-VignonNature2023]:  
**Genome-wide analysis of a collective grave from Mentesh Tepe provides insight into the population structure of early neolithic population in the South Caucasus.** Guarino-Vignon P, Lefeuvre M, Chimènes A, Monnereau A, Guliyev F, Pecqueur L, Jovenet E, Lyonnet B, Bon C. Commun Biol. 2023 Mar 25;6(1):319. doi: 10.1038/s42003-023-04681-w. PMID: 36966245; PMCID: PMC10039893.  
  
[GuntherPLoSBiology2018]:  
**Population genomics of Mesolithic Scandinavia: Investigating early postglacial migration routes and high-latitude adaptation.** Günther T, Malmström H, Svensson EM, Omrak A, Sánchez-Quinto F, Kılınç GM, Krzewińska M, Eriksson G, Fraser M, Edlund H, Munters AR, Coutinho A, Simões LG, Vicente M, Sjölander A, Jansen Sellevold B, Jørgensen R, Claes P, Shriver MD, Valdiosera C, Netea MG, Apel J, Lidén K, Skar B, Storå J, Götherström A, Jakobsson M. PLoS Biol. 2018 Jan 9;16(1):e2003703. doi: 10.1371/journal.pbio.2003703. eCollection 2018 Jan.   
  
[GuntherPNAS2015]:  
**Ancient genomes link early farmers from Atapuerca in Spain to modern-day Basques.** Günther T, Valdiosera C, Malmström H, Ureña I, Rodriguez-Varela R, Sverrisdóttir ÓO, Daskalaki EA, Skoglund P, Naidoo T, Svensson EM, Bermúdez de Castro JM, Carbonell E, Dunn M, Storå J, Iriarte E, Arsuaga JL, Carretero JM, Götherström A, Jakobsson M. Proc Natl Acad Sci U S A. 2015 Sep 22;112(38):11917-22. doi: 10.1073/pnas.1509851112. Epub 2015 Sep 8.   
  
[HaberAJHG2017]:  
**Continuity and Admixture in the Last Five Millennia of Levantine History from Ancient Canaanite and Present-Day Lebanese Genome Sequences.** Haber M, Doumet-Serhal C, Scheib C, Xue Y, Danecek P, Mezzavilla M, Youhanna S, Martiniano R, Prado-Martinez J, Szpak M, Matisoo-Smith E, Schutkowski H, Mikulski R, Zalloua P, Kivisild T, Tyler-Smith C. Am J Hum Genet. 2017 Aug 3;101(2):274-282. doi: 10.1016/j.ajhg.2017.06.013. Epub 2017 Jul 27. PubMed PMID: 28757201; PubMed Central PMCID: PMC5544389.   
  
[HaberAJHG2018]:  
**A Transient Pulse of Genetic Admixture from the Crusaders in the Near East Identified from Ancient Genome Sequences.** Haber M, Doumet-Serhal C, Scheib CL, Xue Y, Mikulski R, Martiniano R, Fischer-Genz B, Schutkowski H, Kivisild T, Tyler-Smith C. Am J Hum Genet. 2019 May 2;104(5):977-984. doi: 10.1016/j.ajhg.2019.03.015. Epub 2019 Apr 18. PMID: 31006515.  
[HaberAJHG2020]:  
**A Genetic History of the Near East from an aDNA Time Course Sampling Eight Points in the Past 4,000 Years.** Haber M, Nassar J, Almarri MA, Saupe T, Saag L, Griffith SJ, Doumet-Serhal C, Chanteau J, Saghieh-Beydoun M, Xue Y, Scheib CL, Tyler-Smith C. Am J Hum Genet. 2020 Jul 2;107(1):149-157. doi: 10.1016/j.ajhg.2020.05.008. Epub 2020 May 28. PMID: 32470374; PMCID: PMC7332655.  
  
[HajdinjakNature2018]:  
**Reconstructing the genetic history of late Neanderthals.** Hajdinjak M, Fu Q, Hübner A, Petr M, Mafessoni F, Grote S, Skoglund P, Narasimham V, Rougier H, Crevecoeur I, Semal P, Soressi M, Talamo S, Hublin JJ, Gušić I, Kućan Ž, Rudan P, Golovanova LV, Doronichev VB, Posth C, Krause J, Korlević P, Nagel S, Nickel B, Slatkin M, Patterson N, Reich D, Prüfer K, Meyer M, Pääbo S, Kelso J. Nature. 2018 Mar 29;555(7698):652-656. doi: 10.1038/nature26151. Epub 2018 Mar 21.  
  
[HajdinjakNature2021]:  
**Initial Upper Palaeolithic humans in Europe had recent Neanderthal ancestry. .** Hajdinjak M, Mafessoni F, Skov L, Vernot B, Hübner A, Fu Q, Essel E, Nagel S, Nickel B, Richter J, Moldovan OT, Constantin S, Endarova E, Zahariev N, Spasov R, Welker F, Smith GM, Sinet-Mathiot V, Paskulin L, Fewlass H, Talamo S, Rezek Z, Sirakova S, Sirakov N, McPherron SP, Tsanova T, Hublin JJ, Peter BM, Meyer M, Skoglund P, Kelso J, Pääbo S. Nature. 2021 Apr;592(7853):253-257. doi: 10.1038/s41586-021-03335-3. Epub 2021 Apr 7. PMID: 33828320; PMCID: PMC8026394.  
  
[HarneyBioRxiv2022]:  
**Technical Report on Ancient DNA analysis of 27 African Americans from Catoctin Furnace, Maryland.** Éadaoin Harney, Iñigo Olalde, Kari Bruwelheide, Kathryn G. Barca, Roslyn Curry, Elizabeth Comer, Nadin Rohland, Douglas Owsley, David Reich bioRxiv 2022.06.12.495320; doi: https://doi.org/10.1101/2022.06.12.495320.  
  
[HarneyScience2023]]:  
**The genetic legacy of African Americans from Catoctin Furnace. Science.** Harney É, Micheletti S, Bruwelheide KS, Freyman WA, Bryc K, Akbari A, Jewett E, Comer E, Gates HL Jr, Heywood L, Thornton J, Curry R, Esselmann SA, Barca KG, Sedig J, Sirak K, Olalde I, Adamski N, Bernardos R, Broomandkhoshbacht N, Ferry M, Qiu L, Stewardson K, Workman JN, Zalzala F, Mallick S, Micco A, Mah M, Zhang Z; 23andMe Research Team†; Rohland N, Mountain JL, Owsley DW, Reich D; 23andMe Research Team. 2023 Aug 4;381(6657):eade4995. doi: 10.1126/science.ade4995. Epub 2023 Aug 4. PMID: 37535739; PMCID: PMC10958645.  
  
[HarneyCheronetGenomeResearch2021]:  
**A minimally destructive protocol for DNA extraction from ancient teeth.** Harney É, Cheronet O, Fernandes DM, Sirak K, Mah M, Bernardos R, Adamski N, Broomandkhoshbacht N, Callan K, Lawson AM, Oppenheimer J, Stewardson K, Zalzala F, Anders A, Candilio F, Constantinescu M, Coppa A, Ciobanu I, Dani J, Gallina Z, Genchi F, Nagy EG, Hajdu T, Hellebrandt M, Horváth A, Király Á, Kiss K, Kolozsi B, Kovács P, Köhler K, Lucci M, Pap I, Popovici S, Raczky P, Simalcsik A, Szeniczey T, Vasilyev S, Virag C, Rohland N, Reich D, Pinhasi R. A minimally destructive protocol for DNA extraction from ancient teeth. Genome Res. 2021 Mar;31(3):472-483. doi: 10.1101/gr.267534.120. Epub 2021 Feb 12. PMID: 33579752; PMCID: PMC7919446.  
  
[HarneyMayNatureCommunications2018]:  
**Ancient DNA from Chalcolithic Israel reveals the role of population mixture in cultural transformation.** Harney É, May H, Shalem D, Rohland N, Mallick S, Lazaridis I, Sarig R, Stewardson K, Nordenfelt S, Patterson N, Hershkovitz I, Reich D. Nat Commun. 2018 Aug 20;9(1):3336. doi: 10.1038/s41467-018-05649-9. Erratum in: Nat Commun. 2018 Sep 20;9(1):3913.   
  
[HarneyNatureCommunications2019]:  
**Ancient DNA from the skeletons of Roopkund Lake reveals Mediterranean migrants in India.** Harney É, Nayak A, Patterson N, Joglekar P, Mushrif-Tripathy V, Mallick S, Rohland N, Sedig J, Adamski N, Bernardos R, Broomandkhoshbacht N, Culleton BJ, Ferry M, Harper TK, Michel M, Oppenheimer J, Stewardson K, Zhang Z, Harashawaradhana, Bartwal MS, Kumar S, Diyundi SC, Roberts P, Boivin N, Kennett DJ, Thangaraj K, Reich D, Rai N. Nat Commun. 2019 Aug 20;10(1):3670. doi: 10.1038/s41467-019-11357-9. PMID: 31431628.  
  
[HofmanovaPNAS2016]:  
**Early farmers from across Europe directly descended from Neolithic Aegeans.** Hofmanová Z, Kreutzer S, Hellenthal G, Sell C, Diekmann Y, Díez-Del-Molino D, van Dorp L, López S, Kousathanas A, Link V, Kirsanow K, Cassidy LM, Martiniano R, Strobel M, Scheu A, Kotsakis K, Halstead P, Triantaphyllou S, Kyparissi-Apostolika N, Urem-Kotsou D, Ziota C, Adaktylou F, Gopalan S, Bobo DM, Winkelbach L, Blöcher J, Unterländer M, Leuenberger C, Çilingiroğlu Ç, Horejs B, Gerritsen F, Shennan SJ, Bradley DG, Currat M, Veeramah KR, Wegmann D, Thomas MG, Papageorgopoulou C, Burger J. Proc Natl Acad Sci U S A. 2016 Jun 21;113(25):6886-91. doi: 10.1073/pnas.1523951113. Epub 2016 Jun 6.  
  
[HuangRingbauer2022]:  
**hapCon: estimating contamination of ancient genomes by copying from reference haplotypes.** Huang Y, Ringbauer H. Bioinformatics. 2022 Aug 2;38(15):3768-3777. doi: 10.1093/bioinformatics/btac390. PMID: 35695771; PMCID: PMC9344841 (software available from: https://haproh.readthedocs.io/en/latest/hapCon.html ).  
  
[ImmelCommBiol2021]:  
**Genome-wide study of a Neolithic Wartberg grave community reveals distinct HLA variation and hunter-gatherer ancestry.** Immel A, Pierini F, Rinne C, Meadows J, Barquera R, Szolek A, Susat J, Böhme L, Dose J, Bonczarowska J, Drummer C, Fuchs K, Ellinghaus D, Kässens JC, Furholt M, Kohlbacher O, Schade-Lindig S, Franke A, Schreiber S, Krause J, Müller J, Lenz TL, Nebel A, Krause-Kyora B. Commun Biol. 2021 Jan 25;4(1):113. doi: 10.1038/s42003-020-01627-4. PMID: 33495542; PMCID: PMC7835224.

[ImmelNature2020]:  
**Gene-flow from steppe individuals into Cucuteni-Trypillia associated populations indicates long-standing contacts and gradual admixture.** Immel A, Țerna S, Simalcsik A, Susat J, Šarov O, Sîrbu G, Hofmann R, Müller J, Nebel A, Krause-Kyora B. Sci Rep. 2020 Mar 6;10(1):4253. doi: 10.1038/s41598-020-61190-0. PMID: 32144348; PMCID: PMC7060214.  
  
[IngmanStockhammerPLoS2021]:  
**Turkey during the 2nd millennium BC: Integration of isotopic and genomic evidence..** Ingman T, Eisenmann S, Skourtanioti E, Akar M, Ilgner J, Gnecchi Ruscone GA, le Roux P, Shafiq R, Neumann GU, Keller M, Freund C, Marzo S, Lucas M, Krause J, Roberts P, Yener KA, Stockhammer PW. Human mobility at Tell Atchana (Alalakh), Hatay, PLoS One. 2021 Jun 30;16(6):e0241883. doi: 10.1371/journal.pone.0241883. PMID: 34191795; PMCID: PMC8244877.  
  
[JacobsCell2019]:  
**Multiple Deeply Divergent Denisovan Ancestries in Papuans.** Jacobs GS, Hudjashov G, Saag L, Kusuma P, Darusallam CC, Lawson DJ, Mondal M, Pagani L, Ricaut FX, Stoneking M, Metspalu M, Sudoyo H, Lansing JS, Cox MP. Cell. 2019 May 2;177(4):1010-1021.e32. doi: 10.1016/j.cell.2019.02.035. Epub 2019 Apr 11. PMID: 30981557.  
  
[JarveCurrentBiology2019]:  
**Shifts in the Genetic Landscape of the Western Eurasian Steppe Associated with the Beginning and End of the Scythian Dominance.** Järve M, Saag L, Scheib CL, Pathak AK, Montinaro F, Pagani L, Flores R, Guellil M, Saag L, Tambets K, Kushniarevich A, Solnik A, Varul L, Zadnikov S, Petrauskas O, Avramenko M, Magomedov B, Didenko S, Toshev G, Bruyako I, Grechko D, Okatenko V, Gorbenko K, Smyrnov O, Heiko A, Reida R, Sapiehin S, Sirotin S, Tairov A, Beisenov A, Starodubtsev M, Vasilev V, Nechvaloda A, Atabiev B, Litvinov S, Ekomasova N, Dzhaubermezov M, Voroniatov S, Utevska O, Shramko I, Khusnutdinova E, Metspalu M, Savelev N, Kriiska A, Kivisild T, Villems R. Curr Biol. 2019 Jul 22;29(14):2430-2441.e10. doi: 10.1016/j.cub.2019.06.019. Epub 2019 Jul 11. PMID: 31303491.  
  
[JensenSchroederNatureCommunications2019]:  
**A 5700 year-old human genome and oral microbiome from chewed birch pitch. .** Jensen TZT, Niemann J, Iversen KH, Fotakis AK, Gopalakrishnan S, Vågene ÅJ, Pedersen MW, Sinding MS, Ellegaard MR, Allentoft ME, Lanigan LT, Taurozzi AJ, Nielsen SH, Dee MW, Mortensen MN, Christensen MC, Sørensen SA, Collins MJ, Gilbert MTP, Sikora M, Rasmussen S, Schroeder H. Nat Commun. 2019 Dec 17;10(1):5520. doi: 10.1038/s41467-019-13549-9. PMID: 31848342; PMCID: PMC6917805.  
  
[JeongCell2020]:  
**A Dynamic 6,000-Year Genetic History of Eurasia's Eastern Steppe.** Jeong C, Wang K, Wilkin S, Taylor WTT, Miller BK, Bemmann JH, Stahl R, Chiovelli C, Knolle F, Ulziibayar S, Khatanbaatar D, Erdenebaatar D, Erdenebat U, Ochir A, Ankhsanaa G, Vanchigdash C, Ochir B, Munkhbayar C, Tumen D, Kovalev A, Kradin N, Bazarov BA, Miyagashev DA, Konovalov PB, Zhambaltarova E, Miller AV, Haak W, Schiffels S, Krause J, Boivin N, Erdene M, Hendy J, Warinner C. A Dynamic 6,000-Year Genetic History of Eurasia's Eastern Steppe. Cell. 2020 Nov 12;183(4):890-904.e29. doi: 10.1016/j.cell.2020.10.015. Epub 2020 Nov 5. PMID: 33157037; PMCID: PMC7664836.  
  
[JeongNatureEcologyEvolution2019]:  
**The genetic history of admixture across inner Eurasia.** Jeong C, Balanovsky O, Lukianova E, Kahbatkyzy N, Flegontov P, Zaporozhchenko V, Immel A, Wang CC, Ixan O, Khussainova E, Bekmanov B, Zaibert V, Lavryashina M, Pocheshkhova E, Yusupov Y, Agdzhoyan A, Koshel S, Bukin A, Nymadawa P, Turdikulova S, Dalimova D, Churnosov M, Skhalyakho R, Daragan D, Bogunov Y, Bogunova A, Shtrunov A, Dubova N, Zhabagin M, Yepiskoposyan L, Churakov V, Pislegin N, Damba L, Saroyants L, Dibirova K, Atramentova L, Utevska O, Idrisov E, Kamenshchikova E, Evseeva I, Metspalu M, Outram AK, Robbeets M, Djansugurova L, Balanovska E, Schiffels S, Haak W, Reich D, Krause J. Nat Ecol Evol. 2019 Jun;3(6):966-976. doi: 10.1038/s41559-019-0878-2. Epub 2019 Apr 29. PMID: 31036896.  
  
[JeongPNAS2016]:  
**Long-term genetic stability and a high-altitude East Asian origin for the peoples of the high valleys of the Himalayan arc.** Jeong C, Ozga AT, Witonsky DB, Malmström H, Edlund H, Hofman CA, Hagan RW, Jakobsson M, Lewis CM, Aldenderfer MS, Di Rienzo A, Warinner C. Proc Natl Acad Sci U S A. 2016 Jul 5;113(27):7485-90. doi: 10.1073/pnas.1520844113. Epub 2016 Jun 20. PMID: 27325755.  
  
[JeongPNAS2018]:  
**Bronze Age population dynamics and the rise of dairy pastoralism on the eastern Eurasian steppe.** Jeong C, Wilkin S, Amgalantugs T, Bouwman AS, Taylor WTT, Hagan RW, Bromage S, Tsolmon S, Trachsel C, Grossmann J, Littleton J, Makarewicz CA, Krigbaum J, Burri M, Scott A, Davaasambuu G, Wright J, Irmer F, Myagmar E, Boivin N, Robbeets M, Rühli FJ, Krause J, Frohlich B, Hendy J, Warinner C. Proc Natl Acad Sci U S A. 2018 Nov 27;115(48):E11248-E11255. doi: 10.1073/pnas.1813608115. Epub 2018 Nov 5. PMID:30397125.  
  
[JonesNatureCommunications2015]:  
**Upper Palaeolithic genomes reveal deep roots of modern Eurasians.** Jones ER, Gonzalez-Fortes G, Connell S, Siska V, Eriksson A, Martiniano R, McLaughlin RL, Gallego Llorente M, Cassidy LM, Gamba C, Meshveliani T, Bar-Yosef O, Müller W, Belfer-Cohen A, Matskevich Z, Jakeli N, Higham TF, Currat M, Lordkipanidze D, Hofreiter M, Manica A, Pinhasi R, Bradley DG. Nat Commun. 2015 Nov 16;6:8912. doi: 10.1038/ncomms9912. PMID: 26567969.   
  
[JonesCurrentBiology2017]:  
**The Neolithic Transition in the Baltic Was Not Driven by Admixture with Early European Farmers.** Jones ER, Zarina G, Moiseyev V, Lightfoot E, Nigst PR, Manica A, Pinhasi R, Bradley DG. Curr Biol. 2017 Feb 20;27(4):576-582.

[KanzawaKiriyamaJHG2016:]  
**A partial nuclear genome of the Jomons who lived 3000 years ago in Fukushima, Japan.** Kanzawa-Kiriyama H, Kryukov K, Jinam TA, Hosomichi K, Saso A, Suwa G, Ueda S, Yoneda M, Tajima A, Shinoda KI, Inoue I, Saitou N. J Hum Genet. 2017 Feb;62(2):213-221. doi: 10.1038/jhg.2016.110. Epub 2016 Sep 1.   
  
[KellerNatureCommunications2012]:  
**New insights into the Tyrolean Iceman's origin and phenotype as inferred by whole-genome sequencing.** Keller A1, Graefen A, Ball M, Matzas M, Boisguerin V, Maixner F, Leidinger P, Backes C, Khairat R, Forster M, Stade B, Franke A, Mayer J, Spangler J, McLaughlin S, Shah M, Lee C, Harkins TT, Sartori A, Moreno-Estrada A, Henn B, Sikora M, Semino O, Chiaroni J, Rootsi S, Myres NM, Cabrera VM, Underhill PA, Bustamante CD, Vigl EE, Samadelli M, Cipollini G, Haas J, Katus H, O'Connor BD, Carlson MR, Meder B, Blin N, Meese E, Pusch CM, Zink A. Nat Commun. 2012 Feb 28;3:698. doi: 10.1038/ncomms1701.Paperpile.   
  
[KennettLipsonPruferNatureCommunications2022]:  
**South-to-north migration preceded the advent of intensive farming in the Maya region.** Kennett DJ, Lipson M, Prufer KM, Mora-Marín D, George RJ, Rohland N, Robinson M, Trask WR, Edgar HHJ, Hill EC, Ray EE, Lynch P, Moes E, O'Donnell L, Harper TK, Kate EJ, Ramos J, Morris J, Gutierrez SM, Ryan TM, Culleton BJ, Awe JJ, Reich D. Nat Commun. 2022 Mar 22;13(1):1530. doi: 10.1038/s41467-022-29158-y. PMID: 35318319; PMCID: PMC8940966.  
  
[KennettNatureCommunications2017]:  
**Archaeogenomic evidence reveals prehistoric matrilineal dynasty.** Kennett DJ, Plog S, George RJ, Culleton BJ, Watson AS, Skoglund P, Rohland N, Mallick S, Stewardson K, Kistler L, LeBlanc SA, Whiteley PM, Reich D, Perry GH. Nat Commun. 2017 Feb 21;8:14115. doi: 10.1038/ncomms14115. PMID: 28221340.   
  
[KilincCurrentBiology2016]:  
**The Demographic Development of the First Farmers in Anatolia.** Kılınç GM, Omrak A, Özer F, Günther T, Büyükkarakaya AM, Bıçakçı E, Baird D, Dönertaş HM, Ghalichi A, Yaka R, Koptekin D, Açan SC, Parvizi P, Krzewińska M, Daskalaki EA, Yüncü E, Dağtaş ND, Fairbairn A, Pearson J, Mustafaoğlu G, Erdal YS, Çakan YG, Togan İ, Somel M, Storå J, Jakobsson M, Götherström A. Curr Biol. 2016 Oct 10;26(19):2659-2666. doi: 10.1016/j.cub.2016.07.057. Epub 2016 Aug 4. PMID: 27498567.  
  
[KilincSciAdv2021]:  
**Human population dynamics and Yersinia pestis in ancient northeast Asia.** Kılınç GM, Kashuba N, Koptekin D, Bergfeldt N, Dönertaş HM, Rodríguez-Varela R, Shergin D, Ivanov G, Kichigin D, Pestereva K, Volkov D, Mandryka P, Kharinskii A, Tishkin A, Ineshin E, Kovychev E, Stepanov A, Dalén L, Günther T, Kırdök E, Jakobsson M, Somel M, Krzewińska M, Storå J, Götherström A. Human population dynamics and Yersinia pestis in ancient northeast Asia. Sci Adv. 2021 Jan 6;7(2):eabc4587. doi: 10.1126/sciadv.abc4587. PMID: 33523963; PMCID: PMC7787494.  
  
[KoptekinCurrentBiology2023]:  
**Spatial and temporal heterogeneity in human mobility patterns in Holocene Southwest Asia and the East Mediterranean.** Koptekin D, Yüncü E, Rodríguez-Varela R, Altınışık NE, Psonis N, Kashuba N, Yorulmaz S, George R, Kazancı DD, Kaptan D, Gürün K, Vural KB, Gemici HC, Vassou D, Daskalaki E, Karamurat C, Lagerholm VK, Erdal ÖD, Kırdök E, Marangoni A, Schachner A, Üstündağ H, Shengelia R, Bitadze L, Elashvili M, Stravopodi E, Özbaşaran M, Duru G, Nafplioti A, Rose CB, Gencer T, Darbyshire G, Gavashelishvili A, Pitskhelauri K, Çevik Ö, Vuruşkan O, Kyparissi-Apostolika N, Büyükkarakaya AM, Oğuzhanoğlu U, Günel S, Tabakaki E, Aliev A, Ibrahimov A, Shadlinski V, Sampson A, Kılınç GM, Atakuman Ç, Stamatakis A, Poulakakis N, Erdal YS, Pavlidis P, Storå J, Özer F, Götherström A, Somel M. Curr Biol. 2023 Jan 9;33(1):41-57.e15. doi: 10.1016/j.cub.2022.11.034. Epub 2022 Dec 8. PMID: 36493775; PMCID: PMC9839366.  
  
[KrzewinskaCurrentBiology2018]:  
**Genomic and Strontium Isotope Variation Reveal Immigration Patterns in a Viking Age Town.** Krzewińska M, Kjellström A, Günther T, Hedenstierna-Jonson C, Zachrisson T, Omrak A, Yaka R, Kılınç GM, Somel M, Sobrado V, Evans J, Knipper C, Jakobsson M, Storå J, Götherström A. Curr Biol. 2018 Sep 10;28(17):2730-2738.e10. doi: 10.1016/j.cub.2018.06.053. Epub 2018 Aug 23. PMID: 30146150.  
  
[KrzewinskaScienceAdvances2018]:  
**Ancient genomes suggest the eastern Pontic-Caspian steppe as the source of western Iron Age nomads.** Krzewińska M, Kılınç GM, Juras A, Koptekin D, Chyleński M, Nikitin AG, Shcherbakov N, Shuteleva I, Leonova T, Kraeva L, Sungatov FA, Sultanova AN, Potekhina I, Łukasik S, Krenz-Niedbała M, Dalén L, Sinika V, Jakobsson M, Storå J, Götherström A. Sci Adv. 2018 Oct 3;4(10):eaat4457. doi: 10.1126/sciadv.aat4457. eCollection 2018 Oct. PMID: 30417088.

[KumarFuScience2022]:  
**Bronze and Iron Age population movements underlie Xinjiang population history.** Kumar V, Wang W, Zhang J, Wang Y, Ruan Q, Yu J, Wu X, Hu X, Wu X, Guo W, Wang B, Niyazi A, Lv E, Tang Z, Cao P, Liu F, Dai Q, Yang R, Feng X, Ping W, Zhang L, Zhang M, Hou W, Liu Y, Bennett EA, Fu Q. Science. 2022 Apr;376(6588):62-69. doi: 10.1126/science.abk1534. Epub 2022 Mar 31. PMID: 35357918.  
  
[KumarMolBioEvo2021]:  
**Genetic Continuity of Bronze Age Ancestry with Increased Steppe-Related Ancestry in Late Iron Age Uzbekistan.** Kumar V, Bennett EA, Zhao D, Liang Y, Tang Y, Ren M, Dai Q, Feng X, Cao P, Yang R, Liu F, Ping W, Zhang M, Ding M, Yang MA, Amridin B, Muttalib H, Wang J, Fu Q. Mol Biol Evol. 2021 Oct 27;38(11):4908-4917. doi: 10.1093/molbev/msab216. PMID: 34320653; PMCID: PMC8557446.  
  
[LamnidisNatureCommunications2018]:  
**Ancient Fennoscandian genomes reveal origin and spread of Siberian ancestry in Europe.** Lamnidis TC, Majander K, Jeong C, Salmela E, Wessman A, Moiseyev V, Khartanovich V, Balanovsky O, Ongyerth M, Weihmann A, Sajantila A, Kelso J, Pääbo S, Onkamo P, Haak W, Krause J, Schiffels S. Nat Commun. 2018 Nov 27;9(1):5018. doi: 10.1038/s41467-018-07483-5. PMID: 30479341.  
  
[LarenaJakobbsonPNAS2021]:  
**Multiple migrations to the Philippines during the last 50,000 years.** Larena M, Sanchez-Quinto F, Sjödin P, McKenna J, Ebeo C, Reyes R, Casel O, Huang JY, Hagada KP, Guilay D, Reyes J, Allian FP, Mori V, Azarcon LS, Manera A, Terando C, Jamero L Jr, Sireg G, Manginsay-Tremedal R, Labos MS, Vilar RD, Latiph A, Saway RL, Marte E, Magbanua P, Morales A, Java I, Reveche R, Barrios B, Burton E, Salon JC, Kels MJT, Albano A, Cruz-Angeles RB, Molanida E, Granehäll L, Vicente M, Edlund H, Loo JH, Trejaut J, Ho SYW, Reid L, Malmström H, Schlebusch C, Lambeck K, Endicott P, Jakobsson M. Multiple migrations to the Philippines during the last 50,000 years. Proc Natl Acad Sci U S A. 2021 Mar 30;118(13):e2026132118. doi: 10.1073/pnas.2026132118. PMID: 33753512; PMCID: PMC8020671.   
  
[LarsColombianSamplesPrepub]:  
  
[LazaridisAlpaslanRoodenbergScience2022]:  
**The genetic history of the Southern Arc: A bridge between West Asia and Europe.**Lazaridis I, Alpaslan-Roodenberg S, Acar A, Açıkkol A, Agelarakis A, Aghikyan L, Akyüz U, Andreeva D, Andrijašević G, Antonović D, Armit I, Atmaca A, Avetisyan P, Aytek Aİ, Bacvarov K, Badalyan R, Bakardzhiev S, Balen J, Bejko L, Bernardos R, Bertsatos A, Biber H, Bilir A, Bodružić M, Bonogofsky M, Bonsall C, Borić D, Borovinić N, Bravo Morante G, Buttinger K, Callan K, Candilio F, Carić M, Cheronet O, Chohadzhiev S, Chovalopoulou ME, Chryssoulaki S, Ciobanu I, Čondić N, Constantinescu M, Cristiani E, Culleton BJ, Curtis E, Davis J, Demcenco TI, Dergachev V, Derin Z, Deskaj S, Devejyan S, Djordjević V, Duffett Carlson KS, Eccles LR, Elenski N, Engin A, Erdoğan N, Erir-Pazarcı S, Fernandes DM, Ferry M, Freilich S, Frînculeasa A, Galaty ML, Gamarra B, Gasparyan B, Gaydarska B, Genç E, Gültekin T, Gündüz S, Hajdu T, Heyd V, Hobosyan S, Hovhannisyan N, Iliev I, Iliev L, Iliev S, İvgin İ, Janković I, Jovanova L, Karkanas P, Kavaz-Kındığılı B, Kaya EH, Keating D, Kennett DJ, Deniz Kesici S, Khudaverdyan A, Kiss K, Kılıç S, Klostermann P, Kostak Boca Negra Valdes S, Kovačević S, Krenz-Niedbała M, Krznarić Škrivanko M, Kurti R, Kuzman P, Lawson AM, Lazar C, Leshtakov K, Levy TE, Liritzis I, Lorentz KO, Łukasik S, Mah M, Mallick S, Mandl K, Martirosyan-Olshansky K, Matthews R, Matthews W, McSweeney K, Melikyan V, Micco A, Michel M, Milašinović L, Mittnik A, Monge JM, Nekhrizov G, Nicholls R, Nikitin AG, Nikolov V, Novak M, Olalde I, Oppenheimer J, Osterholtz A, Özdemir C, Özdoğan KT, Öztürk N, Papadimitriou N, Papakonstantinou N, Papathanasiou A, Paraman L, Paskary EG, Patterson N, Petrakiev I, Petrosyan L, Petrova V, Philippa-Touchais A, Piliposyan A, Pocuca Kuzman N, Potrebica H, Preda-Bălănică B, Premužić Z, Price TD, Qiu L, Radović S, Raeuf Aziz K, Rajić Šikanjić P, Rasheed Raheem K, Razumov S, Richardson A, Roodenberg J, Ruka R, Russeva V, Şahin M, Şarbak A, Savaş E, Schattke C, Schepartz L, Selçuk T, Sevim-Erol A, Shamoon-Pour M, Shephard HM, Sideris A, Simalcsik A, Simonyan H, Sinika V, Sirak K, Sirbu G, Šlaus M, Soficaru A, Söğüt B, Sołtysiak A, Sönmez-Sözer Ç, Stathi M, Steskal M, Stewardson K, Stocker S, Suata-Alpaslan F, Suvorov A, Szécsényi-Nagy A, Szeniczey T, Telnov N, Temov S, Todorova N, Tota U, Touchais G, Triantaphyllou S, Türker A, Ugarković M, Valchev T, Veljanovska F, Videvski Z, Virag C, Wagner A, Walsh S, Włodarczak P, Workman JN, Yardumian A, Yarovoy E, Yavuz AY, Yılmaz H, Zalzala F, Zettl A, Zhang Z, Çavuşoğlu R, Rohland N, Pinhasi R, Reich D, Davtyan R. Science. 2022 Aug 26;377(6609):eabm4247. doi: 10.1126/science.abm4247. Epub 2022 Aug 26. PMID: 36007055.   
  
[LazaridisNature2014]:  
**Ancient human genomes suggest three ancestral populations for present-day Europeans.** Lazaridis I, Patterson N, Mittnik A, Renaud G, Mallick S, Kirsanow K, Sudmant PH, Schraiber JG, Castellano S, Lipson M, Berger B, Economou C, Bollongino R, Fu Q, Bos KI, Nordenfelt S, Li H, de Filippo C, Prüfer K, Sawyer S, Posth C, Haak W, Hallgren F, Fornander E, Rohland N, Delsate D, Francken M, Guinet JM, Wahl J, Ayodo G, Babiker HA, Bailliet G, Balanovska E, Balanovsky O, Barrantes R, Bedoya G, Ben-Ami H, Bene J, Berrada F, Bravi CM, Brisighelli F, Busby GB, Cali F, Churnosov M, Cole DE, Corach D, Damba L, van Driem G, Dryomov S, Dugoujon JM, Fedorova SA, Gallego Romero I, Gubina M, Hammer M, Henn BM, Hervig T, Hodoglugil U, Jha AR, Karachanak-Yankova S, Khusainova R, Khusnutdinova E, Kittles R, Kivisild T, Klitz W, Kučinskas V, Kushniarevich A, Laredj L, Litvinov S, Loukidis T, Mahley RW, Melegh B, Metspalu E, Molina J, Mountain J, Näkkäläjärvi K, Nesheva D, Nyambo T, Osipova L, Parik J, Platonov F, Posukh O, Romano V, Rothhammer F, Rudan I, Ruizbakiev R, Sahakyan H, Sajantila A, Salas A, Starikovskaya EB, Tarekegn A, Toncheva D, Turdikulova S, Uktveryte I, Utevska O, Vasquez R, Villena M, Voevoda M, Winkler CA, Yepiskoposyan L, Zalloua P, Zemunik T, Cooper A, Capelli C, Thomas MG, Ruiz-Linares A, Tishkoff SA, Singh L, Thangaraj K, Villems R, Comas D, Sukernik R, Metspalu M, Meyer M, Eichler EE, Burger J, Slatkin M, Pääbo S, Kelso J, Reich D, Krause J. Nature. 2014 Sep 18;513(7518):409-13. doi: 10.1038/nature13673. PMID: 25230663.   
  
[LazaridisNature2016]:  
**Genomic insights into the origin of farming in the ancient Near East.** Lazaridis I, Nadel D, Rollefson G, Merrett DC, Rohland N, Mallick S, Fernandes D, Novak M, Gamarra B, Sirak K, Connell S, Stewardson K, Harney E, Fu Q, Gonzalez-Fortes G, Jones ER, Roodenberg SA, Lengyel G, Bocquentin F, Gasparian B, Mongce JM, Gregg M, Eshed V, Mizrahi AS, Meiklejohn C, Gerritsen F, Bejenaru L, Blüher M, Campbell A, Cavalleri G, Comas D, Froguel P, Gilbert E, Kerr SM, Kovacs P, Krause J, McGettigan D, Merrigan M, Merriwether DA, O'Reilly S, Richards MB, Semino O, Shamoon-Pour M, Stefanescu G, Stumvoll M, Tönjes A, Torroni A, Wilson JF, Yengo L, Hovhannisyan NA, Patterson N, Pinhasi R, Reich D. Nature. 2016 Aug 25;536(7617):419-24. Epub 2016 Jul 25. PMID: 27459054.  
  
[LazaridisNature2017]:  
**Genetic origins of the Minoans and Mycenaeans.** Lazaridis I, Mittnik A, Patterson N, Mallick S, Rohland N, Pfrengle S, Furtwängler A, Peltzer A, Posth C, Vasilakis A, McGeorge PJP, Konsolaki-Yannopoulou E, Korres G, Martlew H, Michalodimitrakis M, Özsait M, Özsait N, Papathanasiou A, Richards M, Roodenberg SA, Tzedakis Y, Arnott R, Fernandes DM, Hughey JR, Lotakis DM, Navas PA, Maniatis Y, Stamatoyannopoulos JA, Stewardson K, Stockhammer P, Pinhasi R, Reich D, Krause J, Stamatoyannopoulos G. Nature. 2017 Aug 10;548(7666):214-218. doi: 10.1038/nature23310. Epub 2017 Aug 2. PMID: 28783727.

[LazaridisPattersonAnthonyBioRxiv2024]:  
**The Genetic Origin of the Indo-Europeans.** Iosif Lazaridis, Nick Patterson, David Anthony, Leonid Vyazov, Romain Fournier, Harald Ringbauer, Iñigo Olalde, Alexander A. Khokhlov, Egor P. Kitov, Natalia I. Shishlina, Sorin C. Ailincăi, Danila S. Agapov, Sergey A. Agapov, Elena Batieva, Baitanayev Bauyrzhan, Zsolt Bereczki, Alexandra Buzhilova, Piya Changmai, Andrey A. Chizhevsky, Ion Ciobanu, Mihai Constantinescu, Marietta Csányi, János Dani, Peter K. Dashkovskiy, Sándor Évinger, Anatoly Faifert, Pavel N. Flegontov, Alin Frînculeasa, Mădălina N. Frînculeasa, Tamás Hajdu, Tom Higham, Paweł Jarosz, Pavol Jelínek, Valeri I. Khartanovich, Eduard N. Kirginekov, Viktória Kiss, Alexandera Kitova, Alexeiy V. Kiyashko, Jovan Koledin, Arkady Korolev, Pavel Kosintsev, Gabriella Kulcsár, Pavel Kuznetsov, Rabadan Magomedov, Mamedov Aslan Malikovich, Eszter Melis, Vyacheslav Moiseyev, Erika Molnár, Janet Monge, Octav Negrea, Nadezhda A. Nikolaeva, Mario Novak, Maria Ochir-Goryaeva, György Pálfi, Sergiu Popovici, Marina P. Rykun, Tatyana M. Savenkova, Vladimir P. Semibratov, Nikolai N. Seregin, Alena Šefčáková, Mussayeva Raikhan Serikovna, Irina Shingiray, Vladimir N. Shirokov, Angela Simalcsik, Kendra Sirak, Konstantin N. Solodovnikov, Judit Tárnoki, Alexey A. Tishkin, Viktov Trifonov, Sergey Vasilyev, Ali Akbari, Esther S. Brielle, Kim Callan, Francesca Candilio, Olivia Cheronet, Elizabeth Curtis, Olga Flegontova, Lora Iliev, Aisling Kearns, Denise Keating, Ann Marie Lawson, Matthew Mah, Adam Micco, Megan Michel, Jonas Oppenheimer, Lijun Qiu, J. Noah Workman, Fatma Zalzala, Anna Szécsényi-Nagy, Pier Francesco Palamara, Swapan Mallick, Nadin Rohland, Ron Pinhasi, David Reich  
bioRxiv 2024.04.17.589597; doi: https://doi.org/10.1101/2024.04.17.589597  
[LeeGakuhariHumPopGenGeno2024]:  
**Medieval genomes from eastern Mongolia share a stable genetic profile over a millennium.** Lee J, Sato T, Tajima A, Amgalantugs T, Tsogtbaatar B, Nakagome S, Miyake T, Shiraishi N, Jeong C, Gakuhari T. Hum Popul Genet Genom. 2024;4(1):0004. https://doi.org/10.47248/hpgg2404010004.  
  
[LindoFigueiroPNASNexus2022]:  
**The genomic prehistory of the Indigenous peoples of Uruguay.** John Lindo, Rosseirys De La Rosa, Andre L C d Santos, Mónica Sans, Michael DeGiorgio, Gonzalo Figueiro, The genomic prehistory of the Indigenous peoples of Uruguay, PNAS Nexus, Volume 1, Issue 2, May 2022, pgac047, https://doi.org/10.1093/pnasnexus/pgac047.   
  
[LindoPNAS2017]:  
**Ancient individuals from the North American Northwest Coast reveal 10,000 years of regional genetic continuity.** Lindo J, Achilli A, Perego UA, Archer D, Valdiosera C, Petzelt B, Mitchell J, Worl R, Dixon EJ, Fifield TE, Rasmussen M, Willerslev E, Cybulski JS, Kemp BM, DeGiorgio M, Malhi RS. Proc Natl Acad Sci U S A. 2017 Apr 18;114(16):4093-4098. doi: 10.1073/pnas.1620410114. Epub 2017 Apr 4. PMID: 28377518.   
  
[LindoScienceAdvances2018]:  
**The genetic prehistory of the Andean highlands 7000 years BP though European contact.** Lindo J, Haas R, Hofman C, Apata M, Moraga M, Verdugo RA, Watson JT, Viviano Llave C, Witonsky D, Beall C, Warinner C, Novembre J, Aldenderfer M, Di Rienzo A. Sci Adv. 2018 Nov 8;4(11):eaau4921. doi: 10.1126/sciadv.aau4921. eCollection 2018 Nov. PMID: 30417096.   
  
[LinderholmNatureScientificReports2020]:  
**Corded Ware cultural complexity uncovered using genomic and isotopic analysis from south-eastern Poland.** Linderholm A, Kılınç GM, Szczepanek A, Włodarczak P, Jarosz P, Belka Z, Dopieralska J, Werens K, Górski J, Mazurek M, Hozer M, Rybicka M, Ostrowski M, Bagińska J, Koman W, Rodríguez-Varela R, Storå J, Götherström A, Krzewińska M. Sci Rep. 2020 Apr 14;10(1):6885. doi: 10.1038/s41598-020-63138-w. PMID: 32303690; PMCID: PMC7165176.  
  
[LipsonSawchukNature2022]:  
**Ancient DNA and deep population structure in sub-Saharan African foragers.** Lipson M, Sawchuk EA, Thompson JC, Oppenheimer J, Tryon CA, Ranhorn KL, de Luna KM, Sirak KA, Olalde I, Ambrose SH, Arthur JW, Arthur KJW, Ayodo G, Bertacchi A, Cerezo-Román JI, Culleton BJ, Curtis MC, Davis J, Gidna AO, Hanson A, Kaliba P, Katongo M, Kwekason A, Laird MF, Lewis J, Mabulla AZP, Mapemba F, Morris A, Mudenda G, Mwafulirwa R, Mwangomba D, Ndiema E, Ogola C, Schilt F, Willoughby PR, Wright DK, Zipkin A, Pinhasi R, Kennett DJ, Manthi FK, Rohland N, Patterson N, Reich D, Prendergast ME. Nature. 2022 Mar;603(7900):290-296. doi: 10.1038/s41586-022-04430-9. Epub 2022 Feb 23. PMID: 35197631; PMCID: PMC8907066.  
  
[LipsonCurrentBiology2018]:  
**Population Turnover in Remote Oceania Shortly after Initial Settlement.** Lipson M, Skoglund P, Spriggs M, Valentin F, Bedford S, Shing R, Buckley H, Phillip I, Ward GK, Mallick S, Rohland N, Broomandkhoshbacht N, Cheronet O, Ferry M, Harper TK, Michel M, Oppenheimer J, Sirak K, Stewardson K, Auckland K, Hill AVS, Maitland K, Oppenheimer SJ, Parks T, Robson K, Williams TN, Kennett DJ, Mentzer AJ, Pinhasi R, Reich D. Curr Biol. 2018 Apr 2;28(7):1157-1165.e7. doi: 10.1016/j.cub.2018.02.051. Epub 2018 Feb 28. PMID:29501328.  
  
[LipsonCurrentBiology2020]:  
**Three Phases of Ancient Migration Shaped the Ancestry of Human Populations in Vanuatu.** Lipson M, Spriggs M, Valentin F, Bedford S, Shing R, Zinger W, Buckley H, Petchey F, Matanik R, Cheronet O, Rohland N, Pinhasi R, Reich D. Three Phases of Ancient Migration Shaped the Ancestry of Human Populations in Vanuatu. Curr Biol. 2020 Dec 21;30(24):4846-4856.e6. doi: 10.1016/j.cub.2020.09.035. Epub 2020 Oct 15. PMID: 33065004; PMCID: PMC7755836.  
  
[LipsonNature2017]:  
**Parallel palaeogenomic transects reveal complex genetic history of early European farmers.** Lipson M, Szécsényi-Nagy A, Mallick S, Pósa A, Stégmár B, Keerl V, Rohland N, Stewardson K, Ferry M, Michel M, Oppenheimer J, Broomandkhoshbacht N, Harney E, Nordenfelt S, Llamas B, Gusztáv Mende B, Köhler K, Oross K, Bondár M, Marton T, Osztás A, Jakucs J, Paluch T, Horváth F, Csengeri P, Koós J, Sebők K, Anders A, Raczky P, Regenye J, Barna JP, Fábián S, Serlegi G, Toldi Z, GyÖngyvér Nagy E, Dani J, Molnár E, Pálfi G, Márk L, Melegh B, Bánfai Z, Domboróczki L, Fernández-Eraso J, Antonio Mujika-Alustiza J, Alonso Fernández C, Jiménez Echevarría J, Bollongino R, Orschiedt J, Schierhold K, Meller H, Cooper A, Burger J, Bánffy E, Alt KW, Lalueza-Fox C, Haak W, Reich D. Nature. 2017 Nov 16;551(7680):368-372. doi: 10.1038/nature24476. Epub 2017 Nov 8. PMID: 29144465.  
  
[LipsonNature2020]:  
**Ancient West African foragers in the context of African population history.** Lipson M, Ribot I, Mallick S, Rohland N, Olalde I, Adamski N, Broomandkhoshbacht N, Lawson AM, López S, Oppenheimer J, Stewardson K, Asombang RN, Bocherens H, Bradman N, Culleton BJ, Cornelissen E, Crevecoeur I, de Maret P, Fomine FLM, Lavachery P, Mindzie CM, Orban R, Sawchuk E, Semal P, Thomas MG, Van Neer W, Veeramah KR, Kennett DJ, Patterson N, Hellenthal G, Lalueza-Fox C, MacEachern S, Prendergast ME, Reich D. Nature. 2020 Jan;577(7792):665-670. doi: 10.1038/s41586-020-1929-1. Epub 2020 Jan 22. PMID: 31969706.  
  
[LipsonScience2018]:  
**Ancient genomes document multiple waves of migration in Southeast Asian prehistory.** Lipson M, Cheronet O, Mallick S, Rohland N, Oxenham M, Pietrusewsky M, Pryce TO, Willis A, Matsumura H, Buckley H, Domett K, Nguyen GH, Trinh HH, Kyaw AA, Win TT, Pradier B, Broomandkhoshbacht N, Candilio F, Changmai P, Fernandes D, Ferry M, Gamarra B, Harney E, Kampuansai J, Kutanan W, Michel M, Novak M, Oppenheimer J, Sirak K, Stewardson K, Zhang Z, Flegontov P, Pinhasi R, Reich D. Science. 2018 Jul 6;361(6397):92-95. doi: 10.1126/science.aat3188. Epub 2018 May 17. PMID: 29773666.   
  
[LiuDuongMBE2020]:  
**Extensive Ethnolinguistic Diversity in Vietnam Reflects Multiple Sources of Genetic Diversity.** Liu D, Duong NT, Ton ND, Van Phong N, Pakendorf B, Van Hai N, Stoneking M. Mol Biol Evol. 2020 Sep 1;37(9):2503-2519. doi: 10.1093/molbev/msaa099. PMID: 32344428; PMCID: PMC7475039.  
  
[LiuJeongNatComm2022]:  
**Ancient genomes from the Himalayas illuminate the genetic history of Tibetans and their Tibeto-Burman speaking neighbors.** Liu CC, Witonsky D, Gosling A, Lee JH, Ringbauer H, Hagan R, Patel N, Stahl R, Novembre J, Aldenderfer M, Warinner C, Di Rienzo A, Jeong C.Nat Commun. 2022 Mar 8;13(1):1203. doi: 10.1038/s41467-022-28827-2. PMID: 35260549; PMCID: PMC8904508.  
  
[LiuKoStonekingPNASNexus2023]:  
**The genomic diversity of Taiwanese Austronesian groups: Implications for the "Into- and Out-of-Taiwan" models.** Liu D, Ko AM, Stoneking M. PNAS Nexus. 2023 May 16;2(5):pgad122. doi: 10.1093/pnasnexus/pgad122. PMID: 37200801; PMCID: PMC10187666.  
  
[LiuScience2022]:  
**Ancient DNA reveals five streams of migration into Micronesia and matrilocality in early Pacific seafarers.** Liu YC, Hunter-Anderson R, Cheronet O, Eakin J, Camacho F, Pietrusewsky M, Rohland N, Ioannidis A, Athens JS, Douglas MT, Ikehara-Quebral RM, Bernardos R, Culleton BJ, Mah M, Adamski N, Broomandkhoshbacht N, Callan K, Lawson AM, Mandl K, Michel M, Oppenheimer J, Stewardson K, Zalzala F, Kidd K, Kidd J, Schurr TG, Auckland K, Hill AVS, Mentzer AJ, Quinto-Cortés CD, Robson K, Kennett DJ, Patterson N, Bustamante CD, Moreno-Estrada A, Spriggs M, Vilar M, Lipson M, Pinhasi R, Reich D. Science. 2022 Jul;377(6601):72-79. doi: 10.1126/science.abm6536. Epub 2022 Jun 30. PMID: 35771911.  
  
[LlorenteScience2015]:  
**Ancient Ethiopian genome reveals extensive Eurasian admixture throughout the African continent.** Gallego Llorente M, Jones ER, Eriksson A, Siska V, Arthur KW, Arthur JW, Curtis MC, Stock JT, Coltorti M, Pieruccini P, Stretton S, Brock F, Higham T, Park Y, Hofreiter M, Bradley DG, Bhak J, Pinhasi R, Manica A. Science. 2015 Nov 13;350(6262):820-2. doi: 10.1126/science.aad2879. Epub 2015 Oct 8. Erratum in: Science. 2016 Feb 19;351(6275). pii: aaf3945. doi: 10.1126/science.aaf3945. PMID: 26449472.

[LopezNatureCommunications2021]:  
**Evidence of the interplay of genetics and culture in Ethiopia.** López S, Tarekegn A, Band G, van Dorp L, Bird N, Morris S, Oljira T, Mekonnen E, Bekele E, Blench R, Thomas MG, Bradman N, Hellenthal G. Nat Commun. 2021 Jun 11;12(1):3581. doi: 10.1038/s41467-021-23712-w. PMID: 34117245; PMCID: PMC8196081.  
  
[MafessoniPNAS2020]:  
**A high-coverage Neandertal genome from Chagyrskaya Cave.** Mafessoni F, Grote S, de Filippo C, Slon V, Kolobova KA, Viola B, Markin SV, Chintalapati M, Peyrégne S, Skov L, Skoglund P, Krivoshapkin AI, Derevianko AP, Meyer M, Kelso J, Peter B, Prüfer K, Pääbo S. Proc Natl Acad Sci U S A. 2020 Jun 30;117(26):15132-15136. doi: 10.1073/pnas.2004944117. Epub 2020 Jun 16. PMID: 32546518; PMCID: PMC7334501.  
  
[MaierFlegontovELife2023]:  
**On the limits of fitting complex models of population history to f-statistics** eLife 12:e85492. 2023 https://doi.org/10.7554/eLife.85492   
  
[MalaspinasCurrentBiology2014]:  
**Two ancient human genomes reveal Polynesian ancestry among the indigenous Botocudos of Brazil.** Malaspinas AS, Lao O, Schroeder H, Rasmussen M, Raghavan M, Moltke I, Campos PF, Sagredo FS, Rasmussen S, Gonçalves VF, Albrechtsen A, Allentoft ME, Johnson PL, Li M, Reis S, Bernardo DV, DeGiorgio M, Duggan AT, Bastos M, Wang Y, Stenderup J, Moreno-Mayar JV, Brunak S, Sicheritz-Ponten T, Hodges E, Hannon GJ, Orlando L, Price TD, Jensen JD, Nielsen R, Heinemeier J, Olsen J, Rodrigues-Carvalho C, Lahr MM, Neves WA, Kayser M, Higham T, Stoneking M, Pena SD, Willerslev E. Curr Biol. 2014 Nov 3;24(21):R1035-7. doi: 10.1016/j.cub.2014.09.078. Epub 2014 Oct 23. PMID: 25455029.  
  
[MallickNature2016]:  
**The Simons Genome Diversity Project: 300 genomes from 142 diverse populations.** Mallick S, Li H, Lipson M, Mathieson I, Gymrek M, Racimo F, Zhao M, Chennagiri N, Nordenfelt S, Tandon A, Skoglund P, Lazaridis I, Sankararaman S, Fu Q, Rohland N, Renaud G, Erlich Y, Willems T, Gallo C, Spence JP, Song YS, Poletti G, Balloux F, van Driem G, de Knijff P, Romero IG, Jha AR, Behar DM, Bravi CM, Capelli C, Hervig T, Moreno-Estrada A, Posukh OL, Balanovska E, Balanovsky O, Karachanak-Yankova S, Sahakyan H, Toncheva D, Yepiskoposyan L, Tyler-Smith C, Xue Y, Abdullah MS, Ruiz-Linares A, Beall CM, Di Rienzo A, Jeong C, Starikovskaya EB, Metspalu E, Parik J, Villems R, Henn BM, Hodoglugil U, Mahley R, Sajantila A, Stamatoyannopoulos G, Wee JT, Khusainova R, Khusnutdinova E, Litvinov S, Ayodo G, Comas D, Hammer MF, Kivisild T, Klitz W, Winkler CA, Labuda D, Bamshad M, Jorde LB, Tishkoff SA, Watkins WS, Metspalu M, Dryomov S, Sukernik R, Singh L, Thangaraj K, Pääbo S, Kelso J, Patterson N, Reich D. Nature. 2016 Oct 13;538(7624):201-206. doi: 10.1038/nature18964. Epub 2016 Sep 21. PMID: 27654912.  
  
[MalmstromProcBiolSci2019]:  
**The genomic ancestry of the Scandinavian Battle Axe Culture people and their relation to the broader Corded Ware horizon.** Malmström H, Günther T, Svensson EM, Juras A, Fraser M, Munters AR, Pospieszny L , Tõrv M, Lindström J, Götherström A, Storå J, Jakobsson M. Proc Biol Sci. 2019 Oct 9;286(1912):20191528. doi: 10.1098/rspb.2019.1528. Epub 2019 Oct 9. PMID: 31594508.  
  
[MartinianoNatureCommunications2016]:  
**Genomic signals of migration and continuity in Britain before the Anglo-Saxons.** Martiniano R, Caffell A, Holst M, Hunter-Mann K, Montgomery J, Müldner G, McLaughlin RL, Teasdale MD, van Rheenen W, Veldink JH, van den Berg LH, Hardiman O, Carroll M, Roskams S, Oxley J, Morgan C, Thomas MG, Barnes I, McDonnell C, Collins MJ, Bradley DG.  
Nat Commun. 2016 Jan 19;7:10326. doi: 10.1038/ncomms10326. PMID: 26783717.   
  
[MaoCell2021]:  
**The deep population history of northern East Asia from the Late Pleistocene to the Holocene.** Mao X, Zhang H, Qiao S, Liu Y, Chang F, Xie P, Zhang M, Wang T, Li M, Cao P, Yang R, Liu F, Dai Q, Feng X, Ping W, Lei C, Olsen JW, Bennett EA, Fu Q. The deep population history of northern East Asia from the Late Pleistocene to the Holocene. Cell. 2021 Jun 10;184(12):3256-3266.e13. doi: 10.1016/j.cell.2021.04.040. Epub 2021 May 27. PMID: 34048699.  
[MarchiExcoffierCell2022]:  
**The genomic origins of the world's first farmers world.**Marchi N, Winkelbach L, Schulz I, Brami M, Hofmanová Z, Blöcher J, Reyna-Blanco CS, Diekmann Y, Thiéry A, Kapopoulou A, Link V, Piuz V, Kreutzer S, Figarska SM, Ganiatsou E, Pukaj A, Struck TJ, Gutenkunst RN, Karul N, Gerritsen F, Pechtl J, Peters J, Zeeb-Lanz A, Lenneis E, Teschler-Nicola M, Triantaphyllou S, Stefanović S, Papageorgopoulou C, Wegmann D, Burger J, Excoffier L. The genomic origins of the world's first farmers. Cell. 2022 May 26;185(11):1842-1859.e18. doi: 10.1016/j.cell.2022.04.008. Epub 2022 May 12. PMID: 35561686; PMCID: PMC9166250.   
  
[MarcusNatureCommunications2020]:  
**Genetic history from the Middle Neolithic to present on the Mediterranean island of Sardinia.** Marcus JH, Posth C, Ringbauer H, Lai L, Skeates R, Sidore C, Beckett J, Furtwängler A, Olivieri A, Chiang CWK, Al-Asadi H, Dey K, Joseph TA, Liu CC, Der Sarkissian C, Radzevičiūtė R, Michel M, Gradoli MG, Marongiu P, Rubino S, Mazzarello V, Rovina D, La Fragola A, Serra RM, Bandiera P, Bianucci R, Pompianu E, Murgia C, Guirguis M, Orquin RP, Tuross N, van Dommelen P, Haak W, Reich D, Schlessinger D, Cucca F, Krause J, Novembre J. Nat Commun. 2020 Feb 24;11(1):939. doi: 10.1038/s41467-020-14523-6. PMID: 32094358; PMCID: PMC7039977.  
  
[MargaryanNature2020]:  
**Population genomics of the Viking world.** Margaryan A, Lawson DJ, Sikora M, Racimo F, Rasmussen S, Moltke I, Cassidy LM, Jørsboe E, Ingason A, Pedersen MW, Korneliussen T, Wilhelmson H, Buś MM, de Barros Damgaard P, Martiniano R, Renaud G, Bhérer C, Moreno-Mayar JV, Fotakis AK, Allen M, Allmäe R, Molak M, Cappellini E, Scorrano G, McColl H, Buzhilova A, Fox A, Albrechtsen A, Schütz B, Skar B, Arcini C, Falys C, Jonson CH, Błaszczyk D, Pezhemsky D, Turner-Walker G, Gestsdóttir H, Lundstrøm I, Gustin I, Mainland I, Potekhina I, Muntoni IM, Cheng J, Stenderup J, Ma J, Gibson J, Peets J, Gustafsson J, Iversen KH, Simpson L, Strand L, Loe L, Sikora M, Florek M, Vretemark M, Redknap M, Bajka M, Pushkina T, Søvsø M, Grigoreva N, Christensen T, Kastholm O, Uldum O, Favia P, Holck P, Sten S, Arge SV, Ellingvåg S, Moiseyev V, Bogdanowicz W, Magnusson Y, Orlando L, Pentz P, Jessen MD, Pedersen A, Collard M, Bradley DG, Jørkov ML, Arneborg J, Lynnerup N, Price N, Gilbert MTP, Allentoft ME, Bill J, Sindbæk SM, Hedeager L, Kristiansen K, Nielsen R, Werge T, Willerslev E. Nature. 2020 Sep;585(7825):390-396. doi: 10.1038/s41586-020-2688-8. Epub 2020 Sep 16. PMID: 32939067.  
  
[MarotiTorokCurrBio2022]:  
**The genetic origin of Huns, Avars, and conquering Hungarians.** Maróti Z, Neparáczki E, Schütz O, Maár K, Varga GIB, Kovács B, Kalmár T, Nyerki E, Nagy I, Latinovics D, Tihanyi B, Marcsik A, Pálfi G, Bernert Z, Gallina Z, Horváth C, Varga S, Költő L, Raskó I, Nagy PL, Balogh C, Zink A, Maixner F, Götherström A, George R, Szalontai C, Szenthe G, Gáll E, Kiss AP, Gulyás B, Kovacsóczy BN, Gál SS, Tomka P, Török T. The genetic origin of Huns, Avars, and conquering Hungarians. Curr Biol. 2022 Jul 11;32(13):2858-2870.e7. doi: 10.1016/j.cub.2022.04.093. Epub 2022 May 25. PMID: 35617951.  
  
[MartinianoDurbinCellGenomics2024]:  
**Ancient genomes illuminate Eastern Arabian population history and adaptation against malaria.** Martiniano R, Haber M, Almarri MA, Mattiangeli V, Kuijpers MCM, Chamel B, Breslin EM, Littleton J, Almahari S, Aloraifi F, Bradley DG, Lombard P, Durbin R.Cell Genom. 2024 Mar 13;4(3):100507. doi: 10.1016/j.xgen.2024.100507. Epub 2024 Feb 27. PMID: 38417441; PMCID: PMC10943591.  
  
[MartinianoPLoSGenetics2017]:  
**The population genomics of archaeological transition in west Iberia: Investigation of ancient substructure using imputation and haplotype-based methods.** Martiniano R, Cassidy LM, Ó'Maoldúin R, McLaughlin R, Silva NM, Manco L, Fidalgo D, Pereira T, Coelho MJ, Serra M, Burger J, Parreira R, Moran E, Valera AC, Porfirio E, Boaventura R, Silva AM, Bradley DG. PLoS Genet. 2017 Jul 27;13(7):e1006852. doi: 10.1371/journal.pgen.1006852. eCollection 2017 Jul. PMID: 28749934.

[MassilaniPaaboScience2020]:  
**Denisovan ancestry and population history of early East Asians.** Massilani D, Skov L, Hajdinjak M, Gunchinsuren B, Tseveendorj D, Yi S, Lee J, Nagel S, Nickel B, Devièse T, Higham T, Meyer M, Kelso J, Peter BM, Pääbo S. Denisovan ancestry and population history of early East Asians. Science. 2020 Oct 30;370(6516):579-583. doi: 10.1126/science.abc1166. PMID: 33122380.  
  
[MathiesonNature2015]:  
**Genome-wide patterns of selection in 230 ancient Eurasians.** Mathieson I, Lazaridis I, Rohland N, Mallick S, Patterson N, Roodenberg SA, Harney E, Stewardson K, Fernandes D, Novak M, Sirak K, Gamba C, Jones ER, Llamas B, Dryomov S, Pickrell J, Arsuaga JL, de Castro JM, Carbonell E, Gerritsen F, Khokhlov A, Kuznetsov P, Lozano M, Meller H, Mochalov O, Moiseyev V, Guerra MA, Roodenberg J, Vergès JM, Krause J, Cooper A, Alt KW, Brown D, Anthony D, Lalueza-Fox C, Haak W, Pinhasi R, Reich D. Nature. 2015 Dec 24;528(7583):499-503. doi: 10.1038/nature16152. Epub 2015 Nov 23. PMID: 26595274.  
  
[MathiesonNature2018]:  
**The genomic history of southeastern Europe.** Mathieson I, Alpaslan-Roodenberg S, Posth C, Szécsényi-Nagy A, Rohland N, Mallick S, Olalde I, Broomandkhoshbacht N, Candilio F, Cheronet O, Fernandes D, Ferry M, Gamarra B, Fortes GG, Haak W, Harney E, Jones E, Keating D, Krause-Kyora B, Kucukkalipci I, Michel M, Mittnik A, Nägele K, Novak M, Oppenheimer J, Patterson N, Pfrengle S, Sirak K, Stewardson K, Vai S, Alexandrov S, Alt KW, Andreescu R, Antonović D, Ash A, Atanassova N, Bacvarov K, Gusztáv MB, Bocherens H, Bolus M, Boroneanţ A, Boyadzhiev Y, Budnik A, Burmaz J, Chohadzhiev S, Conard NJ, Cottiaux R, Čuka M, Cupillard C, Drucker DG, Elenski N, Francken M, Galabova B, Ganetsovski G, Gély B, Hajdu T, Handzhyiska V, Harvati K, Higham T, Iliev S, Janković I, Karavanić I, Kennett DJ, Komšo D, Kozak A, Labuda D, Lari M, Lazar C, Leppek M, Leshtakov K, Vetro DL, Los D, Lozanov I, Malina M, Martini F, McSweeney K, Meller H, Menđušić M, Mirea P, Moiseyev V, Petrova V, Price TD, Simalcsik A, Sineo L, Šlaus M, Slavchev V, Stanev P, Starović A, Szeniczey T, Talamo S, Teschler-Nicola M, Thevenet C, Valchev I, Valentin F, Vasilyev S, Veljanovska F, Venelinova S, Veselovskaya E, Viola B, Virag C, Zaninović J, Zäuner S, Stockhammer PW, Catalano G, Krauß R, Caramelli D, Zariņa G, Gaydarska B, Lillie M, Nikitin AG, Potekhina I, Papathanasiou A, Borić D, Bonsall C, Krause J, Pinhasi R, Reich D. Nature. 2018 Mar 8;555(7695):197-203. doi: 10.1038/nature25778. Epub 2018 Feb 21. PMID: 29466330.  
  
[MattilaCommBio2023]:  
**Genetic continuity, isolation, and gene flow in Stone Age Central and Eastern Europe.** Mattila TM, Svensson EM, Juras A, Günther T, Kashuba N, Ala-Hulkko T, Chyleński M, McKenna J, Pospieszny Ł, Constantinescu M, Rotea M, Palincaș N, Wilk S, Czerniak L, Kruk J, Łapo J, Makarowicz P, Potekhina I, Soficaru A, Szmyt M, Szostek K, Götherström A, Storå J, Netea MG, Nikitin AG, Persson P, Malmström H, Jakobsson M. Commun Biol. 2023 Aug 9;6(1):793. doi: 10.1038/s42003-023-05131-3. PMID: 37558731; PMCID: PMC10412644.

[McCollScience2018]:  
**The prehistoric peopling of Southeast Asia.** McColl H, Racimo F, Vinner L, Demeter F, Gakuhari T, Moreno-Mayar JV, van Driem G, Gram Wilken U, Seguin-Orlando A, de la Fuente Castro C, Wasef S, Shoocongdej R, Souksavatdy V, Sayavongkhamdy T, Saidin MM, Allentoft ME, Sato T, Malaspinas AS, Aghakhanian FA, Korneliussen T, Prohaska A, Margaryan A, de Barros Damgaard P, Kaewsutthi S, Lertrit P, Nguyen TMH, Hung HC, Minh Tran T, Nghia Truong H, Nguyen GH, Shahidan S, Wiradnyana K, Matsumae H, Shigehara N, Yoneda M, Ishida H, Masuyama T, Yamada Y, Tajima A, Shibata H, Toyoda A, Hanihara T, Nakagome S, Deviese T, Bacon AM, Duringer P, Ponche JL, Shackelford L, Patole-Edoumba E, Nguyen AT, Bellina-Pryce B, Galipaud JC, Kinaston R, Buckley H, Pottier C, Rasmussen S, Higham T, Foley RA, Lahr MM, Orlando L, Sikora M, Phipps ME, Oota H, Higham C, Lambert DM, Willerslev E. Science. 2018 Jul 6;361(6397):88-92. doi: 10.1126/science.aat3628. PMID: 29976827.  
  
[MeyerScience2012]:  
**A high-coverage genome sequence from an archaic Denisovan individual.** Meyer M, Kircher M, Gansauge MT, Li H, Racimo F, Mallick S, Schraiber JG, Jay F, Prüfer K, de Filippo C, Sudmant PH, Alkan C, Fu Q, Do R, Rohland N, Tandon A, Siebauer M, Green RE, Bryc K, Briggs AW, Stenzel U, Dabney J, Shendure J, Kitzman J, Hammer MF, Shunkov MV, Derevianko AP, Patterson N, Andrés AM, Eichler EE, Slatkin M, Reich D, Kelso J, Pääbo S. Science. 2012 Oct 12;338(6104):222-6. doi: 10.1126/science.1224344. Epub 2012 Aug 30. PMID: 22936568.   
  
[MittnikNatureCommunications2018]:  
**The genetic prehistory of the Baltic Sea region.** Mittnik A, Wang CC, Pfrengle S, Daubaras M, Zariņa G, Hallgren F, Allmäe R, Khartanovich V, Moiseyev V, Tõrv M, Furtwängler A, Andrades Valtueña A, Feldman M, Economou C, Oinonen M, Vasks A, Balanovska E, Reich D, Jankauskas R, Haak W, Schiffels S, Krause J. Nat Commun. 2018 Jan 30;9(1):442. doi: 10.1038/s41467-018-02825-9. Erratum in: Nat Commun. 2018 Apr 11;9(1):1494. PMID: 29382937.  
  
[MittnikScience2019]:  
**Kinship-based social inequality in Bronze Age Europe.** Mittnik A, Massy K, Knipper C, Wittenborn F, Friedrich R, Pfrengle S, Burri M, Carlichi-Witjes N, Deeg H, Furtwängler A, Harbeck M, von Heyking K, Kociumaka C, Kucukkalipci I, Lindauer S, Metz S, Staskiewicz A, Thiel A, Wahl J, Haak W, Pernicka E, Schiffels S, Stockhammer PW, Krause J. Science. 2019 Nov 8;366(6466):731-734. doi: 10.1126/science.aax6219. Epub 2019 Oct 10. PMID: 31601705.  
  
[MondalNatureGenetics2016]:  
**Genomic analysis of Andamanese provides insights into ancient human migration into Asia and adaptation.** Mondal M, Casals F, Xu T, Dall'Olio GM, Pybus M, Netea MG, Comas D, Laayouni H, Li Q, Majumder PP, Bertranpetit J. Nat Genet. 2016 Sep;48(9):1066-70. doi: 10.1038/ng.3621. Epub 2016 Jul 25. PMID: 27455350.  
  
[MootsNatEcolEvol2023]:  
**A genetic history of continuity and mobility in the Iron Age central Mediterranean.** Moots HM, Antonio M, Sawyer S, Spence JP, Oberreiter V, Weiß CL, Lucci M, Cherifi YMS, La Pastina F, Genchi F, Praxmeier E, Zagorc B, Cheronet O, Özdoğan KT, Demetz L, Amrani S, Candilio F, De Angelis D, Gasperetti G, Fernandes D, Gao Z, Fantar M, Coppa A, Pritchard JK, Pinhasi R. Nat Ecol Evol. 2023 Sep;7(9):1515-1524. doi: 10.1038/s41559-023-02143-4. Epub 2023 Aug 17. PMID: 37592021.   
  
[MorenoMayarNature2017]:  
**Terminal Pleistocene Alaskan genome reveals first founding population of Native Americans.** Moreno-Mayar JV, Potter BA, Vinner L, Steinrücken M, Rasmussen S, Terhorst J, Kamm JA, Albrechtsen A, Malaspinas AS, Sikora M, Reuther JD, Irish JD, Malhi RS, Orlando L, Song YS, Nielsen R, Meltzer DJ, Willerslev E. Nature. 2018 Jan 11;553(7687):203-207. doi: 10.1038/nature25173. Epub 2018 Jan 3. PMID: 29323294.  
  
[MorenoMayarScience2018]:  
**Early human dispersals within the Americas.** Moreno-Mayar JV, Vinner L, de Barros Damgaard P, de la Fuente C, Chan J, Spence JP, Allentoft ME, Vimala T, Racimo F, Pinotti T, Rasmussen S, Margaryan A, Iraeta Orbegozo M, Mylopotamitaki D, Wooller M, Bataille C, Becerra-Valdivia L, Chivall D, Comeskey D, Devièse T, Grayson DK, George L, Harry H, Alexandersen V, Primeau C, Erlandson J, Rodrigues-Carvalho C, Reis S, Bastos MQR, Cybulski J, Vullo C, Morello F, Vilar M, Wells S, Gregersen K, Hansen KL, Lynnerup N, Mirazón Lahr M, Kjær K, Strauss A, Alfonso-Durruty M, Salas A, Schroeder H, Higham T, Malhi RS, Rasic JT, Souza L, Santos FR, Malaspinas AS, Sikora M, Nielsen R, Song YS, Meltzer DJ, Willerslev E. Science. 2018 Dec 7;362(6419). pii: eaav2621. doi: 10.1126/science.aav2621. Epub 2018 Nov 8. PMID: 30409807.  
  
[NagelePosthScience2020]:  
**Genomic insights into the early peopling of the Caribbean.** Nägele K, Posth C, Iraeta Orbegozo M, Chinique de Armas Y, Hernández Godoy ST, González Herrera UM, Nieves-Colón MA, Sandoval-Velasco M, Mylopotamitaki D, Radzeviciute R, Laffoon J, Pestle WJ, Ramos-Madrigal J, Lamnidis TC, Schaffer WC, Carr RS, Day JS, Arredondo Antúnez C, Rangel Rivero A, Martínez-Fuentes AJ, Crespo-Torres E, Roksandic I, Stone AC, Lalueza-Fox C, Hoogland M, Roksandic M, Hofman CL, Krause J, Schroeder H. Science. 2020 Jul 24;369(6502):456-460. doi: 10.1126/science.aba8697. Epub 2020 Jun 4. PMID: 32499399.  
  
[NakatsukaLuisiNatureCommunications2020]:  
**Ancient genomes in South Patagonia reveal population movements associated with technological shifts and geography.** Nakatsuka N, Luisi P, Motti JMB, Salemme M, Santiago F, D'Angelo Del Campo MD, Vecchi RJ, Espinosa-Parrilla Y, Prieto A, Adamski N, Lawson AM, Harper TK, Culleton BJ, Kennett DJ, Lalueza-Fox C, Mallick S, Rohland N, Guichón RA, Cabana GS, Nores R, Reich D. Ancient genomes in South Patagonia reveal population movements associated with technological shifts and geography. Nat Commun. 2020 Aug 3;11(1):3868. doi: 10.1038/s41467-020-17656-w. PMID: 32747648; PMCID: PMC7400565.  
  
[NakatsukaCell2020]:  
**A Paleogenomic Reconstruction of the Deep Population History of the Andes.** Nakatsuka N, Lazaridis I, Barbieri C, Skoglund P, Rohland N, Mallick S, Posth C, Harkins-Kinkaid K, Ferry M, Harney É, Michel M, Stewardson K, Novak-Forst J, Capriles JM, Durruty MA, Álvarez KA, Beresford-Jones D, Burger R, Cadwallader L, Fujita R, Isla J, Lau G, Aguirre CL, LeBlanc S, Maldonado SC, Meddens F, Messineo PG, Culleton BJ, Harper TK, Quilter J, Politis G, Rademaker K, Reindel M, Rivera M, Salazar L, Sandoval JR, Santoro CM, Scheifler N, Standen V, Barreto MI, Espinoza IF, Tomasto-Cagigao E, Valverde G, Kennett DJ, Cooper A, Krause J, Haak W, Llamas B, Reich D, Fehren-Schmitz L. Cell. 2020 May 28;181(5):1131-1145.e21. doi: 10.1016/j.cell.2020.04.015. Epub 2020 May 7. PMID: 32386546; PMCID: PMC7304944.  
  
[NakatsukaNature2023]:  
**Genetic continuity and change among the Indigenous peoples of California.** Nakatsuka N, Holguin B, Sedig J, Langenwalter PE 2nd, Carpenter J, Culleton BJ, García-Moreno C, Harper TK, Martin D, Martínez-Ramírez J, Porcayo-Michelini A, Tiesler V, Villapando-Canchola ME, Valdes Herrera A, Callan K, Curtis E, Kearns A, Iliev L, Lawson AM, Mah M, Mallick S, Micco A, Michel M, Workman JN, Oppenheimer J, Qiu L, Zalzala F, Rohland N, Punzo Diaz JL, Johnson JR, Reich D. Nature. 2023 Dec;624(7990):122-129. doi: 10.1038/s41586-023-06771-5. Epub 2023 Nov 22. Erratum in: Nature. 2024 Aug;632(8024):E1. doi: 10.1038/s41586-024-07790-6. PMID: 37993721; PMCID: PMC10872549.  
  
[NakatsukaNatureGenetics2017]:  
**The promise of discovering population-specific disease-associated genes in South Asia.** Nakatsuka N, Moorjani P, Rai N, Sarkar B, Tandon A, Patterson N, Bhavani GS, Girisha KM, Mustak MS, Srinivasan S, Kaushik A, Vahab SA, Jagadeesh SM, Satyamoorthy K, Singh L, Reich D, Thangaraj K. Nat Genet. 2017 Sep;49(9):1403-1407. doi: 10.1038/ng.3917. Epub 2017 Jul 17. PMID: 28714977; PMCID: PMC5675555.  
  
[NalchikPostedPubliclyOnline2023]:  
**BioSample: SAMN39854872** https://www.ncbi.nlm.nih.gov/biosample/SAMN39854872?fbclid=IwAR3SVH0UloJnviQMf9AX6sVB8nGoU3kG\_Z3Z\_3adFgv1CD1gunqqQcWJZtE .  
  
[NarasimhanPattersonScience2019]:  
**The formation of human populations in South and Central Asia.** Narasimhan VM, Patterson N, Moorjani P, Rohland N, Bernardos R, Mallick S, Lazaridis I, Nakatsuka N, Olalde I, Lipson M, Kim AM, Olivieri LM, Coppa A, Vidale M, Mallory J, Moiseyev V, Kitov E, Monge J, Adamski N, Alex N, Broomandkhoshbacht N, Candilio F, Callan K, Cheronet O, Culleton BJ, Ferry M, Fernandes D, Freilich S, Gamarra B, Gaudio D, Hajdinjak M, Harney É, Harper TK, Keating D, Lawson AM, Mah M, Mandl K, Michel M, Novak M, Oppenheimer J, Rai N, Sirak K, Slon V, Stewardson K, Zalzala F, Zhang Z, Akhatov G, Bagashev AN, Bagnera A, Baitanayev B, Bendezu-Sarmiento J, Bissembaev AA, Bonora GL, Chargynov TT, Chikisheva T, Dashkovskiy PK, Derevianko A, Dobeš M, Douka K, Dubova N, Duisengali MN, Enshin D, Epimakhov A, Fribus AV, Fuller D, Goryachev A, Gromov A, Grushin SP, Hanks B, Judd M, Kazizov E, Khokhlov A, Krygin AP, Kupriyanova E, Kuznetsov P, Luiselli D, Maksudov F, Mamedov AM, Mamirov TB, Meiklejohn C, Merrett DC, Micheli R, Mochalov O, Mustafokulov S, Nayak A, Pettener D, Potts R, Razhev D, Rykun M, Sarno S, Savenkova TM, Sikhymbaeva K, Slepchenko SM, Soltobaev OA, Stepanova N, Svyatko S, Tabaldiev K, Teschler-Nicola M, Tishkin AA, Tkachev VV, Vasilyev S, Velemínský P, Voyakin D, Yermolayeva A, Zahir M, Zubkov VS, Zubova A, Shinde VS, Lalueza-Fox C, Meyer M, Anthony D, Boivin N, Thangaraj K, Kennett DJ, Frachetti M, Pinhasi R, Reich D. Science. 2019 Sep 6;365(6457). pii: eaat7487. doi: 10.1126/science.aat7487. PMID: 31488661.  
  
[NedoluzhkoPreprint2022]:  
**First ancient DNA analysis of mummies from the post-Scythian Oglakhty cemetery in South Siberia.** Artem Nedoluzhko, Svetlana Pankova, Ekaterina Vergasova et al. First ancient DNA analysis of mummies from the post-Scythian Oglakhty cemetery in South Siberia, 29 August 2022, PREPRINT (Version 1) available at Research Square [https://doi.org/10.21203/rs.3.rs-1993191/v1].  
  
[Nieves-ColonMolecularBiologyandEvolution2020]:  
**Ancient DNA Reconstructs the Genetic Legacies of Precontact Puerto Rico Communities.** Nieves-Colón MA, Pestle WJ, Reynolds AW, Llamas B, de la Fuente C, Fowler K, Skerry KM, Crespo-Torres E, Bustamante CD, Stone AC. Mol Biol Evol. 2020 Mar 1;37(3):611-626. doi: 10.1093/molbev/msz267. PMID: 31710665.  
  
[NikitinLazaridisBioRxiv2024]:  
**A genomic history of the North Pontic Region from the Neolithic to the Bronze Age** Alexey G. Nikitin, Iosif Lazaridis, Nick Patterson, Svitlana Ivanova, Mykhailo Videiko, Valentin Dergachev, Nadiia Kotova, Malcolm Lillie, Inna Potekhina, Marta Krenz-Niedbała, Sylwia Łukasik, Serhij Makhortykh, Virginie Renson, Henry Shephard, Gennadie Sirbu, Sofiia Svyryd, Taras Tkachuk, Piotr Włodarczak, Kim Callan, Elizabeth Curtis, Eadaoin Harney, Lora Iliev, Aisling Kearns, Ann Marie Lawson, Megan Michel, Matthew Mah, Adam Micco, Jonas Oppenheimer, Lijun Qiu, J. Noah Workman, Fatma Zalzala, Swapan Mallick, Nadin Rohland, David Reich bioRxiv 2024.04.17.589600; doi: https://doi.org/10.1101/2024.04.17.589600.  
  
[NikitinPLoSOne2023]:  
**Trypillian farmers and North Pontic forager-pastoralists in Eneolithic central Ukraine.** Nikitin AG, Videiko M, Patterson N, Renson V, Reich D (2023) Interactions between PLoS ONE 18(6): e0285449. https://doi.org/10.1371/journal.pone.0285449.  
  
[NikitinScientificReports2019]:  
**Interactions between earliest Linearbandkeramik farmers and central European hunter gatherers at the dawn of European Neolithization.** Nikitin AG, Stadler P, Kotova N, Teschler-Nicola M, Price TD, Hoover J, Kennett DJ, Lazaridis I, Rohland N, Lipson M, Reich D. Sci Rep. 2019 Dec 20;9(1):19544. doi: 10.1038/s41598-019-56029-2. PMID: 31863024.  
  
[NingCurrentBiology2019]:  
**Ancient Genomes Reveal Yamnaya-Related Ancestry and a Potential Source of Indo-European Speakers in Iron Age Tianshan.** Ning C, Wang CC, Gao S, Yang Y, Zhang X, Wu X, Zhang F, Nie Z, Tang Y, Robbeets M, Ma J, Krause J, Cui Y. Curr Biol. 2019 Aug 5;29(15):2526-2532.e4. doi: 10.1016/j.cub.2019.06.044. Epub 2019 Jul 25. PMID: 31353181.  
  
[NingNatureCommunications2020]:  
**Ancient genomes from northern China suggest links between subsistence changes and human migration.** Ning C, Li T, Wang K, Zhang F, Li T, Wu X, Gao S, Zhang Q, Zhang H, Hudson MJ, Dong G, Wu S, Fang Y, Liu C, Feng C, Li W, Han T, Li R, Wei J, Zhu Y, Zhou Y, Wang CC, Fan S, Xiong Z, Sun Z, Ye M, Sun L, Wu X, Liang F, Cao Y, Wei X, Zhu H, Zhou H, Krause J, Robbeets M, Jeong C, Cui Y. Nat Commun. 2020 Jun 1;11(1):2700. doi: 10.1038/s41467-020-16557-2. PMID: 32483115; PMCID: PMC7264253.  
  
[NovakPLoSOne2021]:  
**Genome-wide analysis of nearly all the victims of a 6200 year old massacre.** Novak M, Olalde I, Ringbauer H, Rohland N, Ahern J, Balen J, Janković I, Potrebica H, Pinhasi R, Reich D. Genome-wide analysis of nearly all the victims of a 6200 year old massacre. PLoS One. 2021 Mar 10;16(3):e0247332. doi: 10.1371/journal.pone.0247332. PMID: 33690651; PMCID: PMC7946188.  
  
[OlaldeCarrionCell2023]:  
**A genetic history of the Balkans from Roman frontier to Slavic migrations.** Olalde I, Carrión P, Mikić I, Rohland N, Mallick S, Lazaridis I, Mah M, Korać M, Golubović S, Petković S, Miladinović-Radmilović N, Vulović D, Alihodžić T, Ash A, Baeta M, Bartík J, Bedić Ž, Bilić M, Bonsall C, Bunčić M, Bužanić D, Carić M, Čataj L, Cvetko M, Drnić I, Dugonjić A, Đukić A, Đukić K, Farkaš Z, Jelínek P, Jovanovic M, Kaić I, Kalafatić H, Krmpotić M, Krznar S, Leleković T, M de Pancorbo M, Matijević V, Milošević Zakić B, Osterholtz AJ, Paige JM, Tresić Pavičić D, Premužić Z, Rajić Šikanjić P, Rapan Papeša A, Paraman L, Sanader M, Radovanović I, Roksandic M, Šefčáková A, Stefanović S, Teschler-Nicola M, Tončinić D, Zagorc B, Callan K, Candilio F, Cheronet O, Fernandes D, Kearns A, Lawson AM, Mandl K, Wagner A, Zalzala F, Zettl A, Tomanović Ž, Keckarević D, Novak M, Harper K, McCormick M, Pinhasi R, Grbić M, Lalueza-Fox C, Reich D. Cell. 2023 Dec 7;186(25):5472-5485.e9. doi: 10.1016/j.cell.2023.10.018. PMID: 38065079; PMCID: PMC10752003.  
  
[OlaldeMBE2015]:  
**A Common Genetic Origin for Early Farmers from Mediterranean Cardial and Central European LBK Cultures.** Olalde I, Schroeder H, Sandoval-Velasco M, Vinner L, Lobón I, Ramirez O, Civit S, García Borja P, Salazar-García DC, Talamo S, María Fullola J, Xavier Oms F, Pedro M, Martínez P, Sanz M, Daura J, Zilhão J, Marquès-Bonet T, Gilbert MT, Lalueza-Fox C. Mol Biol Evol. 2015 Dec;32(12):3132-42. doi: 10.1093/molbev/msv181. Epub 2015 Sep 2. PMID: 26337550.  
  
[OlaldeNature2018]:  
**The Beaker phenomenon and the genomic transformation of northwest Europe.** Olalde I, Brace S, Allentoft ME, Armit I, Kristiansen K, Booth T, Rohland N, Mallick S, Szécsényi-Nagy A, Mittnik A, Altena E, Lipson M, Lazaridis I, Harper TK, Patterson N, Broomandkhoshbacht N, Diekmann Y, Faltyskova Z, Fernandes D, Ferry M, Harney E, de Knijff P, Michel M, Oppenheimer J, Stewardson K, Barclay A, Alt KW, Liesau C, Ríos P, Blasco C, Miguel JV, García RM, Fernández AA, Bánffy E, Bernabò-Brea M, Billoin D, Bonsall C, Bonsall L, Allen T, Büster L, Carver S, Navarro LC, Craig OE, Cook GT, Cunliffe B, Denaire A, Dinwiddy KE, Dodwell N, Ernée M, Evans C, Kuchařík M, Farré JF, Fowler C, Gazenbeek M, Pena RG, Haber-Uriarte M, Haduch E, Hey G, Jowett N, Knowles T, Massy K, Pfrengle S, Lefranc P, Lemercier O, Lefebvre A, Martínez CH, Olmo VG, Ramírez AB, Maurandi JL, Majó T, McKinley JI, McSweeney K, Mende BG, Modi A, KulcsáR G, Kiss V, Czene A, Patay R, Endrődi A, Köhler K, Hajdu T, Szeniczey T, Dani J, Bernert Z, Hoole M, Cheronet O, Keating D, Velemínský P, Dobeš M, Candilio F, Brown F, Fernández RF, Herrero-Corral AM, Tusa S, Carnieri E, Lentini L, Valenti A, Zanini A, Waddington C, Delibes G, Guerra-Doce E, Neil B, Brittain M, Luke M, Mortimer R, Desideri J, Besse M, Brücken G, Furmanek M, Hałuszko A, Mackiewicz M, Rapiński A, Leach S, Soriano I, Lillios KT, Cardoso JL, Pearson MP, Włodarczak P, Price TD, Prieto P, Rey PJ, Risch R, Rojo Guerra MA, Schmitt A, Serralongue J, Silva AM, Smrčka V, Vergnaud L, Zilhão J, Caramelli D, Higham T, Thomas MG, Kennett DJ, Fokkens H, Heyd V, Sheridan A, Sjögren KG, Stockhammer PW, Krause J, Pinhasi R, Haak W, Barnes I, Lalueza-Fox C, Reich D. Nature. 2018 Mar 8;555(7695):190-196. doi: 10.1038/nature25738. Epub 2018 Feb 21. Erratum in: Nature. 2018 Mar 21;555(7697):543. PMID: 29466337.  
  
[OlaldeScience2019]:  
**The genomic history of the Iberian Peninsula over the past 8000 years.** Output encoded/decoded text Olalde I, Mallick S, Patterson N, Rohland N, Villalba-Mouco V, Silva M, Dulias K, Edwards CJ, Gandini F, Pala M, Soares P, Ferrando-Bernal M, Adamski N, Broomandkhoshbacht N, Cheronet O, Culleton BJ, Fernandes D, Lawson AM, Mah M, Oppenheimer J, Stewardson K, Zhang Z, Jiménez Arenas JM, Toro Moyano IJ, Salazar-García DC, Castanyer P, Santos M, Tremoleda J, Lozano M, García Borja P, Fernández-Eraso J, Mujika-Alustiza JA, Barroso C, Bermúdez FJ, Viguera Mínguez E, Burch J, Coromina N, Vivó D, Cebrià A, Fullola JM, García-Puchol O, Morales JI, Oms FX, Majó T, Vergès JM, Díaz-Carvajal A, Ollich-Castanyer I, López-Cachero FJ, Silva AM, Alonso-Fernández C, Delibes de Castro G, Jiménez Echevarría J, Moreno-Márquez A, Pascual Berlanga G, Ramos-García P, Ramos-Muñoz J, Vijande Vila E, Aguilella Arzo G, Esparza Arroyo Á, Lillios KT, Mack J, Velasco-Vázquez J, Waterman A, Benítez de Lugo Enrich L, Benito Sánchez M, Agustí B, Codina F, de Prado G, Estalrrich A, Fernández Flores Á, Finlayson C, Finlayson G, Finlayson S, Giles-Guzmán F, Rosas A, Barciela González V, García Atiénzar G, Hernández Pérez MS, Llanos A, Carrión Marco Y, Collado Beneyto I, López-Serrano D, Sanz Tormo M, Valera AC, Blasco C, Liesau C, Ríos P, Daura J, de Pedro Michó MJ, Diez-Castillo AA, Flores Fernández R, Francès Farré J, Garrido-Pena R, Gonçalves VS, Guerra-Doce E, Herrero-Corral AM, Juan-Cabanilles J, López-Reyes D, McClure SB, Merino Pérez M, Oliver Foix A, Sanz Borràs M, Sousa AC, Vidal Encinas JM, Kennett DJ, Richards MB, Werner Alt K, Haak W, Pinhasi R, Lalueza-Fox C, Reich D. Science. 2019 Mar 15;363(6432):1230-1234. doi: 10.1126/science.aav4040. PMID: 30872528.  
  
[OliveiraNatureEcologyEvolution2022]:  
**Genome-wide variation in the Angolan Namib Desert reveals unique pre-Bantu ancestry.** Oliveira S, Fehn AM, Amorim B, Stoneking M, Rocha J. Sci Adv. 2023 Sep 22;9(38):eadh3822. doi: 10.1126/sciadv.adh3822. Epub 2023 Sep 22. PMID: 37738339; PMCID: PMC10516492.  
  
[OliveiraNatureEcologyEvolution2022]:  
**Ancient genomes from the last three millennia support multiple human dispersals into Wallacea.** Oliveira S, Nägele K, Carlhoff S, Pugach I, Koesbardiati T, Hübner A, Meyer M, Oktaviana AA, Takenaka M, Katagiri C, Murti DB, Putri RS, Mahirta, Petchey F, Higham T, Higham CFW, O'Connor S, Hawkins S, Kinaston R, Bellwood P, Ono R, Powell A, Krause J, Posth C, Stoneking M. Ancient genomes from the last three millennia support multiple human dispersals into Wallacea. Nat Ecol Evol. 2022 Jul;6(7):1024-1034. doi: 10.1038/s41559-022-01775-2. Epub 2022 Jun 9. PMID: 35681000; PMCID: PMC9262713.  
  
[OmrakCurrentBiology2016]:  
**Genomic Evidence Establishes Anatolia as the Source of the European Neolithic Gene Pool.** Omrak A, Günther T, Valdiosera C, Svensson EM, Malmström H, Kiesewetter H, Aylward W, Storå J, Jakobsson M, Götherström A. Curr Biol. 2016 Jan 25;26(2):270-275. doi: 10.1016/j.cub.2015.12.019. Epub 2015 Dec 31. PMID: 26748850.  
  
[PapacScienceAdvances2021]:  
**Dynamic changes in genomic and social structures in third millennium BCE central Europe.** Papac L, Ernée M, Dobeš M, Langová M, Rohrlach AB, Aron F, Neumann GU, Spyrou MA, Rohland N, Velemínský P, Kuna M, Brzobohatá H, Culleton B, Daněček D, Danielisová A, Dobisíková M, Hložek J, Kennett DJ, Klementová J, Kostka M, Krištuf P, Kuchařík M, Hlavová JK, Limburský P, Malyková D, Mattiello L, Pecinovská M, Petriščáková K, Průchová E, Stránská P, Smejtek L, Špaček J, Šumberová R, Švejcar O, Trefný M, Vávra M, Kolář J, Heyd V, Krause J, Pinhasi R, Reich D, Schiffels S, Haak W. Dynamic changes in genomic and social structures in third millennium BCE central Europe. Sci Adv. 2021 Aug 25;7(35):eabi6941. doi: 10.1126/sciadv.abi6941. PMID: 34433570; PMCID: PMC8386934.  
  
[PosthYuNature2023]:  
**Palaeogenomics of Upper Palaeolithic to Neolithic European hunter-gatherers.** Posth C, Yu H, Ghalichi A, Rougier H, Crevecoeur I, Huang Y, Ringbauer H, Rohrlach AB, Nägele K, Villalba-Mouco V, Radzeviciute R, Ferraz T, Stoessel A, Tukhbatova R, Drucker DG, Lari M, Modi A, Vai S, Saupe T, Scheib CL, Catalano G, Pagani L, Talamo S, Fewlass H, Klaric L, Morala A, Rué M, Madelaine S, Crépin L, Caverne JB, Bocaege E, Ricci S, Boschin F, Bayle P, Maureille B, Le Brun-Ricalens F, Bordes JG, Oxilia G, Bortolini E, Bignon-Lau O, Debout G, Orliac M, Zazzo A, Sparacello V, Starnini E, Sineo L, van der Plicht J, Pecqueur L, Merceron G, Garcia G, Leuvrey JM, Garcia CB, Gómez-Olivencia A, Połtowicz-Bobak M, Bobak D, Le Luyer M, Storm P, Hoffmann C, Kabaciński J, Filimonova T, Shnaider S, Berezina N, González-Rabanal B, González Morales MR, Marín-Arroyo AB, López B, Alonso-Llamazares C, Ronchitelli A, Polet C, Jadin I, Cauwe N, Soler J, Coromina N, Rufí I, Cottiaux R, Clark G, Straus LG, Julien MA, Renhart S, Talaa D, Benazzi S, Romandini M, Amkreutz L, Bocherens H, Wißing C, Villotte S, de Pablo JF, Gómez-Puche M, Esquembre-Bebia MA, Bodu P, Smits L, Souffi B, Jankauskas R, Kozakaitė J, Cupillard C, Benthien H, Wehrberger K, Schmitz RW, Feine SC, Schüler T, Thevenet C, Grigorescu D, Lüth F, Kotula A, Piezonka H, Schopper F, Svoboda J, Sázelová S, Chizhevsky A, Khokhlov A, Conard NJ, Valentin F, Harvati K, Semal P, Jungklaus B, Suvorov A, Schulting R, Moiseyev V, Mannermaa K, Buzhilova A, Terberger T, Caramelli D, Altena E, Haak W, Krause J. Nature. 2023 Mar;615(7950):117-126. doi: 10.1038/s41586-023-05726-0. Epub 2023 Mar 1. Erratum in: Nature. 2023 Apr;616(7956):E5. doi: 10.1038/s41586-023-05942-8. PMID: 36859578; PMCID: PMC9977688.  
  
[PattersonNature2021]:  
**Large-scale migration into Britain during the Middle to Late Bronze Age.** Patterson N, Isakov M, Booth T, Büster L, Fischer CE, Olalde I, Ringbauer H, Akbari A, Cheronet O, Bleasdale M, Adamski N, Altena E, Bernardos R, Brace S, Broomandkhoshbacht N, Callan K, Candilio F, Culleton B, Curtis E, Demetz L, Carlson KSD, Edwards CJ, Fernandes DM, Foody MGB, Freilich S, Goodchild H, Kearns A, Lawson AM, Lazaridis I, Mah M, Mallick S, Mandl K, Micco A, Michel M, Morante GB, Oppenheimer J, Özdoğan KT, Qiu L, Schattke C, Stewardson K, Workman JN, Zalzala F, Zhang Z, Agustí B, Allen T, Almássy K, Amkreutz L, Ash A, Baillif-Ducros C, Barclay A, Bartosiewicz L, Baxter K, Bernert Z, Blažek J, Bodružić M, Boissinot P, Bonsall C, Bradley P, Brittain M, Brookes A, Brown F, Brown L, Brunning R, Budd C, Burmaz J, Canet S, Carnicero-Cáceres S, Čaušević-Bully M, Chamberlain A, Chauvin S, Clough S, Čondić N, Coppa A, Craig O, Črešnar M, Cummings V, Czifra S, Danielisová A, Daniels R, Davies A, de Jersey P, Deacon J, Deminger C, Ditchfield PW, Dizdar M, Dobeš M, Dobisíková M, Domboróczki L, Drinkall G, Đukić A, Ernée M, Evans C, Evans J, Fernández-Götz M, Filipović S, Fitzpatrick A, Fokkens H, Fowler C, Fox A, Gallina Z, Gamble M, González Morales MR, González-Rabanal B, Green A, Gyenesei K, Habermehl D, Hajdu T, Hamilton D, Harris J, Hayden C, Hendriks J, Hernu B, Hey G, Horňák M, Ilon G, Istvánovits E, Jones AM, Kavur MB, Kazek K, Kenyon RA, Khreisheh A, Kiss V, Kleijne J, Knight M, Kootker LM, Kovács PF, Kozubová A, Kulcsár G, Kulcsár V, Le Pennec C, Legge M, Leivers M, Loe L, López-Costas O, Lord T, Los D, Lyall J, Marín-Arroyo AB, Mason P, Matošević D, Maxted A, McIntyre L, McKinley J, McSweeney K, Meijlink B, Mende BG, Menđušić M, Metlička M, Meyer S, Mihovilić K, Milasinovic L, Minnitt S, Moore J, Morley G, Mullan G, Musilová M, Neil B, Nicholls R, Novak M, Pala M, Papworth M, Paresys C, Patten R, Perkić D, Pesti K, Petit A, Petriščáková K, Pichon C, Pickard C, Pilling Z, Price TD, Radović S, Redfern R, Resutík B, Rhodes DT, Richards MB, Roberts A, Roefstra J, Sankot P, Šefčáková A, Sheridan A, Skae S, Šmolíková M, Somogyi K, Somogyvári Á, Stephens M, Szabó G, Szécsényi-Nagy A, Szeniczey T, Tabor J, Tankó K, Maria CT, Terry R, Teržan B, Teschler-Nicola M, Torres-Martínez JF, Trapp J, Turle R, Ujvári F, van der Heiden M, Veleminsky P, Veselka B, Vytlačil Z, Waddington C, Ware P, Wilkinson P, Wilson L, Wiseman R, Young E, Zaninović J, Žitňan A, Lalueza-Fox C, de Knijff P, Barnes I, Halkon P, Thomas MG, Kennett DJ, Cunliffe B, Lillie M, Rohland N, Pinhasi R, Armit I, Reich D. Nature. 2022 Jan;601(7894):588-594. doi: 10.1038/s41586-021-04287-4. Epub 2021 Dec 22. PMID: 34937049; PMCID: PMC8889665.  
  
[PattersonGenetics2012]:  
**Ancient admixture in human history.** Patterson N, Moorjani P, Luo Y, Mallick S, Rohland N, Zhan Y, Genschoreck T, Webster T, Reich D. Genetics. 2012 Nov;192(3):1065-93. doi: 10.1534/genetics.112.145037. Epub 2012 Sep 7. PMID: 22960212.  
  
[PeltolaMajanderCell2023]:  
**Genetic admixture and language shift in the medieval Volga-Oka interfluve.** Peltola S, Majander K, Makarov N, Dobrovolskaya M, Nordqvist K, Salmela E, Onkamo P. Curr Biol. 2023 Jan 9;33(1):174-182.e10. doi: 10.1016/j.cub.2022.11.036. Epub 2022 Dec 12. PMID: 36513080.  
  
[PenskeHaakNature2023]:  
**Early contact between late farming and pastoralist societies in southeastern Europe.** Penske S, Rohrlach AB, Childebayeva A, Gnecchi-Ruscone G, Schmid C, Spyrou MA, Neumann GU, Atanassova N, Beutler K, Boyadzhiev K, Boyadzhiev Y, Bruyako I, Chohadzhiev A, Govedarica B, Karaucak M, Krauss R, Leppek M, Manzura I, Privat K, Ross S, Slavchev V, Sobotkova A, Toderaş M, Valchev T, Ringbauer H, Stockhammer PW, Hansen S, Krause J, Haak W. Nature. 2023 Aug;620(7973):358-365. doi: 10.1038/s41586-023-06334-8. Epub 2023 Jul 19. PMID: 37468624; PMCID: PMC10412445.  
  
[PenskeSciRep2024]:  
**Kinship practices at the early bronze age site of Leubingen in Central Germany.** Penske S, Küßner M, Rohrlach AB, Knipper C, Nováček J, Childebayeva A, Krause J, Haak W. Sci Rep. 2024 Feb 16;14(1):3871. doi: 10.1038/s41598-024-54462-6. PMID: 38365887; PMCID: PMC10873355.  
  
[PickrellNatureCommunications2012]:  
**The genetic prehistory of southern Africa.** Pickrell JK, Patterson N, Barbieri C, Berthold F, Gerlach L, Güldemann T, Kure B, Mpoloka SW, Nakagawa H, Naumann C, Lipson M, Loh PR, Lachance J, Mountain J, Bustamante CD, Berger B, Tishkoff SA, Henn BM, Stoneking M, Reich D, Pakendorf B. Nat Commun. 2012;3:1143. doi: 10.1038/ncomms2140. PMID: 23072811.  
  
[PopovicBacaSciAdv2021]:  
**Ancient genomes reveal long-range influence of the pre-Columbian culture and site of Tiwanaku.** Popović D, Molak M, Ziółkowski M, Vranich A, Sobczyk M, Vidaurre DU, Agresti G, Skrzypczak M, Ginalski K, Lamnidis TC, Nakatsuka N, Mallick S, Baca M. Sci Adv. 2021 Sep 24;7(39):eabg7261. doi: 10.1126/sciadv.abg7261. Epub 2021 Sep 24. PMID: 34559567; PMCID: PMC8462900.  
  
[PosthScienceAdvances2021]:  
**The origin and legacy of the Etruscans through a 2000-year archeogenomic time transect.** Posth C, Zaro V, Spyrou MA, Vai S, Gnecchi-Ruscone GA, Modi A, Peltzer A, Mötsch A, Nägele K, Vågene ÅJ, Nelson EA, Radzevičiūtė R, Freund C, Bondioli LM, Cappuccini L, Frenzel H, Pacciani E, Boschin F, Capecchi G, Martini I, Moroni A, Ricci S, Sperduti A, Turchetti MA, Riga A, Zavattaro M, Zifferero A, Heyne HO, Fernández-Domínguez E, Kroonen GJ, McCormick M, Haak W, Lari M, Barbujani G, Bondioli L, Bos KI, Caramelli D, Krause J. Sci Adv. 2021 Sep 24;7(39):eabi7673. doi: 10.1126/sciadv.abi7673. Epub 2021 Sep 24. PMID: 34559560; PMCID: PMC8462907.

[PosthNakatsukaCell2018]:  
**Reconstructing the Deep Population History of Central and South America.** Posth C, Nakatsuka N, Lazaridis I, Skoglund P, Mallick S, Lamnidis TC, Rohland N, Nägele K, Adamski N, Bertolini E, Broomandkhoshbacht N, Cooper A, Culleton BJ, Ferraz T, Ferry M, Furtwängler A, Haak W, Harkins K, Harper TK, Hünemeier T, Lawson AM, Llamas B, Michel M, Nelson E, Oppenheimer J, Patterson N, Schiffels S, Sedig J, Stewardson K, Talamo S, Wang CC, Hublin JJ, Hubbe M, Harvati K, Nuevo Delaunay A, Beier J, Francken M, Kaulicke P, Reyes-Centeno H, Rademaker K, Trask WR, Robinson M, Gutierrez SM, Prufer KM, Salazar-García DC, Chim EN, Müller Plumm Gomes L, Alves ML, Liryo A, Inglez M, Oliveira RE, Bernardo DV, Barioni A, Wesolowski V, Scheifler NA, Rivera MA, Plens CR, Messineo PG, Figuti L, Corach D, Scabuzzo C, Eggers S, DeBlasis P, Reindel M, Méndez C, Politis G, Tomasto-Cagigao E, Kennett DJ, Strauss A, Fehren-Schmitz L, Krause J, Reich D. Cell. 2018 Nov 15;175(5):1185-1197.e22. doi: 10.1016/j.cell.2018.10.027. Epub 2018 Nov 8. PMID: 30415837.  
  
[PosthNatureEcologyEvolution2018]:  
**Language continuity despite population replacement in Remote Oceania.** Posth C, Nägele K, Colleran H, Valentin F, Bedford S, Kami KW, Shing R, Buckley H, Kinaston R, Walworth M, Clark GR, Reepmeyer C, Flexner J, Maric T, Moser J, Gresky J, Kiko L, Robson KJ, Auckland K, Oppenheimer SJ, Hill AVS, Mentzer AJ, Zech J, Petchey F, Roberts P, Jeong C, Gray RD, Krause J, Powell A. Nat Ecol Evol. 2018 Apr;2(4):731-740. doi: 10.1038/s41559-018-0498-2. Epub 2018 Feb 27. PMID: 29487365.  
  
[PrendergastLipsonSawchukScience2019]:  
**Ancient DNA reveals a multistep spread of the first herders into sub-Saharan Africa.** Prendergast ME, Lipson M, Sawchuk EA, Olalde I, Ogola CA, Rohland N, Sirak KA, Adamski N, Bernardos R, Broomandkhoshbacht N, Callan K, Culleton BJ, Eccles L, Harper TK, Lawson AM, Mah M, Oppenheimer J, Stewardson K, Zalzala F, Ambrose SH, Ayodo G, Gates HL Jr, Gidna AO, Katongo M, Kwekason A, Mabulla AZP, Mudenda GS, Ndiema EK, Nelson C, Robertshaw P, Kennett DJ, Manthi FK, Reich D. Science. 2019 Jul 5;365(6448). pii: eaaw6275. doi: 10.1126/science.aaw6275. Epub 2019 May 30. PMID: 31147405.  
  
[PrüferBioinformatics2018]:  
Prüfer K. snpAD: an ancient DNA genotype caller. Bioinformatics. 2018 Dec 15;34(24):4165-4171. doi: 10.1093/bioinformatics/bty507. PMID: 29931305; PMCID: PMC6289138.   
[PrueferNatureEcologyEvolution2021]:  
**A genome sequence from a modern human skull over 45,000 years old from Zlatý kůň in Czechia.** Prüfer K, Posth C, Yu H, Stoessel A, Spyrou MA, Deviese T, Mattonai M, Ribechini E, Higham T, Velemínský P, Brůžek J, Krause J. Nat Ecol Evol. 2021 Jun;5(6):820-825. doi: 10.1038/s41559-021-01443-x. Epub 2021 Apr 7. PMID: 33828249; PMCID: PMC8175239.  
  
[Pruefer2017]:  
**A high-coverage Neandertal genome from Vindija Cave in Croatia.** Prüfer K, de Filippo C, Grote S, Mafessoni F, Korlević P, Hajdinjak M, Vernot B, Skov L, Hsieh P, Peyrégne S, Reher D, Hopfe C, Nagel S, Maricic T, Fu Q, Theunert C, Rogers R, Skoglund P, Chintalapati M, Dannemann M, Nelson BJ, Key FM, Rudan P, Kućan Ž, Gušić I, Golovanova LV, Doronichev VB, Patterson N, Reich D, Eichler EE, Slatkin M, Schierup MH, Andrés AM, Kelso J, Meyer M, Pääbo S. Science. 2017 Nov 3;358(6363):655-658. doi: 10.1126/science.aao1887. Epub 2017 Oct 5. PMID: 28982794.  
  
[PrueferNature2013]:  
**The complete genome sequence of a Neanderthal from the Altai Mountains.** Prüfer K, Racimo F, Patterson N, Jay F, Sankararaman S, Sawyer S, Heinze A, Renaud G, Sudmant PH, de Filippo C, Li H, Mallick S, Dannemann M, Fu Q, Kircher M, Kuhlwilm M, Lachmann M, Meyer M, Ongyerth M, Siebauer M, Theunert C, Tandon A, Moorjani P, Pickrell J, Mullikin JC, Vohr SH, Green RE, Hellmann I, Johnson PL, Blanche H, Cann H, Kitzman JO, Shendure J, Eichler EE, Lein ES, Bakken TE, Golovanova LV, Doronichev VB, Shunkov MV, Derevianko AP, Viola B, Slatkin M, Reich D, Kelso J, Pääbo S. Nature. 2014 Jan 2;505(7481):43-9. doi: 10.1038/nature12886. Epub 2013 Dec 18. PMID: 24352235.

[PugachPNAS2020]:  
**Ancient DNA from Guam and the peopling of the Pacific.** Pugach I, Hübner A, Hung HC, Meyer M, Carson MT, Stoneking M. Ancient DNA from Guam and the peopling of the Pacific. Proc Natl Acad Sci U S A. 2021 Jan 5;118(1):e2022112118. doi: 10.1073/pnas.2022112118. PMID: 33443177; PMCID: PMC7817125.   
  
[QinMBE2015]:  
**Denisovan Ancestry in East Eurasian and Native American Populations.** Qin P, Stoneking M. Mol Biol Evol. 2015 Oct;32(10):2665-74. doi: 10.1093/molbev/msv141. Epub 2015 Jun 23. PMID: 26104010.  
  
[RaghavanNature2013]:  
**Upper Palaeolithic Siberian genome reveals dual ancestry of Native Americans.** Raghavan M, Skoglund P, Graf KE, Metspalu M, Albrechtsen A, Moltke I, Rasmussen S, Stafford TW Jr, Orlando L, Metspalu E, Karmin M, Tambets K, Rootsi S, Mägi R, Campos PF, Balanovska E, Balanovsky O, Khusnutdinova E, Litvinov S, Osipova LP, Fedorova SA, Voevoda MI, DeGiorgio M, Sicheritz-Ponten T, Brunak S, Demeshchenko S, Kivisild T, Villems R, Nielsen R, Jakobsson M, Willerslev E.  
  
[RaghavanNature2014]:  
**Upper Palaeolithic Siberian genome reveals dual ancestry of Native Americans.** Raghavan M, Skoglund P, Graf KE, Metspalu M, Albrechtsen A, Moltke I, Rasmussen S, Stafford TW Jr, Orlando L, Metspalu E, Karmin M, Tambets K, Rootsi S, Mägi R, Campos PF, Balanovska E, Balanovsky O, Khusnutdinova E, Litvinov S, Osipova LP, Fedorova SA, Voevoda MI, DeGiorgio M, Sicheritz-Ponten T, Brunak S, Demeshchenko S, Kivisild T, Villems R, Nielsen R, Jakobsson M, Willerslev E. Nature. 2014 Jan 2;505(7481):87-91. doi: 10.1038/nature12736. Epub 2013 Nov 20. PMID: 24256729.  
  
[RaghavanScience2014]:  
**The genetic prehistory of the New World Arctic.** Raghavan M, DeGiorgio M, Albrechtsen A, Moltke I, Skoglund P, Korneliussen TS, Grønnow B, Appelt M, Gulløv HC, Friesen TM, Fitzhugh W, Malmström H, Rasmussen S, Olsen J, Melchior L, Fuller BT, Fahrni SM, Stafford T Jr, Grimes V, Renouf MA, Cybulski J, Lynnerup N, Lahr MM, Britton K, Knecht R, Arneborg J, Metspalu M, Cornejo OE, Malaspinas AS, Wang Y, Rasmussen M, Raghavan V, Hansen TV, Khusnutdinova E, Pierre T, Dneprovsky K, Andreasen C, Lange H, Hayes MG, Coltrain J, Spitsyn VA, Götherström A, Orlando L, Kivisild T, Villems R, Crawford MH, Nielsen FC, Dissing J, Heinemeier J, Meldgaard M, Bustamante C, O'Rourke DH, Jakobsson M, Gilbert MT, Nielsen R, Willerslev E. Science. 2014 Aug 29;345(6200):1255832. doi: 10.1126/science.1255832. PMID: 25170159.  
  
[RaghavanScience2015]:  
**POPULATION GENETICS. Genomic evidence for the Pleistocene and recent population history of Native Americans.** Raghavan M, Steinrücken M, Harris K, Schiffels S, Rasmussen S, DeGiorgio M, Albrechtsen A, Valdiosera C, Ávila-Arcos MC, Malaspinas AS, Eriksson A, Moltke I, Metspalu M, Homburger JR, Wall J, Cornejo OE, Moreno-Mayar JV, Korneliussen TS, Pierre T, Rasmussen M, Campos PF, de Barros Damgaard P, Allentoft ME, Lindo J, Metspalu E, Rodríguez-Varela R, Mansilla J, Henrickson C, Seguin-Orlando A, Malmström H, Stafford T Jr, Shringarpure SS, Moreno-Estrada A, Karmin M, Tambets K, Bergström A, Xue Y, Warmuth V, Friend AD, Singarayer J, Valdes P, Balloux F, Leboreiro I, Vera JL, Rangel-Villalobos H, Pettener D, Luiselli D, Davis LG, Heyer E, Zollikofer CPE, Ponce de León MS, Smith CI, Grimes V, Pike KA, Deal M, Fuller BT, Arriaza B, Standen V, Luz MF, Ricaut F, Guidon N, Osipova L, Voevoda MI, Posukh OL, Balanovsky O, Lavryashina M, Bogunov Y, Khusnutdinova E, Gubina M, Balanovska E, Fedorova S, Litvinov S, Malyarchuk B, Derenko M, Mosher MJ, Archer D, Cybulski J, Petzelt B, Mitchell J, Worl R, Norman PJ, Parham P, Kemp BM, Kivisild T, Tyler-Smith C, Sandhu MS, Crawford M, Villems R, Smith DG, Waters MR, Goebel T, Johnson JR, Malhi RS, Jakobsson M, Meltzer DJ, Manica A, Durbin R, Bustamante CD, Song YS, Nielsen R, Willerslev E. Science. 2015 Aug 21;349(6250):aab3884. doi: 10.1126/science.aab3884. Epub 2015 Jul 21. PMID: 26198033.  
  
[RasmussenNature2010]:  
**Ancient human genome sequence of an extinct Palaeo-Eskimo.** Rasmussen M, Li Y, Lindgreen S, Pedersen JS, Albrechtsen A, Moltke I, Metspalu M, Metspalu E, Kivisild T, Gupta R, Bertalan M, Nielsen K, Gilbert MT, Wang Y, Raghavan M, Campos PF, Kamp HM, Wilson AS, Gledhill A, Tridico S, Bunce M, Lorenzen ED, Binladen J, Guo X, Zhao J, Zhang X, Zhang H, Li Z, Chen M, Orlando L, Kristiansen K, Bak M, Tommerup N, Bendixen C, Pierre TL, Grønnow B, Meldgaard M, Andreasen C, Fedorova SA, Osipova LP, Higham TF, Ramsey CB, Hansen TV, Nielsen FC, Crawford MH, Brunak S, Sicheritz-Pontén T, Villems R, Nielsen R, Krogh A, Wang J, Willerslev E. Nature. 2010 Feb 11;463(7282):757-62. doi: 10.1038/nature08835. PMID: 20148029.  
  
[RasmussenNature2014]:  
**The genome of a Late Pleistocene human from a Clovis burial site in western Montana.** Rasmussen M, Anzick SL, Waters MR, Skoglund P, DeGiorgio M, Stafford TW Jr, Rasmussen S, Moltke I, Albrechtsen A, Doyle SM, Poznik GD, Gudmundsdottir V, Yadav R, Malaspinas AS, White SS 5th, Allentoft ME, Cornejo OE, Tambets K, Eriksson A, Heintzman PD, Karmin M, Korneliussen TS, Meltzer DJ, Pierre TL, Stenderup J, Saag L, Warmuth VM, Lopes MC, Malhi RS, Brunak S, Sicheritz-Ponten T, Barnes I, Collins M, Orlando L, Balloux F, Manica A, Gupta R, Metspalu M, Bustamante CD, Jakobsson M, Nielsen R, Willerslev E. Nature. 2014 Feb 13;506(7487):225-9. doi: 10.1038/nature13025. PMID: 24522598.  
  
[RasmussenNature2015]:  
**The ancestry and affiliations of Kennewick Man.** Rasmussen M, Sikora M, Albrechtsen A, Korneliussen TS, Moreno-Mayar JV, Poznik GD, Zollikofer CPE, de León MP, Allentoft ME, Moltke I, Jónsson H, Valdiosera C, Malhi RS, Orlando L, Bustamante CD, Stafford TW Jr, Meltzer DJ, Nielsen R, Willerslev E. Nature. 2015 Jul 23;523(7561):455-458. doi: 10.1038/nature14625.   
  
[ReichNature2010]:  
**Genetic history of an archaic hominin group from Denisova Cave in Siberia.** Reich D, Green RE, Kircher M, Krause J, Patterson N, Durand EY, Viola B, Briggs AW, Stenzel U, Johnson PL, Maricic T, Good JM, Marques-Bonet T, Alkan C, Fu Q, Mallick S, Li H, Meyer M, Eichler EE, Stoneking M, Richards M, Talamo S, Shunkov MV, Derevianko AP, Hublin JJ, Kelso J, Slatkin M, Pääbo S. Nature. 2010 Dec 23;468(7327):1053-60. doi: 10.1038/nature09710. PMID: 21179161; PMCID: PMC4306417.  
  
[ReichWorkingPaper2016]:  
**“Ancient DNA analysis of St. Mary’s City Lead Coffin Burials”** https://reich.hms.harvard.edu/sites/reich.hms.harvard.edu/files/inline-files/10\_24\_2016\_Screening\_report\_for\_St\_Marys\_City\_burials\_FINAL\_IL.pdf  
  
[ReitsemaMittnikKylePNAS2022]:  
**The diverse genetic origins of a Classical period Greek army.** Reitsema LJ, Mittnik A, Kyle B, Catalano G, Fabbri PF, Kazmi ACS, Reinberger KL, Sineo L, Vassallo S, Bernardos R, Broomandkhoshbacht N, Callan K, Candilio F, Cheronet O, Curtis E, Fernandes D, Lari M, Lawson AM, Mah M, Mallick S, Mandl K, Micco A, Modi A, Oppenheimer J, Özdogan KT, Rohland N, Stewardson K, Vai S, Vergata C, Workman JN, Zalzala F, Zaro V, Achilli A, Anagnostopoulos A, Capelli C, Constantinou V, Lancioni H, Olivieri A, Papadopoulou A, Psatha N, Semino O, Stamatoyannopoulos J, Valliannou I, Yannaki E, Lazaridis I, Patterson N, Ringbauer H, Caramelli D, Pinhasi R, Reich D. Proc Natl Acad Sci U S A. 2022 Oct 11;119(41):e2205272119. doi: 10.1073/pnas.2205272119. Epub 2022 Oct 3. PMID: 36191217; PMCID: PMC9564095.  
  
[FlegontovNature2019]:  
**Palaeo-Eskimo genetic ancestry and the peopling of Chukotka and North America.** Flegontov P, Altınışık NE, Changmai P, Rohland N, Mallick S, Adamski N, Bolnick DA, Broomandkhoshbacht N, Candilio F, Culleton BJ, Flegontova O, Friesen TM, Jeong C, Harper TK, Keating D, Kennett DJ, Kim AM, Lamnidis TC, Lawson AM, Olalde I, Oppenheimer J, Potter BA, Raff J, Sattler RA, Skoglund P, Stewardson K, Vajda EJ, Vasilyev S, Veselovskaya E, Hayes MG, O'Rourke DH, Krause J, Pinhasi R, Reich D, Schiffels S. Nature. 2019 Jun;570(7760):236-240. doi: 10.1038/s41586-019-1251-y. Epub 2019 Jun 5. PMID: 31168094; PMCID: PMC6942545.  
  
[RivollatNature2023]:  
**Extensive pedigrees reveal the social organization of a Neolithic community.** Rivollat M, Rohrlach AB, Ringbauer H, Childebayeva A, Mendisco F, Barquera R, Szolek A, Le Roy M, Colleran H, Tuke J, Aron F, Pemonge MH, Späth E, Télouk P, Rey L, Goude G, Balter V, Krause J, Rottier S, Deguilloux MF, Haak W. Nature. 2023 Aug;620(7974):600-606. doi: 10.1038/s41586-023-06350-8. Epub 2023 Jul 26. PMID: 37495691; PMCID: PMC10432279.  
  
[RivollatDeguillouxPNAS2022]:  
**Ancient DNA gives new insights into a Norman Neolithic monumental cemetery dedicated to male elites.** Rivollat M, Thomas A, Ghesquière E, Rohrlach AB, Späth E, Pemonge MH, Haak W, Chambon P, Deguilloux MF. Ancient DNA gives new insights into a Norman Neolithic monumental cemetery dedicated to male elites. Proc Natl Acad Sci U S A. 2022 May 3;119(18):e2120786119. doi: 10.1073/pnas.2120786119. Epub 2022 Apr 21. PMID: 35446690; PMCID: PMC9170172.

[RivollatScienceAdvance2020]:  
**Ancient genome-wide DNA from France highlights the complexity of interactions between Mesolithic hunter-gatherers and Neolithic farmers.** Rivollat M, Jeong C, Schiffels S, Küçükkalıpçı İ, Pemonge MH, Rohrlach AB, Alt KW, Binder D, Friederich S, Ghesquière E, Gronenborn D, Laporte L, Lefranc P, Meller H, Réveillas H, Rosenstock E, Rottier S, Scarre C, Soler L, Wahl J, Krause J, Deguilloux MF, Haak W. Sci Adv. 2020 May 29;6(22):eaaz5344. doi: 10.1126/sciadv.aaz5344. PMID: 32523989; PMCID: PMC7259947.  
  
[RobbeetsNingNature2021]:  
**Triangulation supports agricultural spread of the Transeurasian languages.** Robbeets M, Bouckaert R, Conte M, Savelyev A, Li T, An DI, Shinoda KI, Cui Y, Kawashima T, Kim G, Uchiyama J, Dolińska J, Oskolskaya S, Yamano KY, Seguchi N, Tomita H, Takamiya H, Kanzawa-Kiriyama H, Oota H, Ishida H, Kimura R, Sato T, Kim JH, Deng B, Bjørn R, Rhee S, Ahn KD, Gruntov I, Mazo O, Bentley JR, Fernandes R, Roberts P, Bausch IR, Gilaizeau L, Yoneda M, Kugai M, Bianco RA, Zhang F, Himmel M, Hudson MJ, Ning C. TNature. 2021 Nov;599(7886):616-621. doi: 10.1038/s41586-021-04108-8. Epub 2021 Nov 10. PMID: 34759322; PMCID: PMC8612925.  
  
[RodriguezVarelaCurrentBiology2017]:  
**Genomic Analyses of Pre-European Conquest Human Remains from the Canary Islands Reveal Close Affinity to Modern North Africans.** Rodríguez-Varela R, Günther T, Krzewińska M, Storå J, Gillingwater TH, MacCallum M, Arsuaga JL, Dobney K, Valdiosera C, Jakobsson M, Götherström A, Girdland-Flink L. Curr Biol. 2017 Nov 6;27(21):3396-3402.e5. doi: 10.1016/j.cub.2017.09.059. Epub 2017 Oct 26. Erratum in: Curr Biol. 2018 May 21;28(10 ):1677-1679. PMID: 29107554.  
  
[Rodrguez-VarelaScienceDirect2023]:  
**The genetic history of Scandinavia from the Roman Iron Age to the present.** Rodríguez-Varela R, Moore KHS, Ebenesersdóttir SS, Kilinc GM, Kjellström A, Papmehl-Dufay L, Alfsdotter C, Berglund B, Alrawi L, Kashuba N, Sobrado V, Lagerholm VK, Gilbert E, Cavalleri GL, Hovig E, Kockum I, Olsson T, Alfredsson L, Hansen TF, Werge T, Munters AR, Bernhardsson C, Skar B, Christophersen A, Turner-Walker G, Gopalakrishnan S, Daskalaki E, Omrak A, Pérez-Ramallo P, Skoglund P, Girdland-Flink L, Gunnarsson F, Hedenstierna-Jonson C, Gilbert MTP, Lidén K, Jakobsson M, Einarsson L, Victor H, Krzewińska M, Zachrisson T, Storå J, Stefánsson K, Helgason A, Götherström A. Cell. 2023 Jan 5;186(1):32-46.e19. doi: 10.1016/j.cell.2022.11.024. PMID: 36608656.  
  
[RohlandMallickGenomeResearch2022]:  
**Three assays for in-solution enrichment of ancient human DNA at more than a million SNPs.** Rohland N, Mallick S, Mah M, Maier R, Patterson N, Reich D. Genome Res. 2022 Nov-Dec;32(11-12):2068-2078. doi: 10.1101/gr.276728.122. Epub 2022 Dec 14. PMID: 36517229; PMCID: PMC9808625.  
  
[SaagCurrentBiology2017]:  
**Extensive Farming in Estonia Started through a Sex-Biased Migration from the Steppe.** Saag L, Varul L, Scheib CL, Stenderup J, Allentoft ME, Saag L, Pagani L, Reidla M, Tambets K, Metspalu E, Kriiska A, Willerslev E, Kivisild T, Metspalu M.Curr Biol. 2017 Jul 24;27(14):2185-2193.e6. doi: 10.1016/j.cub.2017.06.022. Epub 2017 Jul 14. PMID: 28712569.  
  
[SaagCurrentBiology2019]:  
**The Arrival of Siberian Ancestry Connecting the Eastern Baltic to Uralic Speakers further East.** Saag L, Laneman M, Varul L, Malve M, Valk H, Razzak MA, Shirobokov IG, Khartanovich VI, Mikhaylova ER, Kushniarevich A, Scheib CL, Solnik A, Reisberg T, Parik J, Saag L, Metspalu E, Rootsi S, Montinaro F, Remm M, Mägi R, D'Atanasio E, Crema ER, D'Atanasio E, Crema ER, Díez-Del-Molino D, Thomas MG, Kriiska A, Kivisild T, Villems R, Lang V, Metspalu M, Tambets K. Curr Biol. 2019 May 20;29(10):1701-1711.e16. doi: 10.1016/j.cub.2019.04.026. Epub 2019 May 9. PMID: 31080083.  
  
[SaagMetspaluScience2021]:  
**Genetic ancestry changes in Stone to Bronze Age transition in the East European plain.** Saag L, Vasilyev SV, Varul L, Kosorukova NV, Gerasimov DV, Oshibkina SV, Griffith SJ, Solnik A, Saag L, D'Atanasio E, Metspalu E, Reidla M, Rootsi S, Kivisild T, Scheib CL, Tambets K, Kriiska A, Metspalu M. Genetic ancestry changes in Stone to Bronze Age transition in the East European plain. Sci Adv. 2021 Jan 20;7(4):eabd6535. doi: 10.1126/sciadv.abd6535. PMID: 33523926; PMCID: PMC7817100.  
  
[Sandoval-VelescoAmJHumGenet2023]:  
**The ancestry and geographical origins of St Helena's liberated Africans.** Sandoval-Velasco M, Jagadeesan A, Ramos-Madrigal J, Ávila-Arcos MC, Fortes-Lima CA, Watson J, Johannesdóttir E, Cruz-Dávalos DI, Gopalakrishnan S, Moreno-Mayar JV, Niemann J, Renaud G, Robson Brown KA, Bennett H, Pearson A, Helgason A, Gilbert MTP, Schroeder H. Am J Hum Genet. 2023 Sep 7;110(9):1590-1599. doi: 10.1016/j.ajhg.2023.08.001. Erratum in: Am J Hum Genet. 2023 Oct 5;110(10):1825. doi: 10.1016/j.ajhg.2023.09.007. PMID: 37683613; PMCID: PMC10502851.  
  
[SatoIshidaGenBioEvo2021]:  
**Whole-Genome Sequencing of a 900-Year-Old Human Skeleton Supports Two Past Migration Events from the Russian Far East to Northern Japan.** Sato T, Adachi N, Kimura R, Hosomichi K, Yoneda M, Oota H, Tajima A, Toyoda A, Kanzawa-Kiriyama H, Matsumae H, Koganebuchi K, Shimizu KK, Shinoda KI, Hanihara T, Weber A, Kato H, Ishida H. Genome Biol Evol. 2021 Sep 1;13(9):evab192. doi: 10.1093/gbe/evab192. PMID: 34410389; PMCID: PMC8449830.  
  
[SanchezQuintoPNAS2019]:  
**Megalithic tombs in western and northern Neolithic Europe were linked to a kindred society.** Sánchez-Quinto F, Malmström H, Fraser M, Girdland-Flink L, Svensson EM, Simões LG, George R, Hollfelder N, Burenhult G, Noble G, Britton K, Talamo S, Curtis N, Brzobohata H, Sumberova R, Götherström A, Storå J, Jakobsson M. Proc Natl Acad Sci U S A. 2019 May 7;116(19):9469-9474. doi: 10.1073/pnas.1818037116. Epub 2019 Apr 15. PMID: 30988179.  
  
[SaupeScheibCurrBio2021]:  
**Ancient genomes reveal structural shifts after the arrival of Steppe-related ancestry in the Italian Peninsula.** Saupe T, Montinaro F, Scaggion C, Carrara N, Kivisild T, D'Atanasio E, Hui R, Solnik A, Lebrasseur O, Larson G, Alessandri L, Arienzo I, De Angelis F, Rolfo MF, Skeates R, Silvestri L, Beckett J, Talamo S, Dolfini A, Miari M, Metspalu M, Benazzi S, Capelli C, Pagani L, Scheib CL. Curr Biol. 2021 Jun 21;31(12):2576-2591.e12. doi: 10.1016/j.cub.2021.04.022. Epub 2021 May 10. PMID: 33974848.  
  
[ScheibAnnHumBio2019]:  
**East Anglian early Neolithic monument burial linked to contemporary Megaliths.** Scheib CL, Hui R, D'Atanasio E, Wohns AW, Inskip SA, Rose A, Cessford C, O'Connell TC, Robb JE, Evans C, Patten R, Kivisild T. East Anglian early Neolithic monument burial linked to contemporary Megaliths. Ann Hum Biol. 2019 Mar;46(2):145-149. doi: 10.1080/03014460.2019.1623912. PMID: 31184205; PMCID: PMC6816495.  
  
[ScheibScience2018]:  
**Ancient human parallel lineages within North America contributed to a coastal expansion.** Scheib CL, Li H, Desai T, Link V, Kendall C, Dewar G, Griffith PW, Mörseburg A, Johnson JR, Potter A, Kerr SL, Endicott P, Lindo J, Haber M, Xue Y, Tyler-Smith C, Sandhu MS, Lorenz JG, Randall TD, Faltyskova Z, Pagani L, Danecek P, O'Connell TC, Martz P, Boraas AS, Byrd BF, Leventhal A, Cambra R, Williamson R, Lesage L, Holguin B, Ygnacio-De Soto E, Rosas J, Metspalu M, Stock JT, Manica A, Scally A, Wegmann D, Malhi RS, Kivisild T. Science. 2018 Jun 1;360(6392):1024-1027. doi: 10.1126/science.aar6851. PMID: 29853687.  
  
[ScheunemannNatureCommunications2017]:  
**Ancient Egyptian mummy genomes suggest an increase of Sub-Saharan African ancestry in post-Roman periods.** Schuenemann VJ, Peltzer A, Welte B, van Pelt WP, Molak M, Wang CC, Furtwängler A, Urban C, Reiter E, Nieselt K, Teßmann B, Francken M, Harvati K, Haak W, Schiffels S, Krause J. Nat Commun. 2017 May 30;8:15694. doi: 10.1038/ncomms15694. PMID: 28556824.  
  
[SchiffelsNatureCommunications2016]:  
**Iron Age and Anglo-Saxon genomes from East England reveal British migration history.** Schiffels S, Haak W, Paajanen P, Llamas B, Popescu E, Loe L, Clarke R, Lyons A, Mortimer R, Sayer D, Tyler-Smith C, Cooper A, Durbin R. Nat Commun. 2016 Jan 19;7:10408. doi: 10.1038/ncomms10408. PMID: 26783965.  
  
[SchlebuschScience2017]:  
**Southern African ancient genomes estimate modern human divergence to 350,000 to 260,000 years ago.** Schlebusch CM, Malmström H, Günther T, Sjödin P, Coutinho A, Edlund H, Munters AR, Vicente M, Steyn M, Soodyall H, Lombard M, Jakobsson M. Science. 2017 Nov 3;358(6363):652-655. doi: 10.1126/science.aao6266. Epub 2017 Sep 28. PMID: 28971970.  
  
[SchroederPNAS2015]:  
**Genome-wide ancestry of 17th-century enslaved Africans from the Caribbean.** Schroeder H, Ávila-Arcos MC, Malaspinas AS, Poznik GD, Sandoval-Velasco M, Carpenter ML, Moreno-Mayar JV, Sikora M, Johnson PL, Allentoft ME, Samaniego JA, Haviser JB, Dee MW, Stafford TW Jr, Salas A, Orlando L, Willerslev E, Bustamante CD, Gilbert MT. Proc Natl Acad Sci U S A. 2015 Mar 24;112(12):3669-73. doi: 10.1073/pnas.1421784112. Epub 2015 Mar 9. PMID: 25755263; PMCID: PMC4378422.  
  
[SchroederPNAS2018]:  
**Origins and genetic legacies of the Caribbean Taino.** Schroeder H, Sikora M, Gopalakrishnan S, Cassidy LM, Maisano Delser P, Sandoval Velasco M, Schraiber JG, Rasmussen S, Homburger JR, Ávila-Arcos MC, Allentoft ME, Moreno-Mayar JV, Renaud G, Gómez-Carballa A, Laffoon JE, Hopkins RJA, Higham TFG, Carr RS, Schaffer WC, Day JS, Hoogland M, Salas A, Bustamante CD, Nielsen R, Bradley DG, Hofman CL, Willerslev E. Proc Natl Acad Sci U S A. 2018 Mar 6;115(10):2341-2346. doi: 10.1073/pnas.1716839115. Epub 2018 Feb 20. PMID: 29463742.  
  
[SchroederPNAS2019]:  
**Unraveling ancestry, kinship, and violence in a Late Neolithic mass grave.** Schroeder H, Margaryan A, Szmyt M, Theulot B, Wlodarczak P, Rasmussen S, Gopalakrishnan S, Szczepanek A, Konopka T, Jensen TZT, Witkowska B, Wilk S, Przybyla MM, Pospieszny L, Sjögren KG, Belka Z, Olsen J, Kristiansen K, Willerslev E, Frei KM, Sikora M, Johannsen NN, Allentoft ME. Proc Natl Acad Sci U S A. 2019 May 28;116(22):10705-10710. doi: 10.1073/pnas.1820210116. Epub 2019 May 6. PMID: 31061125.  
  
[ScorranoMacciardiSciRep2022]:  
**Bioarchaeological and palaeogenomic portrait of two Pompeians that died during the eruption of Vesuvius in 79 AD.** Scorrano G, Viva S, Pinotti T, Fabbri PF, Rickards O, Macciardi F. Bioarchaeological and palaeogenomic portrait of two Pompeians that died during the eruption of Vesuvius in 79 AD. Sci Rep. 2022 May 26;12(1):6468. doi: 10.1038/s41598-022-10899-1. PMID: 35618734; PMCID: PMC9135728.   
  
[ScorranoNature2022]:  
**Bioarchaeological and palaeogenomic portrait of two Pompeians that died during the eruption of Vesuvius in 79 AD.** Scorrano G, Viva S, Pinotti T, Fabbri PF, Rickards O, Macciardi F. Sci Rep. 2022 May 26;12(1):6468. doi: 10.1038/s41598-022-10899-1. PMID: 35618734; PMCID: PMC9135728.  
  
[SedigAntiquity2024]:  
**High levels of consanguinity in a child from Paquimé, Chihuahua, Mexico.** Sedig J, Snow M, Searcy M, et al.Antiquity. 2024;98(400):1023-1039. doi:10.15184/aqy.2024.94   
[SeersholmSikoraNature2024]:  
**Repeated plague infections across six generations of Neolithic Farmers.** Seersholm FV, Sjögren KG, Koelman J, Blank M, Svensson EM, Staring J, Fraser M, Pinotti T, McColl H, Gaunitz C, Ruiz-Bedoya T, Granehäll L, Villegas-Ramirez B, Fischer A, Price TD, Allentoft ME, Iversen AKN, Axelsson T, Ahlström T, Götherström A, Storå J, Kristiansen K, Willerslev E, Jakobsson M, Malmström H, Sikora M. Nature. 2024 Aug;632(8023):114-121. doi: 10.1038/s41586-024-07651-2. Epub 2024 Jul 10. PMID: 38987589; PMCID: PMC11291285.  
  
[SeguinOrlandoCurrBio2021]:  
**Heterogeneous Hunter-Gatherer and Steppe-Related Ancestries in Late Neolithic and Bell Beaker Genomes from Present-Day France.** Seguin-Orlando A, Donat R, Der Sarkissian C, Southon J, Thèves C, Manen C, Tchérémissinoff Y, Crubézy E, Shapiro B, Deleuze JF, Dalén L, Guilaine J, Orlando L. Heterogeneous Hunter-Gatherer and Steppe-Related Ancestries in Late Neolithic and Bell Beaker Genomes from Present-Day France. Curr Biol. 2021 Mar 8;31(5):1072-1083.e10. doi: 10.1016/j.cub.2020.12.015. PMID: 33434506.  
  
[Seguin-OrlandoIScience2021]:  
**Heterogeneous Hunter-Gatherer and Steppe-Related Ancestries in Late Neolithic and Bell Beaker Genomes from Present-Day France.** Seguin-Orlando A, Donat R, Der Sarkissian C, Southon J, Thèves C, Manen C, Tchérémissinoff Y, Crubézy E, Shapiro B, Deleuze JF, Dalén L, Guilaine J, Orlando L. Curr Biol. 2021 Mar 8;31(5):1072-1083.e10. doi: 10.1016/j.cub.2020.12.015. PMID: 33434506.  
  
[Seguin-OrlandoScience2014]:   
**Paleogenomics. Genomic structure in Europeans dating back at least 36,200 years.** Seguin-Orlando A, Korneliussen TS, Sikora M, Malaspinas AS, Manica A, Moltke I, Albrechtsen A, Ko A, Margaryan A, Moiseyev V, Goebel T, Westaway M, Lambert D, Khartanovich V, Wall JD, Nigst PR, Foley RA, Lahr MM, Nielsen R, Orlando L, Willerslev E. Paleogenomics. Science. 2014 Nov 28;346(6213):1113-8. doi: 10.1126/science.aaa0114. Epub 2014 Nov 6. PMID: 25378462.  
  
[ShindeNarasimhanCell2019]:  
**An Ancient Harappan Genome Lacks Ancestry from Steppe Pastoralists or Iranian Farmers.** Shinde V, Narasimhan VM, Rohland N, Mallick S, Mah M, Lipson M, Nakatsuka N, Adamski N, Broomandkhoshbacht N, Ferry M, Lawson AM, Michel M, Oppenheimer J, Stewardson K, Jadhav N, Kim YJ, Chatterjee M, Munshi A, Panyam A, Waghmare P, Yadav Y, Patel H, Kaushik A, Thangaraj K, Meyer M, Patterson N, Rai N, Reich D. Cell. 2019 Oct 17;179(3):729-735.e10. doi: 10.1016/j.cell.2019.08.048. Epub 2019 Sep 5. PMID: 31495572.  
  
[SikoraNature2019]:  
**The population history of northeastern Siberia since the Pleistocene.** Sikora M, Pitulko VV, Sousa VC, Allentoft ME, Vinner L, Rasmussen S, Margaryan A, de Barros Damgaard P, de la Fuente C, Renaud G, Yang MA, Fu Q, Dupanloup I, Giampoudakis K, Nogués-Bravo D, Rahbek C, Kroonen G, Peyrot M, McColl H, Vasilyev SV, Veselovskaya E, Gerasimova M, Pavlova EY, Chasnyk VG, Nikolskiy PA, Gromov AV, Khartanovich VI, Moiseyev V, Grebenyuk PS, Fedorchenko AY, Lebedintsev AI, Slobodin SB, Malyarchuk BA, Martiniano R, Meldgaard M, Arppe L, Palo JU, Sundell T, Mannermaa K, Putkonen M, Alexandersen V, Primeau C, Baimukhanov N, Malhi RS, Sjögren KG, Kristiansen K, Wessman A, Sajantila A, Lahr MM, Durbin R, Nielsen R, Meltzer DJ, Excoffier L, Willerslev E. Nature. 2019 Jun;570(7760):182-188. doi: 10.1038/s41586-019-1279-z. Epub 2019 Jun 5. PMID: 31168093.  
  
[SikoraScience2017]:  
**Ancient genomes show social and reproductive behavior of early Upper Paleolithic foragers.** Sikora M, Seguin-Orlando A, Sousa VC, Albrechtsen A, Korneliussen T, Ko A, Rasmussen S, Dupanloup I, Nigst PR, Bosch MD, Renaud G, Allentoft ME, Margaryan A, Vasilyev SV, Veselovskaya EV, Borutskaya SB, Deviese T, Comeskey D, Higham T, Manica A, Foley R, Meltzer DJ, Nielsen R, Excoffier L, Mirazon Lahr M, Orlando L, Willerslev E. Science. 2017 Nov 3;358(6363):659-662. doi: 10.1126/science.aao1807. Epub 2017 Oct 5.   
  
[SilvaRichardsSciRep2021]:  
**Biomolecular insights into North African-related ancestry, mobility and diet in eleventh-century Al-Andalus.** Silva M, Oteo-García G, Martiniano R, Guimarães J, von Tersch M, Madour A, Shoeib T, Fichera A, Justeau P, Foody MGB, McGrath K, Barrachina A, Palomar V, Dulias K, Yau B, Gandini F, Clarke DJ, Rosa A, Brehm A, Flaquer A, Rito T, Olivieri A, Achilli A, Torroni A, Gómez-Carballa A, Salas A, Bryk J, Ditchfield PW, Alexander M, Pala M, Soares PA, Edwards CJ, Richards MB. Biomolecular insights into North African-related ancestry, mobility and diet in eleventh-century Al-Andalus. Sci Rep. 2021 Sep 13;11(1):18121. doi: 10.1038/s41598-021-95996-3. PMID: 34518562; PMCID: PMC8438022.

[SimoesNature2023]:  
**Northwest African Neolithic initiated by migrants from Iberia and Levant.** Simões LG, Günther T, Martínez-Sánchez RM, Vera-Rodríguez JC, Iriarte E, Rodríguez-Varela R, Bokbot Y, Valdiosera C, Jakobsson M. Nature. 2023 Jun;618(7965):550-556. doi: 10.1038/s41586-023-06166-6. Epub 2023 Jun 7. PMID: 37286608; PMCID: PMC10266975.  
  
[SimoesPNAS2024]:  
**Genomic ancestry and social dynamics of the last hunter-gatherers of Atlantic France.** Simões LG, Peyroteo-Stjerna R, Marchand G, Bernhardsson C, Vialet A, Chetty D, Alaçamlı E, Edlund H, Bouquin D, Dina C, Garmond N, Günther T, Jakobsson M. Proc Natl Acad Sci U S A. 2024 Mar 5;121(10):e2310545121. doi: 10.1073/pnas.2310545121. Epub 2024 Feb 26. PMID: 38408241; PMCID: PMC10927518.  
  
[SirakNatureCommunications2021]:  
**Social stratification without genetic differentiation at the site of Kulubnarti in Christian Period Nubia.** Sirak KA, Fernandes DM, Lipson M, Mallick S, Mah M, Olalde I, Ringbauer H, Rohland N, Hadden CS, Harney É, Adamski N, Bernardos R, Broomandkhoshbacht N, Callan K, Ferry M, Lawson AM, Michel M, Oppenheimer J, Stewardson K, Zalzala F, Patterson N, Pinhasi R, Thompson JC, Van Gerven D, Reich D. Nat Commun. 2021 Dec 14;12(1):7283. doi: 10.1038/s41467-021-27356-8. PMID: 34907168; PMCID: PMC8671435.  
  
[SiskaScienceAdvances2017]:  
**Ancient genomes show social and reproductive behavior of early Upper Paleolithic foragers.** Sikora M, Seguin-Orlando A, Sousa VC, Albrechtsen A, Korneliussen T, Ko A, Rasmussen S, Dupanloup I, Nigst PR, Bosch MD, Renaud G, Allentoft ME, Margaryan A, Vasilyev SV, Veselovskaya EV, Borutskaya SB, Deviese T, Comeskey D, Higham T, Manica A, Foley R, Meltzer DJ, Nielsen R, Excoffier L, Mirazon Lahr M, Orlando L, Willerslev E. Science. 2017 Nov 3;358(6363):659-662. doi: 10.1126/science.aao1807. Epub 2017 Oct 5. PMID: 28982795.  
  
[SjogrenPLoSOne2020]:  
**Kinship and social organization in Copper Age Europe. A cross-disciplinary analysis of archaeology, DNA, isotopes, and anthropology from two Bell Beaker cemeteries.** Sjögren KG, Olalde I, Carver S, Allentoft ME, Knowles T, Kroonen G, Pike AWG, Schröter P, Brown KA, Brown KR, Harrison RJ, Bertemes F, Reich D, Kristiansen K, Heyd V. PLoS One. 2020 Nov 16;15(11):e0241278. doi: 10.1371/journal.pone.0241278. PMID: 33196640; PMCID: PMC7668604.  
  
[SkoglundCell2017]:  
**Reconstructing Prehistoric African Population Structure.** Skoglund P, Thompson JC, Prendergast ME, Mittnik A, Sirak K, Hajdinjak M, Salie T, Rohland N, Mallick S, Peltzer A, Heinze A, Olalde I, Ferry M, Harney E, Michel M, Stewardson K, Cerezo-Román JI, Chiumia C, Crowther A, Gomani-Chindebvu E, Gidna AO, Grillo KM, Helenius IT, Hellenthal G, Helm R, Horton M, López S, Mabulla AZP, Parkington J, Shipton C, Thomas MG, Tibesasa R, Welling M, Hayes VM, Kennett DJ, Ramesar R, Meyer M, Pääbo S, Patterson N, Morris AG, Boivin N, Pinhasi R, Krause J, Reich D. Cell. 2017 Sep 21;171(1):59-71.e21. doi: 10.1016/j.cell.2017.08.049. PMID: 28938123.  
  
[SkoglundNature2015]:  
**Genetic evidence for two founding populations of the Americas.** Skoglund P, Mallick S, Bortolini MC, Chennagiri N, Hünemeier T, Petzl-Erler ML, Salzano FM, Patterson N, Reich D. Nature. 2015 Sep 3;525(7567):104-8. doi: 10.1038/nature14895. Epub 2015 Jul 21. PMID: 26196601.  
  
[SkoglundNature2016]:  
**Genomic insights into the peopling of the Southwest Pacific.** Skoglund P, Posth C, Sirak K, Spriggs M, Valentin F, Bedford S, Clark GR, Reepmeyer C, Petchey F, Fernandes D, Fu Q, Harney E, Lipson M, Mallick S, Novak M, Rohland N, Stewardson K, Abdullah S, Cox MP, Friedlaender FR, Friedlaender JS, Kivisild T, Koki G, Kusuma P, Merriwether DA, Ricaut FX, Wee JT, Patterson N, Krause J, Pinhasi R, Reich D. Nature. 2016 Oct 27;538(7626):510-513. doi: 10.1038/nature19844. Epub 2016 Oct 3. PMID: 27698418.

[SkoglundScience2014]:  
**Genomic diversity and admixture differs for Stone-Age Scandinavian foragers and farmers.** Skoglund P, Malmström H, Omrak A, Raghavan M, Valdiosera C, Günther T, Hall P, Tambets K, Parik J, Sjögren KG, Apel J, Willerslev E, Storå J, Götherström A, Jakobsson M. Science. 2014 May 16;344(6185):747-50. doi: 10.1126/science.1253448. Epub 2014 Apr 24. PMID: 24762536.  
  
[SkourtaniotiCell2020]:  
**Genomic History of Neolithic to Bronze Age Anatolia, Northern Levant, and Southern Caucasus.** Skourtanioti E, Erdal YS, Frangipane M, Balossi Restelli F, Yener KA, Pinnock F, Matthiae P, Özbal R, Schoop UD, Guliyev F, Akhundov T, Lyonnet B, Hammer EL, Nugent SE, Burri M, Neumann GU, Penske S, Ingman T, Akar M, Shafiq R, Palumbi G, Eisenmann S, D'Andrea M, Rohrlach AB, Warinner C, Jeong C, Stockhammer PW, Haak W, Krause J. Cell. 2020 May 28;181(5):1158-1175.e28. doi: 10.1016/j.cell.2020.04.044. PMID: 32470401.  
  
[SkourtaniotiRingbauerNatureEcologyEvolution2023]:  
**Ancient DNA reveals admixture history and endogamy in the prehistoric Aegean.** Skourtanioti E, Ringbauer H, Gnecchi Ruscone GA, Bianco RA, Burri M, Freund C, Furtwängler A, Gomes Martins NF, Knolle F, Neumann GU, Tiliakou A, Agelarakis A, Andreadaki-Vlazaki M, Betancourt P, Hallager BP, Jones OA, Kakavogianni O, Kanta A, Karkanas P, Kataki E, Kissas K, Koehl R, Kvapil L, Maran J, McGeorge PJP, Papadimitriou A, Papathanasiou A, Papazoglou-Manioudaki L, Paschalidis K, Polychronakou-Sgouritsa N, Preve S, Prevedorou EA, Price G, Protopapadaki E, Schmidt-Schultz T, Schultz M, Shelton K, Wiener MH, Krause J, Jeong C, Stockhammer PW. Nat Ecol Evol. 2023 Feb;7(2):290-303. doi: 10.1038/s41559-022-01952-3. Epub 2023 Jan 16. PMID: 36646948; PMCID: PMC9911347.  
  
[SlonNature2018]:  
**The genome of the offspring of a Neanderthal mother and a Denisovan father.** Slon V, Mafessoni F, Vernot B, de Filippo C, Grote S, Viola B, Hajdinjak M, Peyrégne S, Nagel S, Brown S, Douka K, Higham T, Kozlikin MB, Shunkov MV, Derevianko AP, Kelso J, Meyer M, Prüfer K, Pääbo S.Nature. 2018 Sep;561(7721):113-116. doi: 10.1038/s41586-018-0455-x. Epub 2018 Aug 22. PMID: 30135579.  
  
[SpyrouNature2022]:  
**The source of the Black Death in fourteenth-century central Eurasia.** Spyrou MA, Musralina L, Gnecchi Ruscone GA, Kocher A, Borbone PG, Khartanovich VI, Buzhilova A, Djansugurova L, Bos KI, Kühnert D, Haak W, Slavin P, Krause J. The source of the Black Death in fourteenth-century central Eurasia. Nature. 2022 Jun;606(7915):718-724. doi: 10.1038/s41586-022-04800-3. Epub 2022 Jun 15. PMID: 35705810; PMCID: PMC9217749.   
  
[SrigyanValdioseraCommBio2022]:  
**Bioarchaeological evidence of one of the earliest Islamic burials in the Levant.** Srigyan M, Bolívar H, Ureña I, Santana J, Petersen A, Iriarte E, Kırdök E, Bergfeldt N, Mora A, Jakobsson M, Abdo K, Braemer F, Smith C, Ibañez JJ, Götherström A, Günther T, Valdiosera C. Bioarchaeological evidence of one of the earliest Islamic burials in the Levant. Commun Biol. 2022 Jun 7;5(1):554. doi: 10.1038/s42003-022-03508-4. PMID: 35672445; PMCID: PMC9174286.   
  
[StolarekGenomeBio2023]:  
**Genetic history of East-Central Europe in the first millennium CE.** Stolarek I, Zenczak M, Handschuh L, Juras A, Marcinkowska-Swojak M, Spinek A, Dębski A, Matla M, Kóčka-Krenz H, Piontek J; Polish Archaeogenomics Consortium Team; Figlerowicz M. Genome Biol. 2023 Jul 24;24(1):173. doi: 10.1186/s13059-023-03013-9. PMID: 37488661; PMCID: PMC10364380.  
  
[SullivanScienceAdvances2018]:  
**Ancient genome-wide analyses infer kinship structure in an Early Medieval Alemannic graveyard.** O'Sullivan N, Posth C, Coia V, Schuenemann VJ, Price TD, Wahl J, Pinhasi R, Zink A, Krause J, Maixner F. Sci Adv. 2018 Sep 5;4(9):eaao1262. doi: 10.1126/sciadv.aao1262. PMID: 30191172; PMCID: PMC6124919.

[SvenssonJakobssonCurrBio2021]:  
**Genome of Peştera Muierii skull shows high diversity and low mutational load in pre-glacial Europe.** Svensson E, Günther T, Hoischen A, Hervella M, Munters AR, Ioana M, Ridiche F, Edlund H, van Deuren RC, Soficaru A, de-la-Rua C, Netea MG, Jakobsson M. Genome of Peştera Muierii skull shows high diversity and low mutational load in pre-glacial Europe. Curr Biol. 2021 Jul 26;31(14):2973-2983.e9. doi: 10.1016/j.cub.2021.04.045. Epub 2021 May 18. PMID: 34010592.  
  
[TeschlerNicolaCommunicationsBiology2020]:  
**Ancient DNA reveals monozygotic newborn twins from the Upper Palaeolithic.** Teschler-Nicola M, Fernandes D, Händel M, Einwögerer T, Simon U, Neugebauer-Maresch C, Tangl S, Heimel P, Dobsak T, Retzmann A, Prohaska T, Irrgeher J, Kennett DJ, Olalde I, Reich D, Pinhasi R. Commun Biol. 2020 Nov 6;3(1):650. doi: 10.1038/s42003-020-01372-8. PMID: 33159107; PMCID: PMC7648643.  
  
[TieslerSedigAntiquity2022]:  
**Life and death in early colonial Campeche: New insights from ancient DNA.** Tiesler, V., Sedig, J., Nakatsuka, N., Mallick, S., Lazaridis, I., Bernardos, R., Broomandkhoshbacht , N., Oppenheimer, J., Marie Lawson, A., Stewardson, K., Rohland, N., Kennett, D., Price, T., Reich, D. (2022). Antiquity, 96(388), 937-954. doi:10.15184/aqy.2022.79   
  
[UllingerNearEasternArchaeology2022]:  
**A Bioarchaeological Investigation of Fraternal Stillborn Twins from Tell el-Hesi.** Jaime Ullinger, Lesley Gregoricka, Rebecca Bernardos, David Reich, Amel Langston, Paige Ferreri, and Brittney Ingram (2022). Near Eastern Archaelogy 85:3, doi: https://doi.org/10.1086/720748.   
  
[UnterlanderNatureCommunications2017]:  
**Ancestry and demography and descendants of Iron Age nomads of the Eurasian Steppe.** Unterländer M, Palstra F, Lazaridis I, Pilipenko A, Hofmanová Z, Groß M, Sell C, Blöcher J, Kirsanow K, Rohland N, Rieger B, Kaiser E, Schier W, Pozdniakov D, Khokhlov A, Georges M, Wilde S, Powell A, Heyer E, Currat M, Reich D, Samashev Z, Parzinger H, Molodin VI, Burger J. Nat Commun. 2017 Mar 3;8:14615. doi: 10.1038/ncomms14615. PMID: 28256537.  
  
[ValdioseraPNAS2018]:  
**Four millennia of Iberian biomolecular prehistory illustrate the impact of prehistoric migrations at the far end of Eurasia.** Valdiosera C, Günther T, Vera-Rodríguez JC, Ureña I, Iriarte E, Rodríguez-Varela R, Simões LG, Martínez-Sánchez RM, Svensson EM, Malmström H, Rodríguez L, Bermúdez de Castro JM, Carbonell E, Alday A, Hernández Vera JA, Götherström A, Carretero JM, Arsuaga JL, Smith CI, Jakobsson M. Proc Natl Acad Sci U S A. 2018 Mar 27;115(13):3428-3433. doi: 10.1073/pnas.1717762115. Epub 2018 Mar 12. PMID: 29531053.  
  
[vandeLoosdrechtScience2018]:  
**Pleistocene North African genomes link Near Eastern and sub-Saharan African human populations.** van de Loosdrecht M, Bouzouggar A, Humphrey L, Posth C, Barton N, Aximu-Petri A, Nickel B, Nagel S, Talbi EH, El Hajraoui MA, Amzazi S, Hublin JJ, Pääbo S, Schiffels S, Meyer M, Haak W, Jeong C, Krause J. Science. 2018 May 4;360(6388):548-552. doi: 10.1126/science.aar8380. Epub 2018 Mar 15.   
  
[VanDenBrink2017]:  
**A Late Bronze Age II clay coffin from Tel Shaddudin the Central Jezreel Valley, Israel: context andhistorical implications.** Edwin C. M. van den Brink, Ron Beeri, Dan Kirzner, Enno Bron, Anat Cohen-Weinberger, Elisheva Kamaisky, Tamar Gonen, Lilly Gershuny, Yossi Nagar, Daphna Ben-Tor,Naama Sukenik, Orit Shamir, Edward F. Maher & David Reich Levant, 49:2, 105-135, DOI:10.1080/00758914.2017.1368204.   
  
[VeeramahPNAS2018]:  
**Population genomic analysis of elongated skulls reveals extensive female-biased immigration in Early Medieval Bavaria.** Veeramah KR, Rott A, Groß M, van Dorp L, López S, Kirsanow K, Sell C, Blöcher J, Wegmann D, Link V, Hofmanová Z, Peters J, Trautmann B, Gairhos A, Haberstroh J, Päffgen B, Hellenthal G, Haas-Gebhard B, Harbeck M, Burger J. Proc Natl Acad Sci U S A. 2018 Mar 27;115(13):3494-3499. doi: 10.1073/pnas.1719880115. Epub 2018 Mar 12. pPMID: 29531040.  
  
[Villa-IslasScience2023]:  
**Demographic history and genetic structure in pre-Hispanic Central Mexico.** Villa-Islas V, Izarraras-Gomez A, Larena M, Campos EMP, Sandoval-Velasco M, Rodríguez-Rodríguez JE, Bravo-Lopez M, Moguel B, Fregel R, Garfias-Morales E, Medina Tretmanis J, Velázquez-Ramírez DA, Herrera-Muñóz A, Sandoval K, Nieves-Colón MA, Zepeda García Moreno G, Villanea FA, Medina EFV, Aguayo-Haro R, Valdiosera C, Ioannidis AG, Moreno-Estrada A, Jay F, Huerta-Sanchez E, Moreno-Mayar JV, Sánchez-Quinto F, Ávila-Arcos MC. Science. 2023 May 12;380(6645):eadd6142. doi: 10.1126/science.add6142. Epub 2023 May 12. PMID: 37167382.  
  
[Villalba-MoucobioRxiv2023]:  
**A 23,000-year-old southern Iberian individual links human groups that lived in Western Europe before and after the Last Glacial Maximum.** Villalba-Mouco V, van de Loosdrecht MS, Rohrlach AB, Fewlass H, Talamo S, Yu H, Aron F, Lalueza-Fox C, Cabello L, Cantalejo Duarte P, Ramos-Muñoz J, Posth C, Krause J, Weniger GC, Haak W. Nat Ecol Evol. 2023 Apr;7(4):597-609. doi: 10.1038/s41559-023-01987-0. Epub 2023 Mar 1. PMID: 36859553; PMCID: PMC10089921.   
[VillalbaMoucoSciAdv2021]:  
**Genomic transformation and social organization during the Copper Age-Bronze Age transition in southern Iberia.** Villalba-Mouco V, Oliart C, Rihuete-Herrada C, Childebayeva A, Rohrlach AB, Fregeiro MI, Celdrán Beltrán E, Velasco-Felipe C, Aron F, Himmel M, Freund C, Alt KW, Salazar-García DC, García Atiénzar G, de Miguel Ibáñez MP, Hernández Pérez MS, Barciela V, Romero A, Ponce J, Martínez A, Lomba J, Soler J, Martínez AP, Avilés Fernández A, Haber-Uriarte M, Roca de Togores Muñoz C, Olalde I, Lalueza-Fox C, Reich D, Krause J, García Sanjuán L, Lull V, Micó R, Risch R, Haak W. Sci Adv. 2021 Nov 19;7(47):eabi7038. doi: 10.1126/sciadv.abi7038. Epub 2021 Nov 17. PMID: 34788096; PMCID: PMC8597998.  
  
[VillalbaMoucoCurrentBiology2019]:  
**Survival of Late Pleistocene Hunter-Gatherer Ancestry in the Iberian Peninsula.** Villalba-Mouco V, van de Loosdrecht MS, Posth C, Mora R, Martínez-Moreno J, Rojo-Guerra M, Salazar-García DC, Royo-Guillén JI, Kunst M, Rougier H, Crevecoeur I, Arcusa-Magallón H, Tejedor-Rodríguez C, García-Martínez de Lagrán I, Garrido-Pena R, Alt KW, Jeong C, Schiffels S, Utrilla P, Krause J, Haak W. Survival of Late Pleistocene Hunter-Gatherer Ancestry in the Iberian Peninsula. Curr Biol. 2019 Apr 1;29(7):1169-1177.e7. doi: 10.1016/j.cub.2019.02.006. Epub 2019 Mar 14. PMID: 30880015.  
  
[VyasAJPA2017/VyasDryadDigitalRepository2017]:  
**Testing support for the northern and southern dispersal routes out of Africa: an analysis of Levantine and southern Arabian populations.** Vyas DN, Al-Meeri A, Mulligan CJ. Am J Phys Anthropol. 2017 Dec;164(4):736-749. doi: 10.1002/ajpa.23312. Epub 2017 Sep 15. PMID: 28913852.  
  
[WaldmanCell2022]:  
**Genome-wide data from medieval German Jews show that the Ashkenazi founder event pre-dated the 14th century.** Waldman S, Backenroth D, Harney É, Flohr S, Neff NC, Buckley GM, Fridman H, Akbari A, Rohland N, Mallick S, Olalde I, Cooper L, Lomes A, Lipson J, Cano Nistal J, Yu J, Barzilai N, Peter I, Atzmon G, Ostrer H, Lencz T, Maruvka YE, Lämmerhirt M, Beider A, Rutgers LV, Renson V, Prufer KM, Schiffels S, Ringbauer H, Sczech K, Carmi S, Reich D. Cell. 2022 Dec 8;185(25):4703-4716.e16. doi: 10.1016/j.cell.2022.11.002. Epub 2022 Nov 30. PMID: 36455558; PMCID: PMC9793425.  
  
[WangbioRxiv2020]:  
**The Genomic Formation of Human Populations in East Asia.** Chuan-Chao Wang, Hui-Yuan Yeh, Alexander N Popov, Hu-Qin Zhang, Hirofumi Matsumura, Kendra Sirak, Olivia Cheronet, Alexey Kovalev, Nadin Rohland, Alexander M. Kim, Rebecca Bernardos, Dashtseveg Tumen, Jing Zhao, Yi-Chang Liu, Jiun-Yu Liu, Matthew Mah, Swapan Mallick, Ke Wang, Zhao Zhang, Nicole Adamski, Nasreen Broomandkhoshbacht, Kimberly Callan, Brendan J. Culleton, Laurie Eccles, Ann Marie Lawson, Megan Michel, Jonas Oppenheimer, Kristin Stewardson, Shaoqing Wen, Shi Yan, Fatma Zalzala, Richard Chuang, Ching-Jung Huang, Chung-Ching Shiung, Yuri G. Nikitin, Andrei V. Tabarev, Alexey A. Tishkin, Song Lin, Zhou-Yong Sun, Xiao-Ming Wu, Tie-Lin Yang, Xi Hu, Liang Chen, Hua Du, Jamsranjav Bayarsaikhan, Enkhbayar Mijiddorj, Diimaajav Erdenebaatar, Tumur-Ochir Iderkhangai, Erdene Myagmar, Hideaki Kanzawa-Kiriyama, Msato Nishino, Ken-ichi Shinoda, Olga A. Shubina, Jianxin Guo, Qiongying Deng, Longli Kang, Dawei Li, Dongna Li, Rong Lin, Wangwei Cai, Rukesh Shrestha, Ling-Xiang Wang, Lanhai Wei, Guangmao Xie, Hongbing Yao, Manfei Zhang, Guanglin He, Xiaomin Yang, Rong Hu, Martine Robbeets, Stephan Schiffels, Douglas J. Kennett, Li Jin, Hui Li, Johannes Krause, Ron Pinhasi, David Reich bioRxiv 2020.03.25.004606; doi: https://doi.org/10.1101/2020.03.25.004606.  
  
[WangBleasdaleNature2022]:  
**4000-year-old hair from the Middle Nile highlights unusual ancient DNA degradation pattern and a potential source of early eastern Africa pastoralists..** Wang K, Bleasdale M, Le Moyne C, Freund C, Krause J, Boivin N, Schiffels S. Sci Rep. 2022 Dec 3;12(1):20939. doi: 10.1038/s41598-022-25384-y. PMID: 36463384; PMCID: PMC9719486.  
  
[WangCell2021]:  
**Human population history at the crossroads of East and Southeast Asia since 11,000 years ago.** Wang T, Wang W, Xie G, Li Z, Fan X, Yang Q, Wu X, Cao P, Liu Y, Yang R, Liu F, Dai Q, Feng X, Wu X, Qin L, Li F, Ping W, Zhang L, Zhang M, Liu Y, Chen X, Zhang D, Zhou Z, Wu Y, Shafiey H, Gao X, Curnoe D, Mao X, Bennett EA, Ji X, Yang MA, Fu Q. Cell. 2021 Jul 8;184(14):3829-3841.e21. doi: 10.1016/j.cell.2021.05.018. Epub 2021 Jun 24. PMID: 34171307.   
  
[WangKrauseCellGenomics2023]:  
**High-coverage genome of the Tyrolean Iceman reveals unusually high Anatolian farmer ancestry.** Wang K, Prüfer K, Krause-Kyora B, Childebayeva A, Schuenemann VJ, Coia V, Maixner F, Zink A, Schiffels S, Krause J. Cell Genom. 2023 Aug 16;3(9):100377. doi: 10.1016/j.xgen.2023.100377. PMID: 37719142; PMCID: PMC10504632.  
  
[WangNature2021]:  
**Genomic insights into the formation of human populations in East Asia.** Wang CC, Yeh HY, Popov AN, Zhang HQ, Matsumura H, Sirak K, Cheronet O, Kovalev A, Rohland N, Kim AM, Mallick S, Bernardos R, Tumen D, Zhao J, Liu YC, Liu JY, Mah M, Wang K, Zhang Z, Adamski N, Broomandkhoshbacht N, Callan K, Candilio F, Carlson KSD, Culleton BJ, Eccles L, Freilich S, Keating D, Lawson AM, Mandl K, Michel M, Oppenheimer J, Özdoğan KT, Stewardson K, Wen S, Yan S, Zalzala F, Chuang R, Huang CJ, Looh H, Shiung CC, Nikitin YG, Tabarev AV, Tishkin AA, Lin S, Sun ZY, Wu XM, Yang TL, Hu X, Chen L, Du H, Bayarsaikhan J, Mijiddorj E, Erdenebaatar D, Iderkhangai TO, Myagmar E, Kanzawa-Kiriyama H, Nishino M, Shinoda KI, Shubina OA, Guo J, Cai W, Deng Q, Kang L, Li D, Li D, Lin R, Nini, Shrestha R, Wang LX, Wei L, Xie G, Yao H, Zhang M, He G, Yang X, Hu R, Robbeets M, Schiffels S, Kennett DJ, Jin L, Li H, Krause J, Pinhasi R, Reich D. Genomic insights into the formation of human populations in East Asia. Nature. 2021 Mar;591(7850):413-419. doi: 10.1038/s41586-021-03336-2. Epub 2021 Feb 22. PMID: 33618348; PMCID: PMC7993749.  
  
[WangNatureCommunications2019]:  
**Ancient human genome-wide data from a 3000-year interval in the Caucasus corresponds with eco-geographic regions.** Wang CC, Reinhold S, Kalmykov A, Wissgott A, Brandt G, Jeong C, Cheronet O, Ferry M, Harney E, Keating D, Mallick S, Rohland N, Stewardson K, Kantorovich AR, Maslov VE, Petrenko VG, Erlikh VR, Atabiev BC, Magomedov RG, Kohl PL, Alt KW, Pichler SL, Gerling C, Meller H, Vardanyan B, Yeganyan L, Rezepkin AD, Mariaschk D, Berezina N, Gresky J, Fuchs K, Knipper C, Schiffels S, Balanovska E, Balanovsky O, Mathieson I, Higham T, Berezin YB, Buzhilova A, Trifonov V, Pinhasi R, Belinskij AB, Reich D, Hansen S, Krause J, Haak W. Nat Commun. 2019 Feb 4;10(1):590. doi: 10.1038/s41467-018-08220-8. PMID: 30713341.  
  
[WangSciAdv2020]:  
**Ancient genomes reveal complex patterns of population movement, interaction, and replacement in sub-Saharan Africa.** Wang K, Goldstein S, Bleasdale M, Clist B, Bostoen K, Bakwa-Lufu P, Buck LT, Crowther A, Dème A, McIntosh RJ, Mercader J, Ogola C, Power RC, Sawchuk E, Robertshaw P, Wilmsen EN, Petraglia M, Ndiema E, Manthi FK, Krause J, Roberts P, Boivin N, Schiffels S. Sci Adv. 2020 Jun 12;6(24):eaaz0183. doi: 10.1126/sciadv.aaz0183. PMID: 32582847; PMCID: PMC7292641.  
  
[WangSkourtaniotiPNAS2023]:  
**Isotopic and DNA analyses reveal multiscale PPNB mobility and migration across Southeastern Anatolia and the Southern Levant.** Wang X, Skourtanioti E, Benz M, Gresky J, Ilgner J, Lucas M, Morsch M, Peters J, Pöllath N, Ringbauer H, le Roux P, Schultz M, Krause J, Roberts P, Stockhammer PW. Proc Natl Acad Sci U S A. 2023 Jan 24;120(4):e2210611120. doi: 10.1073/pnas.2210611120. Epub 2023 Jan 17. PMID: 36649412; PMCID: PMC9942848.  
  
[WangYangScienceAdvances2023]:  
**Human genetic history on the Tibetan Plateau in the past 5100 years.** Wang H, Yang MA, Wangdue S, Lu H, Chen H, Li L, Dong G, Tsring T, Yuan H, He W, Ding M, Wu X, Li S, Tashi N, Yang T, Yang F, Tong Y, Chen Z, He Y, Cao P, Dai Q, Liu F, Feng X, Wang T, Yang R, Ping W, Zhang Z, Gao Y, Zhang M, Wang X, Zhang C, Yuan K, Ko AM, Aldenderfer M, Gao X, Xu S, Fu Q. Sci Adv. 2023 Mar 15;9(11):eadd5582. doi: 10.1126/sciadv.add5582. Epub 2023 Mar 17. PMID: 36930720; PMCID: PMC10022901.  
  
[WegmannCurBio2020]:  
**Low Prevalence of Lactase Persistence in Bronze Age Europe Indicates Ongoing Strong Selection over the Last 3,000 Years.** Burger J, Link V, Blöcher J, Schulz A, Sell C, Pochon Z, Diekmann Y, Žegarac A, Hofmanová Z, Winkelbach L, Reyna-Blanco CS, Bieker V, Orschiedt J, Brinker U, Scheu A, Leuenberger C, Bertino TS, Bollongino R, Lidke G, Stefanović S, Jantzen D, Kaiser E, Terberger T, Thomas MG, Veeramah KR, Wegmann D. Low Prevalence of Lactase Persistence in Bronze Age Europe Indicates Ongoing Strong Selection over the Last 3,000 Years. Curr Biol. 2020 Nov 2;30(21):4307-4315.e13. doi: 10.1016/j.cub.2020.08.033. Epub 2020 Sep 3. PMID: 32888485.  
  
[WangYuCurrentBiology2023]:  
**Middle Holocene Siberian genomes reveal highly connected gene pools throughout North Asia.** Wang K, Yu H, Radzevičiūtė R, Kiryushin YF, Tishkin AA, Frolov YV, Stepanova NF, Kiryushin KY, Kungurov AL, Shnaider SV, Tur SS, Tiunov MP, Zubova AV, Pevzner M, Karimov T, Buzhilova A, Slon V, Jeong C, Krause J, Posth C. Curr Biol. 2023 Feb 6;33(3):423-433.e5. doi: 10.1016/j.cub.2022.11.062. Epub 2023 Jan 12. PMID: 36638796.  
  
[WohnsScience2022]:  
**A unified genealogy of modern and ancient genomes.** Wohns AW, Wong Y, Jeffery B, Akbari A, Mallick S, Pinhasi R, Patterson N, Reich D, Kelleher J, McVean G. Science. 2022 Feb 25;375(6583):eabi8264. doi: 10.1126/science.abi8264. Epub 2022 Feb 25. PMID: 35201891.  
  
[WrightSciAdv2018]:  
**Ancient nuclear genomes enable repatriation of Indigenous human remains.** Wright JL, Wasef S, Heupink TH, Westaway MC, Rasmussen S, Pardoe C, Fourmile GG, Young M, Johnson T, Slade J, Kennedy R, Winch P, Pappin M Sr, Wales T, Bates WB, Hamilton S, Whyman N, van Holst Pellekaan S, McAllister PJ, Taçon PSC, Curnoe D, Li R, Millar C, Subramanian S, Willerslev E, Malaspinas AS, Sikora M, Lambert DM. Sci Adv. 2018 Dec 19;4(12):eaau5064. doi: 10.1126/sciadv.aau5064. PMID: 30585290; PMCID: PMC6300400.  
  
[YakaSomelCurrBio2021]:  
**Variable kinship patterns in Neolithic Anatolia revealed by ancient genomes.** Yaka R, Mapelli I, Kaptan D, Doğu A, Chyleński M, Erdal ÖD, Koptekin D, Vural KB, Bayliss A, Mazzucato C, Fer E, Çokoğlu SS, Lagerholm VK, Krzewińska M, Karamurat C, Gemici HC, Sevkar A, Dağtaş ND, Kılınç GM, Adams D, Munters AR, Sağlıcan E, Milella M, Schotsmans EMJ, Yurtman E, Çetin M, Yorulmaz S, Altınışık NE, Ghalichi A, Juras A, Bilgin CC, Günther T, Storå J, Jakobsson M, de Kleijn M, Mustafaoğlu G, Fairbairn A, Pearson J, Togan İ, Kayacan N, Marciniak A, Larsen CS, Hodder I, Atakuman Ç, Pilloud M, Sürer E, Gerritsen F, Özbal R, Baird D, Erdal YS, Duru G, Özbaşaran M, Haddow SD, Knüsel CJ, Götherström A, Özer F, Somel M. Variable kinship patterns in Neolithic Anatolia revealed by ancient genomes. Curr Biol. 2021 Jun 7;31(11):2455-2468.e18. doi: 10.1016/j.cub.2021.03.050. Epub 2021 Apr 14. PMID: 33857427; PMCID: PMC8210650.  
  
[YangCurrentBiology2017]:  
**40,000-Year-Old Individual from Asia Provides Insight into Early Population Structure in Eurasia.** Yang MA, Gao X, Theunert C, Tong H, Aximu-Petri A, Nickel B, Slatkin M, Meyer M, Pääbo S, Kelso J, Fu Q. Curr Biol. 2017 Oct 23;27(20):3202-3208.e9. doi: 10.1016/j.cub.2017.09.030. Epub 2017 Oct 12. PMID: 29033327.  
  
[YangScience2020]:  
**Ancient DNA indicates human population shifts and admixture in northern and southern China.** Yang MA, Fan X, Sun B, Chen C, Lang J, Ko YC, Tsang CH, Chiu H, Wang T, Bao Q, Wu X, Hajdinjak M, Ko AM, Ding M, Cao P, Yang R, Liu F, Nickel B, Dai Q, Feng X, Zhang L, Sun C, Ning C, Zeng W, Zhao Y, Zhang M, Gao X, Cui Y, Reich D, Stoneking M, Fu Q. Science. 2020 Jul 17;369(6501):282-288. doi: 10.1126/science.aba0909. Epub 2020 May 14. PMID: 32409524.  
  
[YuCell2020]:  
**Paleolithic to Bronze Age Siberians Reveal Connections with First Americans and across Eurasia.** Yu H, Spyrou MA, Karapetian M, Shnaider S, Radzevičiūtė R, Nägele K, Neumann GU, Penske S, Zech J, Lucas M, LeRoux P, Roberts P, Pavlenok G, Buzhilova A, Posth C, Jeong C, Krause J. Cell. 2020 Jun 11;181(6):1232-1245.e20. doi: 10.1016/j.cell.2020.04.037. Epub 2020 May 20. PMID: 32437661.  
  
[YuvandeLoosdrechtiScience2022]:  
**Genomic and dietary discontinuities during the Mesolithic and Neolithic in Sicily.** Yu H, van de Loosdrecht MS, Mannino MA, Talamo S, Rohrlach AB, Childebayeva A, Villalba-Mouco V, Aron F, Brandt G, Burri M, Freund C, Radzeviciute R, Stahl R, Wissgott A, Fewlass H, Tagliacozzo A, Piperno M, Tusa S, Collina C, Schimmenti V, Di Salvo R, Prüfer K, Posth C, Hublin JJ, Gronenborn D, Binder D, Jeong C, Haak W, Krause J. iScience. 2022 Apr 12;25(5):104244. doi: 10.1016/j.isci.2022.104244. PMID: 35494246; PMCID: PMC9051636.  
  
[ZagorcArchaeologicalAnthropologicalSciences2024]:  
**Bioarchaeological Perspectives on Late Antiquity in Dalmatia: Paleogenetic, Dietary, and Population Studies of the Hvar - Radošević burial site** Brina Zagorc, Magdalena Blanz, Pere Gelabert, Susanna Sawyer, Victoria Oberreiter, Olivia Cheronet, Hao Shan Chen, Mario Carić, Eduard Visković, Iňigo Olalde, Maria Ivanova-Bieg, Mario Novak, David Reich, Ron Pinhasi bioRxiv 2024.05.14.594056; doi: https://doi.org/10.1101/2024.05.14.594056   
  
[ZallouaScientificReports2018]:  
**Ancient DNA of Phoenician remains indicates discontinuity in the settlement history of Ibiza.** Zalloua P, Collins CJ, Gosling A, Biagini SA, Costa B, Kardailsky O, Nigro L, Khalil W, Calafell F, Matisoo-Smith E. Sci Rep. 2018 Dec 4;8(1):17567. doi: 10.1038/s41598-018-35667-y. PMID: 30514893.  
  
[ZegaracBurgerbioRxiv2021]:  
**Kinship, acquired and inherited status, and population structure at the Early Bronze Age Mokrin necropolis in northern Serbia.** Aleksandra Žegarac, Laura Winkelbach, Jens Blöcher, Yoan Diekmann, Marija Krečković Gavrilović, Marko Porčić, Biljana Stojković, Lidija Milašinović, Mona Schreiber, Daniel Wegmann, Krishna R. Veeramah, Sofija Stefanović, Joachim Burger  
bioRxiv 2020.05.18.101337; doi: https://doi.org/10.1101/2020.05.18.101337.  
  
[ZengVyazovKimbioRxiv2023]:  
**Postglacial genomes from foragers across Northern Eurasia reveal prehistoric mobility associated with the spread of the Uralic and Yeniseian languages** Tian Chen Zeng, Leonid A. Vyazov, Alexander Kim, Pavel Flegontov, Kendra Sirak, Robert Maier, Iosif Lazaridis, Ali Akbari, Michael Frachetti, Alexey A. Tishkin, Natalia E. Ryabogina, Sergey A. Agapov, Danila S. Agapov, Anatoliy N. Alekseev, Gennady G. Boeskorov, Anatoly P. Derevianko, Viktor M. Dyakonov, Dmitry N. Enshin, Alexey V. Fribus, Yaroslav V. Frolov, Sergey P. Grushin, Alexander A. Khokhlov, Kirill Yu. Kiryushin, Yurii. F. Kiryushin, Egor P. Kitov, Pavel Kosintsev, Igor V. Kovtun, Nikolai P. Makarov, Viktor V. Morozov, Egor N. Nikolaev, Marina P. Rykun, Tatyana M. Savenkova, Marina V. Shchelchkova, Vladimir Shirokov, Svetlana N. Skochina, Olga S. Sherstobitova, Sergey M. Slepchenko, Konstantin N. Solodovnikov, Elena N. Solovyova, Aleksandr D. Stepanov, Aleksei A. Timoshchenko, Aleksandr S. Vdovin, Anton V. Vybornov, Elena V. Balanovska, Stanislav Dryomov, Garrett Hellenthal, Kenneth Kidd, Johannes Krause, Elena Starikovskaya, Rem Sukenik, Tatiana Tatarinova, Mark G. Thomas, Maxat Zhabagin, Kim Callan, Olivia Cheronet, Daniel Fernandes, Denise Keating, Candilio Francesca, Lora Iliev, Aisling Kearns, Kadir Toykan Özdoğan, Matthew Mah, Adam Micco, Megan Michel, Iñigo Olalde, Fatma Zalzala, Swapan Mallick, Nadin Rohland, Ron Pinhasi, Vagheesh Narasimhan, David Reich  
bioRxiv 2023.10.01.560332; doi: https://doi.org/10.1101/2023.10.01.560332 .

[ZhangCurrBio2022]:  
**A Late Pleistocene human genome from Southwest China.** Zhang X, Ji X, Li C, Yang T, Huang J, Zhao Y, Wu Y, Ma S, Pang Y, Huang Y, He Y, Su B. Curr Biol. 2022 Jul 25;32(14):3095-3109.e5. doi: 10.1016/j.cub.2022.06.016. Epub 2022 Jul 14. PMID: 35839766.  
  
[ZhangNature2021]:  
**The genomic origins of the Bronze Age Tarim Basin mummies.** Zhang F, Ning C, Scott A, Fu Q, Bjørn R, Li W, Wei D, Wang W, Fan L, Abuduresule I, Hu X, Ruan Q, Niyazi A, Dong G, Cao P, Liu F, Dai Q, Feng X, Yang R, Tang Z, Ma P, Li C, Gao S, Xu Y, Wu S, Wen S, Zhu H, Zhou H, Robbeets M, Kumar V, Krause J, Warinner C, Jeong C, Cui Y. The genomic origins of the Bronze Age Tarim Basin mummies. Nature. 2021 Nov;599(7884):256-261. doi: 10.1038/s41586-021-04052-7. Epub 2021 Oct 27. PMID: 34707286; PMCID: PMC8580821.   
  
[ZhangNingArchAnthSci2024]:  
**Ancient genomes provide insights into the genetic history in the historical era of southwest China.** Zhang, F., Zhang, X., Bai, B. et al. Archaeol Anthropol Sci 16, 120 (2024). https://doi.org/10.1007/s12520-024-02036-y .  
  
[ZhuiScience2022]:  
**Cultural and demic co-diffusion of Tubo Empire on Tibetan Plateau.** Zhu K, Du P, Li J, Zhang J, Hu X, Meng H, Chen L, Zhou B, Yang X, Xiong J, Allen E, Ren X, Ding Y, Xu Y, Chang X, Yu Y, Han S, Dong G, Wang CC, Wen S. iScience. 2022 Nov 22;25(12):105636. doi: 10.1016/j.isci.2022.105636. PMID: 36582485; PMCID: PMC9792914.