Resource Summary Report

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UniSTS

RRID:SCR_006843
Type: Tool

Proper Citation

UniSTS (RRID:SCR_006843)

Resource Information

URL: http://www.ncbi.nlm.nih.gov/unists

Proper Citation: UniSTS (RRID:SCR_006843)

Description: THIS RESOURCE IS NO LONGER IN SERVICE, documented August 22, 2016. Database of sequence tagged sites (STSs) derived from STS-based maps and other experiments. STSs are defined by PCR primer pairs and are associated with additional information such as genomic position, genes, and sequences. Chromosome maps are labeled by name of the originating organism, the map title, total markers, total UniSTSs and links to view maps as well as research documents available through PubMed, another NCBI database. The search functions within UniSTS allow the user to search by gene marker, chromosome, gene symbol and gene description terms to locate markers on specified genes. A representation of the UniSTS datasets is available by ftp. NOTE: All data from this resource have been moved to the Probe database, http://www.ncbi.nlm.nih.gov/probe. You can retrieve all UniSTS records by searching the probe database using the search term unists(properties). (use brackets insead of parenthesis). Additionally, legacy data remain on the NCBI FTP Site in the UniSTS Repository (ftp://ftp.ncbi.nih.gov/pub/ProbeDB/legacy_unists).

Abbreviations: UniSTS

Synonyms: UniSTS: Integrating Markers and Maps, NCBI UniSTS, Entrez UniSTS

Resource Type: data or information resource, database

Keywords: marker, primer sequence, mapping, sequence tagged site, genomic position, gene, sequence, nucleotide, nucleotide sequence, chromosome, gold standard

Funding:

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: UniSTS

Resource ID: SCR_006843

Alternate IDs: nif-0000-03614

Record Creation Time: 20220129T080238+0000

Record Last Update: 20250424T064848+0000

Ratings and Alerts

No rating or validation information has been found for UniSTS.

No alerts have been found for UniSTS.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 40 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Gu L, et al. (2023) The causal mutation in ARR3 gene for high myopia and progressive color vision defect. Scientific reports, 13(1), 8986.

Takayama J, et al. (2021) Construction and integration of three de novo Japanese human genome assemblies toward a population-specific reference. Nature communications, 12(1), 226.

Kim YM, et al. (2020) The GBA p.G85E mutation in Korean patients with non-neuronopathic Gaucher disease: founder and neuroprotective effects. Orphanet journal of rare diseases, 15(1), 318.

Muhie S, et al. (2019) Molecular alterations induced by Yersinia pestis, dengue virus and Staphylococcal enterotoxin B under severe stress. Brain, behavior, and immunity, 80, 725.

Koohiyan M, et al. (2019) Screening of 10 DFNB Loci Causing Autosomal Recessive Non-Syndromic Hearing Loss in Two Iranian Populations Negative for GJB2 Mutations. Iranian

journal of public health, 48(9), 1704.

Sharifi Z, et al. (2019) Development and validation of a novel panel of 16 STR markers for simultaneous diagnosis of ?-thalassemia, aneuploidy screening, maternal cell contamination detection and fetal sample authenticity in PND and PGD/PGS cases. Scientific reports, 9(1), 7452.

Naseri M, et al. (2018) Genetic Linkage Analysis of DFNB4, DFNB28, DFNB93 Loci in Autosomal Recessive Non-syndromic Hearing Loss: Evidence for Digenic Inheritance in GJB2 and GJB3 Mutations. Iranian journal of public health, 47(1), 95.

Laleh MA, et al. (2017) Diverse pattern of gap junction beta-2 and gap junction beta-4 genes mutations and lack of contribution of DFNB21, DFNB24, DFNB29, and DFNB42 loci in autosomal recessive nonsyndromic hearing loss patients in Hormozgan, Iran. Journal of research in medical sciences : the official journal of Isfahan University of Medical Sciences, 22, 99.

Liu X, et al. (2016) Novel Y-chromosomal microdeletions associated with non-obstructive azoospermia uncovered by high throughput sequencing of sequence-tagged sites (STSs). Scientific reports, 6, 21831.

Fan J, et al. (2016) Quantification of nucleic acid quality in postmortem tissues from a cancer research autopsy program. Oncotarget, 7(41), 66906.

Saghafi H, et al. (2016) Setting up Multiplex Panels for Genetic Testing of Familial Hypertrophic Cardiomyopathy Based on Linkage Analysis. Iranian journal of public health, 45(3), 329.

Reiisi S, et al. (2016) Screening of DFNB3 in Iranian families with autosomal recessive non-syndromic hearing loss reveals a novel pathogenic mutation in the MyTh4 domain of the MYO15A gene in a linked family. Iranian journal of basic medical sciences, 19(7), 772.

Masoudi M, et al. (2016) Genetic Linkage Analysis of DFNB3, DFNB9 and DFNB21 Loci in GJB2 Negative Families with Autosomal Recessive Non-syndromic Hearing Loss. Iranian journal of public health, 45(5), 680.

Omachi T, et al. (2015) Expression of tenocyte lineage-related factors in regenerated tissue at sites of tendon defect. Journal of orthopaedic science : official journal of the Japanese Orthopaedic Association, 20(2), 380.

Thornhill AR, et al. (2015) Karyomapping-a comprehensive means of simultaneous monogenic and cytogenetic PGD: comparison with standard approaches in real time for Marfan syndrome. Journal of assisted reproduction and genetics, 32(3), 347.

Nyegaard M, et al. (2015) A Novel Locus Harbouring a Functional CD164 Nonsense Mutation Identified in a Large Danish Family with Nonsyndromic Hearing Impairment. PLoS genetics, 11(7), e1005386.

Marchi N, et al. (2015) Confirmation of a founder effect in a Northern European population of

a new ?-globin variant: HBB:c.23_26dup (codons 8/9 (+AGAA)). European journal of human genetics : EJHG, 23(9), 1158.

Magalhães M, et al. (2015) Microsatellite alterations are also present in the less aggressive types of adult T-cell leukemia-lymphoma. PLoS neglected tropical diseases, 9(1), e0003403.

Wang C, et al. (2014) Mutation in xyloglucan 6-xylosytransferase results in abnormal root hair development in Oryza sativa. Journal of experimental botany, 65(15), 4149.

Hermetz KE, et al. (2014) Large inverted duplications in the human genome form via a fold-back mechanism. PLoS genetics, 10(1), e1004139.