Resource Summary Report

Generated by dkNET on Aug 26, 2026

SYZYGY

RRID:SCR_002157
Type: Tool

Proper Citation

SYZYGY (RRID:SCR_002157)

Resource Information

URL: http://www.broadinstitute.org/software/syzygy/

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Description: A targeted sequencing post processing analysis software tool that allows: 1. SNP and indel detection; 2. Allele frequency estimation; 3. Single-marker association test; 4. Group-wise marker test association; 5. Experimental QC summary (%dbSNP, Ts/Tv, Ns/S); 6. Power to detect variant. (entry from Genetic Analysis Software)

Abbreviations: Syzygy

Synonyms: Syzygy - SNP and indel calling for pooled and individual targeted resequencing studies

Resource Type: software application, software resource

Defining Citation: PMID:21983784

Keywords: gene, genetic, genomic, variant calling, snp, indel, allele frequency, single-marker association, group-wise marker, quality control, variant

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: SYZYGY

Resource ID: SCR_002157

Alternate IDs: nlx_154668, OMICS_02166

Record Creation Time: 20220129T080211+0000

Record Last Update: 20260821T193637+0000

Ratings and Alerts

No rating or validation information has been found for SYZYGY.

No alerts have been found for SYZYGY.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 5 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET .

Artigas MS, et al. (2017) Targeted Sequencing of Lung Function Loci in Chronic Obstructive Pulmonary Disease Cases and Controls. PloS one, 12(1), e0170222.

Ellis MK, et al. (2015) Rare variants in MYD88, IRAK4 and IKBKG and susceptibility to invasive pneumococcal disease: a population-based case-control study. PloS one, 10(4), e0123532.

Villanueva P, et al. (2015) Exome sequencing in an admixed isolated population indicates NFXL1 variants confer a risk for specific language impairment. PLoS genetics, 11(3), e1004925.

Day-Williams AG, et al. (2011) An evaluation of different target enrichment methods in pooled sequencing designs for complex disease association studies. PloS one, 6(11), e26279.

Raychaudhuri S, et al. (2011) A rare penetrant mutation in CFH confers high risk of age-related macular degeneration. Nature genetics, 43(12), 1232.