Resource Summary Report

Generated by NIF on May 20, 2025

OligoGenome

RRID:SCR_006025
Type: Tool

Proper Citation

OligoGenome (RRID:SCR_006025)

Resource Information

URL: http://oligogenome.stanford.edu/

Proper Citation: OligoGenome (RRID:SCR_006025)

Description: The Stanford Human OligoGenome Project hosts a database of capture oligonucleotides for conducting high-throughput targeted resequencing of the human genome. This set of capture oligonucleotides covers over 92% of the human genome for build 37 / hg19 and over 99% of the coding regions defined by the Consensus Coding Sequence (CCDS). The capture reaction uses a highly multiplexed approach for selectively circularizing and capturing multiple genomic regions using the in-solution method developed in Natsoulis et al, PLoS One 2011. Combined pools of capture oligonucleotides selectively circularize the genomic DNA target, followed by specific PCR amplification of regions of interest using a universal primer pair common to all of the capture oligonucleotides. Unlike multiplexed PCR methods, selective genomic circularization is capable of efficiently amplifying hundreds of genomic regions simultaneously in multiplex without requiring extensive PCR optimization or producing unwanted side reaction products. Benefits of the selective genomic circularization method are the relative robustness of the technique and low costs of synthesizing standard capture oligonucleotide for selecting genomic targets.

Abbreviations: OligoGenome

Synonyms: Stanford Human Oligo Genome Project, Human OligoGenome Resource, Stanford Human Oligo Genome, Human Oligo Genome, Human OligoGenome

Resource Type: database, data or information resource, resource

Defining Citation: PMID:22102592

Keywords: oligonucleotide, genome, probe, coding region, oligonucleotide sequence,

chromosome

Funding: NHGRI RC2 HG005570-01;
NCI R21CA12848;
NCI 5K08CA96879?6;
NIDDK DK56339;
NHGRI 2P01HG000205;
NLM T15-LM007033;
Doris Duke Clinical Foundation ;
Reddere Foundation ;
Liu Bie Ju Cha and Family Fellowship in Cancer ;
Wang Family Foundation ;
Howard Hughes Medical Foundation

Resource Name: OligoGenome

Resource ID: SCR_006025

Alternate IDs: nlx_151422

Record Creation Time: 20220129T080233+0000

Record Last Update: 20250519T203430+0000

Ratings and Alerts

No rating or validation information has been found for OligoGenome .

No alerts have been found for OligoGenome .

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 2 mentions in open access literature.

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

Detwiler LT, et al. (2016) From frames to OWL2: Converting the Foundational Model of Anatomy. Artificial intelligence in medicine, 69, 12.

Myllykangas S, et al. (2011) Targeted sequencing library preparation by genomic DNA circularization. BMC biotechnology, 11, 122.