National Advisory Council for Human Genome Research
Concept Clearance for Genomic Technology Development PAR
September 16 - 17, 2019

Title: Genomic Technology Development PAR (R01, R21 and R43/R44)

Purpose: The purpose of this set of Novel Genomic Technology Development Program Announcements with special Review criteria (PARs) is to catalyze and support major advances in genomic technologies. Progress in basic research and clinical applications of genomics, and more broadly in biomedical research, has been greatly facilitated by significant and sustained genomics technology throughput increases, cost decreases, and improvements in ease of use. The proposed work solicited should allow comprehensive genomic analysis of features not assayable today, completely new ways to assay genomic features, or an increase of no less than an order of magnitude in an existing technology in terms of data quality, throughput, efficiency or comprehensiveness (individually or in combination). Work solicited under the accompanying Technology Development RFAs Concept Clearance will be explicitly excluded from this set of PARs.

New or renewal/modified initiative: Renewal
Some changes reflecting input from town halls, workshops and other strategic planning forums are anticipated for the revised PARs. Switching to every other Council review rather than the current annual cycle is also anticipated to accelerate progress.

Current PARs:

R01:	https://grants.nih.gov/grants/guide/pa-files/PAR-18-777.html
R21:	https://grants.nih.gov/grants/guide/pa-files/PAR-18-778.html
R43/R44:	https://grants.nih.gov/grants/guide/pa-files/PAR-18-779.html

Mechanism of Support: R01, R21 and R43/R44 (see Appendix 1).

Appendix 1: Mechanism Overview
Appendix 2: Novel Genomic Technology Development PAR grants awarded (FY16-FY19).

Appendix 1. Mechanism Overview

Program Announcement with special Review criteria (PAR)

FOA set	Receipt dates	Activity Code(s)	Max award duration
Genomic Technology	FY21-FY23	R01, R21 & R43/R44	4 years

Appendix 2. Novel Genomic Technology Development PAR grants (FY16-FY19).

Grant	PI	Title
R01		
HG009269	Bernstein, Bradley	Single-molecule systems for decoding combinatorial chromatin modifications
HG009276	Regev, Aviv	DNA microscopy for spatially resolved genomic analyses in intact tissue
HG009283	Blainey, Paul	Arrayed single-cell readout of pooled genetic perturbation libraries
HG009285	Mali, Prashant	Next-generation Functional Genetic Screening of Un-screenable Traits
HG009761	Zhang, Feng	Programmable RNA-targeting tools
HG010318	Kim, Sanggu	On-site, high-fidelity target sequencing and absolute quantitation for HIV-1 surveillance
HG010211	Zeitlinger, Julia	A transposase system for integrative ChIP-exo and ATAC-seq analysis at single-cell resolution
HG010647	Chen, Fei	A single cell spatial genomics platform for multi-modal characterization of tissue organization
HG010634	Ecker, Joseph	Development of methods for multi-omic analysis of DNA methylation and chromatin architecture in single cells
HG010646	Kohli, Rahul	Non-destructive epigenetic sequencing with DNA deaminase enzymes
HG010632	Shendure, Jay	Versatile, exponentially scalable methods for single cell molecular profiling
R21		
HG009268	Bulyk, Martha	Surveying transcription factor pioneer interactions with nucleosomal DNA
HG009264	Churchman, Lee	Global measurement of splicing kinetics
HG009274	Ecker, Joseph	Multidimensional Epigenomic Single Cell Analyses
HG009256	Lu, Chang	Ultrasensitive microfluidic ChIP-MethylC-seq for integrative analysis of histone modification and DNA methylation
HG009255	Powers, Scott	High-throughput genetic interaction sequencing in mammalian cells
HG009749	Buenrostro, Jason	In situ ATAC-seq, a novel technology for structural epigenomics
HG009758	Davis, Ronald	Ultra high-throughput DNA synthesis via nano-optical conveyer belts
HG009742	Farnham, Peggy	Development of a novel promoter tagging technology to identify enhancer targets
HG009750	Mitra, Robi	SINGLE-CELL ANALYSIS OF PIONEER BINDING AND FUNCTION DURING LINEAGE REPROGRAMMING
HG009748	Smibert, Peter	Massively Parallel Multi-Modal Single-Cell Phenotyping Using a Portable Device
HG010200	Bulyk, Martha	AVATAR: highly parallel analysis of variation in transcription factors and their DNA binding sites
HG010195	Lu, Chang	Drop-BS: high-throughput single-cell bisulfite sequencing on a microfluidic droplet platform
R43/R44		
HG009768	Keogh, Michael-Christopher	Next-Generation Detection Reagents for Chromatin Immunoprecipitation
HG010237	Jelinek, Mary	Epi-seq: Multiplexed ChIP-seq for personalized medicine and drug discovery
HG009763	Seligmann, Bruce	TempO-Seq Profiling of RNA Epitranscriptomic Modifications