

Resource Summary Report

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[nf-vcf-cataloguer](#)

DOI:10.17504/protocols.io.bkmzku76

Type: Protocol

Proper Citation

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[dx.doi.org/10.17504/protocols.io.bkmzku76](https://doi.org/10.17504/protocols.io.bkmzku76)

Protocol Information

URL: <https://dx.doi.org/10.17504/protocols.io.bkmzku76>

Authors: Israel Aguilar Ordoñez

Group: Whole genome variation in 27 Mexican indigenous populations, demographic and biomedical insights

Summary: 'nf-vcf-cataloguer' is a tool, implemented in Nextflow, that generates a general table description in TSV format of the description of each category and subgroup of a VCF with the extended annotation made by VEP. Furthermore, it plots each subset of the consequences of variants.

Affiliations: Instituto Nacional de Medicina Genómica (INMEGEN)

External URL: <https://github.com/laguilaror/nf-VCF-cataloguer>

Version: 1

Publication Date: 2020

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