

# Resource Summary Report

Generated by NIF on Sep 1, 2026

## VG

RRID:SCR\_013378

Type: Tool

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### Proper Citation

VG (RRID:SCR\_013378)

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### Resource Information

**URL:** <http://pga.gs.washington.edu/VG2.html>

**Proper Citation:** VG (RRID:SCR\_013378)

**Description:** Software program that presents complete raw datasets of individuals' genotype data using a display format with samples as rows and polymorphisms as columns. The color code is: (1) blue: homozygous genotype for the common allele; (2) red: heterozygous genotype; (3) yellow: homozygous genotype for the rare allele; and (4) grey: missing data (entry from Genetic Analysis Software)

**Abbreviations:** VG

**Synonyms:** Visual Genotype

**Resource Type:** software application, software resource

**Keywords:** gene, genetic, genomic

**Resource Name:** VG

**Resource ID:** SCR\_013378

**Alternate IDs:** nlx\_154688

**Record Creation Time:** 20220129T080315+0000

**Record Last Update:** 20260829T183116+0000

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### Ratings and Alerts

No rating or validation information has been found for VG.

No alerts have been found for VG.

## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 3 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [NIF](#) .

Sztangierska W, et al. (2024) Early steps of protein disaggregation by Hsp70 chaperone and class B J-domain proteins are shaped by Hsp110. eLife, 13.

Ragnarsdóttir B, et al. (2010) Toll-like receptor 4 promoter polymorphisms: common TLR4 variants may protect against severe urinary tract infection. PloS one, 5(5), e10734.

Chan TF, et al. (2008) Natural variation in four human collagen genes across an ethnically diverse population. Genomics, 91(4), 307.