# **Resource Summary Report**

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## **BETASEQ**

RRID:SCR\_006401

Type: Tool

### **Proper Citation**

BETASEQ (RRID:SCR\_006401)

#### Resource Information

URL: http://www.unc.edu/~yunmli/betaseq/

**Proper Citation:** BETASEQ (RRID:SCR\_006401)

**Description:** Software to control Type-I error inflation in partially sequenced data for rare variant association testing. It is typically used to combine sequence and genotype data for the two stage design, in which individuals sequenced in stage one for variant detection are solely or predominantly cases then in stage two the discovered variants are genotyped in the remaining individuals. BETASEQ can work with any existing rare variant association methods that use genotypes or imputed genotypes as input.

**Abbreviations: BETASEQ** 

Resource Type: software resource

**Defining Citation:** PMID:24336643

Keywords: variant association testing, variant association, variant

**Funding:** 

Availability: Free, Public

**Resource Name: BETASEQ** 

Resource ID: SCR 006401

Alternate IDs: OMICS\_02213

**Record Creation Time:** 20220129T080236+0000

**Record Last Update:** 20250420T014325+0000

### Ratings and Alerts

No rating or validation information has been found for BETASEQ.

No alerts have been found for BETASEQ.

#### **Data and Source Information**

Source: SciCrunch Registry

## **Usage and Citation Metrics**

We have not found any literature mentions for this resource.