Searching dbSNP in Entrez

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How to construct queries

dbSNP is part of NCBI's network of Entrez databases. As with these other databases, data of interest may be located simply by entering keywords into the dbSNP search box. The Advanced Search page, linked below the dbSNP search box, can assist in the construction of complex queries. To construct a complex query, specify the search terms, their fields, and the Boolean operations to perform on the terms using the following syntax:

```
term[field] OPERATOR term[field]
```

where `term` is the search terms, `field` is the search field, and `OPERATOR` is the Boolean operator ('AND', 'OR', 'NOT'; must be capitalized).

Common Query fields and examples

Field full name	Field aliases	Description	Search term values and rules	Example
All Fields	ALL, *	Search all searchable (indexed) fields	Asterisk (*) in the search term is not interpreted as a wildcard	SNV AND pathogenic
Base Position	POSITION, SNPPOS	Chromosome base position on GRCh38 (current)	A natural number representing the SNP's start coordinate on its chromosome on the latest assembly (ie. GRCh38). Most useful when search in combination with the CHR field.	19956018[POSITION] AND 8[CHR]
Base Position Previous	POSITION_GRCH37, CHRPOS_PREV_ASSM	Chromosome base position on GRCh37 (previous)	A natural number representing the SNP's start coordinate on its chromosome on the previous assembly (ie. GRCh37). Most useful when search in combination with the CHR field.	19813529[POSITION_GRCH37] AND 8[CHR]

Chromosome	CHR, CHRNUM	Chromosomes	One of 1-22, X, Y, MT	7[CHR]
Clinical Significance	CLIN	Variations with defined clinical effects or significances	16 search term values, defined for a relatively small subset of SNPs.	"likely pathogenic"[CLIN]
Filter	FILT, FLTR, SUBSET, SB, FIL	Limits the records returned	A variety of filters is available, including functional, positional, source, etc.	get all dbSNP records "all[sb]" or subsets "splice 5 snp"[Filter]
Function Class	FXN, Function_class, FUNC, FUNCTION, FUNCTION_CLASS	Function class	21 function classes are defined	"frameshift"[Function Class]
Gene Name	GENE, GENE_SYMBOL	Entrez Gene symbol	Corresponds to the Official Symbol field in the Entrez Gene resource	MAPK1[GENE]
Gene ID	GENE_ID	Entrez Gene UID	The numeric ID referencing the Entrez Gene ID	5594[GENE_ID]
Global Minor Allele Frequency	GMAF	Minor Allele Frequency derived from global population (i.e., 1000G); can also be study-wide MAF that is not from global population	Most useful when entered as a range, as in the example	(0.0[GMAF] : 0.01[GMAF])
Project or Submitter Handle	HAN, PROJECT	Submitter Handle or Project Name	Submitter lab or project name including 1000Genomes, GnomAD, and DebNick	1000genomes[Submitter Handle] or 1000genomes[PROJECT]
Reference SNP ID	RS, SNPID	Clustered SNP ID (rs)	The numeric ID must be prefixed with "rs". Also retrieves SNPs that have been merged into the specified SNP.	rs328[RS]
SNP Class	SCLS, SNPCLASS	SNP class	Possible values are: "del", "delins", "ins", "mnv", and "snv".	del[SNPCLASS]
Submitter SNP ID	SS, SSNUM	The ID assigned to each report of a SNP at submission time	Must be prefixed with "ss". Note that the query still returns Reference	ss329[SS]

			SNPs rather than Submitter SNPs.	
Validation Status	VALI, VALIDATE, VALIDATION	Validation status	Possible values are: "by cluster" or "by frequency"	"by cluster"[Validation Status]

Complex queries and others

Description	Query	Note
Variant allele with MAF = 0	"00000.0000"[Global Minor Allele Frequency]	variant allele is homozygous and may be due to differences between assembly versions
Pathogenic variants in BRCA1 with MAF < 0.01	"pathogenic"[Clinical Significance] AND BRCA1 AND 00000.0000:00000.00999[GLOBAL_MAF]	set GLOBAL_MAF range between 0 and 0.00999 for MAF < 0.01
Common variant (MAF => 0.01)	00000.0100[GLOBAL_MAF] : 00001.0000[GLOBAL_MAF]	set GLOBAL_MAF range from 0.0100 and 1.0000 for MAF => 0.01
1000Genomes common variant (MAF => 0.01) not found by TOPMED	"1000genomes"[Submitter Handle] NOT "topmed"[Submitter Handle] AND 00000.0100: 00001.0000[GLOBAL_MAF]	set GLOBAL_MAF range from 0.0100 and 1.0000 for MAF => 0.01

HGVS Search

Users can search dbSNP with HGVS names, as shown with the example: NM_000237.3:c.1421C>G OR NG_013007.1:g.7147G>A