

# How to use gene runner

MS.Daneshpour  
(PhD, molecular genetic)



rs1333049



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### [Rs1333049 - SNPedia](#)

[snpedia.com/index.php/Rs1333049](http://snpedia.com/index.php/Rs1333049)

Dec 27, 2012 – **rs1333049** has been reported in a large study to be associated with heart disease, in particular, coronary artery disease. The risk allele ...

### [Single nucleotide polymorphism rs1333049 on chromosome 9p21.3 ...](#)

[www.ncbi.nlm.nih.gov/pubmed/20427016](http://www.ncbi.nlm.nih.gov/pubmed/20427016)

by JT Yu - 2010 - Cited by 5 - Related articles

Clin Chim Acta. 2010 Sep 6;411(17-18):1204-7. doi: 10.1016/j.cca.2010.04.023. Epub 2010 Apr 26. Single nucleotide polymorphism **rs1333049** on ...

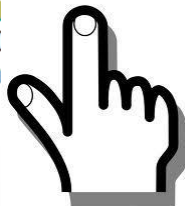
### [Reference SNP\(refSNP\) Cluster Report: rs1333049 \\*\\*Clinical...](#)

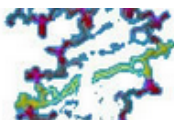
[www.ncbi.nlm.nih.gov/proj](http://www.ncbi.nlm.nih.gov/proj)

The submission ss280150 and was used to instantiate

[.cgi?rs=1333049](#)

... flanking sequence of all cluster members **rs1333049** during BLAST ...





Search for SNP on NCBI Reference Assembly

Search Entrez  for

### Reference SNP(refSNP) Cluster Report: rs1333049

**\*\*Clinical Channel\*\***

RefSNP	Allele	HGVS Names	Links
Organism:human ( <a href="#">Homo sapiens</a> )	<b>Variation Class:</b> SNV: single nucleotide variation	NC_000009.11:g.22125503G>C	
Molecule Type:Genomic		NT_008413.18:g.22115503G>C	
Created/Updated in build:88/137	RefSNP Alleles:C/G		
Map to Genome Build: <a href="#">37.3</a>	Allele Origin:		
<b>Validation Status:</b>	Ancestral Allele:C		
Citation: <a href="#">PubMed</a>	Clinical Channel:Link to <a href="#">VarView</a> pending		
Association: <a href="#">NHGRI GWAS</a> <a href="#">PheGenI</a>	Clinical Significance:NA		
	<b>MAF/MinorAlleleCount:</b> C=0.433/945		
	MAF Source:1000 Genomes		

SNP Details are organized in the following sections:

[GeneView](#) | [Map](#) | [Submission](#) | [Fasta](#) | [Resource](#) | [Diversity](#) | [Validation](#)

**Integrated Maps (Hint: click on 'Chr Pos' or 'Contig Pos' column value to see variation in NCBI sequence viewer)**

Assembly	Genome Build	Chr	Chr Pos	Contig	Contig Pos	SNP to Chr	Contig allele	Contig to Chr	Neighbor SNP	Map Method
GRCh37.p5	37.3	<a href="#">9</a>	<a href="#">22125503</a>	<a href="#">NT_008413.18</a>	<a href="#">22115503</a>	Fwd	G	Fwd	<a href="#">view</a>	remap
reference	36.3	<a href="#">9</a>	<a href="#">22115503</a>	<a href="#">NT_008413.17</a>	<a href="#">22115503</a>	Fwd	G	Fwd	<a href="#">view</a>	blast
Celera	36.3	<a href="#">9</a>	<a href="#">22063860</a>	<a href="#">NW_924062.1</a>	<a href="#">21948379</a>	Fwd	C	Fwd	<a href="#">view</a>	blast
HuRef	36.3	<a href="#">9</a>	<a href="#">22088777</a>	<a href="#">NW_001839149.2</a>	<a href="#">13779444</a>	Fwd	G	Rev	<a href="#">view</a>	blast

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Fasta sequence (Legend)

gnl|dbSNP|rs1333049|allelePos=501|totalLen=1001|taxid=9606|snpclass=1|alleles='C/G'|mol=Genomic|build=137

```
CTCTCAGTCT CTCTCTATGT TTCTCTCTCA CATGTACGTG CATGCACGCA CACGTGTGCA
CACACACATA TGCTCACATC ATTTTAAGAT ACATCTCATT TTTAACCCAA ACCATTTTAT
CTTGCTTGAT AACCAATTTT ATTTGTTAGA TGACTTGGCT ATAAATGCCT TTGGCTATCA
GGAAAATCAA ATCAAAATTA AAAGACACTG TTACTACTGA AGAAGTAAAA AAAGAATGGG
CTGCTGACTC TGAAGATCAT ACCCGAAGTA GAGCTGCAAA GATATTTGGA ATATTGGTAA
TATCCAATAA AGAATGACCT TCAIGCTATT TTGAGGAGAT GTTTAAATGT CGAATTATTG
AAATATTTAT AAAATACAAA TAAACTAACT CTGCTTCATA TTCCAACITG TGTATGACAC
TTCTIAGGCT ATCATTTCAT TCCAAATTTA TGGTCACTAC CCTACTGICA TTCCTCATAc
TAACCATATG ATCAACAGTT
```

```
S
AAAAGCAGCC ACTCGCAGAG GTAAGCAAGA TATATGGTAA ATACTGTGTT GACAAAAGTA
TGCAGAAGCA GTCACATTTA TACAGTAGTG AAGGAAATGT AAATGGGACA AACTTTTTGG
AAGATAAGTT GAGAATGTCA AAAATCAAAA CACACTTTCT GTTTATTICA GCAATTATGA
GCCCTTTGTT TTACAGCTAT GCTCACAAAT ATATACAAAC ATGTATGCAC AATTATGTTC
ACTGTGGTAT TGCGCTAGAA AAATACTAAA AACAAACCAA ATGTTCAICA ATAGGGAAAT
TGTTCAACAA ATTACAGTAT ATCTAAAAAA AGAATAATAT ATAACAACTG AAAAAATAAA
ATAGTTGATA TAAGCAGATA TTCCAAGATC TGCCAGACAT ATTGTTAAAC GAAAAATCTA
GATACAAAAT TGTTTATAGT TCTCTTTCAT ACTATAGCCA AAGAAAATTC AGAAAAAACT
ACTTACAGTT GATCCTTGAA
```



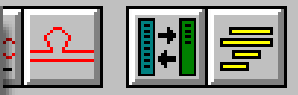


Gene Runner

File Edit View Analysis Tables Graph Options Window Help

- New
  - Open... Ctrl+F12
  - Close Ctrl+F4
  - Save Shift+F12
  - Save As... F12
  - Delete
  - Sort... Alt+F12
  - Protect
  - Unprotect
  - Print Ctrl+Shift+F12
  - Print setup...
  - Exit Alt+F4
- 1 D:\GENERUNR\WORK\NUC4.SEQ
  - 2 D:\GENERUNR\WORK\LAMBDA.SEQ
  - 3 D:\GENERUNR\WORK\NUC2.SEQ
  - 4 D:\GENERUNR\WORK\NUC1.SEQ

- Nucleic acid sequence
- Protein sequence
- Sequence assembly project...
- Multiple Alignment project...

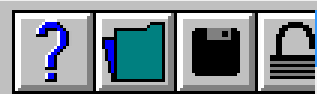












- Nucleic acid ▶
  - Restriction sites... Ctrl+R
  - Protein ▶
    - Fragments... Ctrl+F
  - Contigs ▶
    - Open reading frames... Ctrl+O
  - Alignment ▶
    - Site-directed mutagenesis... Ctrl+B
  - Composition Ctrl+K
    - Sequencing primers & Hybridization probes... Ctrl+S
  - Oligo... Ctrl+L
    - PCR primers... Ctrl+P
  - Clone... Ctrl+N
    - Motif search... Ctrl+J
    - Codon frequency... Ctrl+Q
    - Properties graphs...
    - Melting temperature...

0000 d

1	GNDBSNRSAS	TT				
	CNHUSNYSTS	AA				
101	CACCAAACTG	ATGAATATTT	GCCTTGTATA	ATCTTTTTTGT	AGTTTTTTTTTA	TGAA
	GTGGTTTGAC	TACTTATAAA	CGGAACATAT	TAGAAAAACA	TCAAAAAAAT	ACTT



51  
TAGT  
ATCA

TGAA  
ACTT

**Primer parameters:**

Shortest primers only

Primer length  $\geq$  18

Primer length  $\leq$  22

Primer  $T_m \geq$  40.0

Primer  $T_m \leq$  65.0

Primer  $T_m$  dif  $\leq$  5.0

Primer %GC  $\geq$  35.0

Primer %GC  $\leq$  60.0

3' Nucleotides: S C or G

dG Temp: 25.0

Probe C. [pMol]: 250.0

Salt con (mMol): 50.0

3' end dG  $\geq$  -9.0

3' end dG  $\leq$  -3.0

3' end length: 7

**Search region:**

From base #: 201

To base #: 900

Product must include region:

From: 401 To: 700

**Product:**

Product length  $\geq$  300

Product length  $\leq$  700

Product  $T_m \geq$  68.0

Product  $T_m \leq$  77.5

Product %GC  $\geq$  25.3

Product %GC  $\leq$  45.3

Optimal  $T_m \geq$  45.0

Optimal  $T_m \leq$  75.0

**Discard primers with:**

Hairpin loops stem  $\geq$  3

Hairpin loop dG  $\leq$  -1.0

Dimers with dG  $\leq$  -10.0

Primer-primer complementarity

3' end dimers w/dG  $\leq$  -3.0

Primer-3' end complementarity

Palindromes  $\geq$  8

Base runs  $\geq$  4

Non-unique 3' end

Sense 5' ext: 0

A-Sns 5' ext: 0

RE sequences: NONE

All sense combinations  All antisense combinations

OK

CANCEL

HELP

Primers

Defaults

# 990 primer

d:\generun\work\nuc7.pcr

SORT		ANALYZE			SELECT			SEL ALL			DELETE		FILTERS		OLIGOS	GO TO	CREATE
Prod#	Start	Stop	Length	Prod-GC	Prod-Tm	Tm-Dif	Opt-Tm	Sns-Tm	ASn-Tm	Sns-GC	ASn-GC	S-3'dG	A-3'dG				
1	401	714	314	34.7	72.0	1.8	47.7	42.4	40.6	40.0	35.0	-4.5	-5.6				
	TTCCAACCTTGTGTATGACAC 20 -27.0 -133.4 -349.0 TATATTTGTGAGCATAGCTG 20 -27.5 -142.9 -379.4																
2	400	714	315	34.6	71.9	3.1	47.7	43.7	40.6	38.1	35.0	-4.5	-5.6				
	ATTCCAACTTGTGTATGACAC 21 -28.5 -142.0 -372.9 TATATTTGTGAGCATAGCTG 20 -27.5 -142.9 -379.4																
3	399	714	316	34.5	71.9	3.7	47.6	44.3	40.6	36.4	35.0	-4.5	-5.6				
	TATTCCAACTTGTGTATGACAC 22 -29.4 -148.0 -389.8 TATATTTGTGAGCATAGCTG 20 -27.5 -142.9 -379.4																
4	397	714	318	34.6	72.0	3.4	47.7	44.0	40.6	36.4	35.0	-3.5	-5.6				
	CATATTCCAACTTGTGTATGAC 22 -29.6 -150.1 -396.4 TATATTTGTGAGCATAGCTG 20 -27.5 -142.9 -379.4																
5	393	714	322	34.8	72.1	4.1	47.7	44.7	40.6	40.0	35.0	-4.9	-5.6				
	GCTTCATATTCCAACTTGTG 20 -29.3 -144.7 -379.6 TATATTTGTGAGCATAGCTG 20 -27.5 -142.9 -379.4																
6	392	714	323	34.7	72.0	2.5	47.7	43.2	40.6	36.8	35.0	-5.5	-5.6				
	TGCTTCATATTCCAACTTG 19 -28.0 -138.2 -362.3 TATATTTGTGAGCATAGCTG 20 -27.5 -142.9 -379.4																
7	391	714	324	34.9	72.1	4.3	47.8	45.0	40.6	40.0	35.0	-5.5	-5.6				
	CTGCTTCATATTCCAACTTG 20 -29.6 -146.0 -383.1 TATATTTGTGAGCATAGCTG 20 -27.5 -142.9 -379.4																
8	389	714	326	35.0	72.2	1.0	47.8	41.6	40.6	42.1	35.0	-6.7	-5.6				
	CTCTGCTTCATATTCCAAC 19 -27.4 -136.7 -359.7 TATATTTGTGAGCATAGCTG 20 -27.5 -142.9 -379.4																
9	388	714	327	34.9	72.1	2.6	47.8	43.2	40.6	40.0	35.0	-6.7	-5.6				
	ACTCTGCTTCATATTCCAAC 20 -28.7 -143.2 -377.0 TATATTTGTGAGCATAGCTG 20 -27.5 -142.9 -379.4																
10	387	714	328	34.8	72.1	4.8	47.8	45.4	40.6	38.1	35.0	-6.7	-5.6				
	AACTCTGCTTCATATTCCAAC 21 -30.6 -152.3 -401.0 TATATTTGTGAGCATAGCTG 20 -27.5 -142.9 -379.4																
11	401	747	347	34.6	72.1	0.9	48.3	42.4	43.2	40.0	40.0	-4.5	-6.6				
	TTCCAACCTTGTGTATGACAC 20 -27.0 -133.4 -349.0 CACAGTGAACATAATTGTGC 20 -27.5 -135.8 -355.1																
12	400	747	348	34.5	72.1	0.4	48.5	43.7	43.2	38.1	40.0	-4.5	-6.6				



**Primer parameters:**

Shortest primers only

Primer length  $\geq$

Primer length  $\leq$

Primer  $T_m \geq$   48

Primer  $T_m \leq$   62

Primer  $T_m$  dif  $\leq$   2.0

Primer %GC  $\geq$

Primer %GC  $\leq$

3' Nucleotides:

dG Temp:

Probe C. [pMol]:

Salt con (mMol):

3' end dG  $\geq$   -7.0

3' end dG  $\leq$   -5.0

3' end length:

**Search region:**

From base #:

To base #:

**Product:**

Product length  $\geq$

Product length  $\leq$   400

Product  $T_m \geq$

Product  $T_m \leq$

Product %GC  $\geq$

Product %GC  $\leq$

Optimal  $T_m \geq$

Optimal  $T_m \leq$

Sense 5' ext:

A-Sns 5' ext:

RE sequences:

All sense combinations

All antisense combinations

Product must include region:

From:  To:

**Discard primers with:**

Hairpin loops stem  $\geq$

Hairpin loop dG  $\leq$

Dimers with dG  $\leq$

Primer-primer complementarity

3' end dimers w/dG  $\leq$

Primer-3' end complementarity

Palindromes  $\geq$

Base runs  $\geq$

Non-unique 3' end

Prod#	Start	Stop	Length	Prod-GC	Prod-Tm	Tm-Dif	Opt-Tm	Sns-Tm	ASn-Tm	Sns-GC	ASn-GC	S-3'dG	A-3'dG
1	389	749	361	34.9	72.3	0.5	50.4	48.7	49.2	40.9	40.9	-5.5	-6.6
CTCTGCTTCATATTCCAACCTG 22 -32.8 -159.4 -417.4 ACCACAGTGAACATAATTGTGC 22 -31.9 -153.3 -399.0													
2	389	762	374	35.0	72.5	0.4	50.3	48.7	48.4	40.9	45.0	-5.5	-6.1
CTCTGCTTCATATTCCAACCTG 22 -32.8 -159.4 -417.4 TTTCTAGCGCAATACCCACAG 20 -31.6 -152.4 -397.5													

**Oligo Analysis** [X]

Oligo: CTCTGCTTCATATTCCAACCTG

Mol Wt:	6691.4	<Sense oligo>	Strand	Molecule
Tm:	48.7	From: 389	<input checked="" type="radio"/> Top	<input checked="" type="radio"/> DNA
Filter Tm:	41.1	Len: 22	<input type="radio"/> Comp	<input type="radio"/> RNA
%GC Tm:	46.0	<input type="button" value="Edit antisense"/> <input checked="" type="button" value="Switch oligos"/>		
GC+AT Tm:	62.0	Free energy (dG) Temp:	25.0	
nMol/A260:	5.1	Probe con (pico Mol):	250.00	
ug/A260:	34.5	Salt con (milli Mol):	50.00	
%GC:	40.9	% Formamide:	0.0	
dG:	-32.8	3'-end len: 7	Base run >=	4
dH:	-159.4	Pal len >= 8	Stem len >=	3
dS:	-417.4	Base runs / Palindromes:		
3'-end dG:	-5.5			

0 of 0 << >> - Sort Tm: dG:

Hairpin loops  Dimers  Bulge loops  Internal loops

OK CANCEL HELP Print Defaults

# window

GGGGGGGGTGTACACCCCCCATT

1 of 2 << >> Other Sort Tm: 44.5 dG: -23.6

Hairpin loops  Dimers  Bulge loops  Internal loops

```
5' GGGGGGGTGTACACCCCCCATT 3'
      | | | | |           | | | | |
3' TTTACCCCCACATGTGGGGGGG 5'
STACK AT 1 IS 19 BP LONG.
```