

**Когда известно название  
гена**

Search:  for

e.g. Carboxy\* or chx28

### Favourite genomes

 <b>Arabidopsis thaliana</b> TAIR10	 <b>Oryza sativa Japonica</b> IRGSP-1.0
 <b>Triticum aestivum</b> TGACv1	 <b>Hordeum vulgare</b> ASM32608v1
 <b>Zea mays</b> AGPv4	 <b>Physcomitrella patens</b> ASM242v1

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### All genomes

-- Select a species --

[View full list of all Ensembl Plants species](#)

### What's New in Release 35

- Updated genomes

## New Bread Wheat Genome Assembly

A new genome assembly of *Triticum aestivum* cv. Chinese Spring is now available in Ensembl Plants. The assembly (TGACv1) and it's accompanying annotation was produced by the [Earlham Institute](#), formerly The Centre for Genome Analysis (TGAC), as part of the [Triticeae Genomics for Sustainable Agriculture](#) project.

The assembly has a scaffold N50 of 88 Kbp and a total length of 13.4 Gbp in contigs greater than 500 bp ([read more](#)). The gene model annotation consists of 217,907 loci and 273,739 transcripts. A total of 104,049 protein coding genes (154,798 transcripts) and 10,156 long ncRNAs have been annotated with high confidence ([read more](#)). Approximately 99,000 genes (99% of the total) annotated on the previous IWGSC CSS assembly (MIPS) have been mapped to the new assembly.

The Axiom 35k and 820k SNP marker sets have been provided by [CerealsDB](#) and located on the new assembly ([read more](#)).

## Ensembl Plants Archive Site

Alongside release 32 we have launched a new [archive site](#), where we will keep selected previous releases of Ensembl Plants publicly available. The first release available on the archive site is release 31, and includes the previous assemblies for wheat and maize.

Ensembl Plants is developed in coordination with other plant genomics and bioinformatics groups via the EBI's role in the [transPLANT](#) consortium. The transPLANT project is funded by the [European Commission](#) within its [7th Framework Programme](#), under the thematic area "Infrastructures", contract number [283496](#).



## Search results for 'VIT\_01s0011g00960'

Showing 1 Gene found in Ensembl Plants

### VIT\_01s0011g00960

Description	Putative uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:F6HEY8]
Gene ID	<a href="#">VIT_01s0011g00960</a>
Species	<a href="#">Vitis vinifera</a>
Location	<a href="#">1:812008-816090</a>
Gene trees	<a href="#">EPIGT00820000103231</a> (Plant Compara) <a href="#">EGGT001300000085269</a> (Pan-taxonomic Compara)

Ensembl Plants release 35 - April 2017 © [EMBL-EBI](#)

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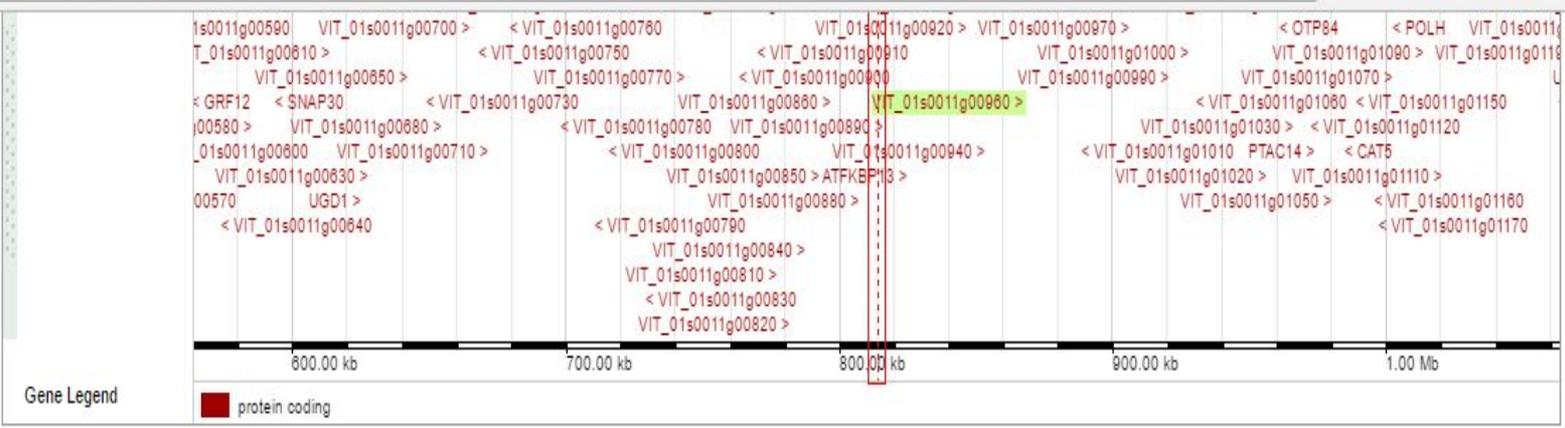
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Ensembl Plants is produced in collaboration with Gramene



Location:   Gene:

Navigation controls: left, right, zoom in (+), zoom out (-), reset (↔)

Drag/Select: ↔

812kb 813kb 814kb 815kb 816kb

Forward strand

Genes

VIT\_01s0011g00960.t01 > protein coding

Contigs

< FN595752.1

Region: 1:811959-814575

Mark region (2617 bp)

Variant - All sources

%GC

No Sequence variants (all sources)

Jump to region (2617 bp)

Reverse strand

Gene Legend

■ protein coding

There are currently 46 tracks turned off.

Ensembl Plants Vitis vinifera version 88.3 (IGGP\_12x) Chromosome 1: 811,192 - 816,906

Configure this page

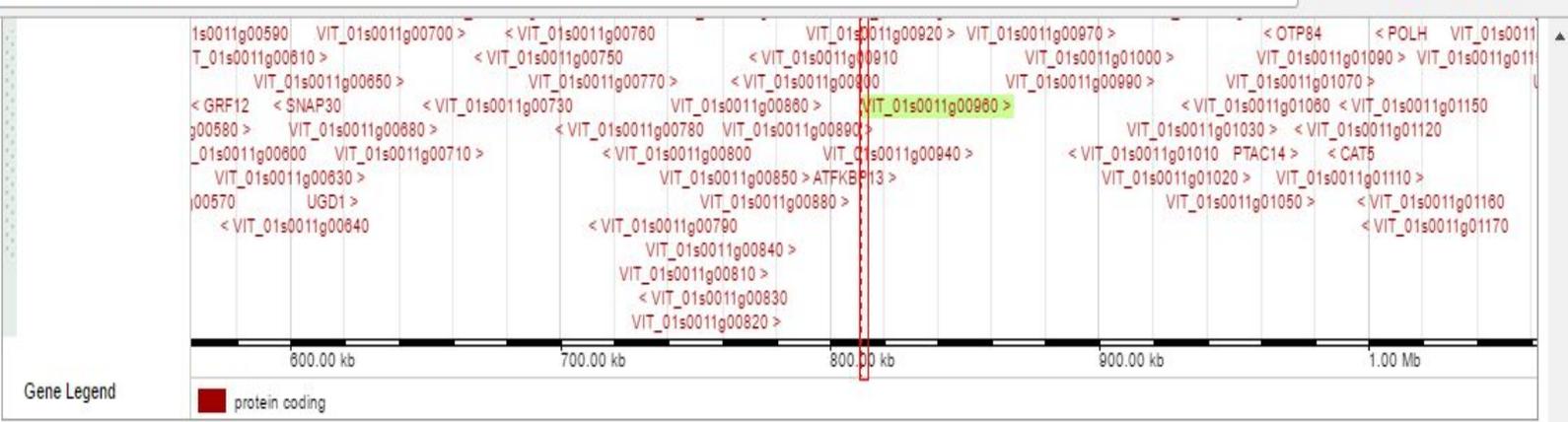
Custom tracks

Export data

Share this page

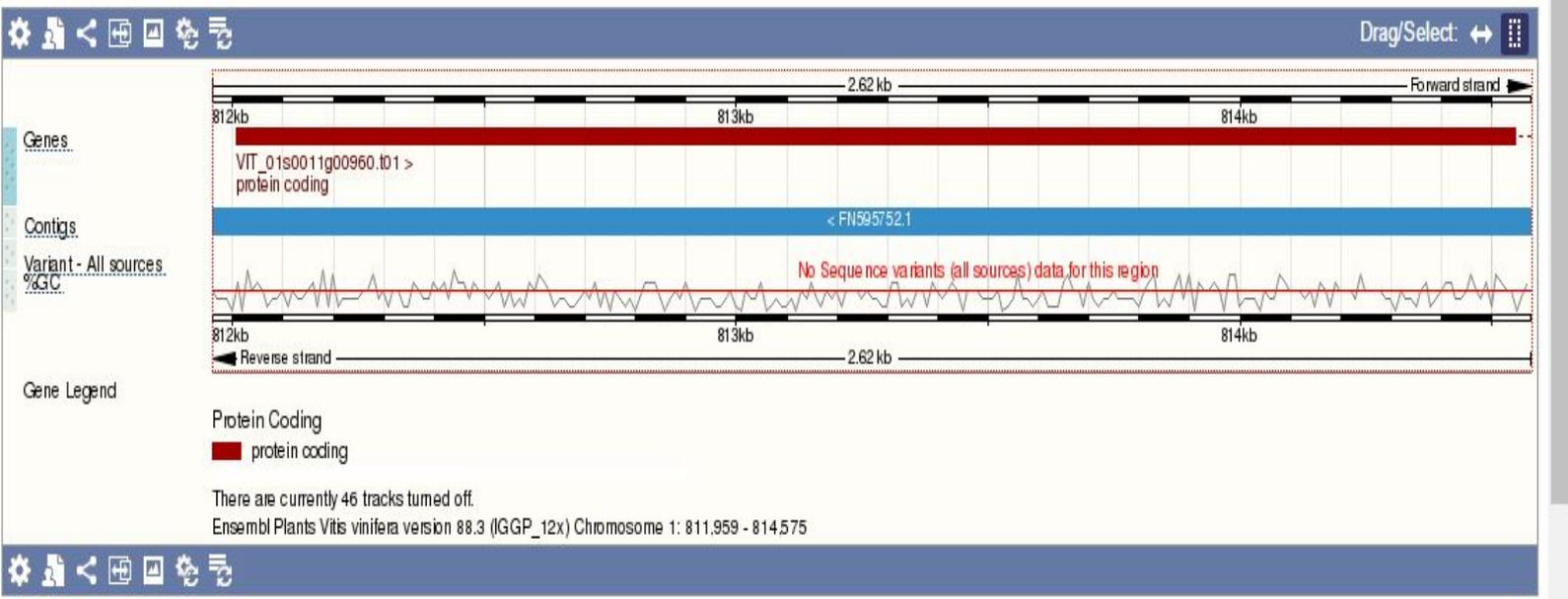
Bookmark this page

Ensembl Plants is produced in collaboration with Gramene



Location:   Gene:

Navigation controls: back, forward, zoom in, zoom out, home, end



Configure this page

Custom tracks

Export

Share

Bookmarks

Ensembl collaborator

VIT_01s0011g00590	VIT_01s0011g00700	VIT_01s0011g00780	VIT_01s0011g00820	VIT_01s0011g00970	VIT_01s0011g01000	VIT_01s0011g01090	VIT_01s0011g01100
T_01s0011g00810	VIT_01s0011g00850	VIT_01s0011g00750	VIT_01s0011g00770	VIT_01s0011g00910	VIT_01s0011g00990	VIT_01s0011g01070	VIT_01s0011g01170

Export data

Export Configuration - Feature List

Location to export: chromosome:IGGP\_12x:1:811959:814575:1

Output: FASTA sequence \*

Select location: 1 \* 811959 \* 814575 \* 1

5' Flanking sequence (upstream): 0 \* (Maximum of 1000000)

3' Flanking sequence (downstream): 0 \* (Maximum of 1000000)

**Next >**

Fields marked \* are required

Options for FASTA sequence

Genomic: Unmasked \*

Fields marked \* are required

TGAGGATGTTCTTGACCTGTTGAGGCTCGATCAAGAA  
 GCGTCACTCCATCAACAACCTGATACAGGATATTGAC  
 GACAAAGGAGAGGATCGCAGCATGGCCCTCCTATTCA  
 CCTTCATGTGAGAATGGCTCCTTTGTTCAATTGGTAAT  
 GCCTACAATAAGCTGGTTCTTGGGCCTGGAACCG  
 CGTGGTGGGGATGGCTGGACTGGGGAAGACAACCTCT  
 GAAGCAGAACCTTGATTGCCATGTCTGGACCACAGCC  
 TATCTTATGGACCTTGTAGTAGAGGAATTGGCTGT  
 GGTGCTCTGACGCATAAGCTGCGAAAAATTTCAAC  
 TGATGACTTATGGGTAAGATGTGGGAGTCCATT  
 GGACAGTAGAATAATTACTACAAGGAGAGGCGAT  
 TGATTCTATTGATATCCACAAGCTTCAGCCACTGTCA  
 CTATAAGAAAGCTTTCTAAGAAATGGCAGATGCTCT  
 ATCCATTTACAGAAATGTGATGGATTACCACTTGGG  
 GTCCATTAAGGCTCAACTAAAAATGAGTGGAAAAAT  
 ATTGAGAAGCAGTGGTGAAGCTTTCAAATATTTGAAAG  
 TTTACCTTACCATCTCAAGTATTGTTCTTGTACATG  
 AGTTAAGCGAAGAGACTTATTCGGCTATGGATAGCT  
 AGGCAAAACGCTTGAAGAGGTTGGGGAAGAGTACCTG  
 GATAAAGGCAATGAAATGGATTTGATGGAAGGCCG  
 CATGTTGAAGATGATTCTCTCAGTCTCACATGAGGAG  
 GGCAGTAAGAAAGTTGACTGAGAATACCCGCCCTAT  
 TGTGCTCAGGACTTACCCTGTGTTGCAACCTTCTCA  
 GATTGGTTCCAATTTCAAACCTATTGAAGGCTTGGAC  
 ATTTCCGAGTGAATTACAGATCTTCTGCTCTGAGG  
 TATAAGGAGAAATCCCTCGTCCCTCGGTGACCTTCA  
 GCAGACTCTGGTAACAAAGGTACCTAAAGAAGTCTAG  
 GCTGGTTTATCGCTACAATATGGAAAGTGTCTTACCT  
 GGCACCAAGAGGATGGGCGCATTGAAGAACCACAAA  
 TGGGACGACAGAAATGAGTCGGCAGCACAGTATGATC  
 GTTGAGGAAGCTGGGCATTGTAGAAGTGGCAAAAGAA  
 AATTGTGAAGATGCGAAATCTCATTCTTGAATGTG  
 TCTAGAGCTTGATGCAATGACCAATCCGCGCCCTT  
 GCCTTTGAAAGGTTTCAAAGTGGGTATCTTCTAG  
 AAAATGGTCTTCACTCGCAGAAGACCGATTGCAAGCT  
 GGAGCTGCAGCTGCTTATGCATACACTGGAACCCAGT  
 TCAGAAGCTTAAAGATATTAGACCTCAGCAATTGGAAG  
 AGAAGGCACATTGCTTGCCTACAAGGCTGATCATAAGCCACTGTAGCAAGCTGGTGCA  
 GGTCCCTACAGGATTGACAAGCTCATTACCTCCAAATGCTGCTGCTGCACGATATGCC  
 CGAACCATTTGTGATCAGGCTGAGGAAAAATGGCGGTGATTGCGCCGTTTGGTTCACCA  
 CATTCCGTGATTCAATCATATAATCAGGGCCAGTTG

PrimersDesign — Блокнот

Файл Правка Формат Вид Справка

```
>1 dna:chromosome chromosome:IGGP_12x:1:811959:814575:1
AC TTGAGGCTTT CGCAAGTAGAGAATGGAATTTGCAGGAAAAATCAAAATGGCAGTCCA
AAATTTAGGACGCGAGCTGCGGAGCATTGAAGCCCTACTGAGAGATGCTGCTTCAAAGAA
AGAGCATGATCACC AATTCACAGTCTGGATTCAAAATGTCCGTGATCAAGCTTATGCCAT
TGAGGATGTTCTTGACCTGTTGAGGCTCGATCAAGAATCAGTGTGGCGCCGCTTGAAAAAT
GCGTCACTCCATCAACAACCTGATACAGGATATTGACTGGAGTCTCAAATAATTCAGCG
GACAAAGGAGAGGATCGCAGCATGGCCCTCCTATTCAACCAATGCTGGCAACAACACATA
CCTTCATGTGAGAATGGCTCCTTTGTTCAATTGGTAAATGTTGATACCGTGGGCATTGAGGA
GCCACAATAAGCTGGTTTCTTGGGCCTTGAACCGAAACAGAGGCTTGAGGTGATGTT
CGTGGTGGGGATGGCTGGACTGGGGAAGACAACCTTGTCCACAGCGTGTATGAGAGGGT
GAAGCAGAACCTTGATTGCCATGTCTGGACCACAGCCTCAAAGTCCAAAACCAAACCTCGA
TATCTTATGGACCTTGTAGTAGAGGAATGGGCTGTACAATCACACAGGGGGCCGATGT
GGTTGCTCTGACGCATAAGCTGCGAAAAATTTCTCAAACAACAAACGGTATGTCATAGTCT
TGATGACTTATGGGTAAGATGTGGGAGTCCATTAGACTAGCCTTGCCAAATGGTAA
GGACAGTAGAATAATTACTACAAGGAGAGGCGATATAGCTAATTC TTGTAGAGATGA
TGATTCTATTGATATCCACAAGCTTCAGCCACTGTCACCGCAAAGGGCTGAGCAACTCTT
CTATAAGAAAGCTTTCTAAGAAATGGCAGATGCTCCTCAGGTTTGGAGGAAGTCTCCAA
ATCCATTTTACAGAAATGTGATGGATTACCACTTGGGATTATTGAAATCGGTAGACTTTT
GTCCATTAAGGCTCAACTAAAAATGAGTGGAAAAATATTACATGATAGCCTTGAGTCTGA
ATTGAGAAGCAGTGGTGAAGCTTTCAAATATTGAAAGTGTGCTGCAAGTTACAATGA
TTTACCTTACCATCTCAAGTATTGTTCTTGTACATGAGCATCTTCTGAGAGCAACCC
AGTTAAGCGAAGAGACTTATTCGGCTATGGATAGCTGAAGGTTTGTGATAGAGAAAAAG
AGGCAAAACGCTTGAAGAGGTTGGGGAAGAGTACCTGAATGAGCTGATTGACAGGAATCT
GATAAAGGCAATGAAATGGATTTTGTGGAAGGCCGACAAGTGTGGGAGTTCATAGTCT
CATGTTGAAGATGATTCTCTCAGTCTCACATGAGGAGAACTTTTGTACTGTCCGTACAGG
GGCAGTAAGAAAGTTGACTGAGAATACCCGCCCTATCTATCCAGAAGGAAGATTTTGA
TG TGTCTCAGGACTTACCCTGTGTTGCAACCTTCTCAGTTTCTCAGTATGCGATAGGCAAAGTAAAG
```

# Primer3 (v. 0.4.0) Pick primers from a DNA sequence.

[Checks for mispriming in template.](#)

[disclaimer](#)

[Primer3 Home](#)

[Primer3plus interface](#)

[cautions](#)

[FAQ/WIKI](#)

There is a newer version of Primer3 available at <http://primer3.ut.ee>

Paste source sequence below (5' to 3', string of ACGTNacgtn -- other letters treated as N -- numbers and blanks ignored). FASTA format ok. Please N-out undesirable sequence (vector, ALUs, LINEs, etc.) or use a [Mispriming Library \(repeat library\)](#):

```
ACTTGAGGCTTTCGCAAGTAGAGAATGGAATTTGCAGGAAAATATCAAAATGGCAGTCCA
AAATTTAGGACGCGAGCTGCGGAGCATTGAAGCCCTACTGAGAGATGCTGCTTCAAAGAA
AGAGCATGATCACCAATTCACAGTCTGGATTCAAAATGTCCGTGATCAAGCTTATGCCAT
TGAGGATGTTCTTGACCTGTTGAGGCTCGATCAAGAATCAGTGTGGCGCCGCTTGAAAAT
GCGTCACTCCATCAACAACCTTGATACAGGATATTGACTGGAGTCTCCAAAATATTCAGCG
GACAAAGGAGAGGTATCGCAGCATGGCTCCTATTCAACCAATGCTGGCAACAACACATA
```

<input checked="" type="checkbox"/> Pick left primer, or use left primer below:	<input type="checkbox"/> Pick hybridization probe (internal oligo), or use oligo below:	<input checked="" type="checkbox"/> Pick right primer, or use right primer below (5' to 3' on opposite strand):
<input type="text"/>	<input type="text"/>	<input type="text"/>

Sequence Id:  A string to identify your output.

Targets:  E.g. 50,2 requires primers to surround the 2 bases at positions 50 and 51. Or mark the [source sequence](#) with [ and ]: e.g. ...ATCT[CCCC]TCAT.. means that primers must flank the central CCCC.

Excluded Regions:  E.g. 401,7 68,3 forbids selection of primers in the 7 bases starting at 401 and the 3 bases at 68. Or mark the [source sequence](#) with < and >: e.g. ...ATCT<CCCC>TCAT.. forbids primers in the central CCCC.

Product Size Ranges

Number To Return  Max 3' Stability

Max Repeat Mispriming  Pair Max Repeat Mispriming

Max Template Mispriming  Pair Max Template Mispriming

2521 CGAACCATTTGTGATCAGGCTGAGGAAAAATGGCGGTCGATTGCGCCGTTTGGTTCACCA

2581 CATTCCGTGATTTCATCATATAATCAGGGCCAGTTG

KEYS (in order of precedence):

>>>> left primer
<<<<< right primer

ADDITIONAL OLIGOS

	start	len	tm	gc%	any	3' seq
1 LEFT PRIMER	304	20	59.98	50.00	3.00	1.00 AAAGGAGAGGTATCGCAGCA
RIGHT PRIMER	2344	20	60.04	45.00	7.00	1.00 CTGAAATTTTCCCGACCTGA
PRODUCT SIZE: 2041, PAIR ANY COMPL: 4.00, PAIR 3' COMPL: 1.00						
2 LEFT PRIMER	304	20	59.98	50.00	3.00	1.00 AAAGGAGAGGTATCGCAGCA
RIGHT PRIMER	2345	20	60.04	45.00	7.00	1.00 TCTGAAATTTTCCCGACCTG
PRODUCT SIZE: 2042, PAIR ANY COMPL: 4.00, PAIR 3' COMPL: 2.00						
3 LEFT PRIMER	374	20	59.93	45.00	3.00	2.00 ATGGCTCCTTTGTTTCATTGG
RIGHT PRIMER	2383	20	59.99	45.00	6.00	1.00 CAGCTGTCCAATTGCTGAA
PRODUCT SIZE: 2010, PAIR ANY COMPL: 5.00, PAIR 3' COMPL: 3.00						
4 LEFT PRIMER	396	20	60.08	45.00	3.00	1.00 ATGTTGATACCGTGGGCATT
RIGHT PRIMER	2383	20	59.99	45.00	6.00	1.00 CAGCTGTCCAATTGCTGAA
PRODUCT SIZE: 1988, PAIR ANY COMPL: 3.00, PAIR 3' COMPL: 2.00						

Statistics

	con	too	in	in	no	tm	tm	high	high	high	high		
	sid	many	tar	excl	bad	GC	too	too	any	3'	poly	end	
	ered	Ns	get	reg	GC%	clamp	low	high	compl	compl	X	stab	ok
Left	6394	0	0	0	0	0	1828	2695	0	1	0	105	1765
Right	6294	0	0	0	2	0	1825	2762	0	2	0	114	1589

Pair Stats:
considered 52, unacceptable product size 44, ok 8
primer3 release 1.1.4

**Oligo Calc: Oligonucleotide Properties**

Enter Oligonucleotide Sequence: AAA GGA GAG GTA TCG CAG CA  
*OD calculations are for single-stranded DNA*

**Nucleotide base codes**  
 AAA GGA GAG GTA TCG CAG CA

**Reverse Complement Strand (5' to 3') is:**  
 TGC TGC GAT ACC TCT CCT TT

5' modification (if any):   
 3' modification (if any):

50 nM Primer  
 50 mM Salt (Na<sup>+</sup>)  
 1 Measured Absorbance

**Calculate** **Swap Strands** **BLAST**

---

**Physical Constants**

Length:  20 Molecular Weight:  6224.14 GC content:  50%  
 1 ml of a sol'n with an Absorbance of  1 at 260 nm  
 is  4.105 microMolar and contains  25.5 micrograms.

**Melting Temperature (T<sub>M</sub>) Calculations**

1	51.8 °C (Basic)
2	58.4 °C (Salt Adjusted)
3	54.28 °C (Nearest Neighbor)

**Thermodynamic Constants Conditions: 1 M NaCl at 25°C at pH 7.**

RlnK	<input type="text"/> 33.404 cal/(°K*mol)	deltaH	<input type="text"/> 161.4 Kcal/mol
deltaG	<input type="text"/> 26.2 Kcal/mol	deltaS	<input type="text"/> 419.6 cal/(°K*mol)

**Deprecated Hairpin/self dimerization calculations**

5 (Minimum base pairs required for single primer self-dimerization)  
 4 (Minimum base pairs required for a hairpin)

**Check Self-Complementarity**

---

Citation: Kibbe WA. 'OligoCalc: an online oligonucleotide properties calculator'. (2007)  
*Nucleic Acids Res.* **35**(webserver issue): May 25. ([Abstract/Full text](#))

**Oligo Self Complementarity Check - Google Chrome**

about:blank

Minimum base pairs required for single primer self-dimerization: 5.  
 Minimum base pairs required for a hairpin: 4.

**Potential hairpin formation :**

None !

3' Complementarity:  
 None !

All potential self-annealing sites are marked in red (allowing 1 mis-match):  
 None !

Со всеми обратным праймерами проблемы, поэтому нужно подобрать другие им на замену.



2521 CGAACCATTGTGATCAGGCTGAGGAAAAATGGCGGTGATTGCGCCGTTTGGTTCACCA

2581 CATTCCGTGTATTCATTATATAATCAGGGCCAGTTG

KEYS (in order of precedence):

>>>>> left primer  
<<<<<< right primer

ADDITIONAL OLIGOS

	start	len	tm	gc%	any	3'	seq
1 LEFT PRIMER	81	20	59.84	55.00	3.00	1.00	GGAGCATTGAAGCCCTACTG
RIGHT PRIMER	2414	20	60.08	45.00	4.00	1.00	GCAATGTGCCTTCTCCATT
PRODUCT SIZE: 2334, PAIR ANY COMPL: 5.00, PAIR 3' COMPL: 2.00							
2 LEFT PRIMER	146	20	59.90	40.00	4.00	2.00	TGGATTCAAAATGTCCGTGA
RIGHT PRIMER	2505	20	59.70	45.00	3.00	2.00	AGCAGCATTGGAGGTGAAT
PRODUCT SIZE: 2360, PAIR ANY COMPL: 6.00, PAIR 3' COMPL: 1.00							
3 LEFT PRIMER	81	20	59.84	55.00	3.00	1.00	GGAGCATTGAAGCCCTACTG
RIGHT PRIMER	2426	20	59.73	45.00	3.00	2.00	TTTGTAGGCAAGGCAATGTG
PRODUCT SIZE: 2346, PAIR ANY COMPL: 5.00, PAIR 3' COMPL: 1.00							
4 LEFT PRIMER	146	20	59.90	40.00	4.00	2.00	TGGATTCAAAATGTCCGTGA
RIGHT PRIMER	2532	20	59.65	45.00	4.00	2.00	ACAAATGGTTCGGGCATATC
PRODUCT SIZE: 2387, PAIR ANY COMPL: 5.00, PAIR 3' COMPL: 2.00							

Statistics

	con	too	in	in	no	tm	tm	high	high	high			
	sid	many	tar	excl	bad	GC	too	too	any	3'	poly	end	
	ered	Ns	get	reg	GC%	clamp	low	high	compl	compl	X	stab	ok
Left	2886	0	0	0	0	0	821	1190	1	4	0	39	831
Right	2839	0	0	0	2	0	795	1277	0	2	0	45	718

Pair Stats:

considered 329, unacceptable product size 304, high end compl 6, ok 19  
primer3 release 1.1.4

Chromosome 1: 811,959 x plants.ensembl.org/Vitis x primer3 - Поиск в Google x Primer3 Input (version 0. x OligoCalc: Oligonucleotide x

← → ↻ ⤴ ⤵ ⓘ biotools.nubic.northwestern.edu/OligoCalc.html

### Oligo Calc: Oligonucleotide

Enter Oligonucleotide  
OD calculations are for single

Nucleotide base codes  
AGC AGC ATT TGG AGG TGA AT

**Reverse Complement Strand(5' to 3') is:**  
ATT CAC CTC CAA ATG CTG CT

5' modification (if any) 3' modification (if any)

50 nM Primer 1 Measure  
50 mM Salt (Na<sup>+</sup>)

**Calculate** **Swap Strands** **BLAS**

#### Physical Constants

Length: 20 Molecular Weight: 6221.14 GC con  
1 ml of a sol'n with an Absorbance of 1 at 260 nm  
is 4.322 microMolar and contains 26.9 micrograms.

#### Thermodynamic Constants Conditions: 1 M NaCl at 25°C at pH 7.

RlnK 33.404 cal/(°K\*mol) deltaH 157.6 Kcal/mol  
deltaG 25 Kcal/mol deltaS 411.4 cal/(°K\*mol)

#### Depreciated Hairpin/self dimerization calculations

5 (Minimum base pairs required for single primer self-dimerization)  
4 (Minimum base pairs required for a hairpin)

**Check Self-Complementarity**

Citation: Kibbe WA. 'OligoCalc: an online oligonucleotide properties calculator'. (2007) *Nucleic Acids Res.* 35(webserver issue): May 25. ([Abstract/Full text](#))

### Oligo Self Complementarity Check - Google Chrome

about:blank

Minimum base pairs required for single primer self-dimerization: 5.  
Minimum base pairs required for a hairpin: 4.

**Potential hairpin formation :**

None !

3' Complementarity:

None !

All potential self-annealing sites are marked in red (allowing 1 mis-match):

None !

- Остальные два праймера тоже хорошо подходят, но тут нужно выбирать в зависимости от цели, какой длины ПЦР продукт нужен.

# Primer-BLAST *A tool for finding specific primers*

NCBI/Primer-BLAST: Finding primers specific to your PCR template (using Primer3 and BLAST).

## PCR Template

[Reset page](#) [Save search parameters](#) [Retrieve recent results](#) [Publication](#) [Tips for finding specific primers](#)

Enter accession, gi, or FASTA sequence (A refseq record is preferred) [Clear](#)

```
ACTTGAGGCTTTGCAAGTAGAGAAATGGAATTTGCAGGAAAAATCAAAATGGCAGTCCA
AAATTTAGGACGCGAGCTGCGGAGCATTGAAGCCCTACTGAGAGATGCTGCTTCAAAGAA
AGAGCATGATACCAATTACAGTCTGGATTCAAATGTCGGTGATCAAGCTTATGCCAT
TGAGGATGTTCTTGACCTGTTCAAGGCTCGATCAAGAATCAGTGTGGCGCCGTTGAAAAAT
GCGTCACTCCATCAACAACCTTGATACAGGATATTGACTGGAGTCTCCAAAATATTCAGCG
```

Range

	From	To	
Forward primer	<input type="text"/>	<input type="text"/>	<a href="#">Clear</a>
Reverse primer	<input type="text"/>	<input type="text"/>	

Or, upload FASTA file

Файл не выбран

## Primer Parameters

Use my own forward primer (5'→3' on plus strand)

[Clear](#)

Use my own reverse primer (5'→3' on minus strand)

[Clear](#)

PCR product size

Min	Max
<input type="text" value="70"/>	<input type="text" value="1000"/>

# of primers to return

Primer melting temperatures (T<sub>m</sub>)

Min	Opt	Max	Max T <sub>m</sub> difference
<input type="text" value="57.0"/>	<input type="text" value="60.0"/>	<input type="text" value="63.0"/>	<input type="text" value="3"/> <a href="#">Clear</a>

## Exon/intron selection

A refseq mRNA sequence as PCR template input is required for options in the section [Clear](#)

Exon junction span

[Clear](#)

Exon junction match

Exon at 5' side    Exon at 3' side

Minimal number of bases that must anneal to exons at the 5' or 3' side of the junction [Clear](#)

Intron inclusion

Primer pair must be separated by at least one intron on the corresponding genomic DNA [Clear](#)

Intron length range

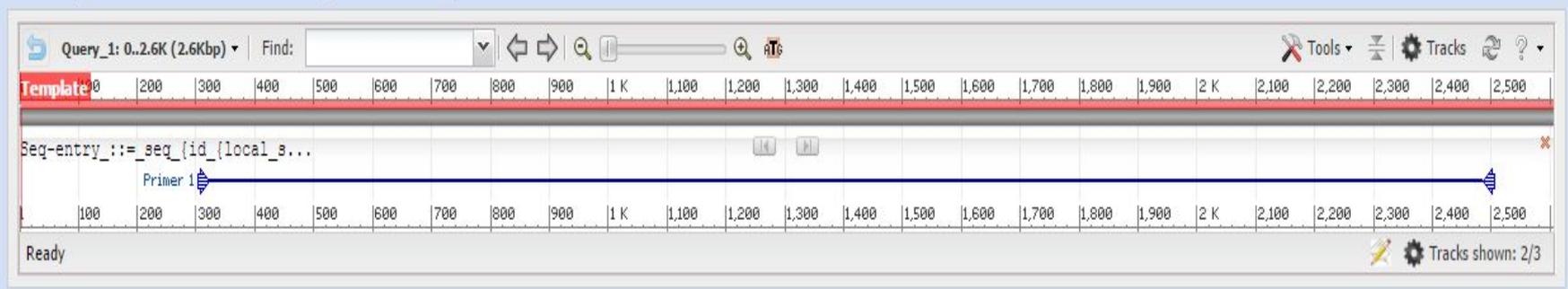
Min	Max
<input type="text" value="1000"/>	<input type="text" value="1000000"/> <a href="#">Clear</a>

NCBI/Primer-BLAST : results: Job id=GhDFARnbFHMzTQ5IAyqgenkzO0hUICBVVQ [more...](#)

Input PCR template  
 Range  
 Specificity of primers  
 Other reports

1 - 2617  
 primers may **not** be specific to the input PCR template as targets were found in selected database:Refseq mRNA (Organism limited to Homo sapiens)...[help on specific primers](#)  
[Search Summary](#)

## Graphical view of primer pairs



## Detailed primer reports

### Primer pair 1

	Sequence (5'→3')	Template strand	Length	Start	Stop	Tm	GC%	Self complementarity	Self 3' complementarity
Forward primer	AAAGGAGAGGTATCGCAGCA	Plus	20	304	323	58.80	50.00	3.00	1.00
Reverse primer	AGCAGCATTTGGAGGTGAAT	Minus	20	2505	2486	57.77	45.00	3.00	2.00
Product length	2202								

### Products on potentially unintended templates

>[XM\\_017024298.1](#) PREDICTED: Homo sapiens dishevelled segment polarity protein 2 (DVL2), transcript variant X5, mRNA

product length = 136  
 Forward primer 1 AAAGGAGAGGTATCGCAGCA 20  
 Template 707 TG.....G...C..... 688

# Когда есть «неизвестная» последовательность ДНК

На примере гена NBS-LRR гена детекции патогенов у люцерны (давайте сделаем вид, что сиквенс действительно случайный)

BLAST/BLAT

- Web Tools
  - Web Tools
  - BLAST
  - Variant Effect Predictor
  - Assembly Converter
  - ID History Converter

Configure this page

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Export data

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Bookmark this page

Ensembl Plants is produced in collaboration with Gramene

### BLAST search

Sequence data:

Search against:

Search tool:

Search Sensitivity:

```
>
TTTCAAATGGGTGGATTGCCTTCCAACCTGGCCGACCTTTATATAGAGAATTGCCCAAAA
CTGATTCGCTTCRAGAAGGAGTGGGGTTTGTTCCAACTCAATTCCTTGAAGTCATTCTTC
ATCAGTAATGAGTTTGAAAACGTGGAGTCATCCAGAGAAGAATCTGCTGCCACCACT
CTTCAAACCTCTTTGTATTAAATGATTGTTCAAAGCTAAGAATAATGAACAACAGGGTTTT
CTCCACCTCAATCTCTCATAGAACTACATAATTTGGAAGTGTCTATTCTTGAGCGCTTG
CCAGAGGAGGCTCTACCCAACACCCTTACTTCTATTGAAATTTCCGATTGTCCATTARTT
AAAGGGAAGTATGAAAAGGAGGGAGGAGAATTGGCATACAATTAGTCACATCCCTCAT
GTGACGATTGACGGAATTGAGCAGAAATGAGCTAA
```

[Add more sequences](#) (1 sequence added, 29 more sequences allowed)

DNA

Protein

 Medicago truncatula X

[Add/remove species](#)

DNA database

Protein database

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  - BLAST
  - Variant Effect Predictor
  - Assembly Converter
  - ID History Converter

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### BLAST search

New job

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Analysis	Jobs	Submitted at
BLASTN	BLASTN against Medicago truncatula MedtrA17_4.0 (Genomic sequence) <span>Done: 237 hits found</span> <a href="#">View results</a>	15/05/2017, 11:07 (BST)

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## Results for BLASTN against Medicago truncatula MedtrA17\_4.0 (Genomic sequence) ⓘ

### Job details ⓘ

Job name: BLASTN against Medicago truncatula MedtrA17\_4.0 (Genomic sequence)

Species: Medicago truncatula

Assembly: MedtrA17\_4.0

Search type: BLASTN (NCBI BLAST)

Download results file

### Results table ⓘ

Show All entries      Show/hide columns (4 hidden)      Filter

Genomic Location	Overlapping Gene(s)	Orientation	Length	Score	E-val	%ID
<a href="#">scaffold2053:198-652</a> [Sequence]	<a href="#">MTR_2053s0010</a>	Forward	455 [Sequence]	455	0.0	100.0 [Alignment]
<a href="#">scaffold1643:3-133</a> [Sequence]		Reverse	131 [Sequence]	99	1.1E-48	93.9 [Alignment]
<a href="#">3:6733583-6733716</a> [Sequence]	<a href="#">MTR_3g022600</a>	Reverse	134 [Sequence]	94	1.0E-45	92.5 [Alignment]
<a href="#">3:6941721-6941824</a> [Sequence]	<a href="#">MTR_3g023020</a>	Reverse	104 [Sequence]	72	1.4E-32	92.3 [Alignment]
<a href="#">3:8571018-8571148</a> [Sequence]	<a href="#">MTR_3g027420</a>	Forward	131 [Sequence]	67	1.3E-29	87.8 [Alignment]
<a href="#">3:6523624-6523683</a> [Sequence]	<a href="#">MTR_3g022230</a>	Forward	60 [Sequence]	60	2.0E-25	100.0 [Alignment]
<a href="#">3:6945053-6945156</a> [Sequence]	<a href="#">MTR_3g023030</a>	Reverse	104 [Sequence]	60	2.0E-25	89.4 [Alignment]
<a href="#">3:6782319-6782389</a> [Sequence]	<a href="#">MTR_3g022730</a>	Forward	71 [Sequence]	55	1.9E-22	94.4 [Alignment]
<a href="#">3:8469378-8469448</a> [Sequence]	<a href="#">MTR_3g027250</a>	Reverse	71 [Sequence]	55	1.9E-22	94.4 [Alignment]
<a href="#">3:6782473-6782529</a> [Sequence]	<a href="#">MTR_3g022730</a>	Forward	57 [Sequence]	53	3.0E-21	98.2 [Alignment]
<a href="#">3:7585704-7585759</a> [Sequence]	<a href="#">MTR_3g024460</a>	Reverse	56 [Sequence]	52	1.2E-20	98.2 [Alignment]
<a href="#">scaffold0425:9753-9823</a> [Sequence]	<a href="#">MTR_0425s0020</a>	Forward	71 [Sequence]	51	4.7E-20	93.0 [Alignment]
<a href="#">3:7595470-7595524</a> [Sequence]	<a href="#">MTR_3_g024460</a> <a href="#">MTR_3_g024460</a>	Reverse	55 [Sequence]	51	1.7E-20	93.0 [Alignment]



Далее возвращаемся к разделу Primer3 и делаем как делали ранее.

То есть все то же самое, только если бы у Вас не было названия гена, а был какой-то его сиквенс.

Но. Если есть название гена, который пересекается с нашим сиквенсом, то можно сделать точно также, как мы делали с самого

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### Results for BLASTN against Medicago truncatula Medtra17\_4.0 (Genomic sequence) ?

Job details

Job name: BLASTN against Medicago truncatula Medtra17\_4.0 (Genomic sequence)

Species: Medicago truncatula

Assembly: Medtra17\_4.0

Search type: BLASTN (NCBI BLAST)

Download results file

### Results table

Show All entries

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Genomic Location	Overlapping Gene(s)	Orientation	Length	Score	E-val	%ID
<a href="#">scaffold2053:198-652</a> [Sequence]	<a href="#">MTR_2053s0010</a>	Forward	455 [Sequence]	455	0.0	100.0 [Alignment]
<a href="#">scaffold1643:3-133</a> [Sequence]		Reverse	131 [Sequence]	99	1.1E-48	93.9 [Alignment]
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<a href="#">3:6523624-6523683</a> [Sequence]	<a href="#">MTR_3g022230</a>	Forward	60 [Sequence]	60	2.0E-25	100.0 [Alignment]
<a href="#">3:6945053-6945156</a> [Sequence]	<a href="#">MTR_3g023030</a>	Reverse	104 [Sequence]	60	2.0E-25	89.4 [Alignment]
<a href="#">3:6782319-6782389</a> [Sequence]	<a href="#">MTR_3g022730</a>	Forward	71 [Sequence]	55	1.9E-22	94.4 [Alignment]
<a href="#">3:8469378-8469448</a> [Sequence]	<a href="#">MTR_3g027250</a>	Reverse	71 [Sequence]	55	1.9E-22	94.4 [Alignment]
<a href="#">3:6782473-6782529</a> [Sequence]	<a href="#">MTR_3g022730</a>	Forward	57 [Sequence]	53	3.0E-21	98.2 [Alignment]
<a href="#">3:7585704-7585759</a> [Sequence]	<a href="#">MTR_3g024460</a>	Reverse	56 [Sequence]	52	1.2E-20	98.2 [Alignment]
<a href="#">scaffold0425:9753-9823</a> [Sequence]	<a href="#">MTR_0425s0020</a>	Forward	71 [Sequence]	51	4.7E-20	93.0 [Alignment]

# Смотрим первый слайд.

Nucleotide BLAST: Search x e! Gene: MTR\_2053s0010 - x

plants.ensembl.org/Medicago\_truncatula/Gene/Summary?db=core:g=MTR\_2053s0010;r=scaffold2053:204-647;t=KEH15144;tl=VPv2HPtFZOqOlGFR-1785891

**Medicago truncatula (MedtrA17\_4.0)**

Location: scaffold2053:204-647 Gene: MTR\_2053s0010 Transcript: KEH15144 BLAST/BLAT results

## Gene-based displays

- Summary
  - Splice variants
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  - Secondary Structure
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- Pan-taxonomic Compara
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- Ontologies
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  - GO: Cellular component
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  - Variant table
  - Variant image
  - Structural variants
- Gene expression
- Regulation
- External references
- Supporting evidence
- ID History
  - Gene history

## Gene: MTR\_2053s0010

Description: NBS-LRR resistance protein

Location: [SuperContig scaffold2053: 204-647 forward strand.](#)

About this gene: This gene has 1 transcript ([splice variant](#)), [10 orthologues](#) and [7 paralogues](#).

Transcripts: [Show transcript table](#)

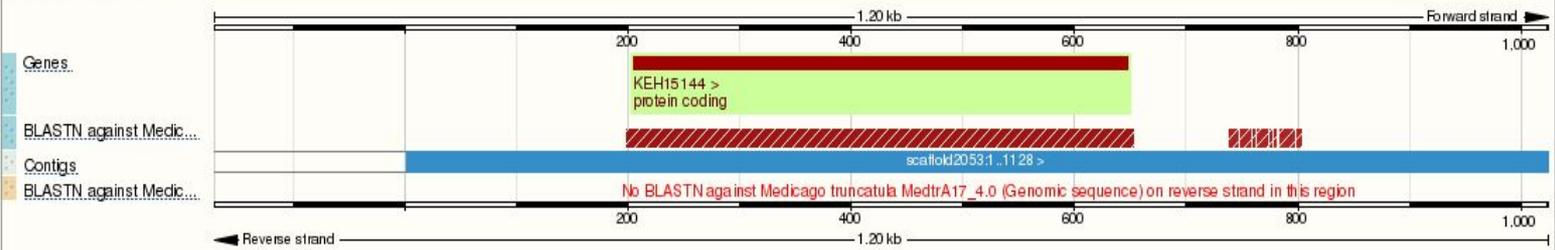
## Summary

Gene type: Protein coding

Annotation method: Protein-coding genes annotation was carried out by the [International Medicago Genome Annotation Group](#) (IMGAG)

 [Go to Region in Detail](#) for more tracks and navigation options (e.g. zooming)

Drag/Select: ← →



1.20 kb Forward strand

200 400 600 800 1,000

Genes: KEH15144 > protein coding

BLASTN against Medic... 

Contigs: scaffold2053:1..1128 >

BLASTN against Medic... No BLASTN aga inst Medicago truncatula MedtrA17\_4.0 (Genomic sequence) on reverse strand in this region

Reverse strand

200 400 600 800 1,000

1.20 kb

Gene Legend

Protein Coding  protein coding