

ID or sequence input

This E-RNAi option allows to search for desired target genes by gene identifier or sequence input (but not by both at the same time).

Page contents

- Selection of reagent and organism
- Search by gene identifier
- Paste or upload a sequence

Selection of reagent and organism

De-novo design by sequence or sequence identifier [Help]

1. Select type of RNAi reagent

long dsRNA

2. Select organism

D. melanogaster (FlyBase r5.19)

3. Enter gene identifiers (max. 50)

Examples: [twl](#), [CG11992](#), [FBgn0036141](#)

... or enter target nucleotide sequences in raw or FASTA format (max. 50 sequences), in raw format newlines separate different queries

Examples: [FASTA](#), [RAW](#)

... or upload a file in FASTA format (*.fa, *.fasta and *.txt)

Choose File no file selected

[Help]

Reset Submit

Select type of RNAi reagent

Choose **long dsRNAs** for the design of long dsRNAs (including esiRNAs) or **siRNAs** for the design of short interfering RNAs.

Select organism

Select the organism used for the RNAi experiment.

Search by gene identifier

The types of available gene identifiers depend on the database, where the annotations were retrieved from:

Organism

Source

Available query identifiers

D. melanogaster

FlyBase

FBgn, CG identifiers and gene symbols (e.g. CG11992, FBgn0014018 or rel)

A. pisum

AphidBase

ACYPI, XM and LOC identifiers (from 'official gene consensus set', e.g. ACYPI006699, XM_001944230 or LOC100165774)

H. sapiens

NCBI RefSeq

Gene names, Entrez gene identifiers and RefSeq identifiers (e.g. RPS11, 6205 or NM_001015.3)

S. mediterranea

SmedGD

MAKER identifiers (mk4, from SmedGD) will work (e.g. mk4.023206.00)

S. cerevisiae, *S. pombe*

EnsemblFungi

Ensembl gene identifiers (e.g. YHR055C for budding yeast, SPMIT.05 for fission yeast)

C. elegans

WormBase

WBGene identifiers, sequence names and gene names (e.g. WBGene00006763, JC8.10 or unc-26)

C. briggsae

WormBase

WBGene identifiers, transcript identifiers (e.g. WBGene00032891, CBG11841)

A. gambiae

VectorBase

AGAP gene identifiers (e.g. AGAP000009)

A. aegypti

VectorBase

AAEL gene identifiers (e.g. AAEL000068)

M. musculus

NCBI RefSeq

Gene names, Entrez gene identifiers and RefSeq identifiers (e.g. Axin1, 12005 or NM_009733.2)

A. mellifera

BeeBase

GB gene identifiers (e.g. GB15421)

T. castaneum

BeetleBase

TC and GLEAN-prediction gene identifiers (e.g. TC004684 or GLEAN_04684)

Examples with identifiers specific to the selected organism are available as direct links on top of the identifier text-box.

In the example below the *D. melanogaster* genes FBgn0014018, *wls*, CG2956 and CG99999 were queried for the design of long dsRNAs.

De-novo design by sequence or sequence identifier [\[Help\]](#)

1. Select type of RNAi reagent

long dsRNA 

2. Select organism

D. melanogaster (FlyBase r5.19) 

3. Enter gene identifiers (max. 50)

Examples: [twl](#), [CG11992](#), [FBgn0036141](#)

FBgn0014018
wls
CG2956
CG99999|

... or enter target nucleotide sequences in raw or FASTA format (max. 50 sequences), in raw format newlines separate different queries

Examples: [FASTA](#), [RAW](#)

... or upload a file in FASTA format (*.fa, *.fasta and *.txt)

no file selected

[\[Help\]](#)

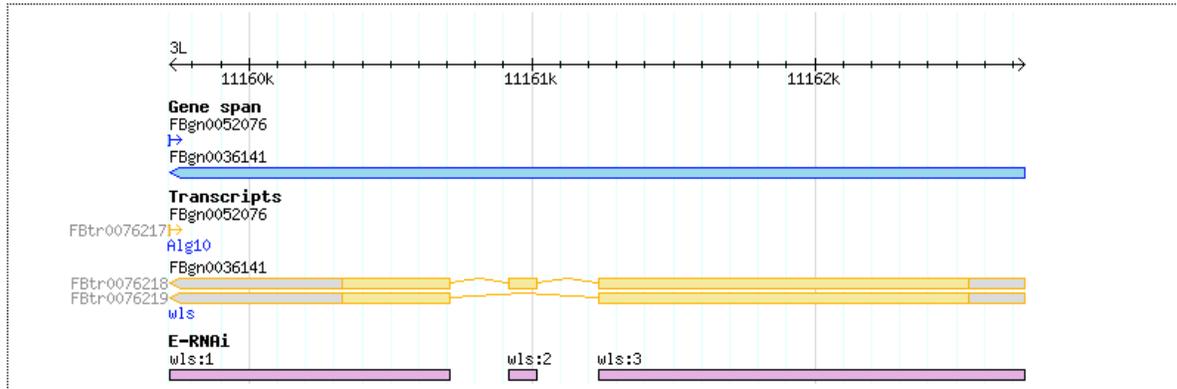
After submitting the query, E-RNAi shows the queried target genes as genome browser visualization including annotated isoforms and exons. Now sequences for the complete target gene, whole transcripts or certain exons can be selected as target sites. The selection of multiple sequences is possible. Queried identifiers that were not found in the database (here CG99999) are listed in red at the top of the page.

De-novo design: sequence selection

Please select RNAi target sequences (whole genes, whole transcripts or exons) from below.

Queried identifiers not found in database: **CG99999**.

Query wls



Gene sequences (click here)

Transcript sequence (click here)

Exon sequence (click here)

>wls:1

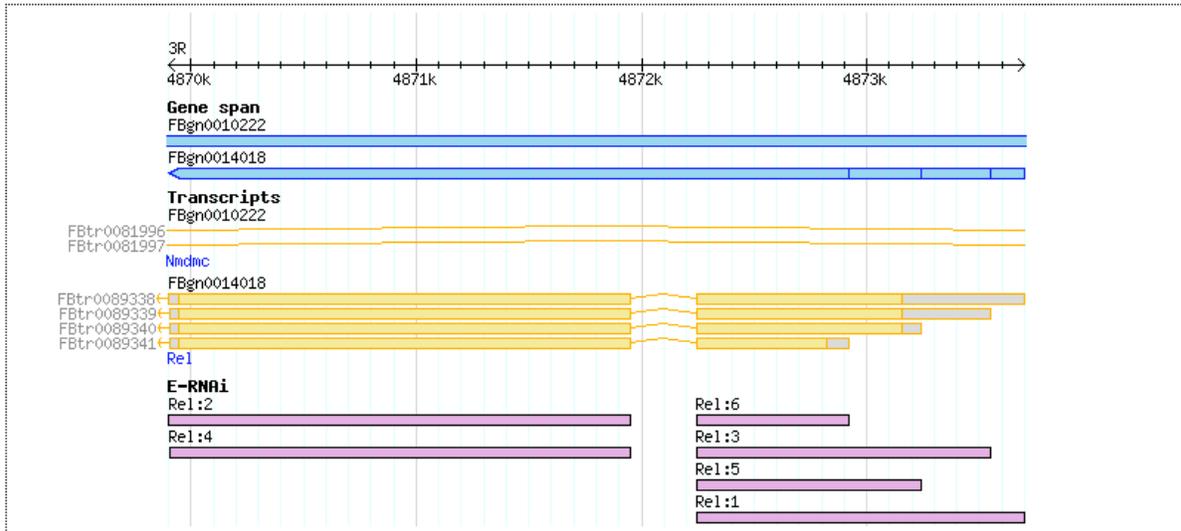
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```

>wls:2

>wls:3

```
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Query Rel



Gene sequences (click here)

Transcript sequence (click here)

Exon sequence (click here)

>Rel:1

>Rel:2

```
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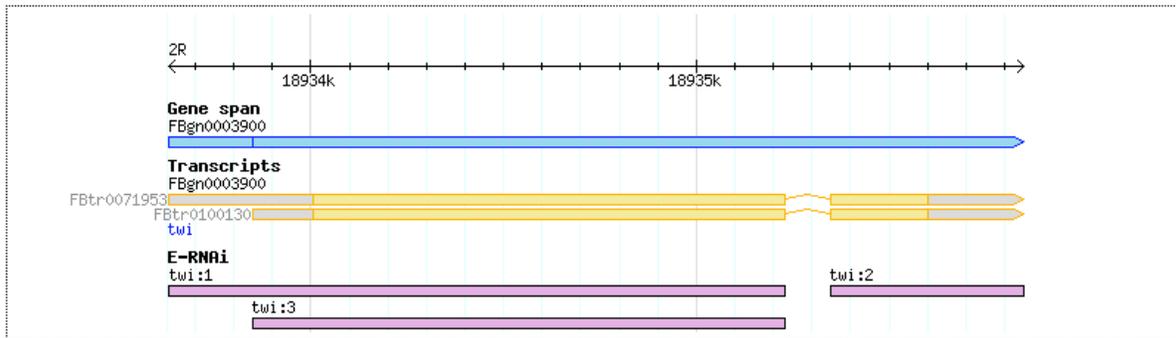
>Rel:3

>Rel:4

>Rel:5

>Rel:6

Query twi



Gene sequences (click here)

>twi

```
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TGGGAGCCGGATGGCAAGACAAGCGAGCGAGCGGGACGACGATAGAGCGGGCGGACGCGAATGGCCGTCGAGCAGCCGCAAAATGTCAATTTGAGCAATGG
CCGGAAGGATCTCGCTCAGTTGCGTTCCGTAAGTGCCTGCGAGCAGATCGATCCAGCAAACCGGGCGTGAAGAAATATCTACGGAGTTATACAGTTCC
GAAATAAGAAATATATTGTTAGTACCACAAATCTAACTGAAGAAGTGCCTAAAAAGCCAAGCAAGATCACCAAATGATGAGCGCTCGCTCGGTGTCGC
CAAAGTGTGCTGGACATAAGCTACAAGCCACACTGCCCAACATCATGGAGCTGCAGAACATGTGATCAAGCTGATACAGGTGGAGCAGCAGGCCCTA
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ATCTAACGGAGGAGTCAATGTCGCCCGCTGCTTGGCGGATGACGGCAGTCCCGGAGTTTGTGGACGGATCCGATGCCGGCGGAAAGGCCCTCCGCCAA
GCCAGCTCGCCGGCTGAAGCGGAAGCCAGCAAGACGGAGGAGACGGACGAGTTTCAGCAACCCAGCGGGTCAATGGCCAAATGTGAGGGAGCCGACGCCACC
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CCCAGAAAGCTGAGTTATCTGTTTCGGGGTGTGGCGCATGGAGGGCGACCGCAGCACCAGAAGGCATAGCGGGGATCAGGACACTATAGTCCGAGAGGG
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TAAGATGCTAAGCCTAAAAACCTACTGTAAATGCCTATTAATGTCATAGTCTAAACTAAATTAATTGTA AAAAGCCAACAGCCAGGAAACAAAGAAA
GCCCATGAACAAAACCCAGA
```

Transcript sequence (click here)

Exon sequence (click here)

Submit Selection

The 'Submit Selection' button links to the settings page.

Paste or upload a sequence

E-RNAi can also be queried with sequences. It is recommended to paste sequences in FASTA format. Raw sequences can also be pasted, however a query sequence must not contain any newline (each newline is interpreted as new query by E-RNAi). Example sequences specific to the selected organism can be pasted in the sequence text-box by clicking the 'FASTA' or 'RAW' links.

Alternatively, sequences can also be uploaded from file. Files must contain sequences in FASTA format (*.fa, *.fasta and *.txt file extensions are allowed).

In the example below sequences from the genes *Ras85D* and *Nc* were pasted in FASTA format.

De-novo design by sequence or sequence identifier [Help]

1. Select type of RNAi reagent

long dsRNA

2. Select organism

D. melanogaster (FlyBase r5.19)

3. Enter gene identifiers (max. 50)

Examples: [twj](#), [CG11992](#), [FBqn0036141](#)

... or enter target nucleotide sequences in raw or FASTA format (max. 50 sequences), in raw format newlines separate different queries

... or upload a file in FASTA format (*.fa, *.fasta and *.txt)

no file selected

[Help]

Examples: FASTA, RAW

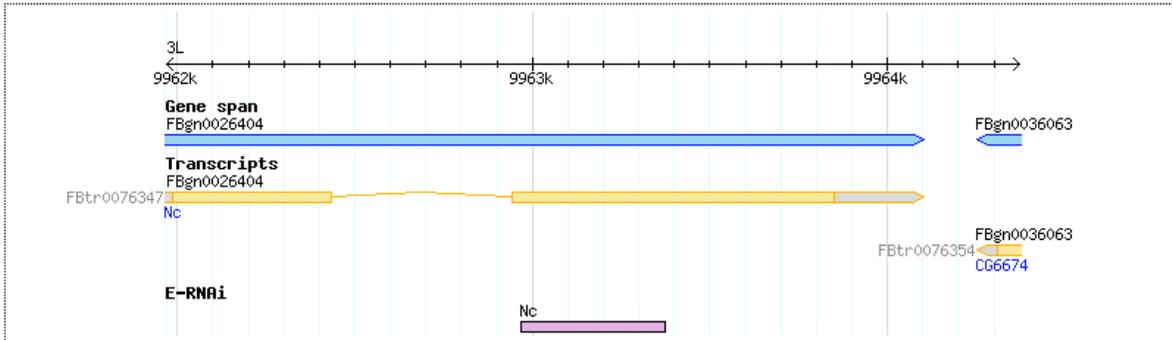
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CAGCAAGTCGTTGATACACTGTTTCAAGAAGTGAATTTACGATT
TTCCCTATGGGAACGTGAATCAGGATCAGTTCTTAAACTTCTGA
CAATGGTGACCTCCTCGTGTATGTGCAGAATACCGAGTGTTCGT
AATGGTACTGATGACACACCGCAACAGTGTGGAGGAAAAGAGAA
GGTGGAGTTTTGCGATGGATCTGTGGTCGATATGCA
>Ras85D
TTACATTTAAATCTACGATTCGGCTTGTTTCATTTTGGGCCCTCC
```

After submitting the query, E-RNAi shows the queried sequences as genome browser visualization (if they could be mapped).

De-novo design: sequence selection

Please select for which of the queried sequences RNAi reagents should be calculated.

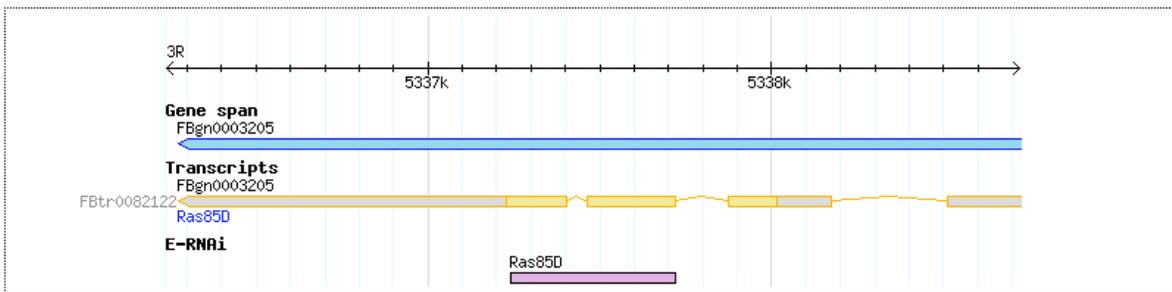
Query Nc



>Nc

```
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GCAGAATACCGAGTGTTCGTAATGGTACTGATGACACACGGCAACAGTGTGGAGGGAAAAGAGAAGGTGGAGTTTTGCGATGGATCTGTGGTCGATATG
CA
```

Query Ras85D



>Ras85D

```
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GGCATCCTTACCGCGCTTGATCTGCTCAGGTAGTCCGATATCCTCGAAGGACTTCGCACTGTTGACGGCAAAGACCAGCAGGAATCCCTCGCCAGTC
CGCATATAGTATCCGCATGGCCGAGTACTCCTCTTGGCGGGCGGTGCCAGGATGTCCAGCAGGCAGGTCTCTCCATCT
```

Submit Selection

The 'Submit Selection' button links to the [settings](#) page.