

Sequence Allocator

<https://puffer.genpat.uu.se/WORKBENCH/allocator/>

This is how the GUI of Sequence Allocator looks like:

Start new Allocator run

Non-redundant region allocator does the following:

- **STEP 1: Identifies repeat-free regions in the input sequence**
The input sequence is processed by *RepeatMasker* and repeat-free regions longer than a minimum PCR product length are selected for further refinement. Processing can be skipped by checking the *Sequence is pre-masked* box below.
 - **STEP 2: Finds out if the repeat-free regions are non-redundant in the human genome**
Every selected repeat-free region is blasted against the draft sequence of the human genome at NCBI. Sequence is non-redundant if only one hit is found (the "self match"), otherwise the redundant parts are removed. Remaining regions longer than a minimum PCR product length are kept.
 - **STEP 3: Designs primer pairs in the non-redundant regions**
For each of the non-redundant regions, *primer3* is invoked to find PCR primers. If a non-redundant region is larger than a desired maximum PCR product, the region is split into several sections, and primers are designed for each section. Re-prime manually if specific sequence intervals need to be covered.
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continued

Paste a sequence (in FASTA format) into the text window below ([less than 100 kb](#)):

102400 characters left

OR upload a sequence file:

Sequence is pre-masked

Blast Parameters

Use Blast algorithm:

Minimum match percentage:

Minimum match length:

Primer Design Parameters

Minimum product length: Maximum product length:

Number of primer pairs per region: Maximum 3'-end stability:

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Typical Output:

Table of repeat-free and non-redundant regions

The table displays:

- positions of the regions referring to the input sequence,
- fasta files of the regions,
- Blast results for the repeat-free regions,
- *primer3* results for the non-redundant regions.

Blast summary

Single contig

Allocator parameters

Your job ID is **0A10606151816** .

The uploaded sequence length is **140001** base pairs.

Minimum size of repeat-free region: **100** base pairs.

Blast algorithm: **Standard BLAST W=11 E=1.0**

Blast match criteria: at least **80** % in more than **50** base pairs.

Minimum size of non-redundant region: **100** base pairs.

PCR products are sought each **500** base pairs.

Product length must be at least **100** base pairs, but not more than **500** base pairs.

Number of primer pairs per region: **5** ; Maximum 3'-end stability: **6.0**

Important files: [Input sequence](#) [Masked sequence](#) [List of repeats](#) [Summary of repeats](#)

Region	From	To	Length (repeat-free)	Length (non-redundant)	Fasta	Blast	Blast filter	Hits	Perfect matches	Primers
1	4225	4391	167	167	here	here	On	1	1	here
2	5018	5182	165	165	here	here	On	1	1	here
3	6714	6964	251		here	here	On	2	1	
3.1	6840	6964		125	here	here	On	1	1	here
4	7073	7302	230	230	here	here	On	1	1	here
5	7348	7760	413	413	here	here	On	1	1	here
6	8057	8175	119	119	here	here	On	1	1	none found