

# Collect Motifs with SeqPos Element

Finds motifs enriched in a set of regions.

**Element type:** seqpos-id

## Parameters

Parameter	Description	Default value	Parameter in Workflow File	Type
<b>Output directory</b>	The directory to store seqpos results.		<b>output-dir</b>	<i>string</i>
<b>Genome assembly version</b>	UCSC database version (GENOME).	hg19	<b>assembly</b>	<i>string</i>
<b>Output file name</b>	Name of the output file which stores new motifs found during a de novo search (-n).	Default	<b>out_name</b>	<i>string</i>
<b>De novo motifs</b>	Run de novo motif search (-d).	False	<b>de_novo</b>	<i>boolean</i>
<b>Motif database</b>	Known motif collections. (-m). Warning: computation time increases with selecting additional databases. It is recommended to use cistrome.xml. It is a comprehensive collection of motifs from the other databases with similar motifs deleted.	cistrome.xml	<b>motif_db</b>	<i>string</i>
<b>Region width</b>	Width of the region to be scanned for motifs; depends on a resolution of assay (-w).	600	<b>reg_width</b>	<i>numeric</i>
<b>Pvalue cutoff</b>	Pvalue cutoff for the motif significance (-p).	0.001	<b>p_val</b>	<i>numeric</i>

## Input/Output Ports

The element has 1 *input port*.

**Name in GUI:** SeqPos data

**Name in Workflow File:** in-data

**Slots:**

Slot In GUI	Slot in Workflow File	Type
Input regions	<b>cp_treat-ann</b>	<i>ann-table-list</i>