

# Annotate Peaks with peak2gene Element

Gets refGenes near the ChIP regions identified by a peak-caller.

**Element type:** peak2gene-id

## Parameters

Parameter	Description	Default value	Parameter in Workflow File	Type
<b>Genome file</b>	Select a genome file (sqlite3 file) to search refGenes. (--genome).	hg19	<b>genome</b>	<i>string</i>
<b>Output file</b>	Select which type of genes need to output. up for genes upstream to peak summit, down for genes downstream to peak summit, all for both up and down. (--op).	all	<b>outpos</b>	<i>string</i>
<b>Official gene symbols</b>	Output official gene symbol instead of refseq name. (--symbol).	False	<b>symbol</b>	<i>boolean</i>
<b>Distance</b>	Set a number which unit is base. It will get the refGenes in n bases from peak center. (--distance).	3000	<b>distance</b>	<i>numeric</i>

## Input/Output Ports

The element has 1 *input port*:

**Name in GUI:** Peak2gene data

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

**Slots:**

Slot In GUI	Slot in Workflow File	Type
<b>Treatment features</b>	<b>_treat-ann</b>	<i>ann-table-list</i>

And 1 *output port*:

**Name in GUI:** Peak2gene output data

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

**Slots:**

Slot In GUI	Slot in Workflow File	Type
<b>Gene regions</b>	<b>gene-annotation</b>	<i>ann-table-list</i>
<b>Peak regions</b>	<b>peak-annotation</b>	<i>ann-table-list</i>