

# Annotate Peaks with peak2gene Element

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

## Parameters in GUI

Parameter	Description	Default value
<b>Genome file</b>	Select a genome file (sqlite3 file) to search refGenes. (--genome).	hg19
<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>Official gene symbols</b>	Output official gene symbol instead of refseq name. (--symbol).	False
<b>Distance</b>	Set a number which unit is base. It will get the refGenes in n bases from peak center. (--distance).	3000

# Parameters in Workflow File

Type: peak2gene-id

Parameter	Parameter in the GUI	Type
genome	Genome file	string
outpos	Output file	string
symbol	Official gene symbols	boolean
distance	Distance	numeric

## 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
Treatment features	_treat-ann	<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
Gene regions	gene-annotation	<i>ann-table-list</i>
Peak regions	peak-annotation	<i>ann-table-list</i>