# Problem 03 – Genome

*Every living creature on Earth has genomes in it body. The genome is the total genetic material of an organism and includes both the genes and non-coding sequences. The genome size, and the number of genes it encodes varies widely between organisms (e.g. viruses and viroids have the smallest amount of genomes).*

The next task of candidate-intern Tanya is called „Genome“ and you have to help. You will receive different amount of **encrypted** genes each on a separate line. Until you receive a line “**Stop!**” you have to decrypt the information given and save some data that you will need later on. Each valid information about a gene should consist of:

* **Name of the gene** may contain some of the following characters between its letters (!@#$?). Example for valid names: “!@pro?#line!#” (proline)
* **Length of the name** with a “=” before it. (e.g. =12; =5…)
* **Count of genes** with a “--” before it. (e.g. --800; --142)
* **Organism that it belongs to with** “<<” before it. (e.g. <<cat; <<dog)

**Note: the info will be in that exact order. If something is missing the input is invalid and you should ignore it. If the length of the name does not match with the actual name given, the input is considered invalid and you should ignore it.**

Examples for **valid** input:

“!cad$$he!rins!@=9--30229<<human”

“!@leu?#cine!#=7--800<<cat”

Examples of **invalid** input:

“bx!=4--421<<bison” – the length 4 does not match with the actual length

“#nms!n--126<<dog” – the length is missing

**Store** the information about the genes and print all the organisms you have encountered with their **total** amount of genes.

## Input

* You will receive encrypted lines of input storing information about a gene until you receive “**Stop!**”
* all names will always be **lower-case** characters, **only Latin letters**
* the input will always be **valid** (no whitespaces)

## Output

* Print every organism with their total amount of genes (genome) in **descending order**
* For every organism print “**{organism name} has genome size of {genes count}**”
* If genes count equal -> **save the order** of the input

## Constraints

* all numbers will be in range [1 - 10000]
* name will be string [1 - 1000]

## Examples

|  |  |
| --- | --- |
| **Input** | **Output** |
| !@ab?si?di!a@=7--152<<human  b!etu?la@=6--321<<dog  !curtob@acter##ium$=14--230<<dog  !some@thin@g##=9<<human  Stop! | dog has genome size of 551  human has genome size of 152 |
| =12<<cat  !vi@rus?=2--142  ?!cur##viba@cter!!=11--800<<cat  !fre?esia#=7--450<<mouse  @pa!rcuba@cteria$=13--351<<mouse  !richel#ia??=8--900<<human  Stop! | human has genome size of 900  mouse has genome size of 801  cat has genome size of 800 |
| !@ру?би#=4--57<<polecat  ?do?@#ri#=4--89<<polecat  =12<<cat  !vi@rus?=2--142  @pa!rcu>ba@cteria$=13--234<<mouse  ?!cur##viba@cter!!=11--680<<cat  Stop! | cat has genome size of 680  polecat has genome size of 89 |