## How do you account for aliases for genes and targets?

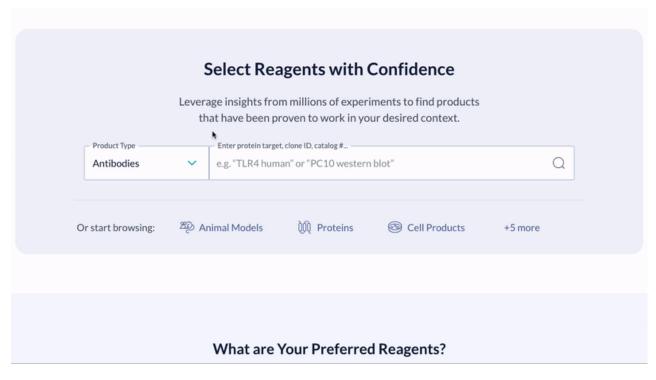
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The ASCEND platform is backed by a proprietary bioinformatics database to account for, track, and link the different syntaxes and aliases of a target/protein

There's no need to ask yourself, "Should this target name have a space, a comma, or maybe a dash?" and run separate searches for each variation. You'll receive comprehensive results regardless of how your search term was referred to in the literature or vendor catalogs.

Selector uses a **preferred name** for a gene and links it to all known species-specific aliases from our bioinformatics database. The preferred gene name is linked to related products and proteins on our platform, each of which has its own set of aliases

For example, you can search for **RIPK2**, **RIPK 2**, **CARD3**, **Card 3**, **RIP2**, and **RIP-Like-Interacting CLARP Kinase** and have confidence you'll see the same results because our platform knows you're referring to the same target.



ASCEND's comprehensive bioinformatic mapping not only applies to target proteins but also to the experimental context used to narrow down your search. This gives you the ability to use alternate names or abbreviations to search for **applications**, **organisms**, **tissues**, **cell types**, **cell lines**, and **diseases** within the Figure Usage Data filters.

By default, aliases will remain hidden. However, you can choose to display aliases by clicking the "See Aliases" button within a filter.

