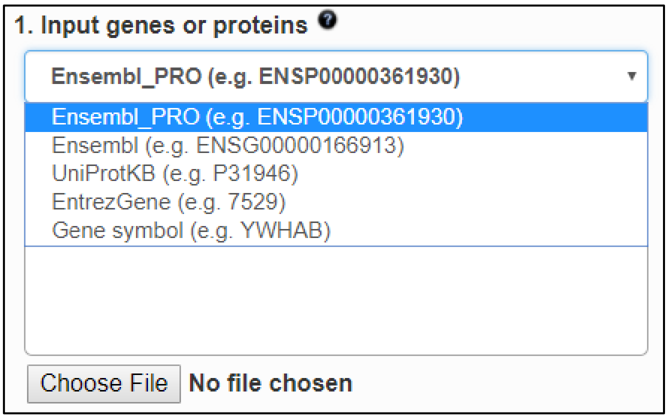
INTERSPIA tutorial for using the main analysis interface

Configuring the analysis using user's data

(1) Entering the list of genes or proteins

(1-1) Selecting the type of the input genes or proteins

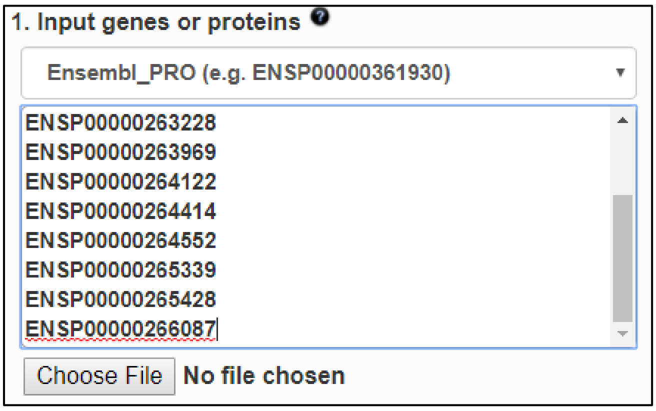
User can select the type of the input genes or proteins among Ensembl protein identifier (Ensembl_PRO), Ensembl gene identifier (Ensembl), Gene ID (EntrezGene), Gene symbol, and UniProt accession (UniprotKB).



(1-2) Entering the list of genes or proteins manually

User can enter the list of genes or proteins in the text box as shown below. The format of genes or proteins need to match with the selected type above.

When user enters genes or proteins with the type of the Ensembl identifier, target species is automatically selected.

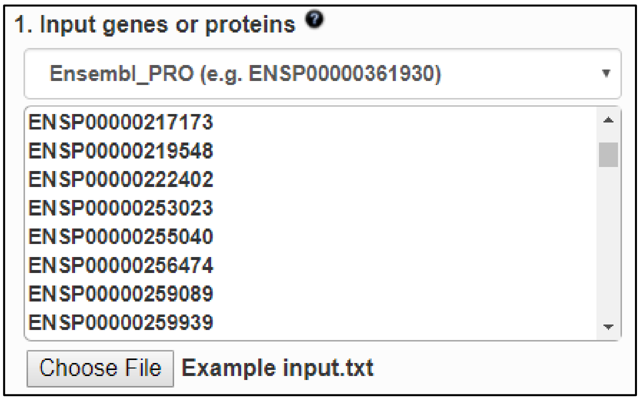


ENSP00000263228
ENSP00000263969
ENSP00000264122
ENSP00000264414
ENSP00000264552
ENSP00000265339
ENSP00000265428
ENSP00000266087

(1-3) Uploading a file with the list of genes or proteins

User can upload the file contained the list of genes or proteins.

When user uploads genes or proteins with the type of the Ensembl identifier, target species is automatically selected.



1. Input genes or proteins

Ensembl_PRO (e.g. ENSP00000361930)

ENSP00000217173
ENSP00000219548
ENSP00000222402
ENSP00000253023
ENSP00000255040
ENSP00000256474
ENSP00000259089
ENSP00000259939

Choose File Example input.txt

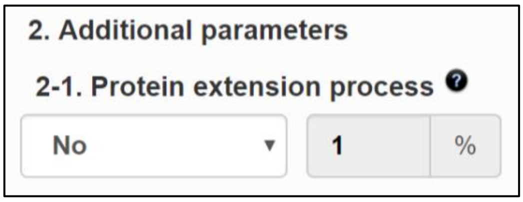
(2) Additional parameters

(2-1) Protein extension process

User can optional select whether the protein extension process based on the random walk with restart algorithm is used or not.

The default setting is "No" (do not use the protein extension process). It means that only the input genes or proteins are used in the analysis.

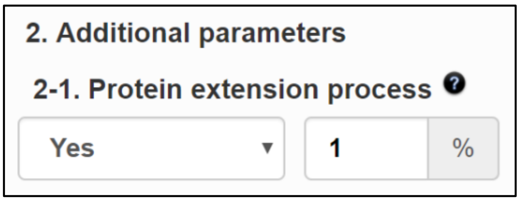
When user selects "Yes", the percentage value between (0.1% to 10%) must be selected. This value is used as a cutoff filtering top cutoff percentage of extended proteins to include this analysis.



2. Additional parameters

2-1. Protein extension process

No 1 %



2. Additional parameters

2-1. Protein extension process

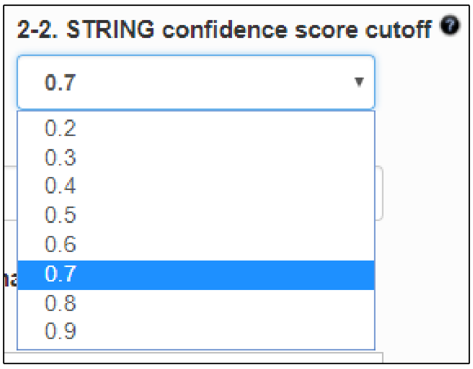
Yes 1 %

(2-2) STRING confidence score cutoff

User can select the confidence cutoff score used in the STRING database.

"0.7" is the most widely used cutoff score.

When user selects a cutoff score, interactions with a confidence score greater than or equal to the cutoff score are considered as "existing interactions". On the other hand, interactions with a



2-2. STRING confidence score cutoff

0.7

0.2
0.3
0.4
0.5
0.6
0.7
0.8
0.9

confidence score less than the cutoff are considered as “not existed interactions”.

The STRING database contains direct (physical) as well as indirect (functional) interactions.

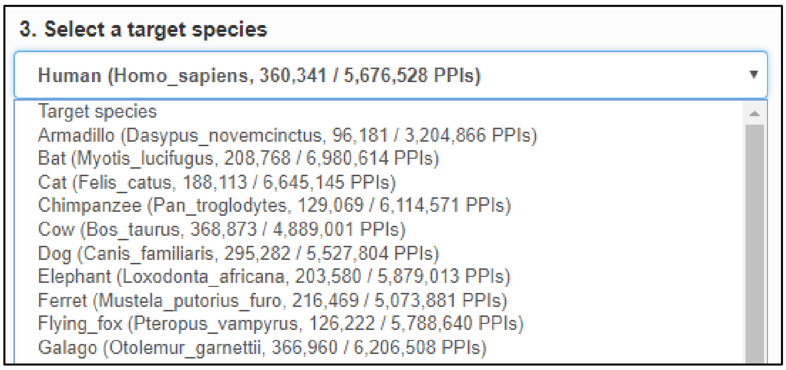
(3) Selecting a target species

User can select the target species for this analysis. The target species needs to match with the input genes or proteins.

The list of target species also provides the number of protein-protein interactions (PPIs) supported by our web server.

The numbers before and after the slash in parentheses represent the number of PPIs with the STRING confidence score greater than or equal to the user selected cutoff and the number of all PPIs in the STRING database respectively.

The number of PPIs is automatically updated as user selects a different STRING confidence score cutoff.



3. Select a target species

Human (Homo_sapiens, 360,341 / 5,676,528 PPIs) ▾

Target species
Armadillo (Dasypus_novemcinctus, 96,181 / 3,204,866 PPIs)
Bat (Myotis_lucifugus, 208,768 / 6,980,614 PPIs)
Cat (Felis_catus, 188,113 / 6,645,145 PPIs)
Chimpanzee (Pan_troglodytes, 129,069 / 6,114,571 PPIs)
Cow (Bos_taurus, 368,873 / 4,889,001 PPIs)
Dog (Canis_familiaris, 295,282 / 5,527,804 PPIs)
Elephant (Loxodonta_africana, 203,580 / 5,879,013 PPIs)
Ferret (Mustela_putorius_furo, 216,469 / 5,073,881 PPIs)
Flying_fox (Pteropus_vampyrus, 126,222 / 5,788,640 PPIs)
Galago (Otolemur_garnettii, 366,960 / 6,206,508 PPIs)

(4) Selecting other species for comparison

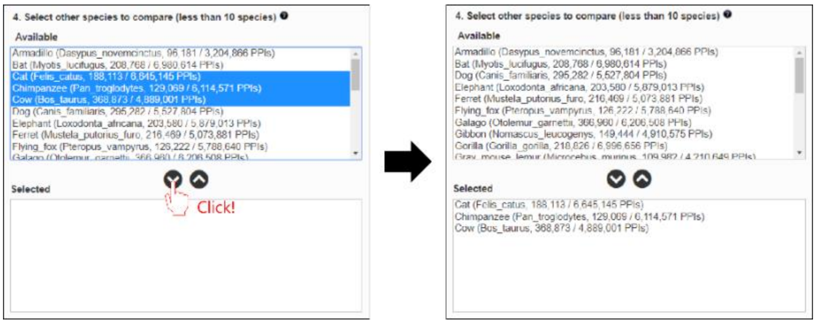
User can select less than 10 species to compare with the target species.

The list of species also provides the number of protein-protein interactions (PPIs) supported by our web server.

User can click and drag a mouse, or use a mouse click holding down the shift key to highlight multiple species adjacent to each other, or highlight multiple interspersed species by mouse click holding down the ctrl key.

The highlighted species need to be moved to the below panel by clicking the “v” button.

If user selects the wrong species in the selected box, user can remove them using the “ʌ” button.



4. Select other species to compare (less than 10 species)

Available
Armadillo (Dasypus_novemcinctus, 96,181 / 3,204,866 PPIs)
Bat (Myotis_lucifugus, 208,768 / 6,980,614 PPIs)
Cat (Felis_catus, 188,113 / 6,645,145 PPIs)
Chimpanzee (Pan_troglodytes, 129,069 / 6,114,571 PPIs)
Cow (Bos_taurus, 368,873 / 4,889,001 PPIs)
Dog (Canis_familiaris, 295,282 / 5,527,804 PPIs)
Elephant (Loxodonta_africana, 203,580 / 5,879,013 PPIs)
Ferret (Mustela_putorius_furo, 216,469 / 5,073,881 PPIs)
Flying_fox (Pteropus_vampyrus, 126,222 / 5,788,640 PPIs)
Galago (Otolemur_garnettii, 366,960 / 6,206,508 PPIs)

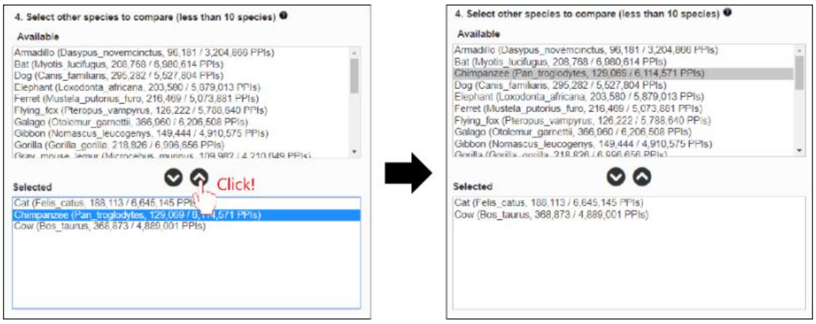
Selected

4. Select other species to compare (less than 10 species)

Available
Armadillo (Dasypus_novemcinctus, 96,181 / 3,204,866 PPIs)
Bat (Myotis_lucifugus, 208,768 / 6,980,614 PPIs)
Dog (Canis_familiaris, 295,282 / 5,527,804 PPIs)
Elephant (Loxodonta_africana, 203,580 / 5,879,013 PPIs)
Ferret (Mustela_putorius_furo, 216,469 / 5,073,881 PPIs)
Flying_fox (Pteropus_vampyrus, 126,222 / 5,788,640 PPIs)
Galago (Otolemur_garnettii, 366,960 / 6,206,508 PPIs)
Gibbon (Nomascus_leucogenys, 149,444 / 4,910,575 PPIs)
Gorilla (Gorilla_gorilla, 218,826 / 6,996,656 PPIs)
Gray_mouse_lemur (Microcebus_murinus, 109,982 / 4,210,649 PPIs)

Selected
Cat (Felis_catus, 188,113 / 6,645,145 PPIs)
Chimpanzee (Pan_troglodytes, 129,069 / 6,114,571 PPIs)
Cow (Bos_taurus, 368,873 / 4,889,001 PPIs)

[Selecting other species to compare]



4. Select other species to compare (less than 10 species)

Available

Armadillo (Dasypus_novemcinctus, 96,181 / 3,204,866 PPIs)
Bat (Myotis_lucifugus, 208,768 / 6,980,614 PPIs)
Dog (Canis_familiaris, 295,282 / 5,527,804 PPIs)
Elephant (Loxodonta_africana, 203,580 / 5,879,013 PPIs)
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Galago (Otolemur_garnettii, 366,960 / 6,206,508 PPIs)
Gibbon (Nomascus_leucogenys, 149,444 / 4,910,575 PPIs)
Gorilla (Gorilla_gorilla, 218,826 / 6,996,656 PPIs)

Selected

Cat (Felis_catus, 188,113 / 6,645,145 PPIs)
Chimpanzee (Pan_troglodytes, 129,069 / 6,114,571 PPIs)
Cow (Bos_taurus, 368,873 / 4,889,001 PPIs)

4. Select other species to compare (less than 10 species)

Available

Armadillo (Dasypus_novemcinctus, 96,181 / 3,204,866 PPIs)
Bat (Myotis_lucifugus, 208,768 / 6,980,614 PPIs)
Chimpanzee (Pan_troglodytes, 129,069 / 6,114,571 PPIs)
Dog (Canis_familiaris, 295,282 / 5,527,804 PPIs)
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Flying_fox (Pteropus_vampyrus, 126,222 / 5,788,640 PPIs)
Galago (Otolemur_garnettii, 366,960 / 6,206,508 PPIs)
Gibbon (Nomascus_leucogenys, 149,444 / 4,910,575 PPIs)

Selected

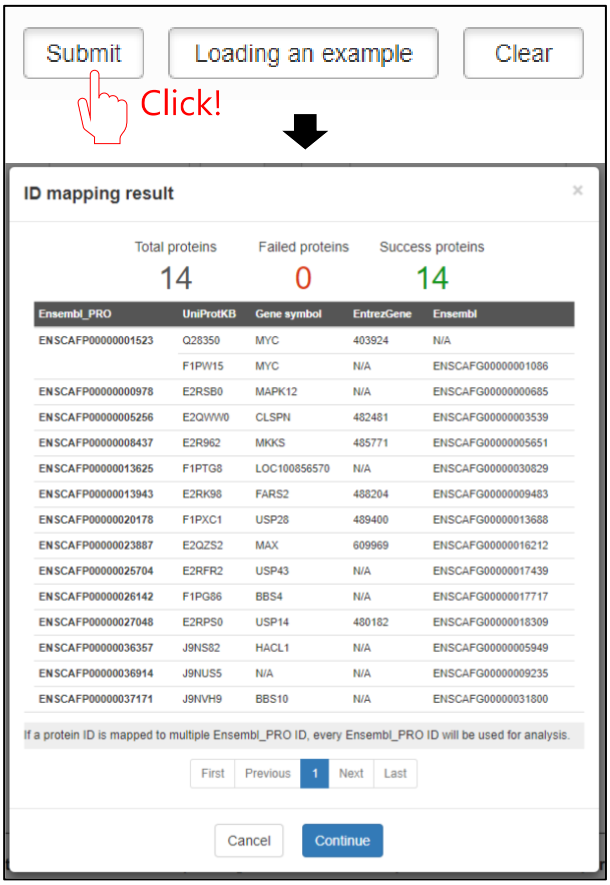
Cat (Felis_catus, 188,113 / 6,645,145 PPIs)
Cow (Bos_taurus, 368,873 / 4,889,001 PPIs)

[Unselecting the chosen species]

(5) Clicking the “Submit” button to start the analysis

If user clicks this button, the results of ID mapping are showing in a separate window.

When clicking the “Continue” button in a separate window as shown below, the analysis begins using input genes or proteins and chosen parameters.



ID mapping result

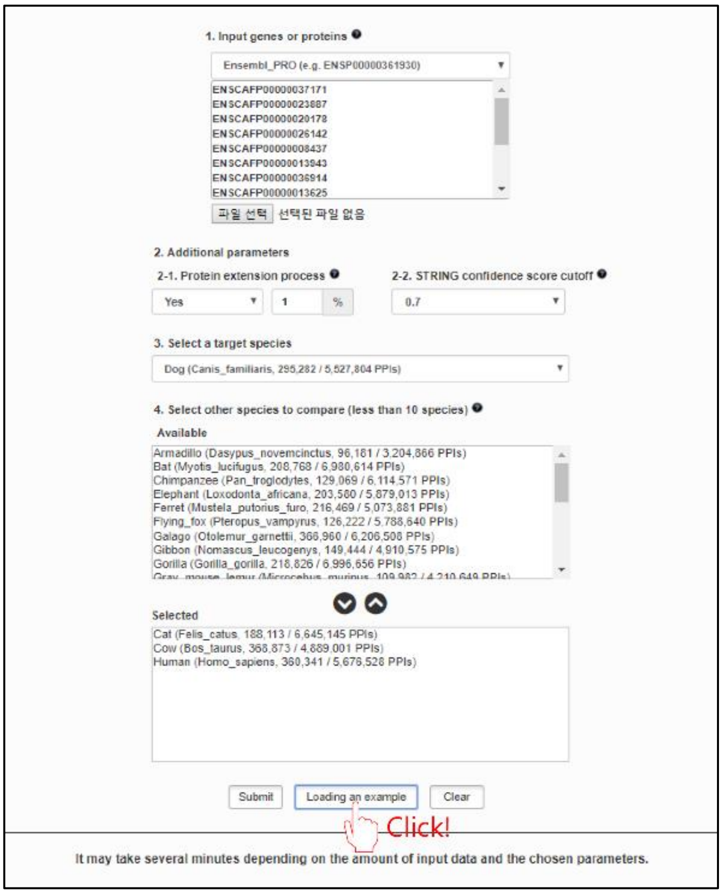
Total proteins	Failed proteins	Success proteins
14	0	14

Ensembl_PRO	UniProtKB	Gene symbol	EntrezGene	Ensembl
ENSCAFP00000001523	Q28350	MYC	403924	N/A
	F1PW15	MYC	N/A	ENSCAFG00000001086
ENSCAFP00000000978	E2RSB0	MAPK12	N/A	ENSCAFG00000000685
ENSCAFP00000005256	E2QWW0	CLSPN	482481	ENSCAFG00000003539
ENSCAFP00000008437	E2R962	MKKS	485771	ENSCAFG00000005651
ENSCAFP00000013625	F1PTG8	LOC100856570	N/A	ENSCAFG00000030829
ENSCAFP00000013943	E2RK98	FARS2	488204	ENSCAFG00000009483
ENSCAFP00000020178	F1PXC1	USP28	489400	ENSCAFG00000013688
ENSCAFP00000023887	E2QZS2	MAX	609969	ENSCAFG00000016212
ENSCAFP00000025704	E2RFR2	USP43	N/A	ENSCAFG00000017439
ENSCAFP00000026142	F1PG86	BBS4	N/A	ENSCAFG00000017717
ENSCAFP00000027048	E2RPS0	USP14	480182	ENSCAFG00000018309
ENSCAFP00000036357	J9NS82	HACL1	N/A	ENSCAFG00000005949
ENSCAFP00000036914	J9NUS5	N/A	N/A	ENSCAFG00000009235
ENSCAFP00000037171	J9NVH9	BBS10	N/A	ENSCAFG00000031800

If a protein ID is mapped to multiple Ensembl_PRO ID, every Ensembl_PRO ID will be used for analysis.

(6) An example data of the INTERSPIA analysis

When clicking the “Load an example” button, parameters of the analysis using example data are automatically filled.



1. Input genes or proteins

Ensembl_PRO (e.g. ENSP00000361930)

ENSCAFP00000037171
ENSCAFP00000023887
ENSCAFP00000020178
ENSCAFP00000026142
ENSCAFP00000008437
ENSCAFP00000013943
ENSCAFP00000036914
ENSCAFP00000013625

파일 선택 선택된 파일 없음

2. Additional parameters

2-1. Protein extension process: Yes, 1 %

2-2. STRING confidence score cutoff: 0.7

3. Select a target species

Dog (Canis_familiaris, 295,282 / 5,527,804 PPIs)

4. Select other species to compare (less than 10 species)

Available

Armadillo (Dasypus_novemcinctus, 96,181 / 3,204,866 PPIs)
Bat (Myotis_lucifugus, 208,768 / 6,980,614 PPIs)
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Selected

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Cow (Bos_taurus, 368,873 / 4,889,001 PPIs)
Human (Homo_sapiens, 360,341 / 5,676,528 PPIs)

It may take several minutes depending on the amount of input data and the chosen parameters.

(7) Refreshing the analysis page

When the “Clear” button is clicked, all data are cleared and chosen parameter values are reset to default values.