

SPRINT-MAI: Predicting lysine malonylation sites of proteins using sequence and predicted structural features.

[Check the current Queue to prevent DUPLICATE submits](#)

E-mail address (Optional):

Target ID (optional):

Input your protein sequence:

Select Protein Species:

**** If you have do not have any information about protein species, please select Mouse. ****

[Output Example](#)

(One protein sequence at a time in [FASTA format](#): [an example](#).)

Submit

Clear

[Download Dataset](#)

***** The use of this server means that you have read and accepted *****