SUB-CELLULAR LOCALISATION OF PROTEIN SEQUENCE

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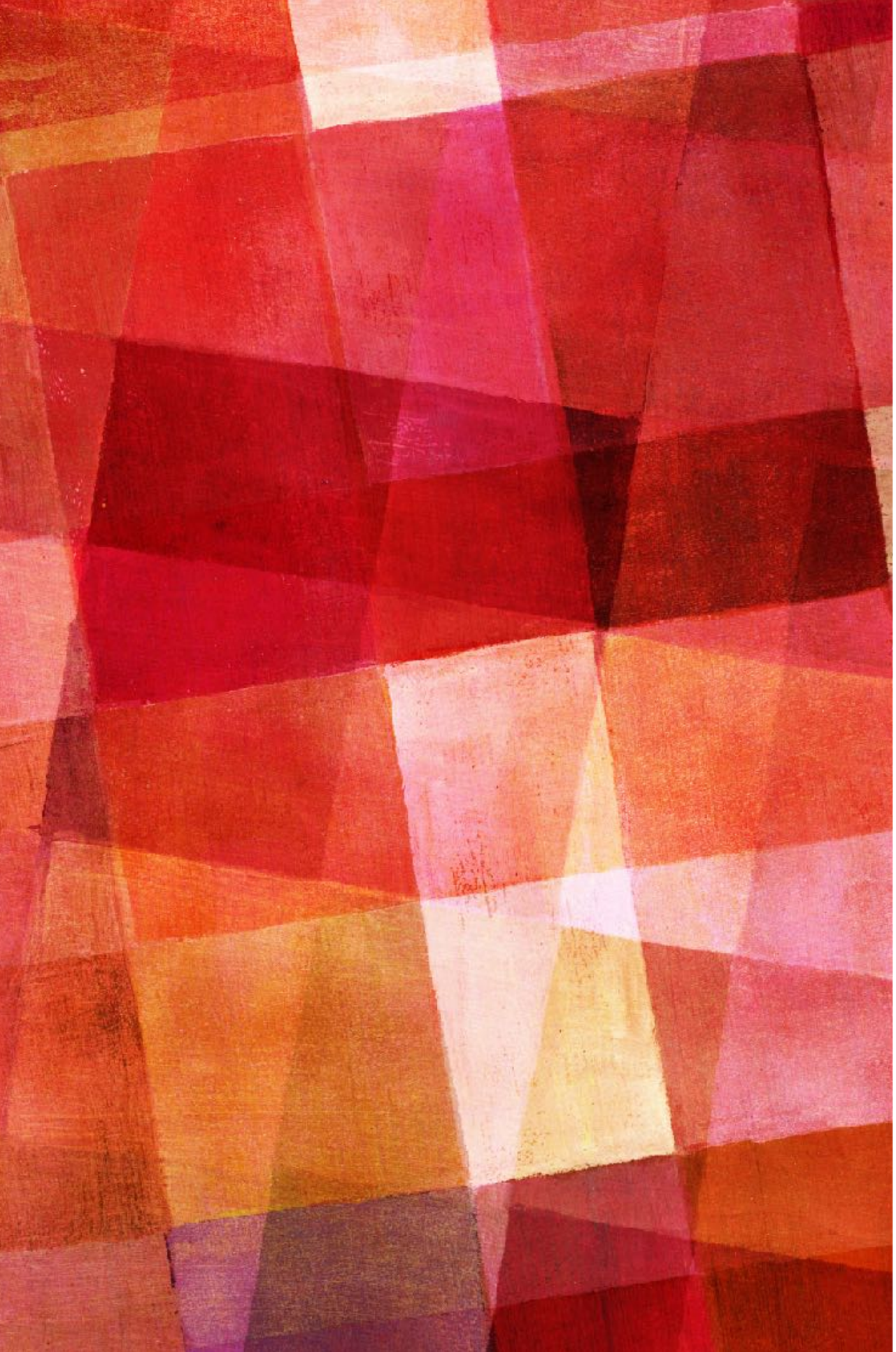
HOW TO GIVE INPUT

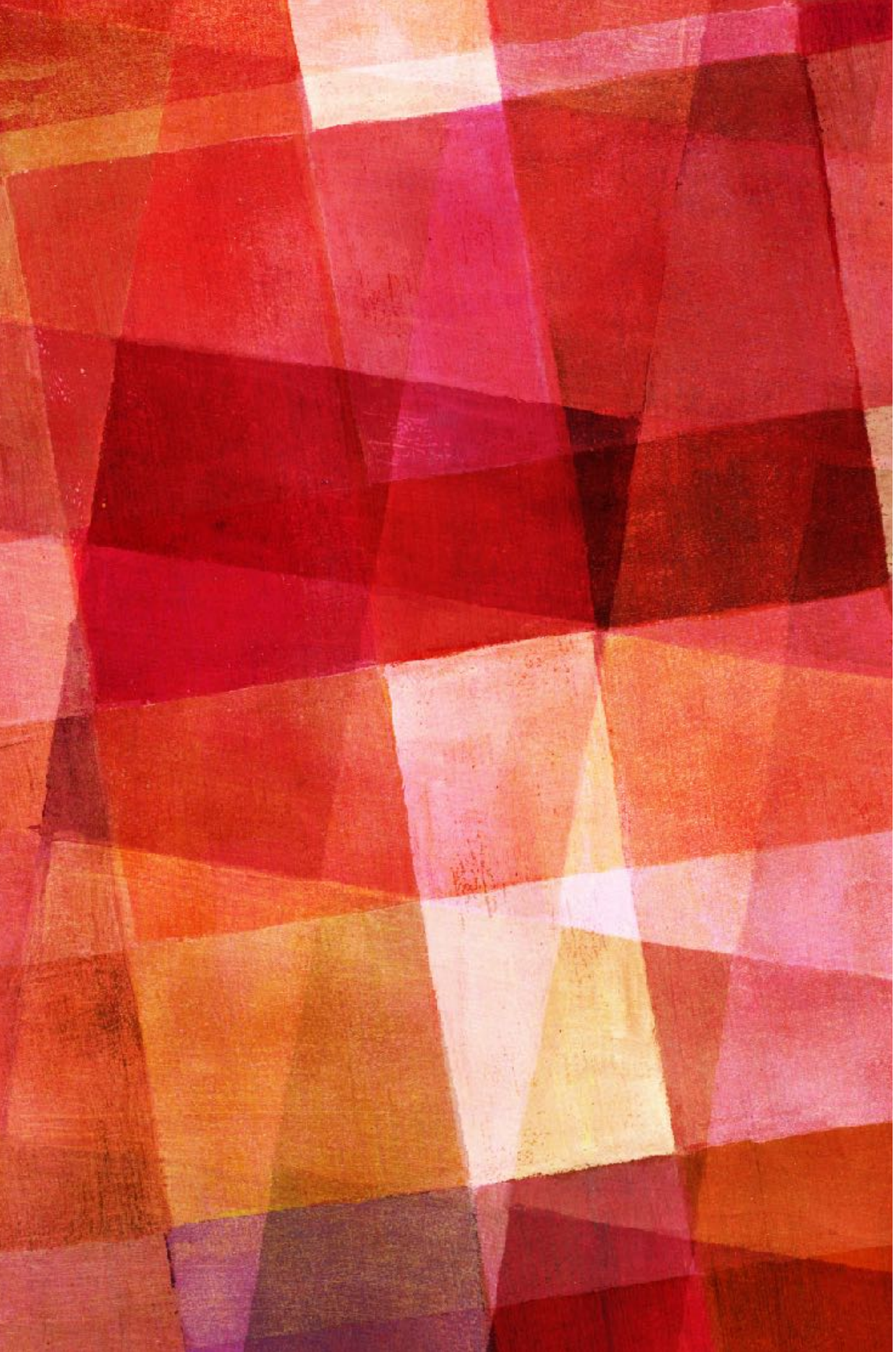
You can either give the protein sequence or the accession id of the known protein sequence as a input to the program.

The protein sequence can be a known sequence or an unknown sequence.



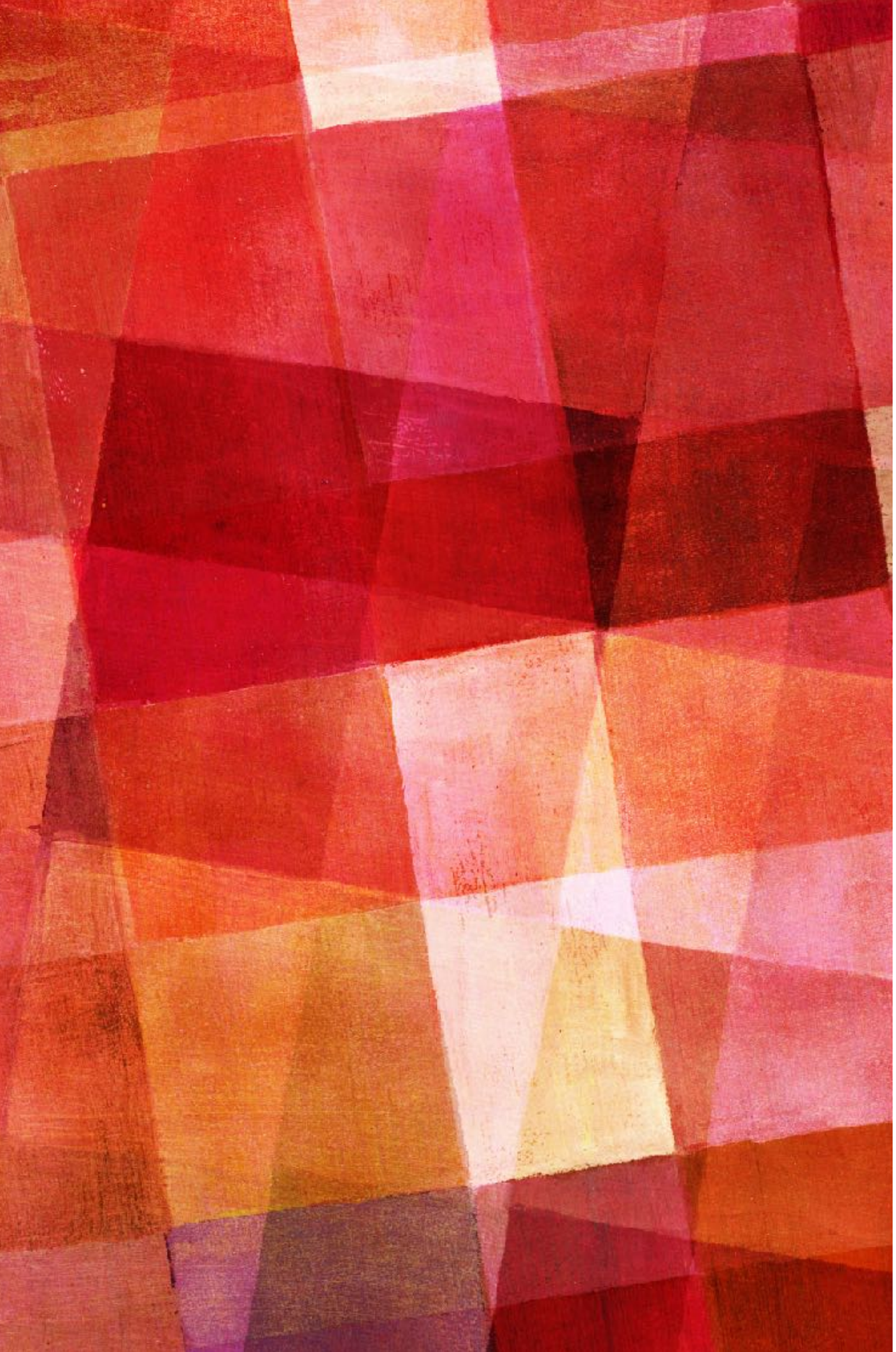
PROCEDURE

- First we run the unknown sequence on BLAST which will provides you with the protein sequence most similar to the input sequence .
- Then we run that output sequence on wolf Psort. Since its a known protein sequence so its localisation is known and that can be found by running the known sequence on wolf Psort.
- As a result we will get the exact sub-cellular localisation of the unknown sequence provided by the user.This method is based on the concept that similar protein sequence have similar sub-cellular localisation.



BLAST

- BLAST finds the region of similarity between biological sequences.This program compares nucleotide or protein sequence to sequence database and calculates the statistical significance.
- BLAST(Basic Local Algorithm Search Tool) can be used to infer functional and evolutionary relationship between sequences as well as help identify members of gene families.



WOLF PSORT

- Wolf PSORT is an extension of PSORT 2 program for protein sub-cellular localisation prediction, which is based on PSORT principle.
- Wolf PSORT converts protein's amino acid sequences into numerical localisation features based on sorting signals, amino acid composition and functional motifs.
- After conversion a simple K-nearest neighbour classifier is used for prediction.

OUTPUT

You will get the sub-cellular localisation of the given sequence.It will tell you all the possible localisations where the sequence can be found along with percentage.

Higher the percentage higher the chances that the particular sequence can be found in that particular organelle.The percentage along with the name of the organelle will be ordered in decreasing order.