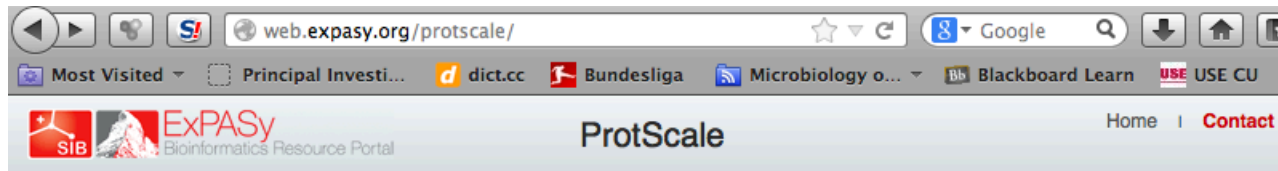


ProtScale: The website is part of the larger ExPASy group of software that does **both** Hydrophobicity and Chou-Fasman Secondary Structure predictions. URL:

<https://web.expasy.org/protscale/>

NOTE: The URL for the TMHMM part of the exercise is: <http://www.cbs.dtu.dk/services/TMHMM/>



ProtScale

ProtScale [Reference / Documentation] allows you to compute and represent the profile produced by any amino acid scale on a selected protein.

An **amino acid scale** is defined by a numerical value assigned to each type of amino acid. The most frequently used scales are the hydrophobicity or hydrophilicity scales and the secondary structure conformational parameters scales, but many other scales exist which are based on different chemical and physical properties of the amino acids. This program provides 57 predefined scales entered from the literature.

Enter a UniProtKB/Swiss-Prot or UniProtKB/TrEMBL accession number (AC) (e.g. **P05130**) or a sequence identifier (ID) (e.g. **KPC1_DROME**):

Or you can paste your own sequence in the box below:

```
>sp|Q9JKM5|S1PR5_RAT Sphingosine 1-phosphate
receptor 5 Rattus norvegicus
MESGLLRPAPVSEVIVLHNYTGKLRGARYQPGAGLRADAACVAVCAFI
VLENLAVLLV
LGRHPRFHAPMFLLLGSLTSLDLAGAAYATNILLSGPLTLRLSPALWFA
REGGVFVALA
ASVLSLLAIALERHLMARRGPAPAASRARTLAMAVAAWGLSLLGLLPA
LGWNCLGRLE
ACSTVLPYAKAYVLCVLAFLGILAAICALYARIYCQVRANARLRAGP
```

Paste amino acid
sequence into form.
Accepts fasta format.

Please choose an amino acid scale from the following list. To display information about a scale (author, reference, amino acid scale values) you can click on its name.

- | | |
|--|---|
| <input type="radio"/> Molecular weight | <input type="radio"/> Number of codon(s) |
| <input type="radio"/> Bulkiness | <input type="radio"/> Polarity / Zimmerman |
| <input type="radio"/> Polarity / Grantham | <input type="radio"/> Refractivity |
| <input type="radio"/> Recognition factors | <input type="radio"/> Hphob. / Eisenberg et al. |
| <input type="radio"/> Hphob. OMH / Sweet et al. | <input type="radio"/> Hphob. / Hopp & Woods |
| <input checked="" type="radio"/> Hphob. / Kyte & Doolittle | <input type="radio"/> Hphob. / Manavalan et al. |
| <input type="radio"/> Hphob. / Abraham & Leo | <input type="radio"/> Hphob. / Black |

- Antiparallel beta-strand
- A.A. composition
- Relative mutability

- Parallel beta-strand
- A.A. comp. in Swiss-Prot

Window size:

Changes size of sliding window

Relative weight of the window edges compared to the window center (in %):

Weight variation model (if the relative weight at the edges is < 100%): linear exponential

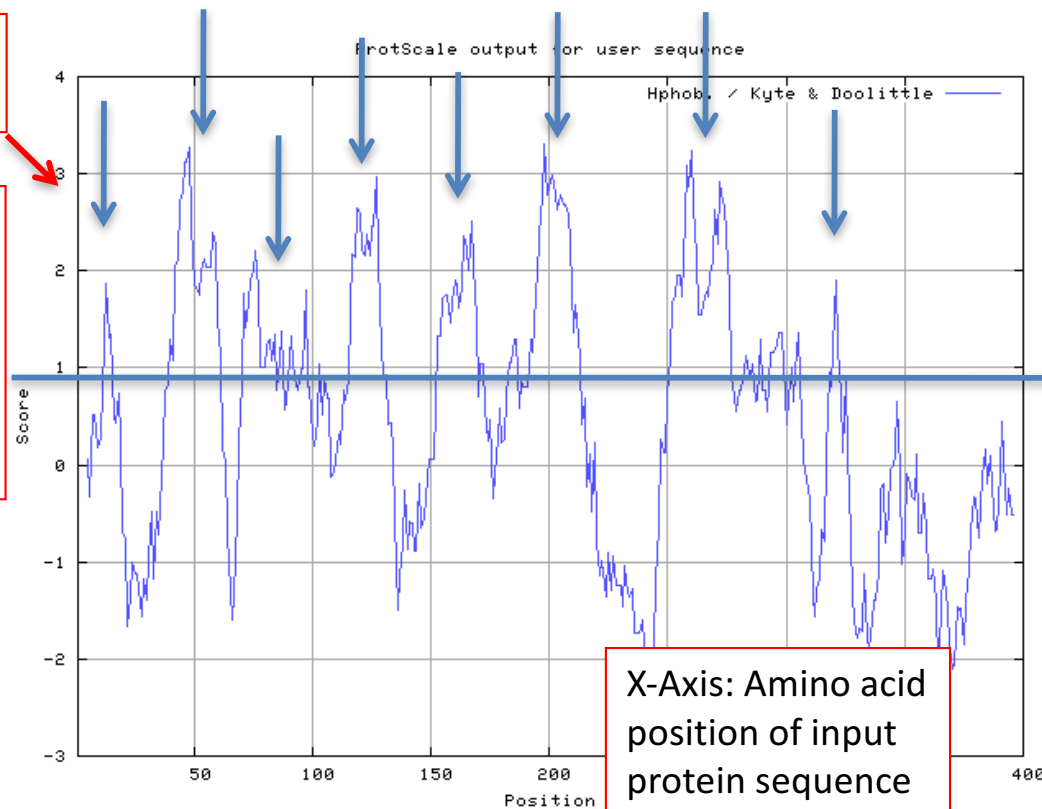
Do you want to normalize the scale from 0 to 1? yes no

If you need more information about how to set these parameters, please click [here](#).

Hit Submit
Produces predictions

Y-Axis:
Hydrophobicity
Score. The higher
the peak the
more hydrophobic
the region.

Peaks indicate predicted regions of Hydrophobicity



X-Axis: Amino acid
position of input
protein sequence

Select a different radio button to perform **alpha-helix**, **beta-sheet**, or many other single-sequence protein analyses.

- Molecular weight
- Bulkiness
- Polarity / Grantham
- Recognition factors
- Hphob. OMH / Sweet et al.
- Hphob. / Kyte & Doolittle
- Hphob. / Abraham & Leo
- Hphob. / Bull & Breese
- Hphob. / Guy
- Hphob. / Miyazawa et al.
- Hphob. / Roseman
- Hphob. / Wolfenden et al.
- Hphob. HPLC / Wilson & al
- Hphob. HPLC pH3.4 / Cowan
- Hphob. / Rf mobility
- HPLC / TFA retention
- HPLC / retention pH 2.1
- % buried residues
- Hphob. / Chothia
- Ratio hetero end/side
- Average flexibility
- beta-sheet / Chou & Fasman
- alpha-helix / Deleage & Roux
- beta-turn / Deleage & Roux
- alpha-helix / Levitt
- beta-turn / Levitt
- Antiparallel beta-strand
- A.A. composition
- Relative mutability
- Number of codon(s)
- Polarity / Zimmerman
- Refractivity
- Hphob. / Eisenberg et al.
- Hphob. / Hopp & Woods
- Hphob. / Manavalan et al.
- Hphob. / Black
- Hphob. / Fauchere et al.
- Hphob. / Janin
- Hphob. / Rao & Argos
- Hphob. / Tanford
- Hphob. / Welling & al
- Hphob. HPLC / Parker & al
- Hphob. HPLC pH7.5 / Cowan
- HPLC / HFBA retention
- Transmembrane tendency
- HPLC / retention pH 7.4
- % accessible residues
- Hphob. / Rose & al
- Average area buried
- alpha-helix / Chou & Fasman
- beta-turn / Chou & Fasman
- beta-sheet / Deleage & Roux
- Coil / Deleage & Roux
- beta-sheet / Levitt
- Total beta-strand
- Parallel beta-strand
- A.A. comp. in Swiss-Prot

For alpha-helix predictions