

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: URL for the TMHMM part -> <https://dtu.biolib.com/DeepTMHMM>

Expasy ProtScale Home | [Contact](#)

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:

```
MGPTSVPLVKAHRSSVSDYVNYDIIVRHNYTGKLNISADKENSITKLTSTV
VFILICCFIILENIFVLLTIWKTKKFHRPMYYFIGNLALSDLLAGVAYTA
NLLLSGATTYKLTQAQWFLREGSMFVALSASVFSLLAIAIERYITMLKMK
LHNGSNNFRLFLLISACWVLSLILGGLPIMGWNCISALSSCSTVLPYHK
HYILFCTTVFTLLLSIVILYCRITYSLVTRSRRLTFRKNISKASRSSEK
SLALLKTVIIVLSVFIACWAPLFILLLLDVGCKVKTCDILFRAEYFLVLA
VLNSGTNPIIYTLTNKEMRRAFIRIMSCCKCPSGDSAGKFKRPIIAGMEF
SRSKSDNSSHPQKDEGDPETIMSSGNVNSS
```

Paste amino acid sequence into form. Use the sequence without the title line for best results.

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"/> Hydropath. / 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

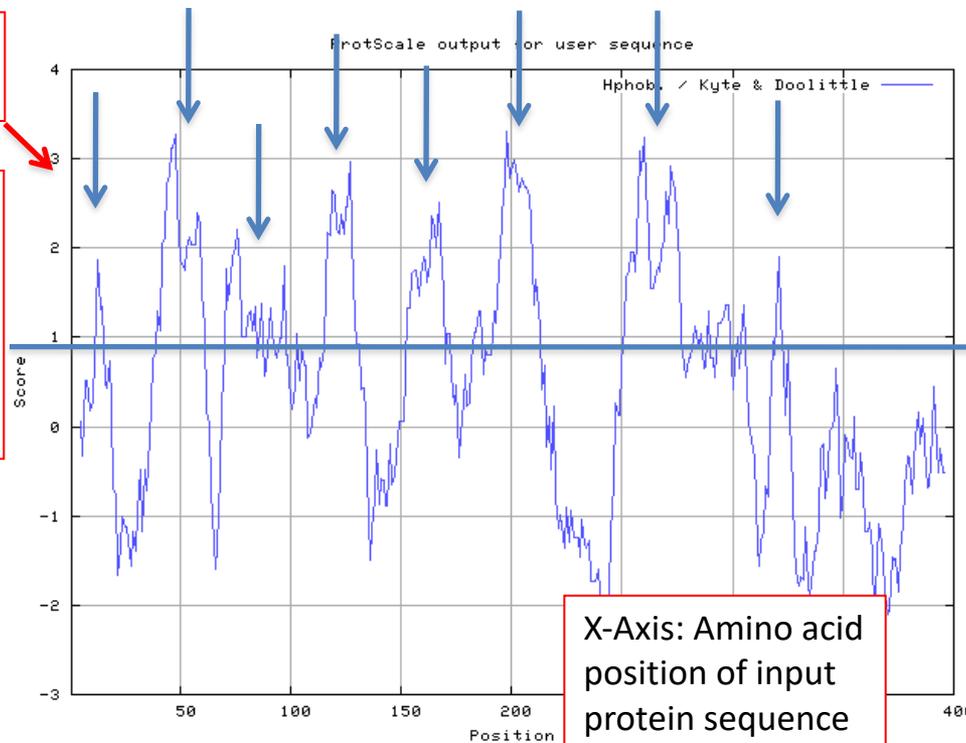
Do you want to normalize the scale from 0 to 1? yes no

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.

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

For alpha-helix predictions