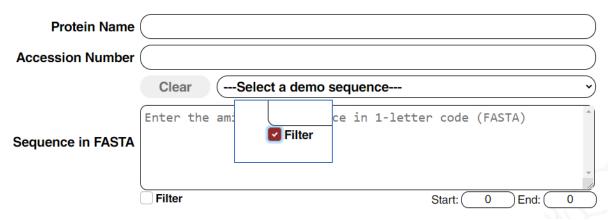# EpiStat – Operation Manual

What is EpiStat?

EpiStat is a simple program used to analyse the amino acid content of protein/peptide sequences. It also produces reports on various types of amino acids that comprise the protein.

Entering the Data

To analyse the sequence, simply **Paste** it into the **Sequence** window . We recommend also entering the accession number of the sequence you use and the name of your sequence or project. This data will be present in all **Results** you save after the analysis.

If your sequence contains gaps (may appear due to formatting) or contains abnormal signs (punctuation/letters that are not amino acid code) the analysis will be aborted. To avoid it, keep the "Filter" option selected.

To analyse only a fragment of the sequence, please enter the position number of the first and the last amino acids of the fragment you want to analyse. Please be aware that the numeration of the sequence starts from the first amino acid of the original sequence and will be kept during the analysis of the fragment. For example, if the first aa of the fragment was 101 it will be indicated as 101 in all further analysis and Results.

However, if you paste a sequence fragment into the sequence window, its first amino acid will be referred to as position 1, not the position in the original sequence- - source of the fragment.

You may **Paste** not only a single sequence, but several sequences, i.e. a set of peptides. The program will produce a result of the entire massive of the entered sequences.

Viewing and saving the Results

The results of the analysis are in tabular form:

Protein Composition

Save data

Protein name: Human AG: NS1, partial [Dengue virus 2]
Sequence length: 380aa
Fragment: 1 - 150

Amino acid composition

Aminoacid			Q-ty	%
Alanine	Ala	A	5	3.33
Arginine	Arg	R	7	4.67
Asparagine	Asn	N	6	4.00
Aspartate	Asp	D	3	2.00
Cysteine	Cys	C	3	2.00
Glutamine	Gln	Q	8	5.33
Glutamate	Glu	E	10	6.67
Glycine	Gly	G	11	7.33
Histidine	His	H	3	2.00
Isoleucine	Ile	I	10	6.67
Leucine	Leu	L	13	8.67
Lysine	Lys	K	13	8.67
Methionine	Met	M	5	3.33
Phenylalanine	Phe	F	2	1.33
Proline	Pro	P	4	2.67
Serine	Ser	S	16	10.67
Threonine	Thr	T	11	7.33
Tyrosine	Tyr	Y	3	2.00
Valine	Val	V	13	8.67
Tryptophan	Trp	W	4	2.67

Types of aminoacids

Type of aminoacid	Codes	Q-ty	%
Very hydrophobic	F, I, W, L, V, M	47	31.33
Hydrophobic	Y, C, A	11	7.33
Neutral	T, S, G, Q, H	49	32.67
Hydrophilic	R, K, N, E, P, D	43	28.67
		150	100.00

Type of aminoacid	Codes	Q-ty	%
Aromatic	F, W, Y	9	6.00
Aliphatic	I, L, V, A	41	27.33
Neutral side chains	M, C, T, S, Q, N	49	32.67
Basic with charged side chains	H, R, K	23	15.33
Acidic, charged side chains	E, D	13	8.67
Unique	G, P	15	10.00
		150	100.00

You may *Save* the report for your records as a standalone HTML document that may be further converted into other formats.