

## Using Amino Acid Analysis for Protein Identification



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Complete hydrolysis of a protein to its component amino acids allows automated separation and quantification at the pmole to nanomole level. Although sequence information is lost, compositional data provides a protein specific fingerprint for identification purposes.

Compositional data of peptides and proteins can be determined using an amino acid analyser.

If the identity of a protein is unknown, the compositional data of the protein can be used in searching protein databases.

A programme that provides this function is the AA Compldent tool from the Swiss Institute of Bioinformatics. This database can be found at [www.expasy.ch/tools/aacomp](http://www.expasy.ch/tools/aacomp).

The tool can be used to identify a protein from its amino acid composition. Swiss-Prot and/or TrEMBL databases are used to search for amino acid compositions that are closest to the amino acid composition given (1)

As an experiment, the human insulin beta chain was chosen as the test protein and the amino acid composition of the this protein was input into the AA Compldent tool (see tables 1 and 2).

Choosing a protein of known composition allowed us to test the accuracy of the AA Compldent tool, and determine whether using the amino acid composition would allow us to identify the correct protein from the database.


The programme matches the percentage empirically measured amino acid composition of the protein against the theoretical percentage amino acid composition of proteins. Results tables are emailed to the user (see Table 3 for the returned table). The score represents the degree of difference between the composition of the

Species searched	HOMO SAPIENS
pI	7.00
Mw	5000

Amino Acid	% composition
Asp	0.00
Gln	3.30
Gly	10.00
Pro	0.00
Val	10.00
Ile	0.00
Phe	0.00
Asp	3.30
Ser	3.30
Thr	6.70
Tyr	6.70
Met	0.00
Leu	13.30
Lys	3.30
Glu	6.70
His	6.70
Ala	3.30
Arg	3.30
Cys	6.70
Trp	0.00

**Table 1 and 2. Data input into the AA Compldent tool**

unknown protein and a protein in the database. The score is calculated for each database entry by the sum of the squared difference between the percentage amino acid composition for all amino acids of the unknown protein and the database entry.



Rank	Score	Protein	Description
1	11	<u>INS_HUMAN</u>	Insulin B chain
2	112	<u>ZDH4_HUMAN</u>	Zn finger DHHC domain containing
3	136	<u>CIW1_HUMAN</u>	Potassium channel subfamily K member 1
4	140	<u>CTE2_HUMAN</u>	Protein C20orf142
5	143	<u>2B14_HUMAN</u>	HLA class II histocompatibility antigen
6	145	<u>PLCC_HUMAN</u>	1-acyl-sn-glycerol-3-phosphate
7	150	<u>DER7_HUMAN</u>	31680 Dermal papilla derived protein 7.
8	151	<u>2B32_HUMAN</u>	HLA class II histocompatibility antigen
9	152	<u>SPR1_HUMAN</u>	Sphingosylphosphorylcholine receptor
10	152	<u>C151_HUMAN</u>	Platelet-endothelial tetraspan antigen 3
11	154	<u>GP42_HUMAN</u>	Probable G protein-coupled receptor
12	154	<u>ICE2_HUMAN</u>	Caspase-2 subunit p18.
13	156	<u>2B31_HUMAN</u>	HLA class II histocompatibility antigen
14	157	<u>MYPR_HUMAN</u>	Myelin proteolipid protein (PLP)
15	158	<u>2B18_HUMAN</u>	HLA class II histocompatibility antigen
16	160	<u>GP97_HUMAN</u>	Probable G protein-coupled receptor 97
17	160	<u>B4G4_HUMAN</u>	Beta-1,4-galactosyltransferase 4
18	161	<u>ZDHF_HUMAN</u>	Zinc finger DHHC domain containing
19	163	<u>GP41_HUMAN</u>	Putative G protein-coupled receptor
20	163	<u>ADR1_HUMAN</u>	Adiponectin receptor protein

**Table 3. Output emailed to user**

All proteins in the database are ranked according to their score, from lowest (best match) to highest (worst match), see table 3.

The AACompident Tool ranks Insulin Beta Chain as the highest match (marked with a star), which gives us confidence in using this tool to identify unknown proteins using amino acid composition.

Using the Biochrom 30 Amino Acid Analyser to identify proteins provides an additional application for the instrument.

## Reference

1. **Boeckmann B., Bairoch A., Apweiler R., Blatter M.-C., Estreicher A., Gasteiger E., Martin M.J., Michoud K., O'Donovan C., Phan I., Pilbout S., Schneider M.**

**The SWISS-PROT protein knowledgebase and its supplement TrEMBL in 2003  
Nucleic Acids Res. 31:365-370 (2003).**