

## **Guidelines for Feed Analysis Laboratories: Importing a Lab Analysis into AminoCow (Revised September 18, 2008)**

The AminoCow program can now automatically load feed analysis sample results attached to e-mails directly into the program. This document provides guidelines to laboratories contemplating providing this service to their customers. Any laboratory interesting in participating in this program and desiring more information should contact Robert Patton at Nittany Dairy Nutrition ([nittanydairynutrition.com](http://nittanydairynutrition.com)).

### **Basic Requirements**

All feed imports into AminoCow are in the form of text files, which must adhere to a prescribed format. Feed laboratories desiring to export lab samples to users of AminoCow must be able to produce files in this format. The AminoCow lab sample import procedure is based on the general assumption that text files are e-mailed to the user and are stored in a designated folder on the user's machine. However, if it is more convenient for the lab and the user, methods other than e-mail can be used to transfer the text file. The procedures for using the lab sample text file in AminoCow are given in separate user documentation and are not the responsibility of laboratories.

### **The Structure of Lab Analysis Text File**

AminoCow uses a standard text file structure for all feed data imports and it is a general requirement that any text file conform to this structure. The following rules apply:

1. The file must be named with the .txt extension.
2. The only delimiter allowed in a text file is the <tab> character.
3. The text file is divided into sections, with the sections described below.
4. Text files can contain multiple samples for different users.
5. Within certain limitations, laboratories can define the header information for each sample. The limitations are that lab header information must contain information sufficient to allow the user to identify the client and the feed included in the sample. Typically, this will be the client name or code as known to the laboratory and the feed name or code as known to the laboratory.
6. The name of each nutrient must conform to the name of the nutrient as it is used in AminoCow. However, except for the name of the feed there are no required nutrients and nutrients can be in any order.
7. Section delimiters such as "Lab Information" must appear on their own line and are case sensitive. Nutrient names are not case sensitive.
8. Nutrients must be expressed in the same units as AminoCow. For example, AminoCow expresses Soluble Protein and RDP as a % of CP rather than as % of DM. A full list of available AminoCow nutrients and their units of expression are included in this document.

AminoCow lab analysis files contain three sections: a file header, a lab header, and a nutrient section. There is one file header per file and a lab header and nutrient section for each sample included in the file.

### **The File Header Section**

The header section appears as the first lines in the file and is required. The lines are as follows:

[Español]

AminoCow Lab Analysis File

Version 3.5.2 [LBS]

Decimal Symbol = 0

Line 1 indicates the language of the file. It is optional and if it is not included, the language is assumed to be English. If the language is other than English, it must be included the language section and it must be enclosed in [ ]. Line 2 tells AminoCow what kind of feed is being imported. Line 3 specifies the import format. The value in brackets indicates the system of measurement used for energy and vitamins. If the system of measurement is not included, LBS is assumed. The three possible values for this field are [LBS], [KG], and [MJ]. Use LBS if the energy density is expressed in MCal per lb, KG if the density is expressed in MCal per kg and MJ if it is expressed in MJ per kg. All samples in a file must use the same unit of measurement. Line 4 specifies the decimal format. A value of 0 indicates that the "." is used as the decimal separator, while a value of 1 indicates that the "," is used as the decimal separator. There is only one header section per file although the file may contain multiple feed samples.

Following the header section are the Lab Section and the Nutrient Section. The combination of these two sections defines the feed analysis to be imported. All data lines in the Lab Section and the Nutrient Section are tab delimited with the following structure:

```
<label><tab><data>
```

Every line must have a label followed by the tab character. The data field is optional and can contain data, contain a -1 indicating missing data or simply be left blank.

### Lab Header Section

The Lab Header Section always begins with the "Lab Information" line This section of the data file contains lab information regarding the sample. Up to 6 lines in this section will appear on the user's screen and in the lab queue. The required elements and order for this section are a line identifying the lab performing the analysis, an account or other reference, the dairy/client name, the name or description of the feed, the date of the analysis, and the lab's identification of the feed type. The labels for items in this section can differ from the labels in the example below, but the data must appear in the order specified. The information in this section will play a critical role in allowing a nutritionist to correctly match a lab analysis with an AminoCow feed.

A maximum of 25 characters is displayed for the item label as well as for the item. The format for each line in this section is: <item label><tab><item>.

There are four rules for the Lab header:

1. The Lab Header Section must begin with the delimiter "Lab Information" and end with the delimiter "End Lab".
2. The first six lines following "Lab Information" must be in this order with the following recommended labels: "Lab", "Reference", "Dairy/Client Name", "Feed Description", "Analysis Date" and "Feed Type" if available.
3. The "Lab" field should uniquely identify your lab and should be the same for all samples, while the "Reference" should be a unique identifier for each sample produced by your lab. "Reference" is an alpha numeric field and there are no restrictions on length.
4. If FeedType is not a part of the analysis, the "FeedType" line should be included with no data.

The following is an example of how this section might look.

```
Lab Information  
Lab<tab>AAForageLab  
Reference<tab>1234  
Dairy/Client<tab>AAA Holsteins  
Feed Description<tab>Bunk #2 Corn silage  
Analysis Date<tab>07/17/06  
FeedType<tab>CS
```

End Lab

While there can be additional fields in this section, only the first 6 fields will be saved by AminoCow. Laboratories use different codes and methods for providing feed type information and where this field is not applicable, the "FeedType" line with the <tab> delimiter must be included, but the data field can be left blank.

### **Nutrient Information Section**

The last section contains nutrient information. In this section each line must begin with a nutrient label and this label must correspond to the name of a nutrient field as found in the AminoCow database. The order of the nutrient lines is not important and nutrients for which there are no data values (1) can be skipped (i.e. not reported), or (2) the data field can be left blank or (3) the data field can be given a value of -1 to indicate missing data. In this context "0", meaning the nutrient was measured and not detected, is regarded as a legitimate value for a nutrient and should not be used to indicate a missing value. AminoCow assumes that the "Nutrient Information Section" begins immediately after the "End Lab" line.

The only required line in the nutrient section is the feed line, which gives the name of the feed. Usually this will be the name of the feed as used by the lab. The format for this line is: Feed<tab>feed name. AminoCow accepts a maximum of 30 characters for a feed name including the "-" and "\_". Apostrophes are not allowed in feed names. Laboratory feed names longer than 30 characters will be truncated to the first 30 characters and apostrophes will be removed.

The end of the Nutrient Section is marked by the phrase "End Feed". If there are multiple feeds in the file, the next sample with its associated Lab Section can begin immediately after "End Feed". A nutrient map with the AminoCow nutrient labels is included in the next section of this document. If a nutrient name is included, a tab must follow the nutrient name even though no value is given for the nutrient.

#### **Rules for the Nutrient Information Section:**

1. Feed name is the only required nutrient value.
2. Nutrients must conform to AminoCow nutrient names
3. Nutrients must be expressed in same units as AminoCow units
4. Nutrients must be followed by a <tab> even where no value is reported.
5. The section must end with "End Feed"
6. 0 cannot be used to indicate a missing value.

The following is an example of a sample nutrient section.

```
Feed<tab>Bunk #2 Corn Silage
DM%<tab>27.3
CP<tab>7.5
ADF<tab>22.99
NDF<tab>39.24
ASH<tab>5.79
FAT<tab>2.90
NEL<tab>0.73
CA<tab>0.23
P<tab>0.20
MG<tab>0.18
K<tab>0.68
NA<tab>-1
CL<tab>-1
S<tab>0.11
ADCP<tab>0.89
LIGNIN<tab>
```

End Feed

The "End Feed" line can be followed by "Lab Information" if there are additional samples. If the sample is the last sample in the file, "End Feed" is followed by "End Feeds" and then "End File." The following is the required end of file sequence.

End Feed  
End Feeds  
End File

"End Feeds" indicates that all feeds have been processed and is used to maintain consistency with other Import/Export functions in AminoCow. "End File" is a simple way of marking the end of the data and is also used to maintain consistency with other Import/Export functions in AminoCow.

### **AminoCow Nutrient Codes**

The following are the AminoCow nutrient codes for most items that might be included in a nutrient analysis. Field names in italics are calculated fields and any lab analysis values for these fields will be ignored. Items marked with an \* are important components of the calculation of the amino acid content of rations and their inclusion is particularly helpful in AminoCow. Field names are not case sensitive.

<b>Code</b>	<b>Description/Note</b>
FEED	The name of the feed
DM%	% DM*
NEL	Mcal/lb or Mcal/kg
NEM	Mcal/lb or Mcal/kg
NEG	Mcal/lb or Mcal/kg
CP	Crude protein % of DM*
<i>RUP</i>	Undegradable crude protein - % of CP
<i>RDP</i>	Degradable crude protein - % of CP
ADF	% DM*
NDF	% DM*
<i>NFC</i>	NFC is calculated by difference
<i>TDN</i>	Calculated, % DM
EE	Fat - % of DM*, this is crude fat, not true fatty acid
ASH	% of DM*
CA	% of DM
P	% of DM
MG	% of DM
K	% of DM
NA	% of DM
CL	% of DM
S	% of DM
CO	PPM
CU	PPM
FE	PPM
I	PPM
MN	PPM
ZN	PPM
SE	PPM
STARCH	% DM
SUGAR	% DM

FMSTARCH	fermentability of starch - % Starch
VFA	% DM
EFFNDF	Effective NDF - % DM
LIGNIN	% DM*
<i>SOLPROTEIN</i>	Soluble intake protein - % CP
ADICP	Acid detergent crude protein - % DM*
NDICP	Neutral Detergent Crude Protein - % DM*
VIT A	KIU/lb or KIU/kg
VIT D	KIU/lb or KIU/kg
VIT E	IU/lb or IU/kg
CHOLINE	mg/lb or mg/kg
NIACIN	mg/lb or mg/kg

### **Verification**

Laboratories interested in participating in this program should submit samples of text files to Nittany Dairy Nutrition for verification. The verification process is designed to insure that text files meet the requirements stated above and can be read and processed by AminoCow. The verification process is not concerned with the content of any given feed analysis or with the methodology used to perform the analysis. For more information on verification, contact Robert Patton at [nittanydairynutrition.com](http://nittanydairynutrition.com).