# MILLENNIUM APPLICATION BRIEF

## TOPIC: Calculation of [redacted]s Using the Millennium Custom Calculation Feature

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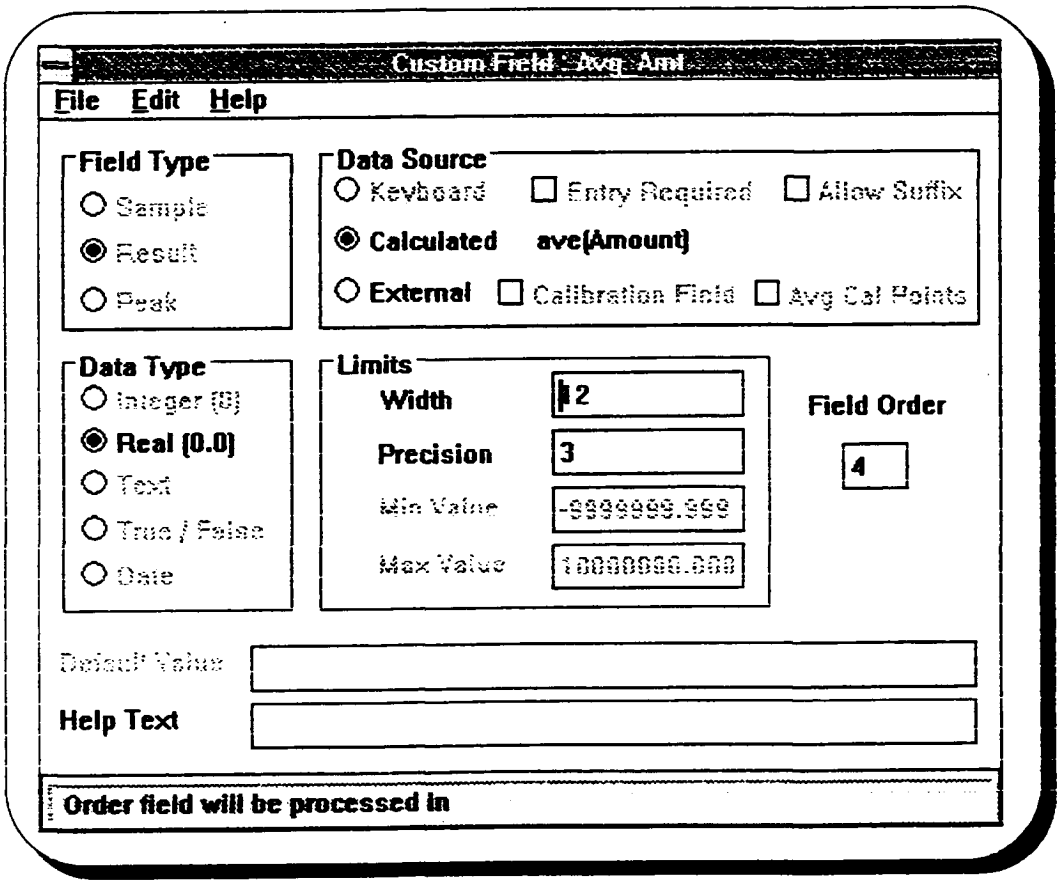
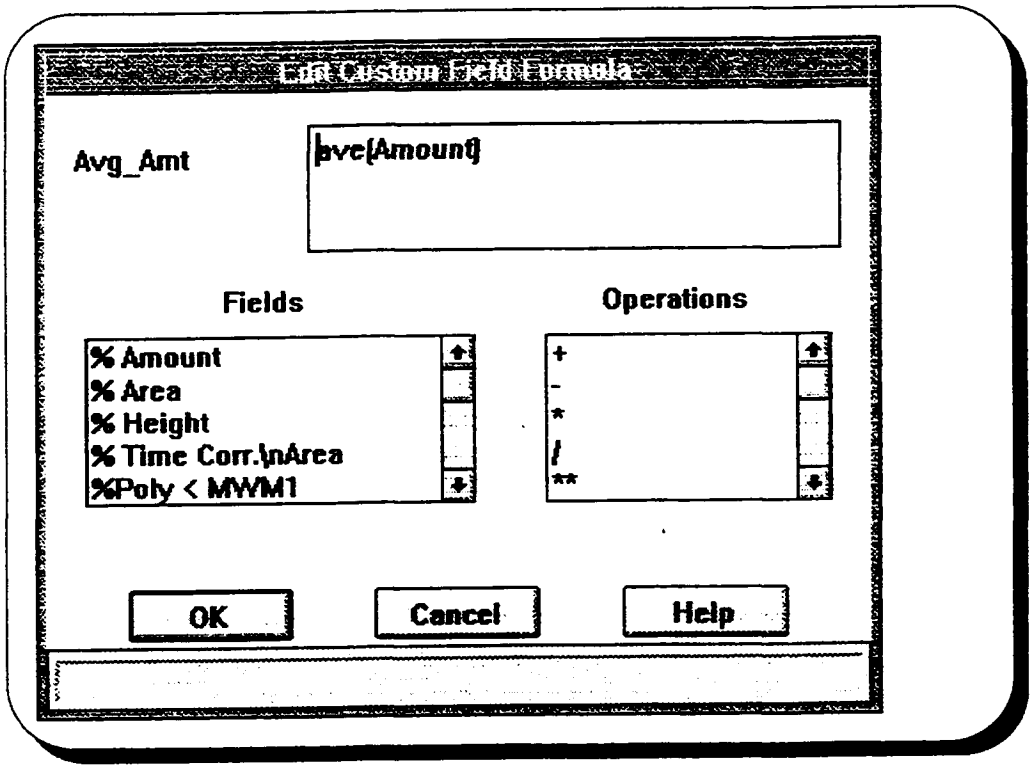
**Introduction:**

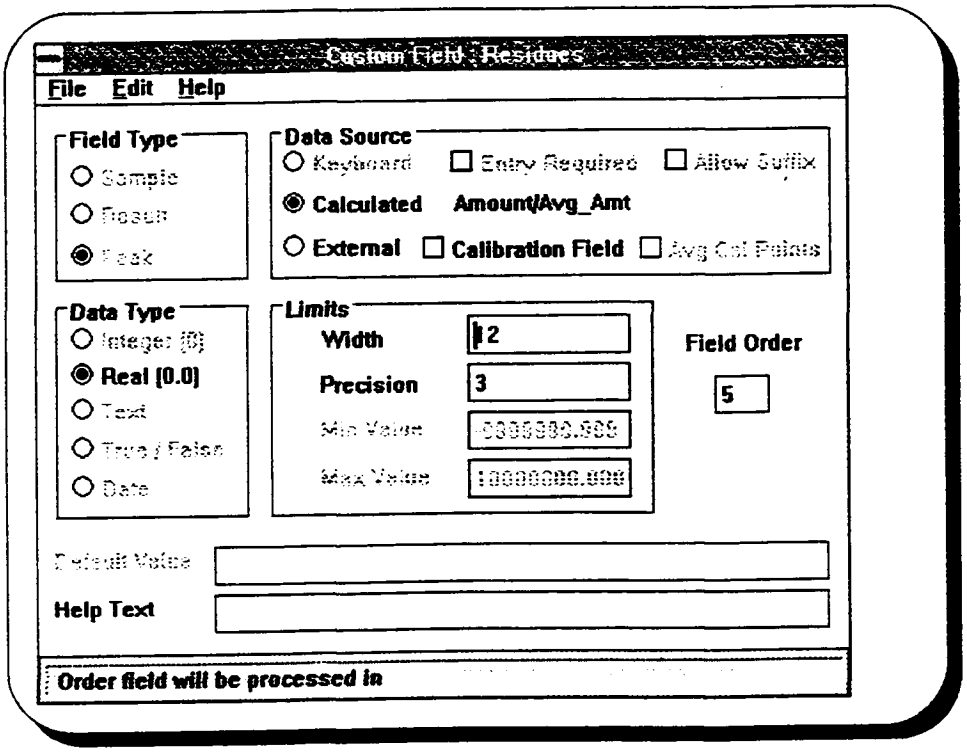
Recently a customer using our [redacted] system was interested in being able to calculate the number of residues of each amino acid present in their original peptide or protein sample. This calculation is very easy to do using the millennium custom calculation feature. This calculation is simple the average number of all amino acids present in the sample divided into each amino acid amount. To do this in millennium you first need to make sure that you have set the AMQ and NH3 peaks to none for quantitate by in the integration method. Second, you need to create a custom field for the average amount present by creating a custom result field (Avg_Amt) as shown below.

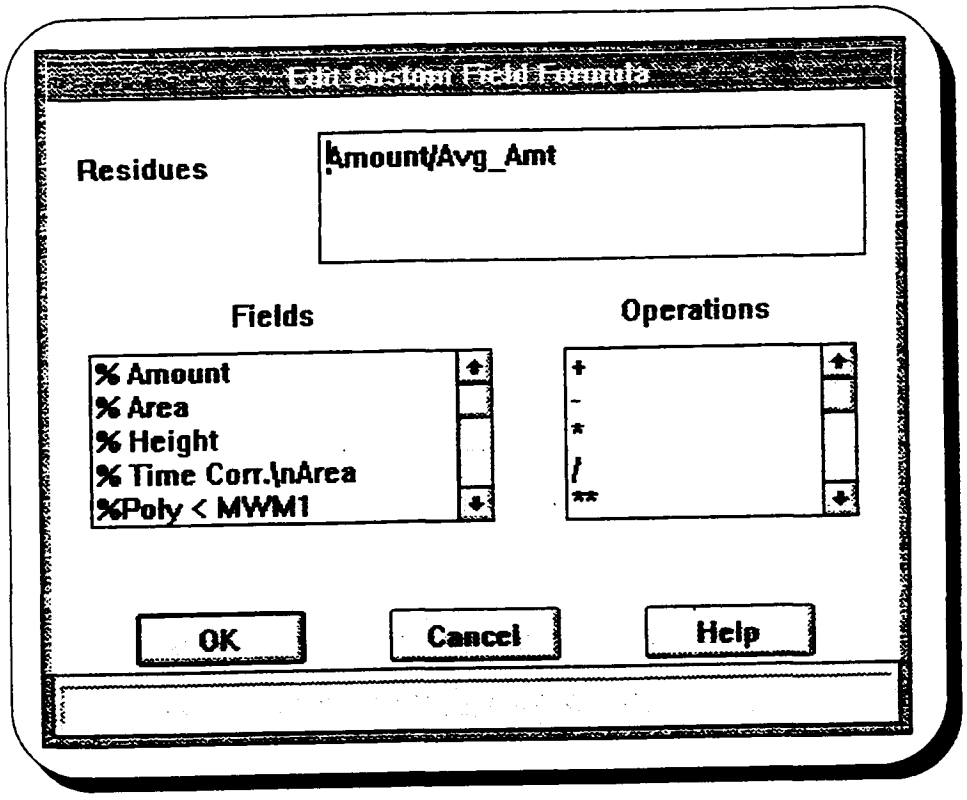


Next, you need to set up the average amount calculation by selecting formula and entering the following formula.




Finally, you need to now set up a peak custom field which divides each peak amount by the Avg_Amt field you just created. Shown below is the field and formula used.

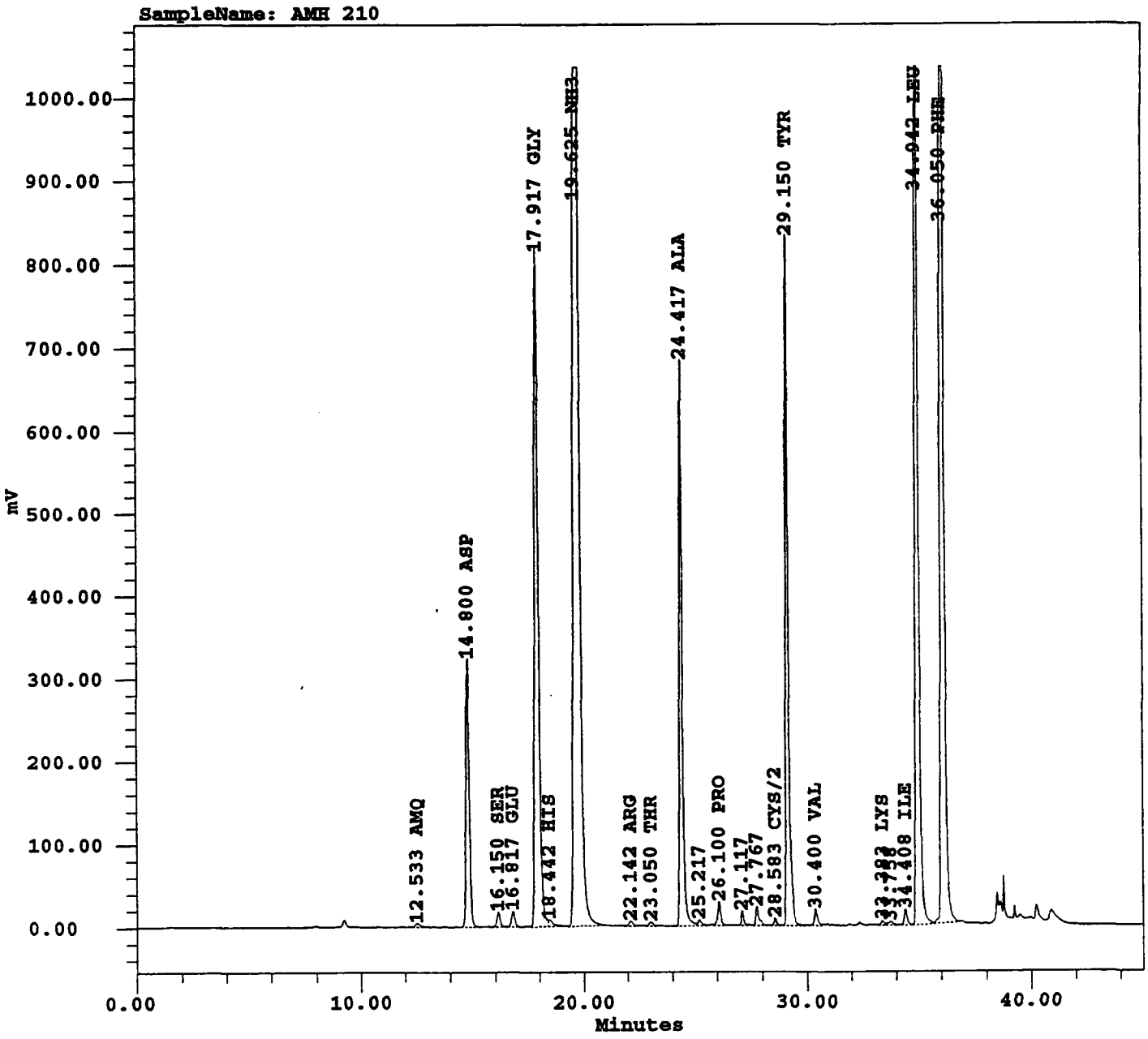





Attached is an example report which incorporates this new field in the report showing not only pmol of each amino acid present but also the residue numbers. Once set up this field can be used for all future projects.

AccQ*Tag Method Sample Information

| | | | |
|---|---|---|---|
| Sample Name: | AMH 210 | | |
| Vial: | 3 | Sample Type: | Unknown |
| Injection: | 1 | Run Time: | 45.0 min |
| Volume: | 10.00 | Channel: | SATIN |
| Set Name 17 | | Channel Descr. 474 ex 250nm em395 | |
| Project Name: | AccQTag_NE | | |
| Acq Meth Set: | AccQ_Tag_MS2 | Date Acquired: | 03/17/95 11:42:52 AM |
| Processing Method: | AccQ_Tag_PM3a | Date Processed: | 03/20/95 11:14:09 PM |



Result Table Information

SampleName AMH 210 Vial 3 Injection 1

Set Name 17

Processing Method: AccQ_Tag_PM3a

*Peak Results*

| # | Amino Acid | Ret Time (min) | Area (uV*sec) | Height (uV) | Pmol | Residues |
|---|---|---|---|---|---|---|
| 1 | AMQ | 12.53 | 58397 | 4128 | | |
| 2 | ASP | 14.80 | 3317675 | 327406 | 158.03 | 2.172 |
| 3 | SER | 16.15 | 184833 | 17435 | 6.40 | 0.088 |
| 4 | GLU | 16.82 | 194659 | 18439 | 8.10 | 0.111 |
| 5 | GLY | 17.92 | 9576438 | 822847 | 354.88 | 4.877 |
| 6 | HIS | 18.44 | 105973 | 7454 | 2.58 | 0.035 |
| 7 | NH3 | 19.62 | 21934737 | 1035023 | | |
| 8 | ARG | 22.14 | 65913 | 5786 | 1.77 | 0.024 |
| 9 | THR | 23.05 | 54192 | 4834 | 1.55 | 0.021 |
| 10 | ALA | 24.42 | 6049472 | 700452 | 166.45 | 2.288 |
| 11 | | 25.22 | 86275 | 7375 | | |
| 12 | PRO | 26.10 | 271478 | 28778 | 14.24 | 0.196 |
| 13 | | 27.12 | 120273 | 17261 | | |
| 14 | | 27.77 | 207457 | 23159 | | |
| 15 | CYS/2 | 28.58 | 64802 | 8832 | 6.87 | 0.094 |
| 16 | TYR | 29.15 | 6633751 | 844483 | 167.88 | 2.307 |
| 17 | VAL | 30.40 | 189566 | 19812 | 2.77 | 0.038 |
| 18 | MET | 30.88 | | | | |
| 19 | LYS | 33.38 | 47356 | 5529 | 1.54 | 0.021 |
| 20 | | 33.76 | 56088 | 4047 | | |
| 21 | ILE | 34.41 | 169008 | 18886 | 1.94 | 0.027 |
| 22 | LEU | 34.94 | 11840549 | 1034862 | 140.13 | 1.926 |
| 23 | PHE | 36.05 | 13619184 | 1033248 | 129.02 | 1.773 |