```c
/* Peptide Fragment Size Calculation program */
/* To calculate the theoretical different peptide fragments */
/* by the given amino acid sequence and enzyme cleaveage sites */
/* Program Composer: Alex Tzuu-Wang Chang */

#define Max_Protein_Sequence_Length 500
char BoNTA_LC[449] =
 { 'M','P','F','V','N','K','Q','F','N','Y','K','D','P','V','N',
   'G','V','D','I','A','Y','I','K','I','P','N','A','G','Q','M',
   'Q','P','V','K','A','F','K','I','H','N','K','I','W','V','I',
   'P','E','R','D','T','F','T','N','P','E','E','G','D','L','N',
   'P','P','P','E','A','K','Q','V','P','V','S','Y','Y','D','S',
   'T','Y','L','S','T','D','N','E','K','D','N','Y','L','K','G',
   'V','T','K','L','F','E','R','I','Y','S','T','D','L','G','R',
   'M','L','L','T','S','I','V','R','G','I','P','F','W','G','G',
   'S','T','I','D','T','E','L','K','V','I','D','T','N','C','I',
   'N','V','I','Q','P','D','G','S','Y','R','S','E','E','L','N',
   'L','V','I','I','G','P','S','A','D','I','I','Q','F','E','C',
   'K','S','F','G','H','E','V','L','N','L','T','R','N','G','Y',
   'G','S','T','Q','Y','I','R','F','S','P','D','F','T','F','G',
   'F','E','E','S','L','E','V','D','T','N','P','L','L','G','A',
   'G','K','F','A','T','D','P','A','V','T','L','A','H','E','L',
   'I','H','A','G','H','R','L','Y','G','I','A','I','N','P','N',
   'R','V','F','K','V','N','T','N','A','Y','Y','E','M','S','G',
   'L','E','V','S','F','E','E','L','R','T','F','G','G','H','D',
   'A','K','F','I','D','S','L','Q','E','N','E','F','R','L','Y',
   'Y','Y','N','K','F','K','D','I','A','S','T','L','N','K','A',
   'K','S','I','V','G','T','T','A','S','L','Q','Y','M','K','N',
   'V','F','K','E','K','Y','L','L','S','E','D','T','S','G','K',
   'F','S','V','D','K','L','K','F','D','K','L','Y','K','M','L',
   'T','E','I','Y','T','E','D','N','F','V','K','F','F','K','V',
   'L','N','R','K','T','Y','L','N','F','D','K','A','V','F','K',
   'I','N','I','V','P','K','V','N','Y','T','I','Y','D','G','F',
   'N','L','R','N','T','N','L','A','A','N','F','N','G','Q','N',
   'T','E','I','N','N','M','N','F','T','K','L','K','N','F','T',
   'G','L','F','E','F','Y','K','L','L','C','V','R','G','I','I',
   'T','S','K','T','K','S','L','D','K','G','Y','N','K',''\0' };
int Pepsin_Sites[106]=
 {0,2,7,35,51,58,77,78,87,88,93,94,102,103,106,108,116,126,127,
  148,149,150,151,162,163,167,173,174,175,192,193,194,195,196,
  199,200,206,208,212,213,220,221,224,242,255,256,259,260,262,
  263,265,272,273,276,277,281,282,284,289,290,296,297,309,310,
  317,321,323,330,331,335,336,338,340,341,344,353,354,356,357,
  360,367,368,369,374,389,390,391,392,396,397,400,401,412,413,
  415,416,418,421,422,423,424,425,427,428,441,448};
int Chymotrypsin_Sites[111]=
 {0,3,8,10,21,30,36,39,43,51,59,72,73,77,78,87,88,94,95,99,103,
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       106,107,108,117,118,127,144,149,151,163,168,170,173,175,180,
       185,188,192,194,196,200,207,208,213,221,223,225,227,230,232,
       233,243,250,251,253,256,260,263,266,273,277,282,284,285,286,
       287,290,297,310,312,313,317,321,322,323,331,336,338,341,342,
       344,345,349,354,357,358,361,366,367,369,374,384,387,390,392,
       397,401,411,413,416,419,422,423,425,426,428,429,442,446,448};
  int Trypsin_Sites[55]=
   {0,6,11,23,34,37,41,48,66,84,89,93,97,105,113,128,145,166,177,
       187,212,231,241,244,264,272,283,289,291,299,301,314,318,320,
       330,335,337,340,343,356,359,363,364,371,375,381,393,415,417,
       427,432,438,440,444,448};

  main()
  {
     static char PeptideFragment[500];
     int index,first,last,i,j,k,w,counter;
     float MW;
     char AA;

     printf("BoNT/A Light Chain Sequence:\n");
     for (index=0; index<449; index++)
      { printf("%c", BoNTA_LC[index]);}
     printf("\n");

     printf("\n\n\n");
     i=0; j=1; k=0; w=0; first=0; last=0;
     printf("BoNT-A_LC Digested by Pepsin\n");
     for (i=0; i<106; i++)
      {
        first=Pepsin_Sites[i];
        for (j=i+1; j<106; j++)
         {
     last=Pepsin_Sites[j];
     w=0;
  /*  printf("first=%d, last=%d ", first, last);     */
    printf("Pepsin: ");
    MW=0.0; counter=0;
    for (k=first; k<=last-1; k++)
     {
        PeptideFragment[w]=BoNTA_LC[k];
        counter++;
        AA=PeptideFragment[w];
        switch (AA)
         {
            case 'A':
             MW=MW+89.09;
             break;
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                    MW=MW+181.19;
                 break;
                case 'V':
                    MW=MW+117.15;
                 break;
                default:
                    printf("Unknown Amino Acid\n");
            }
        printf("%c", PeptideFragment[w++]);
        }
    MW=(MW-((counter-1)*18))/1000;
    printf(" <From %d To %d>", first+1, k);
    printf(" MW=%4.3f KDa\n", MW);
/*  printf("\n");    */
        }
    }
    printf("\n\n\n");
    i=0; j=1; k=0; w=0; first=0; last=0;
    printf("BoNT-A_LC Digested by Chymotrypsin\n");
    for (i=0; i<111; i++)
    {
        first=Chymotrypsin_Sites[i];
        for (j=i+1; j<111; j++)
        {
    last=Chymotrypsin_Sites[j];
    w=0;
/*  printf("first=%d, last=%d ", first, last);    */
    printf("Chymotrypsin: ");
    MW=0.0; counter=0;
    for (k=first; k<=last-1; k++)
    {
        PeptideFragment[w]=BoNTA_LC[k];
        counter++;
        AA=PeptideFragment[w];
        switch (AA)
        {
            case 'A':
             MW=MW+89.09;
             break;
            case 'R':
                MW=MW+174.20;
             break;
            case 'D':
                MW=MW+133.10;
             break;
            case 'N':
                MW=MW+132.12;
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                    case 'V':
                        MW=MW+117.15;
                     break;
                    default:
                        printf("Unknown Amino Acid\n");
                }
            printf("%c", PeptideFragment[w++]);
        }
     MW=(MW-((counter-1)*18))/1000;
     printf(" <From %d To %d>", first+1, k);
     printf(" MW=%4.3f KDa\n", MW);
 /*  printf("\n");    */
            }
        }
     printf("\n\n\n");
     i=0; j=1; k=0; w=0; first=0; last=0;
     printf("BoNT-A_LC Digested by Trypsin\n");
     for (i=0; i<55; i++)
     {
         first=Trypsin_Sites[i];
         for (j=i+1; j<55; j++)
         {
     last=Trypsin_Sites[j];
     w=0;
 /*  printf("first=%d, last=%d ", first, last);     */
     printf("Trypsin: ");
     MW=0.0; counter=0;
     for (k=first; k<=last-1; k++)
     {
         PeptideFragment[w]=BoNTA_LC[k];
         counter++;
         AA=PeptideFragment[w];
         switch (AA)
         {
             case 'A':
              MW=MW+89.09;
              break;
             case 'R':
                 MW=MW+174.20;
              break;
             case 'D':
                 MW=MW+133.10;
              break;
             case 'N':
                 MW=MW+132.12;
              break;
             case 'C':
```