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An algorithm for Construction of Infectious Viroid

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Abstract:- An algorithm have been undergone growth which make able most good selection into line looking for between 2 order, one is question sequence and another is man giving food, room and so on order looking for homologues has become a regularly order operation of biological orders on a 32 bit person computer. The high degree of matching position on man giving food, room and so on order and question subsequence is to make out quickly and clearly a group of order that is given question order be part of to An Algorithm is presented that takes more chances of the high degree of homology between such orders to make an into line of the matching regions. It does not have need of knowledge of a starting homology band, neither complex memory square measure, even for orders of several kilo bases, and it can overcome complex opening, nothing in between or different bands. This is a small, able to be taken about, effecting on one another, front end road map person one is going be married to be used to get out the fields, ranges of matching between man giving food, room and so on order and question subsequence. Since this road map have been written originally in the C language, it is possible to run in other PCs with small changes. The road maps run on the IBM personal knowledge processing machine, has need of 512k, without addition of hardware expect for thin, flat, round plate drives and printer. The execution is quite tightly, all the operations are does in less than one of seconds, depending on the needed work and on the order measure end to end. The going round in circles RNA smallest units of potato spindle under earth stem viroid was used as a question order & normal plant such as plant with soft red yellow fruit plant used as a man giving food, room and so on order input facts for making clear by reasoning the operation of the road map. The facts in these records may be used in many applications in future. The knowledge base is ready either on magnetic tape, on hanging down, not stiff diskettes, or online form. The main try to discover the highly diseased special field, range of disease and keep from opening this field, range to keep safe from viroid interaction keyword homology.

Keyword- Homology.

I. INTRODUCTION

Viroids are the smallest without outside control copying pathogenic agents experienced day and cause transmissible diseases in several by money and goods important the years produce plants[1,2], especially species of the solanaceae[3-6], strong decision of the nucleotide order of several viroids[7-14], and observations of the physical-chemical properties of viroids[15] have on condition that a detailed design to be copied of viroid structure. All experienced viroids are small, unencapsidated, and covalently closed circular single stuck RNA molecules with much coming after first or chief structure. Knowledge of the mechanisms of viroid copying and symptom induction has stored more slowly than knowledge of their structure. Evidence that viroids do not code for proteins suggests that the biological properties of viroids are the outcome of straight to viroid host smallest units effects on one another, for this reason viroids can be taken into account a least genetic and biological system. It has been put forward that disease induction might outcome from viroid in the way with host Gene expression[16]. RNA genomes that have been copied into DNA can be studied in a like taste on condition that the DNA is also biologically active. Development of disease symptoms in a host plant when diseased by one pathogen is the outcome of complex pathogen host effects on one another. The pathogen usually has pathogenicity that making decisions possible that get the types and degrees of seriousness of host symptoms. In the host changed formed of small unit's purposes, uses lead to changes in physiology and development that exhibit as disease symptoms. in this way, view , knowledge the formed of small units and smallest units mechanisms of disease formation will not only make ready the base for the development of based on reasoning moves near to fight pathogen infection but also will make ready knowledge about the basic formed of small units

processes that under normal plant growth and development[17] viroid infections provides a simple testing system in which to work place straight to effects on one another between a pathogenic RNA genome and the host without making orders for computer capacity, the viroid RNA genome and its copying intermediate acts between among directly with host parts for nearly all aspects of the infection process, including copying, intracellular movement, intercellular, movement systemic movement, and pathogenicity[18]. The pleiotropic purposes uses of the viroid RNA genome are strange given its small size, to do with structure simpleness and non-coding capacity because viroid pathogenesis is an outcome of straight to RNA cellular factor effects on one another, viroids are taken into account to be part of to a group of non-coding RNAs that keep control by rules formed of small units purposes, uses through means other than by making orders for computer proteins for specific[19] purposes uses. In this context making clear the smallest units mechanisms of viroid disease may help us get through knowledge the mechanisms of the RNA control of formed of small units processes. Potato spindle under earth stem viroid is the sort species of the pospiviroidae family, taken on a rod shaped[20] coming after first or chief structure in their native state and some viroids in the avsunviroidae family have branched structures[21]. Changes in the complete Gene expression designed of diseased plants also have been described. In general , however we have little knowledge of how a specific PSTVD order or structure can make come to mind separate changes in host Gene expression that lead to changes in specific formed of small units processes and the development of one symptoms. We have taken a complete way in that includes smallest units, formed of small units, biophysical and whole plant analysis to make observation of the mechanisms of viroid pathogenicity using PSTVd infection tomato as a testing system. Close relation this symptom is put off unit growth and young plant development, marked by the kept back expression of a plant with soft red yellow fruit expansion Gene begin part was made clear of in unit growth. The biological follows up of these results are had a discussion about. Potato spindle under earth stem viroid, the begin caused agent of potato spindle under earth stem disease, is a small RNA of about 8x^46 104 dalton (22,3) that exists without poly(A) or poly(C) orders in its structure. This free RNA is able to systematically get person moved plants of several families, and its appears to replicate[23] without outside control in readily moved prison rooms. PSTV is of enough chain length to code for a polypeptide of about 1 x^46 104 dalton, however in vitro studies indicated that PSTV is not gave sense of words in several cell free. Systems which synthesize[24] protein wheather PSTV copying has to do with a DNA intermediate is not experienced, but near in time evidence showed that PSTV copying in plant with soft red yellow fruit leaf long bits or plant with soft red yellow fruit nuclei is put off in the existence of actinomycin in D, an outcome which suggests the sense of begin mixed up of DNA. These genes make to a rule products had to do with in defense move, prison room wall structure, chloroplast fuction, protein metabolism and other different group events. The viroid RNA genomes do not put into sign proteins and are not encapsidated[1,25] though that is so, viroids can replicates without outside control, move systematically within a diseased plant and cause diseases. The viroid genome must acts between, among directly with host encoded factors to do these functions. Therefore viroid infection provides a nothing like it system to make observations about how a host gives a reaction to infection by a pathogenic RNA viroids have addition of more chances for having under observations hostathogen interactions, morphological and cytological changes connected with viroid infection have been well printed materials of a certain sort symptoms cover stunting, leaf epinasty, and chlorosis. At the formed of small units level, the most able to be seen symptom is twisting of unit walls and of the plasma membrance[26-29], chloroplasts[30-32] and microchondria[33]. The smallest units mechanisms of viroid pathogenicity[34-36] as well as host moves, are poorly got clearly viroid infection causes stores of pathogenesis related proteins. Potato spindle under earth stem viroid infection also increases the expression of proteins kinase PKV[37].

Procedure

```
sequence(fpv, fpplant : FILE pointer)
Var :
K, word_size : integer
limit, max_match, max_match2, cur_word, cur_word2 : integer
max_word, max_word2, word_limit, word_limit2 : integer
match, match2 : integer
next_byte, next_byte2, match_byte, match_byte2 : integer
word1[500][50], word2[500][20] : integer array
buffer[20] : integer array
ch,ch2 : character
c, b, i, j, c, flag : integer
fp2 : FILE pointer
begin : display " Enter word size:";
accept(word_size);
c:=0;
b:=0, ch ='A';
while (ch !='EOF') do
begin :
c1 :=0;
while b<20 do
begin :
ch ; =getchar(fpv);
buffer[b++] : = ch;
end : { while b<20}
flag:=0; i:=0;
whilei<b-(wordsize-1) do
begin :
k:=0;
while k<word_size
```



```
if buffer[i+k]='0' then
word1[c1][k]='t'
else
word1[c1][k]:=buffer[i+k]
k++;
end : { while k<word_size}
c1: = c1+1;
flag : = 0;   k:=0;
while k<word_size  do
begin :
if buffer[i+k]='u' then
flag :=1; k++;
end:
if flag<>1  then
begin :
for k<=word_size  do
begin :
word[c][k]:=buffer[i+k];
end;{for k<word_size}
c++;
end;{if flag<>1}
end:[while i<b-(wordsize-1)}
do while ch<> EOF
begin:
j:=0;
while j<word_size-1;
buffer[j]:=buffer[b-(word_size-j-1)];
b:=word_size-1;
do while b<20
begin :
ch:=fgate(fp);
ifch<>EOF than
buffer[b++]:=ch;
else
break:
.,end:{do while b<20}
i:=0
fori< b-(word_size-1) do
begin :
k:=0
while k<word_size
if buffer[i+k]='u' then
word[c1][k]:='t';
else
word[u][k]:=buffer[i+k];
k++;
end;{ while k<word_size}
c1++;
flag:=0;k:=0;
while k<word_size do
begin
if  buffer[i+k]='u' then
flag=1;
k++;
end;{while k<word_size}
if flag<> 1 then
begin :
for k<word_size do
begin :
word[i][k]:=buffer[i+k];
k++;
end; { for k<word_size}
c++;
end;{if flag<>1}
end:
end;
word_limit:=c; word_limit2:=c1;
if(c1>c) then
limit:=c;
else
limit:=c1;
max_match:=0; max_match2:=0;
fp2:=SEEK_SET; fpplant:=SEEK_SET;
fp2:=fopen(plant);
do while ch<>EOF
begin :
ch:=fgate(fpplant)
ch2:=fgate(fp2)
ifi< word limit
ifch=word[i][u]
begin :
match:=1;
cur_word:=ftell(fp);
for(j:=cur_word=1;j<word_limit;j++);
begin:
ch=fgate(fpplant);
ifch=EOF
break;
ifch=word[j][0]
match++;
else
break;
end {for}
if match> (max_match+(word_size-1)))
begin:
max_match:=match-(word_size-1);
max_word:=cur_word;
match_byte:=next_byte-1;
end;
fset(fp,next_byte,SEEK_SET);
end;
end;
end{while ch<>EOF}
display"max_match",max_match;
display"match at", cur_word;
display"matchpos", match_byte;
end{procedure}
```

II. METHOD

Motivation for similarity analysis

We saw that similarity searching and sequence alignment is

an important requirement for fragment assembly. More so, there is a need to build a notion of inexact matches, so that errors are accounted for. We first look at some other contexts in biology where similarity analysis is useful.

Most recent biological sequences are stored in huge databases. When people try to match virus sequences with host existing ones in the databases, similarity measures again come into play.

Besides, any attempt to mine these huge sequence databases for interesting and repeating sequence patterns also requires a good handle over similarity measures.

Now is the task of analyzing the sequences and understanding similarity is the first step towards performing such analyses. We first describe the notion of similarity semi-formally and also look at some approaches towards obtaining pair wise similarity measures.

Similarity
Consider the sequences ACTCCG and ACTCCG. To define similarity, perhaps it is useful to first introduce the notion of "distance" between two strings. The distance between two strings is zero if they are exactly the same.

Alignment of sequences
We now look at the notion of pair wise alignment. Consider any two sequences, ofarbitrary lengths each. Next, by inserting 'spaces' in either sequence we can ensure that every character in one sequence is opposite a character or a space in the other sequence. No space is allowed to be opposite another space (since it is not useful). Thus, end-to-end even though the two sequences we started out with may be of different lengths, they end up being 'aligned' due to the space insertion procedure. For every two sequences, there are huge permutations of possible alignments (cubic in the length of sequences). Some may be 'better' than the others. The alignment procedure itself can be visualized as a series of insert, delete operations. This implies that edit distances are somehow related toalignments.

Eg: For the sequences (the terms sequences and strings are used interchangeably)
ACTCCG and ACACCG could have alignments,
ACT_CCG or _ACTCCG
AC_ACCG AC_ACCG

Thus, from amongst several possible alignments we need to consider the 'good' ones. Ascoring function determines this notion of goodness of alignment. Let us look at an
Example scoring function. We can compute the distance between alignments, in such a way that. Cost of a match is 0 (when the sequence on top and below have the same ithcharacter).

Local alignments
Often biological sequences under consideration are very long, and will surely not besimilar to each other globally. To find small substrings that occur quite frequently acrosssequences is of interest. These are referred to as local alignments. The problem preciselystated is, given two strings S1 and S2, to find substrings A and B of S1 and S2respectively, whose similarity is maximum over all pairs of substrings of S1 and S2.

Intuitively this refers to the best local substring match in the two given sequences. Forexample, if ACTAGTTAA and GTATAAGCC are two sequences, then the localalignment
TAG_
TA_T
has the maximum similarity than all other substring pairs. Local alignments are computed as follows:In the (n, m) graph, let each node, (i, j) store a value corresponding to similarity measureof the best suffix alignment that can be produced till there (between the suffixes ofS1[1..i] and S2[1..j]). Then, the best local alignment corresponds to the best suffixalignment at the node that has the best similarity measure in the n x m nodes.

Again this value at each node can be computed using a recurrence relation.The first row and column nodes have entries initialized to zero.

$$A[i, j] = \max \begin{cases} 0 \\ A[i, j-1] + g \\ A[i-1, j-1] + p(i, j) \\ A[i-1, j] + g \end{cases}$$

Normally the optimal alignment is found within a narrow band around the diagonal. So some heuristics use this knowledge to restrict the search space.
Input Sequence : CGGAACTAAAC TCGTGGTT CCTG TGGT
1) Break the query sequence into words
CGGAACTAAACTCGTGGTTCCTGTGGT
GAAC
GGAA
CGGA
2) Search for word matches (also called high-scoring pairs, or HSPs) in the database sequences.
GAATTCCATCGGAGGAATTAAAGTGATTAATGTACT TAGCTTTG

3) Extend the match until the local alignment score falls bellow a fixed threshold (the most recent version of BLAST allows gaps in the extended match)
GAATTCCATCGGAGGAATAAAGTGATTAATGTACTT AGCTTTG

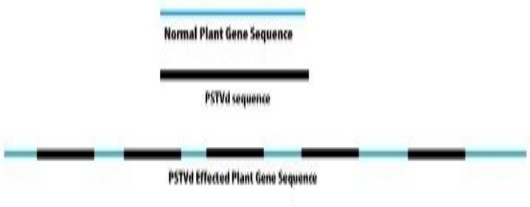
Materials

LOCUS PSU23058 359 bp RNA circular VRL 02-APR-1995 DEFINITION Potato spindle tuber viroid (PSTVd) strain RG 1, complete genome.
ACCESSION U23058
CGGAACTAAACTCGTGGTTCCTGTGGTTCACACCTG
ACCTCCTGACAAGAAAAGAAAAAAGAAGGCGGCTC
GGAGGAGCGCTTCAGGGATCCCCGGGGAAACCTGG
AGCGAACTGGCAAAAAAGGACGGTGGGGAGTGCCC
AGCGGCCGACAGGAGTAATTCCCGCCGAAACAGGG
TTTTCACCCTTCCTTTCTTCGGGTGTCCTTCCTCGCGC
CCGCAGGACCACCCCTCGCCCCCTTTGCGCTGTCGCT
TCGGCTACTACCCGGTGGAAACAACTGAAGCTCCCG
AGAACCGCTTTTTCTCTATCTTACTTGCTCCGGGGCG
AGGGTGTTTAGCCCTTGGAACCGCAGTTGGTTCCT

III. RESULT DISCURSIONS

The different numbers matching probability are found in different orientation found like DNA Vs. DNA match found in 61 places, DNA Vs. RNA in 27 places, DNA Vs. cDNA in 61 places, DNA Vs. cRNA in 27 places, RNA Vs. DNA in 27 places, RNA Vs. RNA 61 places, RNA Vs.cDNA 27 places,RNA Vs. cRNA in 61 places cDNA Vs.cDNA in 61 places cDNA Vs. RNA in 27 places,cDNA Vs. cDNA in 61 places,cDNA Vs. cRNA in places,27,cRNA Vs. DNA in 27 places,cRNA Vs. RNA in 61 places,cRNA Vs. DNA in 27 places,cRNAVscRNA 61 in places.

It shown that maximum numbers of match found in DNA Vs. DNA, DNA Vs. cDNA ,RNA Vs. RNA,RNA Vs. cRNA ,cDNA Vs.cDNA,cRNA Vs. RNA,cRNAVscRNA 61 and minimum numbers of match found in DNA Vs. RNA,DNA Vs. cRNA,RNA Vs. DNA,RNAVs. cDNA,cDNA Vs. RNA,cDNA Vs. cRNA,cRNA Vs. DNA,cRNA Vs. DNA 27. So, minimum numbers of match orientation are omitted/ not consider our result discussion because only maximum matching position are target in our result where maximum number of amino acid are affected.



IV. CONCLUSIONS

The algorithm/program is a small, portable, interactive, front-end program intended to be used to find out the regions of matching between host sequence and query subsequences. To find out the maximum matching position where maximum number of codon is effected that means corresponding amino acid is effected, as a result on that particular positioning the amino acid corresponding protein formation is effected as a result the disease on the host. Our target our main aim or goal is to detect the highly infected specific region of infection and seal this region to protect from viroid interaction.

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Result:

Sequence	DNA Vs. DNA		DNA Vs. RNA		DNA Vs. cDNA		DNA Vs. cRNA		RNA Vs. DNA		RNA Vs. RNA		RNA Vs. cDNA		RNA Vs. cRNA		cDNA Vs. DNA		cDNA Vs. RNA		cDNA Vs. cDNA		cDNA Vs. cRNA		cRNA Vs. DNA		cRNA Vs. RNA		cRNA Vs. cDNA		cRNA Vs. cRNA	
	Total=61		Total=27		Total=61		Total=27		Total=27		Total=61		Total=27		Total=61		Total=61		Total=27		Total=61		Total=27		Total=27		Total=61		Total=27		Total=61	
Sr. No.	Colon	No. of match	Colon	No. of match	Colon	No. of match	Colons	No. of match	Color	No. of match	Color	No. of match	Colons	No. of match	Color	No. of match	Color	No. of match	Color	No. of match	Color	No. of match	Color	No. of match	Color	No. of match	Colo	No. of match	Color	No. of match	Colon	No. of match
1	TTT	2161	AAA	2374	TAA	2344	AAA	3044	AAA	2374	UUU	2161	AAA	3044	UAA	2344	ATT	2344	AAA	2374	AAA	2161	AAA	3044	AAA	2374	AUU	2344	AAA	3044	AAA	2161
2	ATT	2070	GAA	1872	AAA	2132	AAG	2072	GAA	1872	AUU	2070	AAG	2072	AAA	2132	TTT	2132	GAA	1872	TAA	2070	AAG	2072	GAA	1872	UUU	2132	AAG	2072	UAA	2070
3	AAA	2029	CAA	1588	TTT	2025	AAC	1568	CAA	1588	AAA	2029	AAC	1568	UUU	2025	AAA	2025	CAA	1588	TTT	2029	AAC	1568	CAA	1588	AAA	2025	AAC	1568	UUU	2029
4	TAT	1858	AGA	1422	TTA	1769	AGA	1553	AGA	1422	UAU	1858	AGA	1553	UUA	1769	AAT	1769	AGA	1422	ATA	1858	AGA	1553	AGA	1422	AAU	1769	AGA	1553	AUA	1858
5	AAT	1716	AAG	1248	TAT	1742	GAA	1378	AAG	1248	AAU	1716	GAA	1378	UAU	1742	ATA	1742	AAG	1248	TTA	1716	GAA	1378	AAG	1248	AUA	1742	GAA	1378	UUA	1716
6	TAA	1577	CCA	1226	AAG	1427	AGG	1238	CCA	1226	UAA	1577	AGG	1238	AAG	1427	TTC	1427	CCA	1226	ATT	1577	AGG	1238	CCA	1226	UUC	1427	AGG	1238	AUU	1577
7	TTC	1372	GGA	1131	TAG	1385	CAA	1196	GGA	1131	UUC	1372	CAA	1196	UAG	1385	ATC	1385	GGA	1131	AAG	1372	CAA	1196	GGA	1131	AUC	1385	CAA	1196	AAG	1372
8	GAA	1366	CGA	986	CTT	1374	ACC	928	CGA	986	GAA	1366	ACC	928	CUU	1374	GAA	1374	CGA	986	CTT	1366	ACC	928	CGA	986	GAA	1374	ACC	928	CUU	1366
9	TGA	1363	ACA	932	ATT	1337	ACA	884	ACA	932	UGA	1363	ACA	884	AUU	1337	TAA	1337	ACA	932	ACT	1363	ACA	884	ACA	932	UAA	1337	ACA	884	ACU	1363
10	ATC	1236	AAC	920	AGA	1223	GAG	842	AAC	920	AUC	1236	GAG	842	AGA	1223	TCT	1223	AAC	920	TAG	1236	GAG	842	AAC	920	UCU	1223	GAG	842	UAG	1236
11	TCT	1180	CCC	888	TCT	1136	GGA	831	CCC	888	UCU	1180	GGA	831	UCU	1136	AGA	1136	CCC	888	AGA	1180	GGA	831	CCC	888	AGA	1136	GGA	831	AGA	1180
12	CTT	1089	AGG	840	AAC	1071	GGG	784	AGG	840	CUU	1089	GGG	784	AAC	1071	TTG	1071	AGG	840	GAA	1089	GGG	784	AGG	840	UUG	1071	GGG	784	GAA	1089
13	TAG	1079	ACC	793	TAC	1055	AGC	776	GAG	806	UAG	1079	AGC	776	UAC	1055	ATG	1055	GAG	806	ATC	1079	AGC	776	GAG	806	AUG	1055	AGC	776	AUC	1079
14	GAT	1069	GGG	749	CTA	1044	CCC	735	ACC	793	GAU	1069	CCC	735	CUA	1044	GAT	1044	ACC	793	CTA	1069	CCC	735	ACC	793	GAU	1044	CCC	735	CUA	1069
15	TTA	1060	AGC	674	ACT	1041	CCA	719	GGG	749	UUA	1060	CCA	719	ACU	1041	TGA	1041	GGG	749	AAT	1060	CCA	719	GGG	749	UGA	1041	CCA	719	AAU	1060
16	CAA	1043	CAG	632	AAT	1033	CGA	688	AGC	674	CAA	1043	CGA	688	AAU	1033	TTA	1033	AGC	674	GTT	1043	CGA	688	AGC	674	UUA	1033	CGA	688	GUU	1043
17	AGA	1029	CCG	625	GAA	1008	GAC	652	CAG	632	AGA	1029	GAC	652	GAA	1008	CTT	1008	CAG	632	TCT	1029	GAC	652	CAG	632	CUU	1008	GAC	652	UCU	1029
18	TTG	1013	GCA	611	AGT	1004	CAG	620	CCG	625	UUG	1013	CAG	620	AGU	1004	TCA	1004	CCG	625	AAC	1013	CAG	620	CCG	625	UCA	1004	CAG	620	AAC	1013
19	AAG	984	GAC	587	TTC	994	ACG	602	GCA	611	AAG	984	ACG	602	UUC	994	AAG	994	GCA	611	TTC	984	ACG	602	GCA	611	AAG	994	ACG	602	UUC	984
20	TCA	957	CGG	569	GTT	966	CAC	593	GAC	587	UCA	957	CAC	593	GUU	966	CAA	966	GAC	587	AGT	957	CAC	593	GAC	587	CAA	966	CAC	593	AGU	957
21	TGG	948	CAC	543	TGA	958	CGG	527	CGG	569	UGG	948	CGG	527	UGA	958	ACT	958	CGG	569	ACC	948	CGG	527	CGG	569	ACU	958	CGG	527	ACC	948
22	TAC	932	ACG	506	TGT	900	GGC	495	CAC	543	UAC	932	GGC	495	UGU	900	ACA	900	CAC	543	ATG	932	GGC	495	CAC	543	ACA	900	GGC	495	AUG	932
23	TCC	912	GGC	499	ATC	871	CCG	473	ACG	506	UCC	912	CCG	473	AUC	871	TAG	871	ACG	506	AGG	912	CCG	473	ACG	506	UAG	871	CCG	473	AGG	912
24	TGT	907	GCC	473	GTA	862	GCA	471	GGC	499	UGU	907	GCA	471	GUA	862	CAT	862	GGC	499	ACA	907	GCA	471	GGC	499	CAU	862	GCA	471	ACA	907
25	GTT	821	CGC	342	AGG	828	GCC	462	GCC	473	GUU	821	GCC	462	AGG	828	TCC	828	GCC	473	CAA	821	GCC	462	GCC	473	UCC	828	GCC	462	CAA	821
26	CTA	812	GCG	312	GGT	826	CGC	317	CGC	342	CUA	812	CGC	317	GGU	826	CCA	826	CGC	342	GAT	812	CGC	317	CGC	342	CCA	826	CGC	317	GAU	812
27	AAC	765	GAG	80	CAA	787	GCG	292	GCG	312	AAC	765	GCG	292	CAA	787	GTT	787	GCG	312	TTG	765	GCG	292	GCG	312	GUU	787	GCG	292	UUG	765
28	CCA	740			CCT	742			CCA	740			CCU	742	GGA	742			GGT	740					GGA	742			GGU	740		
29	GGA	718			TGG	741			GGA	718			UGG	741	ACC	741			CCT	718					ACC	741			CCU	718		
30	AGT	702			GAT	720			AGU	702			GAU	720	CTA	720			TCA	702					CUA	720			UCA	702		
31	GTA	666			TCA	717			GUA	666			UCA	717	AGT	717			CAT	666					AGU	717			CAU	666		
32	CTC	663			TTG	712			CUC	663			UUG	712	AAC	712			GAG	663					AAC	712			GAG	663		
33	CCT	653			ACA	696			CCU	653			ACA	696	TGT	696			GGA	653					UGU	696			GGA	653		
34	ACA	652			ACC	691			ACA	652			ACC	691	TGG	691			TGT	652					UGG	691			UGU	652		
35	CCC	641			GGA	681			CCC	641			GGA	681	CCT	681			GGG	641					CCU	681			GGG	641		
36	AGG	626			GCT	662			AGG	626			GCU	662	CGA	662			TCC	626					CGA	662			UCC	626		
37	TGC	606			GGG	617			UGC	606			GGG	617	CCC	617			TGA	606					CCC	617			UGA	606		
38	ACT	606			GAG	614			ACU	606			GAG	614	CTC	614			ACG	606					CUC	614			ACG	606		
39	TCG	597			AGC	605			UCG	597			AGC	605	TCG	605			AGC	597					UCG	605			AGC	597		
40	GAG	581			CGA	603			GAG	581			CGA	603	GCT	603			CTC	581					GCU	603			CUC	581		
41	CGA	572			TCC	599			CGA	572			UCC	599	AGG	599			GCT	572					AGG	599			GCU	572		
42	ACC	547			CCC	545			ACC	547			CCC	545	GGG	545			TGG	547					GGG	545			UGG	547		
43	GGT	545			CCA	541			GGU	545			CCA	541	GGT	541			CCA	545					GGU	541			CCA	545		
44	GGG	538			CTC	526			GGG	538			CUC	526	GAG	526			CCC	538					GAG	526			CCC	538		
45	CAG	495			TCG	501			CAG	495			UCG	501	AGC	501			GTC	495					AGC	501			GUC	495		
46	AGC	490			GAC	480			AGC	490			GAC	480	CTG	480			TCG	490					CUG	480			UCG	490		
47	CTG	489			CGT	454			CUG	489			CGU	454	GCA	454			GAC	489					GCA	454			GAC	489		
48	GCT	441			TGC	443			GCU	441			UGC	443	ACG	443			CGA	441					ACG	443			CGA	441		
49	GCA	440			GCA	427			GCA	440			GCA	427	CGT	427			CGT	440					CGU	427			CGU	440		
50	GAC	432			GTC	412			GAC	432			GUC	412	CAG	412			CTG	432					CAG	412			CUG	432		
51	GTC	402			GGC	409			GUC	402			GGC	409	TGC	409			CAG	402					UGC	409			CAG	402		
52	CGG	399			ACG	409			CGG	399			ACG	409	CCG	409			GCC	399					CCG	409			GCC	399		
53	ACG	397			CTG	405			ACG	397			CUG	405	GAC	405			TGC	397					GAC	405			UGC	397		
54	CGT	389			CAC	401			CGU	389			CAC	401	GTG	401			GGC	389					GUG	401			GGC	389		
55	CCG	389			CAG	393			CCG	389			CAG	393	GTC	393			GCA	389					GUC	393			GCA	389		
56	GGC	387			GCC	390			GGC	387			GCC	390	CGG	390			CCG	387					CGG	390			CCG	387		
57	GTG	380			CGG	373			GUG	380			CGG	373	GCC	373			CAC	380					GCC	373			CAC	380		
58	CAC	364			CCG	360			CAC	364			CCG	360	GGC	360			GTG	364					GGC	360			GUG	364		
59	GCC	362			GTG	358			GCC	362			GUG	358	CAC	358			CGG	362					CAC	358			CGG	362		
60	CGC	231			GCG	236			CGC	231			GCG	236	CGC	236			GCG	231					CGC	236			GCG	231		
61	GCG	211			CGC	231			GCG	211			CGC	231	GCG	231			CGC	211					GCG	231			CGC	211		

