DNA or RNA Sequence Analysis and Modification through the

TRICHROMATIC THEORY OF EQUILIBRIUM OF SYSTEMS

1st Chapter (Second Part):

Analysis of 19 Sequences of Insulin Chain A

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INTRODUCTION

In this Chapter, it will be proven how the **TRICHROMATIC THEORY OF EQUILIBRIUM OF SYSTEMS** (**T.T.E.S.**) can be applied to the **DNA or RNA sequence analysis and modification**.

Before starting to read the following Chapter, it is necessary to read the Introduction and Paragraphs 1.1 e 1.2 of Chapter I° First Part [(Analysis and modification of DNA or RNA sequences with T.T.E.S. (Chapter I° - First Part)].

Starting from the DNA or RNA **original sequence** (specifically **Insulin Chain A**), the **T.T.E.S.** software (for further information see also the web site www.ttesystems.eu/index.php) produces many different **new** DNA or RNA **sequences that accurately follow the many different "non-obvious trends" of the original sequence**.

In the following pages, a ***significant amount of results obtained through the analysis of the Original Sequence of DNA*** is displayed .

In particular, here the results of all the ***significant alignments*** obtained by the ***19 new DNA base sequences generated*** by the ***19 specific*** "non-obvious trends" of the *original sequence* are presented.

These **19 new sequences** are constituted by almost totally different bases from those of the **original sequence**.

The **hypothesis** to validate is that the **19 new sequences have strong connections with the features of the original sequence**.

Therefore, from this paper's standpoint, every *organism*, in which a significant alignment with the **19 new produced sequences** has been found, should be connected, indirectly or directly, with

1) the **original sequence** (**Insulin Chain A**);
2) those *organisms* that have been identified with Blast research carried out on **Insulin Chain A**;
3) as well as, partly, to those *organisms* in which significant alignments with the **19 new produced sequences** have been found.

Chapter I° First Part has analyzed only **Sequence n°1/1** out of the **19 new produced sequences.**

The results of **BLAST** research (*Basic Local Alignment Search Tool* (1)) on **Sequence n°1/1** have pointed out significant alignments with the DNA (or RNA) of different *organisms* (see Paragraphs 1.7, 1.8 e 1.9 in Chapter I° First Part and Paragraphs 1.3 e 1.42 in this Chapter).

Chapter I° First Part has delved into the significant alignment of **two** species of *organisms*: some species of **Pseudomonas** bacteria and the nematode **Heligmosomoides polygyrus** (both *organisms* were formed by DNA bases of the new generated sequence: **Sequence n°1/1**).

The **bibliographic research** proves the existence of **important relations** between the characteristics of *Pseudomonas* and *Heligmosomoides polygyrus*, identified with BLAST research carried out on **Sequence n°1/1**, and some of the functional characteristics of Insulin.

As we shall see in this Chapter, the analysis (through the **T.T.E.S.**) of the *original sequence* – based upon its **19** "non-obvious trends" (***Trend n°1, n°2…n°19***) – and the creation of **19** *new DNA sequences* (**Sequences n°1/1, n°2/1,…n°19/1**) from ***19 Trends*** of the *original sequence*, deserve *further studies and bibliographic researches.*

The **comparative analysis** of all the *sequences* and "*organisms*" *identified by Blast research carried out on Insulin Chain A and by Blast research carried out on 19 new sequences* paves the way for a new perspective on genetic research and its uncountable applications.

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(1) Altschul S. F., Madden T. L., Schaffer A. A., Zhang J., Zhang Z., Miller W. and D. J. Lipman. Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. Nucleic Acids Res., 1997, 25 (17) :3389-3402. PMID: 9254694. https://www.ncbi.nlm.nih.gov/pmc/articles/PMC146917/

1st CHAPTER
(Second Part)

New Blast Research on the DNA Sequence of Insulin Chain A

1.1 NEW BLAST RESEARCH ON THE 63 DNA BASE SEQUENCE OF INSULIN CHAIN A

The **63 DNA base** sequence of **Insulin Chain A**, obtained directly from the website of the **NCBI** [(*National Center for Biotechnology Information* (1)], has been subjected to a new and more extensive **BLAST** research (in comparison to that carried out in Chapter I° First Part, Hitlist size ***1000***, rather than ***100***).

Parameters of BLAST research carried out in date 9/04/2019:

Programme	*Blastn*
Word size	*11*
Expect value	*10*
Hitlist size	*1000*
Match/Mismatch scores	*2,-3*
Gapcosts	*5,2*
Low Complexity Filter	*Yes*
Filter string	*L;m;*
Genetic Code	*1*

Results of BLAST research:

Query = ggcatcgtggagcagtgctgcaccagcatctgttccctctaccagctggagaactactgcaac

Length = 63

PLEASE NOTE:

Blast research underscores that **849 sequences** have **significant alignments** with **Insulin Chain A**. Considering the tremendous amount of such results, here, it was preferred to discuss **only those sequences** related to **the same "organism" species** that is to say, those identified by significant alignments with the **sequences** of **19 new Blast researches**. These new researches refer to the **19 sequences** out of the **63 DNA bases** generated by the **TRICHROMATIC THEORY OF EQUILIBRIUM OF SYSTEMS** (**T.T.E.S.**), through the analysis and modification of the original sequence of **Insulin Chain A**, in faithful observance of their **19 different "non-obvious trends"**.

Here, "**the organisms found to be in common**" between the results of BLAST research carried out on **Insulin Chain A** and results of BLAST research carried out **only on one** of the *19 generated sequences*, were highlighted in **Red**.

As well, "**the organisms found to be in common**" between the results of BLAST research carried out on **Insulin Chain A** and results of BLAST research carried out **more on than one** of the *19 generated sequences*, were highlighted in **Green**.

Finally, "**the denomination of the sequence**" (1/1, 2/1, ... 19/1) of the "**organism found to be in common**" between the results of BLAST research carried out on the **Insulin Chain A** and results of BLAST research carried out on *19 generated sequences*, were highlighted in **Yellow**.

(1) National Center for Biotechnology Information (**NCBI**)[Internet]. Bethesda (MD): National Library of Medicine (US), National Center for Biotechnology Information; [1988]. Available from: https://www.ncbi.nlm.nih.gov/

Sequences producing significant alignments:

Selected seq	Description	Max score	Total score	Query cover	E value	Ident	Accession
XM_020883287.1 **6/1**	PREDICTED: Odocoileus virginianus texanus insulin (LOC110130982), transcript variant X2, mRNA	110	110	100%	6e-21	98%	XM_020883287.1
XM_020883286.1 **6/1**	PREDICTED: Odocoileus virginianus texanus insulin (LOC110130982), transcript variant X1, mRNA	110	110	100%	6e-21	98%	XM_020883286.1
XM_015434180.1 **2/1 3/1 8/1 17/1**	PREDICTED: Macaca fascicularis insulin (INS), transcript variant X1, mRNA	110	110	100%	6e-21	98%	XM_015434180.1
XM_015113354.1 **2/1 3/1 8/1 17/1**	PREDICTED: Macaca mulatta insulin (INS), mRNA	110	110	100%	6e-21	98%	XM_015113354.1
XM_011721319.1 **2/1 3/1 8/1 17/1**	PREDICTED: Macaca nemestrina insulin (INS), transcript variant X4, mRNA	110	110	100%	6e-21	98%	XM_011721319.1
XM_011721318.1 **2/1 3/1 8/1 17/1**	PREDICTED: Macaca nemestrina insulin (INS), transcript variant X3, mRNA	110	110	100%	6e-21	98%	XM_011721318.1
XM_011721317.1 **2/1 3/1 8/1 17/1**	PREDICTED: Macaca nemestrina insulin (INS), transcript variant X2, mRNA	110	110	100%	6e-21	98%	XM_011721317.1
XM_011721316.1 **2/1 3/1 8/1 17/1**	PREDICTED: Macaca nemestrina insulin (INS), transcript variant X1, mRNA	110	110	100%	6e-21	98%	XM_011721316.1
XM_012041172.1 **10/1 12/1**	PREDICTED: Cercocebus atys insulin (INS), transcript variant X3, mRNA	110	110	100%	6e-21	98%	XM_012041172.1
XM_012041171.1 **10/1 12/1**	PREDICTED: Cercocebus atys insulin (INS), transcript variant X2, mRNA	110	110	100%	6e-21	98%	XM_012041171.1
XM_012041169.1 **10/1 12/1**	PREDICTED: Cercocebus atys insulin (INS), transcript variant X1, mRNA	110	110	100%	6e-21	98%	XM_012041169.1

Sequences producing significant alignments:

Selected seq	Description	Max score	Total score	Query cover	E value	Ident	Accession
XM_008004634.1 **8/1**	PREDICTED: Chlorocebus sabaeus insulin (INS), transcript variant X2, mRNA	110	110	100%	6e-21	98%	XM_008004634.1
XM_008004561.1 **8/1**	PREDICTED: Chlorocebus sabaeus insulin (INS), transcript variant X1, mRNA	110	110	100%	6e-21	98%	XM_008004561.1
NM_001284919.1 **2/1 3/1 8/1 17/1**	Macaca fascicularis insulin (INS), mRNA	110	110	100%	6e-21	98%	NM_001284919.1
XM_021152514.1 **1/1 6/1 8/1 10/1 13/1 17/1 18/1**	PREDICTED: Mus caroli insulin-1 (LOC110286053), mRNA	105	105	100%	8e-20	97%	XM_021152514.1
DQ250565.1 **1/1 6/1 8/1 10/1 13/1 17/1 18/1**	Mus caroli preproinsulin 1 (Ins1) gene, complete cds	105	105	100%	8e-20	97%	DQ250565.1
XM_022507720.1 **1/1**	PREDICTED: Enhydra lutris kenyoni insulin (LOC111150279), mRNA	101	101	100%	3e-18	95%	XM_022507720.1
XM_021685179.1 **1/1**	PREDICTED: Neomonachus schauinslandi insulin (INS), mRNA	101	101	100%	3e-18	95%	XM_021685179.1
XM_021215010.1 **1/1 6/1 8/1 10/1 13/1 17/1 18/1**	PREDICTED: Mus pahari insulin-1 (LOC110333420), mRNA	101	101	100%	3e-18	95%	XM_021215010.1
NM_008386.4 **1/1 6/1 8/1 10/1 13/1 17/1 18/1**	Mus musculus insulin I (Ins1), mRNA	101	101	100%	3e-18	95%	NM_008386.4
XM_012743999.1 **9/1**	PREDICTED: Microcebus murinus insulin (INS), mRNA	101	101	100%	3e-18	95%	XM_012743999.1
XM_006910977.1 **17/1**	PREDICTED: Pteropus alecto insulin (LOC102881117), mRNA	101	101	100%	3e-18	95%	XM_006910977.1
XM_006750095.1 **1/1**	PREDICTED: Leptonychotes weddellii insulin (INS), mRNA	101	101	100%	3e-18	95%	XM_006750095.1
BC145868.1 **1/1 6/1 8/1 10/1 13/1 17/1 18/1**	Mus musculus insulin I, mRNA (cDNA clone MGC:175755 IMAGE:40131171), complete cds	101	101	100%	3e-18	95%	BC145868.1

Sequences producing significant alignments:

Selected seq	Description	Max score	Total score	Query cover	E value	Ident	Accession
DQ250563.1 **17/1**	Rattus losea preproinsulin 1 (Ins1) gene, complete cds	101	101	100%	3e-18	95%	DQ250563.1
DQ479923.1 **1/1 6/1 8/1 10/1 13/1 17/1 18/1**	Mus musculus strain BTBR T+ tf/J insulin 1 precursor, gene, complete cds	101	101	100%	3e-18	95%	DQ479923.1
AC163452.12 **1/1 6/1 8/1 10/1 13/1 17/1 18/1**	Mus musculus chromosome 19, clone RP23-405C7, complete sequence	101	101	100%	3e-18	95%	AC163452.12
AC136710.8 **1/1 6/1 8/1 10/1 13/1 17/1 18/1**	Mus musculus chromosome 19, clone RP23-35B13, complete sequence	101	101	100%	3e-18	95%	AC136710.8
AC140320.2 **1/1 6/1 8/1 10/1 13/1 17/1 18/1**	Mus musculus BAC clone RP23-401C13 from chromosome 19, complete sequence	101	101	100%	3e-18	95%	AC140320.2
BC098468.1 **1/1 6/1 8/1 10/1 13/1 17/1 18/1**	Mus musculus insulin I, mRNA (cDNA clone MGC:107382 IMAGE:6432765), complete cds	101	101	100%	3e-18	95%	BC098468.1
AK148541.1 **1/1 6/1 8/1 10/1 13/1 17/1 18/1**	Mus musculus adult pancreas islet cells cDNA, RIKEN full-length enriched library, clone:C820020F18 product:insulin I, full insert sequence	101	101	100%	3e-18	95%	AK148541.1
AK007345.1 **1/1 6/1 8/1 10/1 13/1 17/1 18/1**	Mus musculus 10 day old male pancreas cDNA, RIKEN full-length enriched library, clone:1810005L03 product:INSULIN 1 PRECURSOR, full insert sequence	101	101	100%	3e-18	95%	AK007345.1
X04725.1 **8/1 10/1 13/1 17/1**	Mouse preproinsulin gene I	101	101	100%	3e-18	95%	X04725.1
J02547.1 **8/1 17/1**	Human (synthetic) insulin gene, complete cds	101	101	100%	3e-18	95%	J02547.1
M31026.1 **8/1 17/1**	Synthetic human insulin B and mini-C chains using deactivated silica gel chromatography	101	101	100%	3e-18	95%	M31026.1

Sequences producing significant alignments:

Selected seq	Description	Max score	Total score	Query cover	E value	Ident	Accession
V00082.1 **8/1** **17/1**	Artificial gene for human proinsulin	101	101	100%	3e-18	95%	V00082.1
XM_005351571.2 **1/1**	PREDICTED: Microtus ochrogaster insulin (Ins), mRNA	96.9	96.9	100%	4e-17	94%	XM_005351571.2
XM_028118258.1 **1/1**	PREDICTED: Eumetopias jubatus insulin (LOC114220406), mRNA	96.9	96.9	100%	4e-17	94%	XM_028118258.1
XM_027579931.1 **1/1**	PREDICTED: Zalophus californianus insulin (INS), mRNA	96.9	96.9	100%	4e-17	94%	XM_027579931.1
XM_025879485.1 **1/1**	PREDICTED: Callorhinus ursinus insulin (LOC112829807), mRNA	96.9	96.9	100%	4e-17	94%	XM_025879485.1
XM_023654706.1 **6/1**	PREDICTED: Equus caballus insulin (INS), mRNA	96.9	96.9	100%	4e-17	94%	XM_023654706.1
XM_021168754.1 **1/1** **6/1** **8/1** **10/1** **13/1** **17/1** **18/1**	PREDICTED: Mus caroli insulin-2 (LOC110299132), transcript variant X2, mRNA	96.9	96.9	100%	4e-17	94%	XM_021168754.1
XM_021168753.1 **1/1** **6/1** **8/1** **10/1** **13/1** **17/1** **18/1**	PREDICTED: Mus caroli insulin-2 (LOC110299132), transcript variant X1, mRNA	96.9	96.9	100%	4e-17	94%	XM_021168753.1
AH002190.2 **17/1**	Rattus norvegicus insulin 2 (INS2) gene, complete cds	96.9	96.9	100%	4e-17	94%	AH002190.2
NM_001185084.2 **1/1** **6/1** **8/1** **10/1** **13/1** **17/1** **18/1**	Mus musculus insulin II (Ins2), transcript variant 3, mRNA	96.9	96.9	100%	4e-17	94%	NM_001185084.2
NM_001185083.2 **1/1** **6/1** **8/1** **10/1** **13/1** **17/1** **18/1**	Mus musculus insulin II (Ins2), transcript variant 1, mRNA	96.9	96.9	100%	4e-17	94%	NM_001185083.2
NM_008387.5 **1/1** **6/1** **8/1** **10/1** **13/1** **17/1** **18/1**	Mus musculus insulin II (Ins2), transcript variant 2, mRNA	96.9	96.9	100%	4e-17	94%	NM_008387.5
XM_004403802.1 **1/1**	PREDICTED: Odobenus rosmarus divergens insulin (INS), mRNA	96.9	96.9	100%	4e-17	94%	XM_004403802.1

Sequences producing significant alignments:

Selected seq	Description	Max score	Total score	Query cover	E value	Ident	Accession
JN959239.1 **1/1 6/1 8/1 10/1 13/1 17/1 18/1**	Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Ins2:tm1a(EUCOMM)Wtsi; transgenic	96.9	96.9	100%	4e-17	94%	JN959239.1
JN951270.1 **1/1 6/1 8/1 10/1 13/1 17/1 18/1**	Mus musculus targeted non-conditional, lacZ-tagged mutant allele Ins2:tm1e(EUCOMM)Wtsi; transgenic	96.9	96.9	100%	4e-17	94%	JN951270.1
FQ231224.1 **17/1**	Rattus norvegicus TL0AEA77YF17 mRNA sequence	96.9	96.9	100%	4e-17	94%	FQ231224.1
NM_019129.3 **17/1**	Rattus norvegicus insulin 1 (Ins1), mRNA	96.9	96.9	100%	4e-17	94%	NM_019129.3
NM_019130.2 **17/1**	Rattus norvegicus insulin 2 (Ins2), mRNA	96.9	96.9	100%	4e-17	94%	NM_019130.2
BC145554.1 **1/1 6/1 8/1 10/1 13/1 17/1 18/1**	Mus musculus insulin II, mRNA (cDNA clone MGC:179126 IMAGE:9054118), complete cds	96.9	96.9	100%	4e-17	94%	BC145554.1
BC099934.1 **1/1 6/1 8/1 10/1 13/1 17/1 18/1**	Mus musculus insulin II, mRNA (cDNA clone MGC:107381 IMAGE:6432976), complete cds	96.9	96.9	100%	4e-17	94%	BC099934.1
BC132650.1 **1/1 6/1 8/1 10/1 13/1 17/1 18/1**	Mus musculus insulin II, mRNA (cDNA clone MGC:164281 IMAGE:40130927), complete cds	96.9	96.9	100%	4e-17	94%	BC132650.1
DQ250572.1 **1/1**	Microtus kikuchii preproinsulin (Ins) gene, complete cds	96.9	96.9	100%	4e-17	94%	DQ250572.1
DQ250569.1 **1/1 6/1 8/1 10/1 13/1 17/1 18/1**	Mus caroli preproinsulin 2 (Ins2) gene, complete cds	96.9	96.9	100%	4e-17	94%	DQ250569.1
DQ250567.1 **17/1**	Rattus losea preproinsulin 2 (Ins2) gene, complete cds	96.9	96.9	100%	4e-17	94%	DQ250567.1
AC098563.6 **17/1**	Rattus norvegicus 1 BAC CH230-123A15 (Children's Hospital Oakland Research Institute) complete sequence	96.9	96.9	100%	4e-17	94%	AC098563.6

Sequences producing significant alignments:

Selected seq	Description	Max score	Total score	Query cover	E value	Ident	Accession
AK007612.1 **1/1 6/1 8/1 10/1 13/1 17/1 18/1**	Mus musculus 10 day old male pancreas cDNA, RIKEN full-length enriched library, clone:1810027C14 product:INSULIN 2 PRECURSOR, full insert sequence	96.9	96.9	100%	4e-17	94%	AK007612.1
AK007482.1 **1/1 6/1 8/1 10/1 13/1 17/1 18/1**	Mus musculus 10 day old male pancreas cDNA, RIKEN full-length enriched library, clone:1810013J24 product:INSULIN 1 PRECURSOR, full insert sequence	96.9	96.9	100%	4e-17	94%	AK007482.1
BC066208.1 **1/1 6/1 8/1 10/1 13/1 17/1 18/1**	Mus musculus insulin II, mRNA (cDNA clone IMAGE:6436276)	96.9	96.9	100%	4e-17	94%	BC066208.1
AC012382.14 **1/1 6/1 8/1 10/1 13/1 17/1 18/1**	Mus musculus chromosome 7, clone RP23-92L23, complete sequence	96.9	96.9	100%	4e-17	94%	AC012382.14
X04724.1 **8/1 10/1 13/1 17/1**	Mouse preproinsulin gene II	96.9	96.9	100%	4e-17	94%	X04724.1
AY899305.1 **1/1 6/1 8/1 10/1 13/1 17/1 18/1**	Mus musculus proinsulin mRNA, complete cds, alternatively spliced	96.9	96.9	100%	4e-17	94%	AY899305.1
AC013548.13 **1/1 6/1 8/1 10/1 13/1 17/1 18/1**	Mus musculus chromosome 7, clone RP23-209O22, complete sequence	96.9	96.9	100%	4e-17	94%	AC013548.13
AP003182.2 **1/1 6/1 8/1 10/1 13/1 17/1 18/1**	Mus musculus genomic DNA, chromosome 7 clone:B189M11, complete sequences	96.9	96.9	100%	4e-17	94%	AP003182.2
M12913.1 **8/1 17/1**	Synthetic human proinsulin gene, complete cds	96.9	96.9	100%	4e-17	94%	M12913.1
GQ915612.1 **1/1 6/1 8/1 10/1 13/1 17/1 18/1**	Mus musculus insulin-2 precursor (Ins2) mRNA, partial cds, alternatively spliced	95.1	95.1	98%	1e-16	94%	GQ915612.1

Sequences producing significant alignments:

Selected seq	Description	Max score	Total score	Query cover	E value	Ident	Accession
XM_027409202.1 **1/1**	PREDICTED: Cricetulus griseus insulin (Ins), mRNA	92.4	92.4	100%	2e-15	92%	XM_027409202.1
XM_013112606.2 **1/1**	PREDICTED: Mesocricetus auratus insulin (Ins), mRNA	92.4	92.4	100%	2e-15	92%	XM_013112606.2
XM_021204833.1 **1/1 6/1 8/1 10/1 13/1 17/1 18/1**	PREDICTED: Mus pahari insulin-2 (LOC110326410), transcript variant X2, mRNA	92.4	92.4	100%	2e-15	92%	XM_021204833.1
XM_021204825.1 **1/1 6/1 8/1 10/1 13/1 17/1 18/1**	PREDICTED: Mus pahari insulin-2 (LOC110326410), transcript variant X1, mRNA	92.4	92.4	100%	2e-15	92%	XM_021204825.1
LT733283.1 **8/1 17/1**	Human ORFeome Gateway entry vector pENTR223-INS, complete sequence	92.4	92.4	100%	2e-15	92%	LT733283.1
AH002844.2 **2/1 8/1 9/1 10/1 15/1 17/1**	Homo sapiens insulin (INS) gene, complete cds	92.4	92.4	100%	2e-15	92%	AH002844.2
AH012037.2 **2/1 8/1 9/1 10/1 15/1 17/1**	Homo sapiens haplotype ICa tyrosine hydroxylase (TH) gene, partial sequence; insulin (INS) gene, complete cds; and insulin-like growth factor 2 (IGF2) gene, partial sequence	92.4	92.4	100%	2e-15	92%	AH012037.2
AH011814.2 **6/1**	Pan troglodytes tyrosine hydroxylase (TH) gene, partial cds; and insulin precursor (INS) gene, complete cds	92.4	92.4	100%	2e-15	92%	AH011814.2
XM_016919751.1 **6/1**	PREDICTED: Pan troglodytes insulin (INS), transcript variant X1, mRNA	92.4	92.4	100%	2e-15	92%	XM_016919751.1
NG_050578.1 **2/1 8/1 9/1 10/1 15/1 17/1**	Homo sapiens INS-IGF2 readthrough (INS-IGF2), RefSeqGene on chromosome 11	92.4	92.4	100%	2e-15	92%	NG_050578.1
KR710184.1 **2/1 8/1 9/1 10/1 15/1 17/1**	Synthetic construct Homo sapiens clone CCSBHm_00010257 INS (INS) mRNA, encodes complete protein	92.4	92.4	100%	2e-15	92%	KR710184.1
KR710183.1 **2/1 8/1 9/1 10/1 15/1 17/1**	Synthetic construct Homo sapiens clone CCSBHm_00010256 INS (INS) mRNA, encodes complete protein	92.4	92.4	100%	2e-15	92%	KR710183.1

Sequences producing significant alignments:

Selected seq	Description	Max score	Total score	Query cover	E value	Ident	Accession
KR710182.1 **2/1 8/1 9/1 10/1 15/1 17/1**	Synthetic construct Homo sapiens clone CCSBHm_00010255 INS (INS) mRNA, encodes complete protein	92.4	92.4	100%	2e-15	92%	KR710182.1
KJ891480.1 **2/1 8/1 9/1 10/1 15/1 17/1**	Synthetic construct Homo sapiens clone ccsbBroadEn_00874 INS gene, encodes complete protein	92.4	92.4	100%	2e-15	92%	KJ891480.1
NM_001291897.1 **2/1 8/1 9/1 10/1 15/1 17/1**	Homo sapiens insulin (INS), transcript variant 4, mRNA	92.4	92.4	100%	2e-15	92%	NM_001291897.1
XM_003508080.2 **1/1**	PREDICTED: Cricetulus griseus insulin (Ins), mRNA	92.4	92.4	100%	2e-15	92%	XM_003508080.2
JQ951950.1 **2/1 8/1 9/1 10/1 15/1 17/1**	Homo sapiens preproinsulin (INS) mRNA, complete cds	92.4	92.4	100%	2e-15	92%	JQ951950.1
JF909299.1 **2/1 8/1 9/1 10/1 15/1 17/1**	Homo sapiens insulin (INS) mRNA, partial cds	92.4	92.4	100%	2e-15	92%	JF909299.1
AB587580.1 **2/1 8/1 9/1 10/1 15/1 17/1**	Synthetic construct DNA, clone: pF1KB8864, Homo sapiens INS gene for insulin, without stop codon, in Flexi system	92.4	92.4	100%	2e-15	92%	AB587580.1
NM_001185098.1 **2/1 8/1 9/1 10/1 15/1 17/1**	Homo sapiens insulin (INS), transcript variant 3, mRNA	92.4	92.4	100%	2e-15	92%	NM_001185098.1
NM_001185097.1 **2/1 8/1 9/1 10/1 15/1 17/1**	Homo sapiens insulin (INS), transcript variant 2, mRNA	92.4	92.4	100%	2e-15	92%	NM_001185097.1
NM_001008996.2 **6/1**	Pan troglodytes insulin (INS), mRNA	92.4	92.4	100%	2e-15	92%	NM_001008996.2
NG_007114.1 **2/1 8/1 9/1 10/1 15/1 17/1**	Homo sapiens insulin (INS), RefSeqGene on chromosome 11	92.4	92.4	100%	2e-15	92%	NG_007114.1

Sequences producing significant alignments:

Selected seq	Description	Max score	Total score	Query cover	E value	Ident	Accession
DQ778082.1 **2/1** **8/1** **9/1** **10/1** **15/1** **17/1**	Homo sapiens clone BFC06103 insulin mRNA, complete cds7	92.4	92.4	100%	2e-15	92%	DQ778082.1
DQ896283.2 **2/1** **8/1** **9/1** **10/1** **15/1** **17/1**	Synthetic construct Homo sapiens clone IMAGE:100010743; FLH192918.01L; RZPDo839A1068D insulin (INS) gene, encodes complete protein	92.4	92.4	100%	2e-15	92%	DQ896283.2
NM_000207.2 **2/1** **8/1** **9/1** **10/1** **15/1** **17/1**	Homo sapiens insulin (INS), transcript variant 1, mRNA	92.4	92.4	100%	2e-15	92%	NM_000207.2
BT007778.1 **2/1** **8/1** **9/1** **10/1** **15/1** **17/1**	Synthetic construct Homo sapiens insulin mRNA, partial cds	92.4	92.4	100%	2e-15	92%	BT007778.1
BT006808.1 **2/1** **8/1** **9/1** **10/1** **15/1** **17/1**	Homo sapiens insulin mRNA, complete cds	92.4	92.4	100%	2e-15	92%	BT006808.1
BC005255.1 **2/1** **8/1** **9/1** **10/1** **15/1** **17/1**	Homo sapiens insulin, mRNA (cDNA clone MGC:12292 IMAGE:3950204), complete cds	92.4	92.4	100%	2e-15	92%	BC005255.1
AC132217.15 **2/1** **8/1** **9/1** **10/1** **15/1** **17/1**	Homo sapiens chromosome 11, clone RP11-889I17, complete sequence	92.4	92.4	100%	2e-15	92%	AC132217.15
X61089.1 **6/1**	P.troglodytes gene for preproinsulin	92.4	92.4	100%	2e-15	92%	X61089.1
AC130303.8 **2/1** **8/1** **9/1** **10/1** **15/1** **17/1**	Homo sapiens chromosome 11, clone RP4-539G11, complete sequence	92.4	92.4	100%	2e-15	92%	AC130303.8
AY899304.1 **2/1** **8/1** **9/1** **10/1** **15/1** **17/1**	Homo sapiens proinsulin mRNA, complete cds, alternatively spliced	92.4	92.4	100%	2e-15	92%	AY899304.1

Sequences producing significant alignments:

Selected seq	Description	Max score	Total score	Query cover	E value	Ident	Accession
AJ009655.1 **2/1 8/1 9/1 10/1 15/1 17/1**	Homo sapiens ins gene, partial	92.4	92.4	100%	2e-15	92%	AJ009655.1
X70508.1 **2/1 8/1 9/1 10/1 15/1 17/1**	Homo sapiens mRNA for insulinoma pre-proinsulin	92.4	92.4	100%	2e-15	92%	X70508.1
L15440.1 **2/1 8/1 9/1 10/1 15/1 17/1**	Homo sapiens tyrosine hydroxylase (TH) gene, 3' end; insulin (INS) gene, complete cds; insulin-like growth factor 2 (IGF2) gene, 5' end	92.4	92.4	100%	2e-15	92%	L15440.1
M10039.1 **8/1 17/1**	Human alpha-type insulin gene and 5' flanking polymorphic region	92.4	92.4	100%	2e-15	92%	M10039.1
V00565.1 **8/1 17/1**	Human gene for preproinsulin, from chromosome 11. Includes a highly polymorphic region upstream from the insulin gene containing tandemly repeated sequences	92.4	92.4	100%	2e-15	92%	V00565.1
KR710185.1 **2/1 8/1 9/1 10/1 15/1 17/1**	Synthetic construct Homo sapiens clone CCSBHm_00010262 INS (INS) mRNA, encodes complete protein	90.6	90.6	98%	6e-15	92%	KR710185.1
XM_027959829.1 **6/1 14/1 17/1**	PREDICTED: Ovis aries insulin (INS), mRNA	87.8	87.8	100%	2e-14	90%	XM_027959829.1
XM_027868681.1 **6/1**	PREDICTED: Vombatus ursinus insulin (INS), mRNA	87.8	87.8	100%	2e-14	90%	XM_027868681.1
XM_027532448.1 **3/1 4/1 8/1**	PREDICTED: Bos indicus x Bos taurus insulin (INS), mRNA	87.8	87.8	100%	2e-14	90%	XM_027532448.1
XM_015461330.2 **3/1 4/1 8/1**	PREDICTED: Bos taurus insulin (INS), transcript variant X1, mRNA	87.8	87.8	100%	2e-14	90%	XM_015461330.2
CP027097.1 **3/1 4/1 8/1**	Bos mutus isolate yakQH1 chromosome 29	87.8	87.8	100%	2e-14	90%	CP027097.1
XM_020970881.1 **6/1**	PREDICTED: Phascolarctos cinereus insulin (INS), mRNA	87.8	87.8	100%	2e-14	90%	XM_020970881.1

Sequences producing significant alignments:

Selected seq	Description	Max score	Total score	Query cover	E value	Ident	Accession
XM_019954732.1 **3/1 4/1 8/1**	PREDICTED: Bos indicus insulin (INS), transcript variant X2, mRNA	87.8	87.8	100%	2e-14	90%	XM_019954732.1
XM_019954731.1 **3/1 4/1 8/1**	PREDICTED: Bos indicus insulin (INS), transcript variant X1, mRNA	87.8	87.8	100%	2e-14	90%	XM_019954731.1
M54979.2 **3/1 4/1 8/1**	Bos taurus insulin precursor, mRNA, complete cds	87.8	87.8	100%	2e-14	90%	M54979.2
AH005355.3 **6/1 14/1 17/1**	Ovis aries insulin and insulin-like growth factor II (IGF-II) genes, complete cds	87.8	87.8	100%	2e-14	90%	AH005355.3
XM_012167536.2 **6/1 14/1 17/1**	PREDICTED: Ovis aries musimon insulin (LOC105613195), mRNA	87.8	87.8	100%	2e-14	90%	XM_012167536.2
XM_005903505.2 **3/1 4/1 8/1**	PREDICTED: Bos mutus insulin (LOC102274400), mRNA	87.8	87.8	100%	2e-14	90%	XM_005903505.2
XM_006893212.1 **1/1**	PREDICTED: Elephantulus edwardii insulin (INS), mRNA	87.8	87.8	100%	2e-14	90%	XM_006893212.1
JX041514.1 **3/1 4/1 8/1**	Bos taurus proinsulin mRNA, partial cds	87.8	87.8	100%	2e-14	90%	JX041514.1
NM_001185126.1 **3/1 4/1 8/1**	Bos taurus insulin (INS), transcript variant 2, mRNA	87.8	87.8	100%	2e-14	90%	NM_001185126.1
NM_173926.2 **3/1 4/1 8/1**	Bos taurus insulin (INS), transcript variant 1, mRNA	87.8	87.8	100%	2e-14	90%	NM_173926.2
EU518675.1 **3/1 4/1 8/1**	Bos taurus insulin (INS) and insulin-like growth factor 2 (IGF2) genes, complete cds	87.8	87.8	100%	2e-14	90%	EU518675.1
BC142034.1 **3/1 4/1 8/1**	Bos taurus insulin, mRNA (cDNA clone MGC:159719 IMAGE:8631936), complete cds	87.8	87.8	100%	2e-14	90%	BC142034.1
XM_006860809.1 **11/1**	PREDICTED: Chrysochloris asiatica insulin (INS), mRNA	83.3	83.3	100%	9e-13	89%	XM_006860809.1

Sequences producing significant alignments:

Selected seq	Description	Max score	Total score	Query cover	E value	Ident	Accession
XM_019811180.2 **19/1**	PREDICTED: Felis catus insulin (INS), transcript variant X1, mRNA	74.3	74.3	100%	5e-10	86%	XM_019811180.2
NM_001009272.1 **19/1**	Felis catus insulin (INS), mRNA	74.3	74.3	100%	5e-10	86%	NM_001009272.1
AY986822.1 **19/1**	Felis catus preproinsulin mRNA, partial cds	74.3	74.3	100%	5e-10	86%	AY986822.1
AF050524.1 **2/1 8/1 9/1 10/1 15/1 17/1**	Synthetic Homo sapiens proinsulin-like protein BKRA gene, complete cds	74.3	74.3	100%	5e-10	86%	AF050524.1
AB501190.1 **8/1 17/1**	Synthetic construct hpi gene for human M-proinsulin, complete cds	69.8	69.8	100%	6e-09	84%	AB501190.1
XM_024208870.1 **16/1**	PREDICTED: Terrapene mexicana triunguis insulin (INS), mRNA	63.5	63.5	98%	8e-07	82%	XM_024208870.1
XM_024102171.1 **16/1**	PREDICTED: Chrysemys picta bellii insulin (INS), transcript variant X2, mRNA	63.5	63.5	98%	8e-07	82%	XM_024102171.1
XM_005312381.2 **16/1**	PREDICTED: Chrysemys picta bellii insulin (INS), transcript variant X1, mRNA	63.5	63.5	98%	8e-07	82%	XM_005312381.2
XM_027651359.1 **17/1**	PREDICTED: Corapipo altera insulin (INS), transcript variant X3, mRNA	60.8	60.8	100%	3e-06	81%	XM_027651359.1
XM_027651356.1 **17/1**	PREDICTED: Corapipo altera insulin (INS), transcript variant X2, mRNA	60.8	60.8	100%	3e-06	81%	XM_027651356.1
XM_027651355.1 **17/1**	PREDICTED: Corapipo altera insulin (INS), transcript variant X1, mRNA	60.8	60.8	100%	3e-06	81%	XM_027651355.1
J02544.1 **8/1 17/1**	Human insulin A chain gene (synthetic)	60.8	60.8	100%	3e-06	81%	J02544.1
XM_006134914.3 **6/1**	PREDICTED: Pelodiscus sinensis insulin (INS), mRNA	59.0	59.0	98%	1e-05	81%	XM_006134914.3

Sequences producing significant alignments:

Selected seq	Description	Max score	Total score	Query cover	E value	Ident	Accession
LR535846.1 **17/1**	Mastacembelus armatus genome assembly, chromosome: 14	56.3	56.3	100%	1e-04	79%	LR535846.1
XM_026329134.1 **17/1**	PREDICTED: Mastacembelus armatus insulin (LOC113143484), mRNA	56.3	56.3	100%	1e-04	79%	XM_026329134.1
LR131921.1 **4/1 6/1 7/1 16/1 18/1 19/1**	Cottoperca gobio genome assembly, chromosome: 14	55.4	55.4	100%	1e-04	81%	LR131921.1
CP032586.1 **14/1 16/1 17/1**	Lateolabrax maculatus linkage group 12 sequence	55.4	55.4	100%	1e-04	81%	CP032586.1
CP027266.1 **14/1 16/1 17/1**	Lateolabrax maculatus chromosome Lm5	55.4	55.4	100%	1e-04	81%	CP027266.1
XM_022744743.1 **10/1**	PREDICTED: Seriola dumerili insulin (ins), mRNA	55.4	55.4	100%	1e-04	81%	XM_022744743.1
AB262771.1 **10/1**	Seriola dumerili mRNA for insulin, complete cds, subtype 2	55.4	55.4	100%	1e-04	81%	AB262771.1
XM_019069183.1 **4/1 6/1 17/1**	PREDICTED: Cyprinus carpio insulin-like (LOC109051698), mRNA	52.7	52.7	96%	0.002	79%	XM_019069183.1
LN590733.1 **4/1 6/1 17/1**	Cyprinus carpio genome assembly common carp genome, scaffold 000000053	52.7	103	96%	0.002	79%	LN590733.1
XM_026092712.1 **9/1 14/1**	PREDICTED: Dromaius novaehollandiae insulin (INS), mRNA	51.8	51.8	100%	0.002	78%	XM_026092712.1
XM_026079009.1 **5/1 6/1 17/1**	PREDICTED: Apteryx rowi insulin (INS), mRNA	51.8	51.8	100%	0.002	78%	XM_026079009.1
XM_026036815.1 **9/1 14/1**	PREDICTED: Nothoprocta perdicaria insulin (INS), mRNA	51.8	51.8	100%	0.001	78%	XM_026036815.1
XM_022221651.1 **8/1**	PREDICTED: Acanthochromis polyacanthus insulin (ins), mRNA	51.8	51.8	100%	0.001	78%	XM_022221651.1
XM_020661338.1 **17/1**	PREDICTED: Labrus bergylta insulin-like (LOC110006110), mRNA	51.8	51.8	100%	0.001	78%	XM_020661338.1

Sequences producing significant alignments:

Selected seq	Description	Max score	Total score	Query cover	E value	Ident	Accession
XM_020648941.1 **17/1**	PREDICTED: Labrus bergylta insulin-like (LOC109995271), mRNA	51.8	51.8	100%	0.001	78%	XM_020648941.1
XM_013957848.1 **5/1** **6/1** **17/1**	PREDICTED: Apteryx australis mantelli insulin (INS), mRNA	51.8	51.8	100%	0.001	78%	XM_013957848.1
LK064676.1 **5/1** **6/1** **17/1**	Apteryx australis mantelli genome assembly AptMant0, scaffold scaffold77	51.8	51.8	100%	0.001	78%	LK064676.1
XM_008298714.1 **6/1**	PREDICTED: Stegastes partitus insulin (LOC103369873), mRNA	51.8	51.8	100%	0.001	78%	XM_008298714.1
XM_023968633.1 **9/1**	PREDICTED: Salvelinus alpinus insulin (LOC111950763), mRNA	50.9	50.9	100%	0.005	80%	XM_023968633.1
BT049386.1 **4/1**	Salmo salar clone ssal-rgb2-569-154 Insulin precursor putative mRNA, complete cds	50.9	50.9	100%	0.005	80%	BT049386.1
LR132016.1 **4/1** **10/1** **17/1**	Betta splendens genome assembly, chromosome: 14	47.3	47.3	100%	0.065	76%	LR132016.1
CP026246.1 **10/1** **13/1** **17/1**	Scophthalmus maximus chromosome 4	47.3	47.3	100%	0.065	76%	CP026246.1
XM_020629757.1 **17/1**	PREDICTED: Labrus bergylta insulin-like (LOC109981109), mRNA	47.3	47.3	100%	0.065	76%	XM_020629757.1
LR131917.1 **4/1** **6/1** **7/1** **16/1** **18/1** **19/1**	Cottoperca gobio genome assembly, chromosome: 10	46.4	46.4	100%	0.065	78%	LR131917.1
XM_020615193.1 **15/1** **17/1**	PREDICTED: Monopterus albus insulin (LOC109968712), mRNA	46.4	46.4	100%	0.065	78%	XM_020615193.1

Sequences producing significant alignments:

Selected seq	Description	Max score	Total score	Query cover	E value	Ident	Accession
XM_020111207.1 **4/1**	PREDICTED: Paralichthys olivaceus insulin-like (LOC109645588), mRNA	46.4	46.4	100%	0.065	78%	XM_020111207.1
XM_020108849.1 **4/1**	PREDICTED: Paralichthys olivaceus insulin (ins), transcript variant X2, mRNA	46.4	46.4	100%	0.065	78%	XM_020108849.1
XM_020108848.1 **4/1**	PREDICTED: Paralichthys olivaceus insulin (ins), transcript variant X1, mRNA	46.4	46.4	100%	0.065	78%	XM_020108848.1
XM_014198195.1 **4/1**	PREDICTED: Salmo salar insulin-like (LOC106603941), mRNA	46.4	46.4	100%	0.065	78%	XM_014198195.1
XM_020599783.1 **15/1 17/1**	PREDICTED: Monopterus albus insulin-like (LOC109959979), mRNA	44.6	44.6	93%	0.23	76%	XM_020599783.1
XM_008302867.1 **6/1**	PREDICTED: Stegastes partitus circularly permutated Ras protein 1-like (LOC103373066), transcript variant X2, mRNA	44.6	44.6	46%	0.23	93%	XM_008302867.1
XM_008302866.1 **6/1**	PREDICTED: Stegastes partitus circularly permutated Ras protein 1-like (LOC103373066), transcript variant X1, mRNA	44.6	44.6	46%	0.23	93%	XM_008302866.1
AC021233.9 **2/1 8/1 9/1 10/1 15/1 17/1**	Homo sapiens chromosome 11, clone RP11-215H22, complete sequence	43.7	43.7	41%	0.79	96%	AC021233.9
LR132049.1 **15/1**	Anabas testudineus genome assembly, chromosome: 19	42.8	42.8	69%	0.79	82%	LR132049.1
LR132037.1 **15/1**	Anabas testudineus genome assembly, chromosome: 10	42.8	84.6	100%	0.79	75%	LR132037.1

Sequences producing significant alignments:

Selected seq	Description	Max score	Total score	Query cover	E value	Ident	Accession
XM_026357607.1 **15/1**	PREDICTED: Anabas testudineus insulin (LOC113160385), mRNA	42.8	42.8	100%	0.79	75%	XM_026357607.1
XM_022190895.1 **8/1**	PREDICTED: Acanthochromis polyacanthus circularly permutated Ras protein 1-like (LOC110949057), mRNA	42.8	42.8	44%	0.79	93%	XM_022190895.1
XM_020637557.1 **17/1**	PREDICTED: Labrus bergylta circularly permutated Ras protein 1-like (LOC109986768), transcript variant X2, mRNA	42.8	42.8	44%	0.79	93%	XM_020637557.1
XM_020637556.1 **17/1**	PREDICTED: Labrus bergylta circularly permutated Ras protein 1-like (LOC109986768), transcript variant X1, mRNA	42.8	42.8	44%	0.79	93%	XM_020637556.1
LR535851.1 **17/1**	Mastacembelus armatus genome assembly, chromosome: 19	41.9	41.9	39%	2.8	96%	LR535851.1
XM_026357435.1 **15/1**	PREDICTED: Anabas testudineus insulin-like (LOC113160265), mRNA	41.9	41.9	100%	2.8	77%	XM_026357435.1
XM_026351068.1 **15/1**	PREDICTED: Anabas testudineus circularly permutated Ras protein 1-like (LOC113156131), transcript variant X3, mRNA	41.9	41.9	39%	2.8	96%	XM_026351068.1
XM_026351067.1 **15/1**	PREDICTED: Anabas testudineus circularly permutated Ras protein 1-like (LOC113156131), transcript variant X2, mRNA	41.9	41.9	39%	2.8	96%	XM_026351067.1
XM_026351066.1 **15/1**	PREDICTED: Anabas testudineus circularly permutated Ras protein 1-like (LOC113156131), transcript variant X1, mRNA	41.9	41.9	39%	2.8	96%	XM_026351066.1

Sequences producing significant alignments:

Selected seq	Description	Max score	Total score	Query cover	E value	Ident	Accession
XM_026315125.1 **17/1**	PREDICTED: Mastacembelus armatus circularly permutated Ras protein 1-like (LOC113135260), transcript variant X2, mRNA	41.9	41.9	39%	2.8	96%	XM_026315125.1
XM_026315124.1 **17/1**	PREDICTED: Mastacembelus armatus circularly permutated Ras protein 1-like (LOC113135260), transcript variant X1, mRNA	41.9	41.9	39%	2.8	96%	XM_026315124.1
XM_017440672.2 **12/1**	PREDICTED: Kryptolebias marmoratus insulin (LOC108250678), mRNA	41.9	41.9	100%	2.8	77%	XM_017440672.2
XM_024402922.1 **6/1 10/1 17/1**	PREDICTED: Oncorhynchus tshawytscha insulin-like (LOC112234674), mRNA	41.9	41.9	100%	2.8	77%	XM_024402922.1
XM_024402921.1 **6/1 10/1 17/1**	PREDICTED: Oncorhynchus tshawytscha insulin-like (LOC112234673), mRNA	41.9	41.9	100%	2.8	77%	XM_024402921.1
CP026880.1 **1/1 18/1**	Pseudomonas sp. LH1G9 chromosome, complete genome	41.9	41.9	41%	2.8	96%	CP026880.1
CP025263.1 **1/1 18/1**	Pseudomonas sp. S09G 359 chromosome	41.9	41.9	41%	2.8	96%	CP025263.1
XM_023240193.1 **19/1**	PREDICTED: Felis catus insulin like growth factor 2 (IGF2), transcript variant X2, mRNA	41.9	41.9	95%	2.8	75%	XM_023240193.1
XM_023240192.1 **19/1**	PREDICTED: Felis catus insulin like growth factor 2 (IGF2), transcript variant X1, mRNA	41.9	41.9	95%	2.8	75%	XM_023240192.1
XM_020591214.1 **15/1 17/1**	PREDICTED: Monopterus albus insulin-like (LOC109955249), mRNA	41.9	41.9	95%	2.8	75%	XM_020591214.1

Sequences producing significant alignments:

Selected seq	Description	Max score	Total score	Query cover	E value	Ident	Accession
CP018420.1 **1/1** **18/1**	Pseudomonas veronii strain R02, complete genome	41.9	41.9	41%	2.8	96%	CP018420.1
XM_020464884.1 **6/1** **10/1** **17/1**	PREDICTED: Oncorhynchus kisutch insulin-like (LOC109873252), mRNA	41.9	41.9	100%	2.8	77%	XM_020464884.1
XM_019812848.1 **19/1**	PREDICTED: Felis catus insulin like growth factor 2 (IGF2), transcript variant X4, mRNA	41.9	41.9	95%	2.8	75%	XM_019812848.1
XM_019812847.1 **19/1**	PREDICTED: Felis catus insulin like growth factor 2 (IGF2), transcript variant X3, mRNA	41.9	41.9	95%	2.8	75%	XM_019812847.1
LT599583.1 **1/1** **18/1**	Pseudomonas veronii 1YdBTEX2 genome assembly, chromosome: PVE_r1	41.9	41.9	41%	2.8	96%	LT599583.1
XM_008278129.1 **6/1**	PREDICTED: Stegastes partitus insulin-like (LOC103354683), mRNA	41.9	41.9	100%	2.8	77%	XM_008278129.1
NM_001124670.1 **6/1** **10/1** **17/1**	Oncorhynchus mykiss preproinsulin 2 (LOC100136703), mRNA	41.9	41.9	100%	2.8	77%	NM_001124670.1
L11712.1 **6/1** **10/1** **17/1**	Oncorhynchus keta insulin gene, complete cds	41.9	41.9	100%	2.8	77%	L11712.1
CP026255.1 **10/1** **13/1** **17/1**	Scophthalmus maximus chromosome 13	41.0	41.0	100%	2.8	75%	CP026255.1
XM_017419715.2 **12/1**	PREDICTED: Kryptolebias marmoratus insulin-like (LOC108237967), mRNA	41.0	41.0	100%	2.8	75%	XM_017419715.2
XM_022206846.1 **8/1**	PREDICTED: Acanthochromis polyacanthus insulin-like (LOC110959849), mRNA	41.0	41.0	95%	2.8	77%	XM_022206846.1
CP034516.1 **2/1** **17/1**	Eukaryotic synthetic construct chromosome 13	40.1	80.1	76%	9.6	96%	CP034516.1
CP034491.1 **2/1** **17/1**	Eukaryotic synthetic construct chromosome 13	40.1	80.1	76%	9.6	96%	CP034491.1

Sequences producing significant alignments:

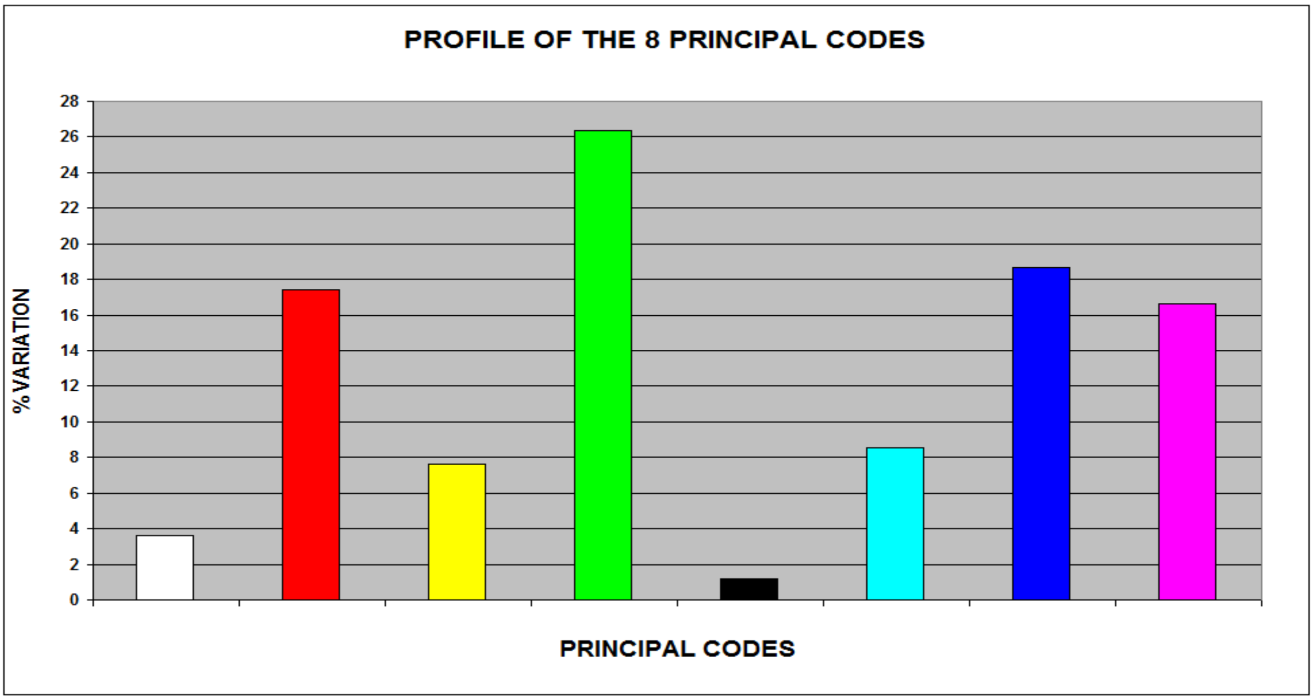
Selected seq	Description	Max score	Total score	Query cover	E value	Ident	Accession
XR_002314985.1 **6/1**	PREDICTED: Odocoileus virginianus texanus uncharacterized LOC110141110 (LOC110141110), transcript variant X3, ncRNA	40.1	40.1	46%	9.6	90%	XR_002314985.1
XM_014136745.1 **4/1**	PREDICTED: Salmo salar insulin (LOC106567474), mRNA	40.1	40.1	90%	9.6	78%	XM_014136745.1
BT049203.1 **4/1**	Salmo salar clone ssal-plnb-020-217 Insulin precursor putative mRNA, complete cds	40.1	40.1	90%	9.6	78%	BT049203.1
BT046764.1 **4/1**	Salmo salar clone ssal-plnb-013-055 Insulin precursor putative mRNA, complete cds	40.1	40.1	90%	9.6	78%	BT046764.1
AC149665.2 **3/1 4/1 8/1**	Bos taurus BAC CH240-60O13 (Children's Hospital Oakland Research Institute Bovine BAC Library (male)) complete sequence	40.1	40.1	46%	9.6	90%	AC149665.2
AL354999.17 **8/1 17/1**	Human DNA sequence from clone RP11-531B22 on chromosome 13, complete sequence	40.1	40.1	38%	9.6	96%	AL354999.17
AL354896.16 **8/1 17/1**	Human DNA sequence from clone RP11-512M17 on chromosome 13, complete sequence	40.1	40.1	38%	9.6	96%	AL354896.16
AK024581.1 **2/1 8/1 9/1 10/1 15/1 17/1**	Homo sapiens cDNA: FLJ20928 fis, clone ADSE01074	40.1	40.1	38%	9.6	96%	AK024581.1
LR132007.1 **4/1 10/1 17/1**	Betta splendens genome assembly, chromosome: 10	39.2	39.2	33%	9.6	100%	LR132007.1
XM_022751952.1 **10/1**	PREDICTED: Seriola dumerili insulin-like (LOC111226678), mRNA	39.2	39.2	33%	9.6	100%	XM_022751952.1
LT594792.1 **9/1 17/1**	Theobroma cacao genome assembly, chromosome: V	39.2	39.2	41%	9.6	92%	LT594792.1

Complete Analysis of Sequence n° 1/1 of Insulin Chain A

1.2 GRAPHIC RESULTS OF THE "NON-OBVIOUS TREND" ANALYSIS OF SEQUENCE n° 1/1 OF INSULIN CHAIN A

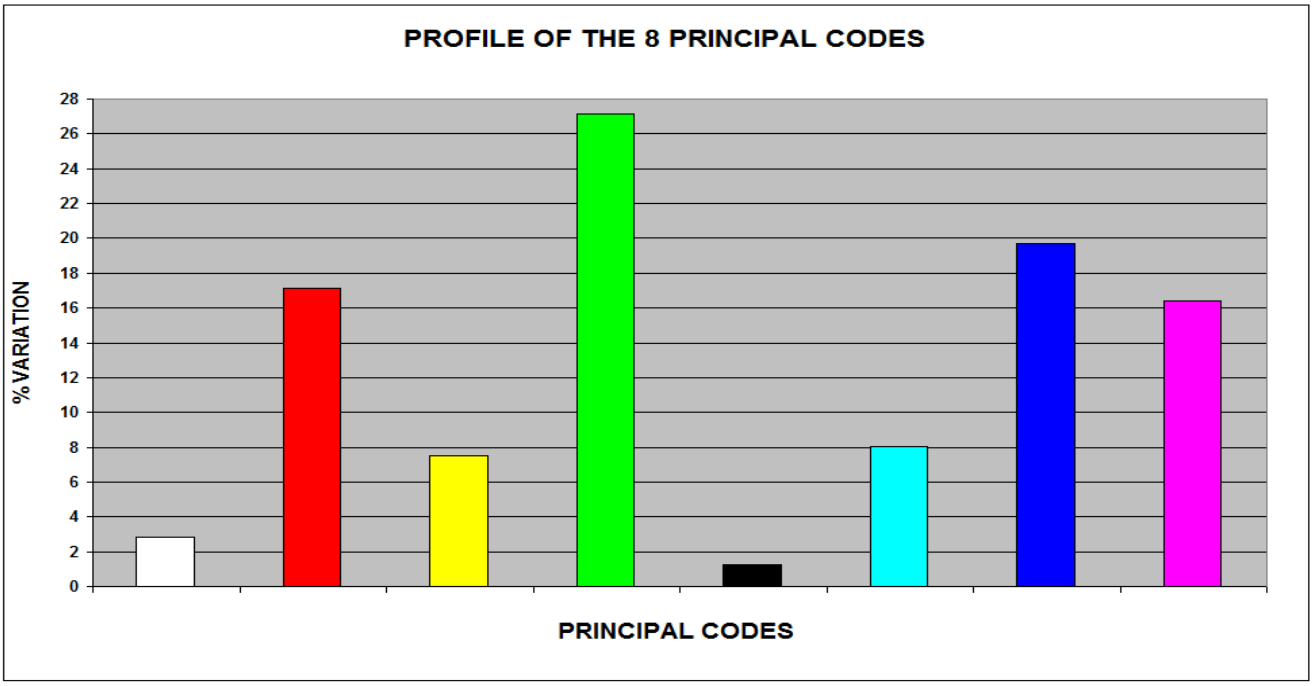
In the Pct. 1 (A e B) two **8 Principal Codes Profiles** are compared.

The chart in Pct. 1 (A) refers to the **original base sequence** of **Insulin Chain A**.



Pct. 1 (A)

The chart in Pct. 1 (B) refers to the **first "new generated sequence"** (**Sequence n° 1/1**) that originates from the original one.

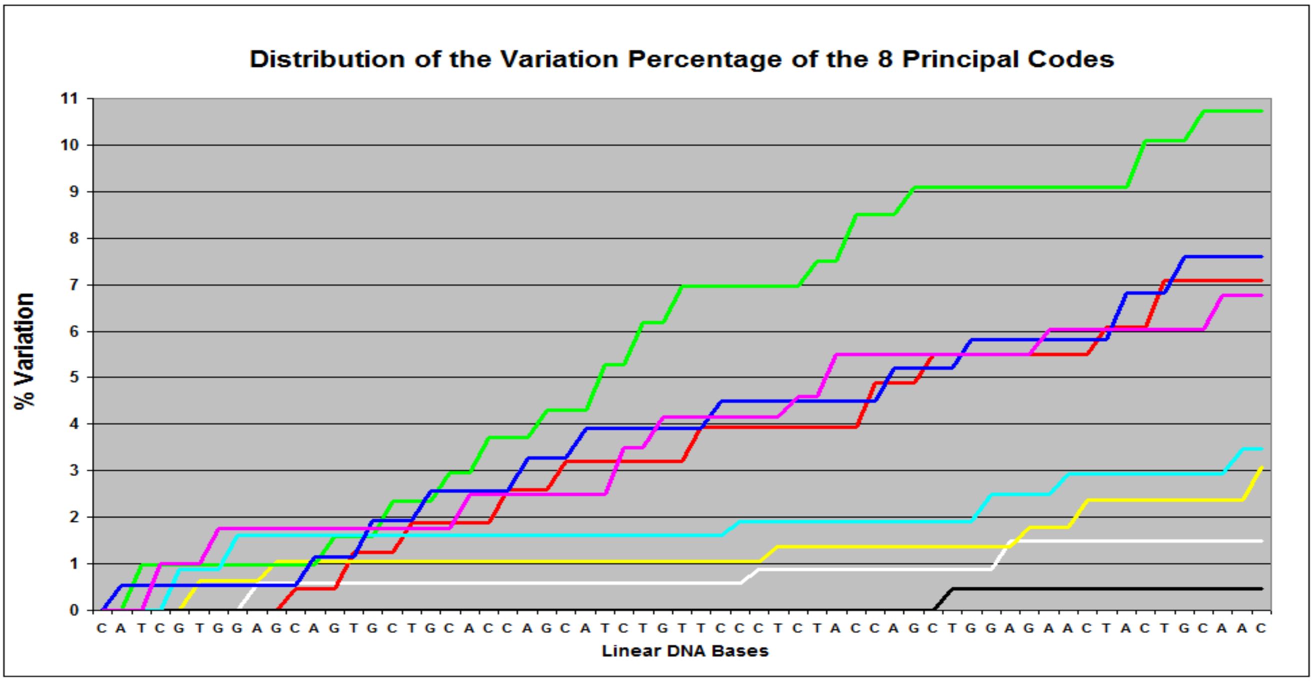


Pct. 1 (B)

As you can see in the charts, the two **8 Main Codes Profiles** of the original sequence and of the new generated sequence arising from the original one, ARE ALMOST IDENTICAL.

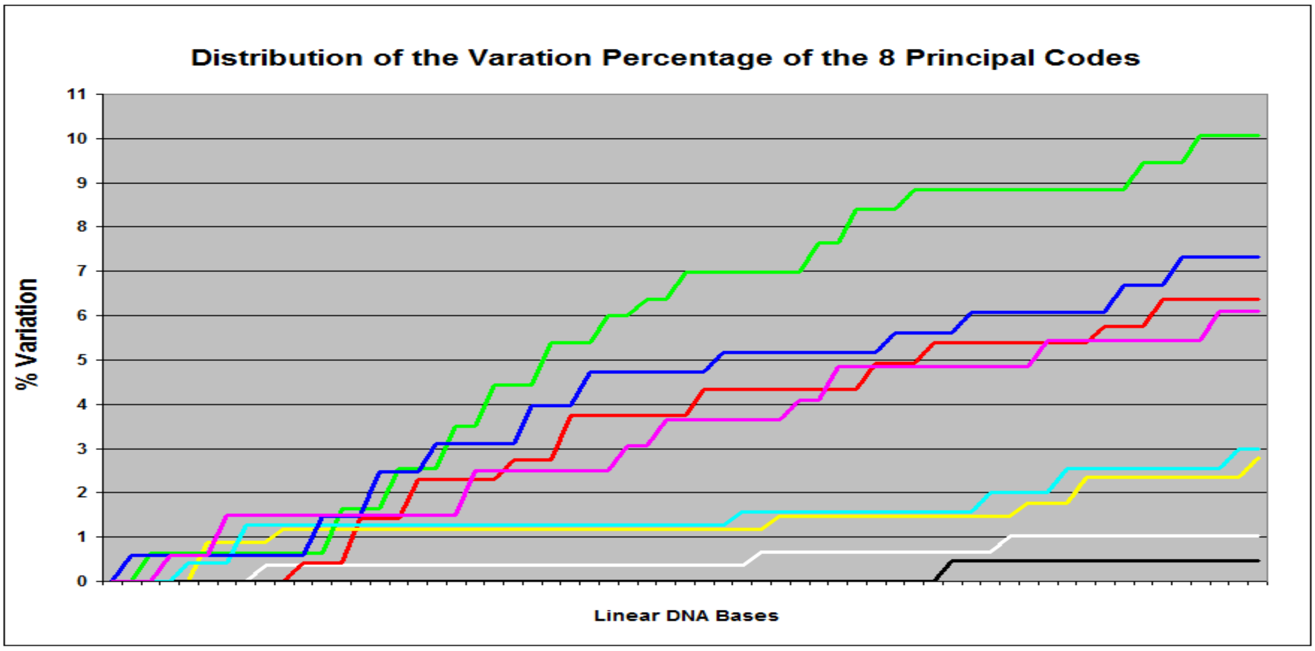
In Pct. 2 (A and B) two charts concerning the **Distribution of the Variation Percentage of the 8 Main Codes** are compared.

The charts in Pct. 2 (A) refers to the **original base sequence** analysed before.



Pct. 2 (A)

The chart in Pct. 2 (B) refers to the **“new generated sequence”** that originates from the original one.

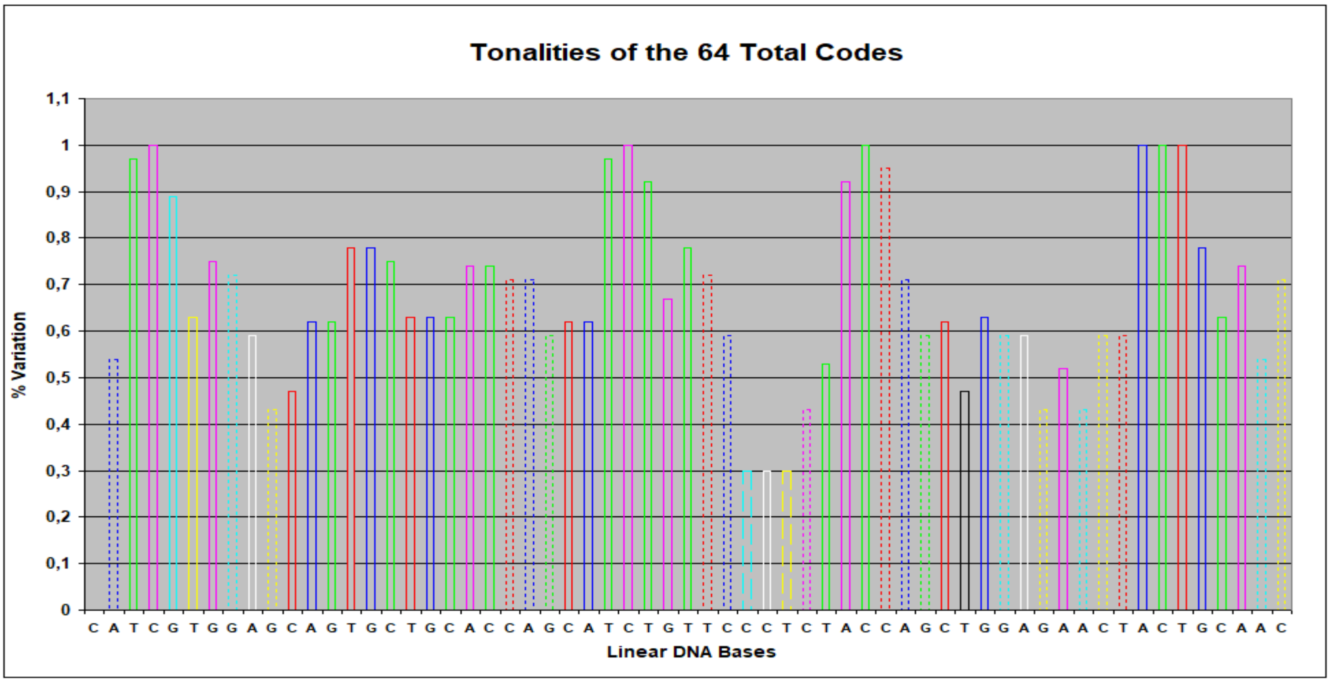


Pct. 2 (B)

As in Pct. 1, the two charts concerning the **Distribution of the Variation Percentage of the 8 Main Codes,** respectively of the **original sequence** and of the **new generated sequence** originating from the original one, <u>ARE ALMOST IDENTICAL.</u>

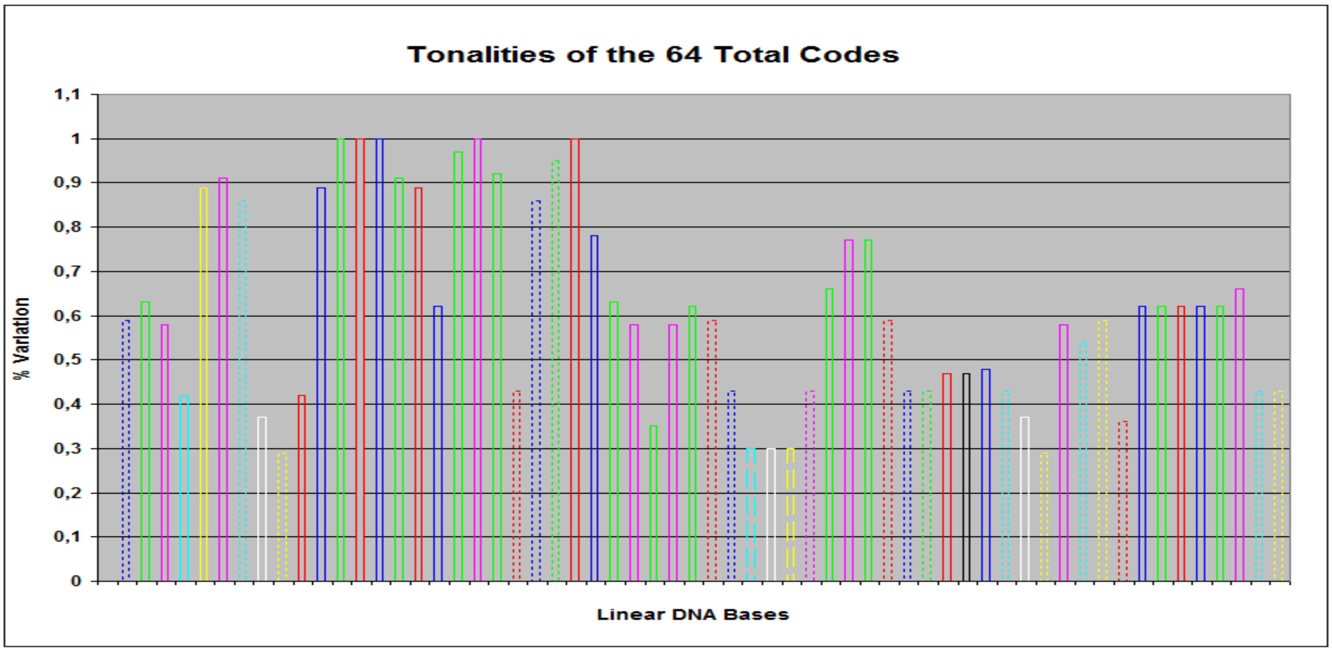
In Pct. 3 (A and B) two charts concerning the single **Tonalities of the 64 Total Codes** are compared.

The chart in Pct. 3 (A) refers to the **original base sequence** analysed before.



Pct. 3 (A)

The chart in Pct. 3 (B) refers to the **"new generated sequence"** that originates from the original one.

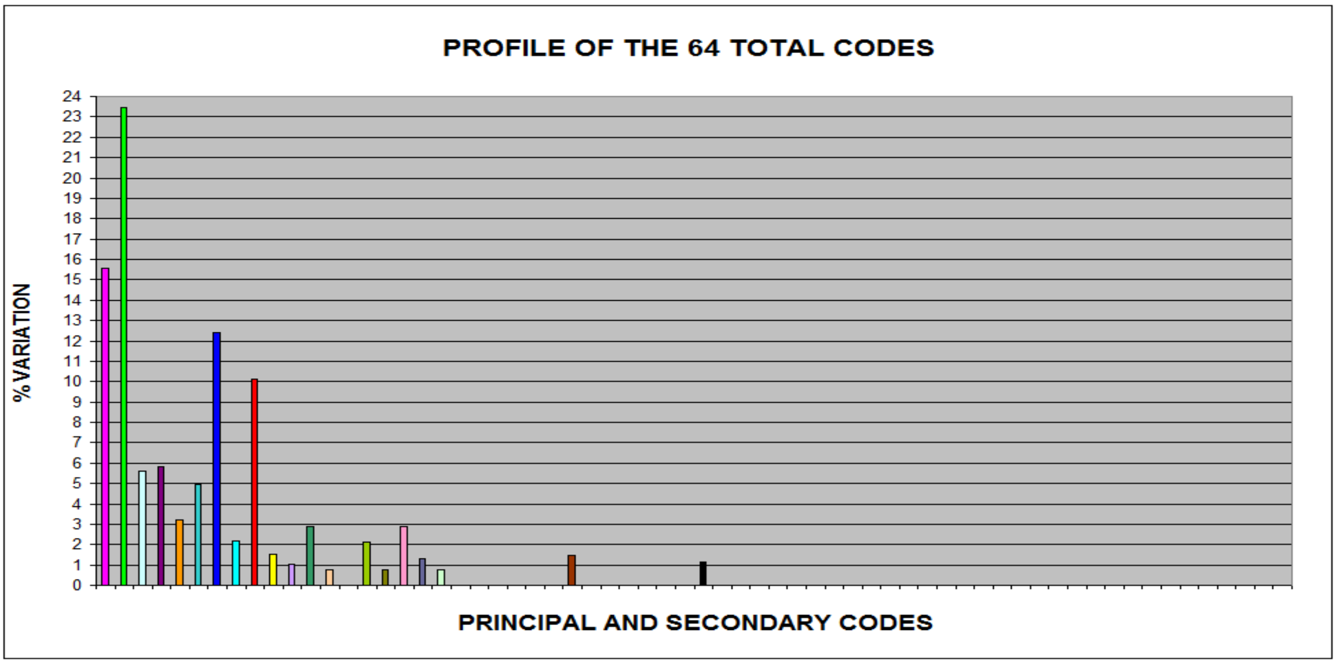


Pct. 3 (B)

DIFFERENTLY FROM THE PREVIOUS CHARTS, the two charts concerning the single **Tonalities of the 64 Total Codes,** respectively of the **original sequence** and of the **new generated sequence** originating from the original one, ARE VERY DIFFERENT FROM ONE ANOTHER.

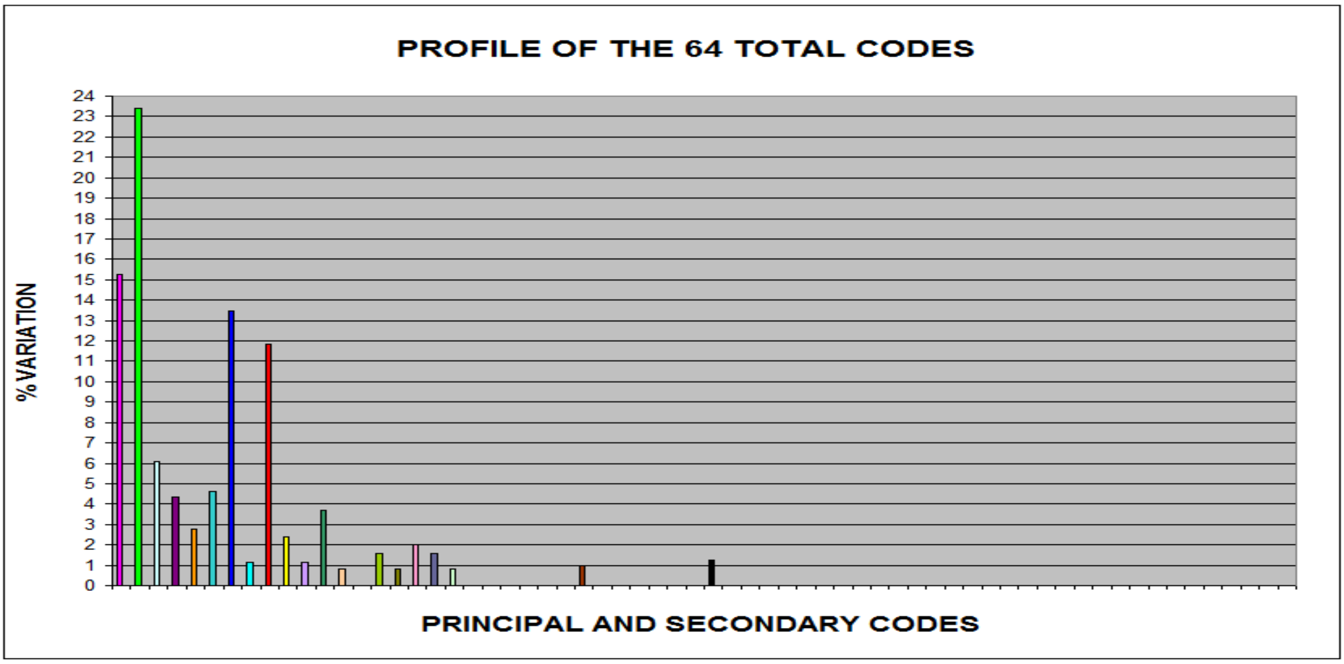
In Pct. 4 (A and B) two charts concerning the **Profile of the 64 Total Codes** are compared.

The chart in Pct. 4 (A) refers to the **original base sequence** analysed before.



Pct. 4 (A)

The chart in Pct. 4 (B) refers to the **"new generated sequence"** originated from the original one.



Pct. 4 (B)

Differently to the previous charts, the two charts concerning the **Profile of the 64 Total Codes,** respectively of the **original sequence** and of the **new generated sequence** produced from the original one, ARE PARTLY SIMILAR.
From the "non-obvious trend" analysis (carried through the **T.T.E.S.**) of **Sequence n°1/1 of Insulin Chain A**, it comes to light that the differences between the "characteristics" of the **original sequence** and those of the **new generated sequence**, that arises from the original one, are noticeably pointed out by the charts concerning the **Tonalities of the 64 Total Codes** (Pct. 3 A and B).

This result is clear considering that the charts of the single **Tonalities of the 64 Total Codes** (Pct. 3 A and B), compared to the other charts, **are *more sensitive to the single base sequences* than to the "non-obvious trend" of the sequences themselves.**

Even the charts related to the **Profiles of the 64 Total Codes (**Pct. 4 A and B) point out some differences, but they are less evident compared to those that emerged from the analysis of the charts of the single **Tonalities of the 64 Total Codes** (Pct. 3 A and B).

From the other charts (Pct. 1 A and B, Pct. 2 A and B), it comes to light a nearly absolute likeness of the "characteristics" of the **original sequence** and the **new generated sequence** that originates from the original one.

This result is remarkable if we consider that, out of the **63** DNA bases of the **new generated sequence**, **Sequence n° 1/1**, ONLY **FOURTEEN BASES** (the **22,22%**)**,** ARE EQUAL (by type and by position in the sequence) TO THOSE OF THE ORIGINAL SEQUENCE (**Insulin Chain A**).

In conclusion, the greater is the level of likeness of the "characteristics" of the **new generated sequence** to the "characteristics" of the **original sequence**, the higher is the likeness of the **8 Main Codes Profiles** (Pct. 1 A and B) and that related to the **Distribution of the Variation Percentage of the 8 Main Codes** (Pct. 2 A and B). ***These charts are both sensitive to the* "non-obvious trend" *of the sequences.***

1. 3 IMPLICATIONS RELATED TO THE GRAPHIC RESULTS OF THE “NON-OBVIOUS TREND” ANALYSIS OF SEQUENCE n° 1/1 OF INSULIN CHAIN A

The **63** DNA base sequence of the **new generated sequence** (**Sequence n° 1/1**) that arises from the **original** one has been subjected to **BLAST** research.

Please note:

Information about the ***significant alignments*** produced by *BLAST research*, related to **Sequence n° 1/1,** and all the data acquired from *GenBank (3)* will be published in the **Appendix,** after the *General Conclusions.*

Query = NEW GENERATED SEQUENCE (Sequence n° 1/1)

Length = 63

Parameters of BLAST research:

Programme	*Blastn*
Word size	*11*
Expect value	*10*
Hitlist size	*100*
Match/Mismatch scores	*2,-3*
Gapcosts	*5,2*
Low Complexity Filter	*Yes*
Filter string	*L;m;*
Genetic Code	*1*

Please note:

Here, “**the organisms found to be in common**” between the results of BLAST research carried out on **Insulin Chain A** and results of BLAST research carried out on **Sequence n° 1/1**, were highlighted in **Red**.

As well, “**the organisms found to be in common**” between the results of BLAST research carried out on **Insulin Chain A**, results of BLAST researches carried out on **Sequence n° 1/1** and results of BLAST research carried out on **at least one** of the *19 generated sequences*, were highlighted in **Green**.

Moreover, “**the denomination of the sequence**” (1/1, 2/1, ... 19/1) of the “**organism found to be in common**” between the results of BLAST research carried out on **Sequence n° 1/1** and results of BLAST research carried out on **at least one** of the *19 new generated sequences*, were highlighted in **Blue**.

Finally, “**the denomination of the sequence**” (1/1, 2/1, ... 19/1) of the “**organism found to be in common**” between the results of BLAST research carried out on **Insulin Chain A** and results of BLAST research carried out on *19 generated sequences*, were highlighted in **Yellow**.

Sequenza n° 1/1

Sequences producing significant alignments:

Selected seq	Description	Max score	Total score	Query cover	E value	Ident	Accession
1 CP010359.1	Pseudomonas plecoglossicida strain NyZ12, complete genome	44.6	44.6	61%	0.22	85%	CP010359.1
2 **18/1** CP007620.1	Pseudomonas putida strain DLL-E4, complete genome	44.6	44.6	61%	0.22	85%	CP007620.1
3 **15/1** XM_017200197.1	PREDICTED: Drosophila ficusphila DNA topoisomerase 2-binding protein 1 (LOC108097709), mRNA	41.0	41.0	55%	2.7	89%	XM_017200197.1
4 XM_027404801.1	PREDICTED: Cricetulus griseus pecanex 2 (Pcnx2), mRNA	40.1	40.1	49%	9.5	88%	XM_027404801.1
5 XM_003496803.4	PREDICTED: Cricetulus griseus pecanex 2 (Pcnx2), mRNA	40.1	40.1	49%	9.5	88%	XM_003496803.4
6 XM_026789982.1	PREDICTED: Microtus ochrogaster pecanex 2 (Pcnx2), transcript variant X2, mRNA	40.1	40.1	49%	9.5	88%	XM_026789982.1
7 XM_013345975.2	PREDICTED: Microtus ochrogaster pecanex 2 (Pcnx2), transcript variant X1, mRNA	40.1	40.1	49%	9.5	88%	XM_013345975.2
8 XM_028095345.1	PREDICTED: Eumetopias jubatus TNFRSF1A associated via death domain (TRADD), mRNA	40.1	40.1	41%	9.5	93%	XM_028095345.1
9 XM_027618249.1	PREDICTED: Zalophus californianus UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 9 (LOC113935781), transcript variant X5, mRNA	40.1	40.1	41%	9.5	93%	XM_027618249.1
10 XM_027618248.1	PREDICTED: Zalophus californianus UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 9 (LOC113935781), transcript variant X4, mRNA	40.1	40.1	41%	9.5	93%	XM_027618248.1
11 XM_025888785.1	PREDICTED: Callorhinus ursinus TNFRSF1A associated via death domain (TRADD), mRNA	40.1	40.1	41%	9.5	93%	XM_025888785.1
12 XM_021703964.1	PREDICTED: Neomonachus schauinslandi TNFRSF1A associated via death domain (TRADD), transcript variant X2, mRNA	40.1	40.1	41%	9.5	93%	XM_021703964.1

Sequences producing significant alignments:

Selected seq	Description	Max score	Total score	Query cover	E value	Ident	Accession
13 XM_021703956.1	PREDICTED: Neomonachus schauinslandi TNFRSF1A associated via death domain (TRADD), transcript variant X1, mRNA	40.1	40.1	41%	9.5	93%	XM_021703956.1
14 15/1 XM_013122036.2	PREDICTED: Mesocricetus auratus pecanex homolog 2 (Drosophila) (Pcnx2), transcript variant X2, mRNA	40.1	40.1	49%	9.5	88%	XM_013122036.2
15 15/1 XM_005064691.3	PREDICTED: Mesocricetus auratus pecanex homolog 2 (Drosophila) (Pcnx2), transcript variant X1, mRNA	40.1	40.1	49%	9.5	88%	XM_005064691.3
16 15/1 XM_021170316.1	PREDICTED: Mus caroli pecanex homolog 2 (Drosophila) (Pcnx2), mRNA	40.1	40.1	49%	9.5	88%	XM_021170316.1
17 15/1 XM_021220388.1	PREDICTED: Mus pahari pecanex homolog 2 (Drosophila) (Pcnx2), mRNA	40.1	40.1	49%	9.5	88%	XM_021220388.1
18 LT629788.1	Pseudomonas moraviensis strain BS3668 genome assembly, chromosome: I	40.1	40.1	61%	9.5	82%	LT629788.1
19 XM_018455918.1	PREDICTED: Trachymyrmex zeteki uncharacterized LOC108727710 (LOC108727710), mRNA	40.1	40.1	38%	9.5	96%	XM_018455918.1
20 XR_001778443.1	PREDICTED: Mus musculus pecanex homolog 2 (Pcnx2), transcript variant X3, misc_RNA	40.1	40.1	49%	9.5	88%	XR_001778443.1
21 XM_011248396.2	PREDICTED: Mus musculus pecanex homolog 2 (Pcnx2), transcript variant X2, mRNA	40.1	40.1	49%	9.5	88%	XM_011248396.2
22 XM_011248395.2	PREDICTED: Mus musculus pecanex homolog 2 (Pcnx2), transcript variant X1, mRNA	40.1	40.1	49%	9.5	88%	XM_011248395.2
23 XM_004393402.2	PREDICTED: Odobenus rosmarus divergens TNFRSF1A-associated via death domain (TRADD), transcript variant X2, mRNA	40.1	40.1	41%	9.5	93%	XM_004393402.2
24 XM_012566139.1	PREDICTED: Odobenus rosmarus divergens TNFRSF1A-associated via death domain (TRADD), transcript variant X1, mRNA	40.1	40.1	41%	9.5	93%	XM_012566139.1

Sequences producing significant alignments:

Selected seq	Description	Max score	Total score	Query cover	E value	Ident	Accession
25 XM_006741502.1	PREDICTED: Leptonychotes weddellii TNFRSF1A-associated via death domain (TRADD), mRNA	40.1	40.1	41%	9.5	93%	XM_006741502.1
26 XM_006531060.1	PREDICTED: Mus musculus pecanex homolog 2 (Pcnx2), transcript variant X4, mRNA	40.1	40.1	49%	9.5	88%	XM_006531060.1
27 NM_175561.4	Mus musculus pecanex homolog 2 (Pcnx2), mRNA	40.1	40.1	49%	9.5	88%	NM_175561.4
28 XM_002620491.1	Ajellomyces dermatitidis SLH14081 peroxisomal ABC transporter, mRNA	40.1	40.1	38%	9.5	96%	XM_002620491.1
29 15/1 BC068235.1	Mus musculus pecanex-like 2 (Drosophila), mRNA (cDNA clone IMAGE:30542978), containing frame-shift errors	40.1	40.1	49%	9.5	88%	BC068235.1
30 AK220342.1	Mus musculus mRNA for mKIAA0435 protein	40.1	40.1	49%	9.5	88%	AK220342.1
31 AK087907.1	Mus musculus 2 days pregnant adult female ovary cDNA, RIKEN full-length enriched library, clone:E330039K12 product:weakly similar to PECANEX 1 [Mus musculus], full insert sequence	40.1	40.1	49%	9.5	88%	AK087907.1
32 AK030215.1	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4933424I21 product:hypothetical Homeodomain-like structure containing protein, full insert sequence	40.1	40.1	49%	9.5	88%	AK030215.1
33 CP026674.1	Pseudomonas sp. SWI44 chromosome, complete genome	39.2	39.2	57%	9.5	83%	CP026674.1
34 CP026676.1	Pseudomonas sp. SWI6 chromosome, complete genome	39.2	39.2	57%	9.5	83%	CP026676.1
35 XM_022492727.1	PREDICTED: Enhydra lutris kenyoni trichohyalin-like (LOC111140481), partial mRNA	39.2	39.2	46%	9.5	88%	XM_022492727.1
36 15/1 XM_020945606.1	PREDICTED: Drosophila serrata uncharacterized LOC110178466 (LOC110178466), mRNA	39.2	39.2	53%	9.5	89%	XM_020945606.1

Sequences producing significant alignments:

Selected seq	Description	Max score	Total score	Query cover	E value	Ident	Accession
37 XM_006880105.1	PREDICTED: Elephantulus edwardii putative scavenger receptor cysteine-rich domain-containing protein LOC619207-like (LOC102868011), mRNA	39.2	39.2	53%	9.5	84%	XM_006880105.1
38 CP003961.1	Pseudomonas sp. VLB120, complete genome	39.2	39.2	57%	9.5	83%	CP003961.1

PLEASE NOTE:

As mentioned in the introduction to this Chapter, Chapter I° First Part delves into only two of the possible significant alignments that have been found, focusing its attention on only **two** species of *organisms*: some species of **Pseudomonas** bacteria and the nematode **Heligmosomoides polygyrus** (*organisms* that are both formed by DNA bases belonging to the new generated sequence: **Sequence n°1/1**).

In date **9 April 2019** the last BLAST research (as a control research carried out to consider possible updates before publishing the present Chapter) has been carried out on all the analysed sequences (the *Insulin Chain A sequence* and the *19 new sequences* obtained through the analysis of their respective 19 "non-obvious trends").

Several months before this last BLAST research, it has been discovered, to our surprise, that **two Sequences**, identified while publishing Chapter I° First Part (videlicet in date 9 January 2018), which showed significant alignments with the nematode **Heligmosomoides polygyrus**, for reasons that are not known, were removed from the National Center for Biotechnology Information (NCBI) archive.

First Sequence removed from the archive:

Sequence producing significant alignments:	***Score (Bits)***	***E Value***	***Identit.***
LL188962.1 Heligmosomoides polygyrus genome assembly H_bakeri_Edinburgh, scaffold HPBE_scaffold0000593	44.6	0.19	93%

Record removed. *This record was removed at the submitter's request. Please contact update@ebi.ac.uk for further details.*

Second Sequence removed from the archive:

Sequence producing significant alignments:	***Score (Bits)***	***E Value***	***Identit.***
LL194531.1 Heligmosomoides polygyrus genome assembly H_bakeri_Edinburgh, scaffold HPBE_contig0000102.........	39.2	8.2	87%

Record removed. *This record was removed at the submitter's request. Please contact update@ebi.ac.uk for further details.*

Comparison between the alignments of Sequence 1/1 and Sequence of Insulin Chain A according to the "Species of Common Organisms":

Alignments Sequence 1/1	Description	Alignments Sequence Insulin Chain A	Description
1 Select seq CP010359.1	Pseudomonas plecoglossicida strain NyZ12, complete genome	Select seq CP026880.1 **18/1**	Pseudomonas sp. LH1G9 chromosome, complete genome
2 Select seq CP007620.1 **18/1**	Pseudomonas putida strain DLL-E4, complete genome	Select seq CP025263.1 **18/1**	Pseudomonas sp. S09G 359 chromosome
18 Select seq LT629788.1	Pseudomonas moraviensis strain BS3668 genome assembly, chromosome: I	Select seq CP018420.1 **18/1**	Pseudomonas veronii strain R02, complete genome
33 Select seq CP026674.1	Pseudomonas sp. SWI44 chromosome, complete genome	Select seq LT599583.1 **18/1**	Pseudomonas veronii 1YdBTEX2 genome assembly, chromosome: PVE_r1
34 Select seq CP026676.1	Pseudomonas sp. SWI6 chromosome, complete genome		
38 Select seq CP003961.1	Pseudomonas sp. VLB120, complete genome		
4 Select seq XM_027404801.1	PREDICTED: Cricetulus griseus pecanex 2 (Pcnx2), mRNA	Select seq XM_027409202.1	PREDICTED: Cricetulus griseus insulin (Ins), mRNA
5 Select seq XM_003496803.4	PREDICTED: Cricetulus griseus pecanex 2 (Pcnx2), mRNA	Select seq XM_003508080.2	PREDICTED: Cricetulus griseus insulin (Ins), mRNA
6 Select seq XM_026789982.1	PREDICTED: Microtus ochrogaster pecanex 2 (Pcnx2), transcript variant X2, mRNA	Select seq XM_005351571.2	PREDICTED: Microtus ochrogaster insulin (Ins), mRNA
7 Select seq XM_013345975.2	PREDICTED: Microtus ochrogaster pecanex 2 (Pcnx2), transcript variant X1, mRNA	Select seq DQ250572.1	Microtus kikuchii preproinsulin (Ins) gene, complete cds

Comparison between the alignments of Sequence 1/1 and Sequence of Insulin Chain A according to the "Species of Common Organisms":

Alignments Sequence 1/1	Description	Alignments Sequence Insulin Chain A	Description
8 Select seq XM_028095345.1	PREDICTED: Eumetopias jubatus TNFRSF1A associated via death domain (TRADD), mRNA	Select seq XM_028118258.1	PREDICTED: Eumetopias jubatus insulin (LOC114220406), mRNA
9 Select seq XM_027618249.1	PREDICTED: Zalophus californianus UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 9 (LOC113935781), transcript variant X5, mRNA	Select seq XM XM_027579931.1	PREDICTED: Zalophus californianus insulin (INS), mRNA
10 Select seq XM_027618248.1	PREDICTED: Zalophus californianus UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 9 (LOC113935781), transcript variant X4, mRNA		
11 Select seq XM_025888785.1	PREDICTED: Callorhinus ursinus TNFRSF1A associated via death domain (TRADD), mRNA	Select seq XM_025879485.1	PREDICTED: Callorhinus ursinus insulin (LOC112829807), mRNA
12 Select seq XM_021703964.1	PREDICTED: Neomonachus schauinslandi TNFRSF1A associated via death domain (TRADD), transcript variant X2, mRNA	Select seq XM XM_021685179.1	PREDICTED: Neomonachus schauinslandi insulin (INS), mRNA
13 Select seq XM_021703956.1	PREDICTED: Neomonachus schauinslandi TNFRSF1A associated via death domain (TRADD), transcript variant X1, mRNA		
14 Select seq XM_013122036.2 **15/1**	PREDICTED: Mesocricetus auratus pecanex homolog 2 (Drosophila) (Pcnx2), transcript variant X2, mRNA	Select seq XM_013112606.2	PREDICTED: Mesocricetus auratus insulin (Ins), mRNA

Comparison between the alignments of Sequence 1/1 and Sequence of Insulin Chain A according to the "Species of Common Organisms":

Alignments Sequence 1/1	Description	Alignments Sequence Insulin Chain A	Description
15 Select seq XM_005064691.3 **15/1**	PREDICTED: Mesocricetus auratus pecanex homolog 2 (Drosophila) (Pcnx2), transcript variant X1, mRNA		
16 Select seq XM_021170316.1 **15/1**	PREDICTED: Mus caroli pecanex homolog 2 (Drosophila) (Pcnx2), mRNA	Select seq XM_021152514.1 **6/1 8/1 10/1** **13/1 17/1 18/1**	PREDICTED: Mus caroli insulin-1 (LOC110286053), mRNA
17 Select seq XM_021220388.1 **15/1**	PREDICTED: Mus pahari pecanex homolog 2 (Drosophila) (Pcnx2), mRNA	Select seq DQ250565.1 **6/1 8/1 10/1** **13/1 17/1 18/1**	Mus caroli preproinsulin 1 (Ins1) gene, complete cds
20 Select seq XR_001778443.1	PREDICTED: Mus musculus pecanex homolog 2 (Pcnx2), transcript variant X3, misc_RNA	Select seq XM_021215010.1 **6/1 8/1 10/1** **13/1 17/1 18/1**	PREDICTED: Mus pahari insulin-1 (LOC110333420), mRNA
21 Select seq XM_011248396.2	PREDICTED: Mus musculus pecanex homolog 2 (Pcnx2), transcript variant X2, mRNA	Select seq NM_008386.4 **6/1 8/1 10/1** **13/1 17/1 18/1**	Mus musculus insulin I (Ins1), mRNA
22 Select seq XM_011248395.2	PREDICTED: Mus musculus pecanex homolog 2 (Pcnx2), transcript variant X1, mRNA	Select seq BC145868.1 **6/1 8/1 10/1** **13/1 17/1 18/1**	Mus musculus insulin I, mRNA (cDNA clone MGC:175755 IMAGE:40131171), complete cds
26 Select seq XM_006531060.1	PREDICTED: Mus musculus pecanex homolog 2 (Pcnx2), transcript variant X4, mRNA	Select seq DQ479923.1 **6/1 8/1 10/1** **13/1 17/1 18/1**	Mus musculus strain BTBR T+ tf/J insulin 1 precursor, gene, complete cds
27 Select seq NM_175561.4	Mus musculus pecanex homolog 2 (Pcnx2), mRNA	Select seq AC163452.12 **6/1 8/1 10/1** **13/1 17/1 18/1**	Mus musculus chromosome 19, clone RP23-405C7, complete sequence
29 Select seq BC068235.1 **15/1**	Mus musculus pecanex-like 2 (Drosophila), mRNA (cDNA clone IMAGE:30542978), containing frame-shift errors	Select seq AC136710.8 **6/1 8/1 10/1** **13/1 17/1 18/1**	Mus musculus chromosome 19, clone RP23-35B13, complete sequence

Comparison between the alignments of Sequence 1/1 and Sequence of Insulin Chain A according to the “Species of Common Organisms”:

Alignments Sequence 1/1	**Description**	**Alignments Sequence Insulin Chain A**	**Description**
30 Select seq AK220342.1	Mus musculus mRNA for mKIAA0435 protein	Select seq AC140320.2 **6/1 8/1 10/1** **13/1 17/1 18/1**	Mus musculus BAC clone RP23-401C13 from chromosome 19, complete sequence
31 Select seq AK087907.1	Mus musculus 2 days pregnant adult female ovary cDNA, RIKEN full-length enriched library, clone:E330039K12 product:weakly similar to PECANEX 1 [Mus musculus], full insert sequence	Select seq BC098468.1 **6/1 8/1 10/1** **13/1 17/1 18/1**	Mus musculus insulin I, mRNA (cDNA clone MGC:107382 IMAGE:6432765), complete cds
32 Select seq AK030215.1	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4933424I21 product:hypothetical Homeodomain-like structure containing protein, full insert sequence	Select seq AK148541.1 **6/1 8/1 10/1** **13/1 17/1 18/1**	Mus musculus adult pancreas islet cells cDNA, RIKEN full-length enriched library, clone:C820020F18 product:insulin I, full insert sequence
		Select seq AK007345.1 **6/1 8/1 10/1** **13/1 17/1 18/1**	Mus musculus 10 day old male pancreas cDNA, RIKEN full-length enriched library, clone:1810005L03 product:INSULIN 1 PRECURSOR, full insert sequence
		Select seq XM_021168754.1 **6/1 8/1 10/1** **13/1 17/1 18/1**	PREDICTED: Mus caroli insulin-2 (LOC110299132), transcript variant X2, mRNA
		Select seq XM_021168753.1 **6/1 8/1 10/1** **13/1 17/1 18/1**	PREDICTED: Mus caroli insulin-2 (LOC110299132), transcript variant X1, mRNA
		Select seq NM_001185084.2 **6/1 8/1 10/1** **13/1 17/1 18/1**	Mus musculus insulin II (Ins2), transcript variant 3, mRNA
		Select seq NM_001185083.2 **6/1 8/1 10/1** **13/1 17/1 18/1**	Mus musculus insulin II (Ins2), transcript variant 1, mRNA

Comparison between the alignments of Sequence 1/1 and Sequence of Insulin Chain A according to the "Species of Common Organisms":

Alignments Sequence 1/1	**Description**	**Alignments Sequence Insulin Chain A**	**Description**
		Select seq NM_008387.5 **6/1 8/1 10/1** **13/1 17/1 18/1**	Mus musculus insulin II (Ins2), transcript variant 2, mRNA
		Select seq JN959239.1 **6/1 8/1 10/1** **13/1 17/1 18/1**	Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Ins2:tm1a(EUCOMM)Wtsi; transgenic
		Select seq JN951270.1 **6/1 8/1 10/1** **13/1 17/1 18/1**	Mus musculus targeted non-conditional, lacZ-tagged mutant allele Ins2:tm1e(EUCOMM)Wtsi; transgenic
		Select seq BC145554.1 **6/1 8/1 10/1** **13/1 17/1 18/1**	Mus musculus insulin II, mRNA (cDNA clone MGC:179126 IMAGE:9054118), complete cds
		Select seq BC099934.1 **6/1 8/1 10/1** **13/1 17/1 18/1**	Mus musculus insulin II, mRNA (cDNA clone MGC:107381 IMAGE:6432976), complete cds
		Select seq BC132650.1 **6/1 8/1 10/1** **13/1 17/1 18/1**	Mus musculus insulin II, mRNA (cDNA clone MGC:164281 IMAGE:40130927), complete cds
		Select seq DQ250569.1 **6/1 8/1 10/1** **13/1 17/1 18/1**	Mus caroli preproinsulin 2 (Ins2) gene, complete cds
		Select seq AK007612.1 **6/1 8/1 10/1** **13/1 17/1 18/1**	Mus musculus 10 day old male pancreas cDNA, RIKEN full-length enriched library, clone:1810027C14 product:INSULIN 2 PRECURSOR, full insert sequence
		Select seq AK007482.1 **6/1 8/1 10/1** **13/1 17/1 18/1**	Mus musculus 10 day old male pancreas cDNA, RIKEN full-length enriched library, clone:1810013J24 product:INSULIN 1 PRECURSOR, full insert sequence
		Select seq BC066208.1 **6/1 8/1 10/1** **13/1 17/1 18/1**	Mus musculus insulin II, mRNA (cDNA clone IMAGE:6436276)

Comparison between the alignments of Sequence 1/1 and Sequence of Insulin Chain A according to the “Species of Common Organisms”:

Alignments Sequence 1/1	Description	Alignments Sequence Insulin Chain A	Description
		Select seq AC012382.14 **6/1 8/1 10/1** **13/1 17/1 18/1**	Mus musculus chromosome 7, clone RP23-92L23, complete sequence
		Select seq AY899305.1 **6/1 8/1 10/1** **13/1 17/1 18/1**	Mus musculus proinsulin mRNA, complete cds, alternatively spliced
		Select seq AC013548.13 **6/1 8/1 10/1** **13/1 17/1 18/1**	Mus musculus chromosome 7, clone RP23-209O22, complete sequence
		Select seq AP003182.2 **6/1 8/1 10/1** **13/1 17/1 18/1**	Mus musculus genomic DNA, chromosome 7 clone:B189M11, complete sequences
		Select seq GQ915612.1 **6/1 8/1 10/1** **13/1 17/1 18/1**	Mus musculus insulin-2 precursor (Ins2) mRNA, partial cds, alternatively spliced
		Select seq XM_021204833.1 **6/1 8/1 10/1** **13/1 17/1 18/1**	PREDICTED: Mus pahari insulin-2 (LOC110326410), transcript variant X2, mRNA
		Select seq XM_021204825.1 **6/1 8/1 10/1** **13/1 17/1 18/1**	PREDICTED: Mus pahari insulin-2 (LOC110326410), transcript variant X1, mRNA
23 Select seq XM_004393402.2	PREDICTED: Odobenus rosmarus divergens TNFRSF1A-associated via death domain (TRADD), transcript variant X2, mRNA	Select seq XM_004403802.1	PREDICTED: Odobenus rosmarus divergens insulin (INS), mRNA
24 Select seq XM_012566139.1	PREDICTED: Odobenus rosmarus divergens TNFRSF1A-associated via death domain (TRADD), transcript variant X1, mRNA		

Comparison between the alignments of Sequence 1/1 and Sequence of Insulin Chain A according to the “Species of Common Organisms”:

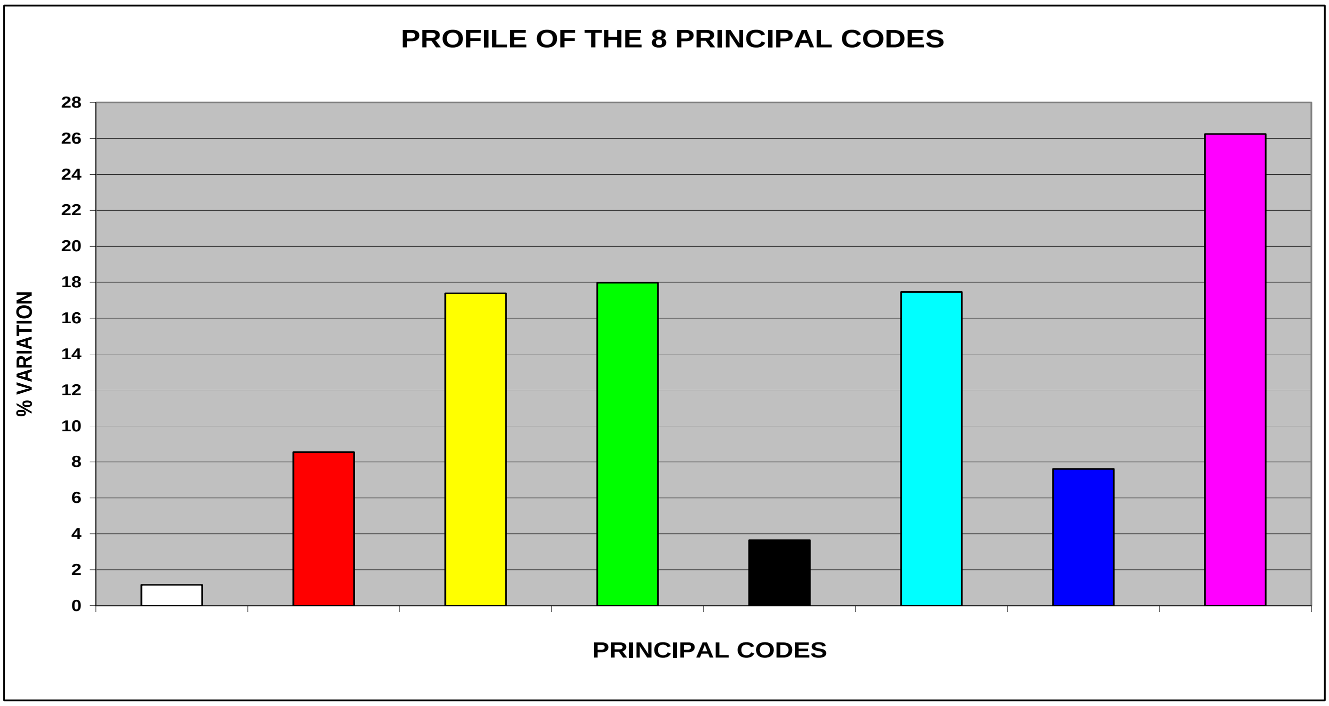
Alignments Sequence 1/1	Description	Alignments Sequence Insulin Chain A	Description
25 Select seq XM_006741502.1	PREDICTED: Leptonychotes weddellii TNFRSF1A-associated via death domain (TRADD), mRNA	Select seq XM_006750095.1	PREDICTED: Leptonychotes weddellii insulin (INS), mRNA
35 Select seq XM_022492727.1	PREDICTED: Enhydra lutris kenyoni trichohyalin-like (LOC111140481), partial mRNA	Select seq XM_022507720.1	PREDICTED: Enhydra lutris kenyoni insulin (LOC111150279), mRNA
37 Select seq XM_006880105.1	PREDICTED: Elephantulus edwardii putative scavenger receptor cysteine-rich domain-containing protein LOC619207-like (LOC102868011), mRNA	Select seq XM_006893212.1	PREDICTED: Elephantulus edwardii insulin (INS), mRNA

Analysis of
Sequence n° 2/1
of Insulin Chain A

1.4 GRAPHIC RESULTS OF THE “NON-OBVIOUS TREND” ANALYSIS OF SEQUENCE n° 2/1 OF INSULIN CHAIN A

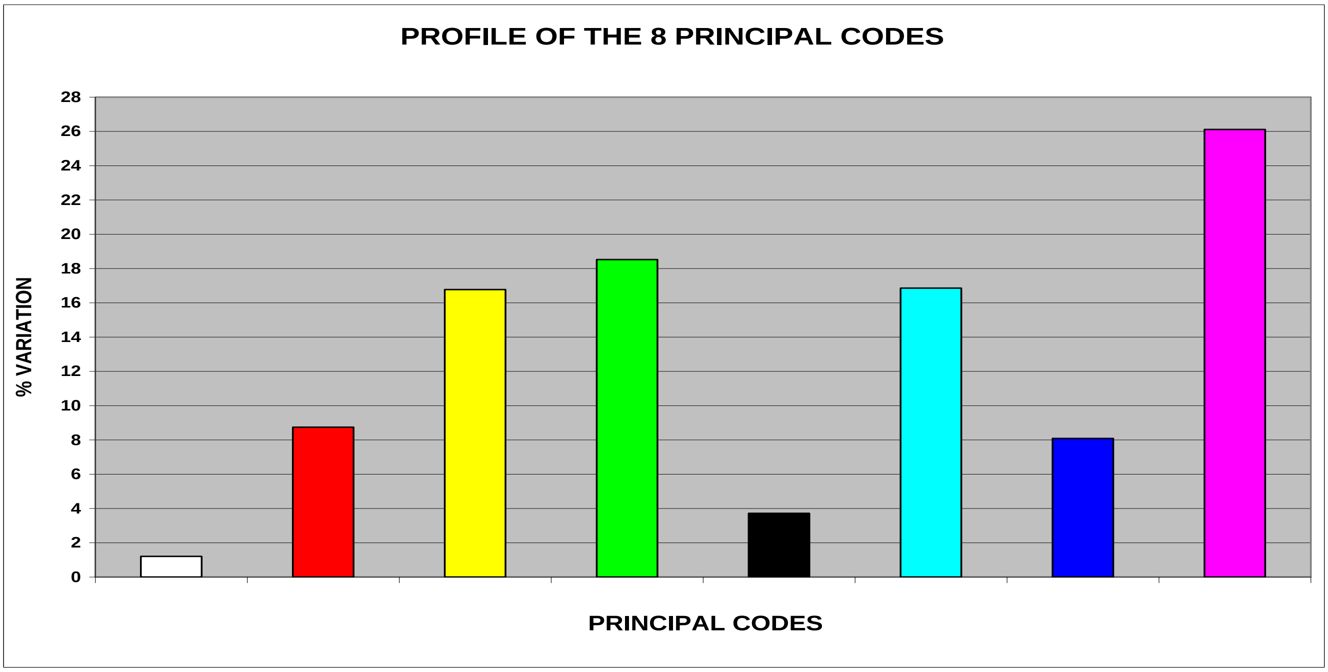
In the Pct. 5 (A e B) two **8 Principal Codes Profiles** are compared.

The chart in Pct. 5 (A) refers to the **original base sequence** of **Insulin Chain A**.



Pct. 5 (A)

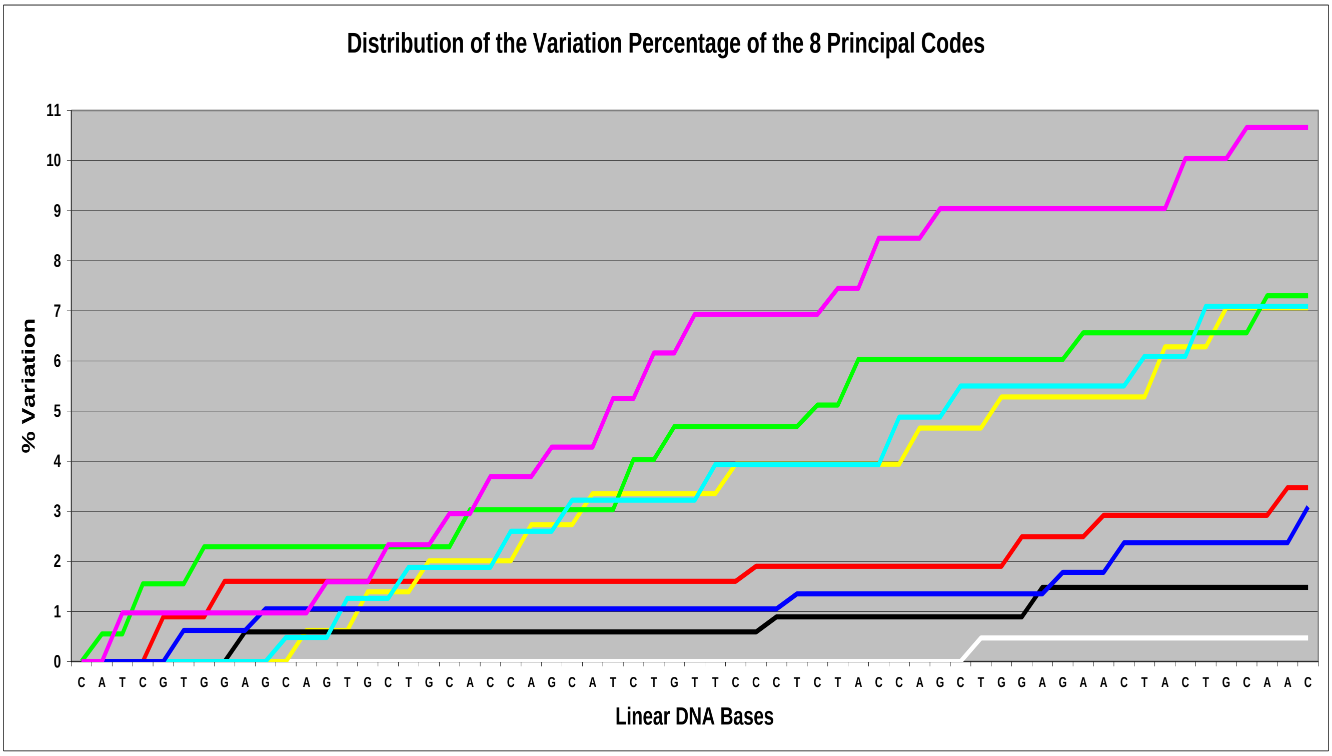
The chart in Pct. 5 (B) refers to the **second** **“new generated sequence”** (**Sequence n° 2/1**) that originates from the original one.



Pct. 5 (B)

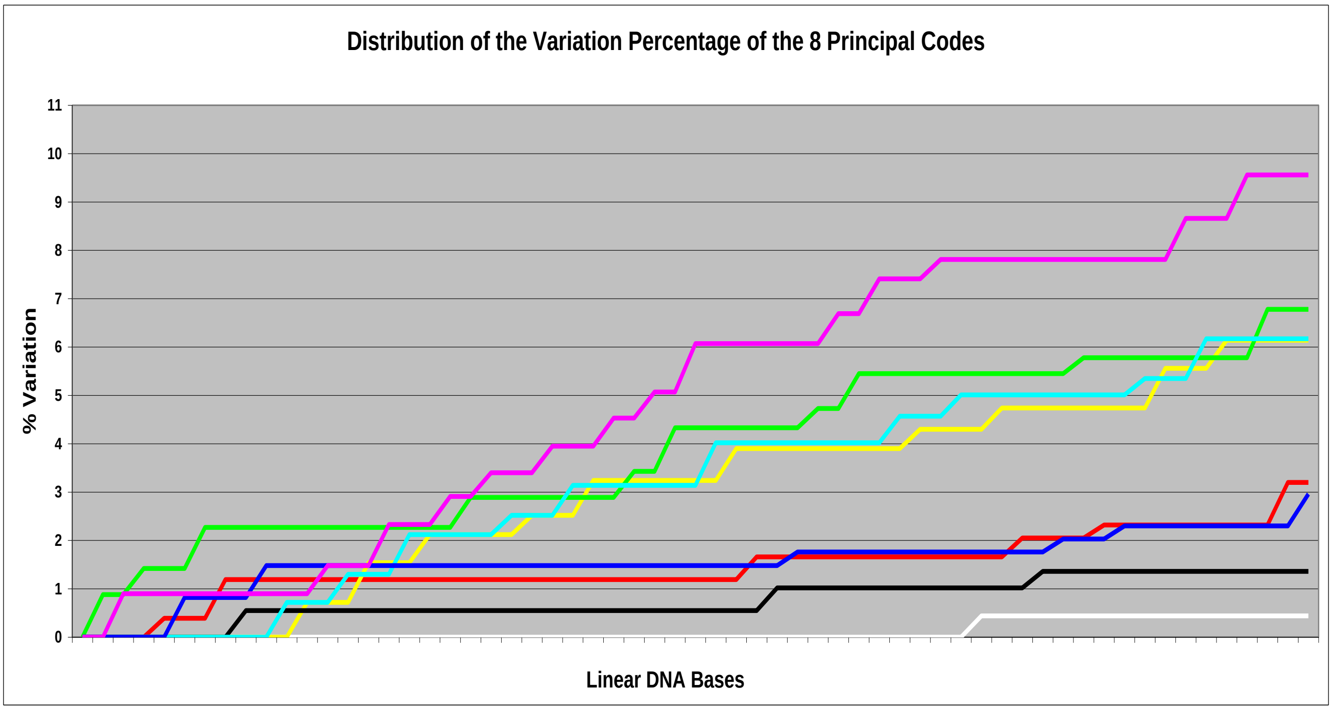
In Pct. 6 (A and B) two charts concerning the **Distribution of the Variation Percentage of the 8 Main Codes** are compared.

The charts in Pct. 6 (A) refers to the **original base sequence** analysed before.



Pct. 6 (A)

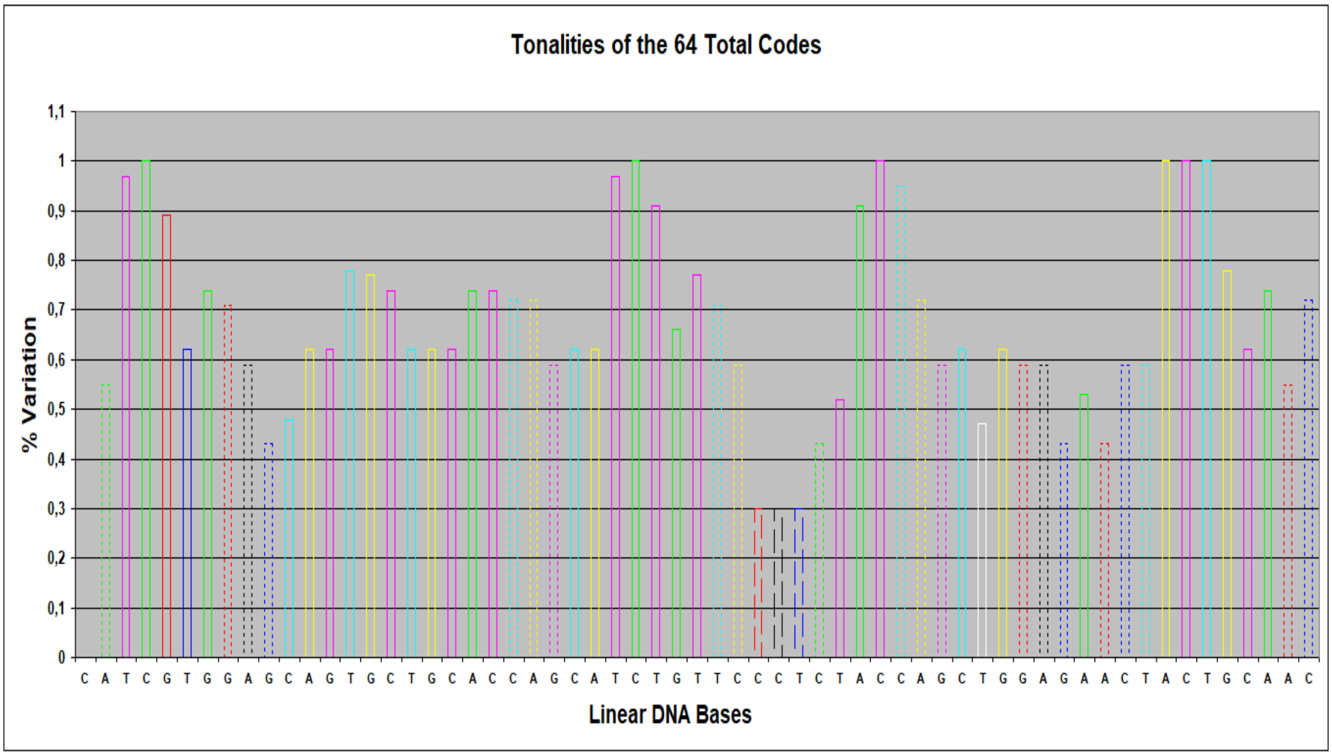
The chart in Pct. 6 (B) refers to the **“new generated sequence”** that originates from the original one.



Pct. 6 (B)

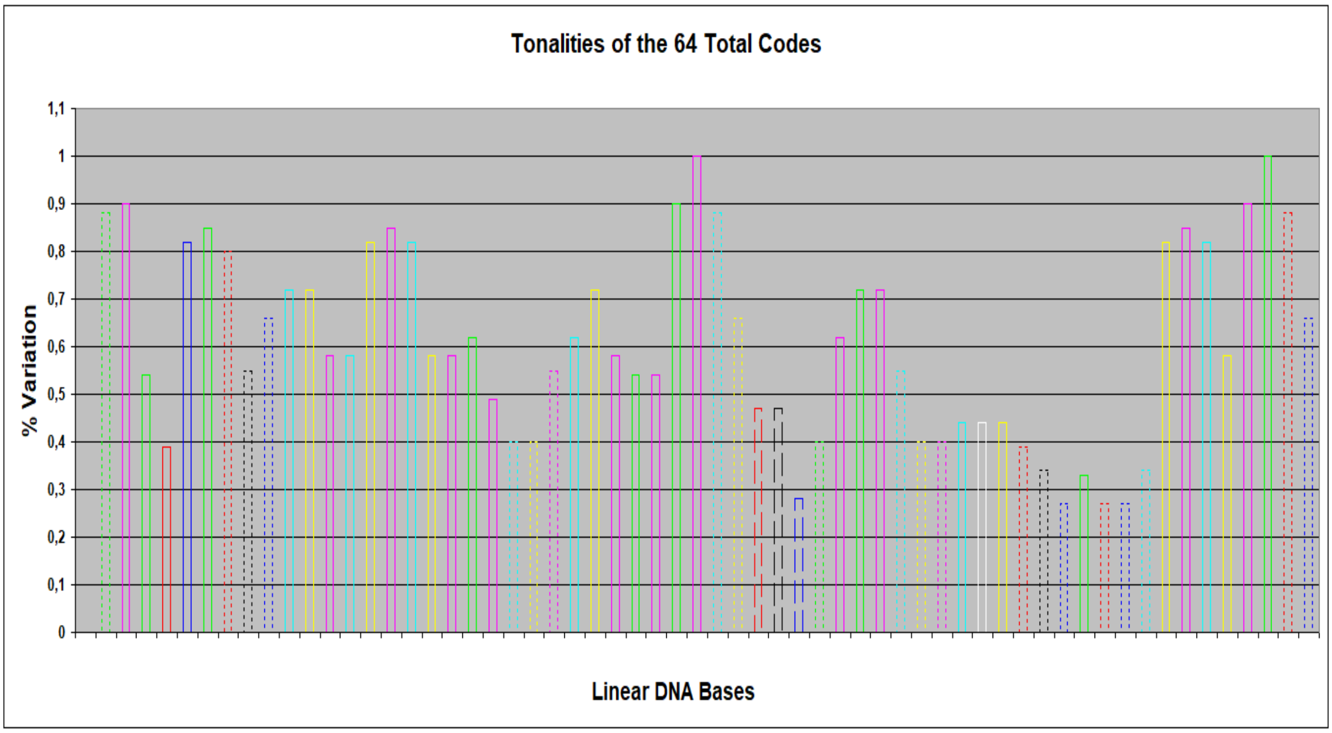
In Pct. 7 (A and B) two charts concerning the single **Tonalities of the 64 Total Codes** are compared.

The chart in Pct. 7 (A) refers to the **original base sequence** analysed before.



Pct. 7 (A)

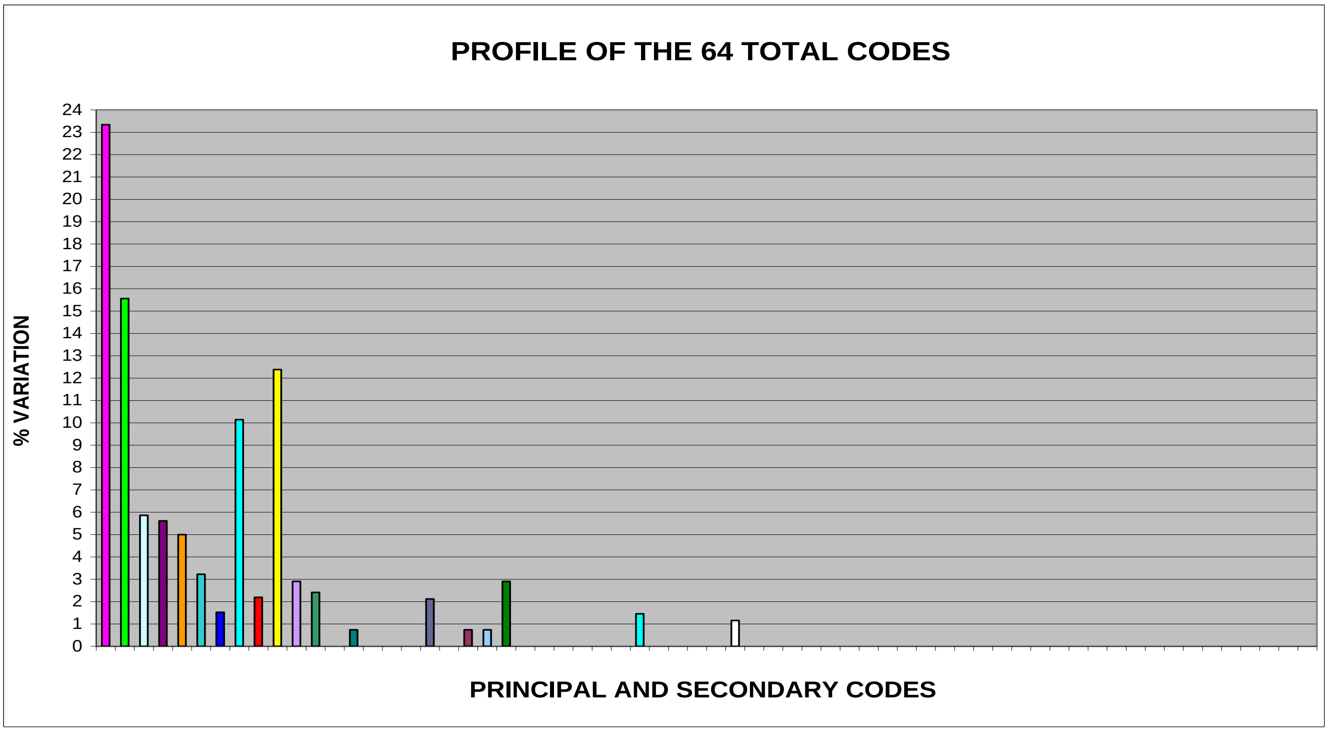
The chart in Pct. 7 (B) refers to the **"new generated sequence"** that originates from the original one.



Pct. 7 (B)

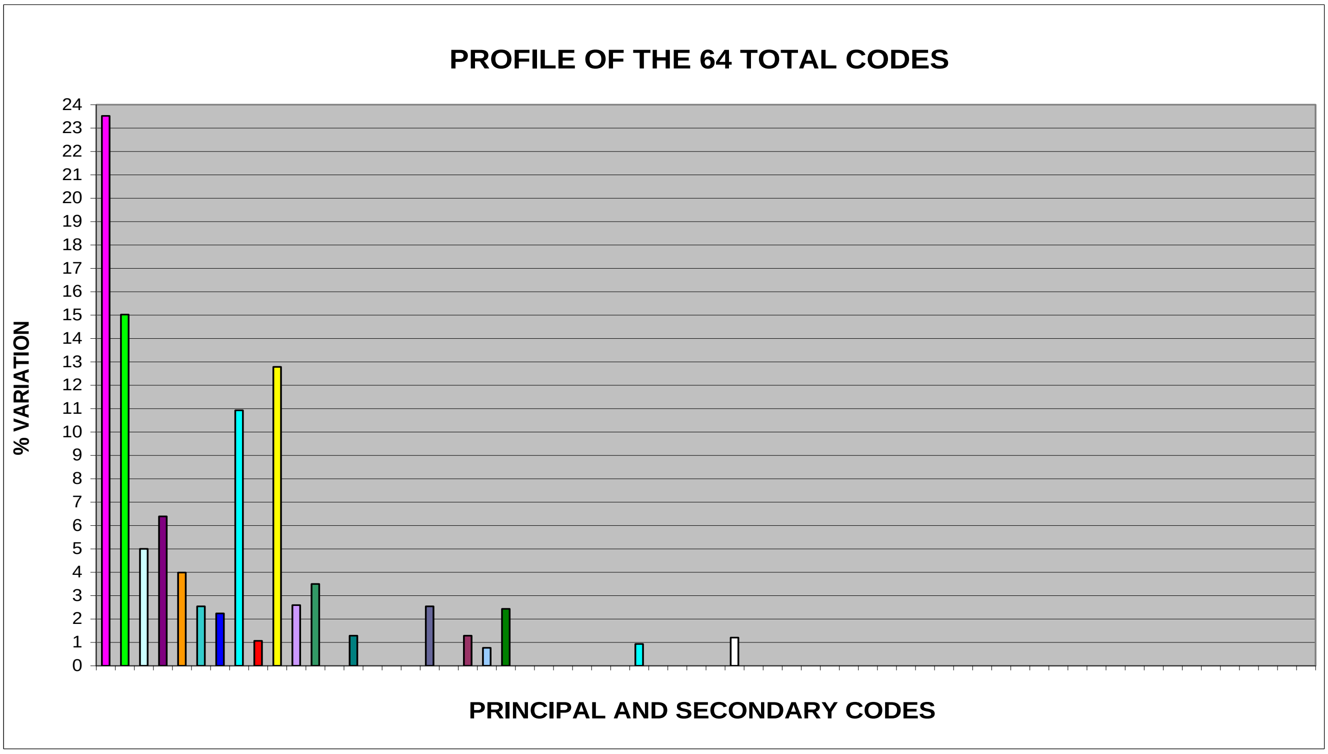
In Pct. 8 (A and B) two charts concerning the **Profile of the 64 Total Codes** are compared.

The chart in Pct. 8 (A) refers to the **original base sequence** analysed before.



Pct. 8 (A)

The chart in Pct. 8 (B) refers to the **“new generated sequence”** originated from the original one.



Pct. 8 (B)

The “non-obvious trend” analysis (obtained through the **T.T.E.S.**) of **Sequence n°2/1 of Insulin Chain A** results in **a comparison among different graphs** that are going to be interpreted in an analogous way to that in which the graphs related to the “non-obvious trend” of **Sequence n° 1/1** were. In order to avoid repetitions, here, the reader is deferred to the interpretation of the **comparisons among the different graphs** presented in the paragraph 1.2 .

Before concluding the paragraph, it is also worth noting that, out of the **63** DNA bases of **Sequence n° 2/1**, ONLY **FOURTEEN BASES** (the **22,22%**)**,** ARE EQUAL (by type and by position in sequence) TO THOSE OF THE ORIGINAL SEQUENCE (**Insulin Chain A**).

1.5 IMPLICATIONS RELATIVE TO THE GRAPHIC RESULTS OF THE "NON-OBVIOUS TREND" ANALYSIS OF SEQUENCE n° 2/1 OF INSULIN CHAIN A

The **63** DNA base sequence of the **new generated sequence** (**Sequence n° 2/1**) that arises from the **original** one has been subjected to **BLAST** research.

Please note:

Information about the ***significant alignments*** produced by *BLAST research*, related to **Sequence n° 2/1,** and all the data acquired from *GenBank (3)* will be published in the **Appendix,** after the *General Conclusions.*

Query = NEW GENERATED SEQUENCE (Sequence n° 2/1)

Length = 63

Parameters of BLAST research:

Programme	*Blastn*
Word size	*11*
Expect value	*10*
Hitlist size	*100*
Match/Mismatch scores	*2,-3*
Gapcosts	*5,2*
Low Complexity Filter	*Yes*
Filter string	*L;m;*
Genetic Code	*1*

Please note:

Here, "**the organisms found to be in common**" between the results of BLAST research carried out on **Insulin Chain A** and results of BLAST research carried out on **Sequence n° 2/1**, were highlighted in **Red**.
As well, "**the organisms found to be in common**" between the results of BLAST research carried out on **Insulin Chain A**, results of BLAST research carried out on **Sequence n° 2/1** and results of BLAST research carried out on **at least one** of the *19 generated sequences*, were highlighted in **Green**.
Moreover, "**the denomination of the sequence**" (1/1, 2/1, ... 19/1) of the "**organism found to be in common**" between the results of BLAST research carried out on **Sequence n° 2/1** and results of BLAST research carried out on **at least one** of the *19 new generated sequences*, were highlighted in **Blue**.
Finally, "**the denomination of the sequence**" (1/1, 2/1, ... 19/1) of the "**organism found to be in common**" between the results of BLAST research carried out on **Insulin Chain A** and results of BLAST research carried out on *19 generated sequences*, were highlighted in **Yellow**.

Sequenza n° 2/1

Sequences producing significant alignments:

Selected seq	Description	Max score	Total score	Query cover	E value	Ident	Accession
1 CP034495.1	Eukaryotic synthetic construct chromosome 17	41.9	41.9	39%	2.7	96%	CP034495.1
2 XR_984267.2	PREDICTED: Macaca nemestrina uncharacterized LOC105476807 (LOC105476807), transcript variant X5, ncRNA	41.9	41.9	39%	2.7	96%	XR_984267.2
3 XR_984264.2	PREDICTED: Macaca nemestrina uncharacterized LOC105476807 (LOC105476807), transcript variant X2, ncRNA	41.9	41.9	39%	2.7	96%	XR_984264.2
4 XR_001440358.1	PREDICTED: Macaca mulatta uncharacterized LOC106993978 (LOC106993978), transcript variant X2, ncRNA	41.9	41.9	39%	2.7	96%	XR_001440358.1
5 XR_001440357.1	PREDICTED: Macaca mulatta uncharacterized LOC106993978 (LOC106993978), transcript variant X1, ncRNA	41.9	41.9	39%	2.7	96%	XR_001440357.1
6 XR_984266.1	PREDICTED: Macaca nemestrina uncharacterized LOC105476807 (LOC105476807), transcript variant X4, ncRNA	41.9	41.9	39%	2.7	96%	XR_984266.1
7 XR_984265.1	PREDICTED: Macaca nemestrina uncharacterized LOC105476807 (LOC105476807), transcript variant X3, ncRNA	41.9	41.9	39%	2.7	96%	XR_984265.1
8 XR_984263.1	PREDICTED: Macaca nemestrina uncharacterized LOC105476807 (LOC105476807), transcript variant X1, ncRNA	41.9	41.9	39%	2.7	96%	XR_984263.1
9 AC015813.12	Homo sapiens, clone RP11-159D12, complete sequence	41.9	41.9	39%	2.7	96%	AC015813.12
10 AC004757.2	Homo sapiens chromosome 17, clone CTB-117K16, complete sequence	41.9	41.9	39%	2.7	96%	AC004757.2
11 AC005962.1	Homo sapiens chromosome 17, clone hRPK.506_H_21, complete sequence	41.9	41.9	39%	2.7	96%	AC005962.1

Comparison between the alignments of Sequence 2/1 and Sequence of Insulin Chain A according to the “Species of Common Organisms”:

Alignments Sequence 2/1	**Description**	**Alignments Sequence Insulin Chain A**	**Description**
1 Select seq CP034495.1	Eukaryotic synthetic construct chromosome 17	Select seq CP034516.1 **17/1**	Eukaryotic synthetic construct chromosome 13
		Select seq CP034491.1 **17/1**	Eukaryotic synthetic construct chromosome 13
2 Select seq XR_984267.2	PREDICTED: Macaca nemestrina uncharacterized LOC105476807 (LOC105476807), transcript variant X5, ncRNA	Select seq XM_015434180.1 **3/1 8/1 17/1**	PREDICTED: Macaca fascicularis insulin (INS), transcript variant X1, mRNA
3 Select seq XR_984264.2	PREDICTED: Macaca nemestrina uncharacterized LOC105476807 (LOC105476807), transcript variant X2, ncRNA	Select seq XM_015113354.1 **3/1 8/1 17/1**	PREDICTED: Macaca mulatta insulin (INS), mRNA
4 Select seq XR_001440358.1	PREDICTED: Macaca mulatta uncharacterized LOC106993978 (LOC106993978), transcript variant X2, ncRNA	Select seq XM_011721319.1 **3/1 8/1 17/1**	PREDICTED: Macaca nemestrina insulin (INS), transcript variant X4, mRNA
5 Select seq XR_001440357.1	PREDICTED: Macaca mulatta uncharacterized LOC106993978 (LOC106993978), transcript variant X1, ncRNA	Select seq XM_011721318.1 **3/1 8/1 17/1**	PREDICTED: Macaca nemestrina insulin (INS), transcript variant X3, mRNA
6 Select seq XR_984266.1	PREDICTED: Macaca nemestrina uncharacterized LOC105476807 (LOC105476807), transcript variant X4, ncRNA	Select seq XM_011721317.1 **3/1 8/1 17/1**	PREDICTED: Macaca nemestrina insulin (INS), transcript variant X2, mRNA
7 Select seq XR_984265.1	PREDICTED: Macaca nemestrina uncharacterized LOC105476807 (LOC105476807), transcript variant X3, ncRNA	Select seq XM_011721316.1 **3/1 8/1 17/1**	PREDICTED: Macaca nemestrina insulin (INS), transcript variant X1, mRNA

Comparison between the alignments of Sequence 2/1 and Sequence of Insulin Chain A according to the "Species of Common Organisms":

Alignments Sequence 2/1	**Description**	**Alignments Sequence Insulin Chain A**	**Description**
8 Select seq XR_984263.1	PREDICTED: Macaca nemestrina uncharacterized LOC105476807 (LOC105476807), transcript variant X1, ncRNA	Select seq NM_001284919.1 **3/1 8/1 17/1**	Macaca fascicularis insulin (INS), mRNA
9 Select seq AC015813.12	Homo sapiens, clone RP11-159D12, complete sequence	Select seq AH002844.2 **8/1 9/1 10/1 15/1 17/1**	Homo sapiens insulin (INS) gene, complete cds
10 Select seq AC004757.2	Homo sapiens chromosome 17, clone CTB-117K16, complete sequence	Select seq AH012037.2 **8/1 9/1 10/1 15/1 17/1**	Homo sapiens haplotype ICa tyrosine hydroxylase (TH) gene, partial sequence; insulin (INS) gene, complete cds; and insulin-like growth factor 2 (IGF2) gene, partial sequence
11 Select seq AC005962.1	Homo sapiens chromosome 17, clone hRPK.506_H_21, complete sequence	Select seq NG_050578.1 **8/1 9/1 10/1 15/1 17/1**	Homo sapiens INS-IGF2 readthrough (INS-IGF2), RefSeqGene on chromosome 11
		Select seq KR710184.1 **8/1 9/1 10/1 15/1 17/1**	Synthetic construct Homo sapiens clone CCSBHm_00010257 INS (INS) mRNA, encodes complete protein
		Select seq KR710183.1 **8/1 9/1 10/1 15/1 17/1**	Synthetic construct Homo sapiens clone CCSBHm_00010256 INS (INS) mRNA, encodes complete protein
		Select seq KR710182.1 **8/1 9/1 10/1 15/1 17/1**	Synthetic construct Homo sapiens clone CCSBHm_00010255 INS (INS) mRNA, encodes complete protein
		Select seq KJ891480.1 **8/1 9/1 10/1 15/1 17/1**	Synthetic construct Homo sapiens clone ccsbBroadEn_00874 INS gene, encodes complete protein
		Select seq NM_001291897.1 **8/1 9/1 10/1 15/1 17/1**	Homo sapiens insulin (INS), transcript variant 4, mRNA

Comparison between the alignments of Sequence 2/1 and Sequence of Insulin Chain A according to the “Species of Common Organisms”:

Alignments Sequence 2/1	**Description**	**Alignments Sequence Insulin Chain A**	**Description**
		Select seq JQ951950.1 **8/1 9/1 10/1 15/1 17/1**	Homo sapiens preproinsulin (INS) mRNA, complete cds
		Select seq JF909299.1 **8/1 9/1 10/1 15/1 17/1**	Homo sapiens insulin (INS) mRNA, partial cds
		Select seq AB587580.1 **8/1 9/1 10/1 15/1 17/1**	Synthetic construct DNA, clone: pF1KB8864, Homo sapiens INS gene for insulin, without stop codon, in Flexi system
		Select seq NM_001185098.1 **8/1 9/1 10/1 15/1 17/1**	Homo sapiens insulin (INS), transcript variant 3, mRNA
		Select seq NM_001185097.1 **8/1 9/1 10/1 15/1 17/1**	Homo sapiens insulin (INS), transcript variant 2, mRNA
		Select seq NG_007114.1 **8/1 9/1 10/1 15/1 17/1**	Homo sapiens insulin (INS), RefSeqGene on chromosome 11
		Select seq DQ778082.1 **8/1 9/1 10/1 15/1 17/1**	Homo sapiens clone BFC06103 insulin mRNA, complete cds
		Select seq DQ896283.2 **8/1 9/1 10/1 15/1 17/1**	Synthetic construct Homo sapiens clone IMAGE:100010743; FLH192918.01L; RZPDo839A1068D insulin (INS) gene, encodes complete protein
		Select seq NM_000207.2 **8/1 9/1 10/1 15/1 17/1**	Homo sapiens insulin (INS), transcript variant 1, mRNA
		Select seq BT007778.1 **8/1 9/1 10/1 15/1 17/1**	Synthetic construct Homo sapiens insulin mRNA, partial cds

Comparison between the alignments of Sequence 2/1 and Sequence of Insulin Chain A according to the "Species of Common Organisms":

Alignments Sequence 2/1	**Description**	**Alignments Sequence Insulin Chain A**	**Description**
		Select seq BT006808.1 **8/1 9/1 10/1 15/1 17/1**	Homo sapiens insulin mRNA, complete cds
		Select seq BC005255.1 **8/1 9/1 10/1 15/1 17/1**	Homo sapiens insulin, mRNA (cDNA clone MGC:12292 IMAGE:3950204), complete cds
		Select seq AC132217.15 **8/1 9/1 10/1 15/1 17/1**	Homo sapiens chromosome 11, clone RP11-889I17, complete sequence
		Select seq AC130303.8 **8/1 9/1 10/1 15/1 17/1**	Homo sapiens chromosome 11, clone RP4-539G11, complete sequence
		Select seq AY899304.1 **8/1 9/1 10/1 15/1 17/1**	Homo sapiens proinsulin mRNA, complete cds, alternatively spliced
		Select seq AJ009655.1 **8/1 9/1 10/1 15/1 17/1**	Homo sapiens ins gene, partial
		Select seq X70508.1 **8/1 9/1 10/1 15/1 17/1**	Homo sapiens mRNA for insulinoma pre-proinsulin
		Select seq L15440.1 **8/1 9/1 10/1 15/1 17/1**	Homo sapiens tyrosine hydroxylase (TH) gene, 3' end; insulin (INS) gene, complete cds; insulin-like growth factor 2 (IGF2) gene, 5' end
		Select seq KR710185.1 **8/1 9/1 10/1 15/1 17/1**	Synthetic construct Homo sapiens clone CCSBHm_00010262 INS (INS) mRNA, encodes complete protein
		Select seq AF050524.1 **8/1 9/1 10/1 15/1 17/1**	Synthetic Homo sapiens proinsulin-like protein BKRA gene, complete cds

Comparison between the alignments of Sequence 2/1 and Sequence of Insulin Chain A according to the "Species of Common Organisms":

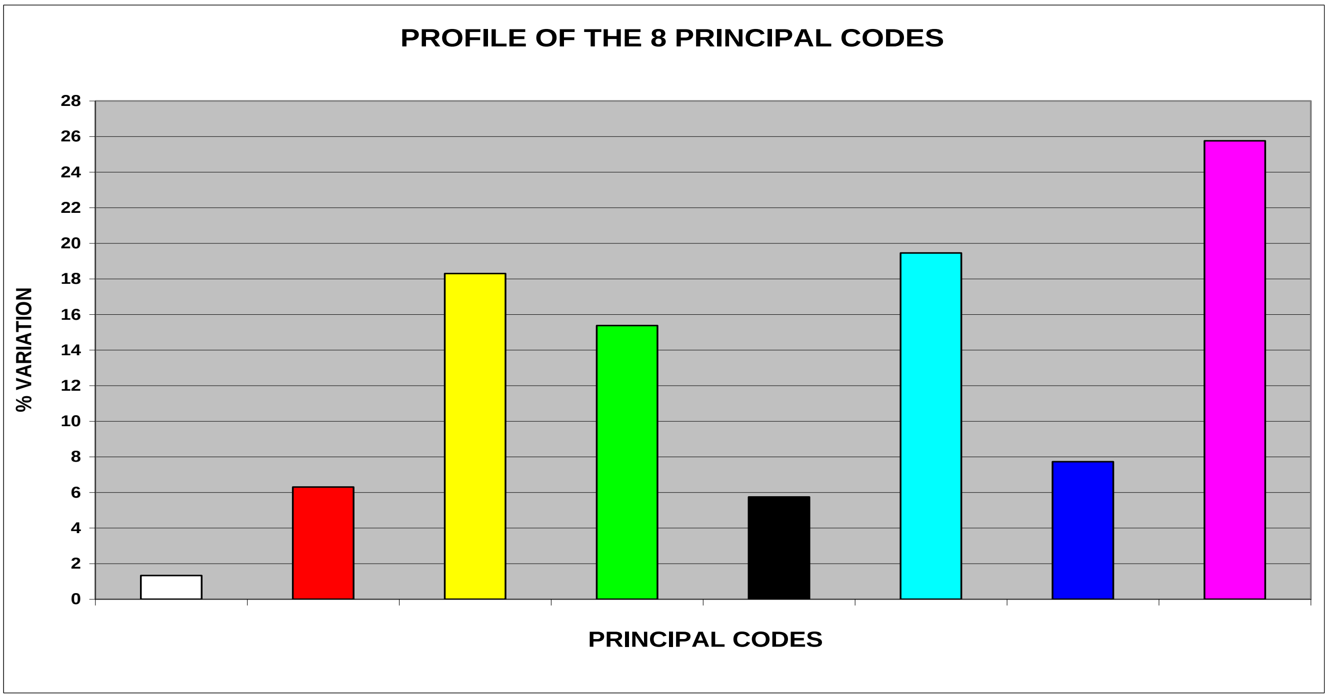
Alignments Sequence 2/1	**Description**	**Alignments Sequence Insulin Chain A**	**Description**
		Select seq AC021233.9 **8/1 9/1 10/1 15/1 17/1**	Homo sapiens chromosome 11, clone RP11-215H22, complete sequence
		Select seq AK024581.1 **8/1 9/1 10/1 15/1 17/1**	Homo sapiens cDNA: FLJ20928 fis, clone ADSE01074

Analysis of Sequence n° 3/1 of Insulin Chain A

1.6 GRAPHIC RESULTS OF THE “NON-OBVIOUS TREND” ANALYSIS OF SEQUENCE n° 3/1 OF INSULIN CHAIN A

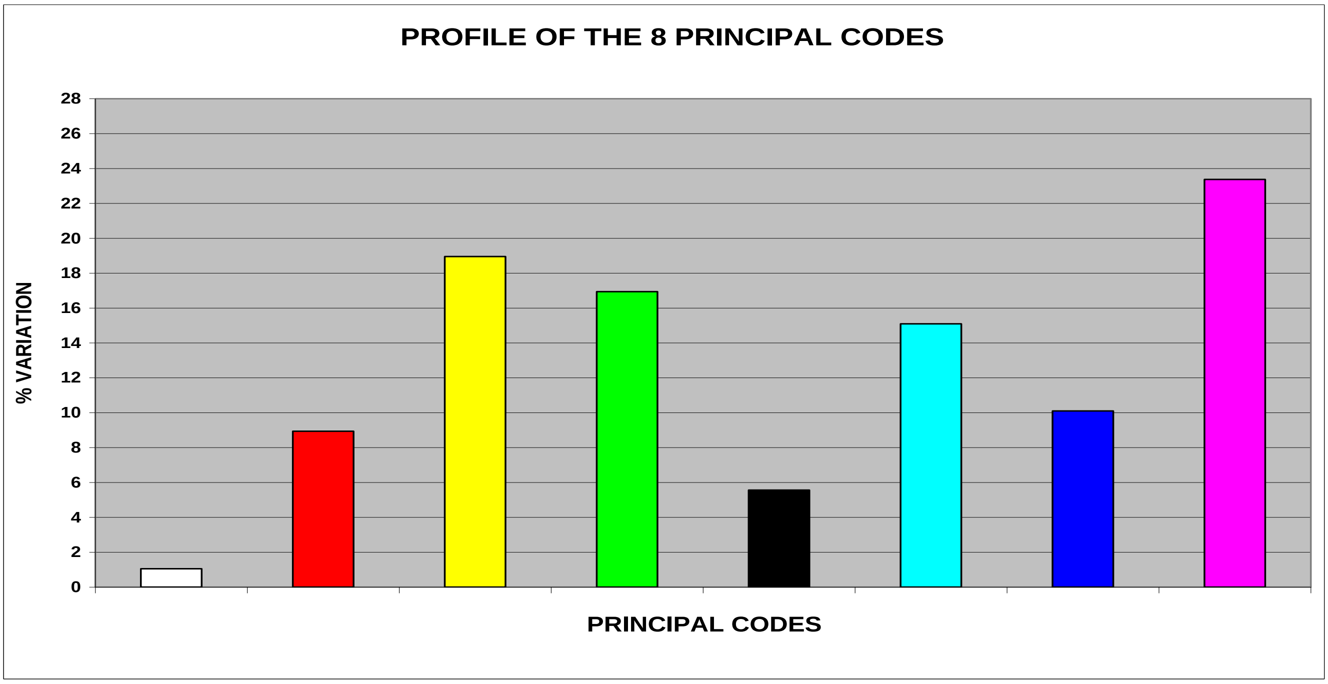
In the Pct. 9 (A e B) two **8 Principal Codes Profiles** are compared.

The chart in Pct. 9 (A) refers to the **original base sequence** of **Insulin Chain A**.



Pct. 9 (A)

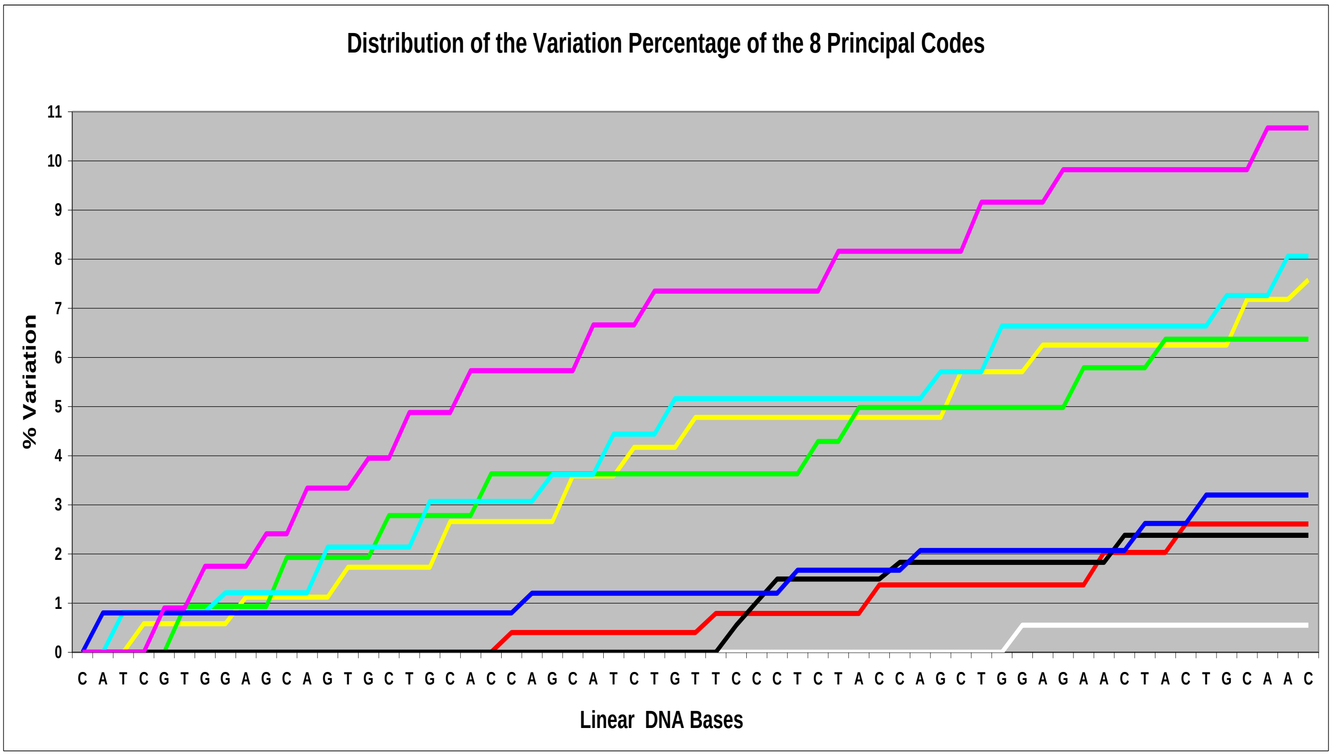
The chart in Pct. 9 (B) refers to the **third “new generated sequence”** (**Sequence n° 3/1**) that originates from the original one.



Pct. 9 (B)

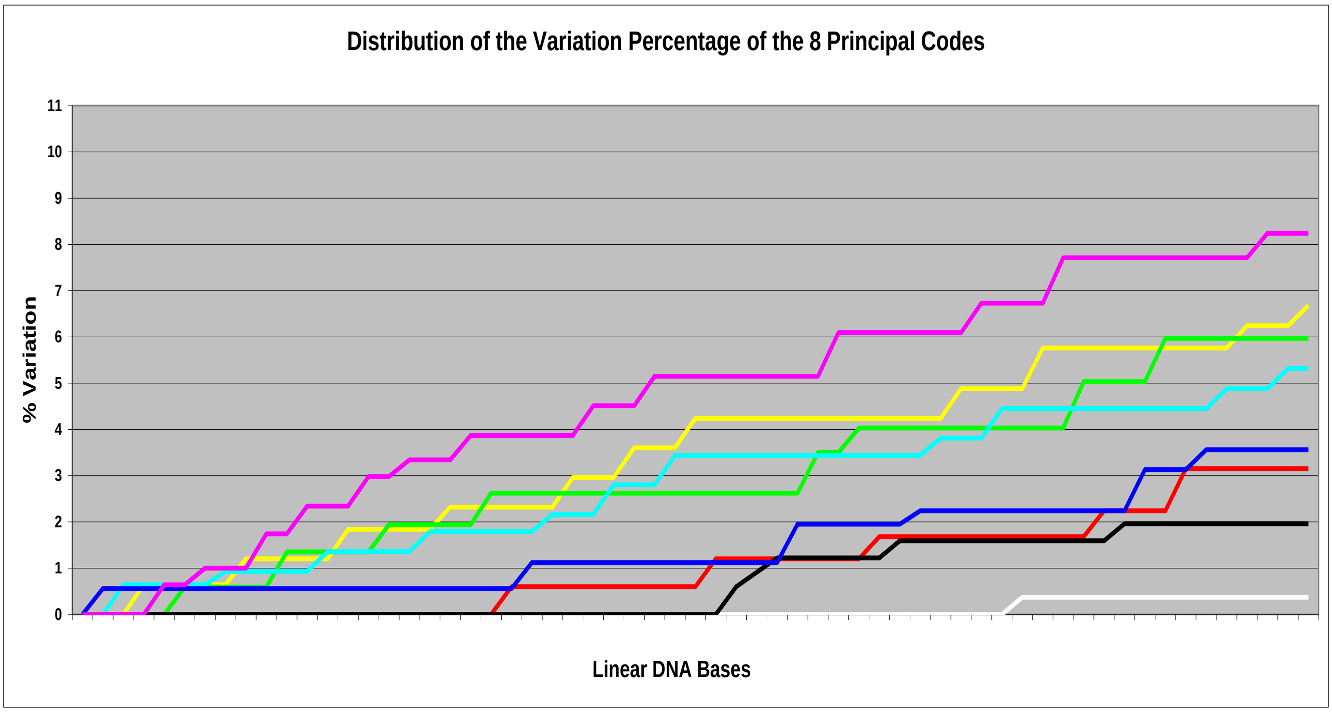
In Pct. 10 (A and B) two charts concerning the **Distribution of the Variation Percentage of the 8 Main Codes** are compared.

The charts in Pct. 10 (A) refers to the **original base sequence** analysed before.



Pct. 10 (A)

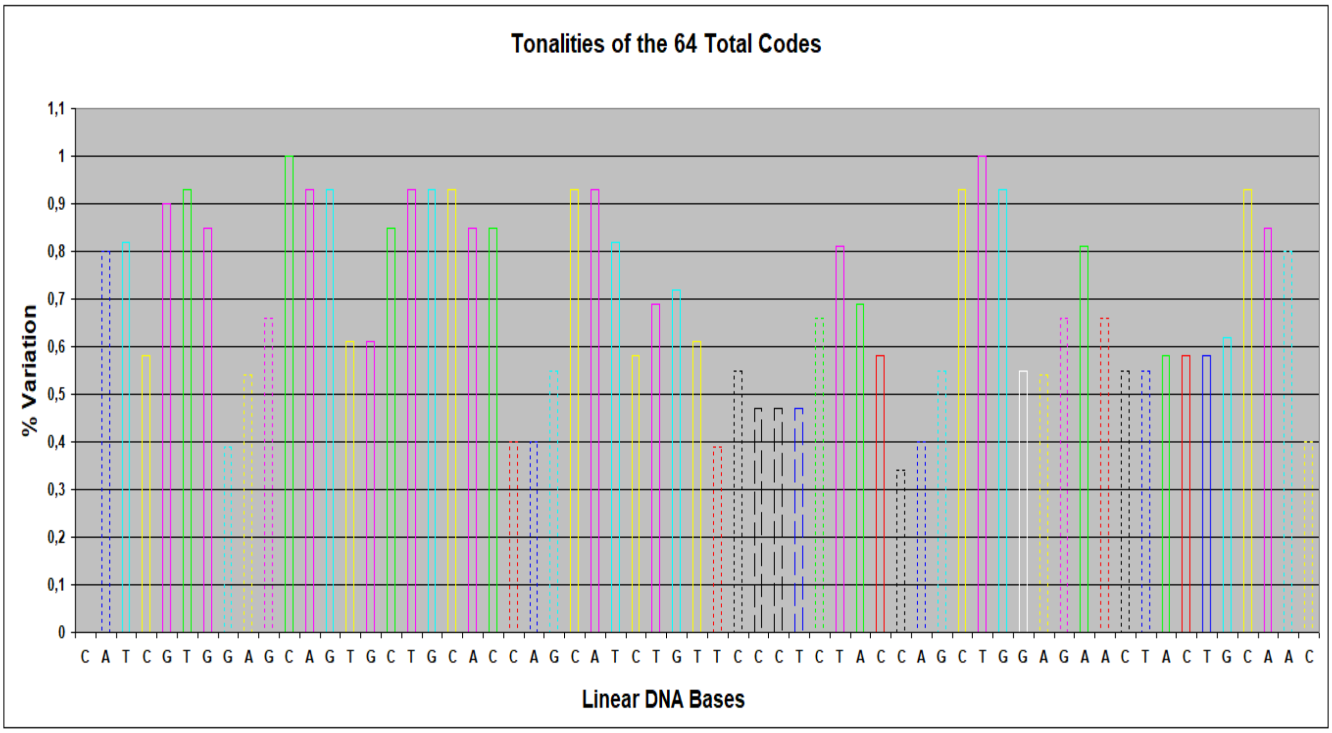
The chart in Pct. 10 (B) refers to the **"new generated sequence"** that originates from the original one.



Pct. 10 (B)

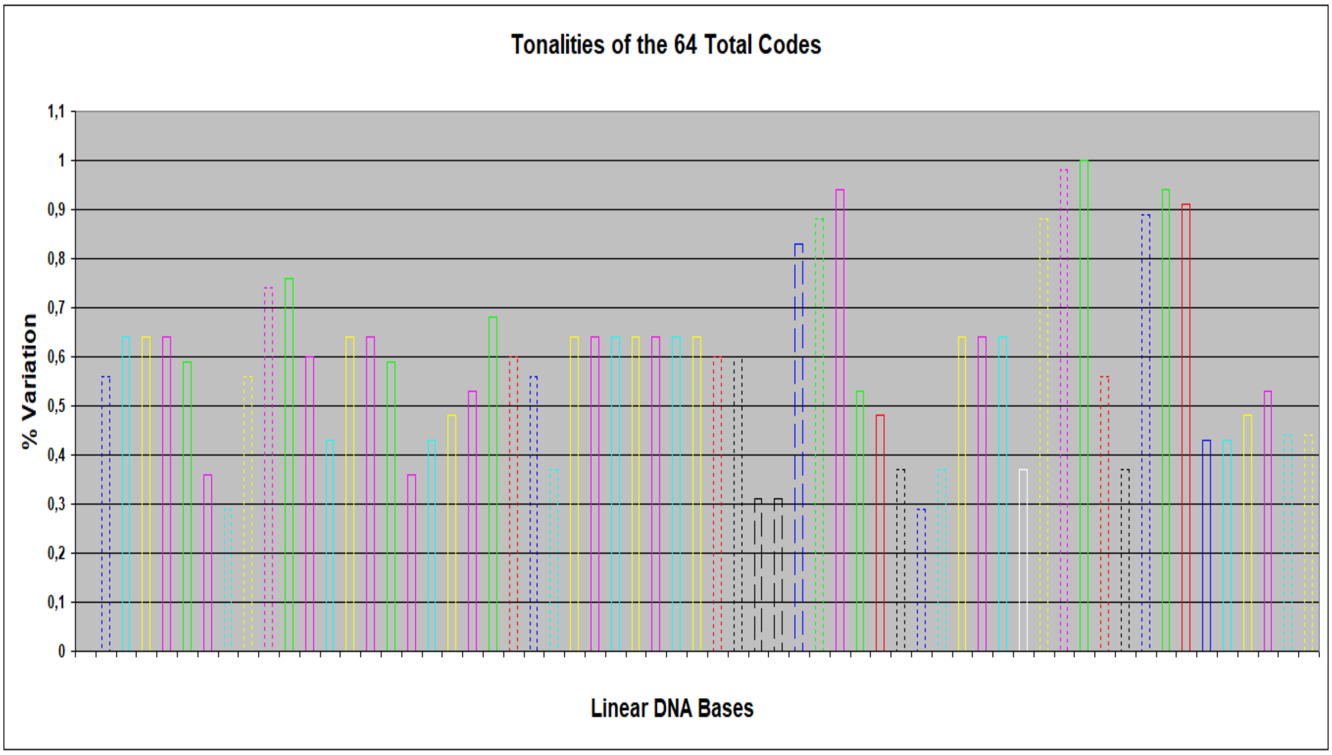
In Pct. 11 (A and B) two charts concerning the single **Tonalities of the 64 Total Codes** are compared.

The chart in Pct. 11 (A) refers to the **original base sequence** analysed before.



Pct. 11 (A)

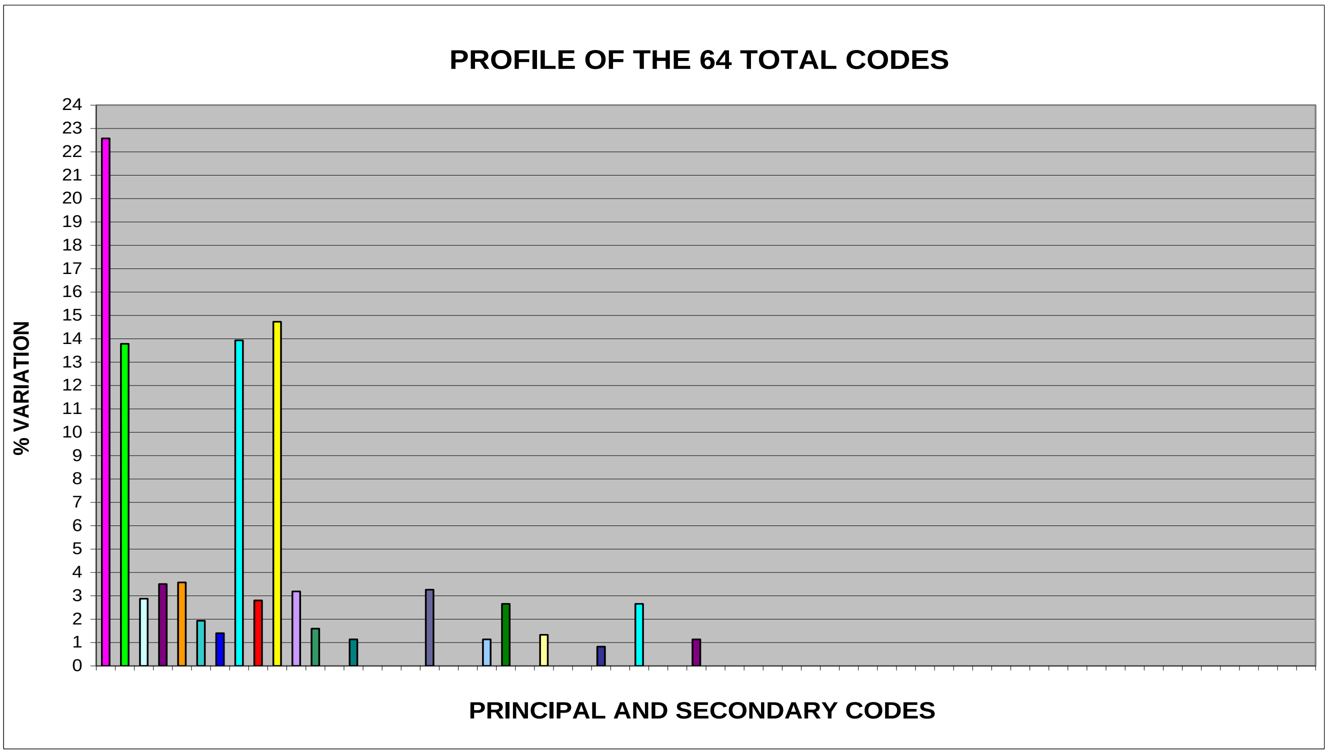
The chart in Pct. 11 (B) refers to the **"new generated sequence"** that originates from the original one.



Pct. 11 (B)

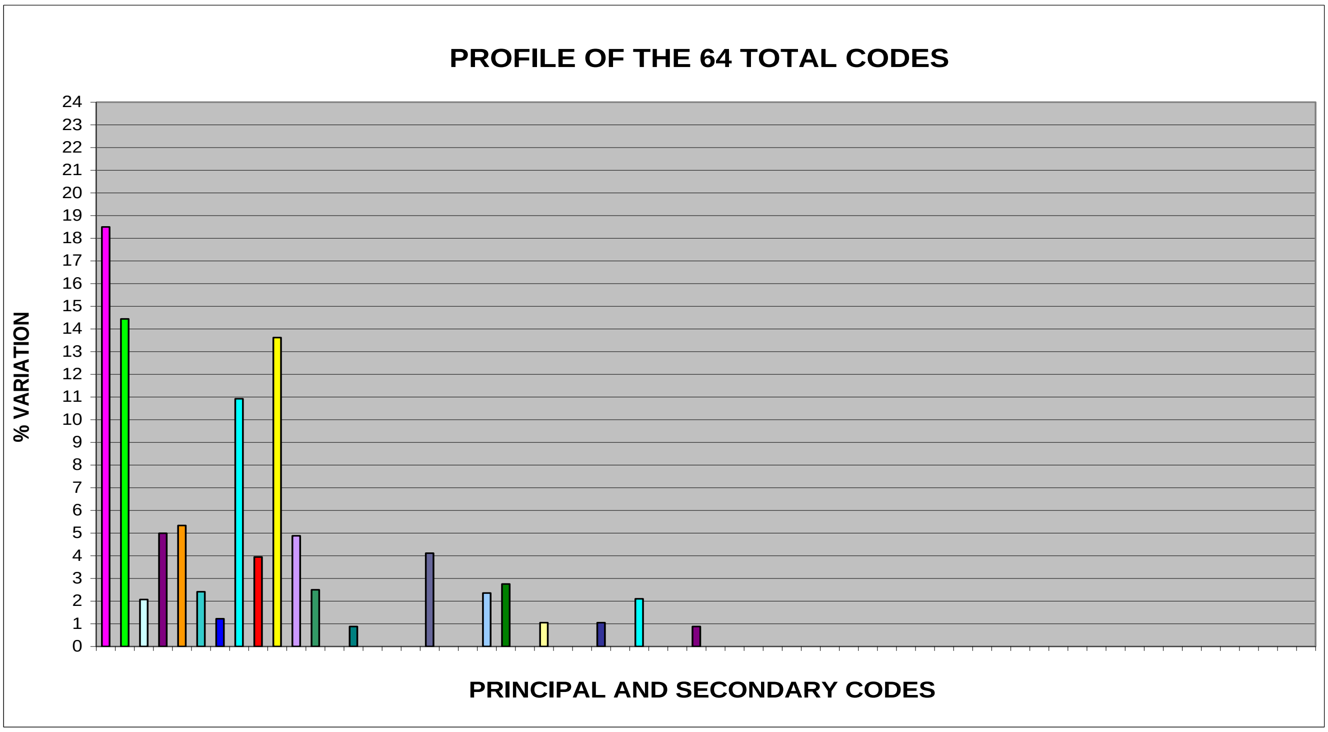
In Pct. 12 (A and B) two charts concerning the **Profile of the 64 Total Codes** are compared.

The chart in Pct. 12 (A) refers to the **original base sequence** analysed before.



Pct. 12 (A)

The chart in Pct. 12 (B) refers to the **“new generated sequence”** originated from the original one.



Pct. 12 (B)

The “non-obvious trend” analysis (obtained through the **T.T.E.S.**) of **Sequence n°3/1 of Insulin Chain A** results in **a comparison among different graphs** that are going to be interpreted in an analogous way to that in which the graphs related to the “non-obvious trend” of **Sequences n° 1/1 and n° 2/1** were. In order to avoid repetitions, here, the reader is deferred to the interpretation of the **comparisons among the different graphs** presented in the paragraph 1.2 .

Before concluding the paragraph, it is worth noting that, out of the **63** DNA bases of **Sequence n° 3/1**, ONLY **SIXTEEN BASES** (the **25,40%**)**,** ARE EQUAL (by type and by position in sequence) TO THOSE OF THE ORIGINAL SEQUENCE (**Insulin Chain A**).

1. 7 IMPLICATIONS RELATIVE TO THE GRAPHIC RESULTS OF THE “NON-OBVIOUS TREND” ANALYSIS OF SEQUENCE n° 3/1 OF INSULIN CHAIN A

The **63** DNA base sequence of the **new generated sequence** (**Sequence n° 3/1**) that arises from the **original** one has been subjected to **BLAST** research.

Please note:

Information about the ***significant alignments*** produced by *BLAST research*, related to **Sequence n° 3/1,** and all the data acquired from *GenBank (3)* will be published in the **Appendix,** after the *General Conclusions.*

Query = NEW GENERATED SEQUENCE (Sequence n° 3/1)

Length = 63

Parameters of BLAST research:

Programme	*Blastn*
Word size	*11*
Expect value	*10*
Hitlist size	*100*
Match/Mismatch scores	*2,-3*
Gapcosts	*5,2*
Low Complexity Filter	*Yes*
Filter string	*L;m;*
Genetic Code	*1*

Please note:

Here, “**the organisms found to be in common**” between the results of BLAST research carried out on **Insulin Chain A** and results of BLAST research carried out on **Sequence n° 3/1**, were highlighted in **Red**.
As well, “**the organisms found to be in common**” between the results of BLAST research carried out on **Insulin Chain A**, results of BLAST research carried out on **Sequence n° 3/1** and results of BLAST research carried out on **at least one** of the *19 generated sequences*, were highlighted in **Green**.
Moreover, “**the denomination of the sequence**” (1/1, 2/1, ... 19/1) of the “**organism found to be in common**” between the results of BLAST research carried out on **Sequence n° 3/1** and results of BLAST research carried out on **at least one** of the *19 new generated sequences*, were highlighted in **Blue**.
Finally, “**the denomination of the sequence**” (1/1, 2/1, ... 19/1) of the “**organism found to be in common**” between the results of BLAST research carried out on **Insulin Chain A** and results of BLAST research carried out on *19 generated sequences*, were highlighted in **Yellow**.

Sequenza n° 3/1

Sequences producing significant alignments:

Selected seq	Description	Max score	Total score	Query cover	E value	Ident	Accession
1 **8/1** LR217737.1	Candidatus Erwinia sp. (ex Cinara spp.) strain ErCipiceae genome assembly, chromosome: 1	44.6	44.6	53%	0.22	88%	LR217737.1
2 AC202851.10	Macaca mulatta BAC CH250-309J8 (Children's Hospital Oakland Research Institute Rhesus macaque Adult Male BAC Library) complete sequence	40.1	80.1	46%	9.5	90%	AC202851.10
3 AC202847.6	Rhesus Macaque BAC CH250-335I24 () complete sequence	40.1	40.1	46%	9.5	90%	AC202847.6
4 **18/1** LR214930.1	Schistosoma mansoni strain Puerto Rico genome assembly, chromosome: 2	39.2	39.2	41%	9.5	92%	LR214930.1
5 XM_027519481.1	PREDICTED: Bos indicus x Bos taurus phospholipid scramblase 3 (PLSCR3), transcript variant X3, mRNA	39.2	39.2	33%	9.5	100%	XM_027519481.1
6 XM_027519480.1	PREDICTED: Bos indicus x Bos taurus phospholipid scramblase 3 (PLSCR3), transcript variant X2, mRNA	39.2	39.2	33%	9.5	100%	XM_027519480.1
7 XM_027519479.1	PREDICTED: Bos indicus x Bos taurus phospholipid scramblase 3 (PLSCR3), transcript variant X1, mRNA	39.2	39.2	33%	9.5	100%	XM_027519479.1
8 **4/1** CP027087.1	Bos mutus isolate yakQH1 chromosome 19	39.2	39.2	33%	9.5	100%	CP027087.1
9 XM_019982110.1	PREDICTED: Bos indicus phospholipid scramblase 3 (PLSCR3), transcript variant X3, mRNA	39.2	39.2	33%	9.5	100%	XM_019982110.1
10 XM_019982108.1	PREDICTED: Bos indicus phospholipid scramblase 3 (PLSCR3), transcript variant X2, mRNA	39.2	39.2	33%	9.5	100%	XM_019982108.1
11 XM_019982107.1	PREDICTED: Bos indicus phospholipid scramblase 3 (PLSCR3), transcript variant X1, mRNA	39.2	39.2	33%	9.5	100%	XM_019982107.1
12 XM_014476435.1	PREDICTED: Bos mutus phospholipid scramblase 3 (PLSCR3), transcript variant X2, mRNA	39.2	39.2	33%	9.5	100%	XM_014476435.1

Sequences producing significant alignments:

Selected seq	Description	Max score	Total score	Query cover	E value	Ident	Accession
13 XM_005889943.2	PREDICTED: Bos mutus phospholipid scramblase 3 (PLSCR3), transcript variant X1, mRNA	39.2	39.2	33%	9.5	100%	XM_005889943.2
14 XM_010847326.1	PREDICTED: Bison bison bison phospholipid scramblase 3 (PLSCR3), transcript variant X2, mRNA	39.2	39.2	33%	9.5	100%	XM_010847326.1
15 GU799624.1	Ictalurus punctatus clone BAC1B immunoglobulin delta heavy chain gene locus, partial sequence	39.2	39.2	49%	9.5	87%	GU799624.1
16 NM_001046053.2	Bos taurus phospholipid scramblase 3 (PLSCR3), mRNA	39.2	39.2	33%	9.5	100%	NM_001046053.2
17 BC114676.1	Bos taurus phospholipid scramblase 3, mRNA (cDNA clone MGC:138060 IMAGE:8087126), complete cds	39.2	39.2	33%	9.5	100%	BC114676.1
18 AF363449.1	Ictalurus punctatus clone IgD6 IgM pseudogene, partial sequence; transposon Tc1, complete sequence; and IgD heavy chain gene, partial sequence	39.2	39.2	49%	9.5	87%	AF363449.1

Comparison between the alignments of Sequence 3/1 and Sequence of Insulin Chain A according to the “Species of Common Organisms”:

Alignments Sequence 3/1	**Description**	**Alignments Sequence Insulin Chain A**	**Description**
2 Select seq AC202851.10	Macaca mulatta BAC CH250-309J8 (Children's Hospital Oakland Research Institute Rhesus macaque Adult Male BAC Library) complete sequence	Select seq XM_015434180.1 **2/1** **8/1** **17/1**	PREDICTED: Macaca fascicularis insulin (INS), transcript variant X1, mRNA
		Select seq XM_015113354.1 **2/1** **8/1** **17/1**	PREDICTED: Macaca mulatta insulin (INS), mRNA
		Select seq XM_011721319.1 **2/1** **8/1** **17/1**	PREDICTED: Macaca nemestrina insulin (INS), transcript variant X4, mRNA
		Select seq XM_011721318.1 **2/1** **8/1** **17/1**	PREDICTED: Macaca nemestrina insulin (INS), transcript variant X3, mRNA
		Select seq XM_011721317.1 **2/1** **8/1** **17/1**	PREDICTED: Macaca nemestrina insulin (INS), transcript variant X2, mRNA
		Select seq XM_011721316.1 **2/1** **8/1** **17/1**	PREDICTED: Macaca nemestrina insulin (INS), transcript variant X1, mRNA
		Select seq NM_001284919.1 **2/1** **8/1** **17/1**	Macaca fascicularis insulin (INS), mRNA
5 Select seq XM_027519481.1	PREDICTED: Bos indicus x Bos taurus phospholipid scramblase 3 (PLSCR3), transcript variant X3, mRNA	Select seq XM_027532448.1 **4/1** **8/1**	PREDICTED: Bos indicus x Bos taurus insulin (INS), mRNA
6 Select seq XM_027519480.1	PREDICTED: Bos indicus x Bos taurus phospholipid scramblase 3 (PLSCR3), transcript variant X2, mRNA	Select seq XM_015461330.2 **4/1** **8/1**	PREDICTED: Bos taurus insulin (INS), transcript variant X1, mRNA
7 Select seq XM_027519479.1	PREDICTED: Bos indicus x Bos taurus phospholipid scramblase 3 (PLSCR3), transcript variant X1, mRNA	Select seq CP027097.1 **4/1** **8/1**	Bos mutus isolate yakQH1 chromosome 29
8 Select seq CP027087.1 4/1	Bos mutus isolate yakQH1 chromosome 19	Select seq XM_019954732.1 **4/1** **8/1**	PREDICTED: Bos indicus insulin (INS), transcript variant X2, mRNA

Comparison between the alignments of Sequence 3/1 and Sequence of Insulin Chain A according to the “Species of Common Organisms”:

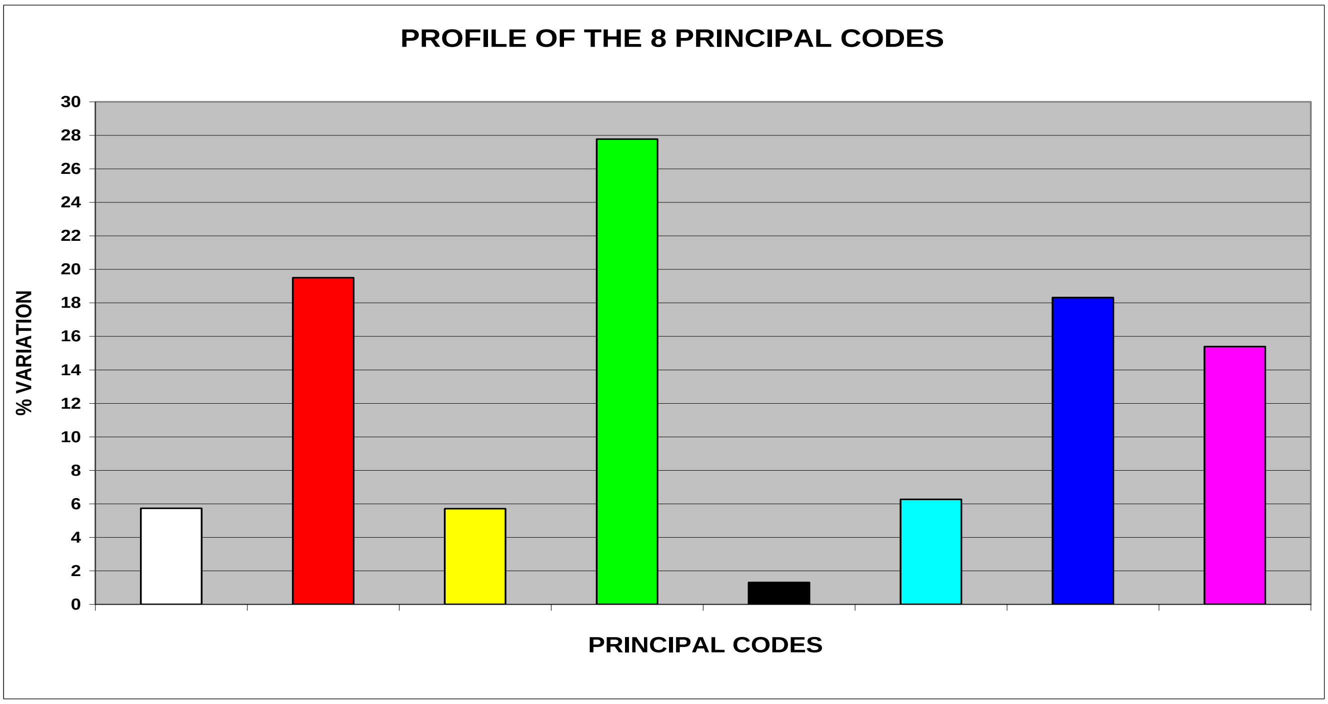
Alignments Sequence 3/1	**Description**	**Alignments Sequence Insulin Chain A**	**Description**
9 Select seq XM_019982110.1	PREDICTED: Bos indicus phospholipid scramblase 3 (PLSCR3), transcript variant X3, mRNA	Select seq XM_019954731.1 **4/1 8/1**	PREDICTED: Bos indicus insulin (INS), transcript variant X1, mRNA
10 Select seq XM_019982108.1	PREDICTED: Bos indicus phospholipid scramblase 3 (PLSCR3), transcript variant X2, mRNA	Select seq M54979.2 **4/1 8/1**	Bos taurus insulin precursor, mRNA, complete cds
11 Select seq XM_019982107.1	PREDICTED: Bos indicus phospholipid scramblase 3 (PLSCR3), transcript variant X1, mRNA	Select seq XM_005903505.2 **4/1 8/1**	PREDICTED: Bos mutus insulin (LOC102274400), mRNA
12 Select seq XM_014476435.1	PREDICTED: Bos mutus phospholipid scramblase 3 (PLSCR3), transcript variant X2, mRNA	Select seq JX041514.1 **4/1 8/1**	Bos taurus proinsulin mRNA, partial cds
13 Select seq XM_005889943.2	PREDICTED: Bos mutus phospholipid scramblase 3 (PLSCR3), transcript variant X1, mRNA	Select seq NM_001185126.1 **4/1 8/1**	Bos taurus insulin (INS), transcript variant 2, mRNA
16 Select seq NM_001046053.2	Bos taurus phospholipid scramblase 3 (PLSCR3), mRNA	Select seq NM_173926.2 **4/1 8/1**	Bos taurus insulin (INS), transcript variant 1, mRNA
17 Select seq BC114676.1	Bos taurus phospholipid scramblase 3, mRNA (cDNA clone MGC:138060 IMAGE:8087126), complete cds	Select seq EU518675.1 **4/1 8/1**	Bos taurus insulin (INS) and insulin-like growth factor 2 (IGF2) genes, complete cds
		Select seq BC142034.1 **4/1 8/1**	Bos taurus insulin, mRNA (cDNA clone MGC:159719 IMAGE:8631936), complete cds
		Select seq AC149665.2 **4/1 8/1**	Bos taurus BAC CH240-60O13 (Children's Hospital Oakland Research Institute Bovine BAC Library (male)) complete sequence

Analysis of
Sequence n° 4/1
of Insulin Chain A

1.8 GRAPHIC RESULTS OF THE "NON-OBVIOUS TREND" ANALYSIS OF SEQUENCE n° 4/1 OF INSULIN CHAIN A

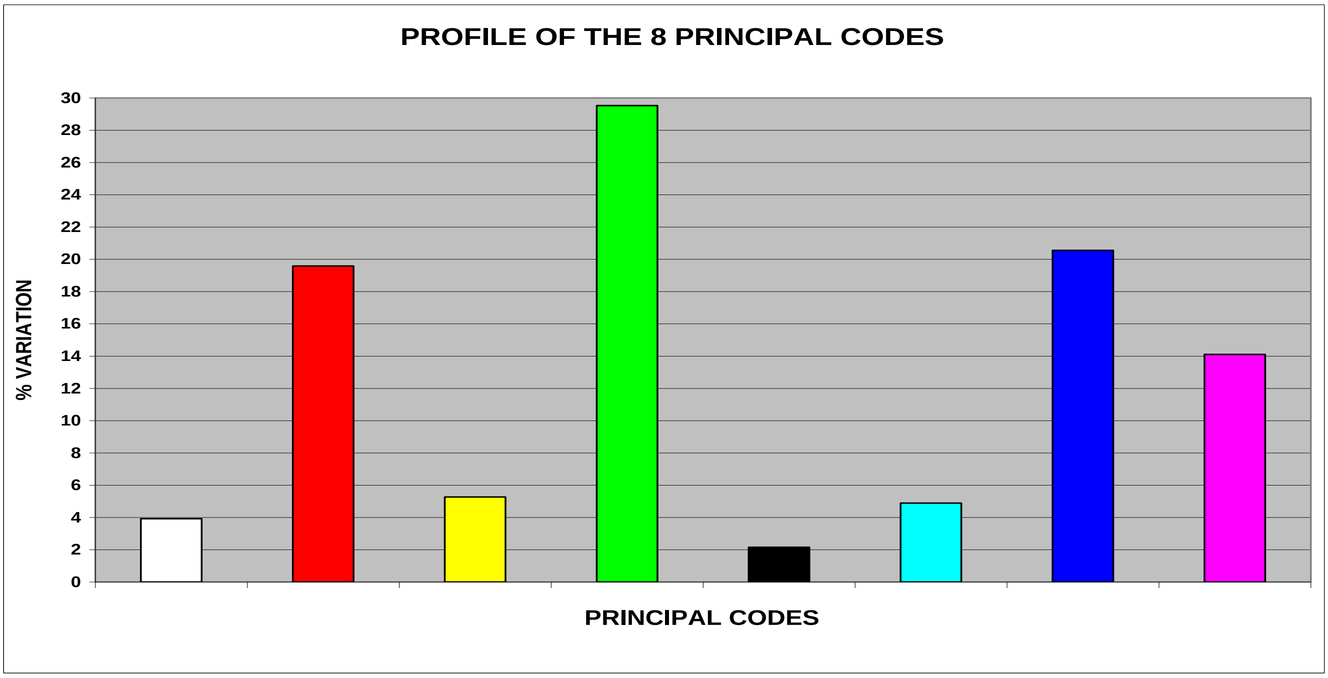
In the Pct. 13 (A e B) two **8 Principal Codes Profiles** are compared.

The chart in Pct. 13 (A) refers to the **original base sequence** of **Insulin Chain A**.



Pct. 13 (A)

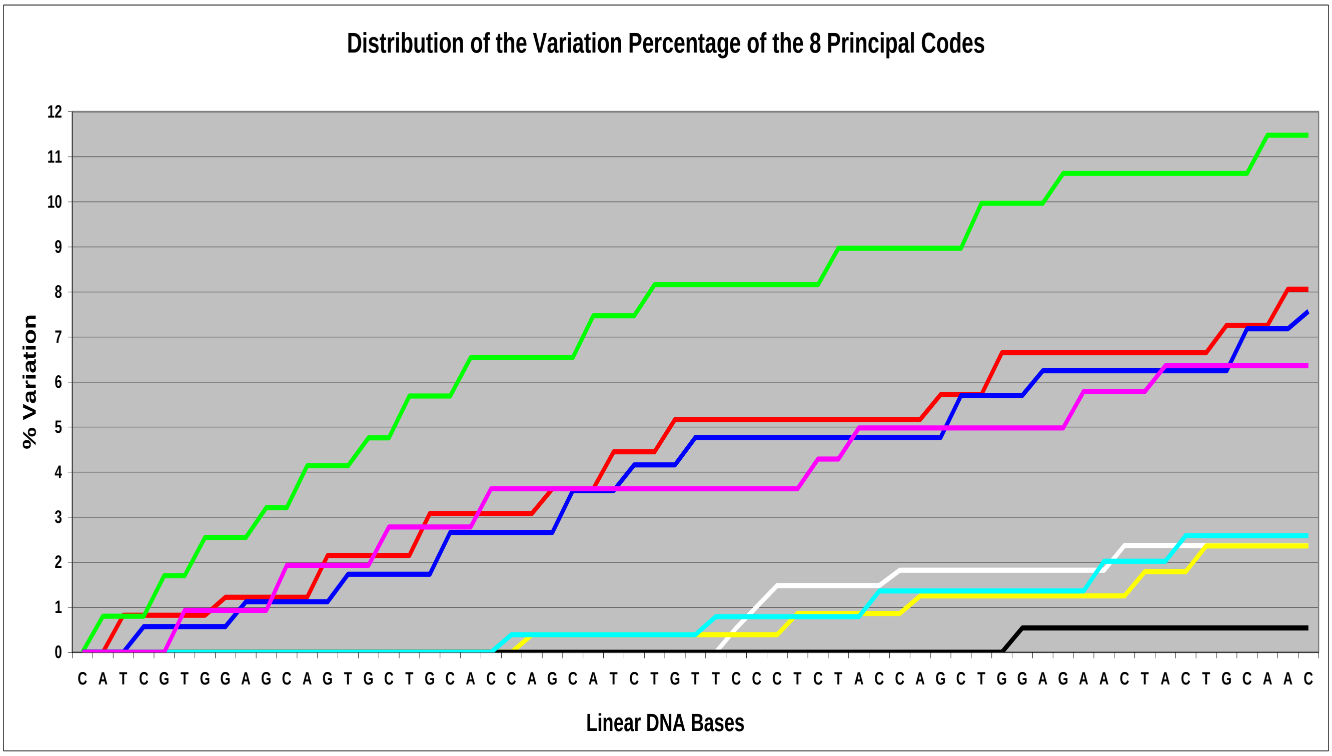
The chart in Pct. 13 (B) refers to the **fourth "new generated sequence"** (**Sequence n° 4/1**) that originates from the original one.



Pct. 13 (B)

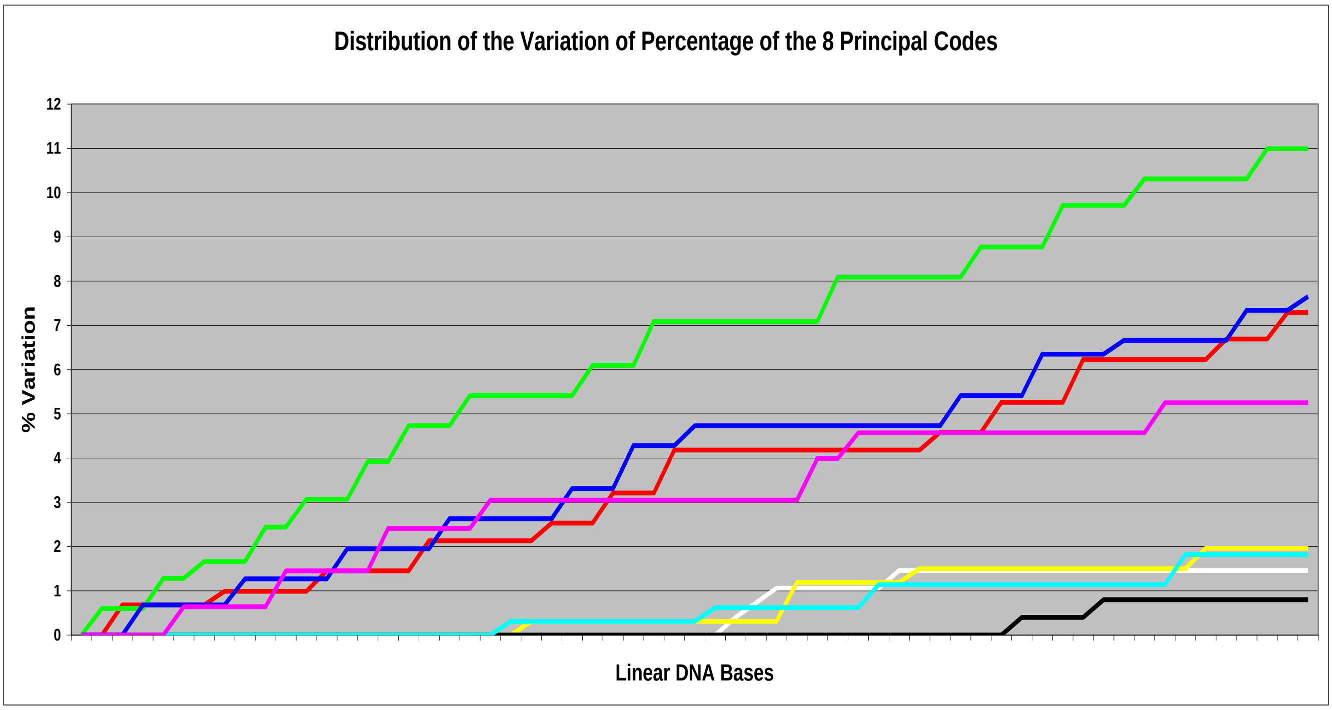
In Pct. 14 (A and B) two charts concerning the **Distribution of the Variation Percentage of the 8 Main Codes** are compared.

The charts in Pct. 14 (A) refers to the **original base sequence** analysed before.



Pct. 14 (A)

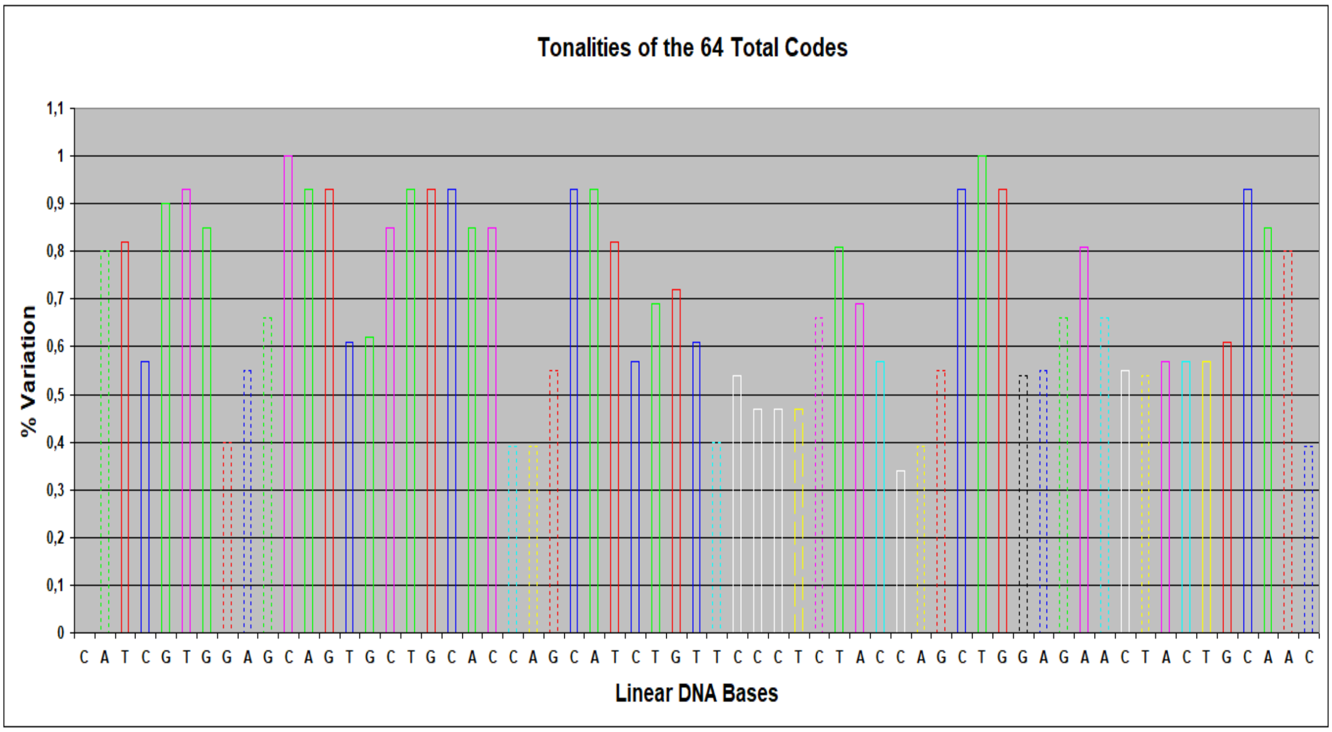
The chart in Pct. 14 (B) refers to the **"new generated sequence"** that originates from the original one.



Pct. 14 (B)

In Pct. 15 (A and B) two charts concerning the single **Tonalities of the 64 Total Codes** are compared.

The chart in Pct. 15 (A) refers to the **original base sequence** analysed before.



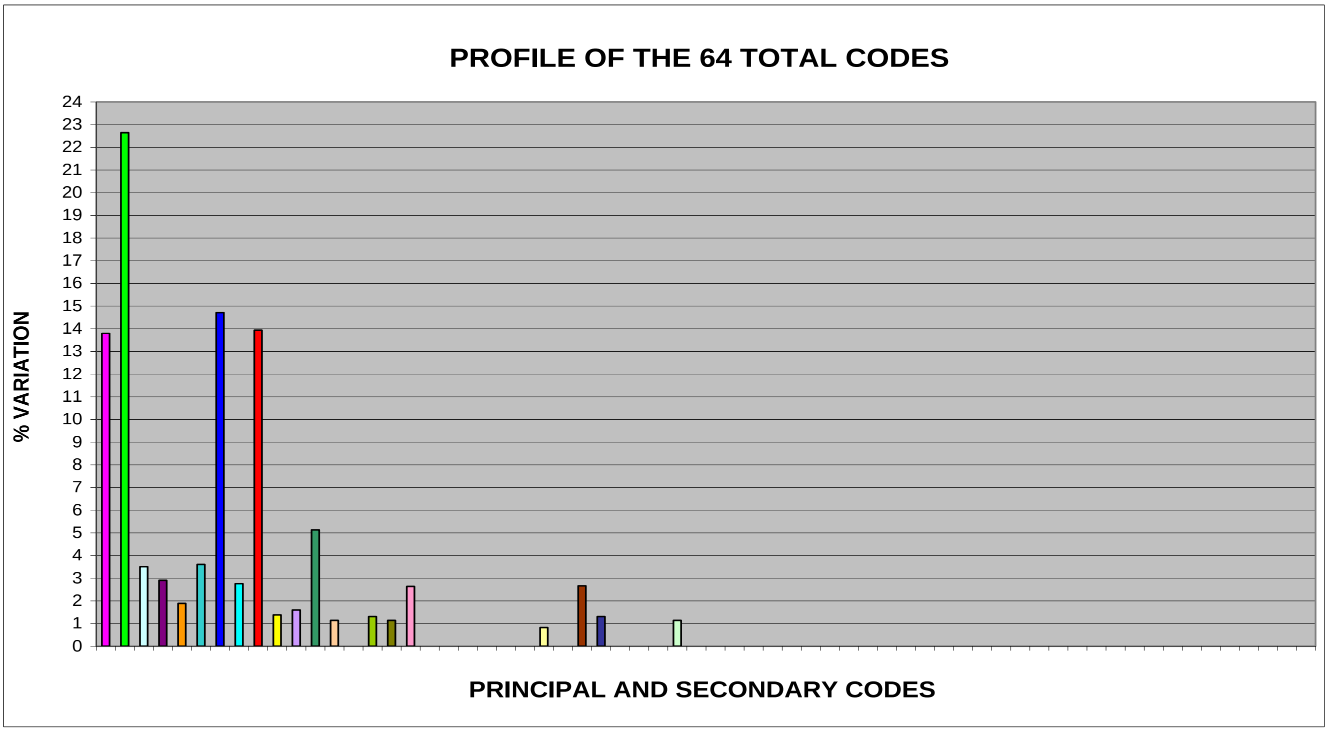
Pct. 15 (A)

The chart in Pct. 15 (B) refers to the **"new generated sequence"** that originates from the original one.

Pct. 15 (B)

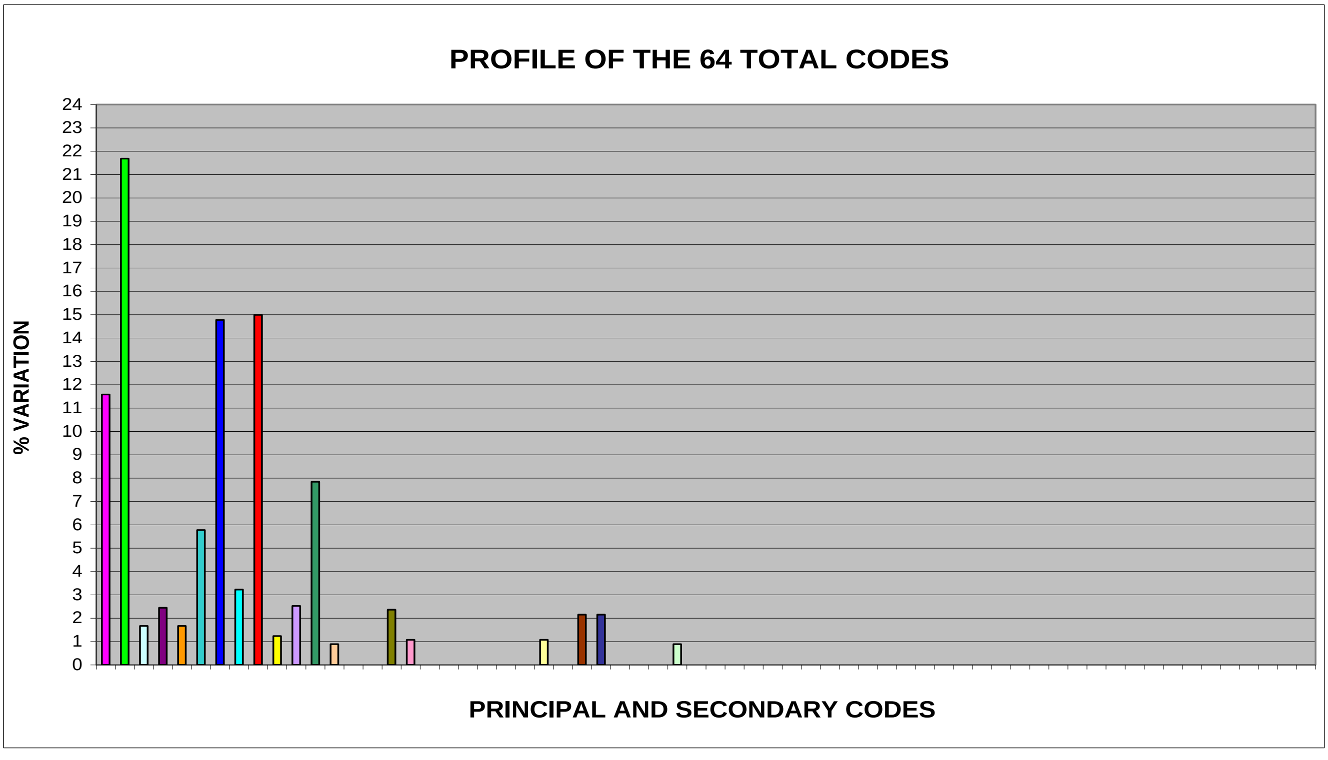
In Pct. 16 (A and B) two charts concerning the **Profile of the 64 Total Codes** are compared.

The chart in Pct. 16 (A) refers to the **original base sequence** analysed before.



Pct. 16 (A)

The chart in Pct. 16 (B) refers to the **"new generated sequence"** originated from the original one.



Pct. 16 (B)

The “non-obvious trend” analysis (obtained through the **T.T.E.S.**) of **Sequence n°4/1 of Insulin Chain A** results in **a comparison among different graphs** that are going to be interpreted in an analogous way to that in which the graphs related to the “non-obvious trend” of the **Sequences** analysed in the previous paragraphs **(n° 1/1, n° 2/1, etc.)**. **n° 1/1** were. In order to avoid repetitions, here, the reader is deferred to the interpretation of the **comparisons among the different graphs** presented in the paragraph 1.2.

Before concluding the paragraph, it is worth noting that, out of the **63** DNA bases of **Sequence n° 4/1**, ONLY **SEVENTEEN BASES** (the **26,98%**)**,** ARE EQUAL (by type and by position in sequence) TO THOSE OF THE ORIGINAL SEQUENCE (**Insulin Chain A**).

1.9 IMPLICATIONS RELATED TO THE GRAPHIC RESULTS OF THE “NON-OBVIOUS TREND” ANALYSIS OF SEQUENCE n° 4/1 OF INSULIN CHAIN A

The **63** DNA base sequence of the **new generated sequence** (**Sequence n° 4/1**) that arises from the **original** one has been subjected to **BLAST** research.

Please note:

Information about the ***significant alignments*** produced by *BLAST research*, related to **Sequence n° 4/1,** and all the data acquired from *GenBank (3)* will be published in the **Appendix,** after the *General Conclusions.*

Query = NEW GENERATED SEQUENCE (Sequence n° 4/1)

Length = 63

Parameters of BLAST research:

Programme	*Blastn*
Word size	*11*
Expect value	*10*
Hitlist size	*100*
Match/Mismatch scores	*2,-3*
Gapcosts	*5,2*
Low Complexity Filter	*Yes*
Filter string	*L;m;*
Genetic Code	*1*

Please note:

Here, “**the organisms found to be in common**” between the results of BLAST research carried out on **Insulin Chain A** and results of BLAST research carried out on **Sequence n° 4/1**, were highlighted in **Red**.
As well, “**the organisms found to be in common**” between the results of BLAST research carried out on **Insulin Chain A**, results of BLAST research carried out on **Sequence n° 4/1** and results of BLAST research carried out on **at least one** of the *19 generated sequences*, were highlighted in **Green**.
Moreover, “**the denomination of the sequence**” (1/1, 2/1, ... 19/1) of the “**organism found to be in common**” between the results of BLAST research carried out on **Sequence n° 4/1** and results of BLAST research carried out on **at least one** of the *19 new generated sequences*, were highlighted in **Blue**.
Finally, “**the denomination of the sequence**” (1/1, 2/1, ... 19/1) of the “**organism found to be in common**” between the results of BLAST research carried out on **Insulin Chain A** and results of BLAST research carried out on *19 generated sequences*, were highlighted in **Yellow**.

Sequenza n° 4/1

Sequences producing significant alignments:

Selected seq	Description	Max score	Total score	Query cover	E value	Ident	Accession
1 LN005780.1 **6/1** **8/1**	Spirometra erinaceieuropaei genome assembly S_erinaceieuropaei, scaffold SPER_scaffold0005729	47.3	47.3	61%	0.061	88%	LN005780.1
2 CP023761.1 **8/1**	Solanum lycopersicum cultivar I-3 chromosome 5	42.8	42.8	53%	0.74	89%	CP023761.1
3 HG975517.1 **8/1**	Solanum lycopersicum chromosome ch05, complete genome	42.8	42.8	53%	0.74	89%	HG975517.1
4 LN590707.1	Cyprinus carpio genome assembly common carp genome, scaffold: LG30, chromosome: 30	41.9	41.9	47%	2.6	90%	LN590707.1
5 CP027418.1	Providencia rettgeri strain FDAARGOS_330 chromosome, complete genome	41.0	41.0	50%	2.6	88%	CP027418.1
6 CP027084.1	Bos mutus isolate yakQH1 chromosome 16	41.0	41.0	42%	2.6	93%	CP027084.1
7 CP023767.1 **8/1**	Solanum lycopersicum cultivar I-3 chromosome 11	41.0	41.0	52%	2.6	88%	CP023767.1
8 CP023759.1 **8/1**	Solanum lycopersicum cultivar I-3 chromosome 3	41.0	41.0	52%	2.6	88%	CP023759.1
9 XM_020086984.1	PREDICTED: Paralichthys olivaceus myb/SANT-like DNA-binding domain-containing protein 4 (LOC109629309), transcript variant X2, mRNA	41.0	41.0	46%	2.6	93%	XM_020086984.1
10 XM_020086983.1	PREDICTED: Paralichthys olivaceus myb/SANT-like DNA-binding domain-containing protein 4 (LOC109629309), transcript variant X1, mRNA	41.0	41.0	46%	2.6	93%	XM_020086983.1
11 CP017671.1	Providencia rettgeri strain RB151, complete genome	41.0	41.0	50%	2.6	88%	CP017671.1
12 CP017817.1	Sclerotinia sclerotiorum chromosome 4, complete sequence	41.0	41.0	34%	2.6	100%	CP017817.1
13 HG975523.1 **8/1**	Solanum lycopersicum chromosome ch11, complete genome	41.0	41.0	52%	2.6	88%	HG975523.1

Sequences producing significant alignments:

Selected seq	Description	Max score	Total score	Query cover	E value	Ident	Accession
14 8/1 HG975515.1	Solanum lycopersicum chromosome ch03, complete genome	41.0	41.0	52%	2.6	88%	HG975515.1
15 8/1 HG975451.1	Solanum pennellii chromosome ch12, complete genome	41.0	41.0	52%	2.6	88%	HG975451.1
16 8/1 HG975448.1	Solanum pennellii chromosome ch09, complete genome	41.0	41.0	52%	2.6	88%	HG975448.1
17 8/1 HG975442.1	Solanum pennellii chromosome ch03, complete genome	41.0	41.0	52%	2.6	88%	HG975442.1
18 LR132017.1	Betta splendens genome assembly, chromosome: 12	40.1	40.1	38%	9.0	96%	LR132017.1
19 3/1 CP027087.1	Bos mutus isolate yakQH1 chromosome 19	40.1	40.1	46%	9.0	90%	CP027087.1
20 CP024962.1	Entomoplasma freundtii strain BARC 318 chromosome, complete genome	40.1	40.1	66%	9.0	84%	CP024962.1
21 CP019108.1	Spirodela polyrhiza strain 9509 chromosome 16 sequence	40.1	40.1	38%	9.0	96%	CP019108.1
22 6/1 8/1 LK787109.1	Dicrocoelium dendriticum genome assembly D_dendriticum_Leon_v1_0_4, scaffold DDEL_scaffold0352685	40.1	40.1	55%	9.0	86%	LK787109.1
23 6/1 8/1 LN001590.1	Spirometra erinaceieuropaei genome assembly S_erinaceieuropaei, scaffold SPER_scaffold0001576	40.1	40.1	46%	9.0	90%	LN001590.1
24 CP002273.2	Eubacterium callanderi strain KIST612, complete genome	40.1	40.1	77%	9.0	78%	CP002273.2
25 6/1 LR131937.1	Cottoperca gobio genome assembly, chromosome: 7	39.2	39.2	41%	9.0	92%	LR131937.1
26 CP021279.1	Legionella pneumophila subsp. fraseri strain F-4198 chromosome, complete genome	39.2	39.2	41%	9.0	92%	CP021279.1
27 CP021277.1	Legionella pneumophila subsp. fraseri strain D-4058 chromosome, complete genome	39.2	39.2	41%	9.0	92%	CP021277.1
28 CP021265.1	Legionella pneumophila subsp. fraseri strain Los Angeles 1 (D-7696) chromosome, complete genome	39.2	39.2	41%	9.0	92%	CP021265.1

Sequences producing significant alignments:

Selected seq	Description	Max score	Total score	Query cover	E value	Ident	Accession
29 CP021264.1	Legionella pneumophila subsp. fraseri strain D-5387 chromosome, complete genome	39.2	39.2	41%	9.0	92%	CP021264.1
30 CP021263.1	Legionella pneumophila subsp. fraseri strain D-3137 chromosome, complete genome	39.2	39.2	41%	9.0	92%	CP021263.1
31 CP021259.1	Legionella pneumophila strain D-7708 chromosome, complete genome	39.2	39.2	41%	9.0	92%	CP021259.1
32 CP021258.1	Legionella pneumophila subsp. fraseri strain D-5744 chromosome, complete genome	39.2	39.2	41%	9.0	92%	CP021258.1
33 CP021257.1	Legionella pneumophila subsp. fraseri strain Lansing 3 chromosome, complete genome	39.2	39.2	41%	9.0	92%	CP021257.1
34 XM_023801497.1	PREDICTED: Paramormyrops kingsleyae C2 calcium-dependent domain-containing protein 4C-like (LOC111838475), mRNA	39.2	39.2	49%	9.0	87%	XM_023801497.1
35 MG779363.1	Bandra megavirus isolate KK-1 genomic sequence	39.2	39.2	41%	9.0	92%	MG779363.1
36 CP017602.1	Legionella pneumophila strain D5945 chromosome, complete genome	39.2	39.2	41%	9.0	92%	CP017602.1
37 CP017601.1	Legionella pneumophila strain D6026 chromosome, complete genome	39.2	39.2	41%	9.0	92%	CP017601.1
38 CP017458.1	Legionella pneumophila subsp. fraseri strain Dallas 1E, complete genome	39.2	39.2	41%	9.0	92%	CP017458.1
39 CP017457.1	Legionella pneumophila subsp. fraseri strain Detroit-1, complete genome	39.2	39.2	41%	9.0	92%	CP017457.1
40 LT594635.1	Plasmodium malariae genome assembly, chromosome: 14	39.2	39.2	49%	9.0	87%	LT594635.1
41 LT594502.1	Plasmodium malariae genome assembly, chromosome: 14	39.2	39.2	49%	9.0	87%	LT594502.1
42 XM_014194504.1	PREDICTED: Salmo salar cytosolic endo-beta-N-acetylglucosaminidase-like (LOC106602056), mRNA	39.2	39.2	41%	9.0	92%	XM_014194504.1

Sequences producing significant alignments:

Selected seq	Description	Max score	Total score	Query cover	E value	Ident	Accession
43 XM_014194503.1	PREDICTED: Salmo salar retinoid-inducible serine carboxypeptidase-like (LOC106602055), mRNA	39.2	39.2	41%	9.0	92%	XM_014194503.1
44 JX885207.1	Megavirus lba isolate LBA111, complete genome	39.2	39.2	41%	9.0	92%	JX885207.1
45 JX975216.1	Megavirus courdo11, complete genome	39.2	39.2	41%	9.0	92%	JX975216.1
46 CP003360.1	Desulfomonile tiedjei DSM 6799, complete genome	39.2	39.2	41%	9.0	92%	CP003360.1
47 JN258408.1	Megavirus chiliensis, complete genome	39.2	39.2	41%	9.0	92%	JN258408.1
48 CP002874.1	Brachyspira intermedia PWS/A, complete genome	39.2	39.2	44%	9.0	93%	CP002874.1
49 **6/1** CP001078.1	Clostridium botulinum E3 str. Alaska E43, complete genome	39.2	39.2	41%	9.0	92%	CP001078.1

Comparison between the alignments of Sequence 4/1 and Sequence of Insulin Chain A according to the "Species of Common Organisms":

Alignments Sequence 4/1	**Description**	**Alignments Sequence Insulin Chain A**	**Description**
4 Select seq LN590707.1	Cyprinus carpio genome assembly common carp genome, scaffold: LG30, chromosome: 30	Select seq XM_019069183.1 **6/1 17/1**	PREDICTED: Cyprinus carpio insulin-like (LOC109051698), mRNA
		Select seq LN590733.1 **6/1 17/1**	Cyprinus carpio genome assembly common carp genome, scaffold 000000053
6 Select seq CP027084.1	Bos mutus isolate yakQH1 chromosome 16	Select seq XM_027532448.1 **3/1 8/1**	PREDICTED: Bos indicus x Bos taurus insulin (INS), mRNA
19 Select seq CP027087.1 **3/1**	Bos mutus isolate yakQH1 chromosome 19	Select seq XM_015461330.2 **3/1 8/1**	PREDICTED: Bos taurus insulin (INS), transcript variant X1, mRNA
		Select seq CP027097.1 **3/1 8/1**	Bos mutus isolate yakQH1 chromosome 29
		Select seq XM_019954732.1 **3/1 8/1**	PREDICTED: Bos indicus insulin (INS), transcript variant X2, mRNA
		Select seq XM_019954731.1 **3/1 8/1**	PREDICTED: Bos indicus insulin (INS), transcript variant X1, mRNA
		Select seq M54979.2 **3/1 8/1**	Bos taurus insulin precursor, mRNA, complete cds
		Select seq XM_005903505.2 **3/1 8/1**	PREDICTED: Bos mutus insulin (LOC102274400), mRNA
		Select seq JX041514.1 **3/1 8/1**	Bos taurus proinsulin mRNA, partial cds
		Select seq NM_001185126.1 **3/1 8/1**	Bos taurus insulin (INS), transcript variant 2, mRNA
		Select seq NM_173926.2 **3/1 8/1**	Bos taurus insulin (INS), transcript variant 1, mRNA
		Select seq EU518675.1 **3/1 8/1**	Bos taurus insulin (INS) and insulin-like growth factor 2 (IGF2) genes, complete cds

Comparison between the alignments of Sequence 4/1 and Sequence of Insulin Chain A according to the “Species of Common Organisms”:

Alignments Sequence 4/1	**Description**	**Alignments Sequence Insulin Chain A**	**Description**
		Select seq BC142034.1 **3/1 8/1**	Bos taurus insulin, mRNA (cDNA clone MGC:159719 IMAGE:8631936), complete cds
		Select seq AC149665.2 **3/1 8/1**	Bos taurus BAC CH240-60O13 (Children's Hospital Oakland Research Institute Bovine BAC Library (male)) complete sequence
9 Select seq XM_020086984.1	PREDICTED: Paralichthys olivaceus myb/SANT-like DNA-binding domain-containing protein 4 (LOC109629309), transcript variant X2, mRNA	Select seq XM_020111207.1	PREDICTED: Paralichthys olivaceus insulin-like (LOC109645588), mRNA
10 Select seq XM_020086983.1	PREDICTED: Paralichthys olivaceus myb/SANT-like DNA-binding domain-containing protein 4 (LOC109629309), transcript variant X1, mRNA	Select seq XM_020108849.1	PREDICTED: Paralichthys olivaceus insulin (ins), transcript variant X2, mRNA
		Select seq XM_020108848.1	PREDICTED: Paralichthys olivaceus insulin (ins), transcript variant X1, mRNA
18 Select seq LR132017.1	Betta splendens genome assembly, chromosome: 12	Select seq LR132016.1 **10/1 17/1**	Betta splendens genome assembly, chromosome: 14
		Select seq LR132007.1 **10/1 17/1**	Betta splendens genome assembly, chromosome: 10
25 Select seq LR131937.1 **6/1**	Cottoperca gobio genome assembly, chromosome: 7	Select seq LR131921.1 **6/1 7/1 16/1 18/1 19/1**	Cottoperca gobio genome assembly, chromosome: 14
		Select seq LR131917.1 **6/1 7/1 16/1 18/1 19/1**	Cottoperca gobio genome assembly, chromosome: 10

Comparison between the alignments of Sequence 4/1 and Sequence of Insulin Chain A according to the "Species of Common Organisms":

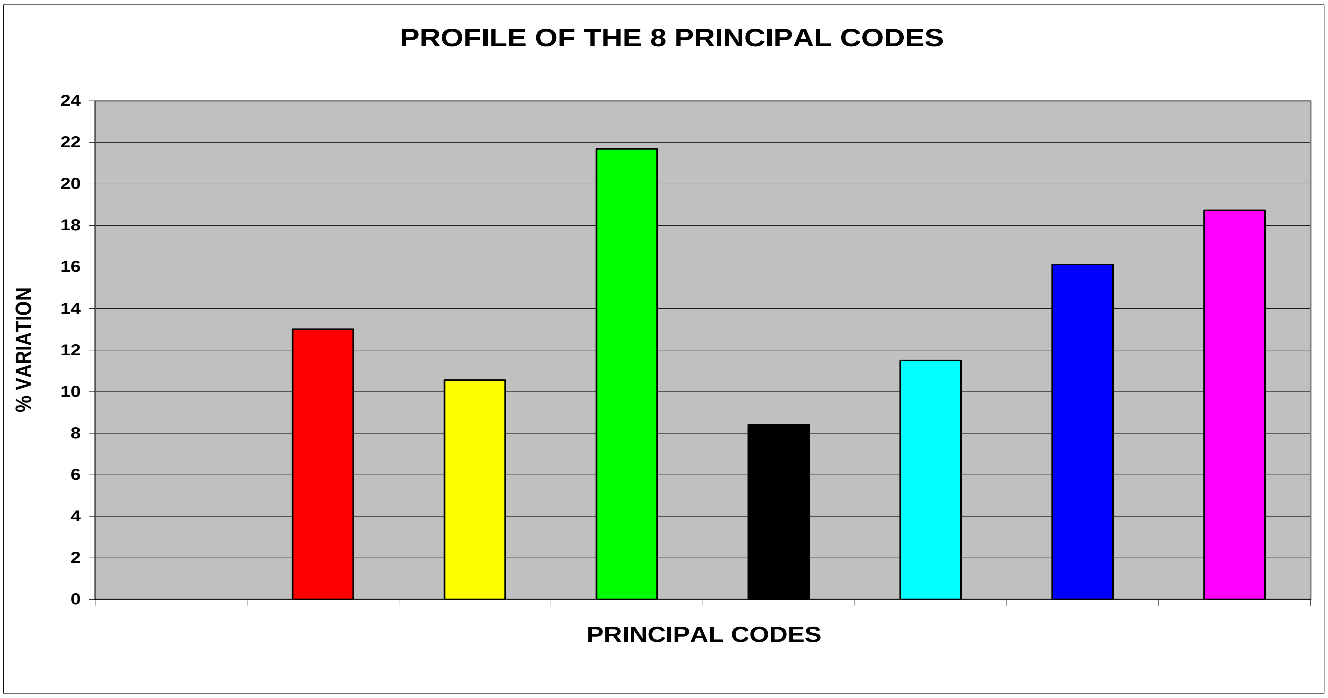
Alignments Sequence 4/1	Description	Alignments Sequence Insulin Chain A	Description
42 Select seq XM_014194504.1	PREDICTED: Salmo salar cytosolic endo-beta-N-acetylglucosaminidase-like (LOC106602056), mRNA	Select seq BT049386.1	Salmo salar clone ssal-rgb2-569-154 Insulin precursor putative mRNA, complete cds
43 Select seq XM_014194503.1	PREDICTED: Salmo salar retinoid-inducible serine carboxypeptidase-like (LOC106602055), mRNA	Select seq XM_014198195.1	PREDICTED: Salmo salar insulin-like (LOC106603941), mRNA
		Select seq XM_014136745.1	PREDICTED: Salmo salar insulin (LOC106567474), mRNA
		Select seq BT049203.1	Salmo salar clone ssal-plnb-020-217 Insulin precursor putative mRNA, complete cds
		Select seq BT046764.1	Salmo salar clone ssal-plnb-013-055 Insulin precursor putative mRNA, complete cds

Analysis of
Sequence n° 5/1
of Insulin Chain A

1.10 GRAPHIC RESULTS OF THE "NON-OBVIOUS TREND" ANALYSIS OF SEQUENCE n° 5/1 OF INSULIN CHAIN A

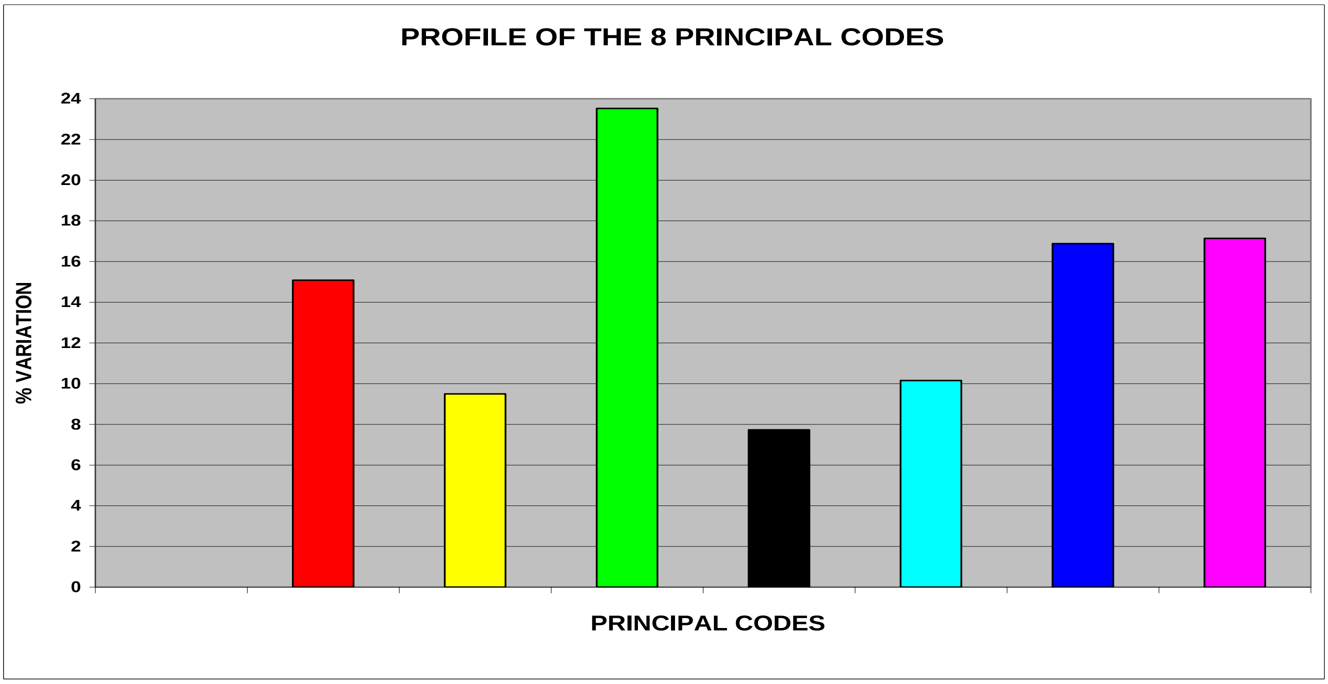
In the Pct. 17 (A e B) two **8 Principal Codes Profiles** are compared.

The chart in Pct. 17 (A) refers to the **original base sequence** of **Insulin Chain A**.



Pct. 17 (A)

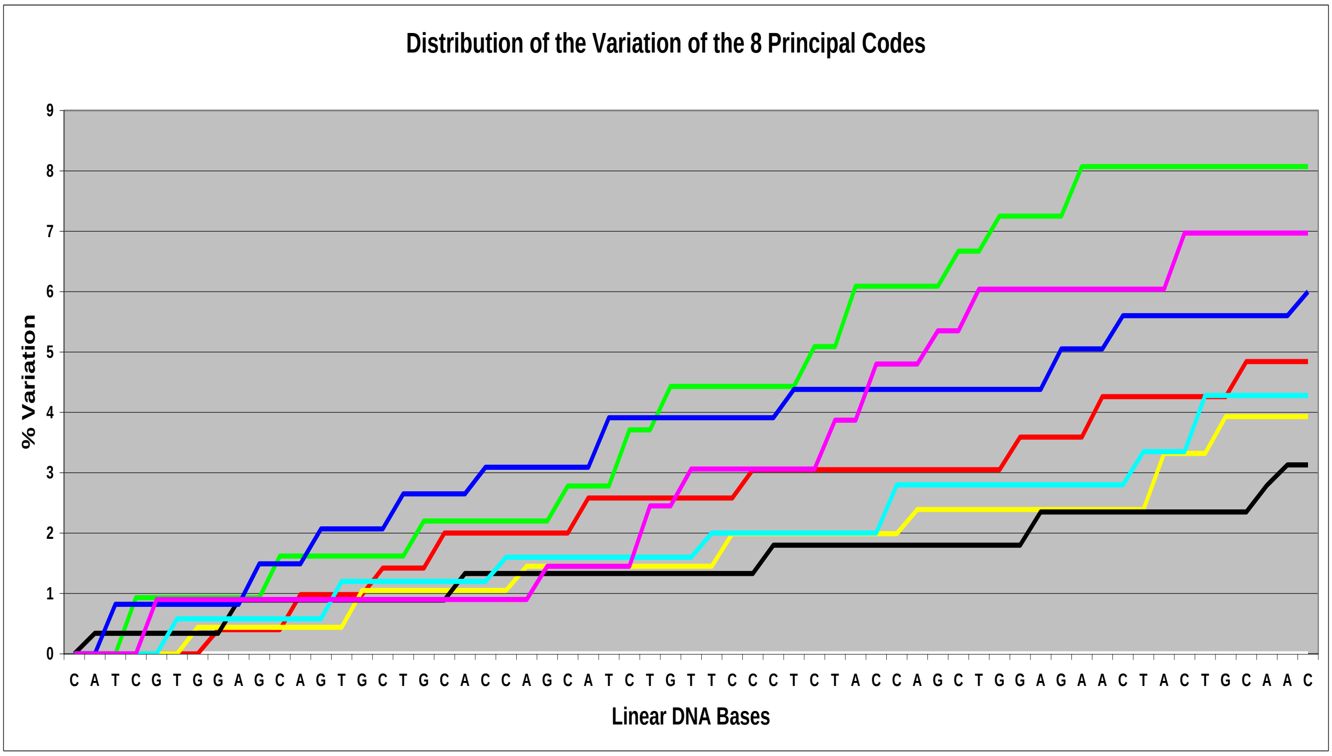
The chart in Pct. 17 (B) refers to the **fifth** **"new generated sequence"** (**Sequence n° 5/1**) that originates from the original one.



Pct. 17 (B)

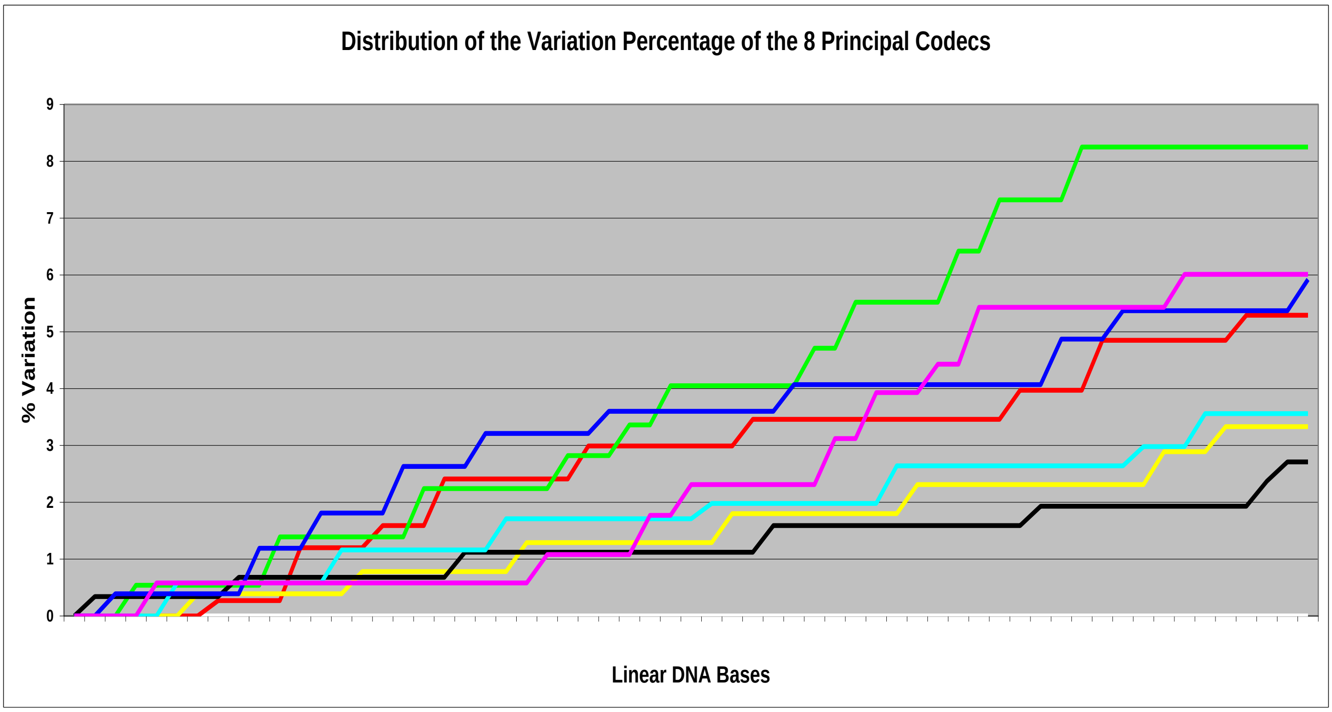
In Pct. 18 (A and B) two charts concerning the **Distribution of the Variation Percentage of the 8 Main Codes** are compared.

The charts in Pct. 18 (A) refers to the **original base sequence** analysed before.



Pct. 18 (A)

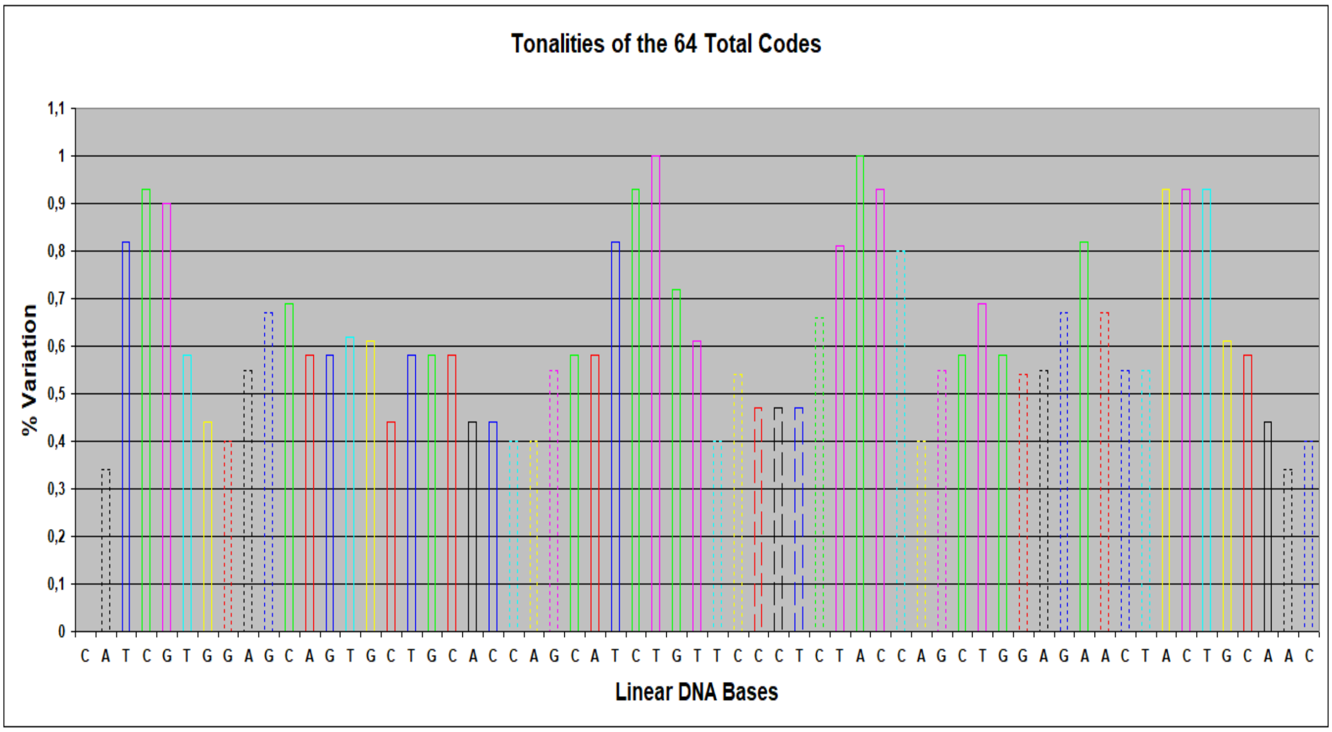
The chart in Pct. 18 (B) refers to the **"new generated sequence"** that originates from the original one.



Pct. 18 (B)

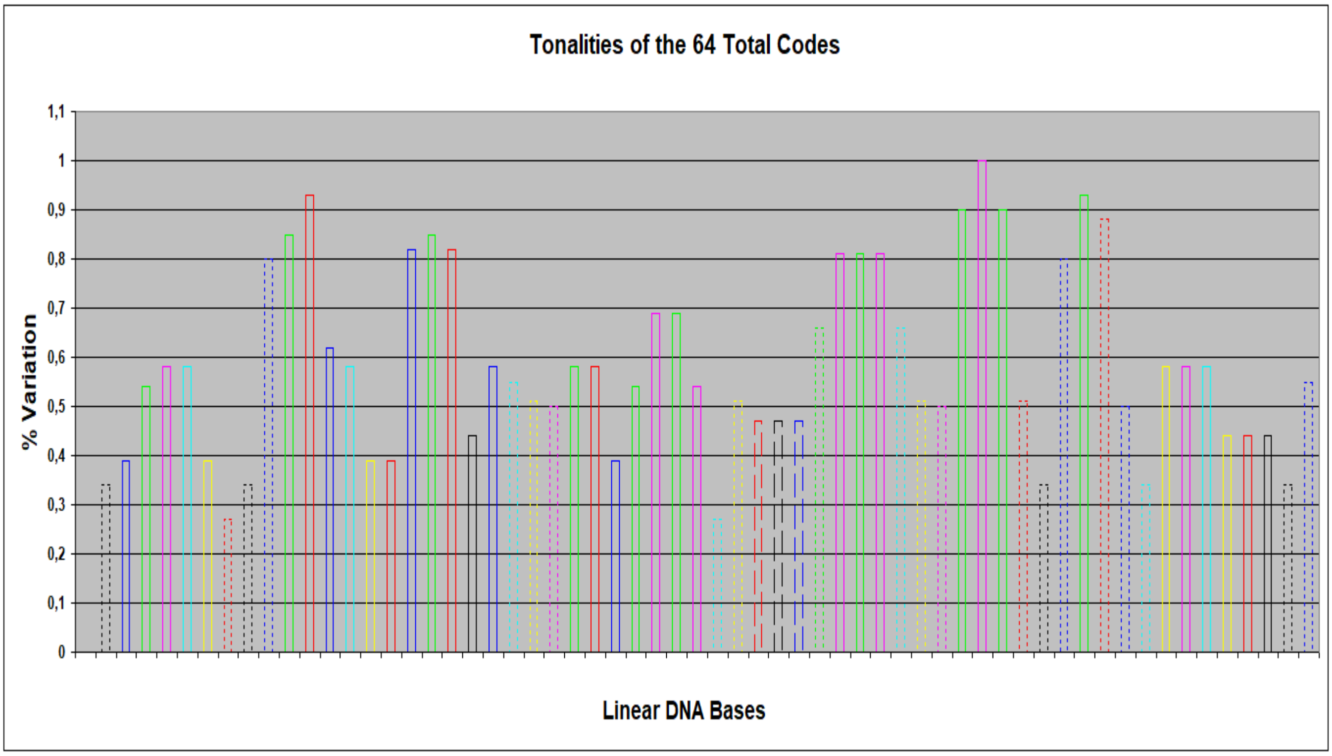
In Pct. 19 (A and B) two charts concerning the single **Tonalities of the 64 Total Codes** are compared.

The chart in Pct. 19 (A) refers to the **original base sequence** analysed before.



Pct. 19 (A)

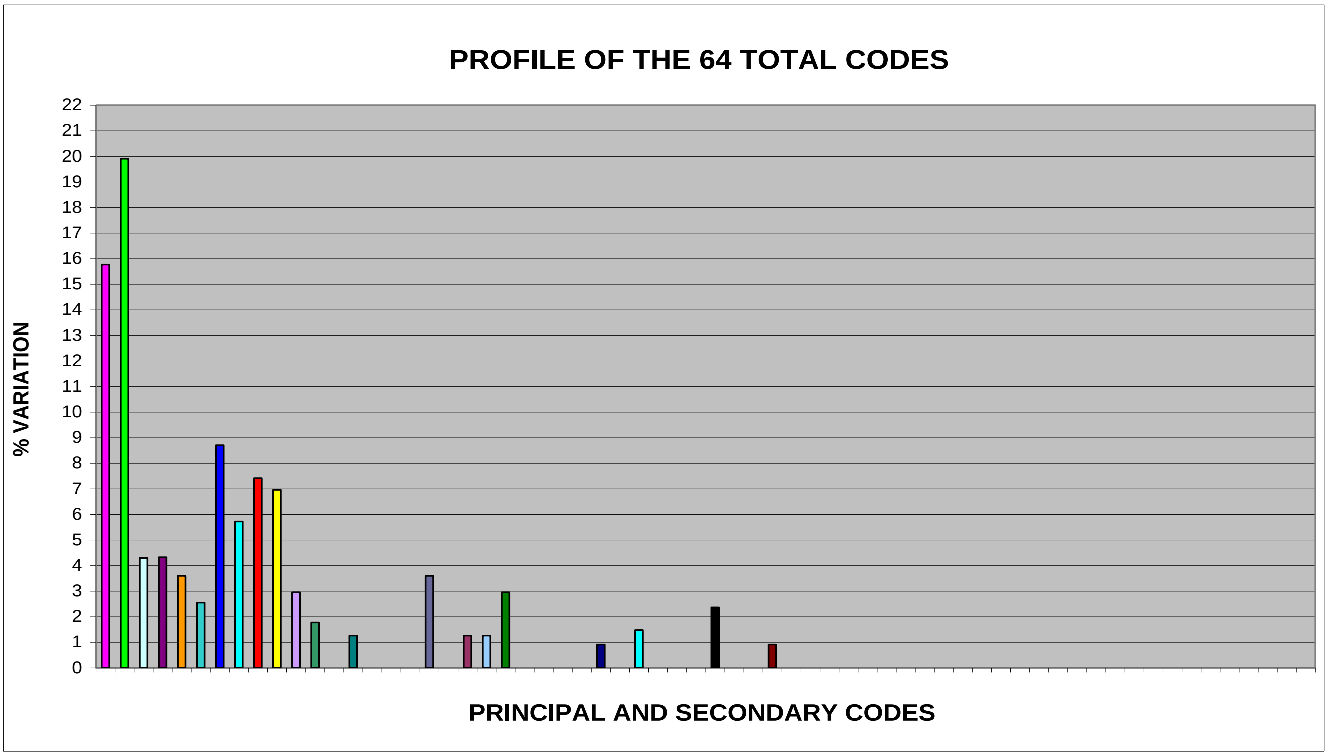
The chart in Pct. 19 (B) refers to the **"new generated sequence"** that originates from the original one.



Pct. 19 (B)

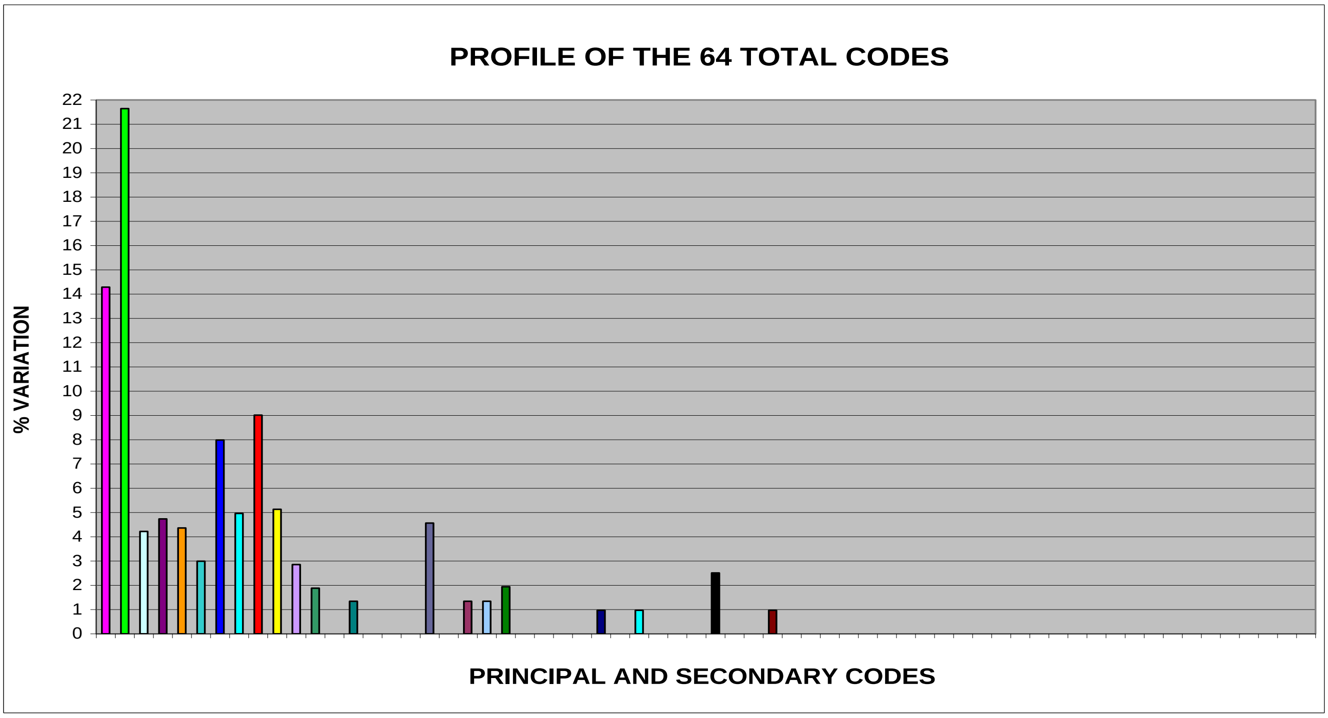
In Pct. 20 (A and B) two charts concerning the **Profile of the 64 Total Codes** are compared.

The chart in Pct. 20 (A) refers to the **original base sequence** analysed before.



Pct. 20 (A)

The chart in Pct. 20 (B) refers to the **“new generated sequence”** originated from the original one.



Pct. 20 (B)

The “non-obvious trend” analysis (obtained through the **T.T.E.S.**) of **Sequence n°2/1 of Insulin Chain A** results in **a comparison among different graphs** that are going to be interpreted in an analogous way to that in which the graphs related to the “non-obvious trend” of the **Sequences** analysed in the previous paragraphs **(n° 1/1, n° 2/1, etc.)** were. In order to avoid repetitions, here, the reader is deferred to the interpretation of the **comparisons among the different graphs** presented in the paragraph 1.2 .

Before concluding the paragraph, it is worth noting that, out of the **63** DNA bases of **Sequence n° 5/1**, ONLY **FOURTEEN BASES** (the **22,22%**)**,** ARE EQUAL (by type and by position in sequence) TO THOSE OF THE ORIGINAL SEQUENCE (**Insulin Chain A**).

1.11 IMPLICATIONS RELATIVE TO THE GRAPHIC RESULTS OF THE "NON-OBVIOUS TREND" ANALYSIS OF SEQUENCE n° 5/1 OF INSULIN CHAIN A

The **63** DNA base sequence of the **new generated sequence** (**Sequence n° 5/1**) that arises from the **original** one has been subjected to **BLAST** research.

Please note:

Information about the ***significant alignments*** produced by *BLAST research*, related to **Sequence n° 5/1,** and all the data acquired from *GenBank (3)* will be published in the **Appendix,** after the *General Conclusions.*

Query = NEW GENERATED SEQUENCE (Sequence n° 5/1)

Length = 63

Parameters of BLAST research:

Programme	*Blastn*
Word size	*11*
Expect value	*10*
Hitlist size	*100*
Match/Mismatch scores	*2,-3*
Gapcosts	*5,2*
Low Complexity Filter	*Yes*
Filter string	*L;m;*
Genetic Code	*1*

Please note:

Here, "**the organisms found to be in common**" between the results of BLAST research carried out on **Insulin Chain A** and results of BLAST research carried out on **Sequence n° 5/1**, were highlighted in **Red**.
As well, "**the organisms found to be in common**" between the results of BLAST research carried out on **Insulin Chain A**, results of BLAST research carried out on **Sequence n° 5/1** and results of BLAST research carried out on **at least one** of the *19 generated sequences*, were highlighted in **Green**.
Moreover, "**the denomination of the sequence**" (1/1, 2/1, ... 19/1) of the "**organism found to be in common**" between the results of BLAST research carried out on **Sequence n° 5/1** and results of BLAST research carried out on **at least one** of the *19 new generated sequences*, were highlighted in **Blue**.
Finally, "**the denomination of the sequence**" (1/1, 2/1, ... 19/1) of the "**organism found to be in common**" between the results of BLAST research carried out on **Insulin Chain A** and results of BLAST research carried out on *19 generated sequences*, were highlighted in **Yellow**.

Sequenza n° 5/1

Sequences producing significant alignments:

Selected seq	Description	Max score	Total score	Query cover	E value	Ident	Accession
1 **18/1** CP035913.1	Massilia lutea strain DSM 17473 chromosome	41.9	41.9	47%	2.7	90%	CP035913.1
2 CP026102.1	Paraburkholderia caribensis strain DSM 13236 chromosome 2, complete sequence	41.0	41.0	42%	2.7	93%	CP026102.1
3 CP013348.1	Paraburkholderia caribensis strain Bcrs1W chromosome 2, complete sequence	41.0	41.0	42%	2.7	93%	CP013348.1
4 CP013103.1	Paraburkholderia caribensis strain MWAP64 chromosome 2, complete sequence	41.0	41.0	42%	2.7	93%	CP013103.1
5 CP012747.1	Paraburkholderia caribensis MBA4 chromosome 2, complete sequence	41.0	41.0	42%	2.7	93%	CP012747.1
6 LK065890.1	Apteryx australis mantelli genome assembly AptMant0, scaffold scaffold1284	41.0	41.0	60%	2.7	89%	LK065890.1
7 XM_013733515.1	PREDICTED: Brassica oleracea var. oleracea glutathione S-transferase T3-like (LOC106297235), mRNA	40.1	40.1	52%	9.5	88%	XM_013733515.1
8 **9/1** **14/1** CP029526.1	Leishmania donovani strain LdCL chromosome LdCL_27, complete sequence	39.2	39.2	47%	9.5	90%	CP029526.1
9 **9/1** **14/1** CP027826.1	Leishmania infantum strain TR01 isolate Lin_TR01 chromosome 27, complete sequence	39.2	39.2	47%	9.5	90%	CP027826.1
10 **9/1** **14/1** CP022642.1	Leishmania donovani strain pasteur chromosome 27, complete sequence	39.2	39.2	47%	9.5	90%	CP022642.1
11 **9/1** **14/1** CP019535.1	Leishmania donovani strain MHOM/IN/1983/AG83 isolate late passage chromosome 27 sequence	39.2	39.2	47%	9.5	90%	CP019535.1
12 **9/1** **14/1** CP018594.1	Leishmania donovani strain MHOM/IN/1983/AG83 isolate early passage chromosome 27 sequence	39.2	39.2	47%	9.5	90%	CP018594.1
13 CP009678.1	Pectobacterium carotovorum subsp. odoriferum strain BC S7, complete genome	39.2	39.2	49%	9.5	87%	CP009678.1
14 XM_008862763.1	Aphanomyces invadans hypothetical protein partial mRNA	39.2	39.2	41%	9.5	92%	XM_008862763.1

Sequences producing significant alignments:

Selected seq	Description	Max score	Total score	Query cover	E value	Ident	Accession
15 **9/1** **14/1** FR799614.1	Leishmania donovani BPK282A1 complete genome, chromosome 27	39.2	39.2	47%	9.5	90%	FR799614.1
16 **9/1** **14/1** FR796423.1	Leishmania major strain Friedlin complete genome, chromosome 27	39.2	39.2	47%	9.5	90%	FR796423.1
17 **9/1** **14/1** FR796459.1	Leishmania infantum JPCM5 genome chromosome 27	39.2	39.2	47%	9.5	90%	FR796459.1

Comparison between the alignments of Sequence 5/1 and Sequence of Insulin Chain A according to the "Species of Common Organisms":

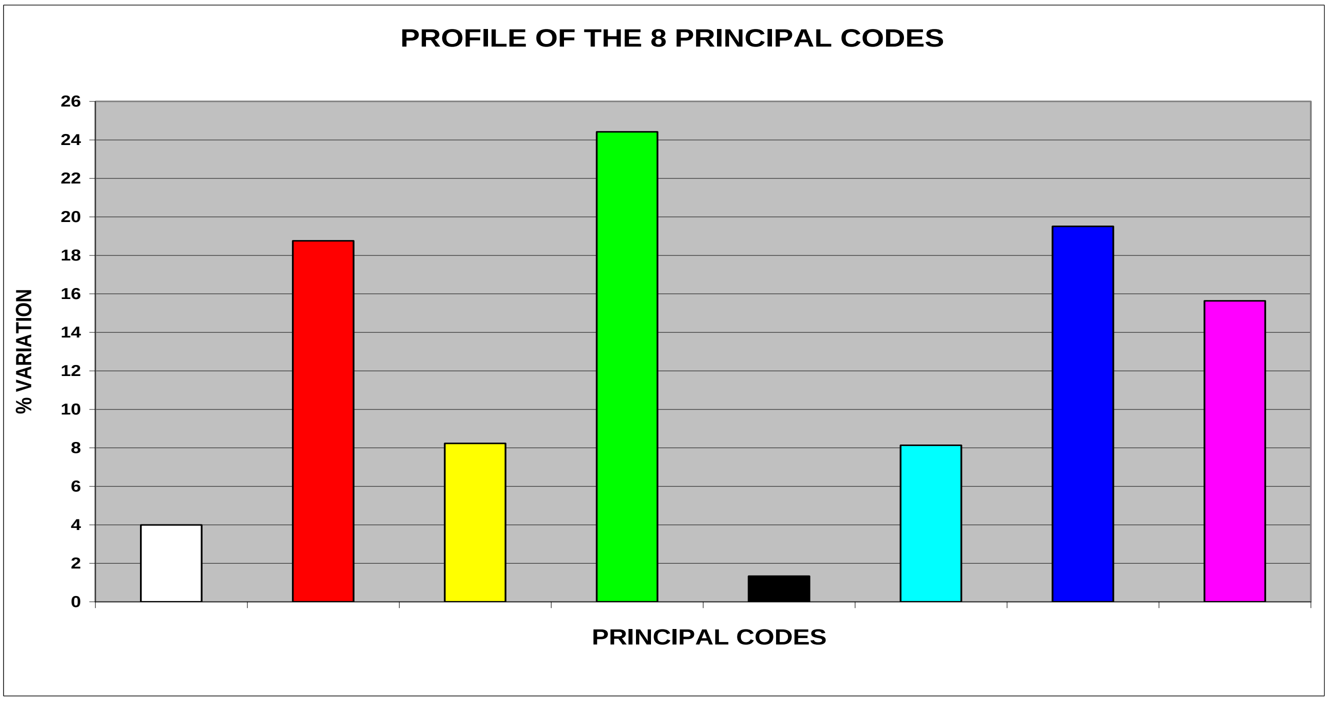
Alignments Sequence 5/1	**Description**	**Alignments Sequence Insulin Chain A**	**Description**
6 Select seq LK065890.1	Apteryx australis mantelli genome assembly AptMant0, scaffold scaffold1284	Select seq XM_026079009.1 **6/1** **17/1**	PREDICTED: Apteryx rowi insulin (INS), mRNA
		Select seq XM_013957848.1 **6/1** **17/1**	PREDICTED: Apteryx australis mantelli insulin (INS), mRNA
		Select seq LK064676.1 **6/1** **17/1**	Apteryx australis mantelli genome assembly AptMant0, scaffold scaffold77

Analysis of
Sequence n° 6/1
of Insulin Chain A

1. 12 GRAPHIC RESULTS OF THE "NON-OBVIOUS TREND" ANALYSIS OF SEQUENCE n° 6/1 OF INSULIN CHAIN A

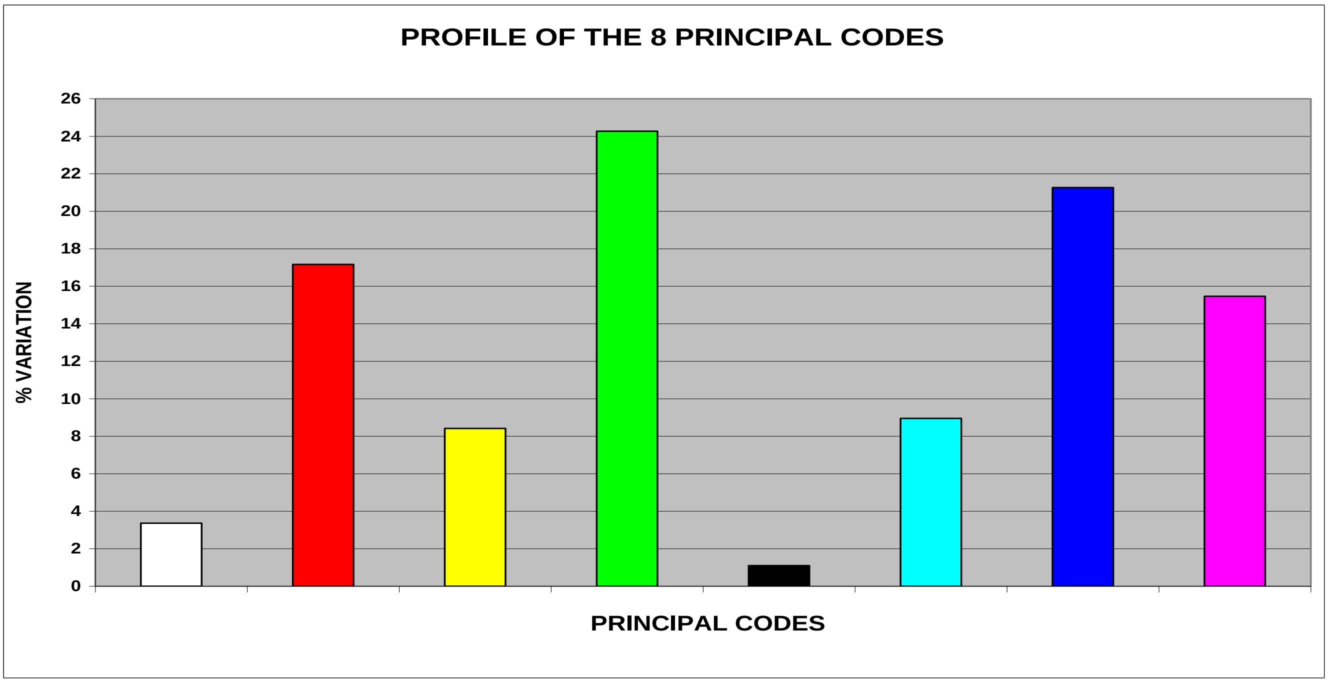
In the Pct. 21 (A e B) two **8 Principal Codes Profiles** are compared.

The chart in Pct. 21 (A) refers to the **original base sequence** of **Insulin Chain A**.



Pct. 21 (A)

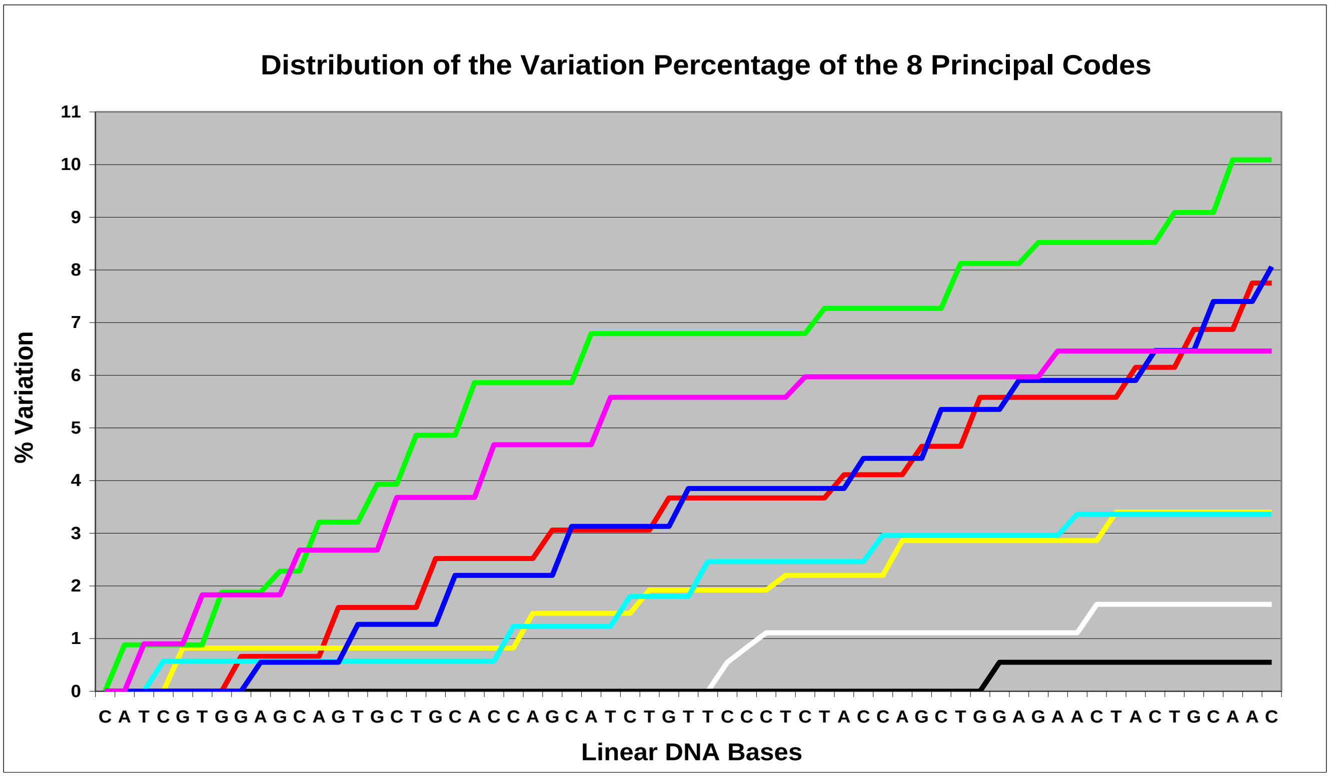
The chart in Pct. 21 (B) refers to the **sixth** **"new generated sequence"** (**Sequence n° 6/1**) that originates from the original one.



Pct. 21 (B)

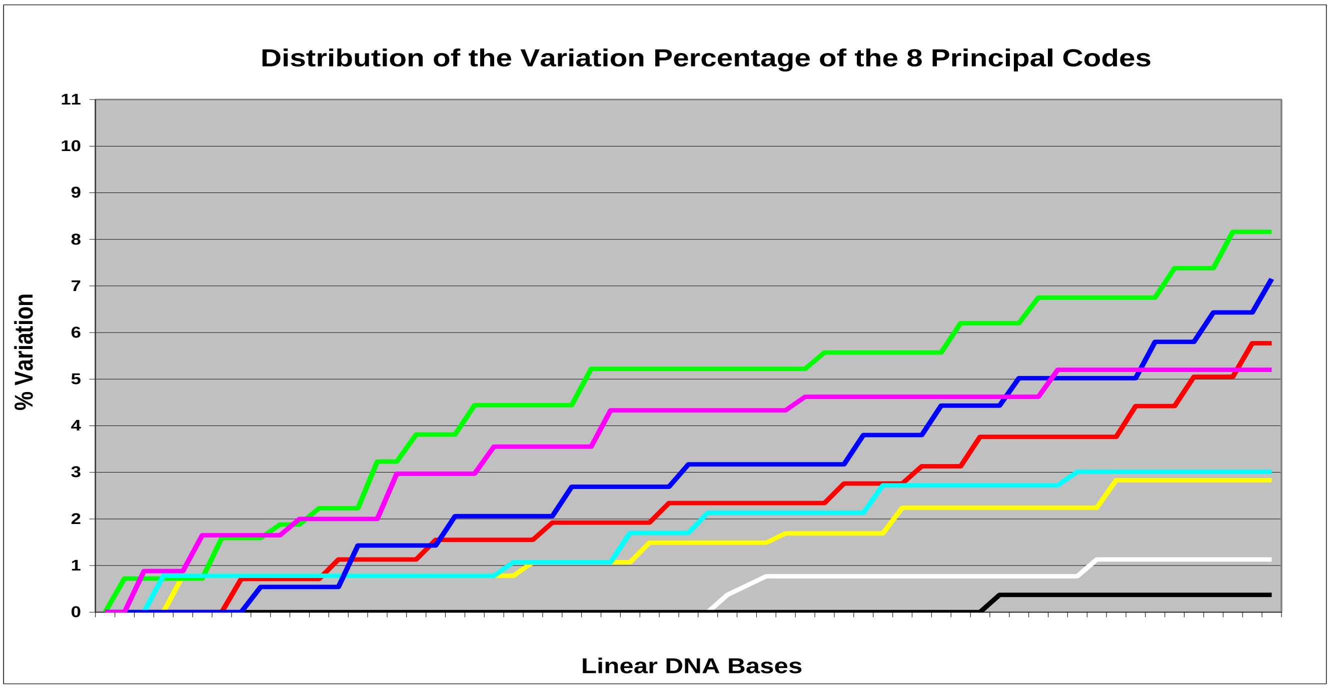
In Pct. 22 (A and B) two charts concerning the **Distribution of the Variation Percentage of the 8 Main Codes** are compared.

The charts in Pct. 22 (A) refers to the **original base sequence** analysed before.



Pct. 22 (A)

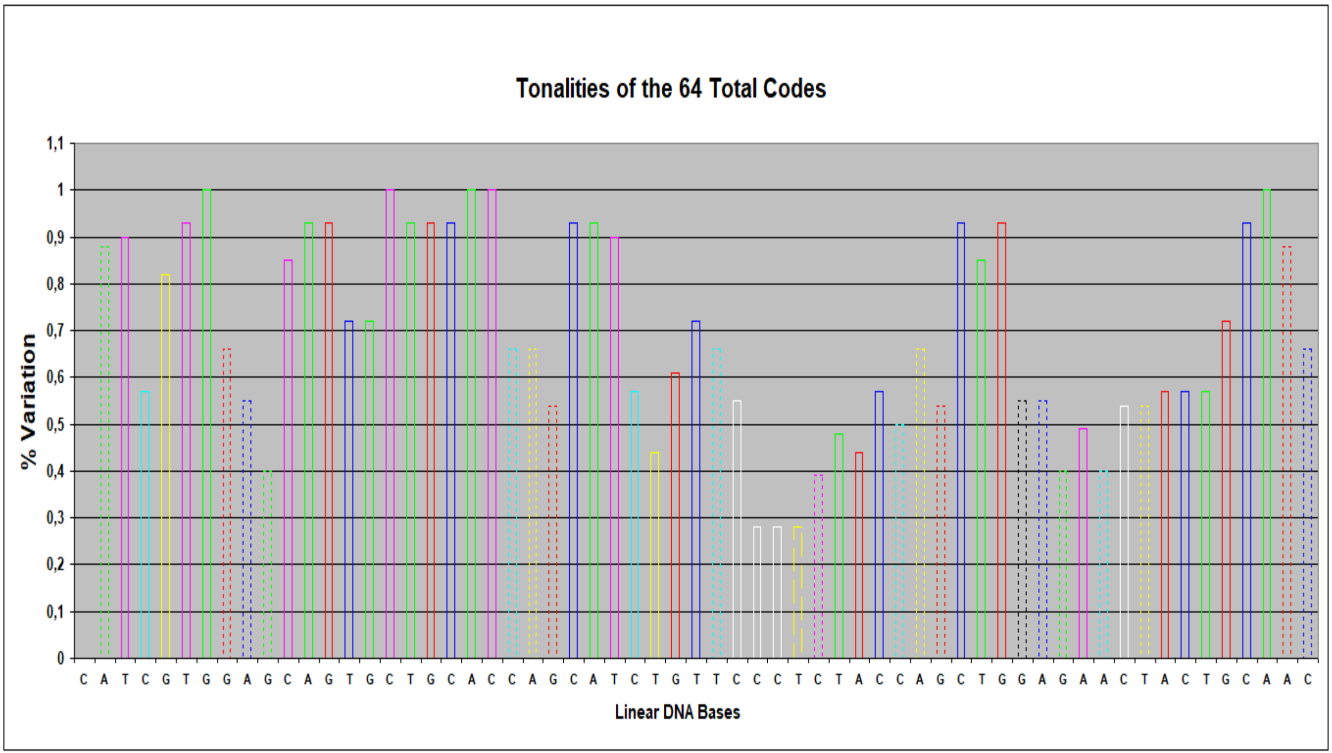
The chart in Pct. 22 (B) refers to the **"new generated sequence"** that originates from the original one.



Pct. 22 (B)

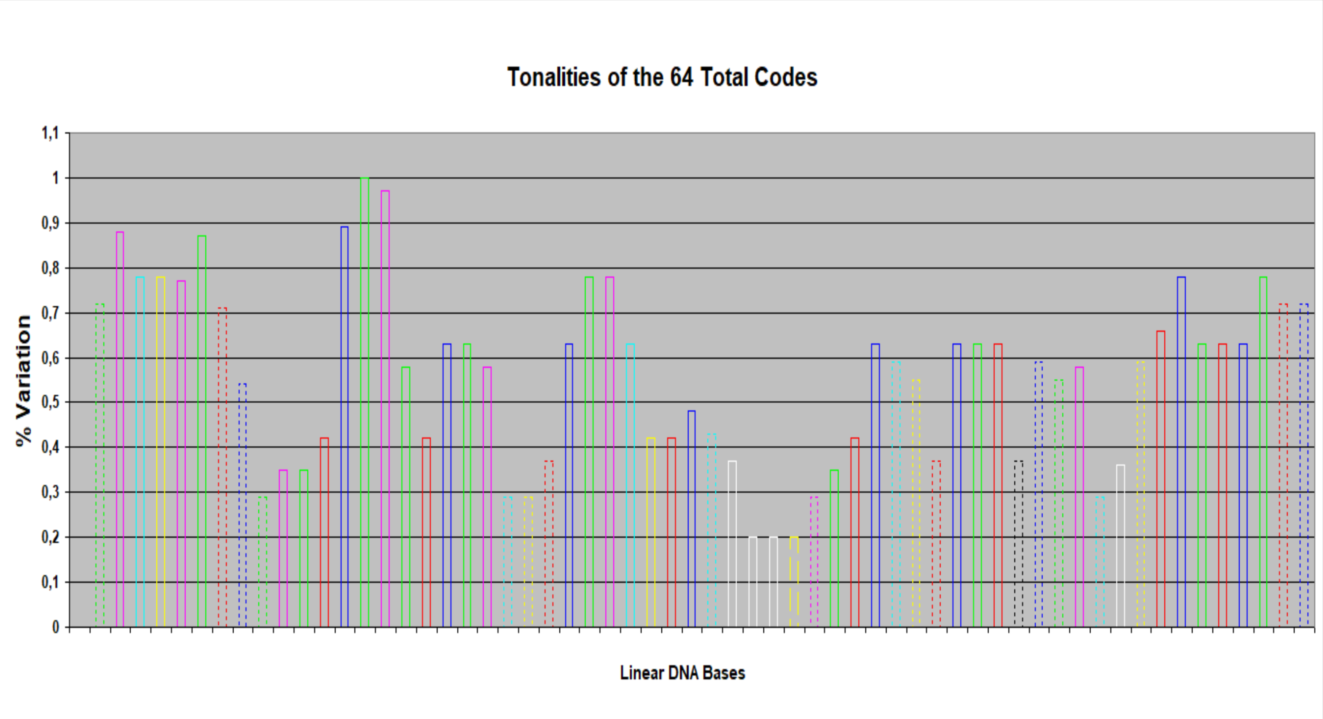
In Pct. 23 (A and B) two charts concerning the single **Tonalities of the 64 Total Codes** are compared.

The chart in Pct. 23 (A) refers to the **original base sequence** analysed before.



Pct. 23 (A)

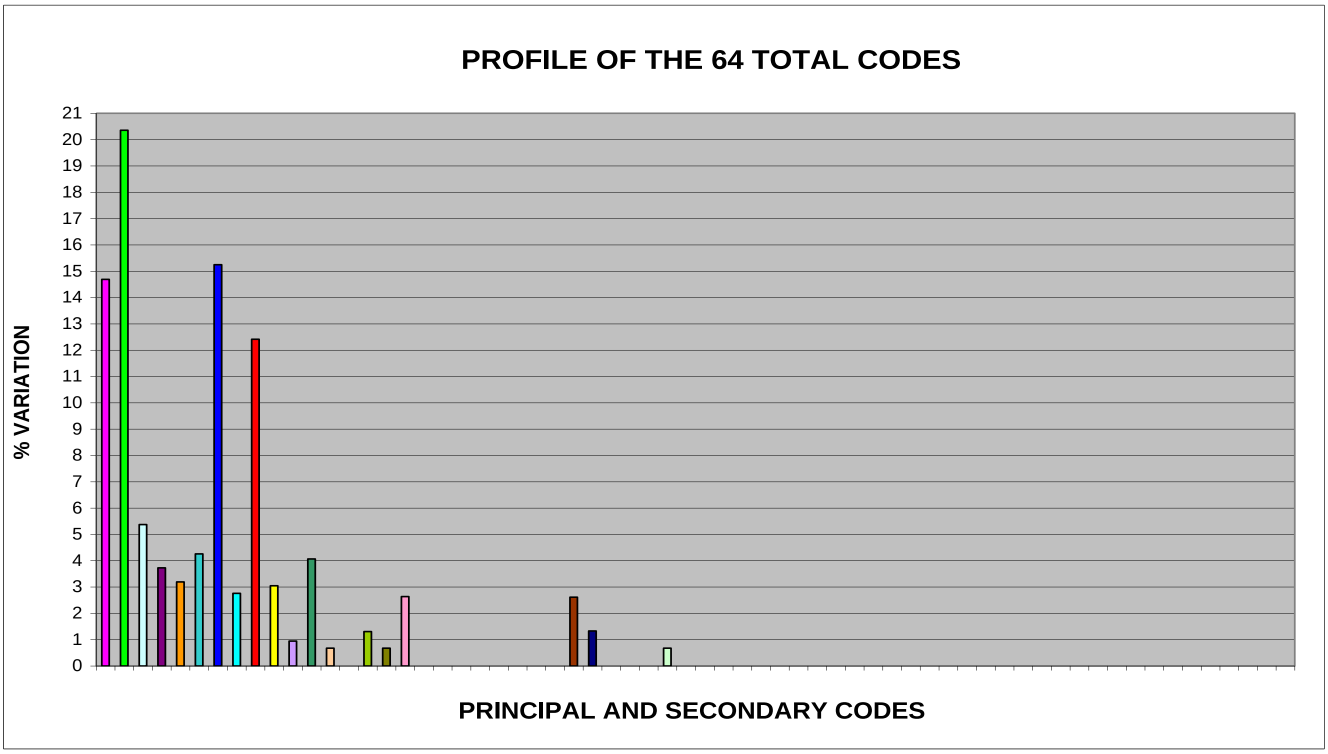
The chart in Pct. 23 (B) refers to the **"new generated sequence"** that originates from the original one.



Pct. 23 (B)

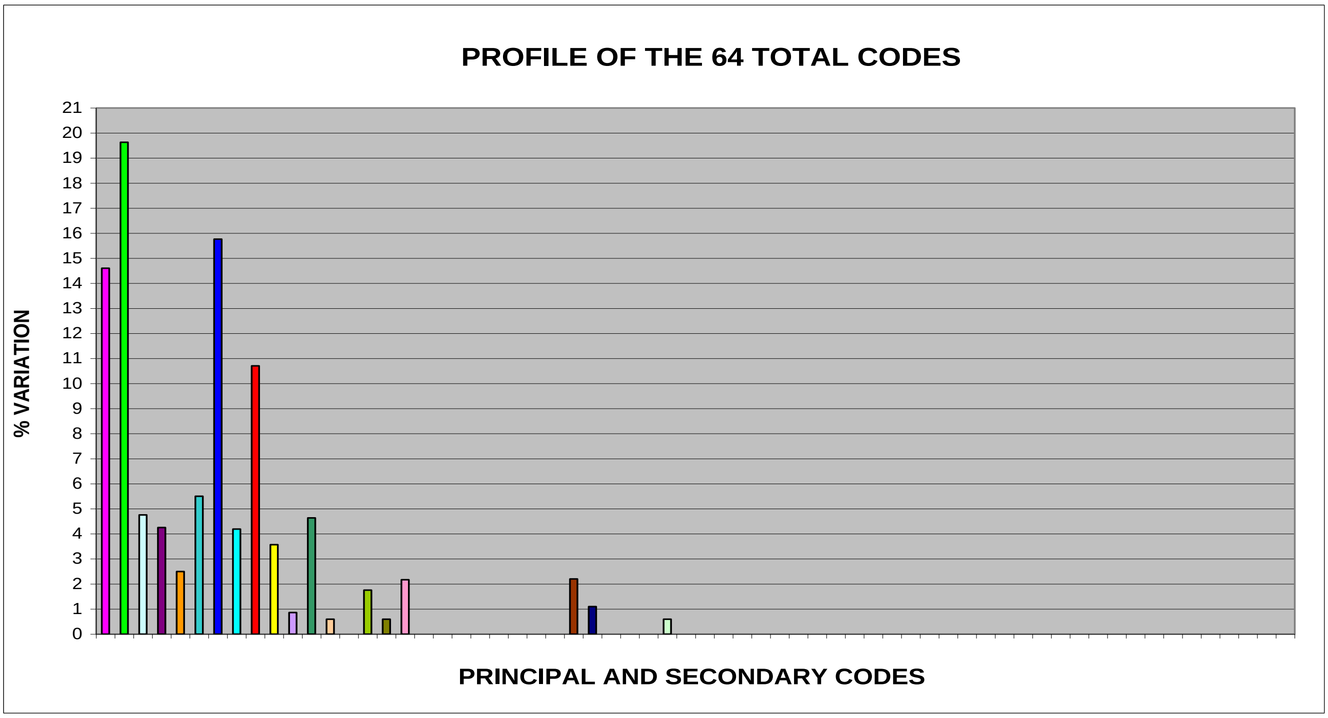
In Pct. 24 (A and B) two charts concerning the **Profile of the 64 Total Codes** are compared.

The chart in Pct. 24 (A) refers to the **original base sequence** analysed before.



Pct. 24 (A)

The chart in Pct. 24 (B) refers to the **"new generated sequence"** originated from the original one.



Pct. 24 (B)

The “non-obvious trend” analysis (obtained through the **T.T.E.S.**) of **Sequence n°6/1 of Insulin Chain A** results in **a comparison among different graphs** that are going to be interpreted in an analogous way to that in which the graphs related to the “non-obvious trend” of the **Sequences** analysed in the previous paragraphs **(n° 1/1, n° 2/1, etc.)** were. In order to avoid repetitions, here, the reader is deferred to the interpretation of the **comparisons among the different graphs** presented in the paragraph 1.2 .

Before concluding the paragraph, it is worth noting that, out of the **63** DNA bases of **Sequence n° 6/1**, ONLY **SEVENTEEN BASES** (the **26,98%**)**,** ARE EQUAL (by type and by position in sequence) TO THOSE OF THE ORIGINAL SEQUENCE (**Insulin Chain A**).

1.13 IMPLICATIONS RELATED TO THE GRAPHIC RESULTS OF THE "NON-OBVIOUS TREND" ANALYSIS OF SEQUENCE n° 6/1 OF INSULIN CHAIN A

The **63** DNA base sequence of the **new generated sequence** (**Sequence n° 6/1**) that arises from the **original** one has been subjected to **BLAST** research.

Please note:

Information about the ***significant alignments*** produced by *BLAST research*, related to **Sequence n° 6/1,** and all the data acquired from *GenBank (3)* will be published in the **Appendix,** after the *General Conclusions.*

Query = NEW GENERATED SEQUENCE (Sequence n° 6/1)

Length = 63

Parameters of BLAST research:

Programme	*Blastn*
Word size	*11*
Expect value	*10*
Hitlist size	*100*
Match/Mismatch scores	*2,-3*
Gapcosts	*5,2*
Low Complexity Filter	*Yes*
Filter string	*L;m;*
Genetic Code	*1*

Please note:

Here, "**the organisms found to be in common**" between the results of BLAST research carried out on **Insulin Chain A** and results of BLAST research carried out on **Sequence n° 6/1**, were highlighted in **Red**.
As well, "**the organisms found to be in common**" between the results of BLAST research carried out on **Insulin Chain A**, results of BLAST research carried out on **Sequence n° 6/1** and results of BLAST research carried out on **at least one** of the *19 generated sequences*, were highlighted in **Green**.
Moreover, "**the denomination of the sequence**" (1/1, 2/1, ... 19/1) of the "**organism found to be in common**" between the results of BLAST research carried out on **Sequence n° 6/1** and results of BLAST research carried out on **at least one** of the *19 new generated sequences*, were highlighted in **Blue**.
Finally, "**the denomination of the sequence**" (1/1, 2/1, ... 19/1) of the "**organism found to be in common**" between the results of BLAST research carried out on **Insulin Chain A** and results of BLAST research carried out on *19 generated sequences*, were highlighted in **Yellow**.

Sequenza n° 6/1

Sequences producing significant alignments:

Selected seq	Description	Max score	Total score	Query cover	E value	Ident	Accession
1 4/1 8/1 LN261386.1	Spirometra erinaceieuropaei genome assembly S_erinaceieuropaei, scaffold SPER_contig0059673	47.3	47.3	84%	0.063	85%	LN261386.1
2 4/1 8/1 LN137640.1	Spirometra erinaceieuropaei genome assembly S_erinaceieuropaei, scaffold SPER_scaffold0126481	47.3	47.3	84%	0.063	85%	LN137640.1
3 LN713262.1	Cucumis melo genomic chromosome, chr_8	45.5	45.5	42%	0.22	96%	LN713262.1
4 LN681876.1	Cucumis melo genomic scaffold, anchoredscaffold00068	45.5	45.5	42%	0.22	96%	LN681876.1
5 LS997567.1	Haemonchus contortus, ISE/inbred ISE, WGS project CAVP01000000 data, chromosome: _X	43.7	43.7	76%	0.77	86%	LS997567.1
6 XR_003088295.1	PREDICTED: Pelodiscus sinensis uncharacterized LOC106731607 (LOC106731607), transcript variant X3, ncRNA	43.7	43.7	76%	0.77	81%	XR_003088295.1
7 XR_003088294.1	PREDICTED: Pelodiscus sinensis uncharacterized LOC106731607 (LOC106731607), transcript variant X2, ncRNA	43.7	43.7	76%	0.77	81%	XR_003088294.1
8 XR_003088293.1	PREDICTED: Pelodiscus sinensis uncharacterized LOC106731607 (LOC106731607), transcript variant X1, ncRNA	43.7	43.7	76%	0.77	81%	XR_003088293.1
9 4/1 LR131937.1	Cottoperca gobio genome assembly, chromosome: 7	42.8	42.8	52%	0.77	88%	LR131937.1
10 XM_020885104.1	PREDICTED: Odocoileus virginianus texanus SEL1L ERAD E3 ligase adaptor subunit (SEL1L), transcript variant X2, mRNA	42.8	42.8	52%	0.77	88%	XM_020885104.1
11 XM_020885103.1	PREDICTED: Odocoileus virginianus texanus SEL1L ERAD E3 ligase adaptor subunit (SEL1L), transcript variant X1, mRNA	42.8	42.8	52%	0.77	88%	XM_020885103.1
12 LN713257.1	Cucumis melo genomic chromosome, chr_3	42.8	42.8	63%	0.77	83%	LN713257.1

Sequences producing significant alignments:

Selected seq	Description	Max score	Total score	Query cover	E value	Ident	Accession
13 LN681823.1	Cucumis melo genomic scaffold, anchoredscaffold00014	42.8	42.8	63%	0.77	83%	LN681823.1
14 XM_027876443.1	PREDICTED: Vombatus ursinus SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily D member 1-like (LOC114053185), mRNA	41.9	41.9	39%	2.7	96%	XM_027876443.1
15 XM_020966077.1	PREDICTED: Phascolarctos cinereus SWI/SNF related, matrix associated, actin dependent regulator of chromatin, …..	41.9	41.9	39%	2.7	96%	XM_020966077.1
16 **14/1** **17/1** CP011900.1	Ovis canadensis canadensis isolate 43U chromosome 15 sequence	41.9	41.9	63%	2.7	83%	CP011900.1
17 LK064741.1	Apteryx australis mantelli genome assembly AptMant0, scaffold scaffold145	41.9	41.9	39%	2.7	96%	LK064741.1
18 **12/1** **17/1** CP025671.1	Ipomoea triloba cultivar NCNSP0323 chromosome 12	41.0	41.0	50%	2.7	88%	CP025671.1
19 **12/1** **17/1** CP025655.1	Ipomoea trifida cultivar NCNSP0306 chromosome 12	41.0	41.0	50%	2.7	88%	CP025655.1
20 **4/1** CP027776.1	Clostridium botulinum strain Mfbjulcb5 chromosome, complete genome	41.0	41.0	63%	2.7	85%	CP027776.1
21 LN713260.1	Cucumis melo genomic chromosome, chr_6	41.0	41.0	53%	2.7	88%	LN713260.1
22 LN681856.1	Cucumis melo genomic scaffold, anchoredscaffold00062	41.0	41.0	53%	2.7	88%	LN681856.1
23 **4/1** **8/1** LK807208.1	Dicrocoelium dendriticum genome assembly D_dendriticum_Leon_v1_0_4, scaffold DDEL_scaffold0367659	41.0	41.0	73%	2.7	83%	LK807208.1
24 LN590718.1	Cyprinus carpio genome assembly common carp genome, scaffold: LG9, chromosome: 9	41.0	41.0	61%	2.7	85%	LN590718.1
25 XR_002800756.1	PREDICTED: Equus caballus uncharacterized LOC102147489 (LOC102147489), transcript variant X2, ncRNA	40.1	40.1	38%	9.4	96%	XR_002800756.1
26 XR_288575.3	PREDICTED: Equus caballus uncharacterized LOC102147489 (LOC102147489), transcript variant X1, ncRNA	40.1	40.1	38%	9.4	96%	XR_288575.3

Sequences producing significant alignments:

Selected seq	Description	Max score	Total score	Query cover	E value	Ident	Accession
27 14/1 XM_013002676.1	PREDICTED: Erythranthe guttatus protein trichome birefringence-like 33 (LOC105977375), mRNA	40.1	40.1	47%	9.4	90%	XM_013002676.1
28 LN713259.1	Cucumis melo genomic chromosome, chr_5	40.1	40.1	60%	9.4	84%	LN713259.1
29 LN681847.1	Cucumis melo genomic scaffold, anchoredscaffold00003	40.1	40.1	60%	9.4	84%	LN681847.1
30 HE803073.1	Cucumis sativus xth23 gene for putative xyloglucan endotransglucosylase/hydrolase, exons 1-5	40.1	40.1	38%	9.4	96%	HE803073.1
31 XM_949121.1	Theileria annulata hypothetical protein partial mRNA	40.1	40.1	49%	9.4	88%	XM_949121.1
32 XM_028321059.1	PREDICTED: Ostrinia furnacalis uncharacterized LOC114364760 (LOC114364760), transcript variant X7, mRNA	39.2	39.2	41%	9.6	92%	XM_028321059.1
33 XM_028321056.1	PREDICTED: Ostrinia furnacalis uncharacterized LOC114364760 (LOC114364760), transcript variant X6, mRNA	39.2	39.2	41%	9.6	92%	XM_028321056.1
34 XM_028321055.1	PREDICTED: Ostrinia furnacalis uncharacterized LOC114364760 (LOC114364760), transcript variant X5, mRNA	39.2	39.2	41%	9.6	92%	XM_028321055.1
35 XM_028321054.1	PREDICTED: Ostrinia furnacalis uncharacterized LOC114364760 (LOC114364760), transcript variant X4, mRNA	39.2	39.2	41%	9.6	92%	XM_028321054.1
36 XM_028321053.1	PREDICTED: Ostrinia furnacalis uncharacterized LOC114364760 (LOC114364760), transcript variant X3, mRNA	39.2	39.2	41%	9.6	92%	XM_028321053.1
37 XM_028321052.1	PREDICTED: Ostrinia furnacalis uncharacterized LOC114364760 (LOC114364760), transcript variant X2, mRNA	39.2	39.2	41%	9.6	92%	XM_028321052.1
38 XM_028321051.1	PREDICTED: Ostrinia furnacalis uncharacterized LOC114364760 (LOC114364760), transcript variant X1, mRNA	39.2	39.2	41%	9.6	92%	XM_028321051.1
39 17/1 CP036230.1	Talaromyces funiculosus strain X33 chromosome 8	39.2	39.2	52%	9.4	88%	CP036230.1
40 8/1 XM_026874233.1	PREDICTED: Trichoplusia ni PDZ and LIM domain protein 3 (LOC113495469), transcript variant X11, mRNA	39.2	39.2	41%	9.4	92%	XM_026874233.1

Sequences producing significant alignments:

Selected seq	Description	Max score	Total score	Query cover	E value	Ident	Accession
41 8/1 XM_026874232.1	PREDICTED: Trichoplusia ni PDZ and LIM domain protein 3 (LOC113495469), transcript variant X10, mRNA	39.2	39.2	41%	9.4	92%	XM_026874232.1
42 8/1 XM_026874231.1	PREDICTED: Trichoplusia ni PDZ and LIM domain protein 3 (LOC113495469), transcript variant X9, mRNA	39.2	39.2	41%	9.4	92%	XM_026874231.1
43 8/1 XM_026874229.1	PREDICTED: Trichoplusia ni PDZ and LIM domain protein 3 (LOC113495469), transcript variant X8, mRNA	39.2	39.2	41%	9.4	92%	XM_026874229.1
44 8/1 XM_026874228.1	PREDICTED: Trichoplusia ni PDZ and LIM domain protein 3 (LOC113495469), transcript variant X7, mRNA	39.2	39.2	41%	9.4	92%	XM_026874228.1
45 8/1 XM_026874227.1	PREDICTED: Trichoplusia ni PDZ and LIM domain protein 3 (LOC113495469), transcript variant X6, mRNA	39.2	39.2	41%	9.4	92%	XM_026874227.1
46 8/1 XM_026874226.1	PREDICTED: Trichoplusia ni PDZ and LIM domain protein 3 (LOC113495469), transcript variant X5, mRNA	39.2	39.2	41%	9.4	92%	XM_026874226.1
47 8/1 XM_026874225.1	PREDICTED: Trichoplusia ni PDZ and LIM domain protein 3 (LOC113495469), transcript variant X4, mRNA	39.2	39.2	41%	9.4	92%	XM_026874225.1
48 8/1 XM_026874224.1	PREDICTED: Trichoplusia ni PDZ and LIM domain protein 3 (LOC113495469), transcript variant X3, mRNA	39.2	39.2	41%	9.4	92%	XM_026874224.1
49 8/1 XM_026874223.1	PREDICTED: Trichoplusia ni PDZ and LIM domain protein 3 (LOC113495469), transcript variant X2, mRNA	39.2	39.2	41%	9.4	92%	XM_026874223.1
50 8/1 XM_026874222.1	PREDICTED: Trichoplusia ni PDZ and LIM domain protein 3 (LOC113495469), transcript variant X1, mRNA	39.2	39.2	41%	9.4	92%	XM_026874222.1
51 XM_026472782.1	PREDICTED: Hyposmocoma kahamanoa PDZ and LIM domain protein 3 (LOC113236620), transcript variant X7, mRNA	39.2	39.2	41%	9.4	92%	XM_026472782.1
52 XM_026472781.1	PREDICTED: Hyposmocoma kahamanoa PDZ and LIM domain protein 3 (LOC113236620), transcript variant X6, mRNA	39.2	39.2	41%	9.4	92%	XM_026472781.1

Sequences producing significant alignments:							
Selected seq	Description	Max score	Total score	Query cover	E value	Ident	Accession
53 XM_026472780.1	PREDICTED: Hyposmocoma kahamanoa PDZ and LIM domain protein 3 (LOC113236620), transcript variant X5, mRNA	39.2	39.2	41%	9.4	92%	XM_026472780.1
54 XM_026472779.1	PREDICTED: Hyposmocoma kahamanoa PDZ and LIM domain protein 3 (LOC113236620), transcript variant X4, mRNA	39.2	39.2	41%	9.4	92%	XM_026472779.1
55 XM_026472778.1	PREDICTED: Hyposmocoma kahamanoa PDZ and LIM domain protein 3 (LOC113236620), transcript variant X3, mRNA	39.2	39.2	41%	9.4	92%	XM_026472778.1
56 XM_026472777.1	PREDICTED: Hyposmocoma kahamanoa PDZ and LIM domain protein 3 (LOC113236620), transcript variant X2, mRNA	39.2	39.2	41%	9.4	92%	XM_026472777.1
57 XM_026472776.1	PREDICTED: Hyposmocoma kahamanoa PDZ and LIM domain protein 3 (LOC113236620), transcript variant X1, mRNA	39.2	39.2	41%	9.4	92%	XM_026472776.1
58 MH430056.1	Cheilosia posjetica voucher MZH:Y1938 large subunit ribosomal RNA gene, partial sequence	39.2	39.2	44%	9.4	93%	MH430056.1
59 XM_022960961.1	PREDICTED: Spodoptera litura PDZ and LIM domain protein 3 (LOC111349736), transcript variant X4, mRNA	39.2	39.2	41%	9.4	92%	XM_022960961.1
60 XM_022960960.1	PREDICTED: Spodoptera litura PDZ and LIM domain protein 3 (LOC111349736), transcript variant X3, mRNA	39.2	39.2	41%	9.4	92%	XM_022960960.1
61 XM_022960959.1	PREDICTED: Spodoptera litura PDZ and LIM domain protein 3 (LOC111349736), transcript variant X2, mRNA	39.2	39.2	41%	9.4	92%	XM_022960959.1
62 XM_022960958.1	PREDICTED: Spodoptera litura PDZ and LIM domain protein 3 (LOC111349736), transcript variant X1, mRNA	39.2	39.2	41%	9.4	92%	XM_022960958.1
63 **17/1** CP017351.1	Talaromyces pinophilus strain 1-95 chromosome 8, complete sequence	39.2	39.2	41%	9.4	92%	CP017351.1

Sequences producing significant alignments:

Selected seq	Description	Max score	Total score	Query cover	E value	Ident	Accession
64 CP017348.1 17/1	Talaromyces pinophilus strain 1-95 chromosome 5, complete sequence	39.2	39.2	41%	9.4	92%	CP017348.1
65 XM_021345372.1	PREDICTED: Helicoverpa armigera PDZ and LIM domain protein 3 (LOC110384210), transcript variant X8, mRNA	39.2	39.2	41%	9.4	92%	XM_021345372.1
66 XM_021345371.1	PREDICTED: Helicoverpa armigera PDZ and LIM domain protein 3 (LOC110384210), transcript variant X7, mRNA	39.2	39.2	41%	9.4	92%	XM_021345371.1
67 XM_021345370.1	PREDICTED: Helicoverpa armigera PDZ and LIM domain protein 3 (LOC110384210), transcript variant X6, mRNA	39.2	39.2	41%	9.4	92%	XM_021345370.1
68 XM_021345369.1	PREDICTED: Helicoverpa armigera PDZ and LIM domain protein 3 (LOC110384210), transcript variant X5, mRNA	39.2	39.2	41%	9.4	92%	XM_021345369.1
69 XM_021345368.1	PREDICTED: Helicoverpa armigera PDZ and LIM domain protein 3 (LOC110384210), transcript variant X4, mRNA	39.2	39.2	41%	9.4	92%	XM_021345368.1
70 XM_021345366.1	PREDICTED: Helicoverpa armigera PDZ and LIM domain protein 3 (LOC110384210), transcript variant X3, mRNA	39.2	39.2	41%	9.4	92%	XM_021345366.1
71 XM_021345365.1	PREDICTED: Helicoverpa armigera PDZ and LIM domain protein 3 (LOC110384210), transcript variant X2, mRNA	39.2	39.2	41%	9.4	92%	XM_021345365.1
72 XM_021345364.1	PREDICTED: Helicoverpa armigera PDZ and LIM domain protein 3 (LOC110384210), transcript variant X1, mRNA	39.2	39.2	41%	9.4	92%	XM_021345364.1
73 XM_020453924.1	PREDICTED: Oncorhynchus kisutch SPRY domain-containing SOCS box protein 3-like (LOC109865612), mRNA	39.2	39.2	57%	9.4	83%	XM_020453924.1
74 CP016087.1 4/1	Clostridium saccharoperbutylacetonicum strain N1-504, complete genome	39.2	39.2	58%	9.4	86%	CP016087.1
75 AP015034.1	Vigna angularis var. angularis DNA, chromosome 1, almost complete sequence, cultivar: Shumari	39.2	39.2	49%	9.4	87%	AP015034.1
76 KM224499.1	Chalcosyrphus valgus voucher MZH:Y1787 28S ribosomal RNA gene, partial sequence	39.2	39.2	44%	9.4	93%	KM224499.1

Sequences producing significant alignments:

Selected seq	Description	Max score	Total score	Query cover	E value	Ident	Accession
77 XM_013332988.1	PREDICTED: Amyelois transitella PDZ and LIM domain protein 2 (LOC106133281), transcript variant X5, mRNA	39.2	39.2	41%	9.4	92%	XM_013332988.1
78 XM_013332980.1	PREDICTED: Amyelois transitella PDZ and LIM domain protein 2 (LOC106133281), transcript variant X4, mRNA	39.2	39.2	41%	9.4	92%	XM_013332980.1
79 XM_013332971.1	PREDICTED: Amyelois transitella PDZ and LIM domain protein 2 (LOC106133281), transcript variant X3, mRNA	39.2	39.2	41%	9.4	92%	XM_013332971.1
80 XM_013332964.1	PREDICTED: Amyelois transitella PDZ and LIM domain protein 2 (LOC106133281), transcript variant X2, mRNA	39.2	39.2	41%	9.4	92%	XM_013332964.1
81 XM_013332955.1	PREDICTED: Amyelois transitella PDZ and LIM domain protein 2 (LOC106133281), transcript variant X1, mRNA	39.2	39.2	41%	9.4	92%	XM_013332955.1
82 LN713265.1	Cucumis melo genomic chromosome, chr_11	39.2	39.2	33%	9.4	100%	LN713265.1
83 LN681912.1	Cucumis melo genomic scaffold, anchoredscaffold00059	39.2	39.2	33%	9.4	100%	LN681912.1
84 **10/1** LM528888.1	Strongyloides papillosus genome assembly S_papillosus_LIN, scaffold SPAL_contig0003209	39.2	39.2	44%	9.4	93%	LM528888.1
85 **17/1** XM_009029397.1	Helobdella robusta hypothetical protein partial mRNA	39.2	39.2	33%	9.4	100%	XM_009029397.1
86 XM_008289952.1	PREDICTED: Stegastes partitus transgelin (tagln), transcript variant X2, mRNA	39.2	39.2	33%	9.4	100%	XM_008289952.1
87 XM_008289951.1	PREDICTED: Stegastes partitus transgelin (tagln), transcript variant X1, mRNA	39.2	39.2	33%	9.4	100%	XM_008289951.1
88 **4/1** CP004121.1	Clostridium saccharoperbutylacetonicum N1-4(HMT), complete genome	39.2	39.2	58%	9.4	86%	CP004121.1
89 DQ401783.1	Hadromyia crawfordi voucher ZMH_DNA_voucher_Y280 28S ribosomal RNA gene, partial sequence	39.2	39.2	44%	9.4	93%	DQ401783.1
90 DQ401780.1	Cacoceria willistoni voucher ZMH_DNA_voucher_Y256 28S ribosomal RNA gene, partial sequence	39.2	39.2	44%	9.4	93%	DQ401780.1

Sequences producing significant alignments:

Selected seq	Description	Max score	Total score	Query cover	E value	Ident	Accession
91 DQ401778.1	Hadromyia crawfordi voucher ZMH_DNA_voucher_Y197 28S ribosomal RNA gene, partial sequence	39.2	39.2	44%	9.4	93%	DQ401778.1
92 DQ401775.1	Chalcosyrphus piger voucher ZMH_DNA_voucher_Y198 28S ribosomal RNA gene, partial sequence	39.2	39.2	44%	9.4	93%	DQ401775.1
93 DQ401773.1	Cacoceria cressoni voucher ZMH_DNA_voucher_Y122 28S ribosomal RNA gene, partial sequence	39.2	39.2	44%	9.4	93%	DQ401773.1
94 DQ401768.1	Chalcosyrphus tuberculifemur voucher ZMH_DNA_voucher_Y165 28S ribosomal RNA gene, partial sequence	39.2	39.2	44%	9.4	93%	DQ401768.1
95 DQ401765.1	Chalcosyrphus rufipes voucher ZMH_DNA_voucher_Y161 28S ribosomal RNA gene, partial sequence	39.2	39.2	44%	9.4	93%	DQ401765.1
96 DQ401764.1	Chalcosyrphus nitidus voucher ZMH_DNA_voucher_Y90 28S ribosomal RNA gene, partial sequence	39.2	39.2	44%	9.4	93%	DQ401764.1
97 DQ401756.1	Chalcosyrphus libo voucher ZMH_DNA_voucher_Y86 28S ribosomal RNA gene, partial sequence	39.2	39.2	44%	9.4	93%	DQ401756.1
98 DQ401755.1	Chalcosyrphus valgus voucher ZMH_DNA_voucher_Y62 28S ribosomal RNA gene, partial sequence	39.2	39.2	44%	9.4	93%	DQ401755.1
99 **17/1** CR925750.13	Zebrafish DNA sequence from clone CH211-242F23 in linkage group 10, complete sequence	39.2	39.2	66%	9.4	85%	CR925750.13
100 AC117702.10	Mus musculus chromosome 10, clone RP23-464I2, complete sequence	39.2	39.2	71%	9.4	82%	AC117702.10
101 AC161283.2	Pan troglodytes BAC clone CH251-354N8 from chromosome 7, complete sequence	39.2	39.2	41%	9.4	92%	AC161283.2
102 AY727421.1	Trillium ovatum trnC-rpoB intergenic spacer, partial sequence; chloroplast	39.2	39.2	49%	9.4	87%	AY727421.1

Comparison between the alignments of Sequence 6/1 and Sequence of Insulin Chain A according to the "Species of Common Organisms":

Alignments Sequence 6/1	**Description**	**Alignments Sequence Insulin Chain A**	**Description**
6 Select seq XR_003088295.1	PREDICTED: Pelodiscus sinensis uncharacterized LOC106731607 (LOC106731607), transcript variant X3, ncRNA	Select seq XM_006134914.3	PREDICTED: Pelodiscus sinensis insulin (INS), mRNA
7 Select seq XR_003088294.1	PREDICTED: Pelodiscus sinensis uncharacterized LOC106731607 (LOC106731607), transcript variant X2, ncRNA		
8 Select seq XR_003088293.1	PREDICTED: Pelodiscus sinensis uncharacterized LOC106731607 (LOC106731607), transcript variant X1, ncRNA		
9 Select seq LR131937.1 **4/1**	Cottoperca gobio genome assembly, chromosome: 7	Select seq LR131921.1 **4/1 7/1 16/1** **18/1 19/1**	Cottoperca gobio genome assembly, chromosome: 14
		Select seq LR131917.1 **4/1 7/1 16/1** **18/1 19/1**	Cottoperca gobio genome assembly, chromosome: 10
10 Select seq XM_020885104.1	PREDICTED: Odocoileus virginianus texanus SEL1L ERAD E3 ligase adaptor subunit (SEL1L), transcript variant X2, mRNA	Select seq XM_020883287.1	PREDICTED: Odocoileus virginianus texanus insulin (LOC110130982), transcript variant X2, mRNA
11 Select seq XM_020885103.1	PREDICTED: Odocoileus virginianus texanus SEL1L ERAD E3 ligase adaptor subunit (SEL1L), transcript variant X1, mRNA	Select seq XM_020883286.1	PREDICTED: Odocoileus virginianus texanus insulin (LOC110130982), transcript variant X1, mRNA
		Select seq XR_002314985.1	PREDICTED: Odocoileus virginianus texanus uncharacterized LOC110141110 (LOC110141110), transcript variant X3, ncRNA

Comparison between the alignments of Sequence 6/1 and Sequence of Insulin Chain A according to the “Species of Common Organisms”:

Alignments Sequence 6/1	**Description**	**Alignments Sequence Insulin Chain A**	**Description**
14 Select seq XM_027876443.1	PREDICTED: Vombatus ursinus SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily D member 1-like (LOC114053185), mRNA	Select seq XM_027868681.1	PREDICTED: Vombatus ursinus insulin (INS), mRNA
15 Select seq XM_020966077.1	PREDICTED: Phascolarctos cinereus SWI/SNF related, matrix associated, actin dependent regulator of chromatin, …..	Select seq XM_020970881.1	PREDICTED: Phascolarctos cinereus insulin (INS), mRNA
16 Select seq CP011900.1 **14/1** **17/1**	Ovis canadensis canadensis isolate 43U chromosome 15 sequence	Select seq XM_027959829.1 **14/1** **17/1**	PREDICTED: Ovis aries insulin (INS), mRNA
		Select seq AH005355.3 **14/1** **17/1**	Ovis aries insulin and insulin-like growth factor II (IGF-II) genes, complete cds
		Select seq XM_012167536.2 **14/1** **17/1**	PREDICTED: Ovis aries musimon insulin (LOC105613195), mRNA
17 Select seq LK064741.1	Apteryx australis mantelli genome assembly AptMant0, scaffold scaffold145	Select seq XM_026079009.1 **5/1** **17/1**	PREDICTED: Apteryx rowi insulin (INS), mRNA
		Select seq XM_013957848.1 **5/1** **17/1**	PREDICTED: Apteryx australis mantelli insulin (INS), mRNA
		Select seq LK064676.1 **5/1** **17/1**	Apteryx australis mantelli genome assembly AptMant0, scaffold scaffold77
24 Select seq LN590718.1	Cyprinus carpio genome assembly common carp genome, scaffold: LG9, chromosome: 9	Select seq XM_019069183.1 **4/1** **17/1**	PREDICTED: Cyprinus carpio insulin-like (LOC109051698), mRNA

Comparison between the alignments of Sequence 6/1 and Sequence of Insulin Chain A according to the “Species of Common Organisms”:

Alignments Sequence 6/1	**Description**	**Alignments Sequence Insulin Chain A**	**Description**
		Select seq LN590733.1 **4/1** **17/1**	Cyprinus carpio genome assembly common carp genome, scaffold 000000053
25 Select seq XR_002800756.1	PREDICTED: Equus caballus uncharacterized LOC102147489 (LOC102147489), transcript variant X2, ncRNA	Select seq XM_023654706.1	PREDICTED: Equus caballus insulin (INS), mRNA
26 Select seq XR_288575.3	PREDICTED: Equus caballus uncharacterized LOC102147489 (LOC102147489), transcript variant X1, ncRNA		
73 Select seq XM_020453924.1	PREDICTED: Oncorhynchus kisutch SPRY domain-containing SOCS box protein 3-like (LOC109865612), mRNA	Select seq XM_024402922.1 **10/1** **17/1**	PREDICTED: Oncorhynchus tshawytscha insulin-like (LOC112234674), mRNA
		Select seq XM_024402921.1 **10/1** **17/1**	PREDICTED: Oncorhynchus tshawytscha insulin-like (LOC112234673), mRNA
		Select seq XM_020464884.1 **10/1** **17/1**	PREDICTED: Oncorhynchus kisutch insulin-like (LOC109873252), mRNA
		Select seq NM_001124670.1 **10/1** **17/1**	Oncorhynchus mykiss preproinsulin 2 (LOC100136703), mRNA
		Select seq L11712.1 **10/1** **17/1**	Oncorhynchus keta insulin gene, complete cds
86 Select seq XM_008289952.1	PREDICTED: Stegastes partitus transgelin (tagln), transcript variant X2, mRNA	Select seq XM_008298714.1	PREDICTED: Stegastes partitus insulin (LOC103369873), mRNA
87 Select seq XM_008289951.1	PREDICTED: Stegastes partitus transgelin (tagln), transcript variant X1, mRNA	Select seq XM_008302867.1	PREDICTED: Stegastes partitus circularly permutated Ras protein 1-like (LOC103373066), transcript variant X2, mRNA

Comparison between the alignments of Sequence 6/1 and Sequence of Insulin Chain A according to the “Species of Common Organisms”:

Alignments Sequence 6/1	**Description**	**Alignments Sequence Insulin Chain A**	**Description**
		Select seq XM_008302866.1	PREDICTED: Stegastes partitus circularly permutated Ras protein 1-like (LOC103373066), transcript variant X1, mRNA
		Select seq XM_008278129.1	PREDICTED: Stegastes partitus insulin-like (LOC103354683), mRNA
100 Select seq AC117702.10	Mus musculus chromosome 10, clone RP23-464I2, complete sequence	Select seq XM_021152514.1 **1/1 8/1 10/1** **13/1 17/1 18/1**	PREDICTED: Mus caroli insulin-1 (LOC110286053), mRNA
		Select seq DQ250565.1 **1/1 8/1 10/1** **13/1 17/1 18/1**	Mus caroli preproinsulin 1 (Ins1) gene, complete cds
		Select seq XM_021215010.1 **1/1 8/1 10/1** **13/1 17/1 18/1**	PREDICTED: Mus pahari insulin-1 (LOC110333420), mRNA
		Select seq NM_008386.4 **1/1 8/1 10/1** **13/1 17/1 18/1**	Mus musculus insulin I (Ins1), mRNA
		Select seq BC145868.1 **1/1 8/1 10/1** **13/1 17/1 18/1**	Mus musculus insulin I, mRNA (cDNA clone MGC:175755 IMAGE:40131171), complete cds
		Select seq DQ479923.1 **1/1 8/1 10/1** **13/1 17/1 18/1**	Mus musculus strain BTBR T+ tf/J insulin 1 precursor, gene, complete cds
		Select seq AC163452.12 **1/1 8/1 10/1** **13/1 17/1 18/1**	Mus musculus chromosome 19, clone RP23-405C7, complete sequence
		Select seq AC136710.8 **1/1 8/1 10/1** **13/1 17/1 18/1**	Mus musculus chromosome 19, clone RP23-35B13, complete sequence

Comparison between the alignments of Sequence 6/1 and Sequence of Insulin Chain A according to the "Species of Common Organisms":

Alignments Sequence 6/1	Description	Alignments Sequence Insulin Chain A	Description
		Select seq AC140320.2 **1/1 8/1 10/1** **13/1 17/1 18/1**	Mus musculus BAC clone RP23-401C13 from chromosome 19, complete sequence
		Select seq BC098468.1 **1/1 8/1 10/1** **13/1 17/1 18/1**	Mus musculus insulin I, mRNA (cDNA clone MGC:107382 IMAGE:6432765), complete cds
		Select seq AK148541.1 **1/1 8/1 10/1** **13/1 17/1 18/1**	Mus musculus adult pancreas islet cells cDNA, RIKEN full-length enriched library, clone:C820020F18 product:insulin I, full insert sequence
		Select seq AK007345.1 **1/1 8/1 10/1** **13/1 17/1 18/1**	Mus musculus 10 day old male pancreas cDNA, RIKEN full-length enriched library, clone:1810005L03 product:INSULIN 1 PRECURSOR, full insert sequence
		Select seq XM_021168754.1 **1/1 8/1 10/1** **13/1 17/1 18/1**	PREDICTED: Mus caroli insulin-2 (LOC110299132), transcript variant X2, mRNA
		Select seq XM_021168753.1 **1/1 8/1 10/1** **13/1 17/1 18/1**	PREDICTED: Mus caroli insulin-2 (LOC110299132), transcript variant X1, mRNA
		Select seq NM_001185084.2 **1/1 8/1 10/1** **13/1 17/1 18/1**	Mus musculus insulin II (Ins2), transcript variant 3, mRNA
		Select seq NM_001185083.2 **1/1 8/1 10/1** **13/1 17/1 18/1**	Mus musculus insulin II (Ins2), transcript variant 1, mRNA
		Select seq NM_008387.5 **1/1 8/1 10/1** **13/1 17/1 18/1**	Mus musculus insulin II (Ins2), transcript variant 2, mRNA
		Select seq JN959239.1 **1/1 8/1 10/1** **13/1 17/1 18/1**	Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Ins2:tm1a(EUCOMM)Wtsi; transgenic

Comparison between the alignments of Sequence 6/1 and Sequence of Insulin Chain A according to the "Species of Common Organisms":

Alignments Sequence 6/1	Description	Alignments Sequence Insulin Chain A	Description
		Select seq JN951270.1 **1/1 8/1 10/1** **13/1 17/1 18/1**	Mus musculus targeted non-conditional, lacZ-tagged mutant allele Ins2:tm1e(EUCOMM)Wtsi; transgenic
		Select seq BC145554.1 **1/1 8/1 10/1** **13/1 17/1 18/1**	Mus musculus insulin II, mRNA (cDNA clone MGC:179126 IMAGE:9054118), complete cds
		Select seq BC099934.1 **1/1 8/1 10/1** **13/1 17/1 18/1**	Mus musculus insulin II, mRNA (cDNA clone MGC:107381 IMAGE:6432976), complete cds
		Select seq BC132650.1 **1/1 8/1 10/1** **13/1 17/1 18/1**	Mus musculus insulin II, mRNA (cDNA clone MGC:164281 IMAGE:40130927), complete cds
		Select seq DQ250569.1 **1/1 8/1 10/1** **13/1 17/1 18/1**	Mus caroli preproinsulin 2 (Ins2) gene, complete cds
		Select seq AK007612.1 **1/1 8/1 10/1** **13/1 17/1 18/1**	Mus musculus 10 day old male pancreas cDNA, RIKEN full-length enriched library, clone:1810027C14 product:INSULIN 2 PRECURSOR, full insert sequence
		Select seq AK007482.1 **1/1 8/1 10/1** **13/1 17/1 18/1**	Mus musculus 10 day old male pancreas cDNA, RIKEN full-length enriched library, clone:1810013J24 product:INSULIN 1 PRECURSOR, full insert sequence
		Select seq BC066208.1 **1/1 8/1 10/1** **13/1 17/1 18/1**	Mus musculus insulin II, mRNA (cDNA clone IMAGE:6436276)
		Select seq AC012382.14 **1/1 8/1 10/1** **13/1 17/1 18/1**	Mus musculus chromosome 7, clone RP23-92L23, complete sequence
		Select seq AY899305.1 **1/1 8/1 10/1** **13/1 17/1 18/1**	Mus musculus proinsulin mRNA, complete cds, alternatively spliced

Comparison between the alignments of Sequence 6/1 and Sequence of Insulin Chain A according to the "Species of Common Organisms":

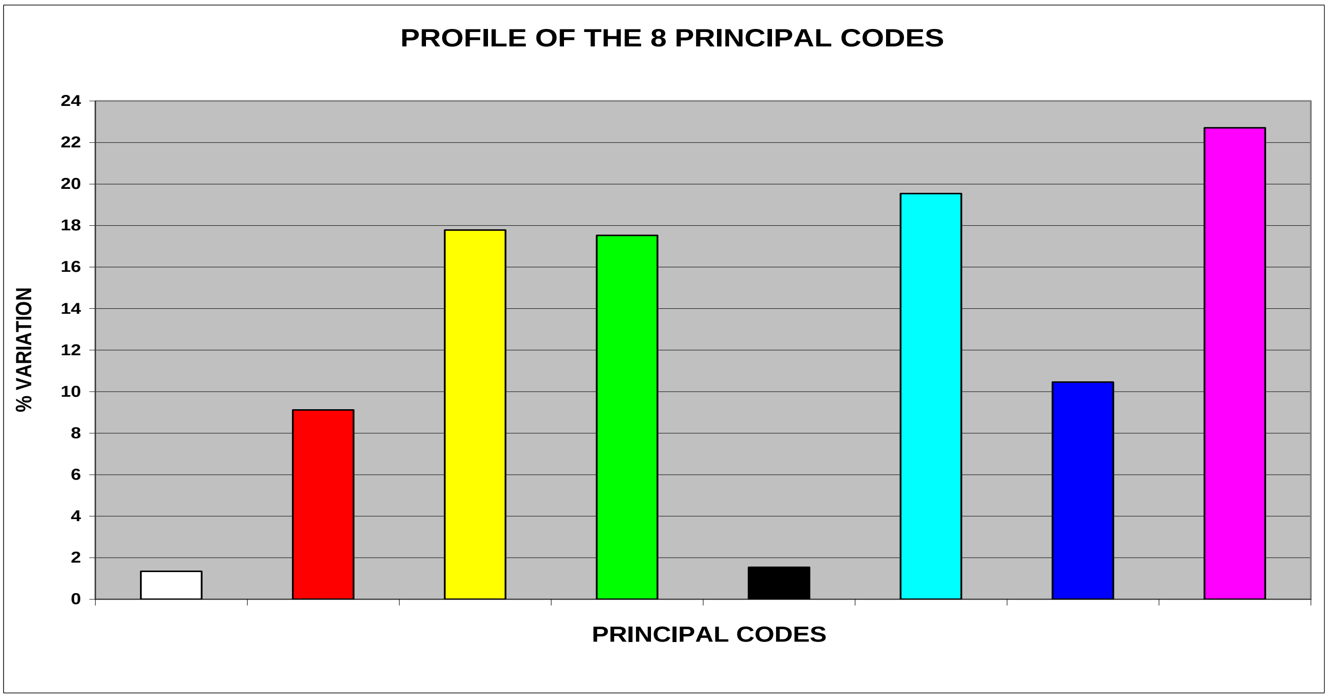
Alignments Sequence 6/1	Description	Alignments Sequence Insulin Chain A	Description
		Select seq AC013548.13 **1/1 8/1 10/1** **13/1 17/1 18/1**	Mus musculus chromosome 7, clone RP23-209O22, complete sequence
		Select seq AP003182.2 **1/1 8/1 10/1** **13/1 17/1 18/1**	Mus musculus genomic DNA, chromosome 7 clone:B189M11, complete sequences
		Select seq GQ915612.1 **1/1 8/1 10/1** **13/1 17/1 18/1**	Mus musculus insulin-2 precursor (Ins2) mRNA, partial cds, alternatively spliced
		Select seq XM_021204833.1 **1/1 8/1 10/1** **13/1 17/1 18/1**	PREDICTED: Mus pahari insulin-2 (LOC110326410), transcript variant X2, mRNA
		Select seq XM_021204825.1 **1/1 8/1 10/1** **13/1 17/1 18/1**	PREDICTED: Mus pahari insulin-2 (LOC110326410), transcript variant X1, mRNA
101 Select seq AC161283.2	Pan troglodytes BAC clone CH251-354N8 from chromosome 7, complete sequence	Select seq AH011814.2	Pan troglodytes tyrosine hydroxylase (TH) gene, partial cds; and insulin precursor (INS) gene, complete cds
		Select seq XM_016919751.1	PREDICTED: Pan troglodytes insulin (INS), transcript variant X1, mRNA
		Select seq NM_001008996.2	Pan troglodytes insulin (INS), mRNA
		Select seq X61089.1	P.troglodytes gene for preproinsulin

Analysis of
Sequence n° 7/1
of Insulin Chain A

1.14 GRAPHIC RESULTS OF THE “NON-OBVIOUS TREND” ANALYSIS OF SEQUENCE n° 7/1 OF INSULIN CHAIN A

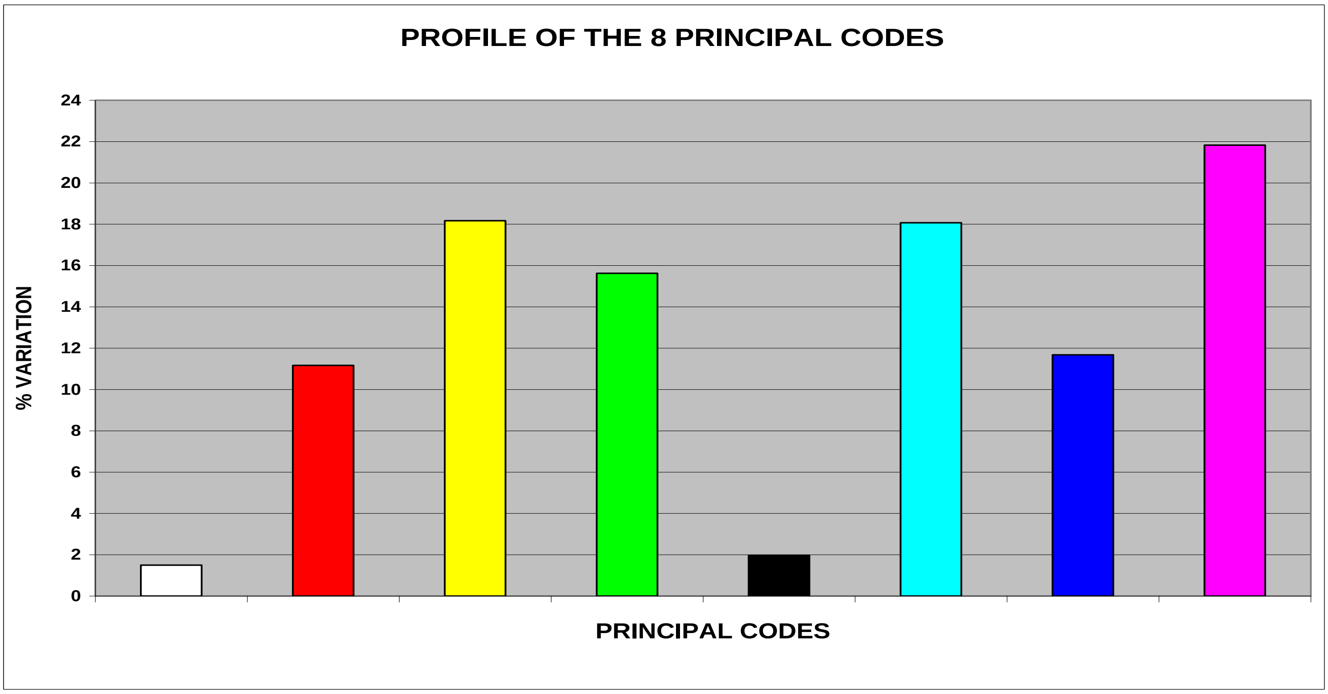
In the Pct. 25 (A e B) two **8 Principal Codes Profiles** are compared.

The chart in Pct. 25 (A) refers to the **original base sequence** of **Insulin Chain A**.



Pct. 25 (A)

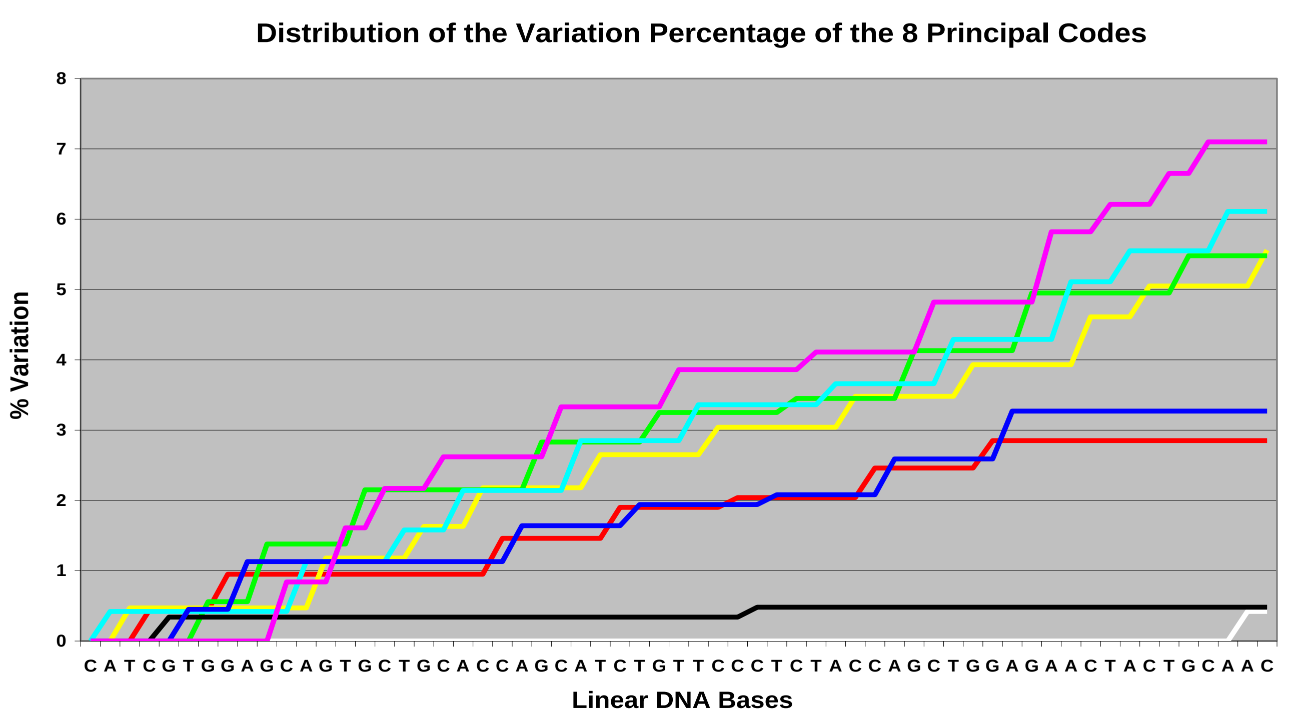
The chart in Pct. 25 (B) refers to the **seventh “new generated sequence”** (**Sequence n° 7/1**) that originates from the original one.



Pct. 25 (B)

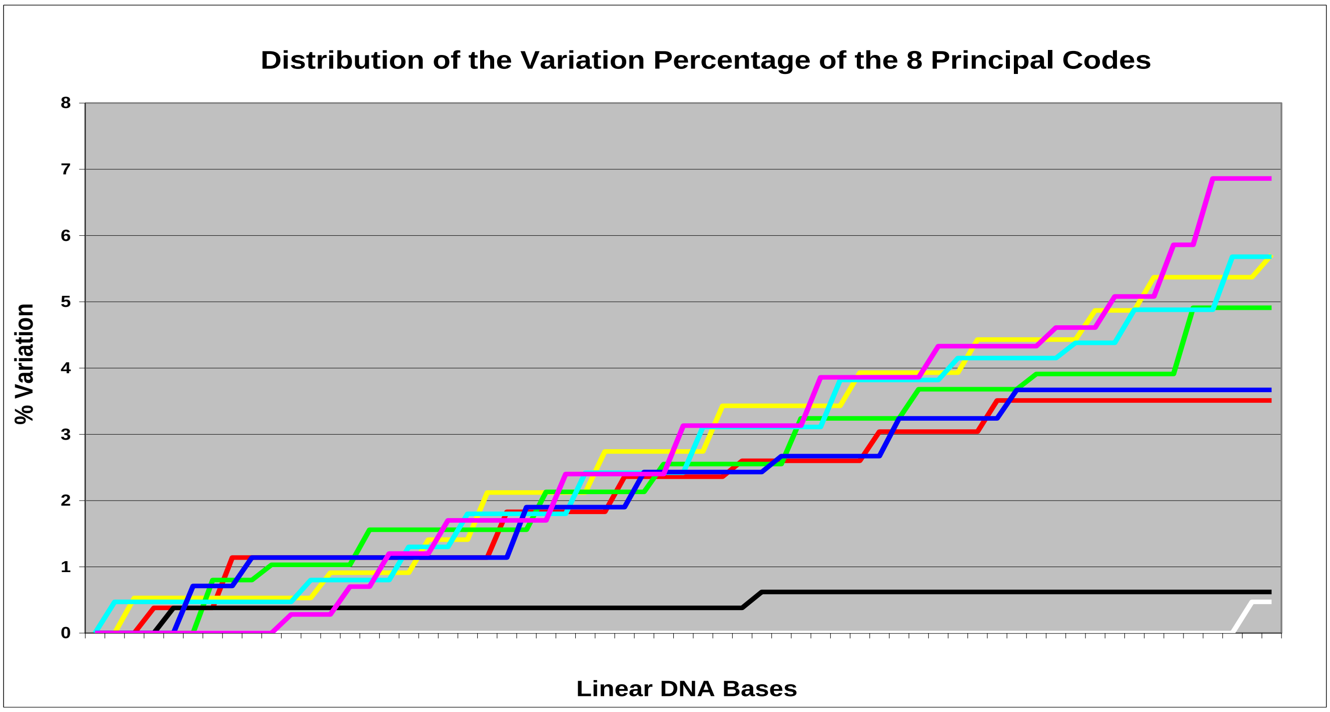
In Pct. 26 (A and B) two charts concerning the **Distribution of the Variation Percentage of the 8 Main Codes** are compared.

The charts in Pct. 26 (A) refers to the **original base sequence** analysed before.



Pct. 26 (A)

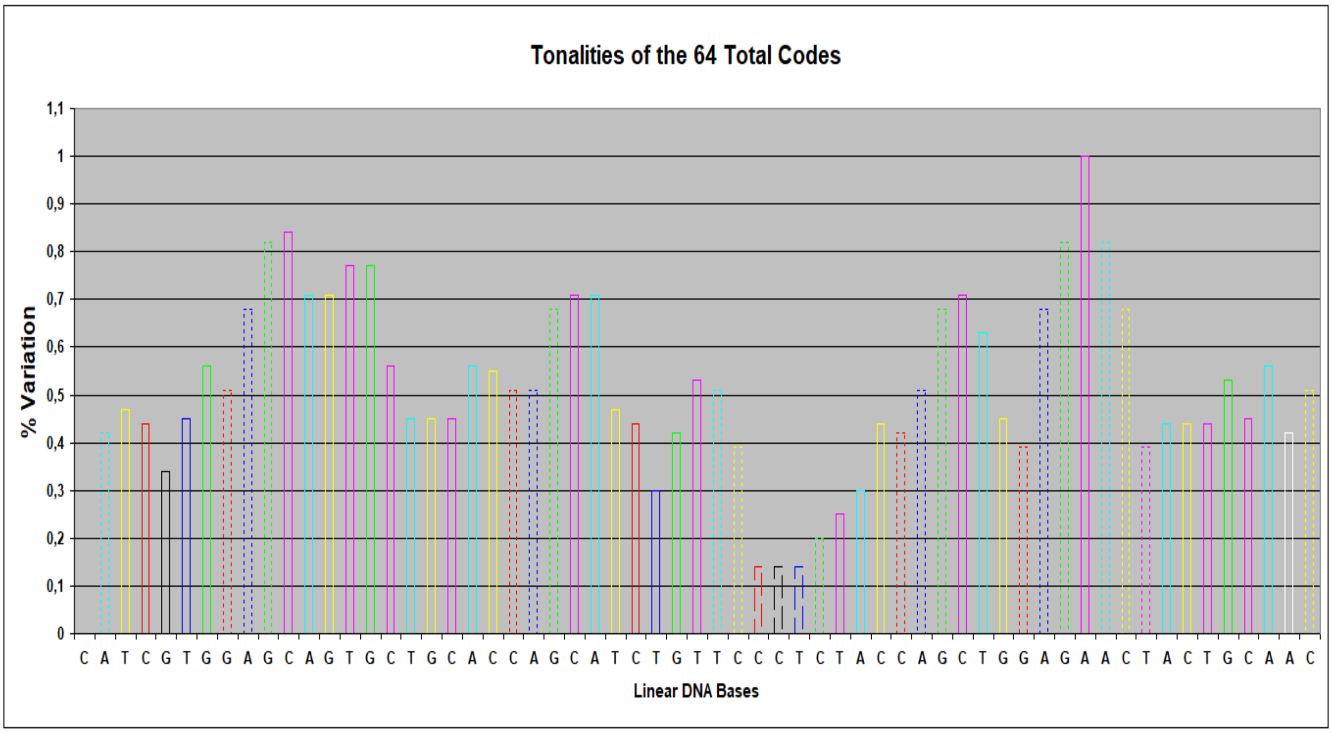
The chart in Pct. 26 (B) refers to the **"new generated sequence"** that originates from the original one.



Pct. 26 (B)

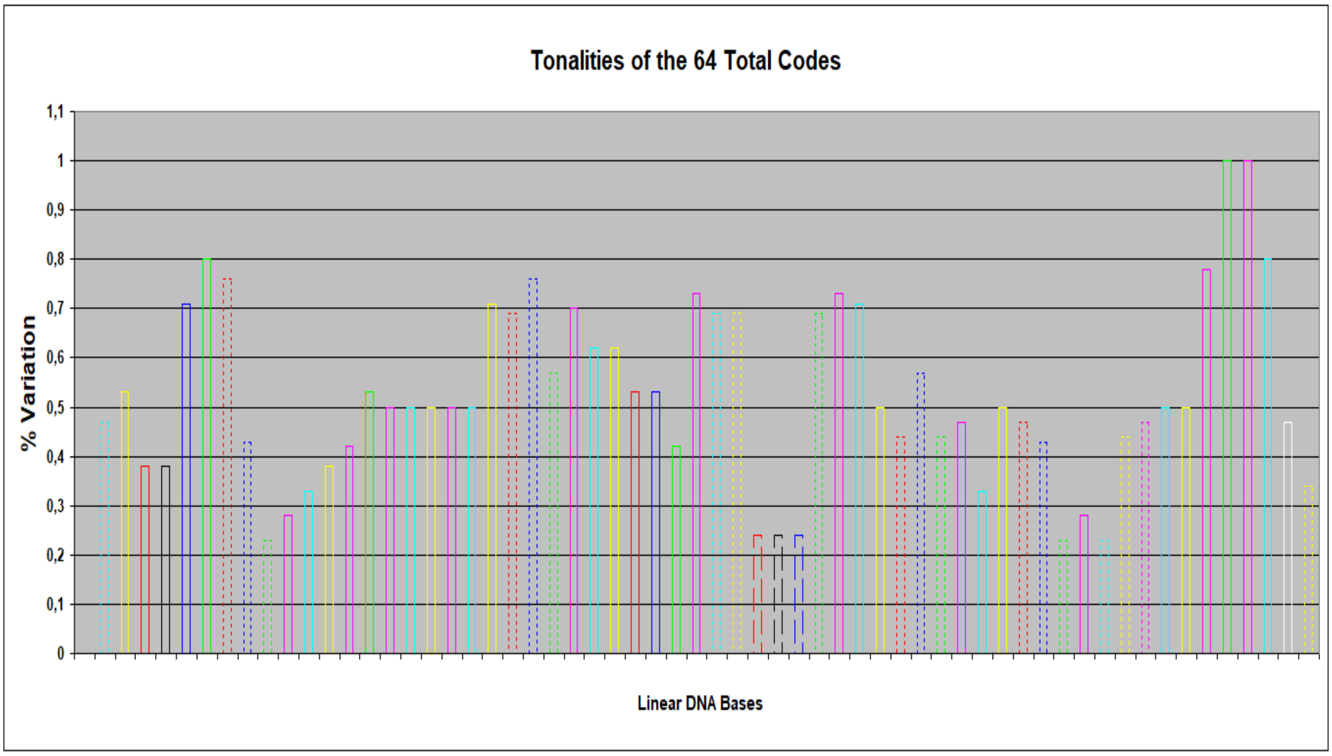
In Pct. 27 (A and B) two charts concerning the single **Tonalities of the 64 Total Codes** are compared.

The chart in Pct. 27 (A) refers to the **original base sequence** analysed before.



Pct. 27 (A)

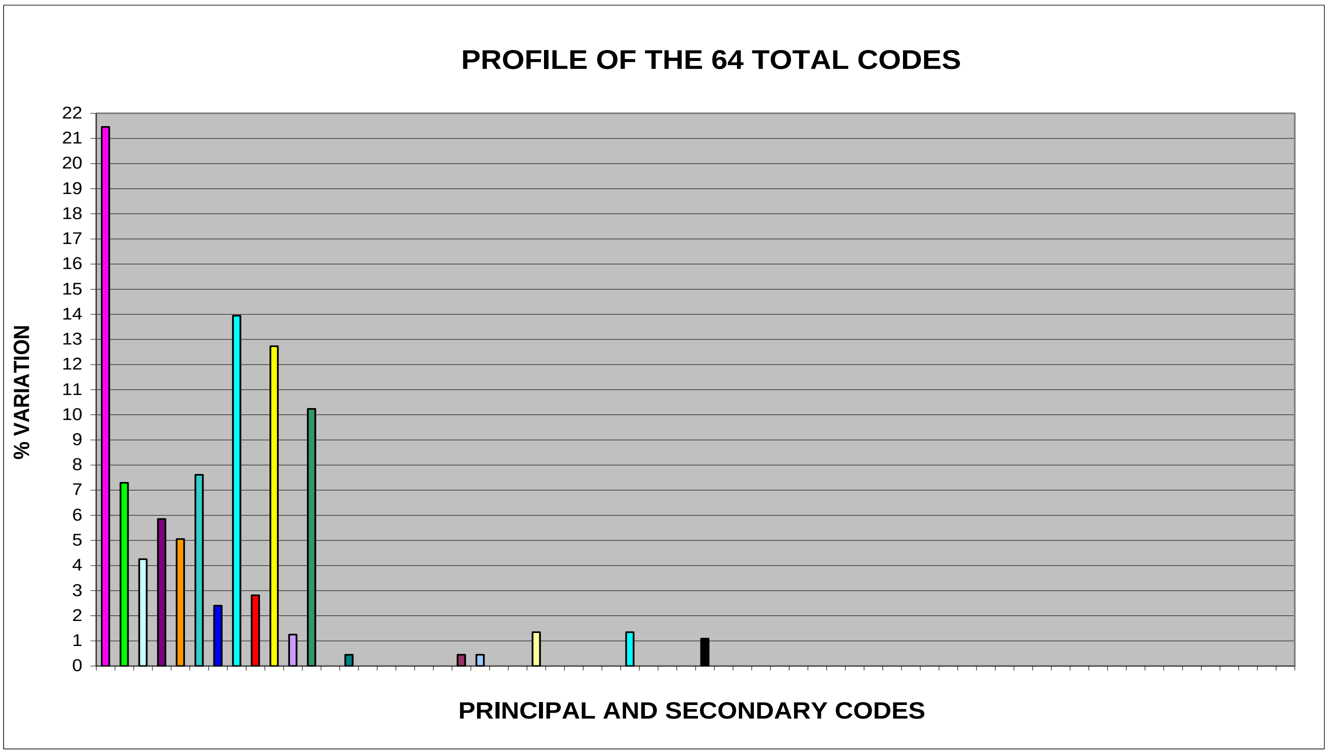
The chart in Pct. 27 (B) refers to the **"new generated sequence"** that originates from the original one.



Pct. 27 (B)

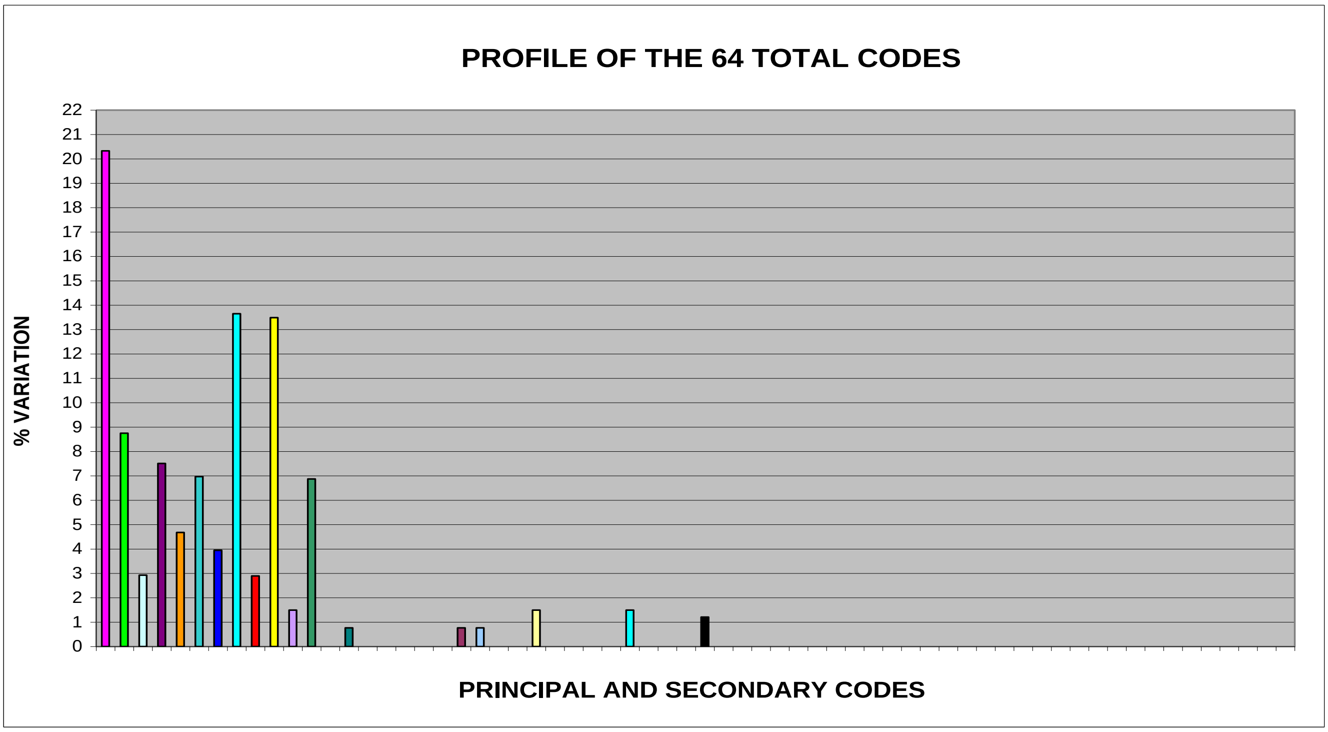
In Pct. 28 (A and B) two charts concerning the **Profile of the 64 Total Codes** are compared.

The chart in Pct. 28 (A) refers to the **original base sequence** analysed before.



Pct. 28 (A)

The chart in Pct. 28 (B) refers to the **“new generated sequence”** originated from the original one.



Pct. 28 (B)

The "non-obvious trend" analysis (obtained through the **T.T.E.S.**) of **Sequence n°7/1 of Insulin Chain A** results in **a comparison among different graphs** that are going to be interpreted in an analogous way to that in which the graphs related to the "non-obvious trend" of the **Sequences** analysed in the previous paragraphs **(n° 1/1, n° 2/1, etc.)** were. In order to avoid repetitions, here, the reader is deferred to the interpretation of the **comparisons among the different graphs** presented in the paragraph 1.2 .

Before concluding the paragraph, it is worth noting that, out of the **63** DNA bases of **Sequence n° 7/1**, ONLY **FOURTEEN BASES** (the **22,22%**)**,** ARE EQUAL (by type and by position in sequence) TO THOSE OF THE ORIGINAL SEQUENCE (**Insulin Chain A**).

1.15 IMPLICATIONS RELATED TO THE GRAPHIC RESULTS OF THE “NON-OBVIOUS TREND” ANALYSIS OF SEQUENCE n° 7/1 OF INSULIN CHAIN A

The **63** DNA base sequence of the **new generated sequence** (**Sequence n° 7/1**) that arises from the **original** one has been subjected to **BLAST** research.

Please note:

Information about the ***significant alignments*** produced by *BLAST research*, related to **Sequence n° 7/1,** and all the data acquired from *GenBank (3)* will be published in the **Appendix,** after the *General Conclusions.*

Query = NEW GENERATED SEQUENCE (Sequence n° 7/1)

Length = 63

Parameters of BLAST research:

Programme	*Blastn*
Word size	*11*
Expect value	*10*
Hitlist size	*100*
Match/Mismatch scores	*2,-3*
Gapcosts	*5,2*
Low Complexity Filter	*Yes*
Filter string	*L;m;*
Genetic Code	*1*

Please note:

Here, “**the organisms found to be in common**” between the results of BLAST research carried out on **Insulin Chain A** and results of BLAST research carried out on **Sequence n° 7/1**, were highlighted in **Red**.
As well, “**the organisms found to be in common**” between the results of BLAST research carried out on **Insulin Chain A**, results of BLAST research carried out on **Sequence n° 7/1** and results of BLAST research carried out on **at least one** of the *19 generated sequences*, were highlighted in **Green**.
Moreover, “**the denomination of the sequence**” (1/1, 2/1, ... 19/1) of the “**organism found to be in common**” between the results of BLAST research carried out on **Sequence n° 7/1** and results of BLAST research carried out on **at least one** of the *19 new generated sequences*, were highlighted in **Blue**.
Finally, “**the denomination of the sequence**” (1/1, 2/1, ... 19/1) of the “**organism found to be in common**” between the results of BLAST research carried out on **Insulin Chain A** and results of BLAST research carried out on *19 generated sequences*, were highlighted in **Yellow**.

Sequenza n° 7/1

Sequences producing significant alignments:

Selected seq	Description	Max score	Total score	Query cover	E value	Ident	Accession
1 LR131921.1	Cottoperca gobio genome assembly, chromosome: 14	39.2	39.2	41%	9.5	92%	LR131921.1
2 XM_006818034.1	PREDICTED: Saccoglossus kowalevskii protein phosphatase Slingshot homolog 2-like (LOC100376065), mRNA	39.2	39.2	49%	9.5	87%	XM_006818034.1

Comparison between the alignments of Sequence 7/1 and Sequence of Insulin Chain A according to the "Species of Common Organisms":

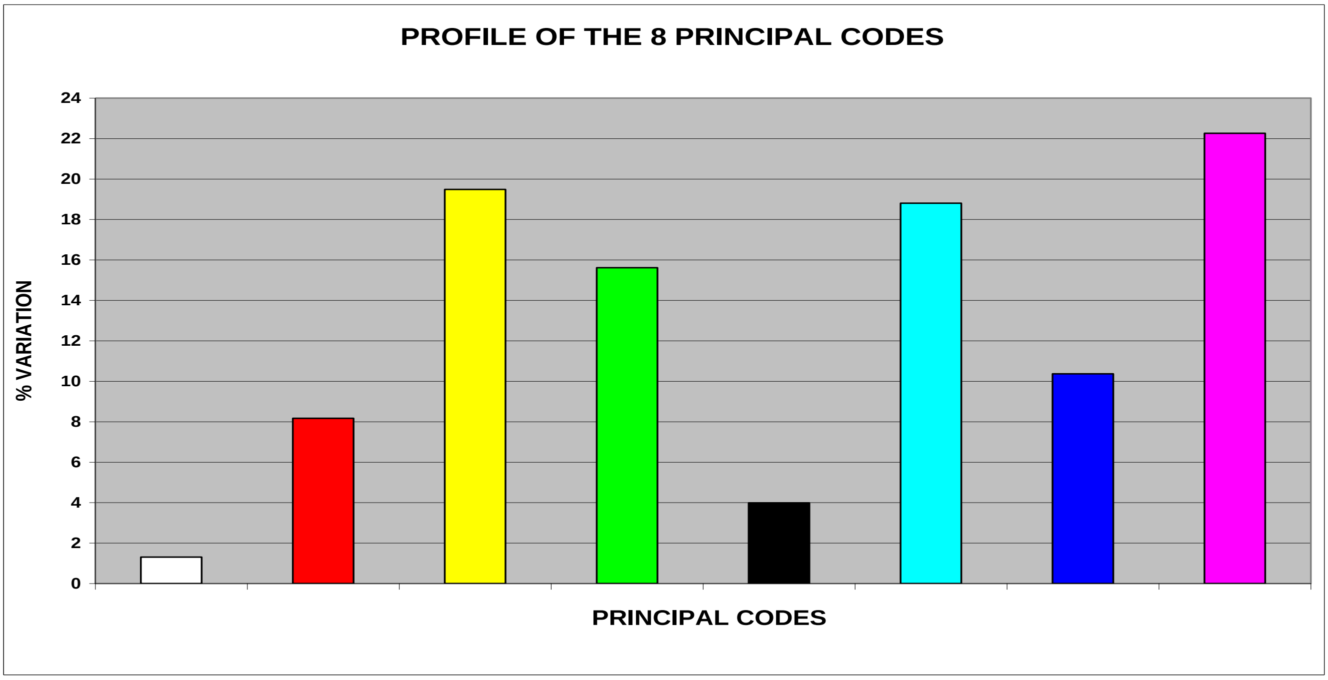
Alignments Sequence 7/1	**Description**	**Alignments Sequence Insulin Chain A**	**Description**
1 Select seq LR131921.1 **19/1**	Cottoperca gobio genome assembly, chromosome: 14	Select seq LR131921.1 **4/1 6/1 16/1** **18/1 19/1**	Cottoperca gobio genome assembly, chromosome: 14
		Select seq LR131917.1 **4/1 6/1 16/1** **18/1 19/1**	Cottoperca gobio genome assembly, chromosome: 10

Analysis of
Sequence n° 8/1
of Insulin Chain A

1. 16 GRAPHIC RESULTS OF THE “NON-OBVIOUS TREND” ANALYSIS OF SEQUENCE n° 8/1 OF INSULIN CHAIN A

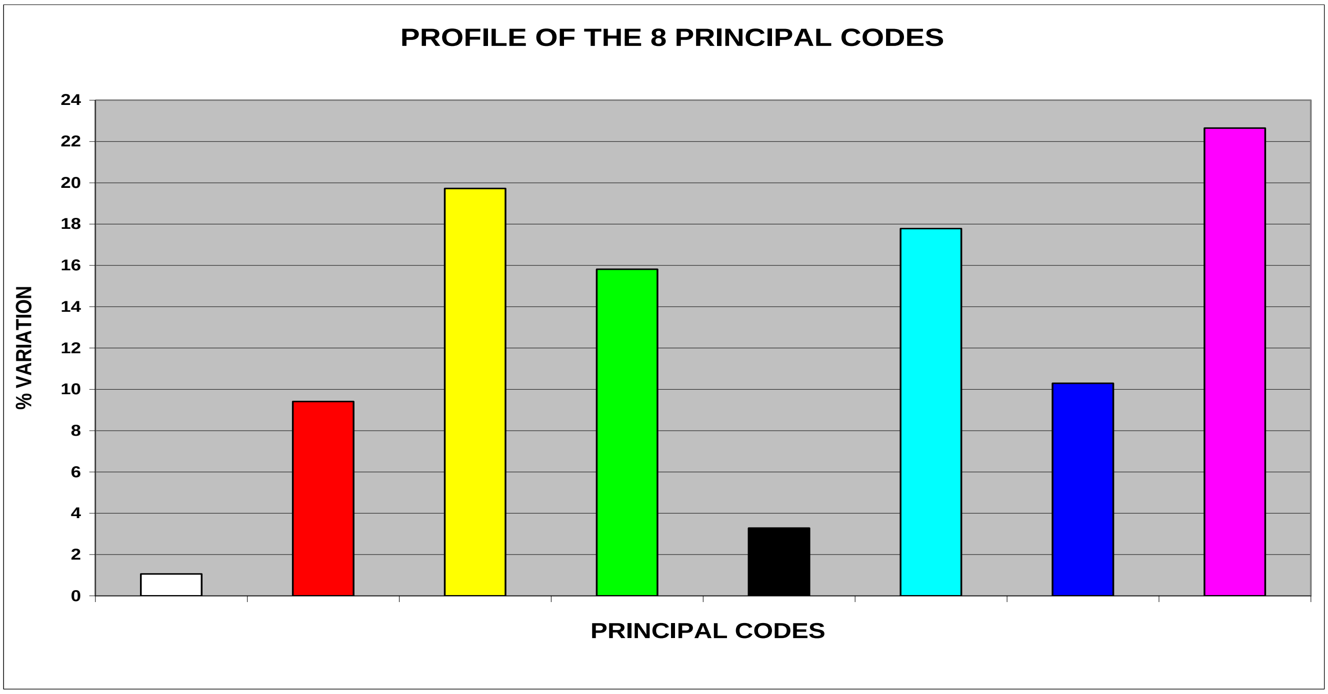
In the Pct. 29 (A e B) two **8 Principal Codes Profiles** are compared.

The chart in Pct. 29 (A) refers to the **original base sequence** of **Insulin Chain A**.



Pct. 29 (A)

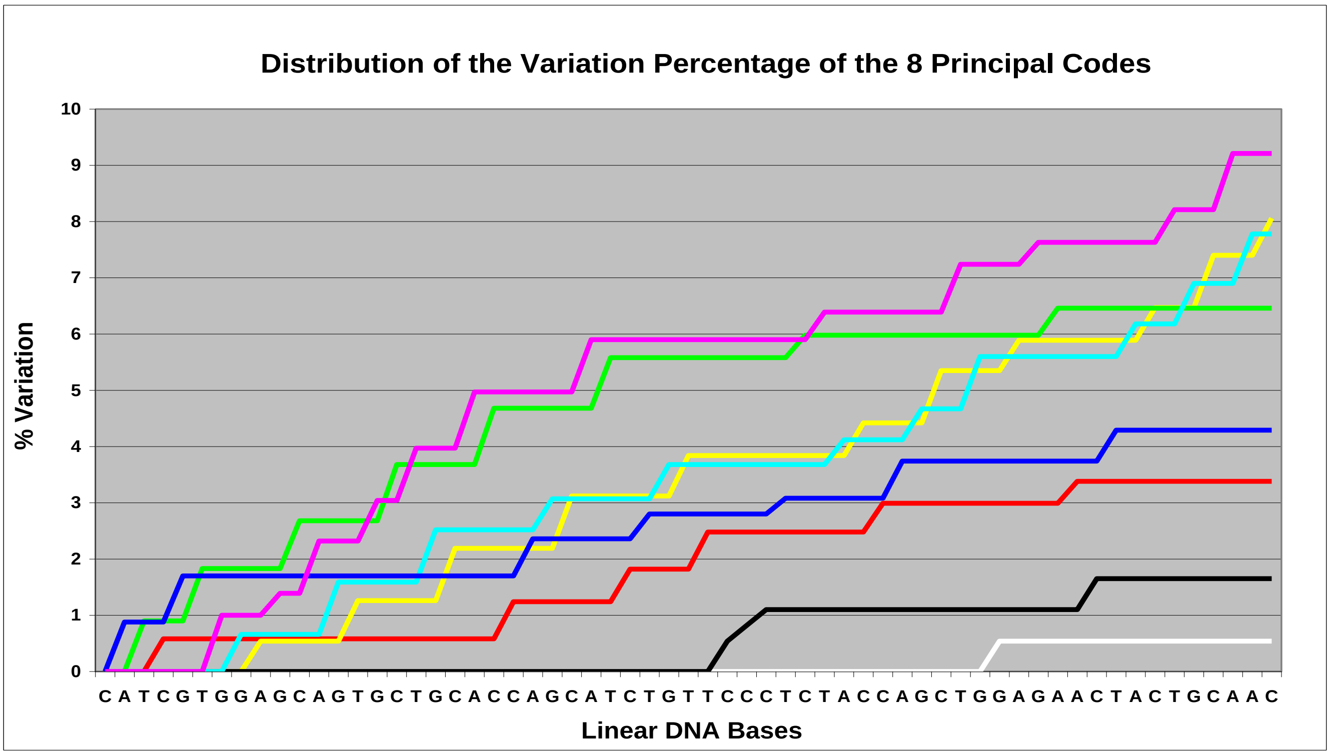
The chart in Pct. 29 (B) refers to the **octave** **“new generated sequence”** (**Sequence n° 8/1**) that originates from the original one.



Pct. 29 (B)

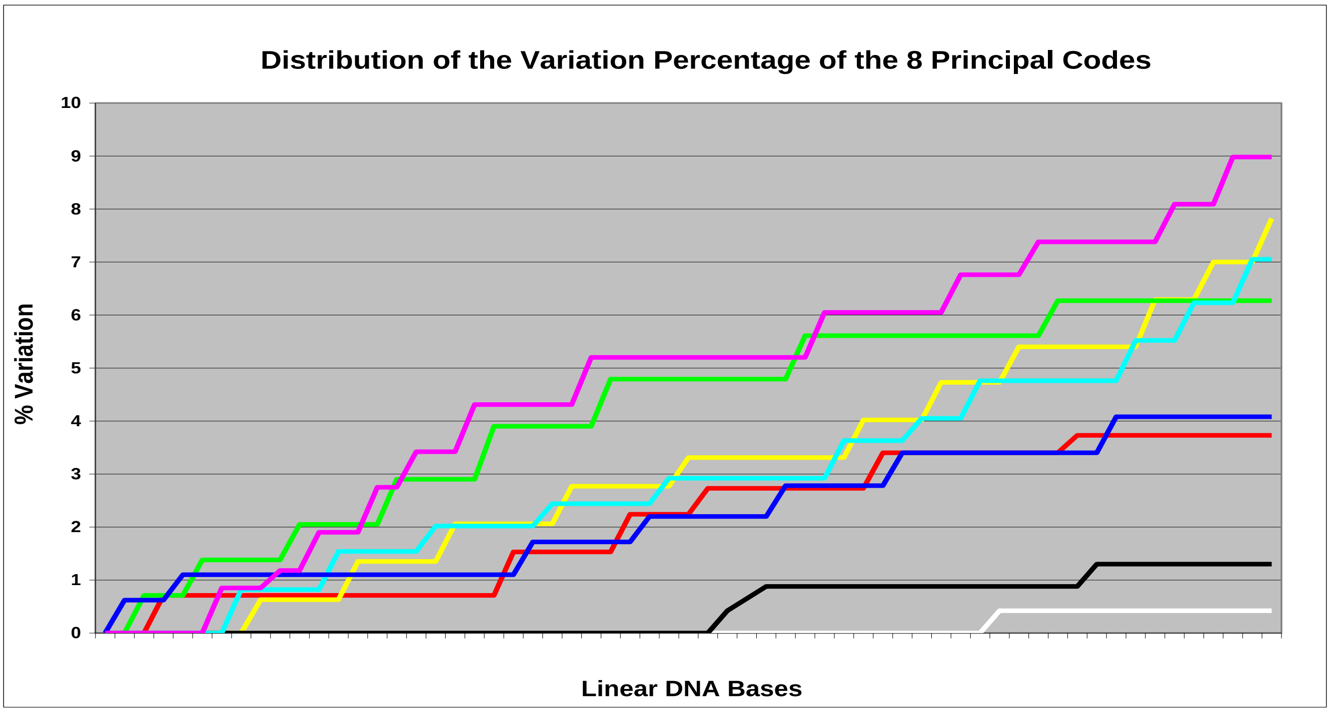
In Pct. 30 (A and B) two charts concerning the **Distribution of the Variation Percentage of the 8 Main Codes** are compared.

The charts in Pct. 30 (A) refers to the **original base sequence** analysed before.



Pct. 30 (A)

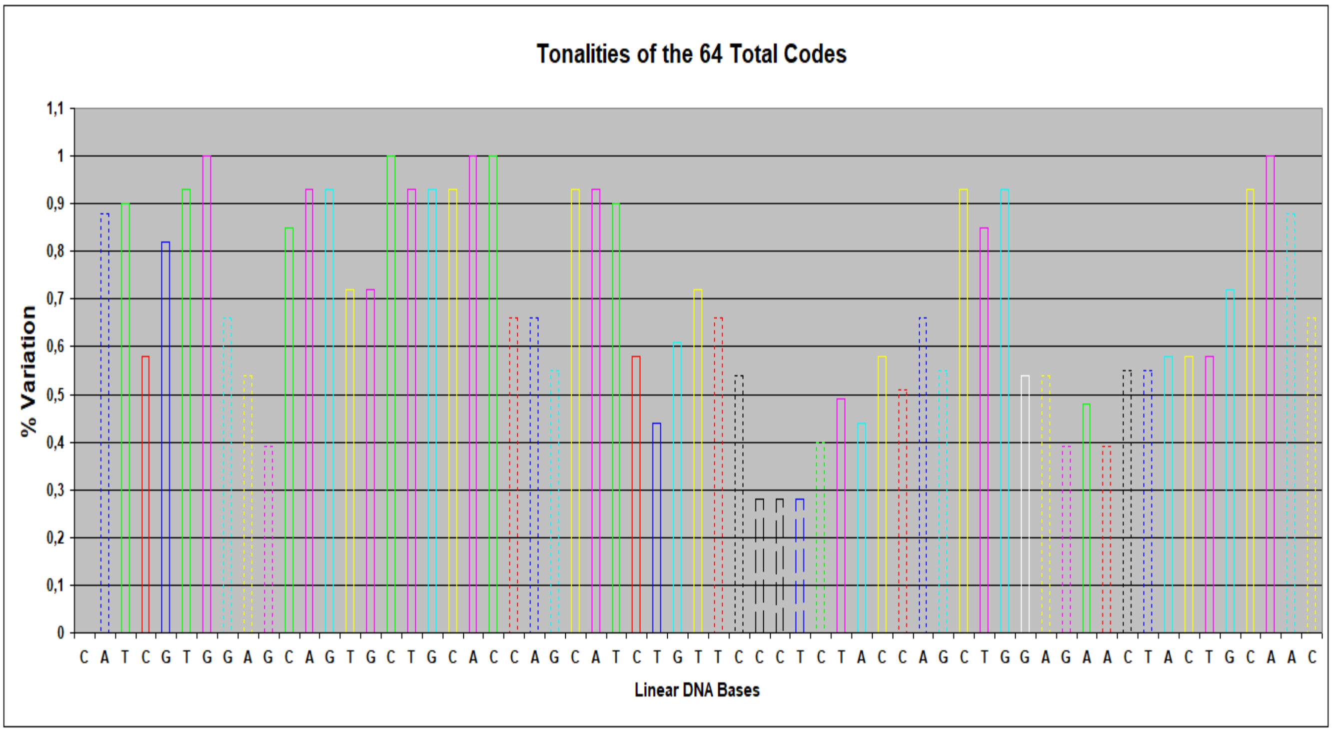
The chart in Pct. 30 (B) refers to the **"new generated sequence"** that originates from the original one.



Pct. 30 (B)

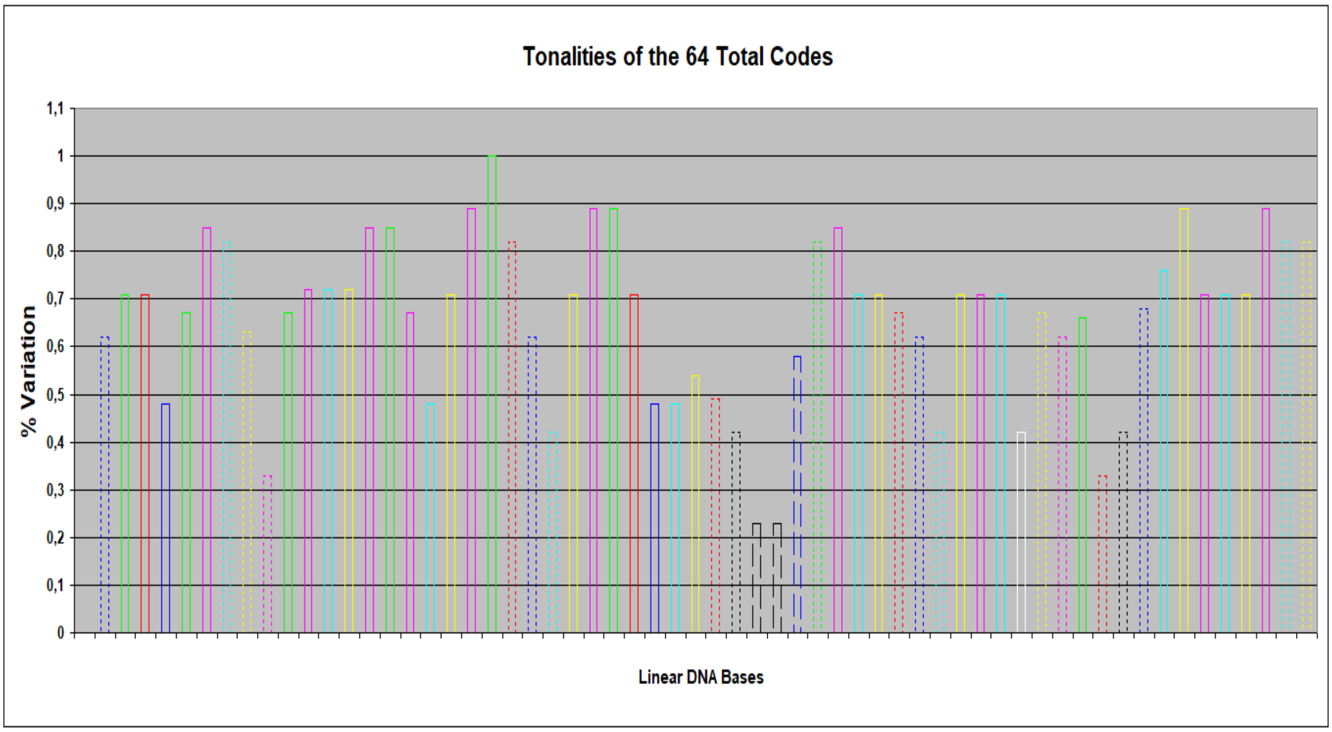
In Pct. 31 (A and B) two charts concerning the single **Tonalities of the 64 Total Codes** are compared.

The chart in Pct. 31 (A) refers to the **original base sequence** analysed before.



Pct. 31 (A)

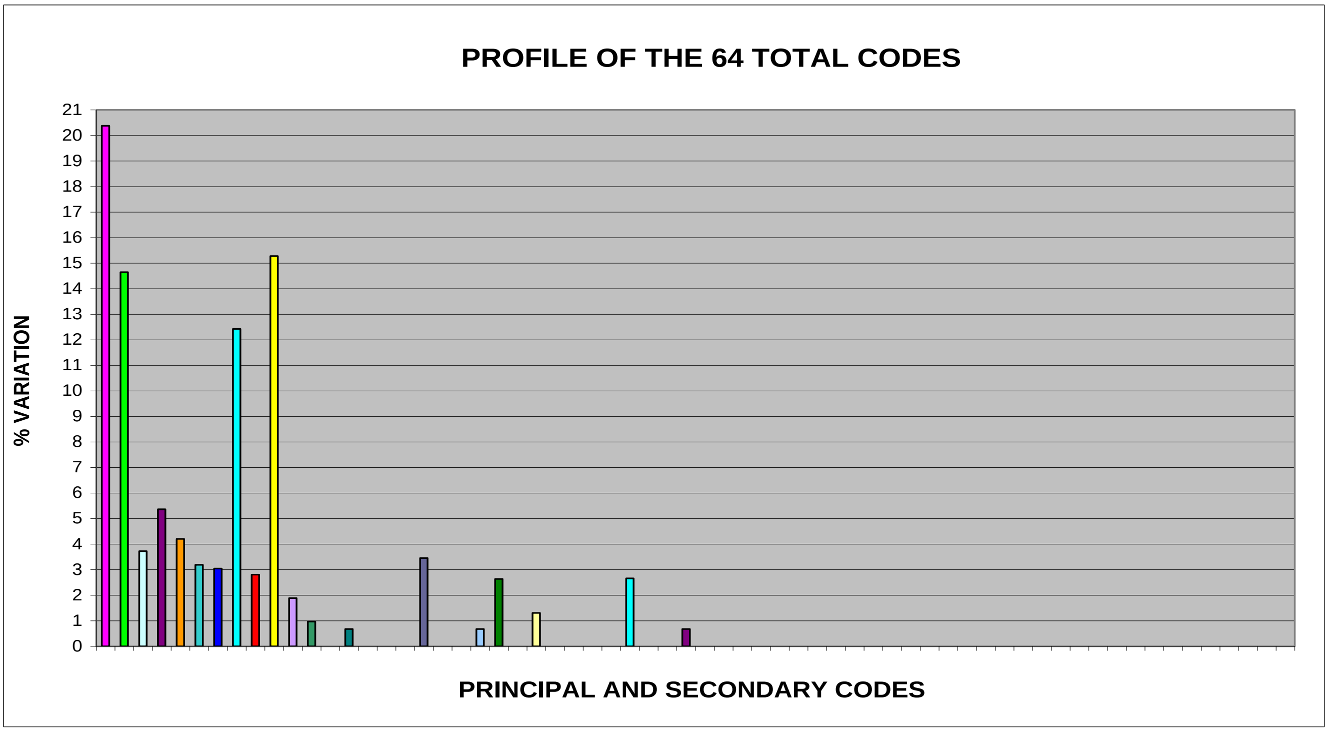
The chart in Pct. 31 (B) refers to the **"new generated sequence"** that originates from the original one.



Pct. 31 (B)

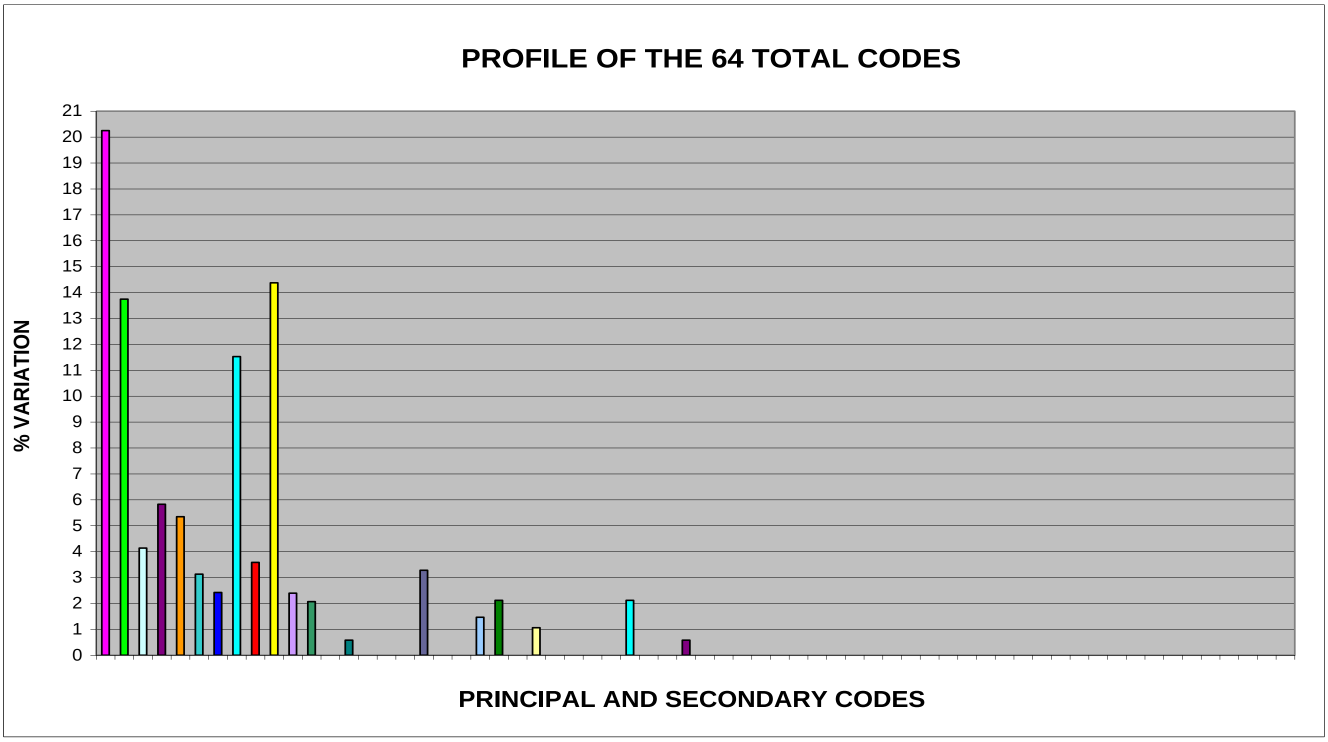
In Pct. 32 (A and B) two charts concerning the **Profile of the 64 Total Codes** are compared.

The chart in Pct. 32 (A) refers to the **original base sequence** analysed before.



Pct. 32 (A)

The chart in Pct. 32 (B) refers to the **“new generated sequence”** originated from the original one.



Pct. 32 (B)

The "non-obvious trend" analysis (obtained through the **T.T.E.S.**) of **Sequence n°8/1 of Insulin Chain A** results in **a comparison among different graphs** that are going to be interpreted in an analogous way to that in which the graphs related to the "non-obvious trend" of the **Sequences** analysed in the previous paragraphs **(n° 1/1, n° 2/1, etc.)** were. In order to avoid repetitions, here, the reader is deferred to the interpretation of the **comparisons among the different graphs** presented in the paragraph 1.2 .

Before concluding the paragraph, it is worth noting that, out of the **63** DNA bases of **Sequence n° 8/1**, ONLY **ELEVEN BASES** (the **17,46%**)**,** ARE EQUAL (by type and by position in sequence) TO THOSE OF THE ORIGINAL SEQUENCE (**Insulin Chain A**).

1.17 IMPLICATIONS RELATIVE TO THE GRAPHIC RESULTS OF THE "NON-OBVIOUS TREND" ANALYSIS OF SEQUENCE n° 8/1 OF INSULIN CHAIN A

The **63** DNA base sequence of the **new generated sequence** (**Sequence n° 8/1**) that arises from the **original** one has been subjected to **BLAST** research.

Please note:

Information about the ***significant alignments*** produced by *BLAST research*, related to **Sequence n° 8/1,** and all the data acquired from *GenBank (3)* will be published in the **Appendix,** after the *General Conclusions.*

Query = NEW GENERATED SEQUENCE (Sequence n° 8/1)

Length = 63

Parameters of BLAST research:

Programme	*Blastn*
Word size	*11*
Expect value	*10*
Hitlist size	*100*
Match/Mismatch scores	*2,-3*
Gapcosts	*5,2*
Low Complexity Filter	*Yes*
Filter string	*L;m;*
Genetic Code	*1*

Please note:

Here, "**the organisms found to be in common**" between the results of BLAST research carried out on **Insulin Chain A** and results of BLAST research carried out on **Sequence n° 8/1**, were highlighted in **Red**.
As well, "**the organisms found to be in common**" between the results of BLAST research carried out on **Insulin Chain A**, results of BLAST research carried out on **Sequence n° 8/1** and results of BLAST research carried out on **at least one** of the *19 generated sequences*, were highlighted in **Green**.
Moreover, "**the denomination of the sequence**" (1/1, 2/1, ... 19/1) of the "**organism found to be in common**" between the results of BLAST research carried out on **Sequence n° 8/1** and results of BLAST research carried out on **at least one** of the *19 new generated sequences*, were highlighted in **Blue**.
Finally, "**the denomination of the sequence**" (1/1, 2/1, ... 19/1) of the "**organism found to be in common**" between the results of BLAST research carried out on **Insulin Chain A** and results of BLAST research carried out on *19 generated sequences*, were highlighted in **Yellow**.

Sequenza n° 8/1

Sequences producing significant alignments:

Selected seq	Description	Max score	Total score	Query cover	E value	Ident	Accession
1 **4/1** HG975449.1	Solanum pennellii chromosome ch10, complete genome	42.8	42.8	44%	0.74	93%	HG975449.1
2 CP027081.1	Bos mutus isolate yakQH1 chromosome 13	41.9	41.9	39%	2.6	96%	CP027081.1
3 **3/1** KP211873.1	Uncultured Candidatus Thalassoarchaea euryarchaeote clone MedDCM-JUL2012-C2515 genomic sequence	41.9	41.9	39%	2.6	96%	KP211873.1
4 FO905645.1	Leptosphaeria biglobosa brassicae b35_scaffold00019 complete sequence	41.9	41.9	47%	2.6	90%	FO905645.1
5 KX822774.1	Xanthorrhoea preissii voucher K:20005062 chloroplast, complete genome	41.0	41.0	52%	2.6	88%	KX822774.1
6 KX754270.1	Racinaea elegans isolate B51 RNA polymerase beta subunit (rpoB) gene, partial cds; rpoB-trnC intergenic spacer, tRNA-Cys (trnC-GCA) gene, and trnC-petN intergenic spacer, complete sequence; and petN gene, partial sequence; plastid	41.0	41.0	52%	2.6	88%	KX754270.1
7 KU053957.1	Coeloseira compressa plastid, complete genome	41.0	41.0	74%	2.6	79%	KU053957.1
8 AL671889.6	Mouse DNA sequence from clone RP23-390M19 on chromosome X, complete sequence	41.0	41.0	77%	2.6	80%	AL671889.6
9 LR131994.1	Gouania willdenowi genome assembly, chromosome: 4	40.1	40.1	38%	9.5	96%	LR131994.1
10 **6/1** XM_026886865.1	PREDICTED: Trichoplusia ni GTP-binding protein 1 (LOC113504522), transcript variant X2, mRNA	40.1	40.1	44%	9.5	93%	XM_026886865.1
11 **6/1** XM_026886864.1	PREDICTED: Trichoplusia ni GTP-binding protein 1 (LOC113504522), transcript variant X1, mRNA	40.1	40.1	44%	9.5	93%	XM_026886864.1
12 XM_023044051.1	PREDICTED: Onthophagus taurus polyprenol reductase (LOC111413171), mRNA	40.1	40.1	39%	9.5	96%	XM_023044051.1
13 **4/1** CP023759.1	Solanum lycopersicum cultivar I-3 chromosome 3	40.1	40.1	53%	9.5	85%	CP023759.1

Sequences producing significant alignments:

Selected seq	Description	Max score	Total score	Query cover	E value	Ident	Accession
14 XM_022220161.1	PREDICTED: Acanthochromis polyacanthus uncharacterized LOC110969974 (LOC110969974), mRNA	40.1	40.1	41%	9.5	96%	XM_022220161.1
15 4/1 6/1 LN134849.1	Spirometra erinaceieuropaei genome assembly S_erinaceieuropaei, scaffold SPER_scaffold0124232	40.1	40.1	63%	9.5	88%	LN134849.1
16 4/1 HG975515.1	Solanum lycopersicum chromosome ch03, complete genome	40.1	40.1	53%	9.5	85%	HG975515.1
17 AC239600.3	Homo sapiens BAC clone RP11-633B17 from chromosome x, complete sequence	40.1	40.1	66%	9.5	84%	AC239600.3
18 17/1 XM_631498.1	Dictyostelium discoideum AX4 IPT/TIG domain-containing protein (tgrM1) mRNA, complete cds	40.1	40.1	46%	9.5	90%	XM_631498.1
19 AL049591.12	Human DNA sequence from clone RP5-878I13 on chromosome Xq23-25 Contains an alpha tubulin pseudogene, complete sequence	40.1	40.1	66%	9.5	84%	AL049591.12
20 LN483848.1	Culicoides sonorensis genome assembly, scaffold: scaffold498	39.2	39.2	41%	9.5	92%	LN483848.1
21 XR_001489186.1	PREDICTED: Macaca fascicularis uncharacterized LOC107129091 (LOC107129091), ncRNA	39.2	39.2	33%	9.5	100%	XR_001489186.1
22 4/1 6/1 LK466226.1	Dicrocoelium dendriticum genome assembly D_dendriticum_Leon_v1_0_4, scaffold DDEL_scaffold0069925	39.2	39.2	41%	9.5	92%	LK466226.1
23 4/1 6/1 LK858215.1	Dicrocoelium dendriticum genome assembly D_dendriticum_Leon_v1_0_4, scaffold DDEL_contig0091947	39.2	39.2	41%	9.5	92%	LK858215.1
24 XR_491488.1	PREDICTED: Chlorocebus sabaeus uncharacterized LOC103218202 (LOC103218202), ncRNA	39.2	39.2	33%	9.5	100%	XR_491488.1

Sequences producing significant alignments:

Selected seq	Description	Max score	Total score	Query cover	E value	Ident	Accession
25 AC109139.15	Mus musculus chromosome 8, clone RP23-47L13, complete sequence	39.2	39.2	41%	9.5	92%	AC109139.15
26 AC113049.22	Mus musculus chromosome 8, clone RP23-248P8, complete sequence	39.2	39.2	41%	9.5	92%	AC113049.22

Comparison between the alignments of Sequence 8/1 and Sequence of Insulin Chain A according to the "Species of Common Organisms":

Alignments Sequence 8/1	Description	Alignments Sequence Insulin Chain A	Description
2 Select seq CP027081.1	Bos mutus isolate yakQH1 chromosome 13	Select seq XM_027532448.1 **3/1 4/1**	PREDICTED: Bos indicus x Bos taurus insulin (INS), mRNA
		Select seq XM_015461330.2 **3/1 4/1**	PREDICTED: Bos taurus insulin (INS), transcript variant X1, mRNA
		Select seq CP027097.1 **3/1 4/1**	Bos mutus isolate yakQH1 chromosome 29
		Select seq XM_019954732.1 **3/1 4/1**	PREDICTED: Bos indicus insulin (INS), transcript variant X2, mRNA
		Select seq XM_019954731.1 **3/1 4/1**	PREDICTED: Bos indicus insulin (INS), transcript variant X1, mRNA
		Select seq M54979.2 **3/1 4/1**	Bos taurus insulin precursor, mRNA, complete cds
		Select seq XM_005903505.2 **3/1 4/1**	PREDICTED: Bos mutus insulin (LOC102274400), mRNA
		Select seq JX041514.1 **3/1 4/1**	Bos taurus proinsulin mRNA, partial cds
		Select seq NM_001185126.1 **3/1 4/1**	Bos taurus insulin (INS), transcript variant 2, mRNA
		Select seq NM_173926.2 **3/1 4/1**	Bos taurus insulin (INS), transcript variant 1, mRNA
		Select seq EU518675.1 **3/1 4/1**	Bos taurus insulin (INS) and insulin-like growth factor 2 (IGF2) genes, complete cds
		Select seq BC142034.1 **3/1 4/1**	Bos taurus insulin, mRNA (cDNA clone MGC:159719 IMAGE:8631936), complete cds
		Select seq AC149665.2 **3/1 4/1**	Bos taurus BAC CH240-60O13 (Children's Hospital Oakland Research Institute Bovine BAC Library (male)) complete sequence

Comparison between the alignments of Sequence 8/1 and Sequence of Insulin Chain A according to the “Species of Common Organisms”:

Alignments Sequence 8/1	**Description**	**Alignments Sequence Insulin Chain A**	**Description**
8 Select seq AL671889.6	Mouse DNA sequence from clone RP23-390M19 on chromosome X, complete sequence	Select seq X04725.1 **10/1 13/1 17/1**	Mouse preproinsulin gene I
		Select seq X04725.1 **10/1 13/1 17/1**	Mouse preproinsulin gene II
14 Select seq XM_022220161.1	PREDICTED: Acanthochromis polyacanthus uncharacterized LOC110969974 (LOC110969974), mRNA	Select seq XM_022221651.1	PREDICTED: Acanthochromis polyacanthus insulin (ins), mRNA
		Select seq XM_022190895.1	PREDICTED: Acanthochromis polyacanthus circularly permutated Ras protein 1-like (LOC110949057), mRNA
		Select seq XM_022206846.1	PREDICTED: Acanthochromis polyacanthus insulin-like (LOC110959849), mRNA
17 Select seq AL049591.12	Homo sapiens BAC clone RP11-633B17 from chromosome x, complete sequence	Select seq AH002844.2 **2/1 9/1 10/1 15/1 17/1**	Homo sapiens insulin (INS) gene, complete cds
		Select seq AH012037.2 **2/1 9/1 10/1 15/1 17/1**	Homo sapiens haplotype ICa tyrosine hydroxylase (TH) gene, partial sequence; insulin (INS) gene, complete cds; and insulin-like growth factor 2 (IGF2) gene, partial sequence
		Select seq NG_050578.1 **2/1 9/1 10/1 15/1 17/1**	Homo sapiens INS-IGF2 readthrough (INS-IGF2), RefSeqGene on chromosome 11
		Select seq KR710184.1 **2/1 9/1 10/1 15/1 17/1**	Synthetic construct Homo sapiens clone CCSBHm_00010257 INS (INS) mRNA, encodes complete protein
		Select seq KR710183.1 **2/1 9/1 10/1 15/1 17/1**	Synthetic construct Homo sapiens clone CCSBHm_00010256 INS (INS) mRNA, encodes complete protein

Comparison between the alignments of Sequence 8/1 and Sequence of Insulin Chain A according to the “Species of Common Organisms”:

Alignments Sequence 8/1	**Description**	**Alignments Sequence Insulin Chain A**	**Description**
		Select seq KR710182.1 **2/1** **9/1** **10/1** **15/1** **17/1**	Synthetic construct Homo sapiens clone CCSBHm_00010255 INS (INS) mRNA, encodes complete protein
		Select seq KJ891480.1 **2/1** **9/1** **10/1** **15/1** **17/1**	Synthetic construct Homo sapiens clone ccsbBroadEn_00874 INS gene, encodes complete protein
		Select seq NM_001291897.1 **2/1** **9/1** **10/1** **15/1** **17/1**	Homo sapiens insulin (INS), transcript variant 4, mRNA
		Select seq JQ951950.1 **2/1** **9/1** **10/1** **15/1** **17/1**	Homo sapiens preproinsulin (INS) mRNA, complete cds
		Select seq JF909299.1 **2/1** **9/1** **10/1** **15/1** **17/1**	Homo sapiens insulin (INS) mRNA, partial cds
		Select seq AB587580.1 **2/1** **9/1** **10/1** **15/1** **17/1**	Synthetic construct DNA, clone: pF1KB8864, Homo sapiens INS gene for insulin, without stop codon, in Flexi system
		Select seq NM_001185098.1 **2/1** **9/1** **10/1** **15/1** **17/1**	Homo sapiens insulin (INS), transcript variant 3, mRNA
		Select seq NM_001185097.1 **2/1** **9/1** **10/1** **15/1** **17/1**	Homo sapiens insulin (INS), transcript variant 2, mRNA
		Select seq NG_007114.1 **2/1** **9/1** **10/1** **15/1** **17/1**	Homo sapiens insulin (INS), RefSeqGene on chromosome 11
		Select seq DQ778082.1 **2/1** **9/1** **10/1** **15/1** **17/1**	Homo sapiens clone BFC06103 insulin mRNA, complete cds

Comparison between the alignments of Sequence 8/1 and Sequence of Insulin Chain A according to the "Species of Common Organisms":

Alignments Sequence 8/1	**Description**	**Alignments Sequence Insulin Chain A**	**Description**
		Select seq DQ896283.2 **2/1 9/1 10/1 15/1 17/1**	Synthetic construct Homo sapiens clone IMAGE:100010743; FLH192918.01L; RZPDo839A1068D insulin (INS) gene, encodes complete protein
		Select seq NM_000207.2 **2/1 9/1 10/1 15/1 17/1**	Homo sapiens insulin (INS), transcript variant 1, mRNA
		Select seq BT007778.1 **2/1 9/1 10/1 15/1 17/1**	Synthetic construct Homo sapiens insulin mRNA, partial cds
		Select seq BT006808.1 **2/1 9/1 10/1 15/1 17/1**	Homo sapiens insulin mRNA, complete cds
		Select seq BC005255.1 **2/1 9/1 10/1 15/1 17/1**	Homo sapiens insulin, mRNA (cDNA clone MGC:12292 IMAGE:3950204), complete cds
		Select seq AC132217.15 **2/1 9/1 10/1 15/1 17/1**	Homo sapiens chromosome 11, clone RP11-889I17, complete sequence
		Select seq AC130303.8 **2/1 9/1 10/1 15/1 17/1**	Homo sapiens chromosome 11, clone RP4-539G11, complete sequence
		Select seq AY899304.1 **2/1 9/1 10/1 15/1 17/1**	Homo sapiens proinsulin mRNA, complete cds, alternatively spliced
		Select seq AJ009655.1 **2/1 9/1 10/1 15/1 17/1**	Homo sapiens ins gene, partial
		Select seq X70508.1 **2/1 9/1 10/1 15/1 17/1**	Homo sapiens mRNA for insulinoma pre-proinsulin

Comparison between the alignments of Sequence 8/1 and Sequence of Insulin Chain A according to the “Species of Common Organisms”:

Alignments Sequence 8/1	**Description**	**Alignments Sequence Insulin Chain A**	**Description**
		Select seq L15440.1 **2/1 9/1 10/1 15/1 17/1**	Homo sapiens tyrosine hydroxylase (TH) gene, 3' end; insulin (INS) gene, complete cds; insulin-like growth factor 2 (IGF2) gene, 5' end
		Select seq KR710185.1 **2/1 9/1 10/1 15/1 17/1**	Synthetic construct Homo sapiens clone CCSBHm_00010262 INS (INS) mRNA, encodes complete protein
		Select seq AF050524.1 **2/1 9/1 10/1 15/1 17/1**	Synthetic Homo sapiens proinsulin-like protein BKRA gene, complete cds
		Select seq AC021233.9 **2/1 9/1 10/1 15/1 17/1**	Homo sapiens chromosome 11, clone RP11-215H22, complete sequence
		Select seq AK024581.1 **2/1 9/1 10/1 15/1 17/1**	Homo sapiens cDNA: FLJ20928 fis, clone ADSE01074
19 Select seq AL049591.12	Human DNA sequence from clone RP5-878I13 on chromosome Xq23-25 Contains an alpha tubulin pseudogene, complete sequence	Select seq J02547.1 **17/1**	Human (synthetic) insulin gene, complete cds
		Select seq M31026.1 **17/1**	Synthetic human insulin B and mini-C chains using deactivated silica gel chromatography
		Select seq V00082.1 **17/1**	Artificial gene for human proinsulin
		Select seq M12913.1 **7/1**	Synthetic human proinsulin gene, complete cds
		Select seq LT733283.1 **17/1**	Human ORFeome Gateway entry vector pENTR223-INS, complete sequence
		Select seq M10039.1 **17/1**	Human alpha-type insulin gene and 5' flanking polymorphic region

Comparison between the alignments of Sequence 8/1 and Sequence of Insulin Chain A according to the “Species of Common Organisms”:

Alignments Sequence 8/1	Description	Alignments Sequence Insulin Chain A	Description
		Select seq V00565.1 **17/1**	Human gene for preproinsulin, from chromosome 11. Includes a highly polymorphic region upstream from the insulin gene containing tandemly repeated sequences
		Select seq AB501190.1 **17/1**	Synthetic construct hpi gene for human M-proinsulin, complete cds
		Select seq J02544.1 **17/1**	Human insulin A chain gene (synthetic)
		Select seq AL354999.17 **17/1**	Human DNA sequence from clone RP11-531B22 on chromosome 13, complete sequence
		Select seq AL354896.16 **17/1**	Human DNA sequence from clone RP11-512M17 on chromosome 13, complete sequence
21 Select seq XR_001489186.1	PREDICTED: Macaca fascicularis uncharacterized LOC107129091 (LOC107129091), ncRNA	Select seq XM_015434180.1 **2/1** **3/1** **17/1**	PREDICTED: Macaca fascicularis insulin (INS), transcript variant X1, mRNA
		Select seq XM_015113354.1 **2/1** **3/1** **17/1**	PREDICTED: Macaca mulatta insulin (INS), mRNA
		Select seq XM_011721319.1 **2/1** **3/1** **17/1**	PREDICTED: Macaca nemestrina insulin (INS), transcript variant X4, mRNA
		Select seq XM_011721318.1 **2/1** **3/1** **17/1**	PREDICTED: Macaca nemestrina insulin (INS), transcript variant X3, mRNA
		Select seq XM_011721317.1 **2/1** **3/1** **17/1**	PREDICTED: Macaca nemestrina insulin (INS), transcript variant X2, mRNA
		Select seq XM_011721316.1 **2/1** **3/1** **17/1**	PREDICTED: Macaca nemestrina insulin (INS), transcript variant X1, mRNA
		Select seq NM_001284919.1 **2/1** **3/1** **17/1**	Macaca fascicularis insulin (INS), mRNA
24 Select seq XR_491488.1	PREDICTED: Chlorocebus sabaeus uncharacterized LOC103218202 (LOC103218202), ncRNA	Select seq XM_008004634.1	PREDICTED: Chlorocebus sabaeus insulin (INS), transcript variant X2, mRNA

Comparison between the alignments of Sequence 8/1 and Sequence of Insulin Chain A according to the "Species of Common Organisms":

Alignments Sequence 8/1	Description	Alignments Sequence Insulin Chain A	Description
		Select seq XM_008004561.1	PREDICTED: Chlorocebus sabaeus insulin (INS), transcript variant X1, mRNA
25 Select seq AC109139.15	Mus musculus chromosome 8, clone RP23-47L13, complete sequence	Select seq XM_021152514.1 1/1 6/1 10/1 13/1 17/1 18/1	PREDICTED: Mus caroli insulin-1 (LOC110286053), mRNA
26 Select seq AC113049.22	Mus musculus chromosome 8, clone RP23-248P8, complete sequence	Select seq DQ250565.1 1/1 6/1 10/1 13/1 17/1 18/1	Mus caroli preproinsulin 1 (Ins1) gene, complete cds
		Select seq XM_021215010.1 1/1 6/1 10/1 13/1 17/1 18/1	PREDICTED: Mus pahari insulin-1 (LOC110333420), mRNA
		Select seq NM_008386.4 1/1 6/1 10/1 13/1 17/1 18/1	Mus musculus insulin I (Ins1), mRNA
		Select seq BC145868.1 1/1 6/1 10/1 13/1 17/1 18/1	Mus musculus insulin I, mRNA (cDNA clone MGC:175755 IMAGE:40131171), complete cds
		Select seq DQ479923.1 1/1 6/1 10/1 13/1 17/1 18/1	Mus musculus strain BTBR T+ tf/J insulin 1 precursor, gene, complete cds
		Select seq AC163452.12 1/1 6/1 10/1 13/1 17/1 18/1	Mus musculus chromosome 19, clone RP23-405C7, complete sequence
		Select seq AC136710.8 1/1 6/1 10/1 13/1 17/1 18/1	Mus musculus chromosome 19, clone RP23-35B13, complete sequence
		Select seq AC140320.2 1/1 6/1 10/1 13/1 17/1 18/1	Mus musculus BAC clone RP23-401C13 from chromosome 19, complete sequence

Comparison between the alignments of Sequence 8/1 and Sequence of Insulin Chain A according to the "Species of Common Organisms":

Alignments Sequence 8/1	Description	Alignments Sequence Insulin Chain A	Description
		Select seq BC098468.1 **1/1 6/1 10/1** **13/1 17/1 18/1**	Mus musculus insulin I, mRNA (cDNA clone MGC:107382 IMAGE:6432765), complete cds
		Select seq AK148541.1 **1/1 6/1 10/1** **13/1 17/1 18/1**	Mus musculus adult pancreas islet cells cDNA, RIKEN full-length enriched library, clone:C820020F18 product:insulin I, full insert sequence
		Select seq AK007345.1 **1/1 6/1 10/1** **13/1 17/1 18/1**	Mus musculus 10 day old male pancreas cDNA, RIKEN full-length enriched library, clone:1810005L03 product:INSULIN 1 PRECURSOR, full insert sequence
		Select seq XM_021168754.1 **1/1 6/1 10/1** **13/1 17/1 18/1**	PREDICTED: Mus caroli insulin-2 (LOC110299132), transcript variant X2, mRNA
		Select seq XM_021168753.1 **1/1 6/1 10/1** **13/1 17/1 18/1**	PREDICTED: Mus caroli insulin-2 (LOC110299132), transcript variant X1, mRNA
		Select seq NM_001185084.2 **1/1 6/1 10/1** **13/1 17/1 18/1**	Mus musculus insulin II (Ins2), transcript variant 3, mRNA
		Select seq NM_001185083.2 **1/1 6/1 10/1** **13/1 17/1 18/1**	Mus musculus insulin II (Ins2), transcript variant 1, mRNA
		Select seq NM_008387.5 **1/1 6/1 10/1** **13/1 17/1 18/1**	Mus musculus insulin II (Ins2), transcript variant 2, mRNA
		Select seq JN959239.1 **1/1 6/1 10/1** **13/1 17/1 18/1**	Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Ins2:tm1a(EUCOMM)Wtsi; transgenic
		Select seq JN951270.1 **1/1 6/1 10/1** **13/1 17/1 18/1**	Mus musculus targeted non-conditional, lacZ-tagged mutant allele Ins2:tm1e(EUCOMM)Wtsi; transgenic

Comparison between the alignments of Sequence 8/1 and Sequence of Insulin Chain A according to the "Species of Common Organisms":

Alignments Sequence 8/1	**Description**	**Alignments Sequence Insulin Chain A**	**Description**
		Select seq BC145554.1 **1/1 6/1 10/1** **13/1 17/1 18/1**	Mus musculus insulin II, mRNA (cDNA clone MGC:179126 IMAGE:9054118), complete cds
		Select seq BC099934.1 **1/1 6/1 10/1** **13/1 17/1 18/1**	Mus musculus insulin II, mRNA (cDNA clone MGC:107381 IMAGE:6432976), complete cds
		Select seq BC132650.1 **1/1 6/1 10/1** **13/1 17/1 18/1**	Mus musculus insulin II, mRNA (cDNA clone MGC:164281 IMAGE:40130927), complete cds
		Select seq DQ250569.1 **1/1 6/1 10/1** **13/1 17/1 18/1**	Mus caroli preproinsulin 2 (Ins2) gene, complete cds
		Select seq AK007612.1 **1/1 6/1 10/1** **13/1 17/1 18/1**	Mus musculus 10 day old male pancreas cDNA, RIKEN full-length enriched library, clone:1810027C14 product:INSULIN 2 PRECURSOR, full insert sequence
		Select seq AK007482.1 **1/1 6/1 10/1** **13/1 17/1 18/1**	Mus musculus 10 day old male pancreas cDNA, RIKEN full-length enriched library, clone:1810013J24 product:INSULIN 1 PRECURSOR, full insert sequence
		Select seq BC066208.1 **1/1 6/1 10/1** **13/1 17/1 18/1**	Mus musculus insulin II, mRNA (cDNA clone IMAGE:6436276)
		Select seq AC012382.14 **1/1 6/1 10/1** **13/1 17/1 18/1**	Mus musculus chromosome 7, clone RP23-92L23, complete sequence
		Select seq AY899305.1 **1/1 6/1 10/1** **13/1 17/1 18/1**	Mus musculus proinsulin mRNA, complete cds, alternatively spliced
		Select seq AC013548.13 **1/1 6/1 10/1** **13/1 17/1 18/1**	Mus musculus chromosome 7, clone RP23-209O22, complete sequence

Comparison between the alignments of Sequence 8/1 and Sequence of Insulin Chain A according to the "Species of Common Organisms":

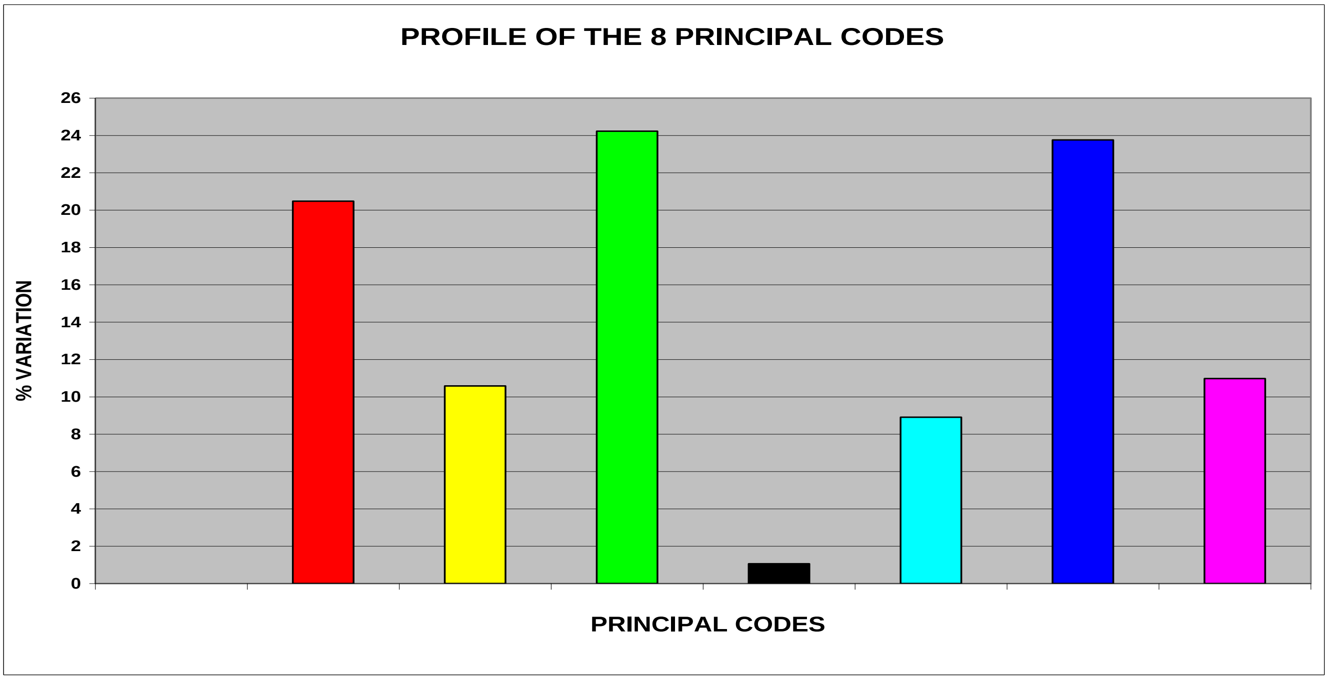
Alignments Sequence 8/1	Description	Alignments Sequence Insulin Chain A	Description
		Select seq AP003182.2 **1/1 6/1 10/1** **13/1 17/1 18/1**	Mus musculus genomic DNA, chromosome 7 clone:B189M11, complete sequences
		Select seq GQ915612.1 **1/1 6/1 10/1** **13/1 17/1 18/1**	Mus musculus insulin-2 precursor (Ins2) mRNA, partial cds, alternatively spliced
		Select seq XM_021204833.1 **1/1 6/1 10/1** **13/1 17/1 18/1**	PREDICTED: Mus pahari insulin-2 (LOC110326410), transcript variant X2, mRNA
		Select seq XM_021204825.1 **1/1 6/1 10/1** **13/1 17/1 18/1**	PREDICTED: Mus pahari insulin-2 (LOC110326410), transcript variant X1, mRNA

Analysis of
Sequence n° 9/1
of Insulin Chain A

1.18 GRAPHIC RESULTS OF THE “NON-OBVIOUS TREND” ANALYSIS OF SEQUENCE n° 9/1 OF INSULIN CHAIN A

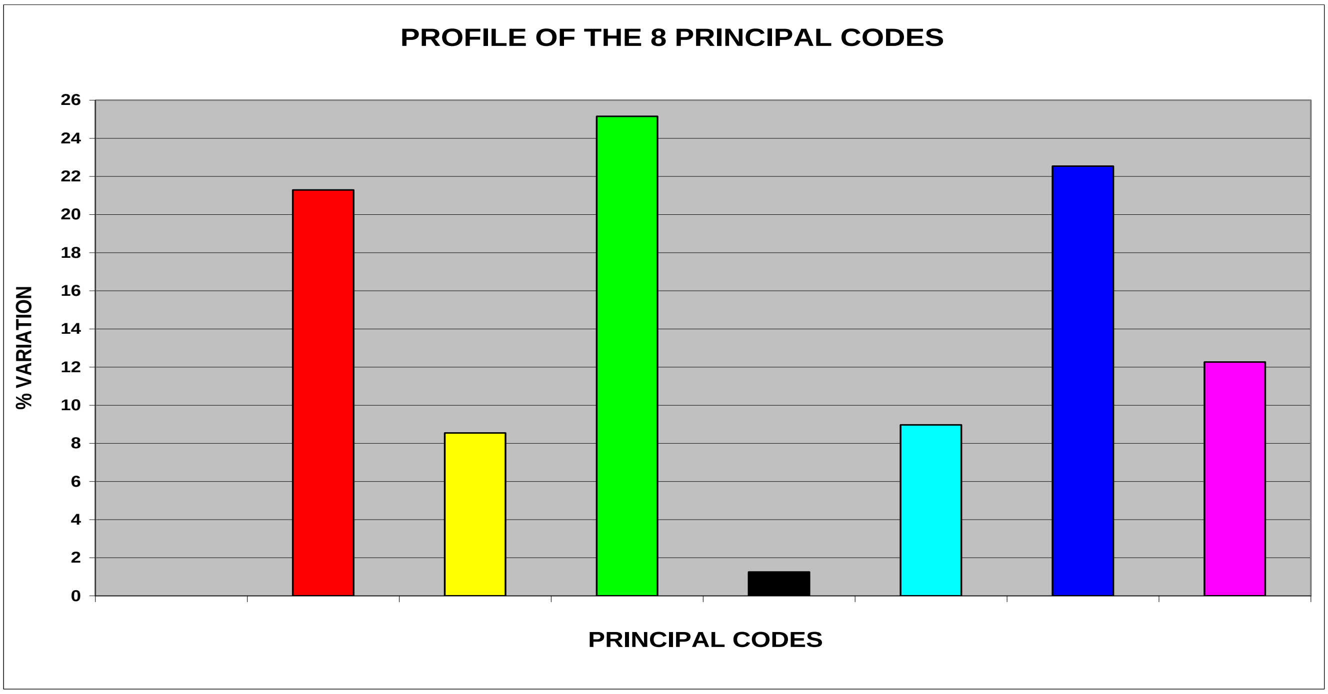
In the Pct. 33 (A e B) two **8 Principal Codes Profiles** are compared.

The chart in Pct. 33 (A) refers to the **original base sequence** of **Insulin Chain A**.



Pct. 33 (A)

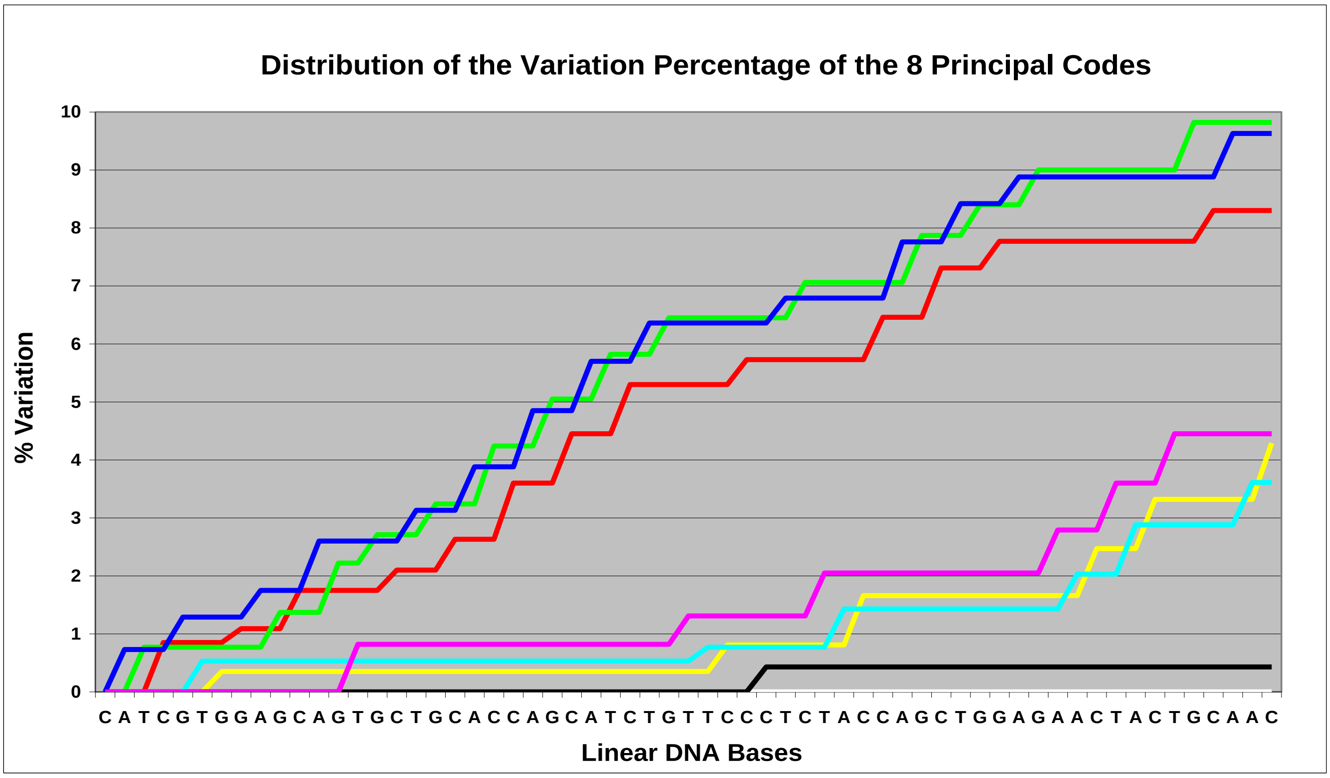
The chart in Pct. 33 (B) refers to the **ninth** **“new generated sequence”** (**Sequence n° 9/1**) that originates from the original one.



Pct. 33 (B)

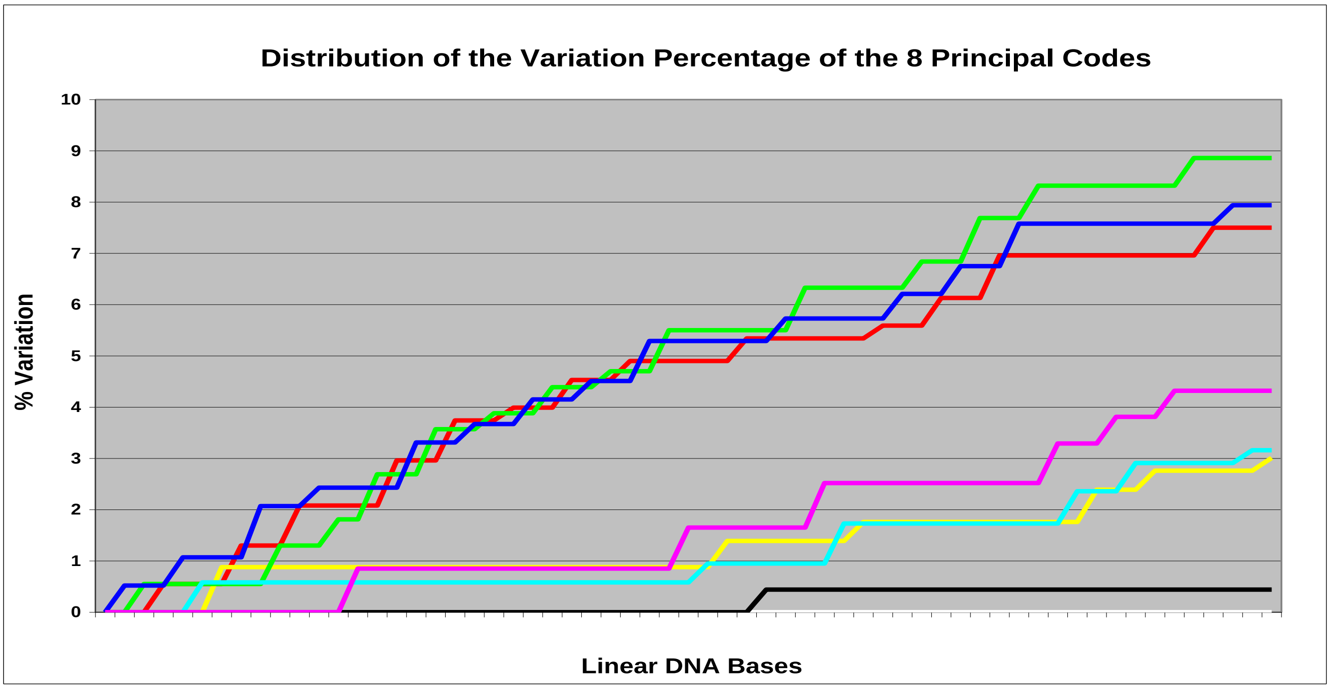
In Pct. 34 (A and B) two charts concerning the **Distribution of the Variation Percentage of the 8 Main Codes** are compared.

The charts in Pct. 34 (A) refers to the **original base sequence** analysed before.



Pct. 34 (A)

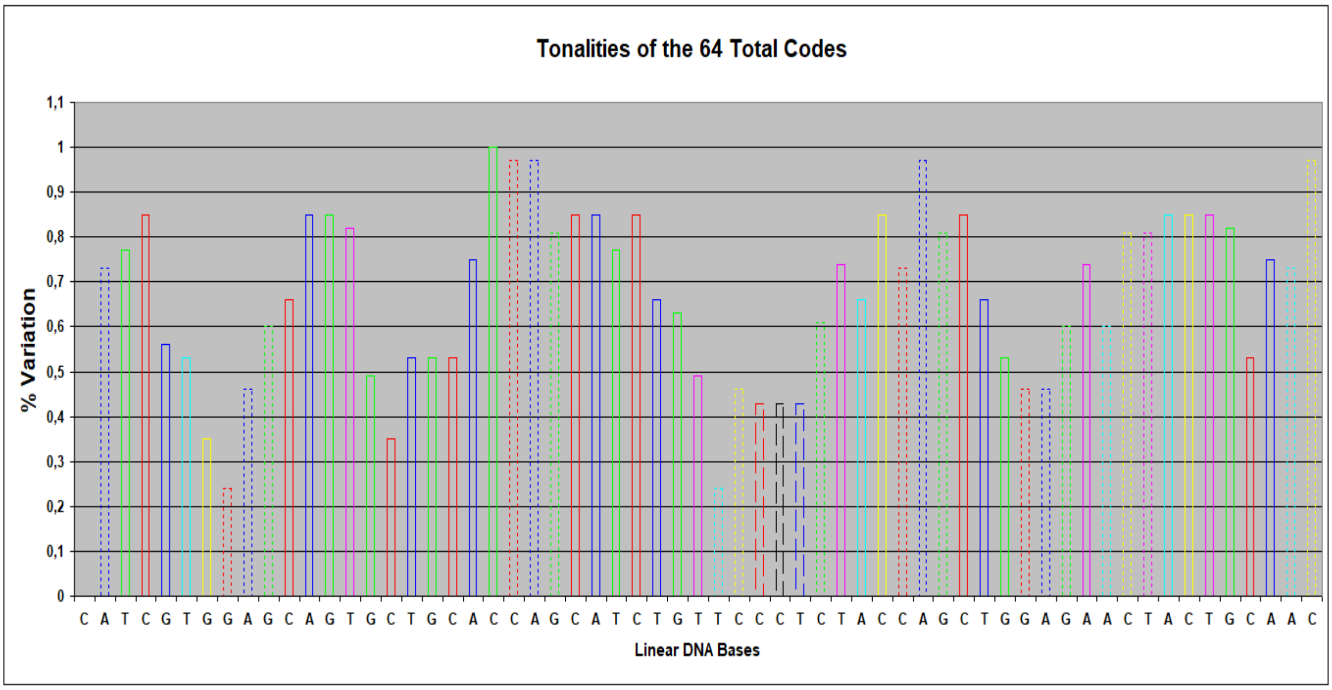
The chart in Pct. 34 (B) refers to the **"new generated sequence"** that originates from the original one.



Pct. 34 (B)

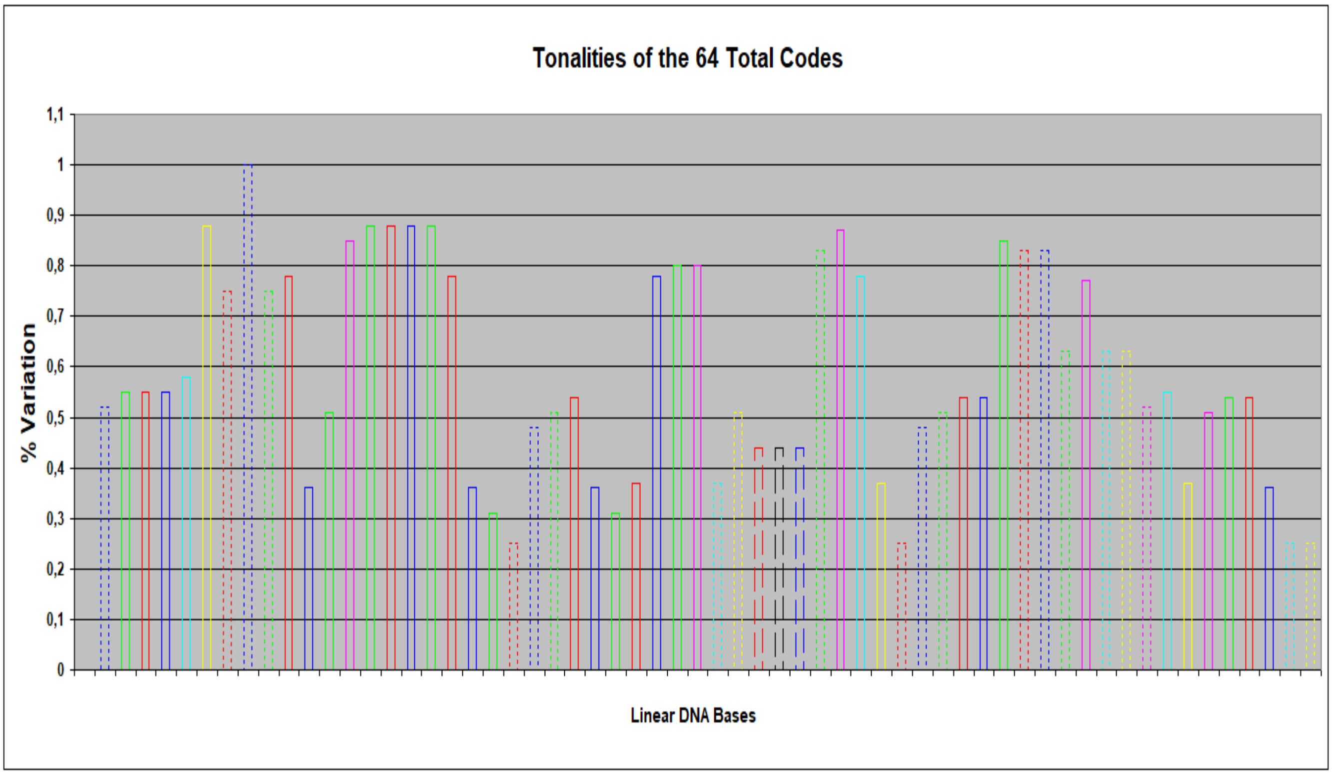
In Pct. 35 (A and B) two charts concerning the single **Tonalities of the 64 Total Codes** are compared.

The chart in Pct. 35 (A) refers to the **original base sequence** analysed before.



Pct. 35 (A)

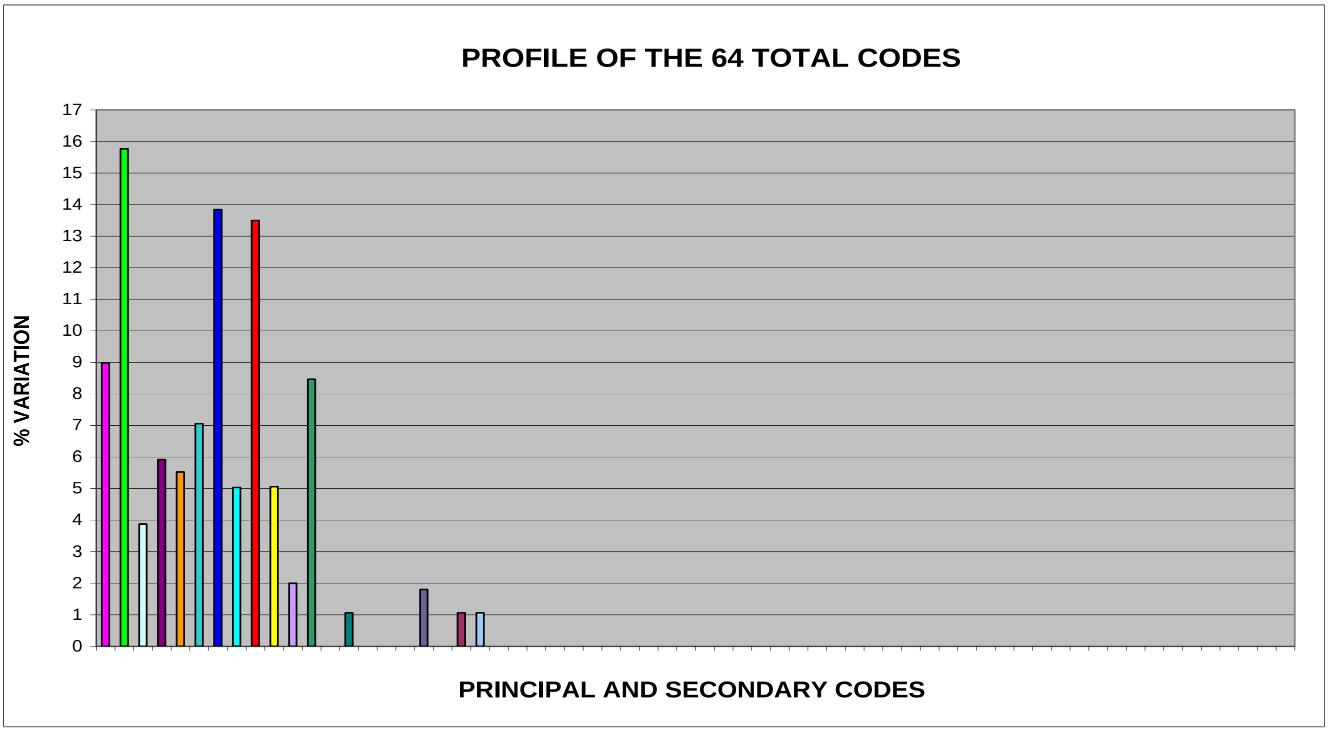
The chart in Pct. 35 (B) refers to the **"new generated sequence"** that originates from the original one.



Pct. 35 (B)

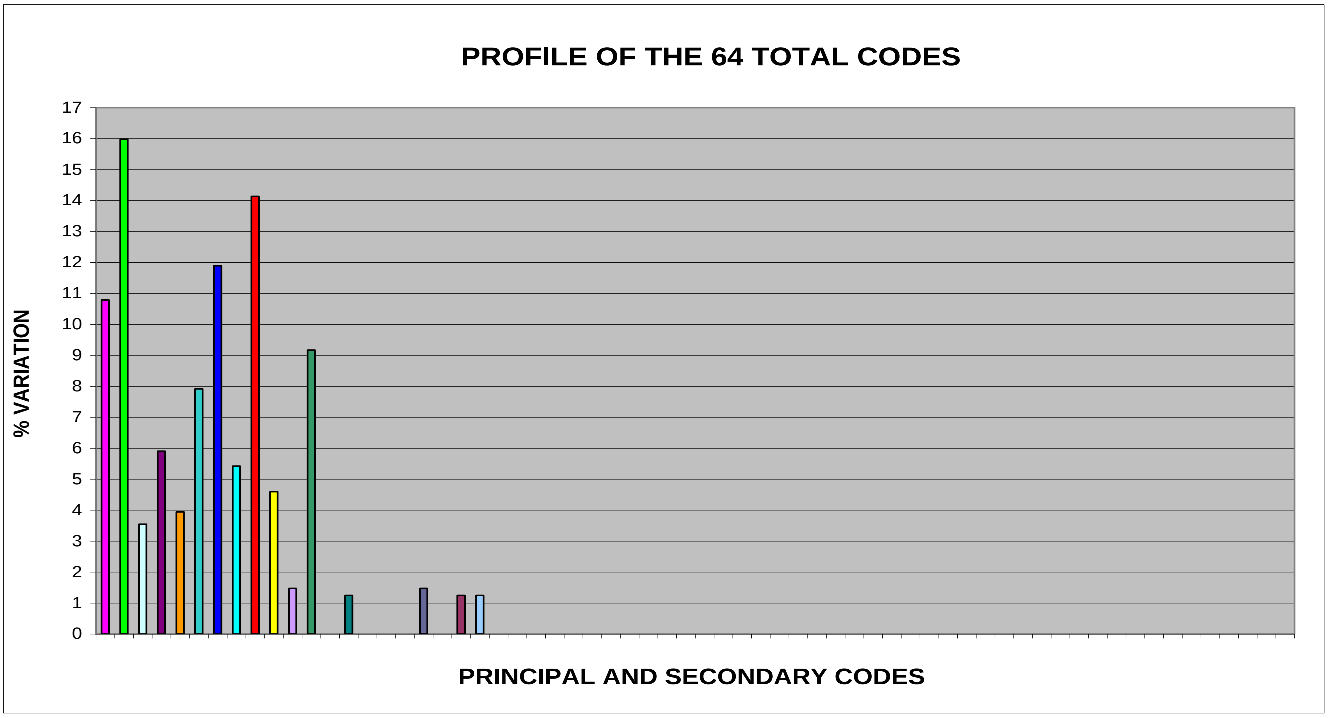
In Pct. 36 (A and B) two charts concerning the **Profile of the 64 Total Codes** are compared.

The chart in Pct. 36 (A) refers to the **original base sequence** analysed before.



Pct. 36 (A)

The chart in Pct. 36 (B) refers to the **“new generated sequence”** originated from the original one.



Pct. 36 (B)

The “non-obvious trend” analysis (obtained through the **T.T.E.S.**) of **Sequence n°9/1 of Insulin Chain A** results in **a comparison among different graphs** that are going to be interpreted in an analogous way to that in which the graphs related to the “non-obvious trend” of the **Sequences** analysed in the previous paragraphs **(n° 1/1, n° 2/1, etc.)** were. In order to avoid repetitions, here, the reader is deferred to the interpretation of the **comparisons among the different graphs** presented in the paragraph 1.2 .

Before concluding the paragraph, it is worth noting that, out of the **63** DNA bases of **Sequence n° 9/1**, ONLY **ELEVEN BASES** (the **17,46%**)**,** ARE EQUAL (by type and by position in sequence) TO THOSE OF THE ORIGINAL SEQUENCE (**Insulin Chain A**).

1.19 IMPLICATIONS RELATED TO THE GRAPHIC RESULTS OF THE "NON-OBVIOUS TREND" ANALYSIS OF SEQUENCE n° 9/1 OF INSULIN CHAIN A

The **63** DNA base sequence of the **new generated sequence** (**Sequence n° 9/1**) that arises from the **original** one has been subjected to **BLAST** research.

Please note:

Information about the ***significant alignments*** produced by *BLAST research*, related to **Sequence n° 9/1,** and all the data acquired from *GenBank (3)* will be published in the **Appendix,** after the *General Conclusions.*

Query = NEW GENERATED SEQUENCE (Sequence n° 9/1)

Length = 63

Parameters of BLAST research:

Programme	*Blastn*
Word size	*11*
Expect value	*10*
Hitlist size	*100*
Match/Mismatch scores	*2,-3*
Gapcosts	*5,2*
Low Complexity Filter	*Yes*
Filter string	*L;m;*
Genetic Code	*1*

Please note:

Here, "**the organisms found to be in common**" between the results of BLAST research carried out on **Insulin Chain A** and results of BLAST research carried out on **Sequence n° 9/1**, were highlighted in **Red**.
As well, "**the organisms found to be in common**" between the results of BLAST research carried out on **Insulin Chain A**, results of BLAST research carried out on **Sequence n° 9/1** and results of BLAST research carried out on **at least one** of the *19 generated sequences*, were highlighted in **Green**.
Moreover, "**the denomination of the sequence**" (1/1, 2/1, ... 19/1) of the "**organism found to be in common**" between the results of BLAST research carried out on **Sequence n° 9/1** and results of BLAST research carried out on **at least one** of the *19 new generated sequences*, were highlighted in **Blue**.
Finally, "**the denomination of the sequence**" (1/1, 2/1, ... 19/1) of the "**organism found to be in common**" between the results of BLAST research carried out on **Insulin Chain A** and results of BLAST research carried out on *19 generated sequences*, were highlighted in **Yellow**.

Sequenza n° 9/1

Sequences producing significant alignments:

Selected seq	Description	Max score	Total score	Query cover	E value	Ident	Accession
1 XM_024001609.1	PREDICTED: Salvelinus alpinus succinyl-CoA:3-ketoacid coenzyme A transferase 1, mitochondrial-like (LOC111974083), mRNA	41.0	41.0	61%	2.7	83%	XM_024001609.1
2 LT594789.1	Theobroma cacao genome assembly, chromosome: II	40.1	40.1	38%	9.5	96%	LT594789.1
3 AC022535.6	Homo sapiens chromosome 10 clone RP11-34C15, complete sequence	40.1	40.1	46%	9.5	90%	AC022535.6
4 XM_028542626.1	PREDICTED: Dendronephthya gigantea E3 ubiquitin-protein ligase HUWE1-like (LOC114522023), transcript variant X3, mRNA	39.2	39.2	41%	9.6	92%	XM_028542626.1
5 XM_028542625.1	PREDICTED: Dendronephthya gigantea E3 ubiquitin-protein ligase HUWE1-like (LOC114522023), transcript variant X2, mRNA	39.2	39.2	41%	9.6	92%	XM_028542625.1
6 XM_028542624.1	PREDICTED: Dendronephthya gigantea E3 ubiquitin-protein ligase HUWE1-like (LOC114522023), transcript variant X1, mRNA	39.2	39.2	41%	9.6	92%	XM_028542624.1
7 XM_027757911.1	Sparassis crispa Ribose-phosphate pyrophosphokinase 2 (SCP_0411840), partial mRNA	39.2	39.2	50%	9.5	88%	XM_027757911.1
8 **14/1** XM_026120534.1	PREDICTED: Dromaius novaehollandiae WD repeat domain 24 (WDR24), mRNA	39.2	39.2	60%	9.5	84%	XM_026120534.1
9 **14/1** XM_026048985.1	PREDICTED: Nothoprocta perdicaria WD repeat domain 24 (WDR24), mRNA	39.2	39.2	60%	9.5	84%	XM_026048985.1
10 XR_002223386.1	PREDICTED: Microcebus murinus uncharacterized LOC109730508 (LOC109730508), ncRNA	39.2	39.2	41%	9.5	92%	XR_002223386.1
11 XM_020316910.1	PREDICTED: Aegilops tauschii subsp. tauschii sodium/hydrogen exchanger 8-like (LOC109758065), transcript variant X7, mRNA	39.2	39.2	33%	9.5	100%	XM_020316910.1

Sequences producing significant alignments:

Selected seq	Description	Max score	Total score	Query cover	E value	Ident	Accession
12 XM_020316908.1	PREDICTED: Aegilops tauschii subsp. tauschii sodium/hydrogen exchanger 8-like (LOC109758065), transcript variant X6, mRNA	39.2	39.2	33%	9.5	100%	XM_020316908.1
13 XM_020316906.1	PREDICTED: Aegilops tauschii subsp. tauschii sodium/hydrogen exchanger 8-like (LOC109758065), transcript variant X4, mRNA	39.2	39.2	33%	9.5	100%	XM_020316906.1
14 XM_020316905.1	PREDICTED: Aegilops tauschii subsp. tauschii sodium/hydrogen exchanger 8-like (LOC109758065), transcript variant X3, mRNA	39.2	39.2	33%	9.5	100%	XM_020316905.1
15 XM_020316904.1	PREDICTED: Aegilops tauschii subsp. tauschii sodium/hydrogen exchanger 8-like (LOC109758065), transcript variant X2, mRNA	39.2	39.2	33%	9.5	100%	XM_020316904.1
16 XM_020316903.1	PREDICTED: Aegilops tauschii subsp. tauschii sodium/hydrogen exchanger 8-like (LOC109758065), transcript variant X1, mRNA	39.2	39.2	33%	9.5	100%	XM_020316903.1
17 XM_007290474.1	Marssonina brunnea f. sp. 'multigermtubi' MB_m1 putative ribose-phosphate pyrophosphokinase 1 (MBM_02647), mRNA	39.2	39.2	50%	9.5	88%	XM_007290474.1
18 **5/1** **14/1** XM_003878010.1	Leishmania mexicana MHOM/GT/2001/U1103 conserved hypothetical protein partial mRNA	39.2	39.2	49%	9.5	87%	XM_003878010.1
19 **14/1** CP002903.1	Spirochaeta thermophila DSM 6578, complete genome	39.2	39.2	49%	9.5	87%	CP002903.1
20 **5/1** **14/1** FR799584.1	Leishmania mexicana MHOM/GT/2001/U1103 complete genome, chromosome 31	39.2	39.2	49%	9.5	87%	FR799584.1

Comparison between the alignments of Sequence 9/1 and Sequence of Insulin Chain A according to the "Species of Common Organisms":

Alignments Sequence 9/1	**Description**	**Alignments Sequence Insulin Chain A**	**Description**
1 Select seq XM_024001609.1	PREDICTED: Salvelinus alpinus succinyl-CoA:3-ketoacid coenzyme A transferase 1, mitochondrial-like (LOC111974083), mRNA	Select seq XM_023968633.1	PREDICTED: Salvelinus alpinus insulin (LOC111950763), mRNA
2 Select seq LT594789.1	Theobroma cacao genome assembly, chromosome: II	Select seq LT594792.1 **17/1**	Theobroma cacao genome assembly, chromosome: V
3 Select seq AC022535.6	Homo sapiens chromosome 10 clone RP11-34C15, complete sequence	Select seq AH002844.2 **2/1 8/1 10/1 15/1 17/1**	Homo sapiens insulin (INS) gene, complete cds
		Select seq AH012037.2 **2/1 8/1 10/1 15/1 17/1**	Homo sapiens haplotype ICa tyrosine hydroxylase (TH) gene, partial sequence; insulin (INS) gene, complete cds; and insulin-like growth factor 2 (IGF2) gene, partial sequence
		Select seq NG_050578.1 **2/1 8/1 10/1 15/1 17/1**	Homo sapiens INS-IGF2 readthrough (INS-IGF2), RefSeqGene on chromosome 11
		Select seq KR710184.1 **2/1 8/1 10/1 15/1 17/1**	Synthetic construct Homo sapiens clone CCSBHm_00010257 INS (INS) mRNA, encodes complete protein
		Select seq KR710183.1 **2/1 8/1 10/1 15/1 17/1**	Synthetic construct Homo sapiens clone CCSBHm_00010256 INS (INS) mRNA, encodes complete protein
		Select seq KR710182.1 **2/1 8/1 10/1 15/1 17/1**	Synthetic construct Homo sapiens clone CCSBHm_00010255 INS (INS) mRNA, encodes complete protein
		Select seq KJ891480.1 **2/1 8/1 10/1 15/1 17/1**	Synthetic construct Homo sapiens clone ccsbBroadEn_00874 INS gene, encodes complete protein

Comparison between the alignments of Sequence 9/1 and Sequence of Insulin Chain A according to the “Species of Common Organisms”:

Alignments Sequence 9/1	Description	Alignments Sequence Insulin Chain A	Description
		Select seq NM_001291897.1 **2/1** **8/1** **10/1** **15/1** **17/1**	Homo sapiens insulin (INS), transcript variant 4, mRNA
		Select seq JQ951950.1 **2/1** **8/1** **10/1** **15/1** **17/1**	Homo sapiens preproinsulin (INS) mRNA, complete cds
		Select seq JF909299.1 **2/1** **8/1** **10/1** **15/1** **17/1**	Homo sapiens insulin (INS) mRNA, partial cds
		Select seq AB587580.1 **2/1** **8/1** **10/1** **15/1** **17/1**	Synthetic construct DNA, clone: pF1KB8864, Homo sapiens INS gene for insulin, without stop codon, in Flexi system
		Select seq NM_001185098.1 **2/1** **8/1** **10/1** **15/1** **17/1**	Homo sapiens insulin (INS), transcript variant 3, mRNA
		Select seq NM_001185097.1 **2/1** **8/1** **10/1** **15/1** **17/1**	Homo sapiens insulin (INS), transcript variant 2, mRNA
		Select seq NG_007114.1 **2/1** **8/1** **10/1** **15/1** **17/1**	Homo sapiens insulin (INS), RefSeqGene on chromosome 11
		Select seq DQ778082.1 **2/1** **8/1** **10/1** **15/1** **17/1**	Homo sapiens clone BFC06103 insulin mRNA, complete cds
		Select seq DQ896283.2 **2/1** **8/1** **10/1** **15/1** **17/1**	Synthetic construct Homo sapiens clone IMAGE:100010743; FLH192918.01L; RZPDo839A1068D insulin (INS) gene, encodes complete protein
		Select seq NM_000207.2 **2/1** **8/1** **10/1** **15/1** **17/1**	Homo sapiens insulin (INS), transcript variant 1, mRNA

Comparison between the alignments of Sequence 9/1 and Sequence of Insulin Chain A according to the "Species of Common Organisms":

Alignments Sequence 9/1	**Description**	**Alignments Sequence Insulin Chain A**	**Description**
		Select seq BT007778.1 **2/1 8/1 10/1 15/1 17/1**	Synthetic construct Homo sapiens insulin mRNA, partial cds
		Select seq BT006808.1 **2/1 8/1 10/1 15/1 17/1**	Homo sapiens insulin mRNA, complete cds
		Select seq BC005255.1 **2/1 8/1 10/1 15/1 17/1**	Homo sapiens insulin, mRNA (cDNA clone MGC:12292 IMAGE:3950204), complete cds
		Select seq AC132217.15 **2/1 8/1 10/1 15/1 17/1**	Homo sapiens chromosome 11, clone RP11-889I17, complete sequence
		Select seq AC130303.8 **2/1 8/1 10/1 15/1 17/1**	Homo sapiens chromosome 11, clone RP4-539G11, complete sequence
		Select seq AY899304.1 **2/1 8/1 10/1 15/1 17/1**	Homo sapiens proinsulin mRNA, complete cds, alternatively spliced
		Select seq AJ009655.1 **2/1 8/1 10/1 15/1 17/1**	Homo sapiens ins gene, partial
		Select seq X70508.1 **2/1 8/1 10/1 15/1 17/1**	Homo sapiens mRNA for insulinoma pre-proinsulin
		Select seq L15440.1 **2/1 8/1 10/1 15/1 17/1**	Homo sapiens tyrosine hydroxylase (TH) gene, 3' end; insulin (INS) gene, complete cds; insulin-like growth factor 2 (IGF2) gene, 5' end
		Select seq KR710185.1 **2/1 8/1 10/1 15/1 17/1**	Synthetic construct Homo sapiens clone CCSBHm_00010262 INS (INS) mRNA, encodes complete protein

Comparison between the alignments of Sequence 9/1 and Sequence of Insulin Chain A according to the “Species of Common Organisms”:

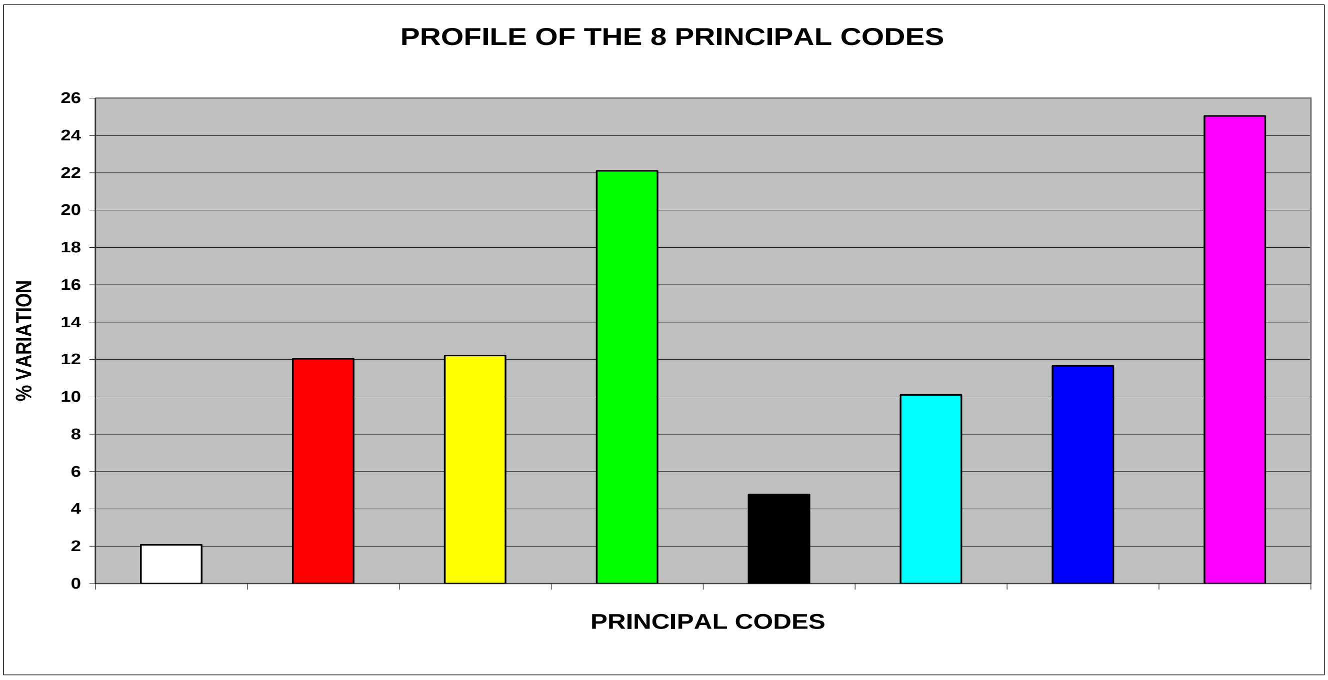
Alignments Sequence 9/1	**Description**	**Alignments Sequence Insulin Chain A**	**Description**
		Select seq AF050524.1 **2/1 8/1 10/1 15/1 17/1**	Synthetic Homo sapiens proinsulin-like protein BKRA gene, complete cds
		Select seq AC021233.9 **2/1 8/1 10/1 15/1 17/1**	Homo sapiens chromosome 11, clone RP11-215H22, complete sequence
		Select seq AK024581.1 **2/1 8/1 10/1 15/1 17/1**	Homo sapiens cDNA: FLJ20928 fis, clone ADSE01074
8 Select seq XM_026120534.1 **14/1**	PREDICTED: Dromaius novaehollandiae WD repeat domain 24 (WDR24), mRNA	Select seq XM_026092712.1 **14/1**	PREDICTED: Dromaius novaehollandiae insulin (INS), mRNA
9 Select seq XM_026048985.1 **14/1**	PREDICTED: Nothoprocta perdicaria WD repeat domain 24 (WDR24), mRNA	Select seq XM_026036815.1 **14/1**	PREDICTED: Nothoprocta perdicaria insulin (INS), mRNA
10 Select seq XR_002223386.1	PREDICTED: Microcebus murinus uncharacterized LOC109730508 (LOC109730508), ncRNA	Select seq XM_012743999.1	PREDICTED: Microcebus murinus insulin (INS), mRNA

Analysis of
Sequence n° 10/1
of Insulin Chain A

1. 20 GRAPHIC RESULTS OF THE “NON-OBVIOUS TREND” ANALYSIS OF SEQUENCE n° 10/1 OF INSULIN CHAIN A

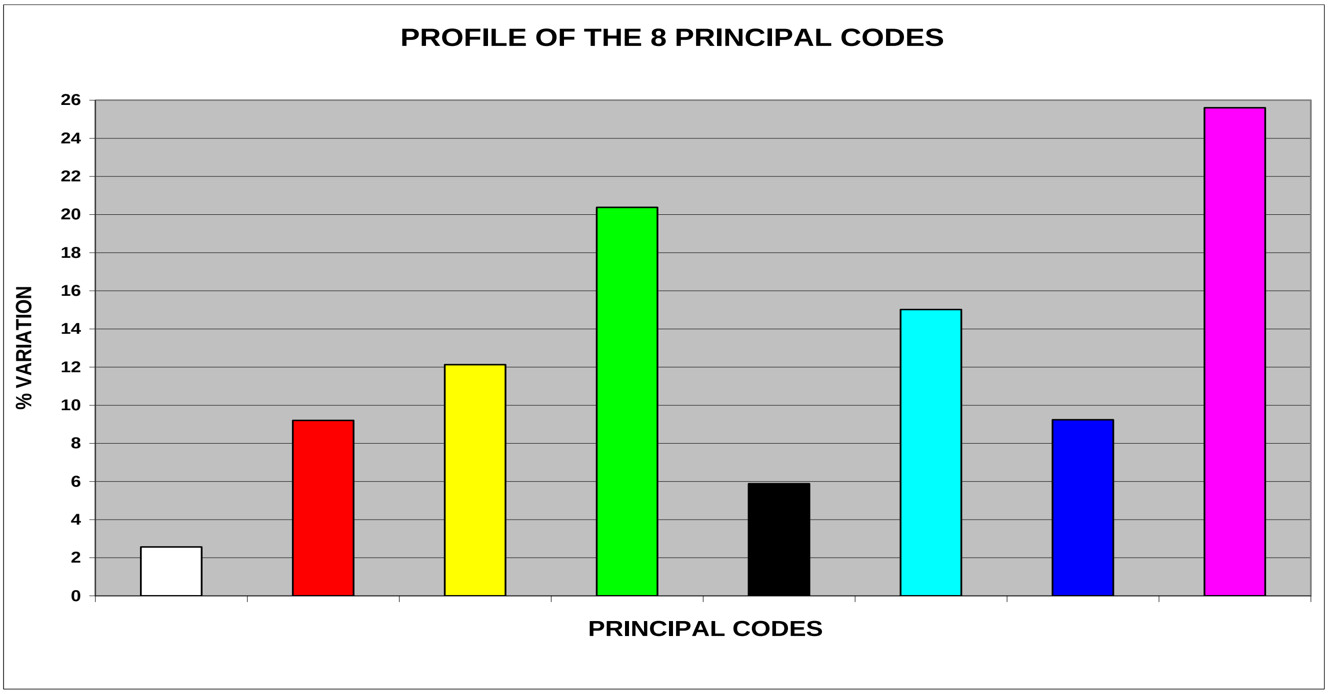
In the Pct. 37 (A e B) two **8 Principal Codes Profiles** are compared.

The chart in Pct. 37 (A) refers to the **original base sequence** of **Insulin Chain A**.



Pct. 37 (A)

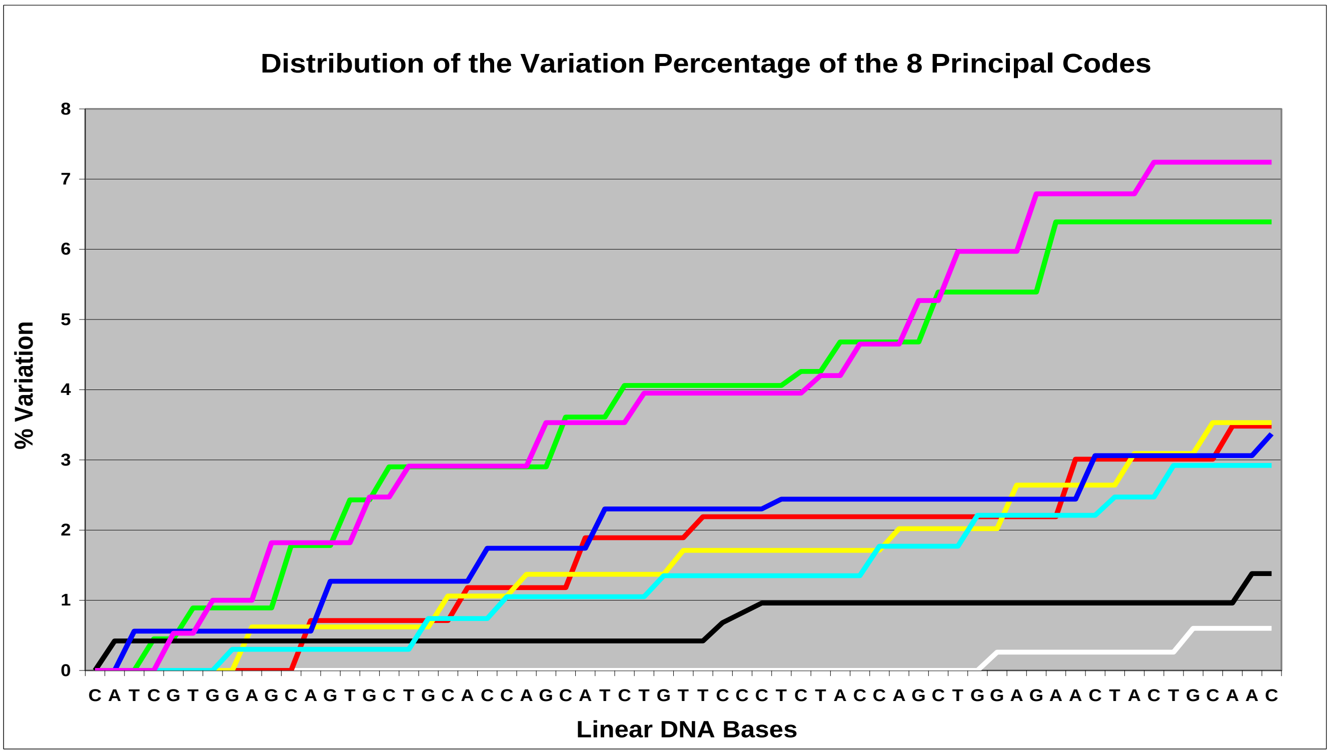
The chart in Pct. 37 (B) refers to the **tithe** **“new generated sequence”** (**Sequence n° 10/1**) that originates from the original one.



Pct. 37 (B)

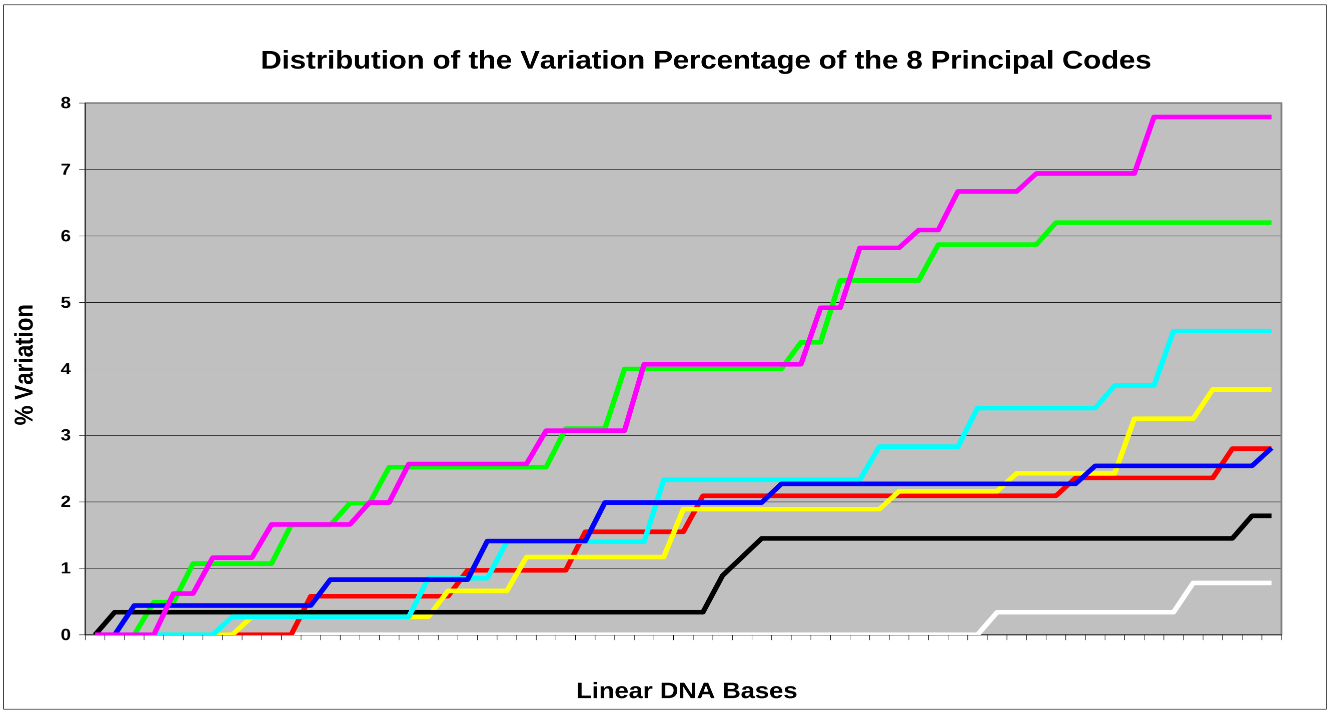
In Pct. 38 (A and B) two charts concerning the **Distribution of the Variation Percentage of the 8 Main Codes** are compared.

The charts in Pct. 38 (A) refers to the **original base sequence** analysed before.



Pct. 38 (A)

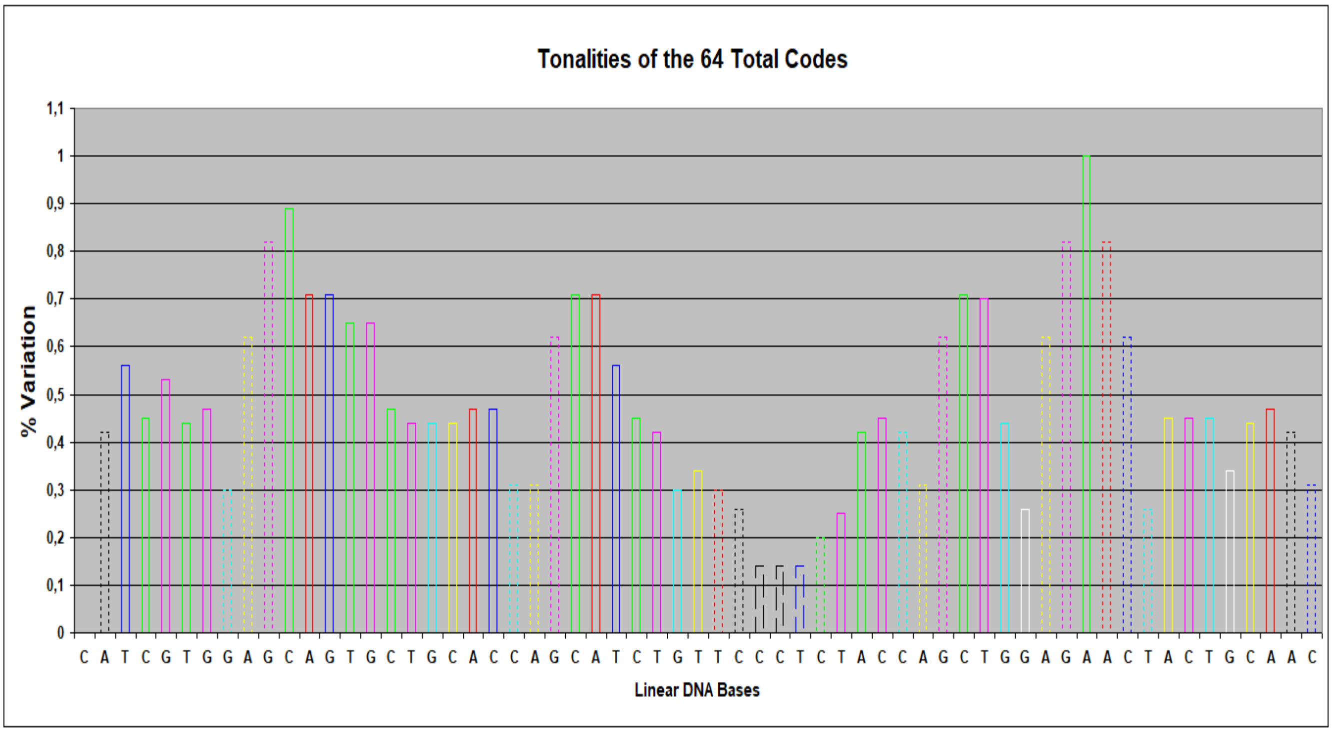
The chart in Pct. 38 (B) refers to the **“new generated sequence”** that originates from the original one.



Pct. 38 (B)

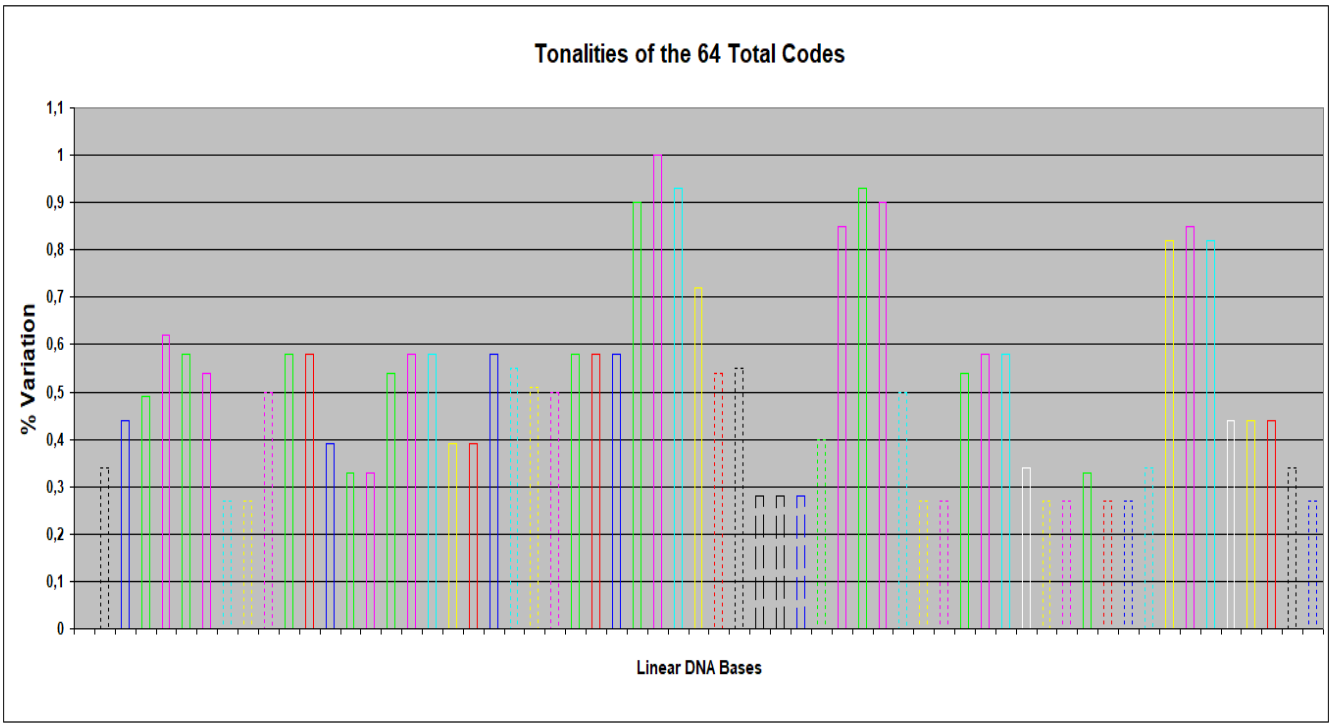
In Pct. 39 (A and B) two charts concerning the single **Tonalities of the 64 Total Codes** are compared.

The chart in Pct. 39 (A) refers to the **original base sequence** analysed before.



Pct. 39 (A)

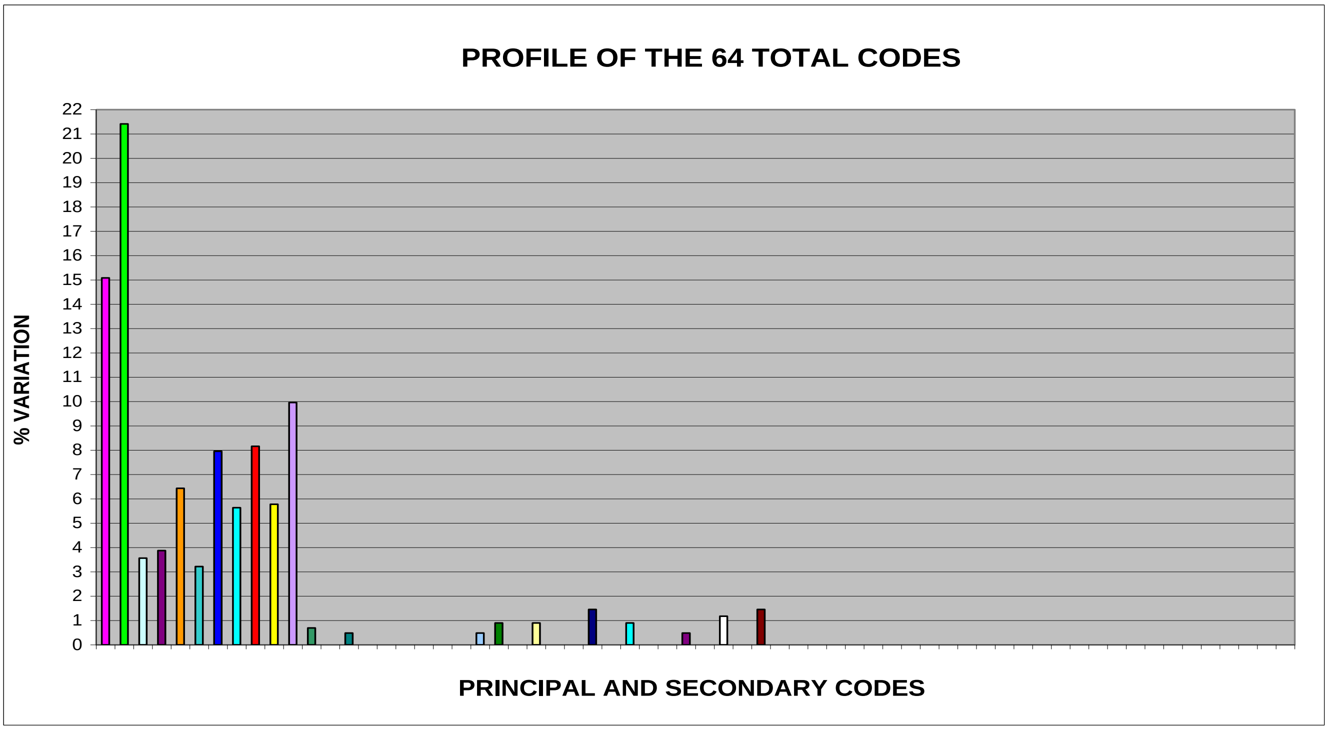
The chart in Pct. 39 (B) refers to the **“new generated sequence”** that originates from the original one.



Pct. 39 (B)

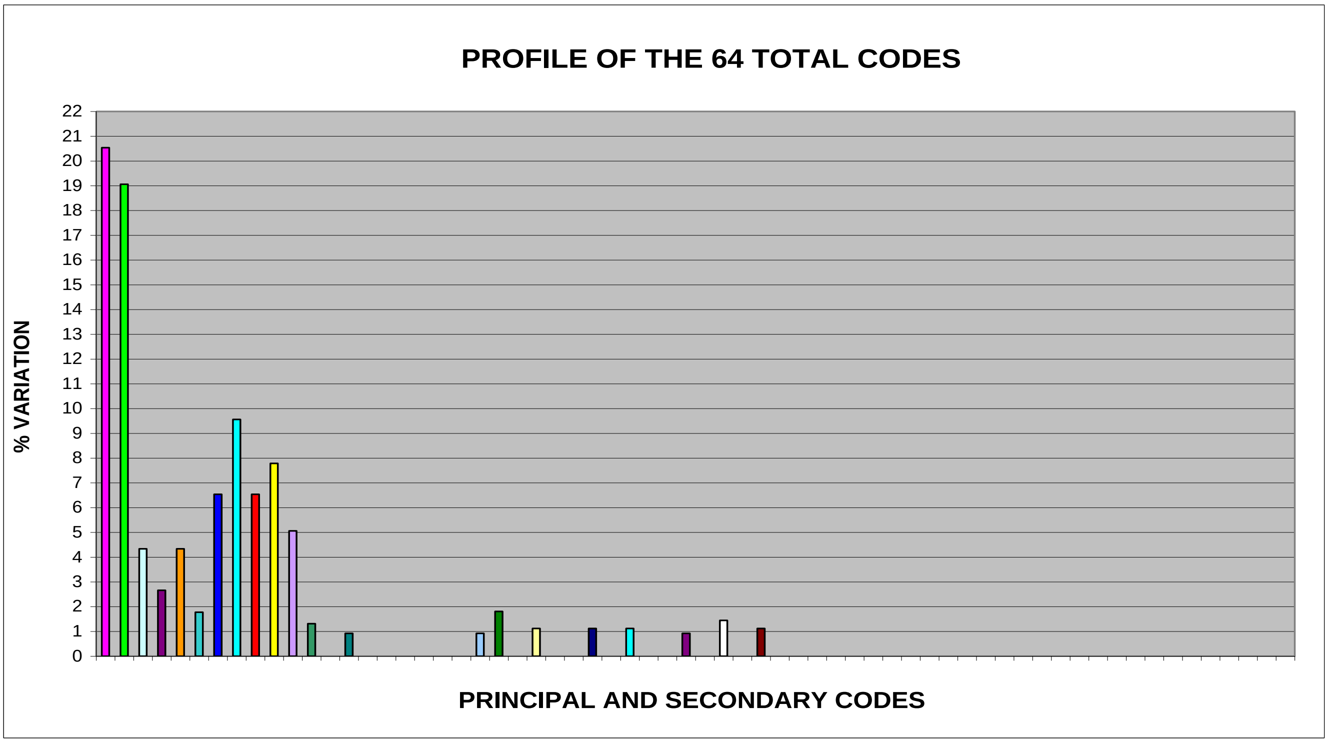
In Pct. 40 (A and B) two charts concerning the **Profile of the 64 Total Codes** are compared.

The chart in Pct. 40 (A) refers to the **original base sequence** analysed before.



Pct. 40 (A)

The chart in Pct. 40 (B) refers to the **“new generated sequence”** originated from the original one.



Pct. 40 (B)

The “non-obvious trend” analysis (obtained through the **T.T.E.S.**) of **Sequence n°10/1 of Insulin Chain A** results in **a comparison among different graphs** that are going to be interpreted in an analogous way to that in which the graphs related to the “non-obvious trend” of the **Sequences** analysed in the previous paragraphs **(n° 1/1, n° 2/1, etc.)** were. In order to avoid repetitions, here, the reader is deferred to the interpretation of the **comparisons among the different graphs** presented in the paragraph 1.2 .

Before concluding the paragraph, it is worth noting that, out of the **63** DNA bases of **Sequence n° 10/1**, ONLY **TWELVE BASES** (the **19,05%**)**,** ARE EQUAL (by type and by position in sequence) TO THOSE OF THE ORIGINAL SEQUENCE (**Insulin Chain A**).

1.21 IMPLICATIONS RELATED TO THE GRAPHIC RESULTS OF THE "NON-OBVIOUS TREND" ANALYSIS OF SEQUENCE n° 10/1 OF INSULIN CHAIN A

The **63** DNA base sequence of the **new generated sequence** (**Sequence n° 10/1**) that arises from the **original** one has been subjected to **BLAST** research.

Please note:

Information about the ***significant alignments*** produced by *BLAST research*, related to **Sequence n° 10/1,** and all the data acquired from *GenBank (3)* will be published in the **Appendix,** after the *General Conclusions.*

Query = NEW GENERATED SEQUENCE (Sequence n° 10/1)

Length = 63

Parameters of BLAST research:

Programme	*Blastn*
Word size	*11*
Expect value	*10*
Hitlist size	*100*
Match/Mismatch scores	*2,-3*
Gapcosts	*5,2*
Low Complexity Filter	*Yes*
Filter string	*L;m;*
Genetic Code	*1*

Please note:

Here, "**the organisms found to be in common**" between the results of BLAST research carried out on **Insulin Chain A** and results of BLAST research carried out on **Sequence n° 10/1**, were highlighted in **Red**.
As well, "**the organisms found to be in common**" between the results of BLAST research carried out on **Insulin Chain A**, results of BLAST research carried out on **Sequence n° 10/1** and results of BLAST research carried out on **at least one** of the *19 generated sequences*, were highlighted in **Green**.
Moreover, "**the denomination of the sequence**" (1/1, 2/1, ... 19/1) of the "**organism found to be in common**" between the results of BLAST research carried out on **Sequence n° 10/1** and results of BLAST research carried out on **at least one** of the *19 new generated sequences*, were highlighted in **Blue**.
Finally, "**the denomination of the sequence**" (1/1, 2/1, ... 19/1) of the "**organism found to be in common**" between the results of BLAST research carried out on **Insulin Chain A** and results of BLAST research carried out on *19 generated sequences*, were highlighted in **Yellow**.

Sequenza n° 10/1

Sequences producing significant alignments:

Selected seq	Description	Max score	Total score	Query cover	E value	Ident	Accession
1 AH011549.2	Mus musculus chromosome 16 thioredoxin reductase (Trxr2) gene, complete cds	41.0	41.0	68%	2.6	82%	AH011549.2
2 AC003067.59	Mus musculus Chromosome 16 BAC Clone tbx3 Syntenic To Homo sapiens 22q11.2 DGCR Region, complete sequence	41.0	41.0	68%	2.6	82%	AC003067.59
3 AC133488.30	Mus musculus strain C57BL/6J clone rp23-432e14, complete sequence	41.0	41.0	68%	2.6	82%	AC133488.30
4 AC003066.18	Mus musculus Chromosome 16 BAC Clone tbx1 Syntenic To Homo sapiens 22q11.2 DGCR Region, complete sequence	41.0	41.0	68%	2.6	82%	AC003066.18
5 AC133487.14	Mus musculus strain C57BL/6J clone rp23-285e22, complete sequence	41.0	41.0	68%	2.6	82%	AC133487.14
6 LR132010.1	Betta splendens genome assembly, chromosome: 7	40.1	40.1	38%	9.5	96%	LR132010.1
7 **13/1** LN649230.1	Fusarium venenatum strain A3/5 genome assembly, chromosome: II	40.1	40.1	60%	9.5	88%	LN649230.1
8 XM_014081268.1	Ogataea parapolymorpha DL-1 hypothetical protein partial mRNA	40.1	40.1	46%	9.5	90%	XM_014081268.1
9 JN958484.1	Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Usp22:tm1a(KOMP)Wtsi; transgenic	40.1	40.1	41%	9.5	96%	JN958484.1
10 JN950499.1	Mus musculus targeted non-conditional, lacZ-tagged mutant allele Usp22:tm1e(KOMP)Wtsi; transgenic	40.1	40.1	41%	9.5	96%	JN950499.1
11 AL646093.9	Mouse DNA sequence from clone RP23-55I2 on chromosome 11, complete sequence	40.1	40.1	41%	9.5	96%	AL646093.9
12 AC025910.19	Mus musculus 11 BAC RP23-40J4 (Roswell Park Cancer Institute Mouse BAC) complete sequence	40.1	40.1	41%	9.5	96%	AC025910.19
13 CP038190.1	Caenorhabditis elegans strain CB4856 chromosome IV	39.2	39.2	41%	9.6	92.31%	CP038190.1

Sequences producing significant alignments:

Selected seq	Description	Max score	Total score	Query cover	E value	Ident	Accession
14 CP026245.1	Scophthalmus maximus chromosome 3	39.2	39.2	41%	9.5	92%	CP026245.1
15 6/1 XM_024644634.1	Strongyloides ratti Neuroglian (SRAE_X000030500), partial mRNA	39.2	39.2	33%	9.5	100%	XM_024644634.1
16 XM_024403100.1	PREDICTED: Oncorhynchus tshawytscha vimentin-like (LOC112234799), mRNA	39.2	39.2	57%	9.5	83%	XM_024403100.1
17 XM_022753695.1	PREDICTED: Seriola dumerili BCL2 like 12 (bcl2l12), mRNA	39.2	39.2	41%	9.5	92%	XM_022753695.1
18 XM_021574948.1	PREDICTED: Oncorhynchus mykiss neurofilament light polypeptide-like (LOC110498314), mRNA	39.2	39.2	57%	9.5	83%	XM_021574948.1
19 XM_020476863.1	PREDICTED: Oncorhynchus kisutch neurofilament light polypeptide-like (LOC109884981), mRNA	39.2	39.2	57%	9.5	83%	XM_020476863.1
20 12/1 XR_001013343.1	PREDICTED: Cercocebus atys pepsin A-like (LOC105581134), misc_RNA	39.2	39.2	33%	9.5	100%	XR_001013343.1
21 XM_011302441.1	PREDICTED: Fopius arisanus nuclear RNA export factor 1-like (LOC105265120), mRNA	39.2	39.2	53%	9.5	89%	XM_011302441.1
22 LK928621.1	Caenorhabditis elegans genome assembly C_elegans_Bristol_N2_v1_5_4, scaffold CELN2_contig0000311	39.2	39.2	41%	9.5	92%	LK928621.1
23 6/1 LN609530.1	Strongyloides ratti genome assembly S_ratti_ED321, chromosome : X	39.2	39.2	33%	9.5	100%	LN609530.1
24 XM_005841697.1	Guillardia theta CCMP2712 hypothetical protein (GUITHDRAFT_63031) mRNA, partial cds	39.2	39.2	44%	9.5	93%	XM_005841697.1
25 Z70284.3	Caenorhabditis elegans Cosmid K07F5, complete sequence	39.2	39.2	41%	9.5	92%	Z70284.3
26 CT978603.1	Synechococcus sp. RCC307 genomic DNA sequence	39.2	39.2	41%	9.5	92%	CT978603.1
27 17/1 BT000771.1	Arabidopsis thaliana clone RAFL08-14-H03 (R11349) putative long-chain acyl-CoA synthetase (At3g16170) mRNA, complete cds	39.2	39.2	65%	9.5	80%	BT000771.1

Comparison between the alignments of Sequence 10/1 and Sequence of Insulin Chain A according to the "Species of Common Organisms":

Alignments Sequence 10/1	Description	Alignments Sequence Insulin Chain A	Description
1 Select seq AH011549.2	Mus musculus chromosome 16 thioredoxin reductase (Trxr2) gene, complete cds	Select seq XM_021152514.1 **1/1 6/1 8/1** **13/1 17/1 18/1**	PREDICTED: Mus caroli insulin-1 (LOC110286053), mRNA
2 Select seq AC003067.59	Mus musculus Chromosome 16 BAC Clone tbx3 Syntenic To Homo sapiens 22q11.2 DGCR Region, complete sequence	Select seq DQ250565.1 **1/1 6/1 8/1** **13/1 17/1 18/1**	Mus caroli preproinsulin 1 (Ins1) gene, complete cds
3 Select seq AC133488.30	Mus musculus strain C57BL/6J clone rp23-432e14, complete sequence	Select seq XM_021215010.1 **1/1 6/1 8/1** **13/1 17/1 18/1**	PREDICTED: Mus pahari insulin-1 (LOC110333420), mRNA
4 Select seq AC003066.18	Mus musculus Chromosome 16 BAC Clone tbx1 Syntenic To Homo sapiens 22q11.2 DGCR Region, complete sequence	Select seq NM_008386.4 **1/1 6/1 8/1** **13/1 17/1 18/1**	Mus musculus insulin I (Ins1), mRNA
5 Select seq AC133487.14	Mus musculus strain C57BL/6J clone rp23-285e22, complete sequence	Select seq BC145868.1 **1/1 6/1 8/1** **13/1 17/1 18/1**	Mus musculus insulin I, mRNA (cDNA clone MGC:175755 IMAGE:40131171), complete cds
9 Select seq JN958484.1	Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Usp22:tm1a(KOMP)Wtsi; transgenic	Select seq DQ479923.1 **1/1 6/1 8/1** **13/1 17/1 18/1**	Mus musculus strain BTBR T+ tf/J insulin 1 precursor, gene, complete cds
10 Select seq JN950499.1	Mus musculus targeted non-conditional, lacZ-tagged mutant allele Usp22:tm1e(KOMP)Wtsi; transgenic	Select seq AC163452.12 **1/1 6/1 8/1** **13/1 17/1 18/1**	Mus musculus chromosome 19, clone RP23-405C7, complete sequence
12 Select seq AC025910.19	Mus musculus 11 BAC RP23-40J4 (Roswell Park Cancer Institute Mouse BAC) complete sequence	Select seq AC136710.8 **1/1 6/1 8/1** **13/1 17/1 18/1**	Mus musculus chromosome 19, clone RP23-35B13, complete sequence
		Select seq AC140320.2 **1/1 6/1 8/1** **13/1 17/1 18/1**	Mus musculus BAC clone RP23-401C13 from chromosome 19, complete sequence

Comparison between the alignments of Sequence 10/1 and Sequence of Insulin Chain A according to the “Species of Common Organisms”:

Alignments Sequence 10/1	**Description**	**Alignments Sequence Insulin Chain A**	**Description**
		Select seq BC098468.1 **1/1 6/1 8/1** **13/1 17/1 18/1**	Mus musculus insulin I, mRNA (cDNA clone MGC:107382 IMAGE:6432765), complete cds
		Select seq AK148541.1 **1/1 6/1 8/1** **13/1 17/1 18/1**	Mus musculus adult pancreas islet cells cDNA, RIKEN full-length enriched library, clone:C820020F18 product:insulin I, full insert sequence
		Select seq AK007345.1 **1/1 6/1 8/1** **13/1 17/1 18/1**	Mus musculus 10 day old male pancreas cDNA, RIKEN full-length enriched library, clone:1810005L03 product:INSULIN 1 PRECURSOR, full insert sequence
		Select seq XM_021168754.1 **1/1 6/1 8/1** **13/1 17/1 18/1**	PREDICTED: Mus caroli insulin-2 (LOC110299132), transcript variant X2, mRNA
		Select seq XM_021168753.1 **1/1 6/1 8/1** **13/1 17/1 18/1**	PREDICTED: Mus caroli insulin-2 (LOC110299132), transcript variant X1, mRNA
		Select seq NM_001185084.2 **1/1 6/1 8/1** **13/1 17/1 18/1**	Mus musculus insulin II (Ins2), transcript variant 3, mRNA
		Select seq NM_001185083.2 **1/1 6/1 8/1** **13/1 17/1 18/1**	Mus musculus insulin II (Ins2), transcript variant 1, mRNA
		Select seq NM_008387.5 **1/1 6/1 8/1** **13/1 17/1 18/1**	Mus musculus insulin II (Ins2), transcript variant 2, mRNA
		Select seq JN959239.1 **1/1 6/1 8/1** **13/1 17/1 18/1**	Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Ins2:tm1a(EUCOMM)Wtsi; transgenic
		Select seq JN951270.1 **1/1 6/1 8/1** **13/1 17/1 18/1**	Mus musculus targeted non-conditional, lacZ-tagged mutant allele Ins2:tm1e(EUCOMM)Wtsi; transgenic

Comparison between the alignments of Sequence 10/1 and Sequence of Insulin Chain A according to the “Species of Common Organisms”:

Alignments Sequence 10/1	**Description**	**Alignments Sequence Insulin Chain A**	**Description**
		Select seq BC145554.1 **1/1 6/1 8/1** **13/1 17/1 18/1**	Mus musculus insulin II, mRNA (cDNA clone MGC:179126 IMAGE:9054118), complete cds
		Select seq BC099934.1 **1/1 6/1 8/1** **13/1 17/1 18/1**	Mus musculus insulin II, mRNA (cDNA clone MGC:107381 IMAGE:6432976), complete cds
		Select seq BC132650.1 **1/1 6/1 8/1** **13/1 17/1 18/1**	Mus musculus insulin II, mRNA (cDNA clone MGC:164281 IMAGE:40130927), complete cds
		Select seq DQ250569.1 **1/1 6/1 8/1** **13/1 17/1 18/1**	Mus caroli preproinsulin 2 (Ins2) gene, complete cds
		Select seq AK007612.1 **1/1 6/1 8/1** **13/1 17/1 18/1**	Mus musculus 10 day old male pancreas cDNA, RIKEN full-length enriched library, clone:1810027C14 product:INSULIN 2 PRECURSOR, full insert sequence
		Select seq AK007482.1 **1/1 6/1 8/1** **13/1 17/1 18/1**	Mus musculus 10 day old male pancreas cDNA, RIKEN full-length enriched library, clone:1810013J24 product:INSULIN 1 PRECURSOR, full insert sequence
		Select seq BC066208.1 **1/1 6/1 8/1** **13/1 17/1 18/1**	Mus musculus insulin II, mRNA (cDNA clone IMAGE:6436276)
		Select seq AC012382.14 **1/1 6/1 8/1** **13/1 17/1 18/1**	Mus musculus chromosome 7, clone RP23-92L23, complete sequence
		Select seq AY899305.1 **1/1 6/1 8/1** **13/1 17/1 18/1**	Mus musculus proinsulin mRNA, complete cds, alternatively spliced
		Select seq AC013548.13 **1/1 6/1 8/1** **13/1 17/1 18/1**	Mus musculus chromosome 7, clone RP23-209O22, complete sequence

Comparison between the alignments of Sequence 10/1 and Sequence of Insulin Chain A according to the "Species of Common Organisms":

Alignments Sequence 10/1	**Description**	**Alignments Sequence Insulin Chain A**	**Description**
		Select seq AP003182.2 **1/1 6/1 8/1** **13/1 17/1 18/1**	Mus musculus genomic DNA, chromosome 7 clone:B189M11, complete sequences
		Select seq GQ915612.1 **1/1 6/1 8/1** **13/1 17/1 18/1**	Mus musculus insulin-2 precursor (Ins2) mRNA, partial cds, alternatively spliced
		Select seq XM_021204833.1 **1/1 6/1 8/1** **13/1 17/1 18/1**	PREDICTED: Mus pahari insulin-2 (LOC110326410), transcript variant X2, mRNA
		Select seq XM_021204825.1 **1/1 6/1 8/1** **13/1 17/1 18/1**	PREDICTED: Mus pahari insulin-2 (LOC110326410), transcript variant X1, mRNA
6 Select seq LR132010.1	Betta splendens genome assembly, chromosome: 7	Select seq LR132016.1 **4/1 17/1**	Betta splendens genome assembly, chromosome: 14
		Select seq LR132007.1 **4/1 17/1**	Betta splendens genome assembly, chromosome: 10
11 Select seq AL646093.9	Mouse DNA sequence from clone RP23-55I2 on chromosome 11, complete sequence	Select seq X04725.1 **8/1 13/1 17/1**	Mouse preproinsulin gene I
		Select seq X04725.1 **8/1 13/1 17/1**	Mouse preproinsulin gene II
14 Select seq CP026245.1	Scophthalmus maximus chromosome 3	Select seq CP026246.1 **13/1 17/1**	Scophthalmus maximus chromosome 4
		Select seq CP026255.1 **13/1 17/1**	Scophthalmus maximus chromosome 13
16 Select seq XM_024403100.1	PREDICTED: Oncorhynchus tshawytscha vimentin-like (LOC112234799), mRNA	Select seq XM_024402922.1 **6/1 17/1**	PREDICTED: Oncorhynchus tshawytscha insulin-like (LOC112234674), mRNA

Comparison between the alignments of Sequence 10/1 and Sequence of Insulin Chain A according to the “Species of Common Organisms”:

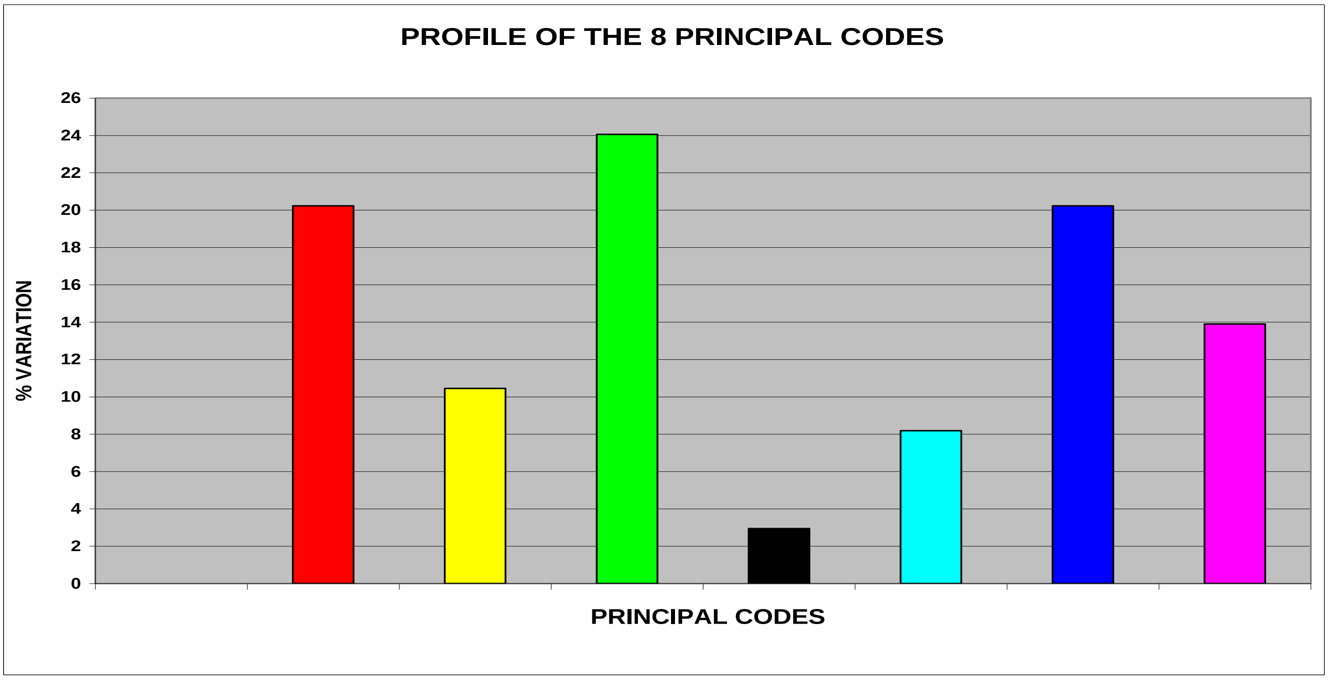
Alignments Sequence 10/1	Description	Alignments Sequence Insulin Chain A	Description
18 Select seq XM_021574948.1	PREDICTED: Oncorhynchus mykiss neurofilament light polypeptide-like (LOC110498314), mRNA	Select seq XM_024402921.1 **6/1 17/1**	PREDICTED: Oncorhynchus tshawytscha insulin-like (LOC112234673), mRNA
19 Select seq XM_020476863.1	PREDICTED: Oncorhynchus kisutch neurofilament light polypeptide-like (LOC109884981), mRNA	Select seq XM_020464884.1 **6/1 17/1**	PREDICTED: Oncorhynchus kisutch insulin-like (LOC109873252), mRNA
		Select seq NM_001124670.1 **6/1 17/1**	Oncorhynchus mykiss preproinsulin 2 (LOC100136703), mRNA
		Select seq L11712.1 **6/1 17/1**	Oncorhynchus keta insulin gene, complete cds
17 Select seq XM_022753695.1	PREDICTED: Seriola dumerili BCL2 like 12 (bcl2l12), mRNA	Select seq XM_022744743.1	PREDICTED: Seriola dumerili insulin (ins), mRNA
		Select seq AB262771.1	Seriola dumerili mRNA for insulin, complete cds, subtype 2
		Select seq XM_022751952.1	PREDICTED: Seriola dumerili insulin-like (LOC111226678), mRNA
20 Select seq XR_001013343.1 **12/1**	PREDICTED: Cercocebus atys pepsin A-like (LOC105581134), misc_RNA	Select seq XM_012041172.1 **12/1**	PREDICTED: Cercocebus atys insulin (INS), transcript variant X3, mRNA
		Select seq XM_012041171.1 **12/1**	PREDICTED: Cercocebus atys insulin (INS), transcript variant X2, mRNA
		Select seq XM_012041169.1 **12/1**	PREDICTED: Cercocebus atys insulin (INS), transcript variant X1, mRNA

Analysis of
Sequence n° 11/1
of Insulin Chain A

1.22 GRAPHIC RESULTS OF THE “NON-OBVIOUS TREND” ANALYSIS OF SEQUENCE n° 11/1 OF INSULIN CHAIN A

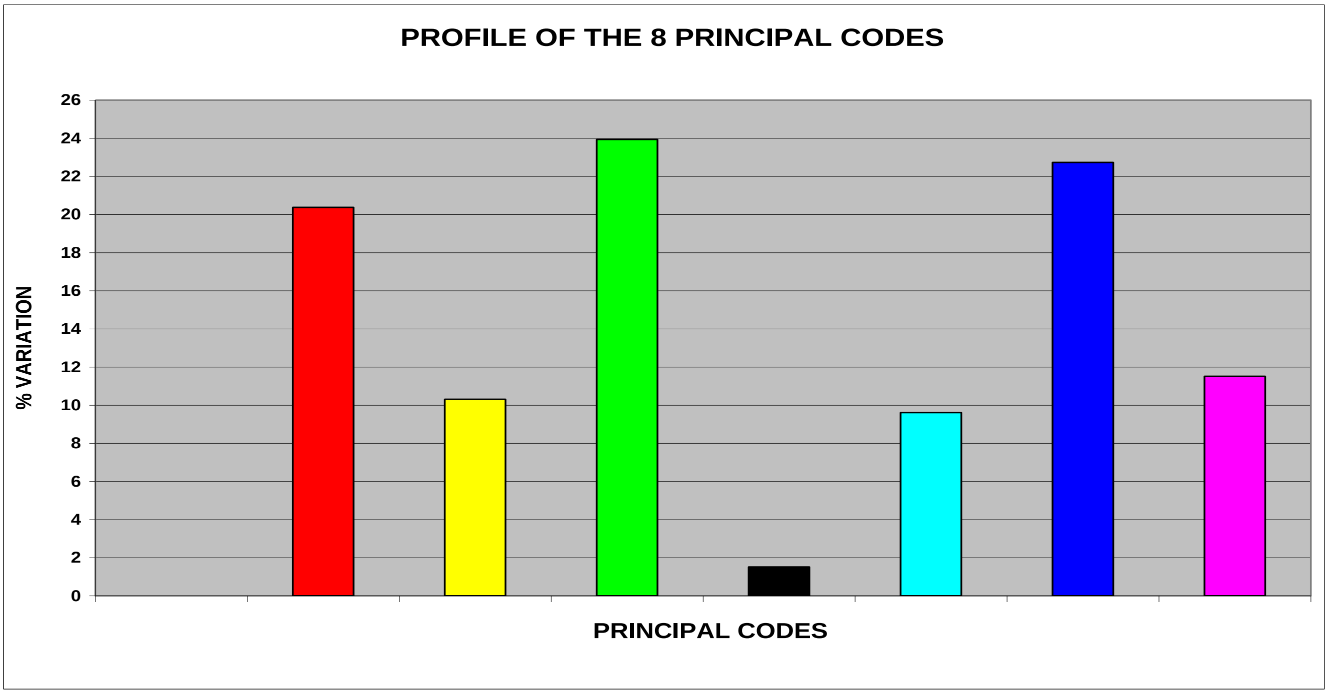
In the Pct. 41 (A e B) two **8 Principal Codes Profiles** are compared.

The chart in Pct. 41 (A) refers to the **original base sequence** of **Insulin Chain A**.



Pct. 41 (A)

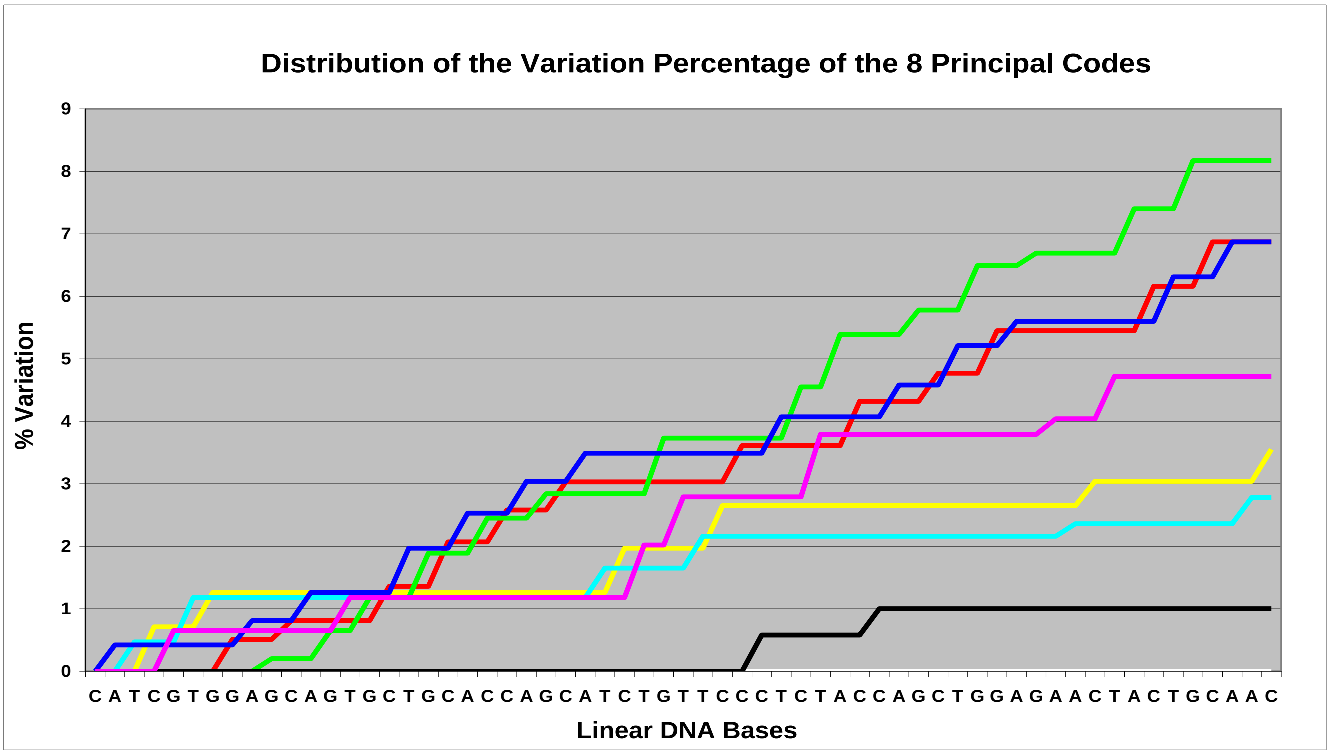
The chart in Pct. 41 (B) refers to the **eleventh** **“new generated sequence”** (**Sequence n°11/1**) that originates from the original one.



Pct. 41 (B)

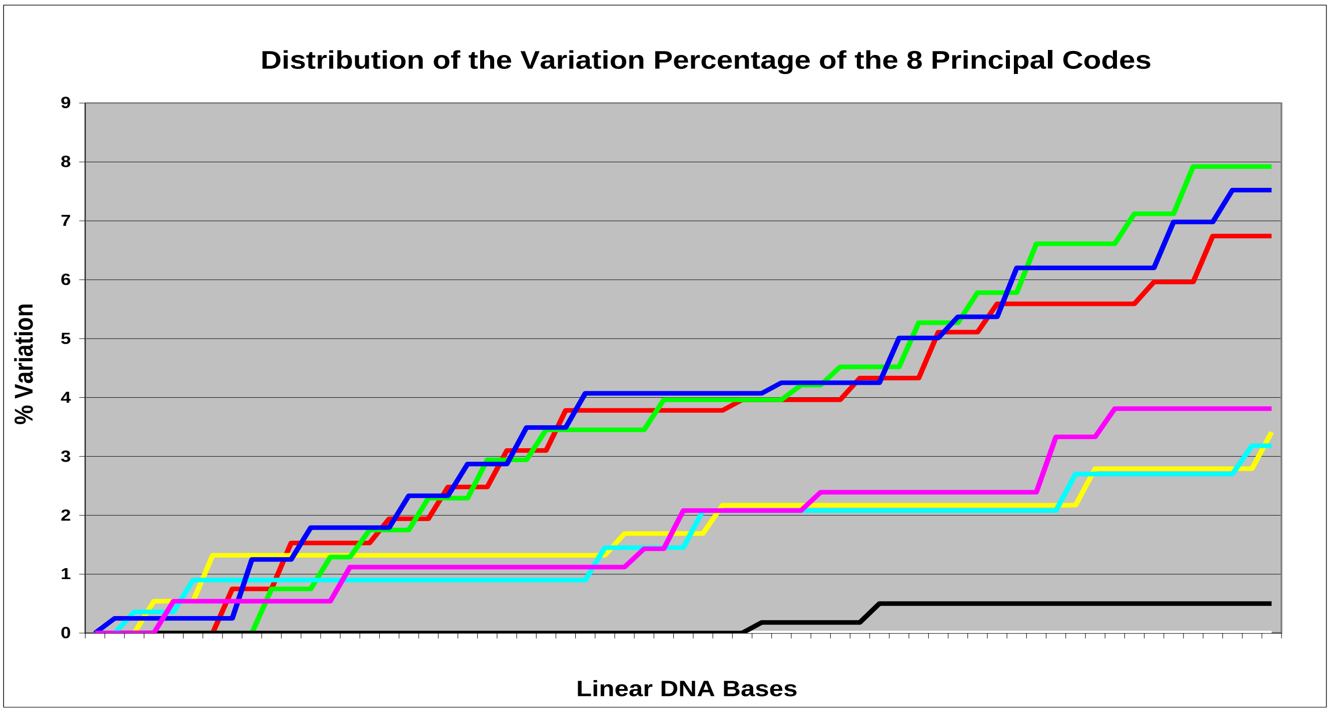
In Pct. 42 (A and B) two charts concerning the **Distribution of the Variation Percentage of the 8 Main Codes** are compared.

The charts in Pct. 42 (A) refers to the **original base sequence** analysed before.



Pct. 42 (A)

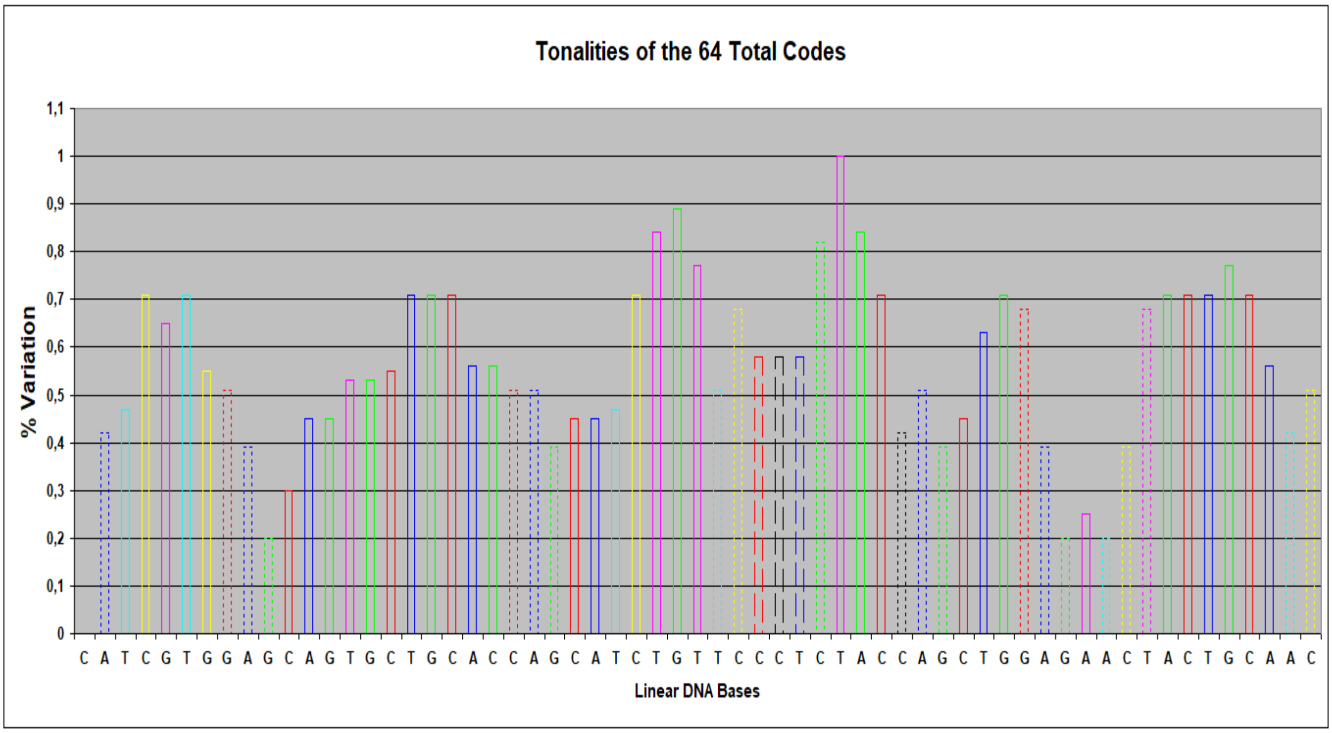
The chart in Pct. 42 (B) refers to the **"new generated sequence"** that originates from the original one.



Pct. 42 (B)

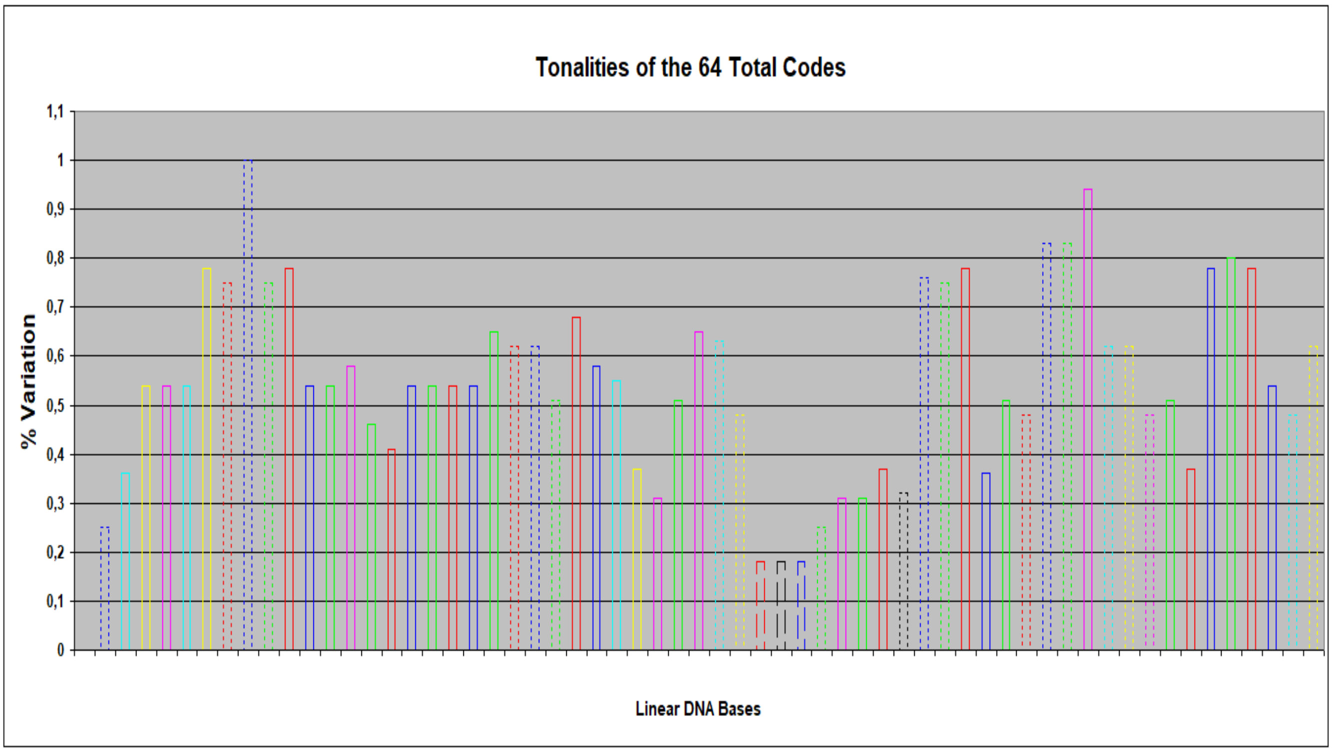
In Pct. 43 (A and B) two charts concerning the single **Tonalities of the 64 Total Codes** are compared.

The chart in Pct. 43 (A) refers to the **original base sequence** analysed before.



Pct. 43 (A)

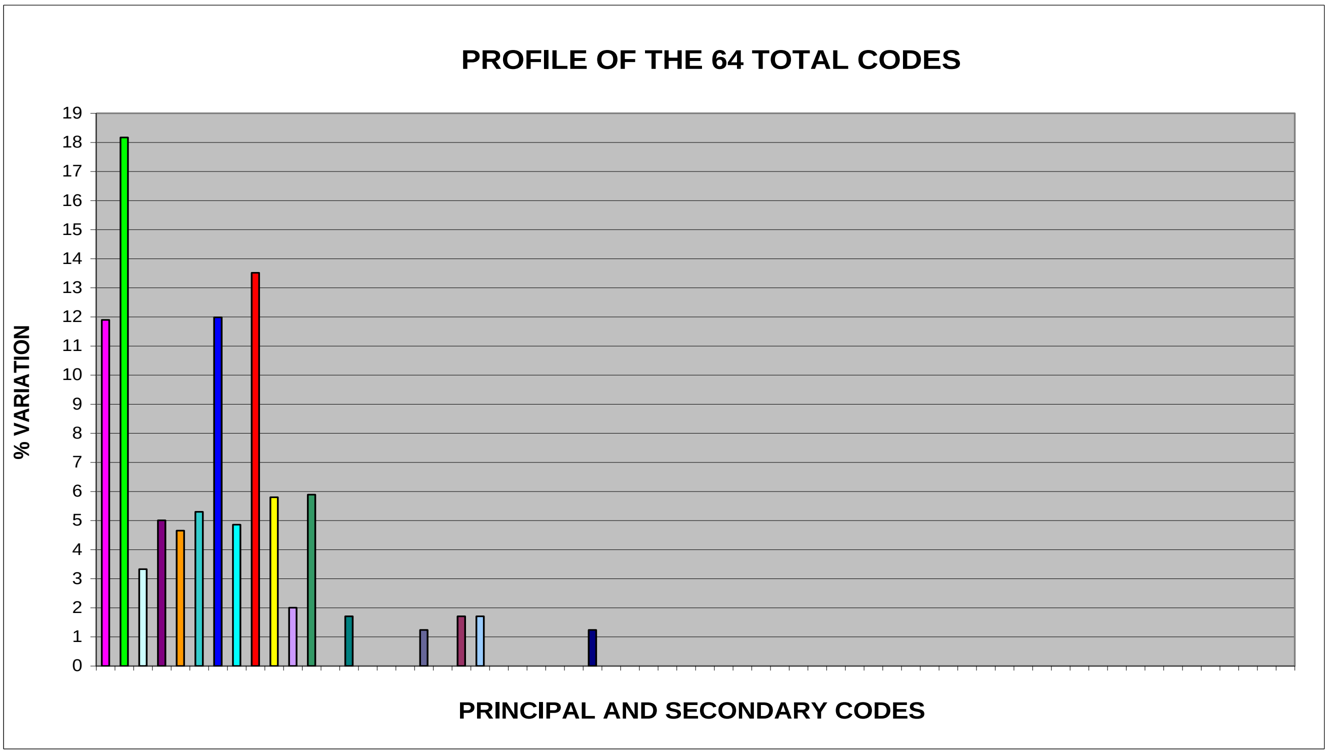
The chart in Pct. 43 (B) refers to the **"new generated sequence"** that originates from the original one.



Pct. 43 (B)

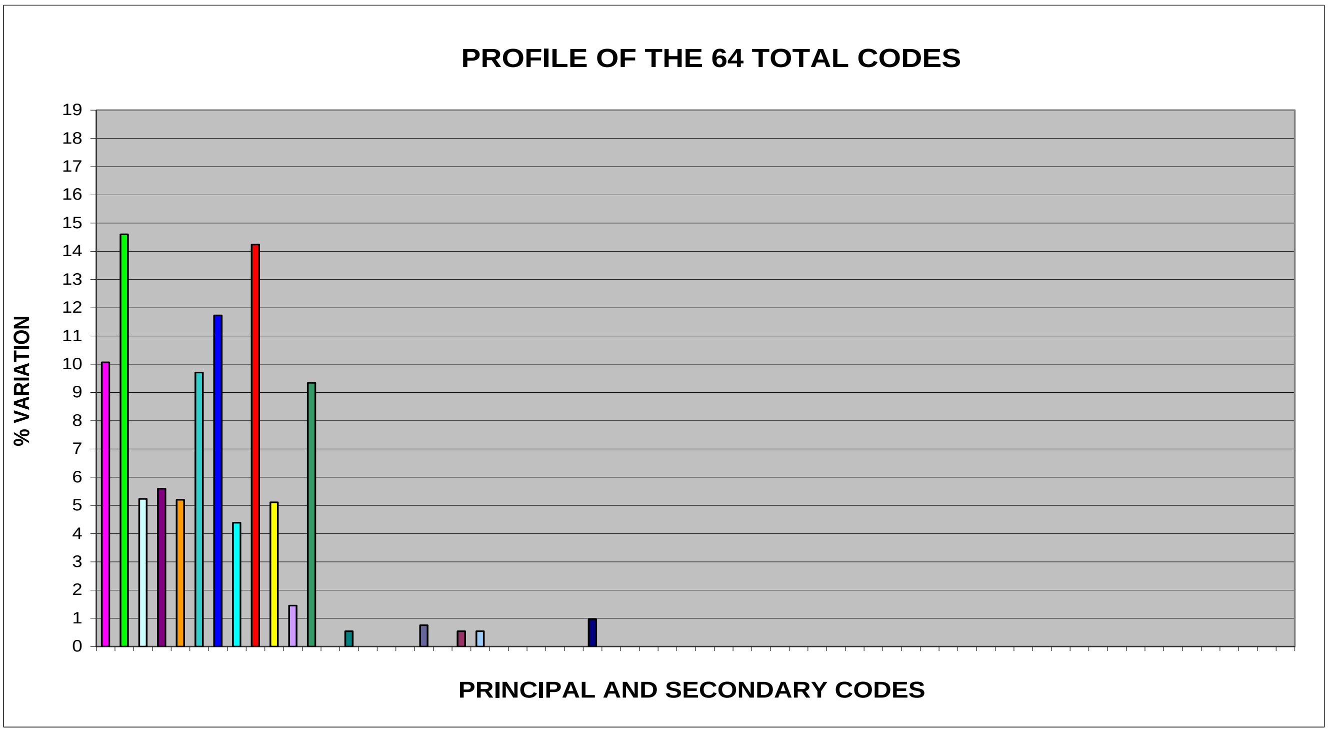
In Pct. 44 (A and B) two charts concerning the **Profile of the 64 Total Codes** are compared.

The chart in Pct. 44 (A) refers to the **original base sequence** analysed before.



Pct. 44 (A)

The chart in Pct. 44 (B) refers to the **"new generated sequence"** originated from the original one.



Pct. 44 (B)

The “non-obvious trend” analysis (obtained through the **T.T.E.S.**) of **Sequence n°11/1 of Insulin Chain A** results in **a comparison among different graphs** that are going to be interpreted in an analogous way to that in which the graphs related to the “non-obvious trend” of the **Sequences** analysed in the previous paragraphs **(n° 1/1, n° 2/1, etc.)** were. In order to avoid repetitions, here, the reader is deferred to the interpretation of the **comparisons among the different graphs** presented in the paragraph 1.2 .

Before concluding the paragraph, it is worth noting that, out of the **63** DNA bases of **Sequence n° 11/1**, ONLY **TEN BASES** (the **15,87%**)**,** ARE EQUAL (by type and by position in sequence) TO THOSE OF THE ORIGINAL SEQUENCE (**Insulin Chain A**).

1.23 IMPLICATIONS RELATED TO THE GRAPHIC RESULTS OF THE "NON-OBVIOUS TREND" ANALYSIS OF SEQUENCE n° 11/1 OF INSULIN CHAIN A

The **63** DNA base sequence of the **new generated sequence** (**Sequence n° 11/1**) that arises from the **original** one has been subjected to **BLAST** research.

Please note:

Information about the ***significant alignments*** produced by *BLAST research*, related to **Sequence n° 11/1,** and all the data acquired from *GenBank (3)* will be published in the **Appendix,** after the *General Conclusions.*

Query = NEW GENERATED SEQUENCE (Sequence n° 11/1)

Length = 63

Parameters of BLAST research:

Programme	*Blastn*
Word size	*11*
Expect value	*10*
Hitlist size	*100*
Match/Mismatch scores	*2,-3*
Gapcosts	*5,2*
Low Complexity Filter	*Yes*
Filter string	*L;m;*
Genetic Code	*1*

Please note:

Here, "**the organisms found to be in common**" between the results of BLAST research carried out on **Insulin Chain A** and results of BLAST research carried out on **Sequence n° 11/1**, were highlighted in **Red**.
As well, "**the organisms found to be in common**" between the results of BLAST research carried out on **Insulin Chain A**, results of BLAST research carried out on **Sequence n° 11/1** and results of BLAST research carried out on **at least one** of the *19 generated sequences*, were highlighted in **Green**.
Moreover, "**the denomination of the sequence**" (1/1, 2/1, ... 19/1) of the "**organism found to be in common**" between the results of BLAST research carried out on **Sequence n° 11/1** and results of BLAST research carried out on **at least one** of the *19 new generated sequences*, were highlighted in **Blue**.
Finally, "**the denomination of the sequence**" (1/1, 2/1, ... 19/1) of the "**organism found to be in common**" between the results of BLAST research carried out on **Insulin Chain A** and results of BLAST research carried out on *19 generated sequences*, were highlighted in **Yellow**.

Sequenza n° 11/1

Sequences producing significant alignments:

Selected seq	Description	Max score	Total score	Query cover	E value	Ident	Accession
1 XM_014704914.1	Bipolaris victoriae FI3 hypothetical protein partial mRNA	41.0	41.0	42%	2.6	93%	XM_014704914.1
2 XM_013459060.1	Exophiala xenobiotica hypothetical protein mRNA	41.0	41.0	42%	2.6	93%	XM_013459060.1
3 XM_007904989.1	PREDICTED: Callorhinchus milii protein tyrosine phosphatase, receptor type, Q (ptprq), mRNA	39.2	39.2	49%	9.5	87%	XM_007904989.1
4 XM_006866173.1	PREDICTED: Chrysochloris asiatica protocadherin alpha subfamily C, 2 (PCDHAC2), transcript variant X1, mRNA	39.2	39.2	41%	9.5	92%	XM_006866173.1

Comparison between the alignments of Sequence 11/1 and Sequence of Insulin Chain A according to the "Species of Common Organisms":

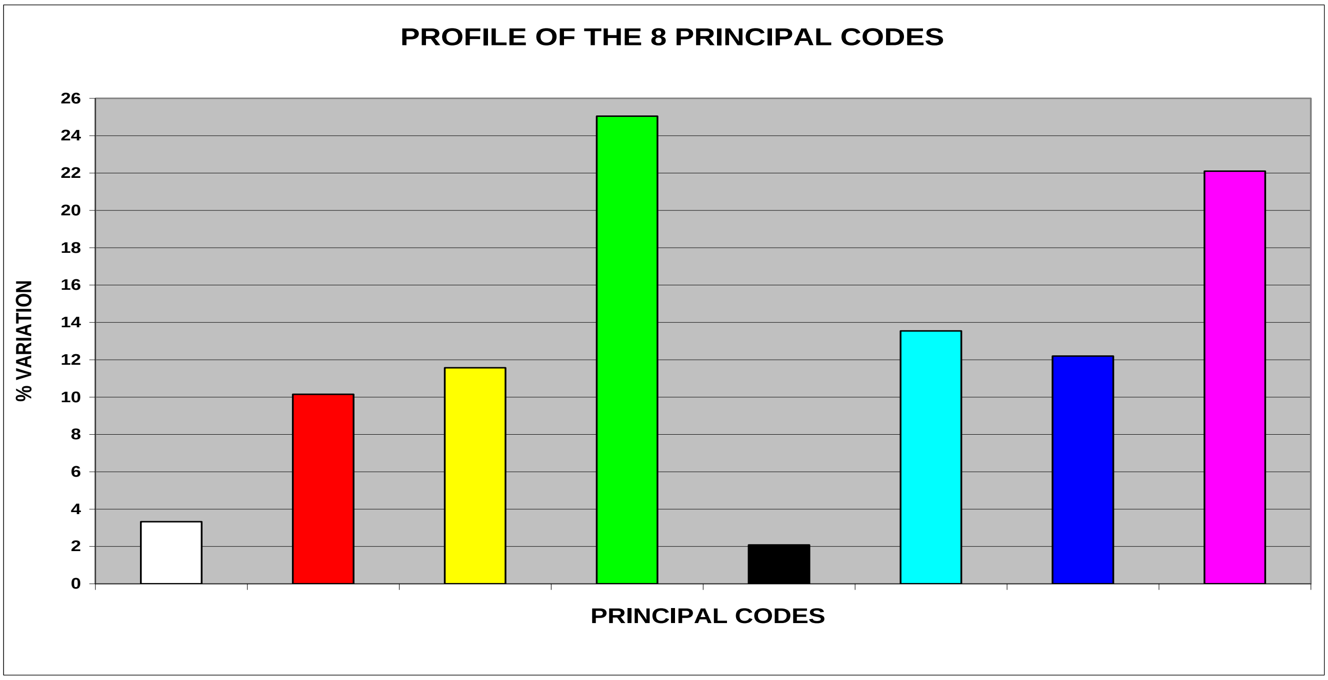
Alignments Sequence 11/1	**Description**	**Alignments Sequence Insulin Chain A**	**Description**
4 Select seq XM_006866173.1	PREDICTED: Chrysochloris asiatica protocadherin alpha subfamily C, 2 (PCDHAC2), transcript variant X1, mRNA	Select seq XM_006860809.1	PREDICTED: Chrysochloris asiatica insulin (INS), mRNA

Analysis of Sequence n° 12/1 of Insulin Chain A

1.24 GRAPHIC RESULTS OF THE “NON-OBVIOUS TREND” ANALYSIS OF SEQUENCE n° 12/1 OF INSULIN CHAIN A

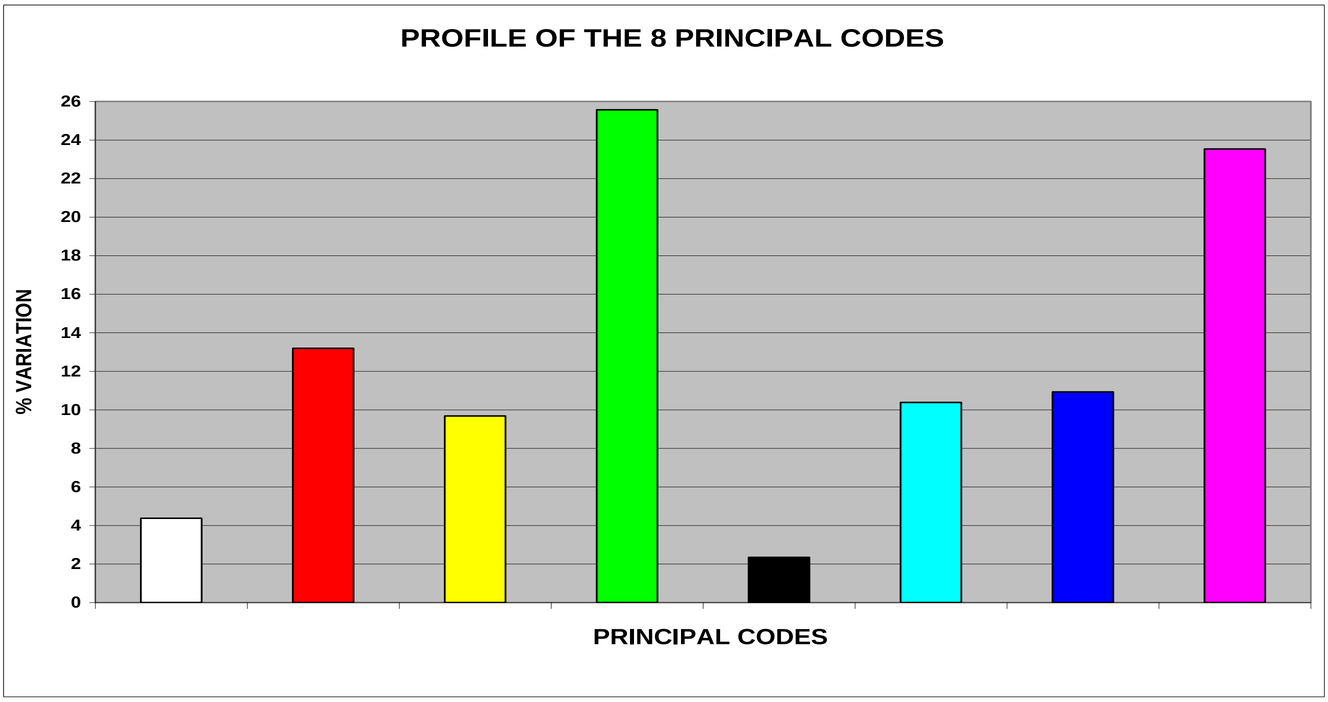
In the Pct. 45 (A e B) two **8 Principal Codes Profiles** are compared.

The chart in Pct. 45 (A) refers to the **original base sequence** of **Insulin Chain A**.



Pct. 45 (A)

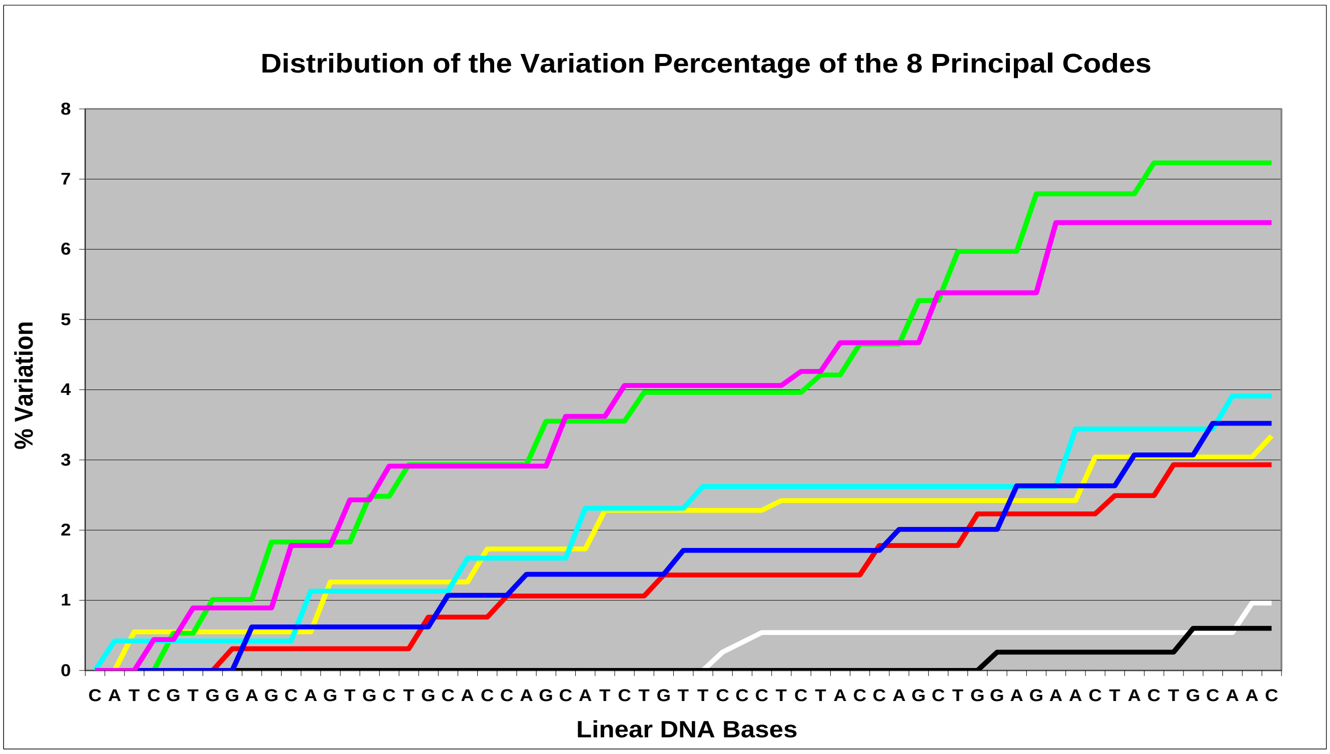
The chart in Pct. 45 (B) refers to the **twelfth “new generated sequence”** (**Sequence n° 12/1**) that originates from the original one.



Pct. 45 (B)

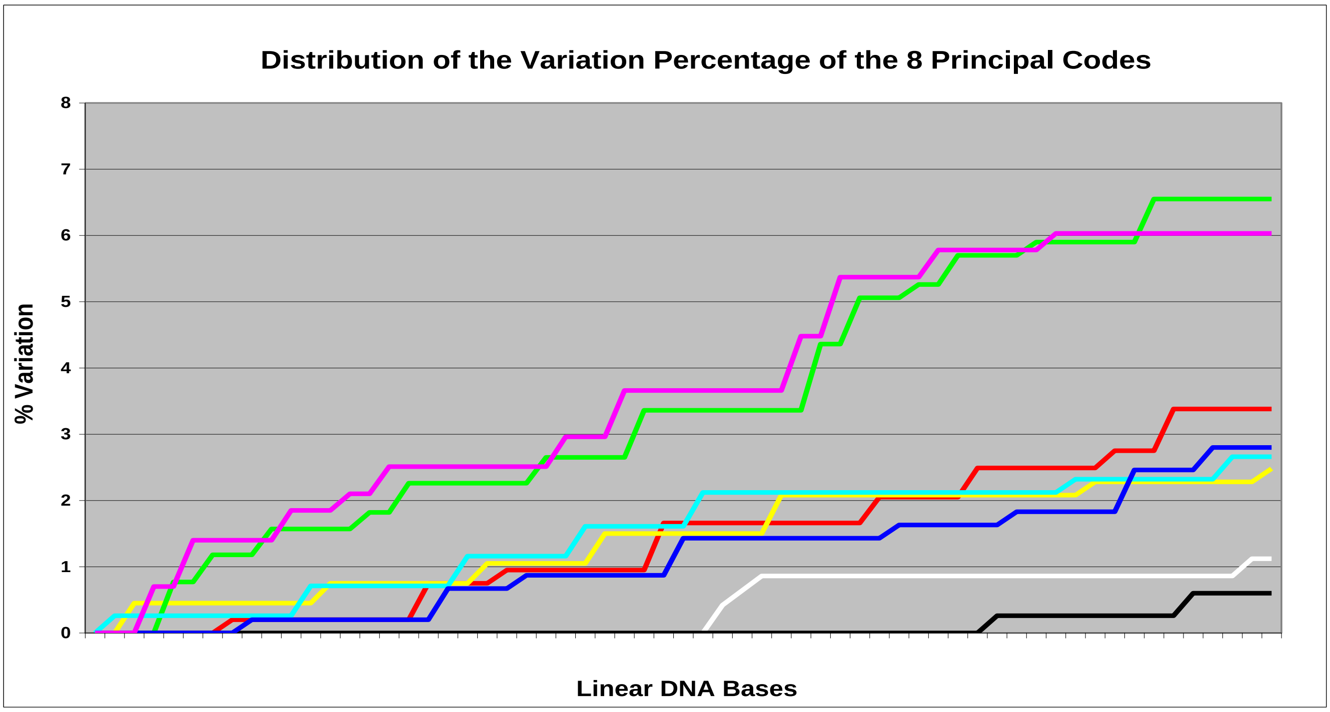
In Pct. 46 (A and B) two charts concerning the **Distribution of the Variation Percentage of the 8 Main Codes** are compared.

The charts in Pct. 46 (A) refers to the **original base sequence** analysed before.



Pct. 46 (A)

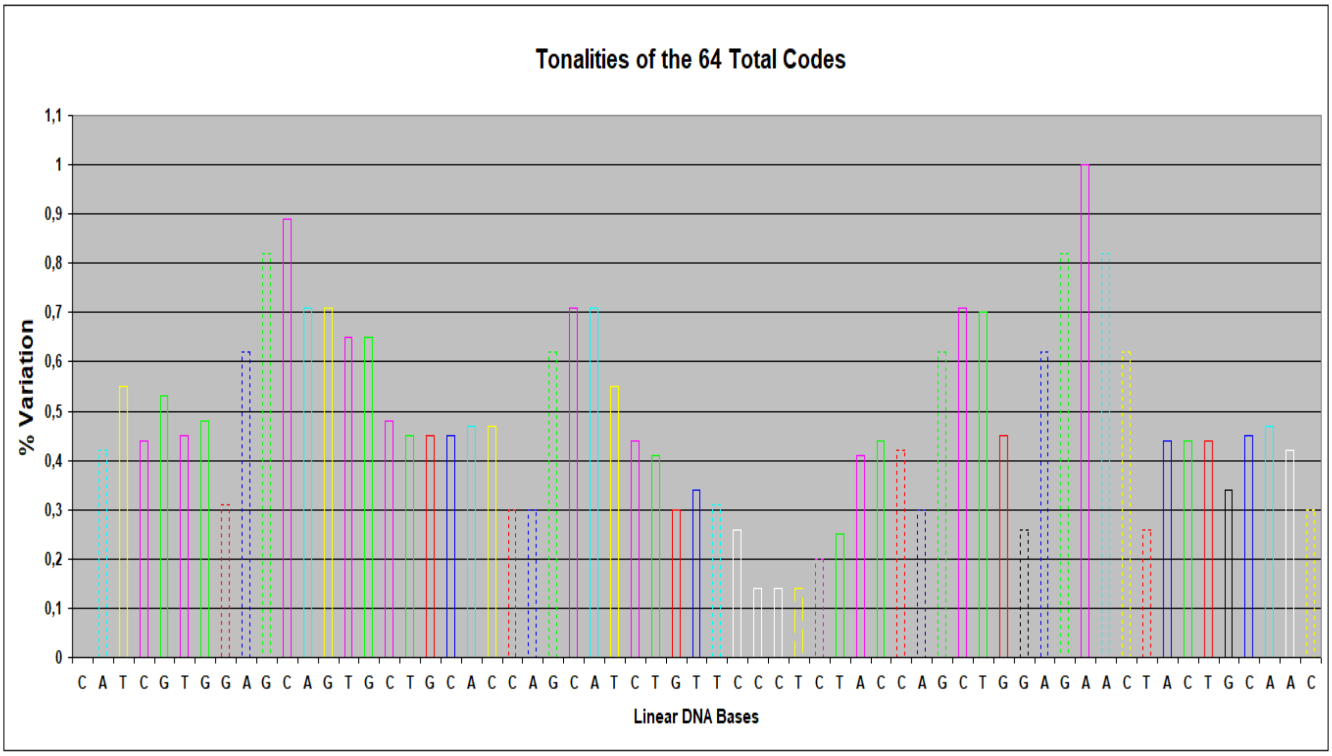
The chart in Pct. 46 (B) refers to the **"new generated sequence"** that originates from the original one.



Pct. 46 (B)

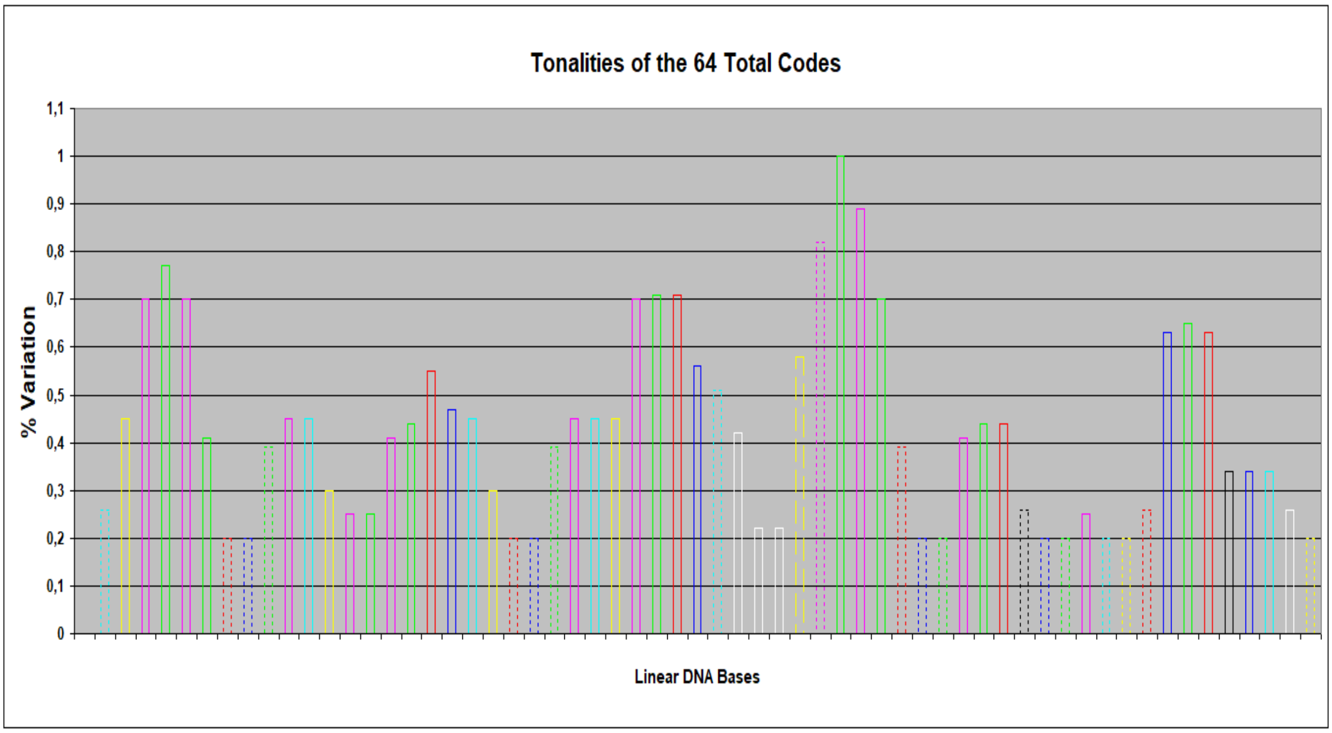
In Pct. 47 (A and B) two charts concerning the single **Tonalities of the 64 Total Codes** are compared.

The chart in Pct. 47 (A) refers to the **original base sequence** analysed before.



Pct. 47 (A)

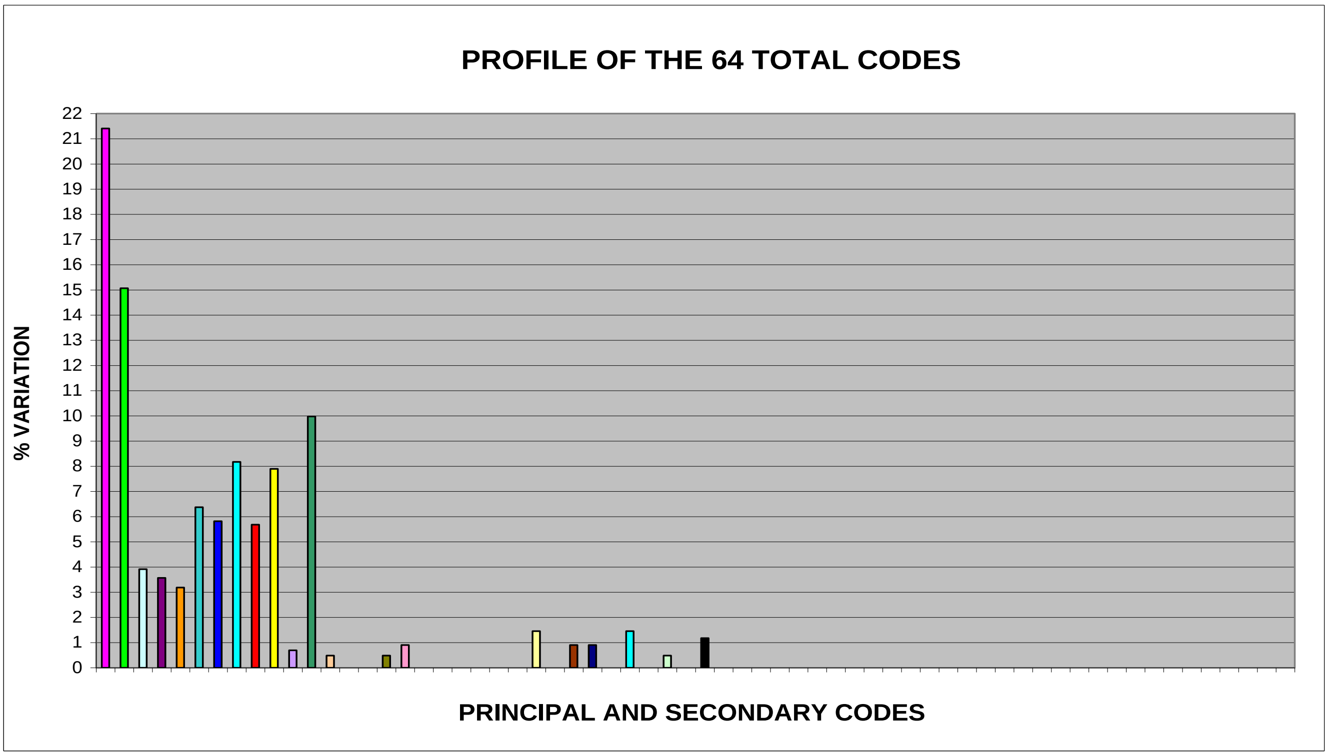
The chart in Pct. 47 (B) refers to the **“new generated sequence”** that originates from the original one.



Pct. 47 (B)

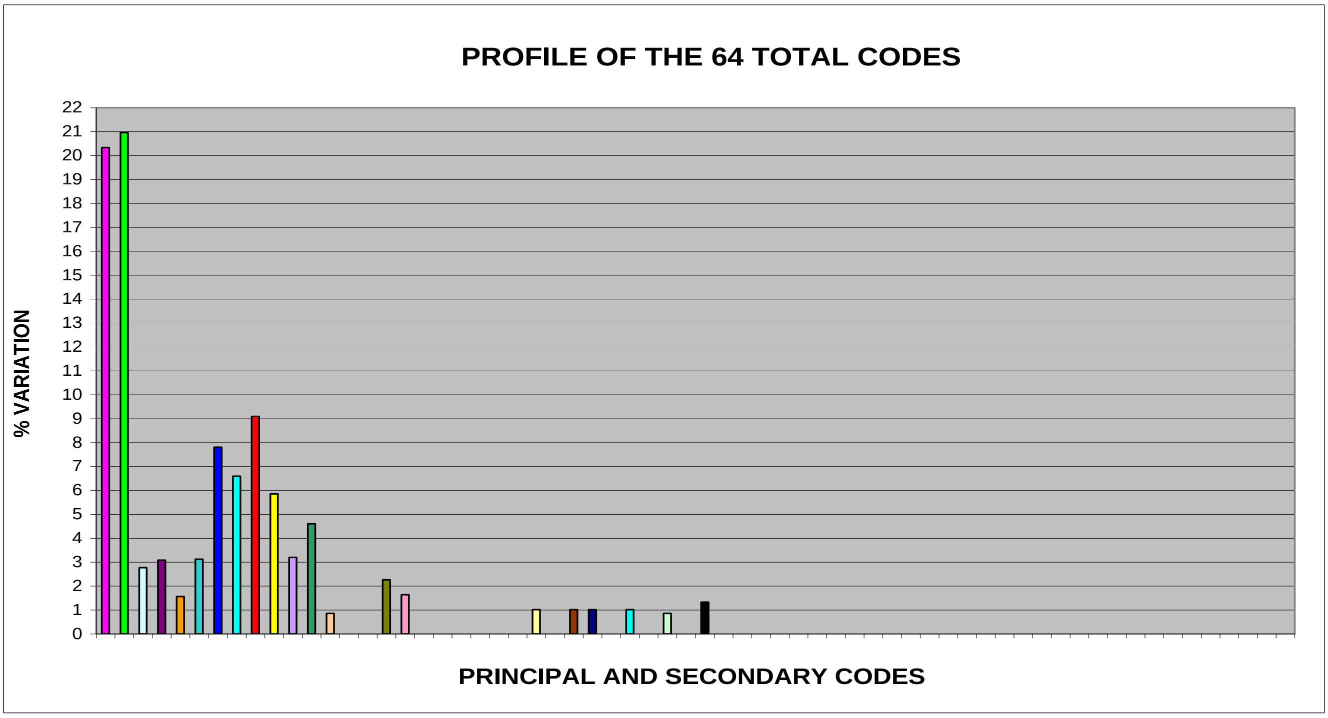
In Pct. 48 (A and B) two charts concerning the **Profile of the 64 Total Codes** are compared.

The chart in Pct. 48 (A) refers to the **original base sequence** analysed before.



Pct. 48 (A)

The chart in Pct. 48 (B) refers to the **"new generated sequence"** originated from the original one.



Pct. 48 (B)

The "non-obvious trend" analysis (obtained through the **T.T.E.S.**) of **Sequence n°12/1 of Insulin Chain A** results in **a comparison among different graphs** that are going to be interpreted in an analogous way to that in which the graphs related to the "non-obvious trend" of the **Sequences** analysed in the previous paragraphs **(n° 1/1, n° 2/1, etc.)** were. In order to avoid repetitions, here, the reader is deferred to the interpretation of the **comparisons among the different graphs** presented in the paragraph 1.2 .

Before concluding the paragraph, it is worth noting that, out of the **63** DNA bases of **Sequence n° 12/1**, ONLY **TEN BASES** (the **15,87%**)**,** ARE EQUAL (by type and by position in sequence) TO THOSE OF THE ORIGINAL SEQUENCE (**Insulin Chain A**).

1.25 IMPLICATIONS RELATED TO THE GRAPHIC RESULTS OF THE "NON-OBVIOUS TREND" ANALYSIS OF SEQUENCE n° 12/1 OF INSULIN CHAIN A

The **63** DNA base sequence of the **new generated sequence** (**Sequence n° 12/1**) that arises from the **original** one has been subjected to **BLAST** research.

Please note:

Information about the ***significant alignments*** produced by *BLAST research*, related to **Sequence n° 12/1,** and all the data acquired from *GenBank (3)* will be published in the **Appendix,** after the *General Conclusions.*

Query = NEW GENERATED SEQUENCE (Sequence n° 12/1)

Length = 63

Parameters of BLAST research:

Programme	*Blastn*
Word size	*11*
Expect value	*10*
Hitlist size	*100*
Match/Mismatch scores	*2,-3*
Gapcosts	*5,2*
Low Complexity Filter	*Yes*
Filter string	*L;m;*
Genetic Code	*1*

Please note:

Here, "**the organisms found to be in common**" between the results of BLAST research carried out on **Insulin Chain A** and results of BLAST research carried out on **Sequence n° 12/1**, were highlighted in **Red**.
As well, "**the organisms found to be in common**" between the results of BLAST research carried out on **Insulin Chain A**, results of BLAST research carried out on **Sequence n° 12/1** and results of BLAST research carried out on **at least one** of the *19 generated sequences*, were highlighted in **Green**.
Moreover, "**the denomination of the sequence**" (1/1, 2/1, ... 19/1) of the "**organism found to be in common**" between the results of BLAST research carried out on **Sequence n° 12/1** and results of BLAST research carried out on **at least one** of the *19 new generated sequences*, were highlighted in **Blue**.
Finally, "**the denomination of the sequence**" (1/1, 2/1, ... 19/1) of the "**organism found to be in common**" between the results of BLAST research carried out on **Insulin Chain A** and results of BLAST research carried out on *19 generated sequences*, were highlighted in **Yellow**.

Sequenza n° 12/1

Sequences producing significant alignments:

Selected seq	Description	Max score	Total score	Query cover	E value	Ident	Accession
1 XM_003063336.1	Micromonas pusilla CCMP1545 predicted protein, mRNA	50.9	50.9	63%	0.005	88%	XM_003063336.1
2 XM_017415237.2	PREDICTED: Kryptolebias marmoratus pericentrin-like (LOC108235288), transcript variant X4, mRNA	46.4	46.4	55%	0.064	89%	XM_017415237.2
3 XM_017415231.2	PREDICTED: Kryptolebias marmoratus pericentrin-like (LOC108235288), transcript variant X3, mRNA	46.4	46.4	55%	0.064	89%	XM_017415231.2
4 XM_017415222.2	PREDICTED: Kryptolebias marmoratus pericentrin-like (LOC108235288), transcript variant X2, mRNA	46.4	46.4	55%	0.064	89%	XM_017415222.2
5 XM_017415214.2	PREDICTED: Kryptolebias marmoratus pericentrin-like (LOC108235288), transcript variant X1, mRNA	46.4	46.4	55%	0.064	89%	XM_017415214.2
6 **13/1** XM_027340696.1	PREDICTED: Dermatophagoides pteronyssinus uncharacterized LOC113790983 (LOC113790983), mRNA	42.8	42.8	57%	0.78	89%	XM_027340696.1
7 CP016189.1	Mycobacteroides immunogenum strain FLAC016 chromosome, complete genome	41.9	41.9	55%	2.7	86%	CP016189.1
8 CP011530.1	Mycobacterium immunogenum strain CCUG 47286, complete genome	41.9	41.9	55%	2.7	86%	CP011530.1
9 CP002538.1	Deinococcus proteolyticus MRP plasmid pDEIPR02, complete sequence	41.9	41.9	39%	2.7	96%	CP002538.1
10 LT854263.1	Zymoseptoria tritici ST99CH_1E4 genome assembly, chromosome: ZT1E4_chr_11	41.0	41.0	42%	2.7	93%	LT854263.1
11 LT853702.1	Zymoseptoria tritici ST99CH_3D7 genome assembly, chromosome: 11	41.0	41.0	42%	2.7	93%	LT853702.1
12 **6/1** **17/1** XM_019301297.1	PREDICTED: Ipomoea nil uncharacterized LOC109153405 (LOC109153405), mRNA	41.0	41.0	50%	2.7	88%	XM_019301297.1
13 XM_018842054.1	Fonsecaea erecta hypothetical protein (AYL99_10548), partial mRNA	41.0	41.0	42%	2.7	93%	XM_018842054.1
14 XM_003848520.1	Zymoseptoria tritici IPO323 hypothetical protein partial mRNA	41.0	41.0	42%	2.7	93%	XM_003848520.1

Sequences producing significant alignments:

Selected seq	Description	Max score	Total score	Query cover	E value	Ident	Accession
15 LR026967.1	Podospora comata strain T genome assembly, chromosome: 4	40.1	40.1	57%	9.5	86%	LR026967.1
16 XM_013606212.2	PREDICTED: Medicago truncatula uncharacterized LOC25491154 (LOC25491154), mRNA	40.1	40.1	46%	9.5	90%	XM_013606212.2
17 **18/1** CP016004.1	Burkholderia sp. KK1 plasmid pkk3 sequence	40.1	40.1	49%	9.5	90%	CP016004.1
18 CP003075.1	Pelagibacterium halotolerans B2, complete genome	40.1	40.1	38%	9.5	96%	CP003075.1
19 CP002840.1	Halopiger xanaduensis SH-6 plasmid pHALXA01, complete genome	40.1	40.1	46%	9.5	90%	CP002840.1
20 XM_002295177.1	Thalassiosira pseudonana CCMP1335 importin alpha 1 subunit-like protein mRNA	40.1	40.1	66%	9.5	80%	XM_002295177.1
21 XM_028198118.1	PREDICTED: Camellia sinensis uncharacterized LOC114258210 (LOC114258210), mRNA	39.2	39.2	49%	9.5	87%	XM_028198118.1
22 **6/1** **17/1** CP025668.1	Ipomoea triloba cultivar NCNSP0323 chromosome 9	39.2	39.2	49%	9.5	87%	CP025668.1
23 CP030984.1	Arachis hypogaea cultivar Shitouqi chromosome A02	39.2	156	41%	9.5	92%	CP030984.1
24 XR_003201898.1	PREDICTED: Arachis hypogaea 2-(3-amino-3-carboxypropyl)histidine synthase subunit 1 pseudogene (LOC112801352), misc_RNA	39.2	39.2	41%	9.5	92%	XR_003201898.1
25 XM_025796929.1	PREDICTED: Arachis hypogaea 2-(3-amino-3-carboxypropyl)histidine synthase subunit 1-like (LOC112748643), transcript variant X10, mRNA	39.2	39.2	41%	9.5	92%	XM_025796929.1
26 XM_025796923.1	PREDICTED: Arachis hypogaea 2-(3-amino-3-carboxypropyl)histidine synthase subunit 1-like (LOC112748643), transcript variant X9, mRNA	39.2	39.2	41%	9.5	92%	XM_025796923.1
27 XM_025796916.1	PREDICTED: Arachis hypogaea 2-(3-amino-3-carboxypropyl)histidine synthase subunit 1-like (LOC112748643), transcript variant X8, mRNA	39.2	39.2	41%	9.5	92%	XM_025796916.1
28 XM_025796911.1	PREDICTED: Arachis hypogaea 2-(3-amino-3-carboxypropyl)histidine synthase subunit 1-like (LOC112748643), transcript variant X7, mRNA	39.2	39.2	41%	9.5	92%	XM_025796911.1

Sequences producing significant alignments:

Selected seq	Description	Max score	Total score	Query cover	E value	Ident	Accession
29 XM_025796903.1	PREDICTED: Arachis hypogaea 2-(3-amino-3-carboxypropyl)histidine synthase subunit 1-like (LOC112748643), transcript variant X6, mRNA	39.2	39.2	41%	9.5	92%	XM_025796903.1
30 XM_025796901.1	PREDICTED: Arachis hypogaea 2-(3-amino-3-carboxypropyl)histidine synthase subunit 1-like (LOC112748643), transcript variant X5, mRNA	39.2	39.2	41%	9.5	92%	XM_025796901.1
31 XM_025796896.1	PREDICTED: Arachis hypogaea 2-(3-amino-3-carboxypropyl)histidine synthase subunit 1-like (LOC112748643), transcript variant X4, mRNA	39.2	39.2	41%	9.5	92%	XM_025796896.1
32 XM_025796888.1	PREDICTED: Arachis hypogaea 2-(3-amino-3-carboxypropyl)histidine synthase subunit 1-like (LOC112748643), transcript variant X3, mRNA	39.2	39.2	41%	9.5	92%	XM_025796888.1
33 XM_025796880.1	PREDICTED: Arachis hypogaea 2-(3-amino-3-carboxypropyl)histidine synthase subunit 1-like (LOC112748643), transcript variant X2, mRNA	39.2	39.2	41%	9.5	92%	XM_025796880.1
34 XM_025796874.1	PREDICTED: Arachis hypogaea 2-(3-amino-3-carboxypropyl)histidine synthase subunit 1-like (LOC112748643), transcript variant X1, mRNA	39.2	39.2	41%	9.5	92%	XM_025796874.1
35 XR_003175031.1	PREDICTED: Arachis hypogaea 2-(3-amino-3-carboxypropyl)histidine synthase subunit 1 pseudogene (LOC112748548), transcript variant X2, misc_RNA	39.2	39.2	41%	9.5	92%	XR_003175031.1
36 XR_003175030.1	PREDICTED: Arachis hypogaea 2-(3-amino-3-carboxypropyl)histidine synthase subunit 1 pseudogene (LOC112748548), transcript variant X1, misc_RNA	39.2	39.2	41%	9.5	92%	XR_003175030.1
37 CP024201.1	Caulobacter mirabilis strain FWC 38 chromosome, complete genome	39.2	39.2	41%	9.5	92%	CP024201.1
38 13/1 CP023743.1	Gossypium hirsutum cultivar TM1 chromosome A11	39.2	39.2	41%	9.5	92%	CP023743.1

Sequences producing significant alignments:

Selected seq	Description	Max score	Total score	Query cover	E value	Ident	Accession
39 XM_021135610.1	PREDICTED: Arachis duranensis 2-(3-amino-3-carboxypropyl)histidine synthase subunit 1-like (LOC107475020), mRNA	39.2	39.2	41%	9.5	92%	XM_021135610.1
40 XM_016346756.2	PREDICTED: Arachis ipaensis 2-(3-amino-3-carboxypropyl)histidine synthase subunit 1 (LOC107643175), mRNA	39.2	39.2	41%	9.5	92%	XM_016346756.2
41 CP016428.1	Bradyrhizobium icense strain LMTR 13, complete genome	39.2	39.2	41%	9.5	92%	CP016428.1
42 XM_016732710.1	Sporothrix schenckii 1099-18 serine/threonineeeee-protein kinase (SPSK_06002), partial mRNA	39.2	39.2	50%	9.5	88%	XM_016732710.1
43 XM_012346141.1	Saprolegnia parasitica CBS 223.65 hypothetical protein partial mRNA	39.2	39.2	53%	9.5	89%	XM_012346141.1
44 **10/1** XR_001013343.1	PREDICTED: Cercocebus atys pepsin A-like (LOC105581134), misc_RNA	39.2	39.2	33%	9.5	100%	XR_001013343.1
45 XM_004346445.1	Acanthamoeba castellanii str. Neff Histone-lysine N-methyltransferase (ACA1_226770) mRNA, complete cds	39.2	39.2	53%	9.5	89%	XM_004346445.1
46 FO082843.1	Nocardia cyriacigeorgica GUH-2 chromosome complete genome	39.2	39.2	47%	9.5	90%	FO082843.1

PLEASE NOTE:

Many months before publishing this new Chapter, to our surprise, a **Sequence** which had already been identified as result of Blast research carried out on **Sequence n° 12/1** and which displayed significant alignments with the nematode **Heligmosomoides polygyrus** (subject of our detailed study and bibliographic research discussed in Chapter I° First Part), for reasons that are not known, was removed from the National Center for Biotechnology Information (NCBI) archive.

Sequence removed from the archive:

Sequence producing significant alignments:	***Score (Bits)***	***E Value***	***Identit.***
LL197912.1 Heligmosomoides polygyrus genome assembly H_bakeri_Edinburgh, scaffold HPBE_scaffold0009137........	41.0	2.3	**93%**

Record removed. *This record was removed at the submitter's request. Please contact update@ebi.ac.uk for further details.*

Comparison between the alignments of Sequence 12/1 and Sequence of Insulin Chain A according to the “Species of Common Organisms”:

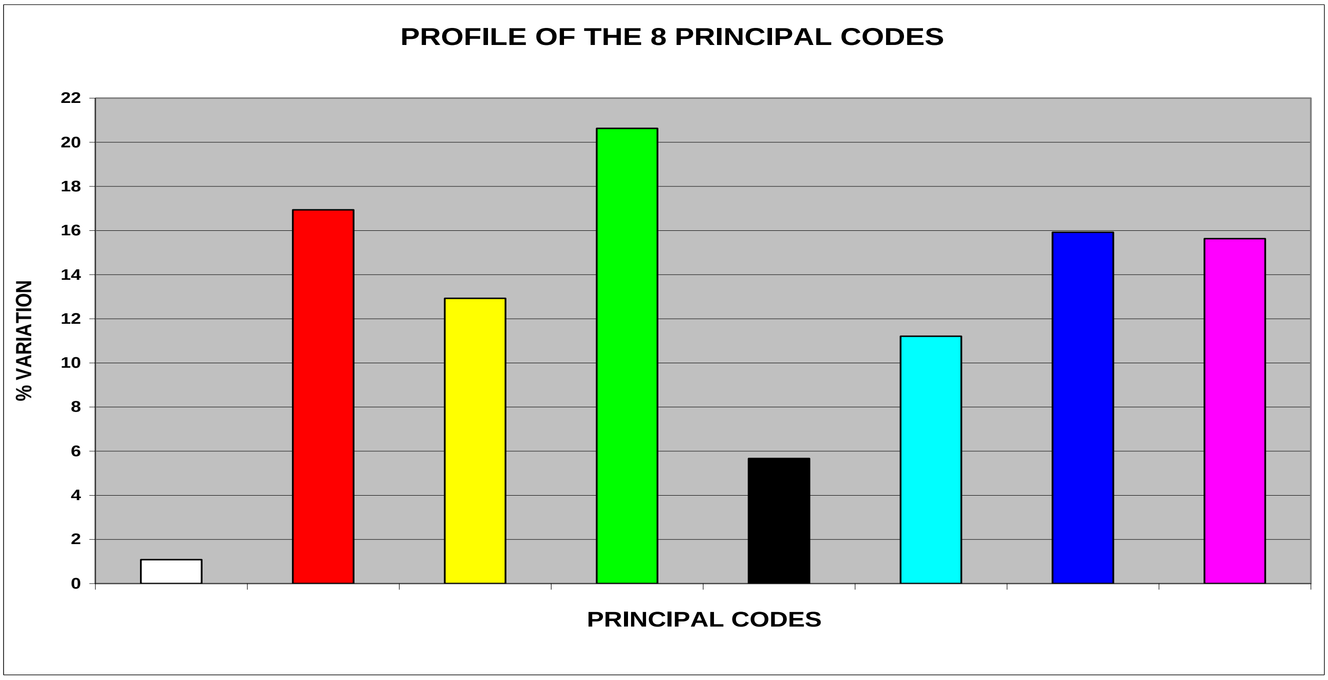
Alignments Sequence 12/1	**Description**	**Alignments Sequence Insulin Chain A**	**Description**
2 Select seq XM_017415237.2	PREDICTED: Kryptolebias marmoratus pericentrin-like (LOC108235288), transcript variant X4, mRNA	Select seq XM_017440672.2	PREDICTED: Kryptolebias marmoratus insulin (LOC108250678), mRNA
3 Select seq XM_017415231.2	PREDICTED: Kryptolebias marmoratus pericentrin-like (LOC108235288), transcript variant X3, mRNA	Select seq XM_017419715.2	PREDICTED: Kryptolebias marmoratus insulin-like (LOC108237967), mRNA
4 Select seq XM_017415222.2	PREDICTED: Kryptolebias marmoratus pericentrin-like (LOC108235288), transcript variant X2, mRNA		
5 Select seq XM_017415214.2	PREDICTED: Kryptolebias marmoratus pericentrin-like (LOC108235288), transcript variant X1, mRNA		
44 Select seq XR_001013343.1 **10/1**	PREDICTED: Cercocebus atys pepsin A-like (LOC105581134), misc_RNA	Select seq XM_012041172.1 **10/1**	PREDICTED: Cercocebus atys insulin (INS), transcript variant X3, mRNA
		Select seq XM_012041171.1 **10/1**	PREDICTED: Cercocebus atys insulin (INS), transcript variant X2, mRNA
		Select seq XM_012041169.1 **10/1**	PREDICTED: Cercocebus atys insulin (INS), transcript variant X1, mRNA

Analysis of
Sequence n° 13/1
of Insulin Chain A

1.26 GRAPHIC RESULTS OF THE "NON-OBVIOUS TREND" ANALYSIS OF SEQUENCE n° 13/1 OF INSULIN CHAIN A

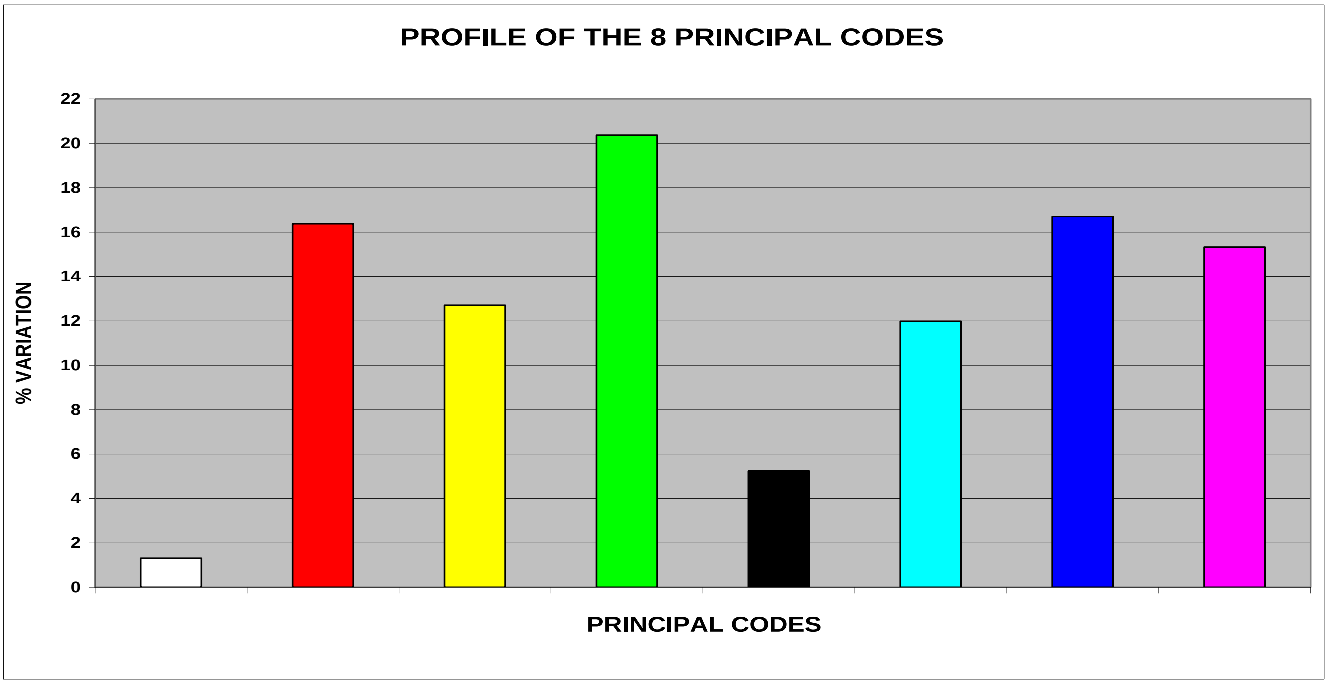
In the Pct. 49 (A e B) two **8 Principal Codes Profiles** are compared.

The chart in Pct. 49 (A) refers to the **original base sequence** of **Insulin Chain A**.



Pct. 49 (A)

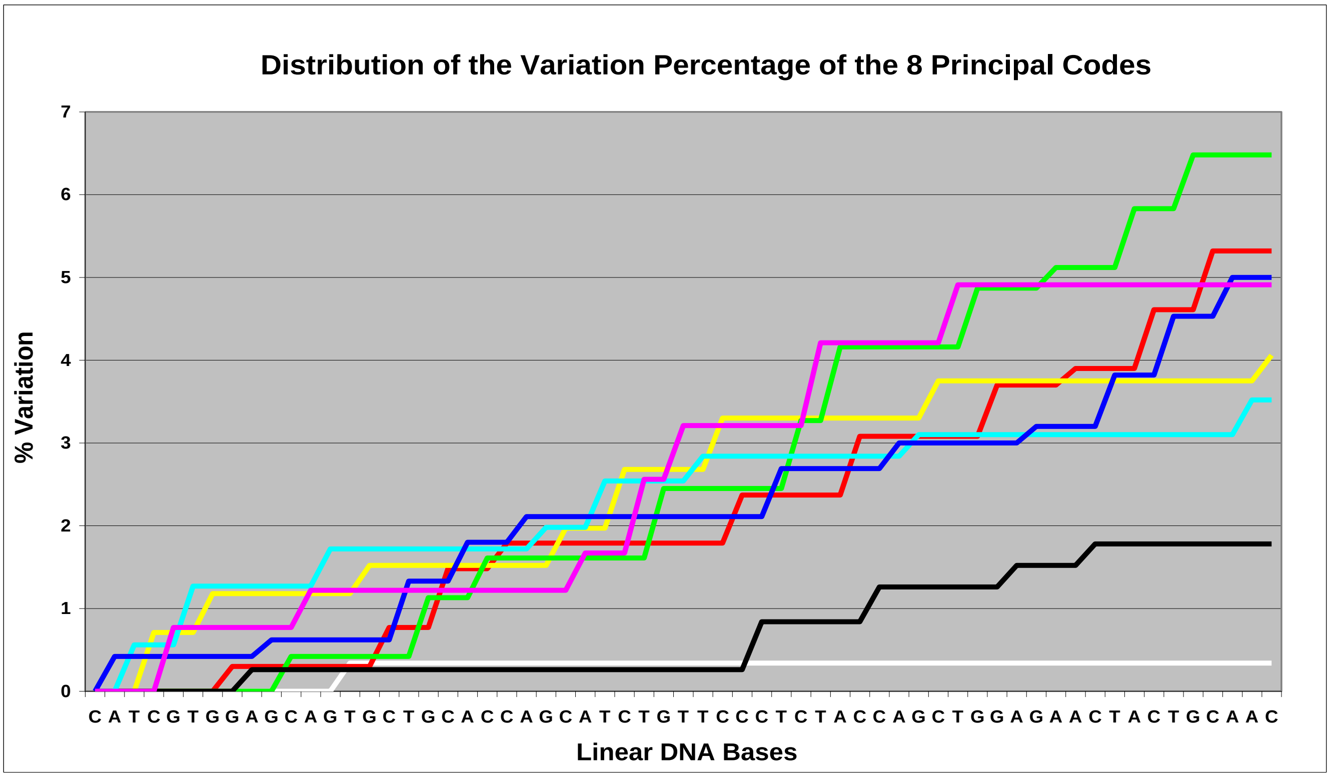
The chart in Pct. 49 (B) refers to the **thirteenth "new generated sequence"** (**Sequence n° 13/1**) that originates from the original one.



Pct. 49 (B)

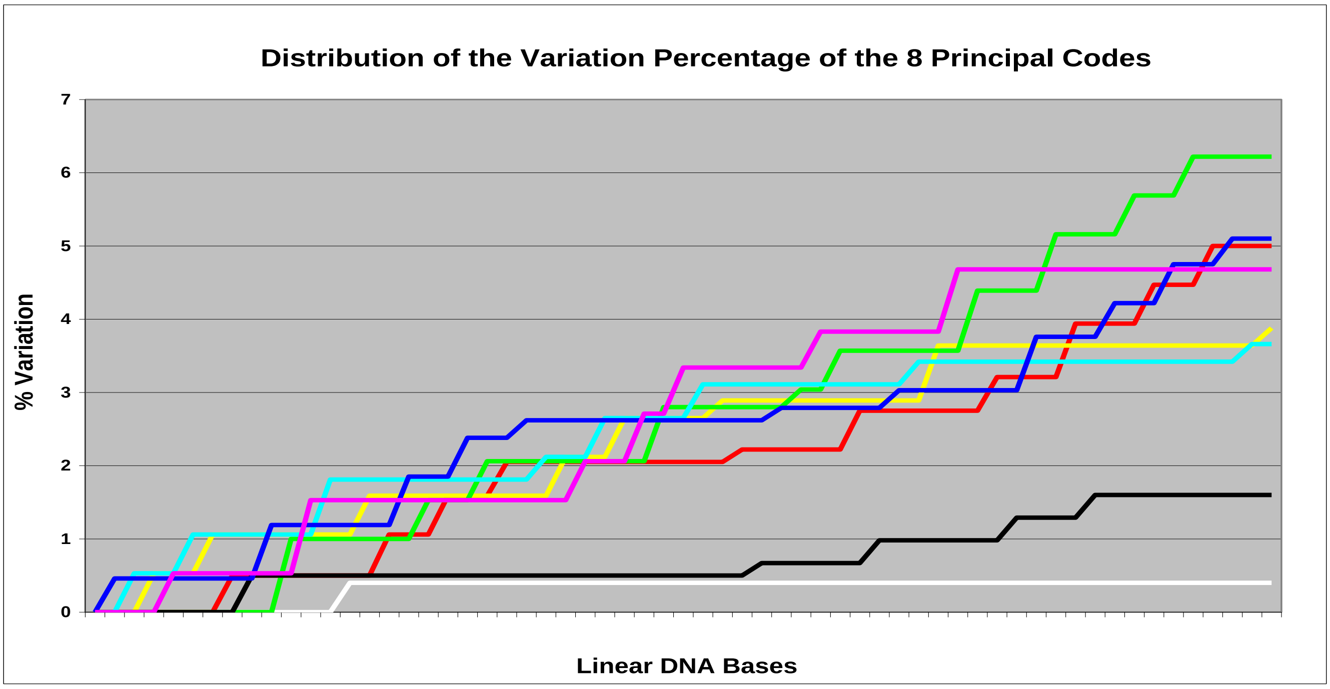
In Pct. 50 (A and B) two charts concerning the **Distribution of the Variation Percentage of the 8 Main Codes** are compared.

The charts in Pct. 50 (A) refers to the **original base sequence** analysed before.



Pct. 50 (A)

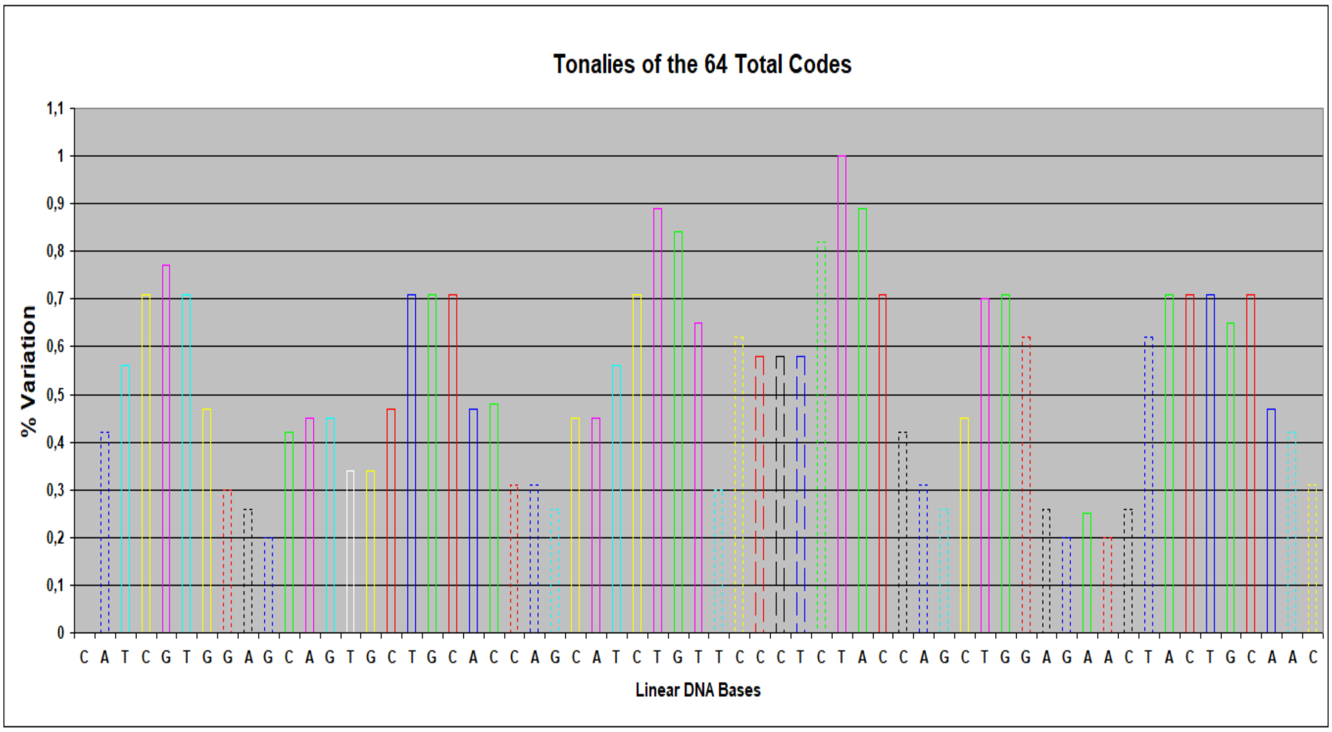
The chart in Pct. 50 (B) refers to the **“new generated sequence”** that originates from the original one.



Pct. 50 (B)

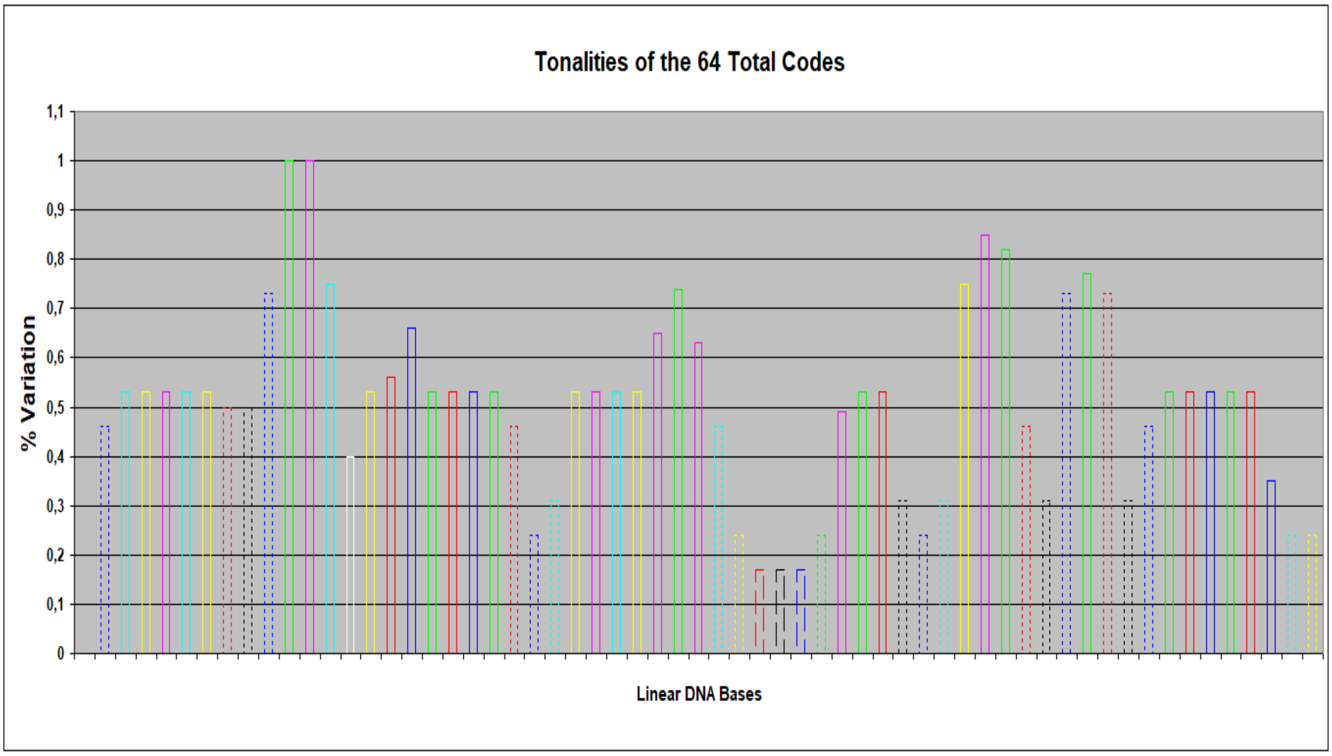
In Pct. 51 (A and B) two charts concerning the single **Tonalities of the 64 Total Codes** are compared.

The chart in Pct. 51 (A) refers to the **original base sequence** analysed before.



Pct. 51 (A)

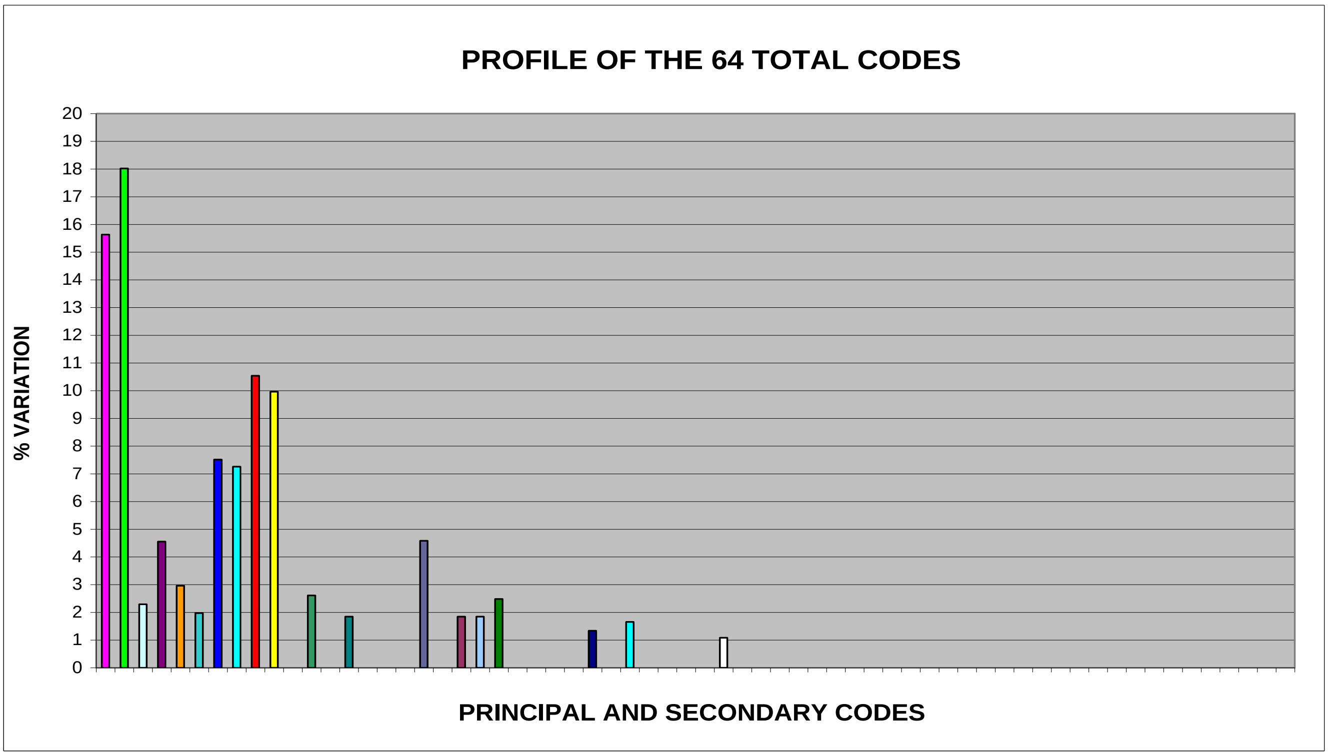
The chart in Pct. 51 (B) refers to the **"new generated sequence"** that originates from the original one.



Pct. 51 (B)

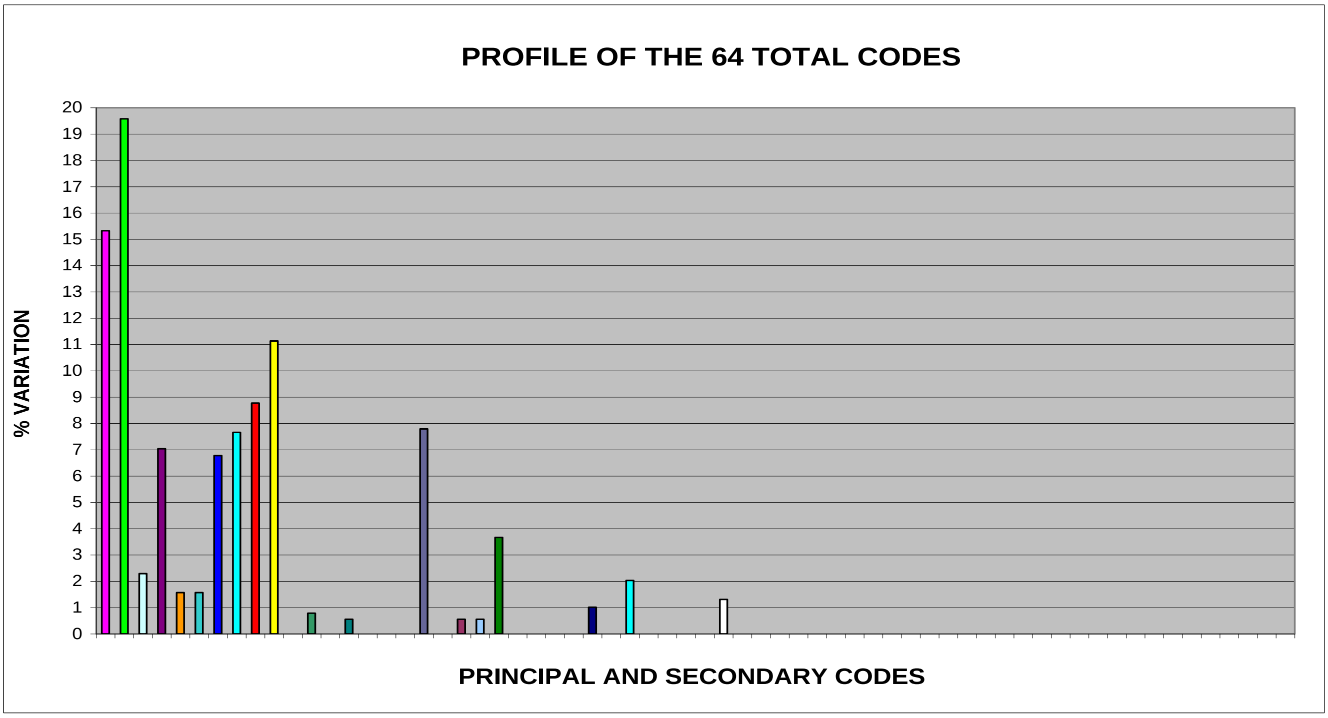
In Pct. 52 (A and B) two charts concerning the **Profile of the 64 Total Codes** are compared.

The chart in Pct. 52 (A) refers to the **original base sequence** analysed before.



Pct. 52 (A)

The chart in Pct. 52 (B) refers to the **"new generated sequence"** originated from the original one.



Pct. 52 (B)

The “non-obvious trend” analysis (obtained through the **T.T.E.S.**) of **Sequence n°13/1 of Insulin Chain A** results in **a comparison among different graphs** that are going to be interpreted in an analogous way to that in which the graphs related to the “non-obvious trend” of the **Sequences** analysed in the previous paragraphs **(n° 1/1, n° 2/1, etc.)** were. In order to avoid repetitions, here, the reader is deferred to the interpretation of the **comparisons among the different graphs** presented in the paragraph 1.2 .

Before concluding the paragraph, it is worth noting that, out of the **63** DNA bases of **Sequence n° 13/1**, ONLY **SIXTEEN BASES** (the **25,40%**)**,** ARE EQUAL (by type and by position in sequence) TO THOSE OF THE ORIGINAL SEQUENCE (**Insulin Chain A**).

1.27 IMPLICATIONS RELATED TO THE GRAPHIC RESULTS OF THE “NON-OBVIOUS TREND” ANALYSIS OF SEQUENCE n° 13/1 OF INSULIN CHAIN A

The **63** DNA base sequence of the **new generated sequence** (**Sequence n° 13/1**) that arises from the **original** one has been subjected to **BLAST** research.

Please note:

Information about the ***significant alignments*** produced by *BLAST research*, related to **Sequence n° 13/1,** and all the data acquired from *GenBank (3)* will be published in the **Appendix,** after the *General Conclusions.*

Query = NEW GENERATED SEQUENCE (Sequence n° 13/1)

Length = 63

Parameters of BLAST research:

Programme	*Blastn*
Word size	*11*
Expect value	*10*
Hitlist size	*100*
Match/Mismatch scores	*2,-3*
Gapcosts	*5,2*
Low Complexity Filter	*Yes*
Filter string	*L;m;*
Genetic Code	*1*

Please note:

Here, “**the organisms found to be in common**” between the results of BLAST research carried out on **Insulin Chain A** and results of BLAST research carried out on **Sequence n° 13/1**, were highlighted in **Red**.
As well, “**the organisms found to be in common**” between the results of BLAST research carried out on **Insulin Chain A**, results of BLAST research carried out on **Sequence n° 13/1** and results of BLAST research carried out on **at least one** of the *19 generated sequences*, were highlighted in **Green**.
Moreover, “**the denomination of the sequence**” (1/1, 2/1, ... 19/1) of the “**organism found to be in common**” between the results of BLAST research carried out on **Sequence n° 13/1** and results of BLAST research carried out on **at least one** of the *19 new generated sequences*, were highlighted in **Blue**.
Finally, “**the denomination of the sequence**” (1/1, 2/1, ... 19/1) of the “**organism found to be in common**” between the results of BLAST research carried out on **Insulin Chain A** and results of BLAST research carried out on *19 generated sequences*, were highlighted in **Yellow**.

Sequenza n° 13/1

Sequences producing significant alignments:

Selected seq	Description	Max score	Total score	Query cover	E value	Ident	Accession
1 **12/1** XM_012624036.1	PREDICTED: Gossypium raimondii dnaJ homolog subfamily B member 1-like (LOC105794733), mRNA	41.9	41.9	47%	2.6	90%	XM_012624036.1
2 AC163349.3	Mus musculus BAC clone RP23-188F5 from chromosome 3, complete sequence	41.9	41.9	39%	2.6	96%	AC163349.3
3 AC150893.3	Mus musculus BAC clone RP24-403H13 from chromosome 3, complete sequence	41.9	41.9	39%	2.6	96%	AC150893.3
4 CP026254.1	Scophthalmus maximus chromosome 12	41.0	41.0	42%	2.6	93%	CP026254.1
5 CP023019.1	Shewanella sp. WE21 chromosome, complete genome	41.0	41.0	34%	2.6	100%	CP023019.1
6 CP015971.1	Arachidicoccus sp. BS20, complete genome	40.1	40.1	46%	9.5	90%	CP015971.1
7 XM_014055903.1	PREDICTED: Thamnophis sirtalis ganglioside induced differentiation associated protein 1 (GDAP1), mRNA	40.1	40.1	61%	9.5	85%	XM_014055903.1
8 AL844491.14	Mouse DNA sequence from clone RP23-173A8 on chromosome 11, complete sequence	40.1	40.1	38%	9.5	96%	AL844491.14
9 **12/1** XM_027348268.1	PREDICTED: Dermatophagoides pteronyssinus dual specificity protein kinase splA-like (LOC113797827), mRNA	39.2	39.2	41%	9.5	92%	XM_027348268.1
10 MK072158.1	Faunusvirus sp. clone Faunusvirus_27 genomic sequence	39.2	39.2	41%	9.5	92%	MK072158.1
11 XM_026937320.1	PREDICTED: Pangasianodon hypophthalmus zinc finger protein 622 (znf622), transcript variant X3, mRNA	39.2	39.2	41%	9.5	92%	XM_026937320.1
12 XM_026937319.1	PREDICTED: Pangasianodon hypophthalmus zinc finger protein 622 (znf622), transcript variant X2, mRNA	39.2	39.2	41%	9.5	92%	XM_026937319.1

Sequences producing significant alignments:

Selected seq	Description	Max score	Total score	Query cover	E value	Ident	Accession
13 XM_026937318.1	PREDICTED: Pangasianodon hypophthalmus zinc finger protein 622 (znf622), transcript variant X1, mRNA	39.2	39.2	41%	9.5	92%	XM_026937318.1
14 CP011391.1	Faecalibaculum rodentium strain Alo17, complete genome	39.2	39.2	41%	9.5	92%	CP011391.1
15 XM_957723.2 17/1	Neurospora crassa OR74A hypothetical protein (NCU07883), mRNA	39.2	39.2	41%	9.5	92%	XM_957723.2
16 HF679027.1 10/1	Fusarium fujikuroi IMI 58289 draft genome, chromosome FFUJ_chr05	39.2	39.2	49%	9.5	87%	HF679027.1
17 XM_003323363.2	Puccinia graminis f. sp. tritici CRL 75-36-700-3 hypothetical protein (PGTG_04948), mRNA	39.2	39.2	41%	9.5	92%	XM_003323363.2
18 AF231375.1	Heteropsylla texana diffusable secreted glycoprotein (wg) gene, partial cds	39.2	39.2	52%	9.5	88%	AF231375.1

Comparison between the alignments of Sequence 13/1 and Sequence of Insulin Chain A according to the “Species of Common Organisms”:

Alignments Sequence 13/1	**Description**	**Alignments Sequence Insulin Chain A**	**Description**
2 Select seq AC163349.3	Mus musculus BAC clone RP23-188F5 from chromosome 3, complete sequence	Select seq XM_021152514.1 **1/1 6/1 8/1 10/1** **17/1 18/1**	PREDICTED: Mus caroli insulin-1 (LOC110286053), mRNA
3 Select seq AC150893.3	Mus musculus BAC clone RP24-403H13 from chromosome 3, complete sequence	Select seq DQ250565.1 **1/1 6/1 8/1 10/1** **17/1 18/1**	Mus caroli preproinsulin 1 (Ins1) gene, complete cds
		Select seq XM_021215010.1 **1/1 6/1 8/1 10/1** **17/1 18/1**	PREDICTED: Mus pahari insulin-1 (LOC110333420), mRNA
		Select seq NM_008386.4 **1/1 6/1 8/1 10/1** **17/1 18/1**	Mus musculus insulin I (Ins1), mRNA
		Select seq BC145868.1 **1/1 6/1 8/1 10/1** **17/1 18/1**	Mus musculus insulin I, mRNA (cDNA clone MGC:175755 IMAGE:40131171), complete cds
		Select seq DQ479923.1 **1/1 6/1 8/1 10/1** **17/1 18/1**	Mus musculus strain BTBR T+ tf/J insulin 1 precursor, gene, complete cds
		Select seq AC163452.12 **1/1 6/1 8/1 10/1** **17/1 18/1**	Mus musculus chromosome 19, clone RP23-405C7, complete sequence
		Select seq AC136710.8 **1/1 6/1 8/1 10/1** **17/1 18/1**	Mus musculus chromosome 19, clone RP23-35B13, complete sequence
		Select seq AC140320.2 **1/1 6/1 8/1 10/1** **17/1 18/1**	Mus musculus BAC clone RP23-401C13 from chromosome 19, complete sequence
		Select seq BC098468.1 **1/1 6/1 8/1 10/1** **17/1 18/1**	Mus musculus insulin I, mRNA (cDNA clone MGC:107382 IMAGE:6432765), complete cds

Comparison between the alignments of Sequence 13/1 and Sequence of Insulin Chain A according to the "Species of Common Organisms":

Alignments Sequence 13/1	Description	Alignments Sequence Insulin Chain A	Description
		Select seq AK148541.1 **1/1 6/1 8/1 10/1 17/1 18/1**	Mus musculus adult pancreas islet cells cDNA, RIKEN full-length enriched library, clone:C820020F18 product:insulin I, full insert sequence
		Select seq AK007345.1 **1/1 6/1 8/1 10/1 17/1 18/1**	Mus musculus 10 day old male pancreas cDNA, RIKEN full-length enriched library, clone:1810005L03 product:INSULIN 1 PRECURSOR, full insert sequence
		Select seq XM_021168754.1 **1/1 6/1 8/1 10/1 17/1 18/1**	PREDICTED: Mus caroli insulin-2 (LOC110299132), transcript variant X2, mRNA
		Select seq XM_021168753.1 **1/1 6/1 8/1 10/1 17/1 18/1**	PREDICTED: Mus caroli insulin-2 (LOC110299132), transcript variant X1, mRNA
		Select seq NM_001185084.2 **1/1 6/1 8/1 10/1 17/1 18/1**	Mus musculus insulin II (Ins2), transcript variant 3, mRNA
		Select seq NM_001185083.2 **1/1 6/1 8/1 10/1 17/1 18/1**	Mus musculus insulin II (Ins2), transcript variant 1, mRNA
		Select seq NM_008387.5 **1/1 6/1 8/1 10/1 17/1 18/1**	Mus musculus insulin II (Ins2), transcript variant 2, mRNA
		Select seq JN959239.1 **1/1 6/1 8/1 10/1 17/1 18/1**	Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Ins2:tm1a(EUCOMM)Wtsi; transgenic
		Select seq JN951270.1 **1/1 6/1 8/1 10/1 17/1 18/1**	Mus musculus targeted non-conditional, lacZ-tagged mutant allele Ins2:tm1e(EUCOMM)Wtsi; transgenic
		Select seq BC145554.1 **1/1 6/1 8/1 10/1 17/1 18/1**	Mus musculus insulin II, mRNA (cDNA clone MGC:179126 IMAGE:9054118), complete cds

Comparison between the alignments of Sequence 13/1 and Sequence of Insulin Chain A according to the "Species of Common Organisms":

Alignments Sequence 13/1	**Description**	**Alignments Sequence Insulin Chain A**	**Description**
		Select seq BC099934.1 **1/1 6/1 8/1 10/1 17/1 18/1**	Mus musculus insulin II, mRNA (cDNA clone MGC:107381 IMAGE:6432976), complete cds
		Select seq BC132650.1 **1/1 6/1 8/1 10/1 17/1 18/1**	Mus musculus insulin II, mRNA (cDNA clone MGC:164281 IMAGE:40130927), complete cds
		Select seq DQ250569.1 **1/1 6/1 8/1 10/1 17/1 18/1**	Mus caroli preproinsulin 2 (Ins2) gene, complete cds
		Select seq AK007612.1 **1/1 6/1 8/1 10/1 17/1 18/1**	Mus musculus 10 day old male pancreas cDNA, RIKEN full-length enriched library, clone:1810027C14 product:INSULIN 2 PRECURSOR, full insert sequence
		Select seq AK007482.1 **1/1 6/1 8/1 10/1 17/1 18/1**	Mus musculus 10 day old male pancreas cDNA, RIKEN full-length enriched library, clone:1810013J24 product:INSULIN 1 PRECURSOR, full insert sequence
		Select seq BC066208.1 **1/1 6/1 8/1 10/1 17/1 18/1**	Mus musculus insulin II, mRNA (cDNA clone IMAGE:6436276)
		Select seq AC012382.14 **1/1 6/1 8/1 10/1 17/1 18/1**	Mus musculus chromosome 7, clone RP23-92L23, complete sequence
		Select seq AY899305.1 **1/1 6/1 8/1 10/1 17/1 18/1**	Mus musculus proinsulin mRNA, complete cds, alternatively spliced
		Select seq AC013548.13 **1/1 6/1 8/1 10/1 17/1 18/1**	Mus musculus chromosome 7, clone RP23-209O22, complete sequence
		Select seq AP003182.2 **1/1 6/1 8/1 10/1 17/1 18/1**	Mus musculus genomic DNA, chromosome 7 clone:B189M11, complete sequences

Comparison between the alignments of Sequence 13/1 and Sequence of Insulin Chain A according to the “Species of Common Organisms”:

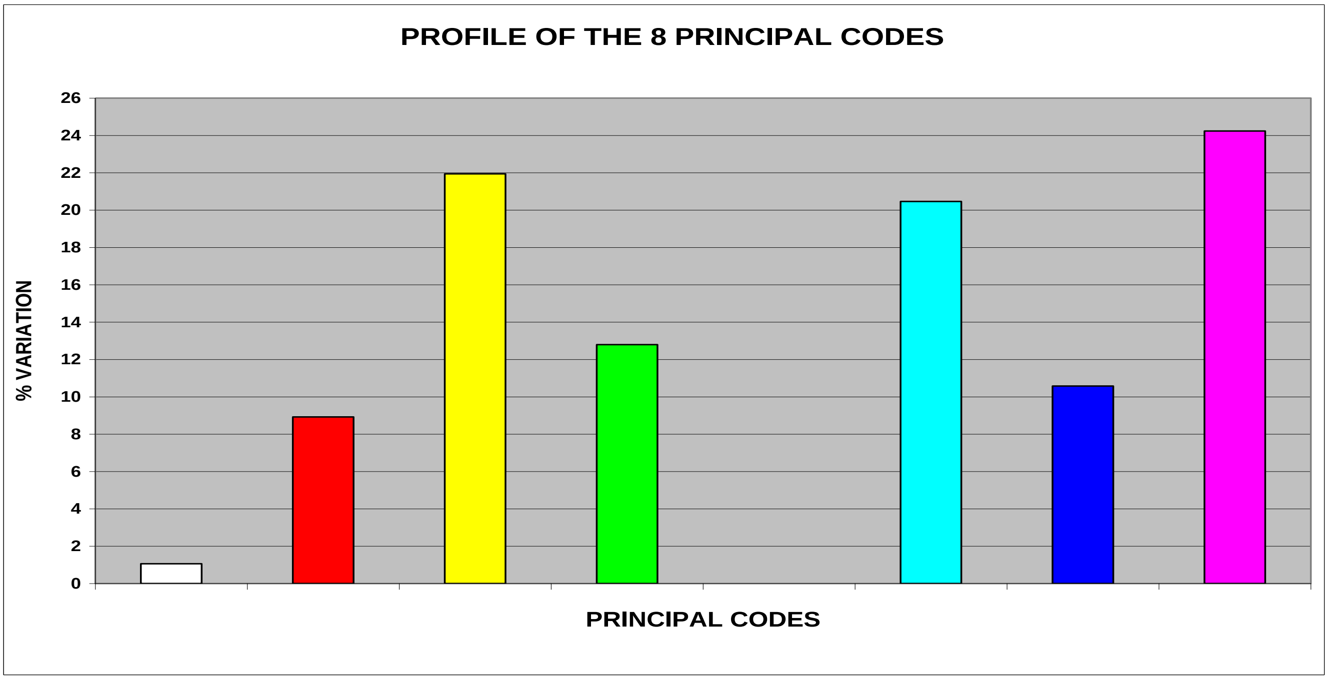
Alignments Sequence 13/1	**Description**	**Alignments Sequence Insulin Chain A**	**Description**
		Select seq GQ915612.1 **1/1 6/1 8/1 10/1** **17/1 18/1**	Mus musculus insulin-2 precursor (Ins2) mRNA, partial cds, alternatively spliced
		Select seq XM_021204833.1 **1/1 6/1 8/1 10/1** **17/1 18/1**	PREDICTED: Mus pahari insulin-2 (LOC110326410), transcript variant X2, mRNA
		Select seq XM_021204825.1 **1/1 6/1 8/1 10/1** **17/1 18/1**	PREDICTED: Mus pahari insulin-2 (LOC110326410), transcript variant X1, mRNA
4 Select seq CP026254.1	Scophthalmus maximus chromosome 12	Select seq CP026246.1 **10/1 17/1**	Scophthalmus maximus chromosome 4
		Select seq CP026255.1 **10/1 17/1**	Scophthalmus maximus chromosome 13
8 Select seq AL844491.14	Mouse DNA sequence from clone RP23-173A8 on chromosome 11, complete sequence	Select seq X04725.1 **8/1 10/1 17/1**	Mouse preproinsulin gene I
		Select seq X04725.1 **8/1 10/1 17/1**	Mouse preproinsulin gene II

Analysis of Sequence n° 14/1 of Insulin Chain A

1.28 GRAPHIC RESULTS OF THE "NON-OBVIOUS TREND" ANALYSIS OF SEQUENCE n° 14/1 OF INSULIN CHAIN A

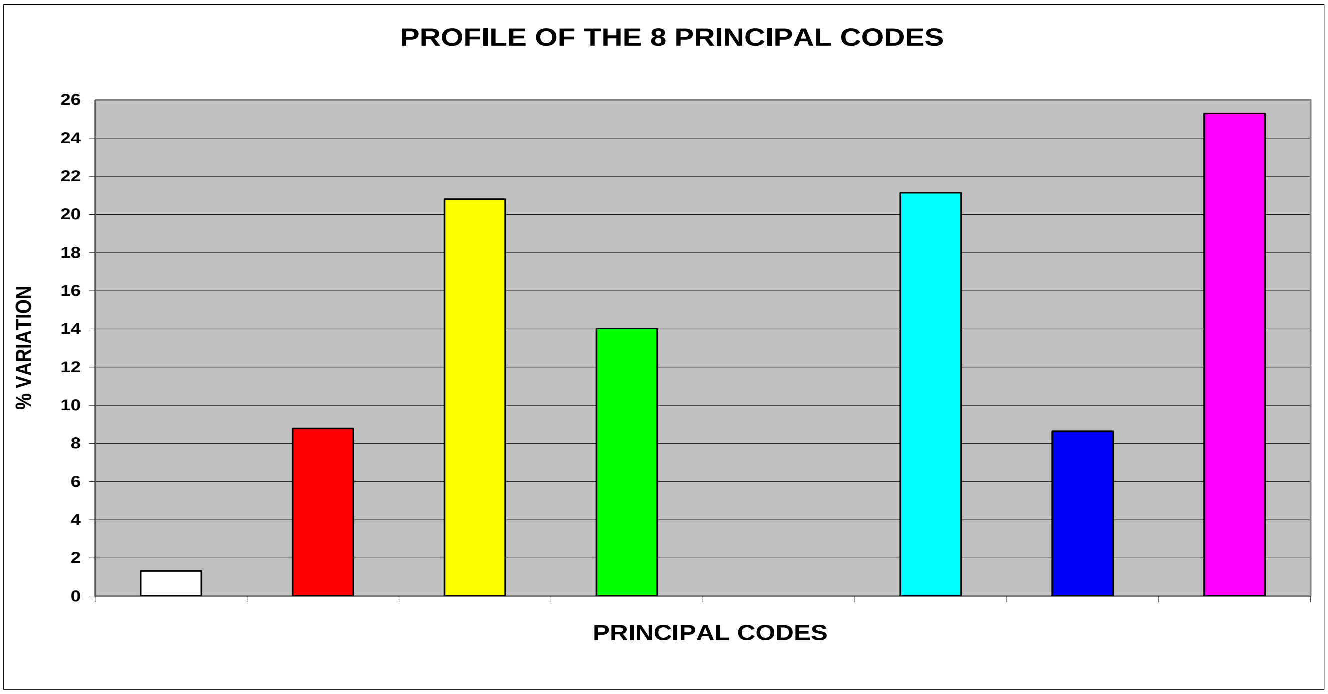
In the Pct. 53 (A e B) two **8 Principal Codes Profiles** are compared.

The chart in Pct. 53 (A) refers to the **original base sequence** of **Insulin Chain A**.



Pct. 53 (A)

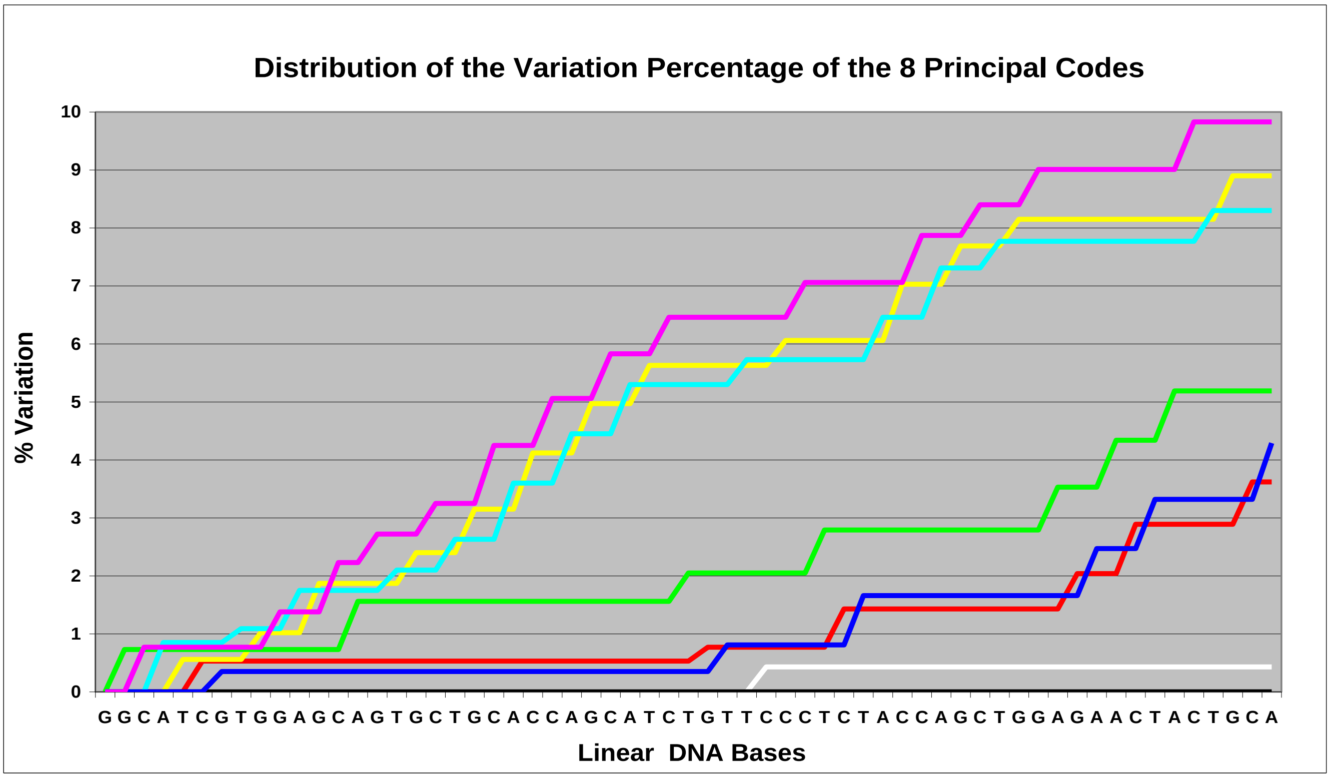
The chart in Pct. 53 (B) refers to the **fourteenth** **"new generated sequence"** (**Sequence n° 14/1**) that originates from the original one.



Pct. 53 (B)

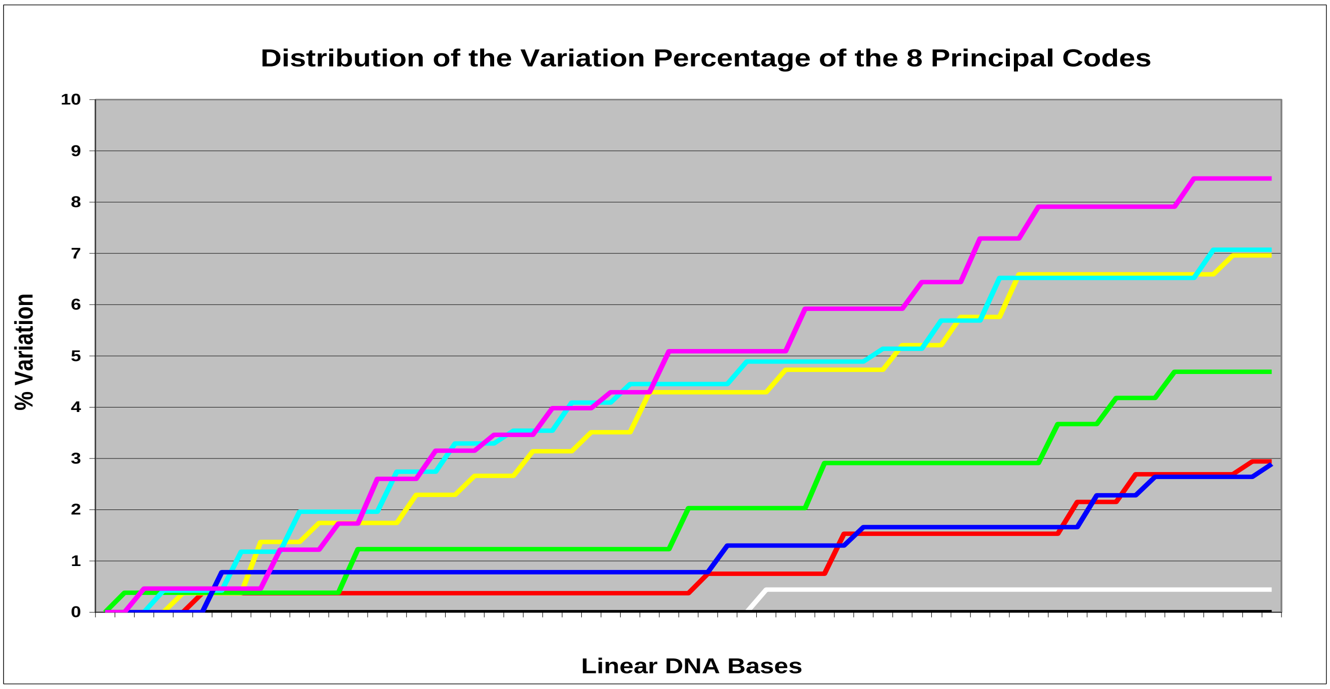
In Pct. 54 (A and B) two charts concerning the **Distribution of the Variation Percentage of the 8 Main Codes** are compared.

The charts in Pct. 54 (A) refers to the **original base sequence** analysed before.



Pct. 54 (A)

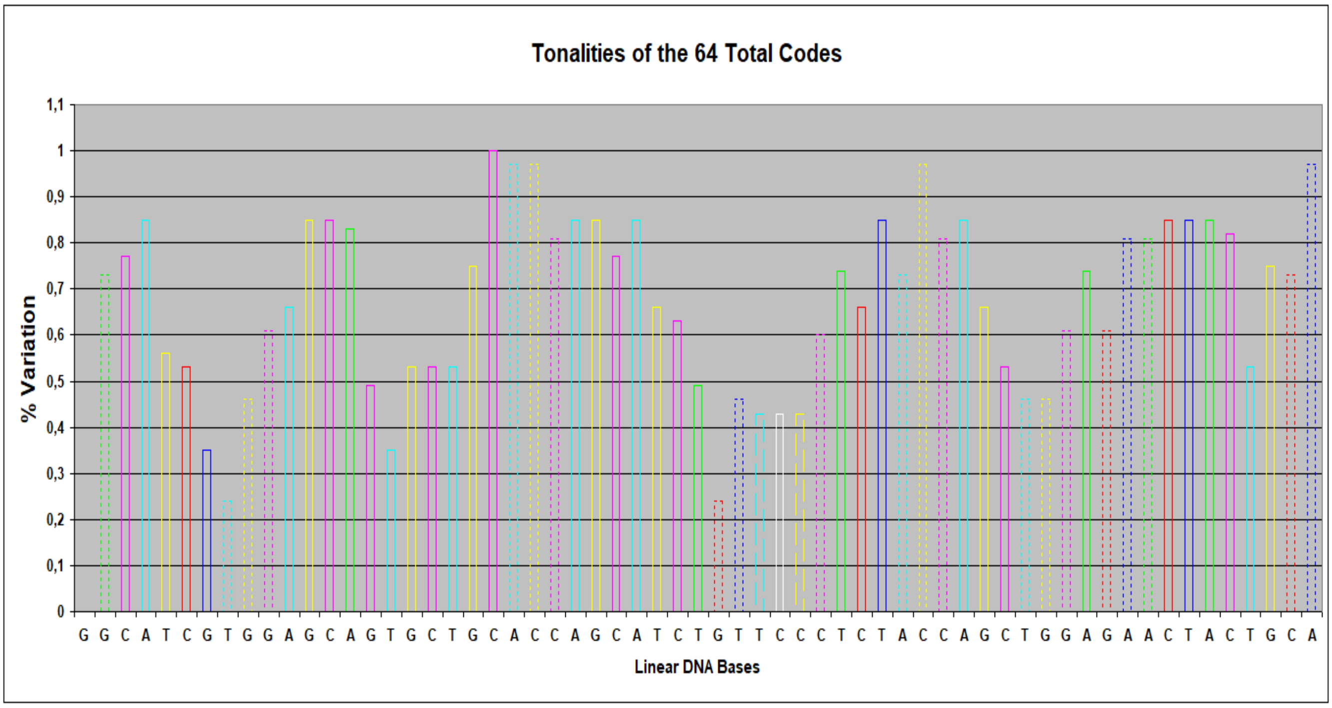
The chart in Pct. 54 (B) refers to the **“new generated sequence”** that originates from the original one.



Pct. 54 (B)

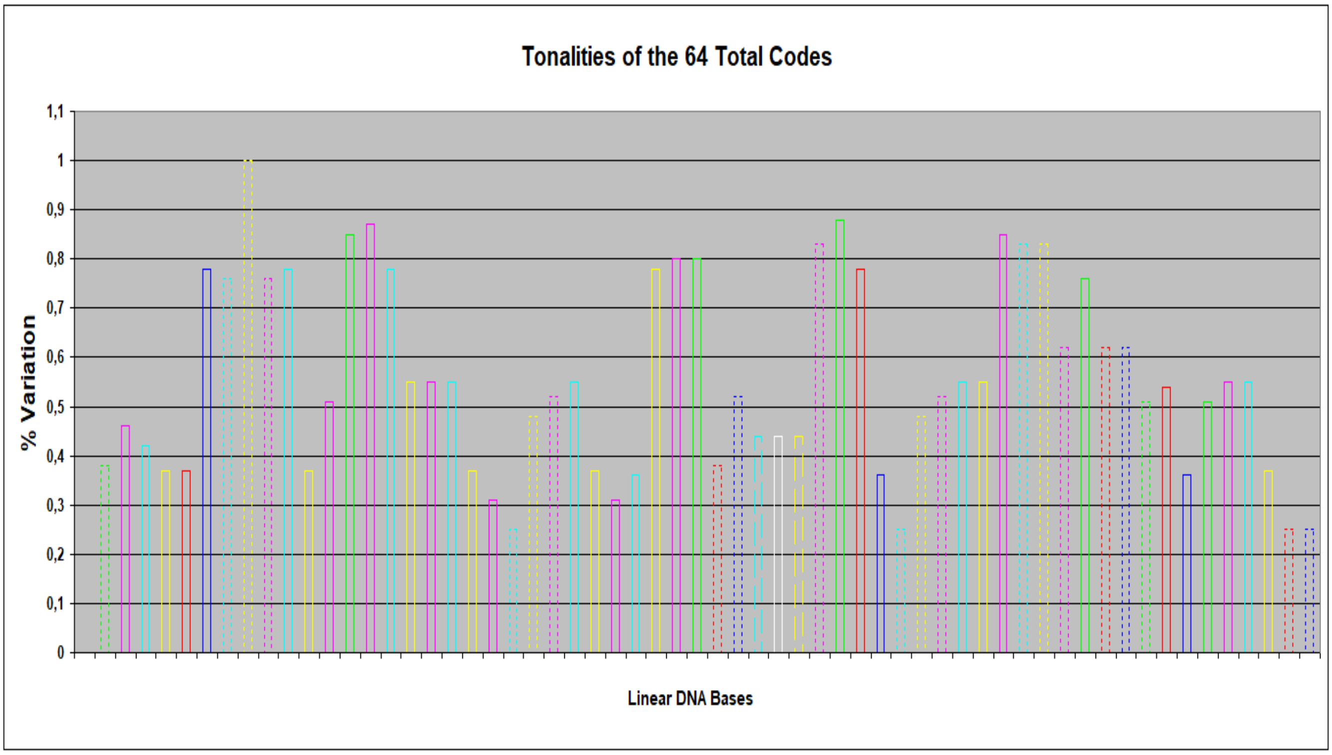
In Pct. 55 (A and B) two charts concerning the single **Tonalities of the 64 Total Codes** are compared.

The chart in Pct. 55 (A) refers to the **original base sequence** analysed before.



Pct. 55 (A)

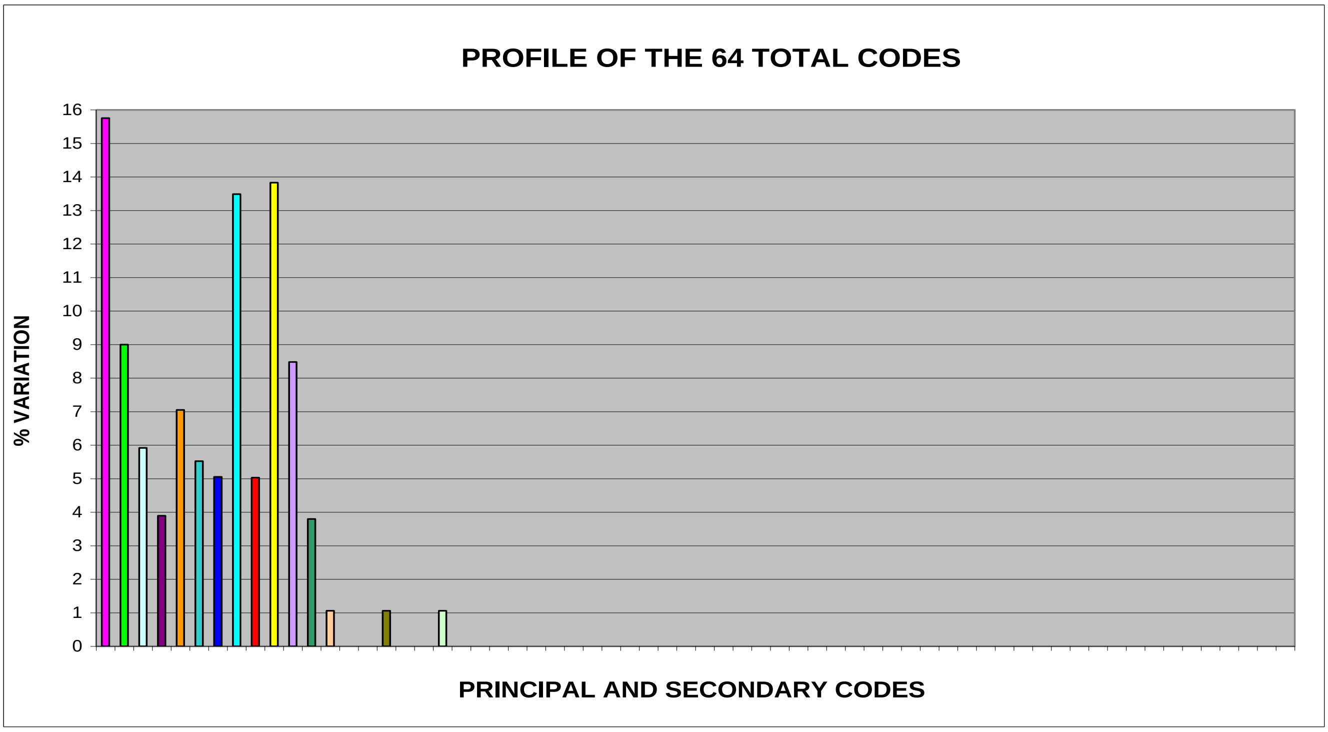
The chart in Pct. 55 (B) refers to the **“new generated sequence”** that originates from the original one.



Pct. 55 (B)

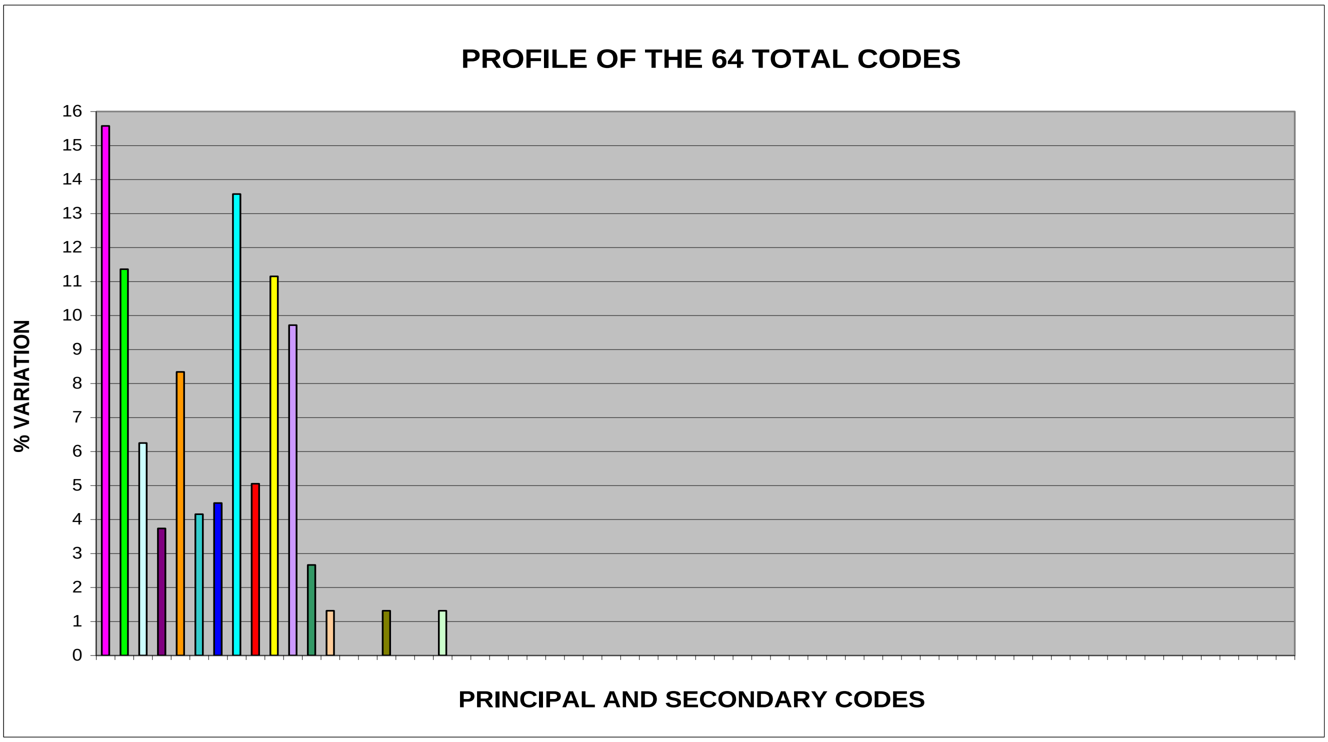
In Pct. 56 (A and B) two charts concerning the **Profile of the 64 Total Codes** are compared.

The chart in Pct. 56 (A) refers to the **original base sequence** analysed before.



Pct. 56 (A)

The chart in Pct. 56 (B) refers to the **"new generated sequence"** originated from the original one.



Pct. 56 (B)

The "non-obvious trend" analysis (obtained through the **T.T.E.S.**) of **Sequence n°14/1 of Insulin Chain A** results in **a comparison among different graphs** that are going to be interpreted in an analogous way to that in which the graphs related to the "non-obvious trend" of the **Sequences** analysed in the previous paragraphs **(n° 1/1, n° 2/1, etc.)** were. In order to avoid repetitions, here, the reader is deferred to the interpretation of the **comparisons among the different graphs** presented in the paragraph 1.2 .

Before concluding the paragraph, it is worth noting that, out of the **63** DNA bases of **Sequence n° 14/1**, ONLY **EIGHT BASES** (the **12,70%**)**,** ARE EQUAL (by type and by position in sequence) TO THOSE OF THE ORIGINAL SEQUENCE (**Insulin Chain A**).

1.29 IMPLICATIONS RELATED TO THE GRAPHIC RESULTS OF THE "NON-OBVIOUS TREND" ANALYSIS OF SEQUENCE n° 14/1 OF INSULIN CHAIN A

The **63** DNA base sequence of the **new generated sequence** (**Sequence n° 14/1**) that arises from the **original** one has been subjected to **BLAST** research.

Please note:

Information about the ***significant alignments*** produced by *BLAST research*, related to **Sequence n° 14/1,** and all the data acquired from *GenBank (3)* will be published in the **Appendix,** after the *General Conclusions.*

Query = NEW GENERATED SEQUENCE (Sequence n° 14/1)

Length = 63

Parameters of BLAST research:

Programme	*Blastn*
Word size	*11*
Expect value	*10*
Hitlist size	*100*
Match/Mismatch scores	*2,-3*
Gapcosts	*5,2*
Low Complexity Filter	*Yes*
Filter string	*L;m;*
Genetic Code	*1*

Please note:

Here, "**the organisms found to be in common**" between the results of BLAST research carried out on **Insulin Chain A** and results of BLAST research carried out on **Sequence n° 14/1**, were highlighted in **Red**.
As well, "**the organisms found to be in common**" between the results of BLAST research carried out on **Insulin Chain A**, results of BLAST research carried out on **Sequence n° 14/1** and results of BLAST research carried out on **at least one** of the *19 generated sequences*, were highlighted in **Green**.
Moreover, "**the denomination of the sequence**" (1/1, 2/1, ... 19/1) of the "**organism found to be in common**" between the results of BLAST research carried out on **Sequence n° 14/1** and results of BLAST research carried out on **at least one** of the *19 new generated sequences*, were highlighted in **Blue**.
Finally, "**the denomination of the sequence**" (1/1, 2/1, ... 19/1) of the "**organism found to be in common**" between the results of BLAST research carried out on **Insulin Chain A** and results of BLAST research carried out on *19 generated sequences*, were highlighted in **Yellow**.

Sequenza n° 14/1

Sequences producing significant alignments:

Selected seq	Description	Max score	Total score	Query cover	E value	Ident	Accession
1 CP023126.1	Lupinus angustifolius cultivar Tanjil chromosome LG-14	41.0	41.0	53%	2.7	88%	CP023126.1
2 CP032589.1	Lateolabrax maculatus linkage group 15 sequence	40.1	40.1	38%	9.5	96%	CP032589.1
3 CP027273.1	Lateolabrax maculatus chromosome Lm12	40.1	40.1	38%	9.5	96%	CP027273.1
4 **6/1** **17/1** CP011906.1	Ovis canadensis canadensis isolate 43U chromosome 21 sequence	40.1	40.1	39%	9.5	96%	CP011906.1
5 **9/1** XM_026120534.1	PREDICTED: Dromaius novaehollandiae WD repeat domain 24 (WDR24), mRNA	39.2	39.2	60%	9.5	84%	XM_026120534.1
6 **9/1** XM_026048985.1	PREDICTED: Nothoprocta perdicaria WD repeat domain 24 (WDR24), mRNA	39.2	39.2	60%	9.5	84%	XM_026048985.1
7 XM_022948735.1	PREDICTED: Stylophora pistillata prefoldin subunit 5-like (LOC111341737), mRNA	39.2	39.2	41%	9.5	92%	XM_022948735.1
8 CP023131.1	Lupinus angustifolius cultivar Tanjil chromosome LG-19	39.2	39.2	44%	9.5	93%	CP023131.1
9 **6/1** XM_012983817.1	PREDICTED: Erythranthe guttatus uncharacterized LOC105959677 (LOC105959677), mRNA	39.2	39.2	49%	9.5	87%	XM_012983817.1
10 **5/1** **9/1** XM_003878010.1	Leishmania mexicana MHOM/GT/2001/U1103 conserved hypothetical protein partial mRNA	39.2	39.2	49%	9.5	87%	XM_003878010.1
11 **9/1** CP002903.1	Spirochaeta thermophila DSM 6578, complete genome	39.2	39.2	49%	9.5	87%	CP002903.1
12 **5/1** **9/1** FR799584.1	Leishmania mexicana MHOM/GT/2001/U1103 complete genome, chromosome 31	39.2	39.2	49%	9.5	87%	FR799584.1

Comparison between the alignments of Sequence 14/1 and Sequence of Insulin Chain A according to the "Species of Common Organisms":

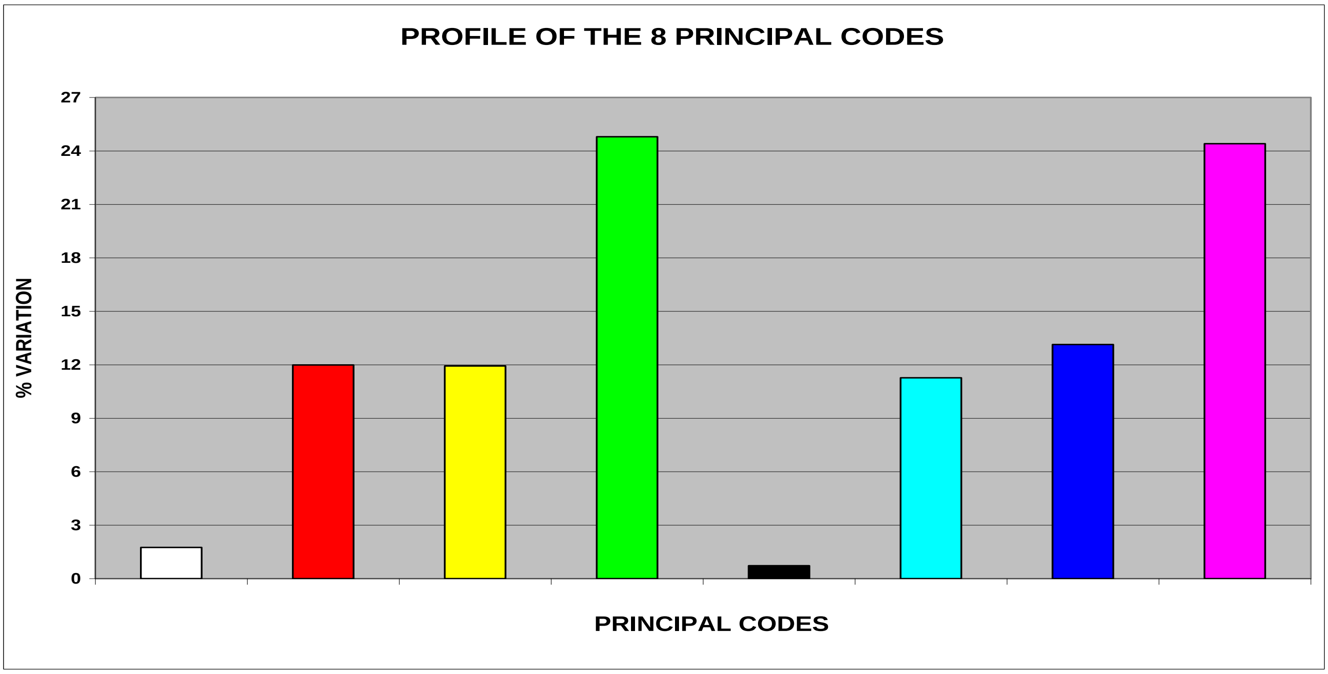
Alignments Sequence 14/1	**Description**	**Alignments Sequence Insulin Chain A**	**Description**
2 Select seq CP032589.1	Lateolabrax maculatus linkage group 15 sequence	Select seq CP032586.1 **16/1 17/1**	Lateolabrax maculatus linkage group 12 sequence
3 Select seq CP027273.1	Lateolabrax maculatus chromosome Lm12	Select seq CP027266.1 **16/1 17/1**	Lateolabrax maculatus chromosome Lm5
4 Select seq CP011906.1 **17/1**	Ovis canadensis canadensis isolate 43U chromosome 21 sequence	Select seq XM_027959829.1 **6/1 17/1**	PREDICTED: Ovis aries insulin (INS), mRNA
		Select seq AH005355.3 **6/1 17/1**	Ovis aries insulin and insulin-like growth factor II (IGF-II) genes, complete cds
		Select seq XM_012167536.2 **6/1 17/1**	PREDICTED: Ovis aries musimon insulin (LOC105613195), mRNA
5 Select seq XM_026120534.1 **9/1**	PREDICTED: Dromaius novaehollandiae WD repeat domain 24 (WDR24), mRNA	Select seq XM_026092712.1 **9/1**	PREDICTED: Dromaius novaehollandiae insulin (INS), mRNA
6 Select seq XM_026048985.1 **9/1**	PREDICTED: Nothoprocta perdicaria WD repeat domain 24 (WDR24), mRNA	Select seq XM_026036815.1 **9/1**	PREDICTED: Nothoprocta perdicaria insulin (INS), mRNA

Analysis of
Sequence n° 15/1
of Insulin Chain A

1.30 GRAPHIC RESULTS OF THE “NON-OBVIOUS TREND” ANALYSIS OF SEQUENCE n° 15/1 OF INSULIN CHAIN A

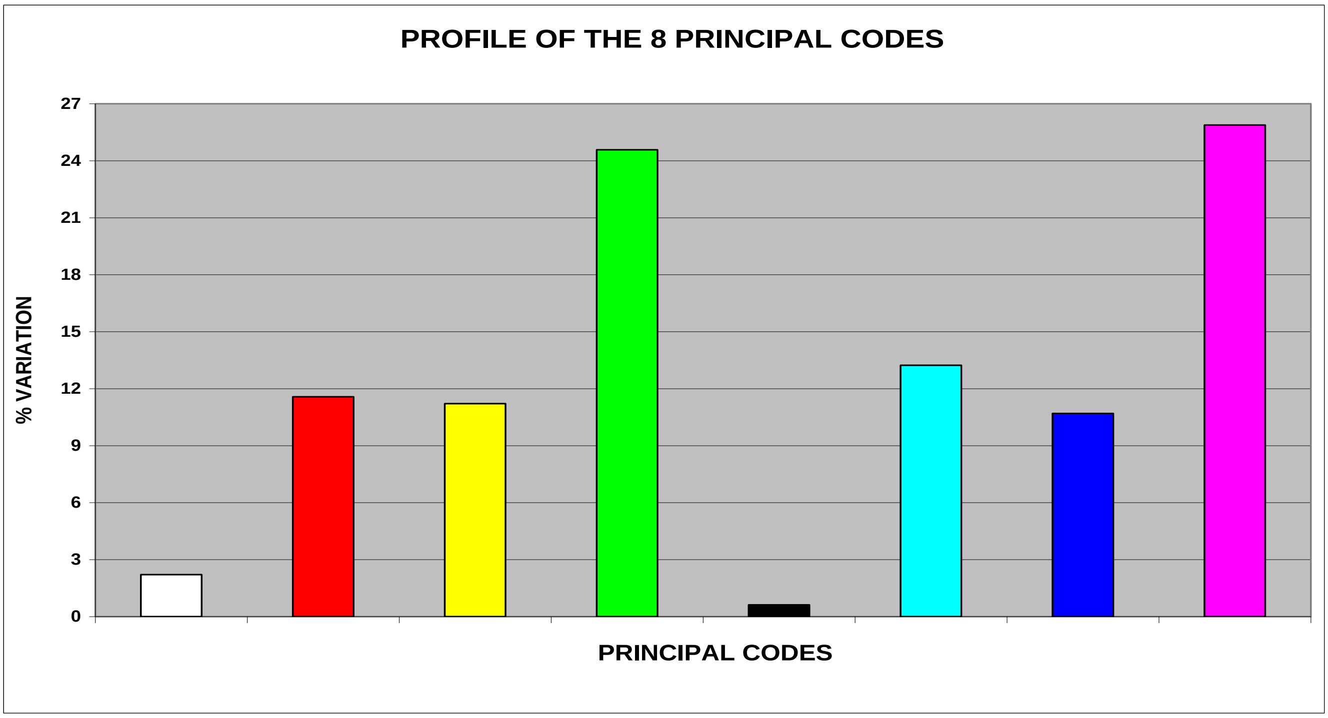
In the Pct. 57 (A e B) two **8 Principal Codes Profiles** are compared.

The chart in Pct. 57 (A) refers to the **original base sequence** of **Insulin Chain A**.



Pct. 57 (A)

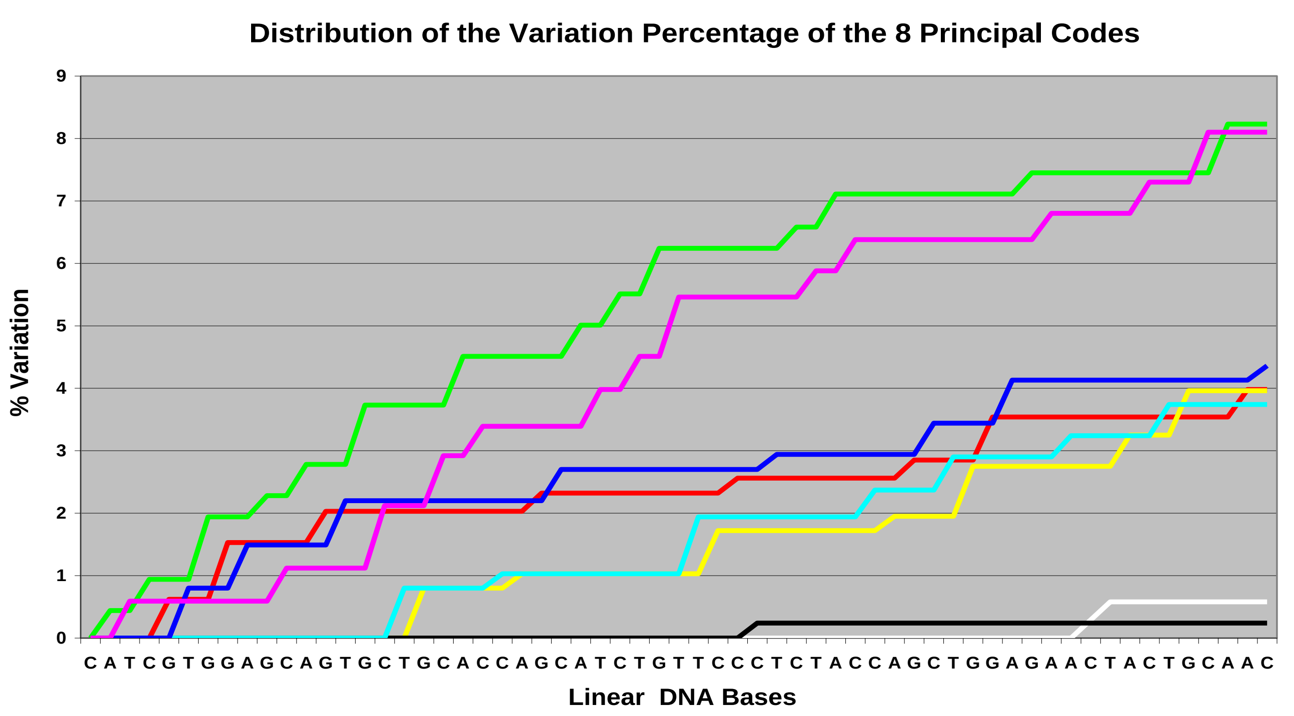
The chart in Pct. 57 (B) refers to the **fifteenth** **“new generated sequence”** (**Sequence n° 15/1**) that originates from the original one.



Pct. 57 (B)

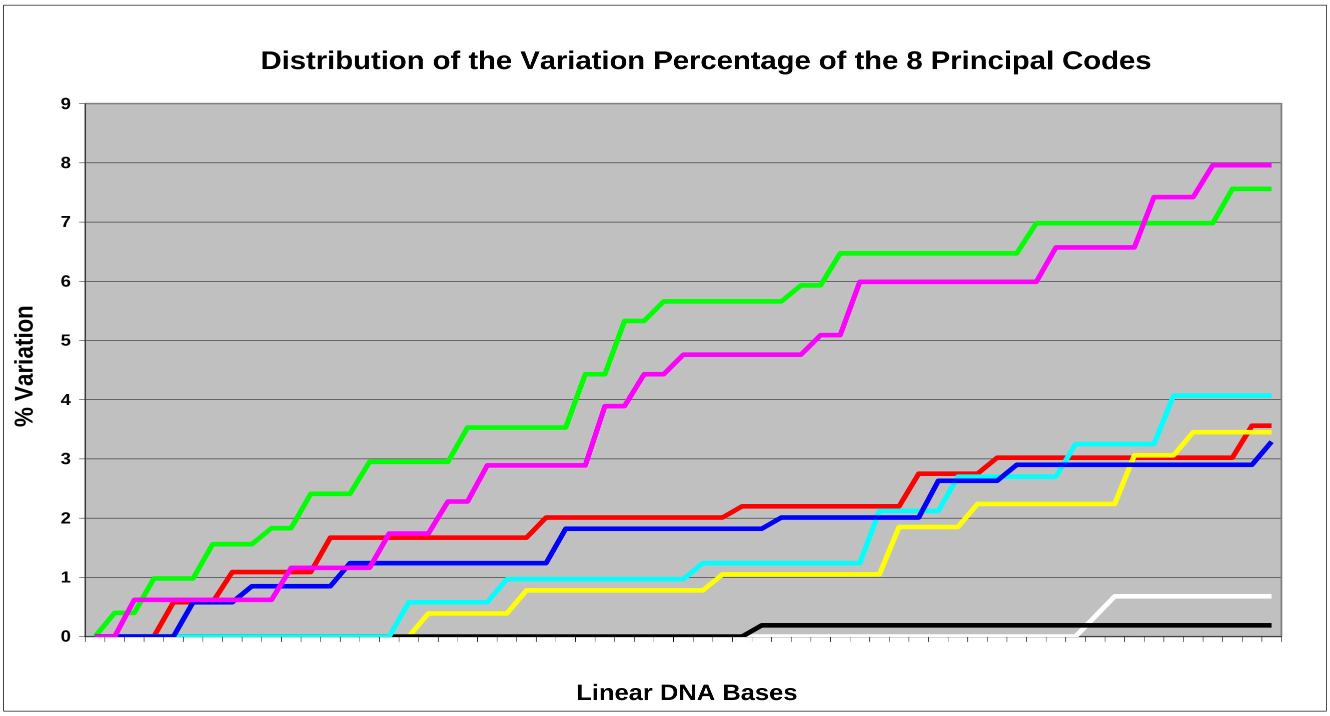
In Pct. 58 (A and B) two charts concerning the **Distribution of the Variation Percentage of the 8 Main Codes** are compared.

The charts in Pct. 58 (A) refers to the **original base sequence** analysed before.



Pct. 58 (A)

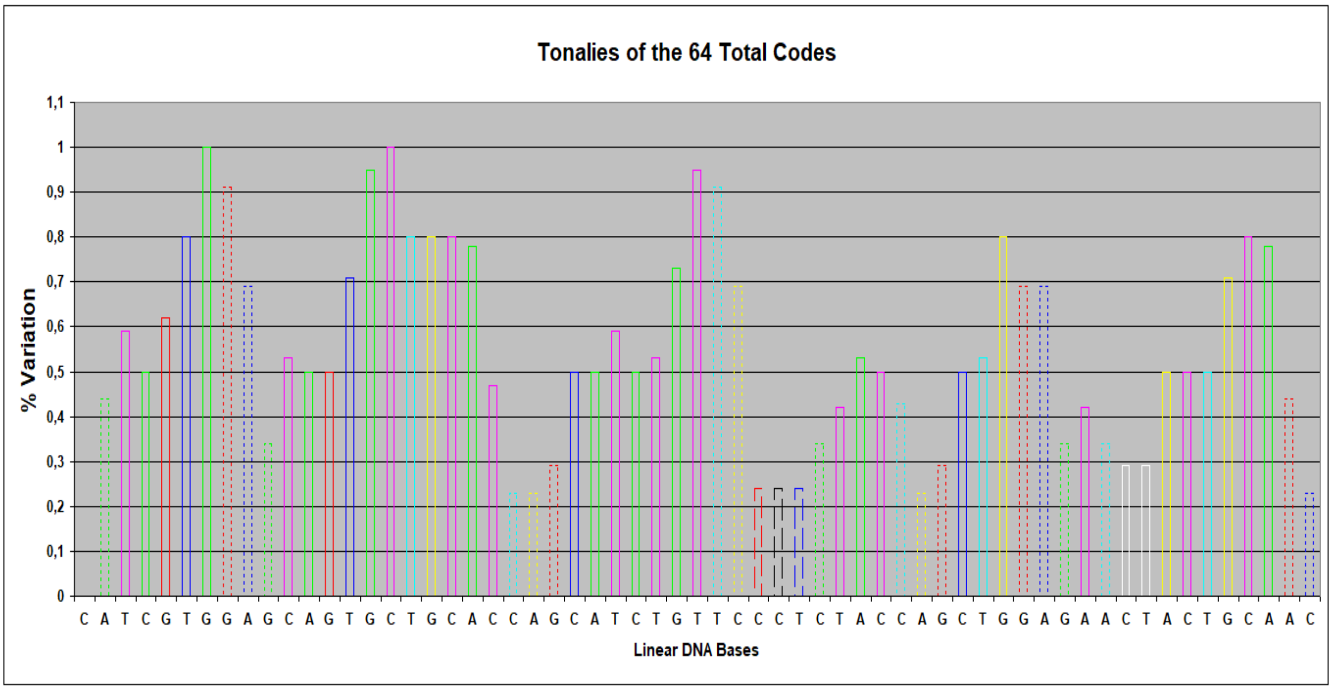
The chart in Pct. 58 (B) refers to the **“new generated sequence”** that originates from the original one.



Pct. 58 (B)

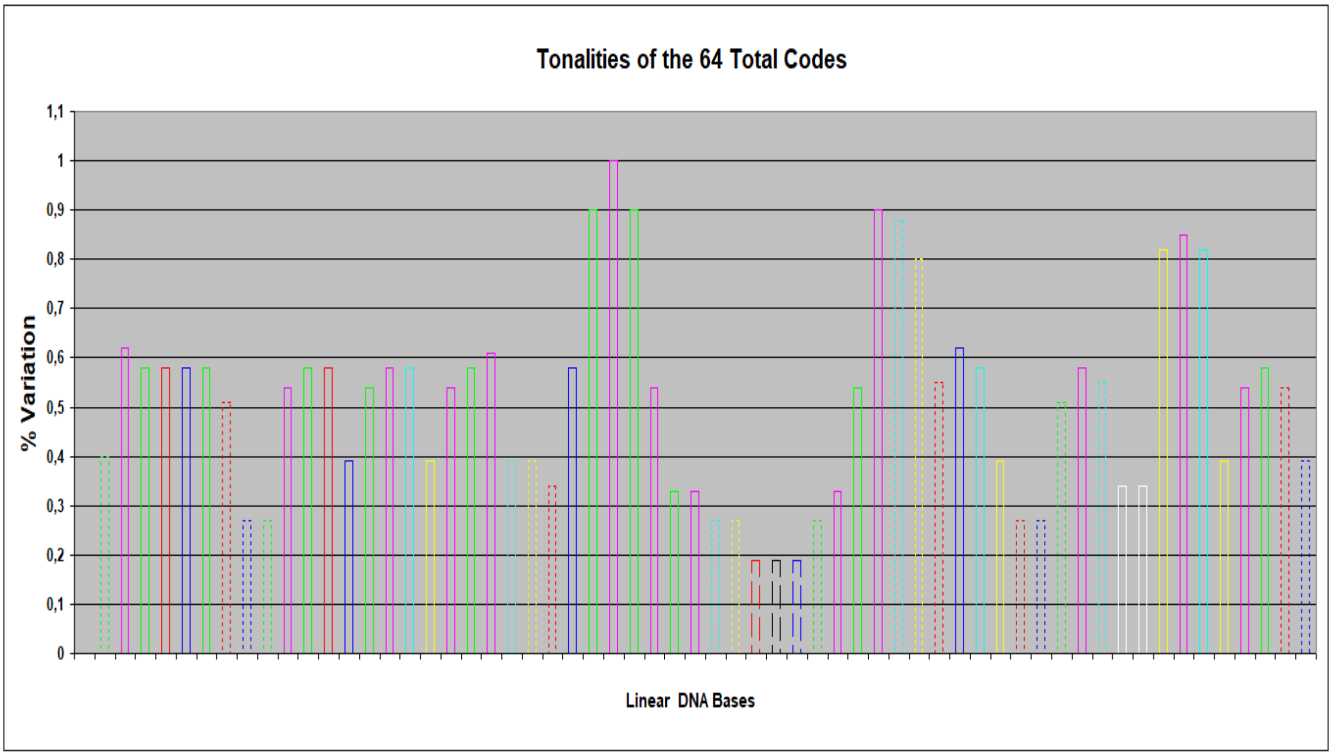
In Pct. 59 (A and B) two charts concerning the single **Tonalities of the 64 Total Codes** are compared.

The chart in Pct. 59 (A) refers to the **original base sequence** analysed before.



Pct. 59 (A)

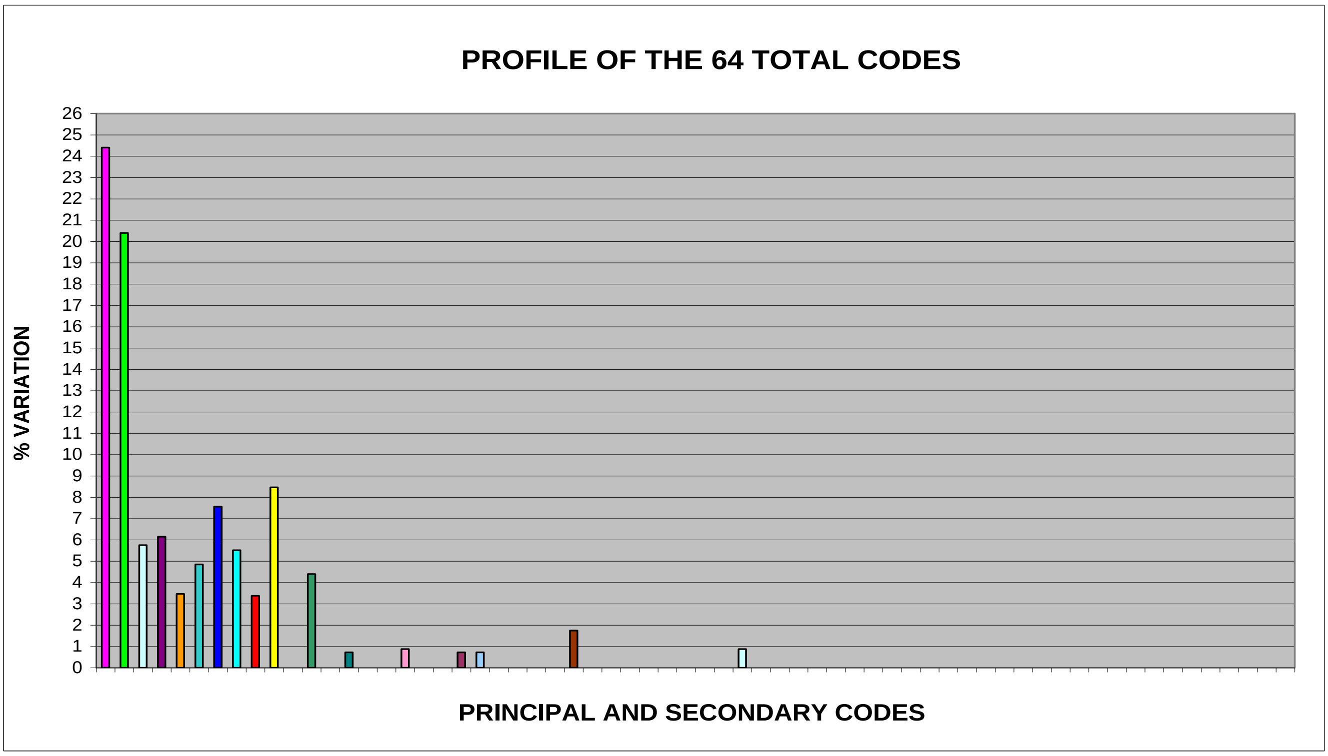
The chart in Pct. 59 (B) refers to the **"new generated sequence"** that originates from the original one.



Pct. 59 (B)

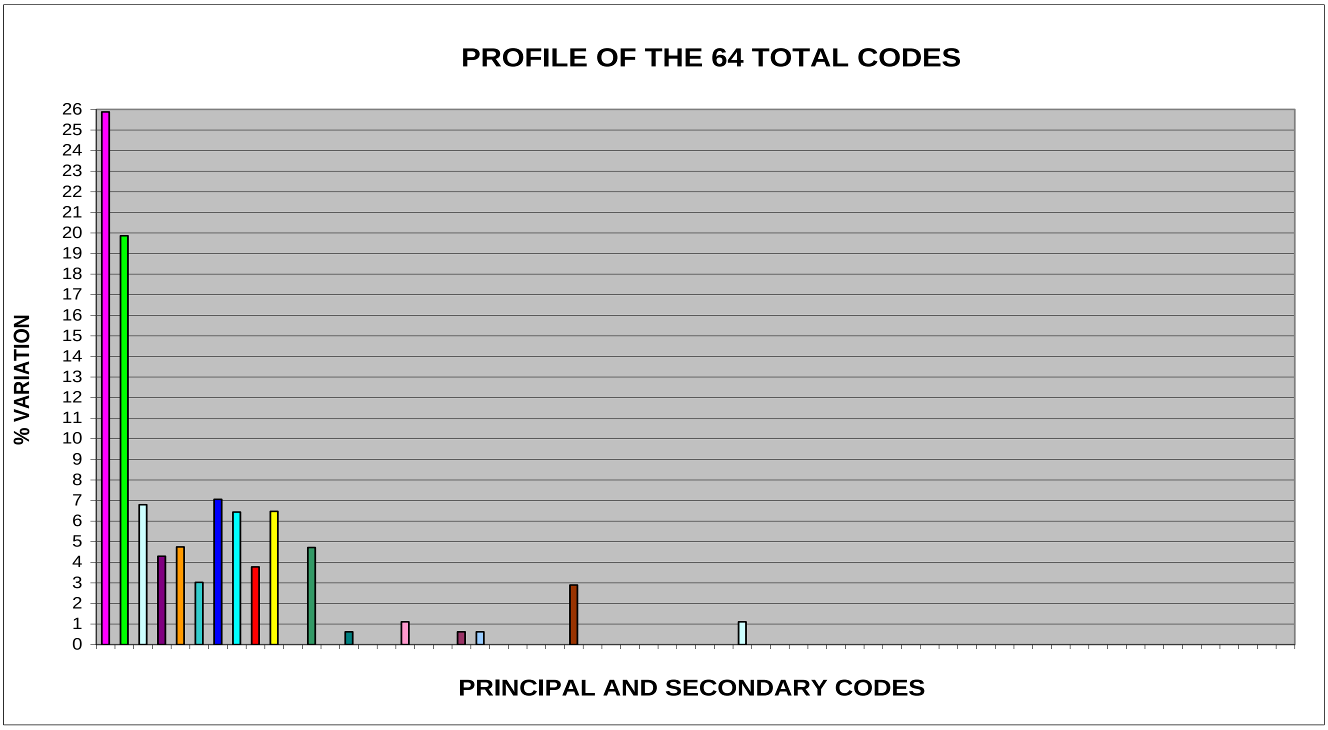
In Pct. 60 (A and B) two charts concerning the **Profile of the 64 Total Codes** are compared.

The chart in Pct. 60 (A) refers to the **original base sequence** analysed before.



Pct. 60 (A)

The chart in Pct. 60 (B) refers to the **“new generated sequence”** originated from the original one.



Pct. 60 (B)

The “non-obvious trend” analysis (obtained through the **T.T.E.S.**) of **Sequence n°15/1 of Insulin Chain A** results in **a comparison among different graphs** that are going to be interpreted in an analogous way to that in which the graphs related to the “non-obvious trend” of the **Sequences** analysed in the previous paragraphs **(n° 1/1, n° 2/1, etc.)** were. In order to avoid repetitions, here, the reader is deferred to the interpretation of the **comparisons among the different graphs** presented in the paragraph 1.2 .

Before concluding the paragraph, it is worth noting that, out of the **63** DNA bases of **Sequence n° 15/1**, ONLY **TEEN BASES** (the **15,87%**), ARE EQUAL (by type and by position in sequence) TO THOSE OF THE ORIGINAL SEQUENCE (**Insulin Chain A**).

1.31 IMPLICATIONS RELATED TO THE GRAPHIC RESULTS OF THE “NON-OBVIOUS TREND” ANALYSIS OF SEQUENCE n° 15/1 OF INSULIN CHAIN A

The **63** DNA base sequence of the **new generated sequence** (**Sequence n° 15/1**) that arises from the **original** one has been subjected to **BLAST** research.

Please note:

Information about the ***significant alignments*** produced by *BLAST research*, related to **Sequence n° 15/1,** and all the data acquired from *GenBank (3)* will be published in the **Appendix,** after the *General Conclusions.*

Query = NEW GENERATED SEQUENCE (Sequence n° 15/1)

Length = 63

Parameters of BLAST research:

Programme	*Blastn*
Word size	*11*
Expect value	*10*
Hitlist size	*100*
Match/Mismatch scores	*2,-3*
Gapcosts	*5,2*
Low Complexity Filter	*Yes*
Filter string	*L;m;*
Genetic Code	*1*

Please note:

Here, “**the organisms found to be in common**” between the results of BLAST research carried out on **Insulin Chain A** and results of BLAST research carried out on **Sequence n° 15/1**, were highlighted in **Red**.
As well, “**the organisms found to be in common**” between the results of BLAST research carried out on **Insulin Chain A**, results of BLAST research carried out on **Sequence n° 15/1** and results of BLAST research carried out on **at least one** of the *19 generated sequences*, were highlighted in **Green**.
Moreover, “**the denomination of the sequence**” (1/1, 2/1, ... 19/1) of the “**organism found to be in common**” between the results of BLAST research carried out on **Sequence n° 15/1** and results of BLAST research carried out on **at least one** of the *19 new generated sequences*, were highlighted in **Blue**.
Finally, “**the denomination of the sequence**” (1/1, 2/1, ... 19/1) of the “**organism found to be in common**” between the results of BLAST research carried out on **Insulin Chain A** and results of BLAST research carried out on *19 generated sequences*, were highlighted in **Yellow**.

Sequenza n° 15/1

Sequences producing significant alignments:

Selected seq	Description	Max score	Total score	Query cover	E value	Ident	Accession
1 XM_020585373.1	PREDICTED: Monopterus albus myoneurin-like (LOC109951089), mRNA	41.9	41.9	50%	2.7	91%	XM_020585373.1
2 MK500381.1	Marseillevirus LCMAC202 genomic sequence	41.0	41.0	42%	2.7	93%	MK500381.1
3 **16/1** LS483476.1	Bacillus lentus strain NCTC4824 genome assembly, chromosome: 1	41.0	41.0	34%	2.7	100%	LS483476.1
4 **18/1** XM_022531200.1	Aspergillus bombycis hypothetical protein (ABOM_004070), partial mRNA	41.0	41.0	42%	2.7	93%	XM_022531200.1
5 FN545254.1	Arsenophonus nasoniae whole genome shotgun assembly, contig scaffold01140	41.0	41.0	58%	2.7	84%	FN545254.1
6 XM_001319644.1	Trichomonas vaginalis G3 hypothetical protein (TVAG_499420) partial mRNA	41.0	41.0	42%	2.7	93%	XM_001319644.1
7 LR132049.1	Anabas testudineus genome assembly, chromosome: 19	40.1	40.1	38%	9.5	96%	LR132049.1
8 CP003616.1	Oscillatoria nigro-viridis PCC 7112 plasmid pOSC7112.02, complete sequence	40.1	40.1	38%	9.5	96%	CP003616.1
9 FO082057.1	Pichia sorbitophila strain CBS 7064 chromosome C complete sequence	40.1	40.1	38%	9.5	96%	FO082057.1
10 **1/1** XM_026987438.1	PREDICTED: Drosophila persimilis serine-rich adhesin for platelets (LOC6593495), transcript variant X3, mRNA	39.2	39.2	92%	9.5	76%	XM_026987438.1
11 CP022854.1	Parastagonospora nodorum isolate Sn79-1087 chromosome 4, complete sequence	39.2	39.2	41%	9.5	92%	CP022854.1
12 CP022832.1	Parastagonospora nodorum isolate Sn2000 chromosome 4 sequence	39.2	39.2	41%	9.5	92%	CP022832.1
13 CP022802.1	Parastagonospora nodorum isolate LDN03-Sn4 chromosome 4, complete sequence	39.2	39.2	41%	9.5	92%	CP022802.1
14 NG_051023.1	Homo sapiens LDL receptor related protein 1B (LRP1B), RefSeqGene on chromosome 2	39.2	39.2	49%	9.5	87%	NG_051023.1
15 **1/1** XM_017299325.1	PREDICTED: Drosophila miranda serine-rich adhesin for platelets (LOC108163827), transcript variant X10, mRNA	39.2	39.2	92%	9.5	76%	XM_017299325.1

Sequences producing significant alignments:

Selected seq	Description	Max score	Total score	Query cover	E value	Ident	Accession
16 **1/1** XM_017299320.1	PREDICTED: Drosophila miranda serine-rich adhesin for platelets (LOC108163827), transcript variant X5, mRNA	39.2	39.2	92%	9.5	76%	XM_017299320.1
17 **1/1** XM_001355767.3	Drosophila pseudoobscura pseudoobscura uncharacterized protein (Dpse\GA21824), mRNA	39.2	39.2	92%	9.5	76%	XM_001355767.3
18 AC073319.4	Homo sapiens BAC clone RP11-279M2 from 2, complete sequence	39.2	39.2	49%	9.5	87%	AC073319.4

Comparison between the alignments of Sequence 15/1 and Sequence of Insulin Chain A according to the “Species of Common Organisms”:

Alignments Sequence 15/1	**Description**	**Alignments Sequence Insulin Chain A**	**Description**
1 Select seq XM_020585373.1	PREDICTED: Monopterus albus myoneurin-like (LOC109951089), mRNA	Select seq XM_020615193.1 **17/1**	PREDICTED: Monopterus albus insulin (LOC109968712), mRNA
		Select seq XM_020599783.1 **17/1**	PREDICTED: Monopterus albus insulin-like (LOC109959979), mRNA
		Select seq XM_020591214.1 **17/1**	PREDICTED: Monopterus albus insulin-like (LOC109955249), mRNA
7 Select seq LR132049.1	Anabas testudineus genome assembly, chromosome: 19	Select seq LR132049.1	Anabas testudineus genome assembly, chromosome: 19
		Select seq LR132037.1	Anabas testudineus genome assembly, chromosome: 10
		Select seq XM_026357607.1	PREDICTED: Anabas testudineus insulin (LOC113160385), mRNA
		Select seq XM_026357435.1	PREDICTED: Anabas testudineus insulin-like (LOC113160265), mRNA
		Select seq XM_026351068.1	PREDICTED: Anabas testudineus circularly permutated Ras protein 1-like (LOC113156131), transcript variant X3, mRNA
		Select seq XM_026351067.1	PREDICTED: Anabas testudineus circularly permutated Ras protein 1-like (LOC113156131), transcript variant X2, mRNA
		Select seq XM_026351066.1	PREDICTED: Anabas testudineus circularly permutated Ras protein 1-like (LOC113156131), transcript variant X1, mRNA
14 Select seq NG_051023.1	Homo sapiens LDL receptor related protein 1B (LRP1B), RefSeqGene on chromosome 2	Select seq AH002844.2 **2/1 8/1 9/1 10/1** **17/1**	Homo sapiens insulin (INS) gene, complete cds

Comparison between the alignments of Sequence 15/1 and Sequence of Insulin Chain A according to the “Species of Common Organisms”:

Alignments Sequence 15/1	**Description**	**Alignments Sequence Insulin Chain A**	**Description**
18 Select seq AC073319.4	Homo sapiens BAC clone RP11-279M2 from 2, complete sequence	Select seq AH012037.2 **2/1 8/1 9/1 10/1 17/1**	Homo sapiens haplotype ICa tyrosine hydroxylase (TH) gene, partial sequence; insulin (INS) gene, complete cds; and insulin-like growth factor 2 (IGF2) gene, partial sequence
		Select seq NG_050578.1 **2/1 8/1 9/1 10/1 17/1**	Homo sapiens INS-IGF2 readthrough (INS-IGF2), RefSeqGene on chromosome 11
		Select seq KR710184.1 **2/1 8/1 9/1 10/1 17/1**	Synthetic construct Homo sapiens clone CCSBHm_00010257 INS (INS) mRNA, encodes complete protein
		Select seq KR710183.1 **2/1 8/1 9/1 10/1 17/1**	Synthetic construct Homo sapiens clone CCSBHm_00010256 INS (INS) mRNA, encodes complete protein
		Select seq KR710182.1 **2/1 8/1 9/1 10/1 17/1**	Synthetic construct Homo sapiens clone CCSBHm_00010255 INS (INS) mRNA, encodes complete protein
		Select seq KJ891480.1 **2/1 8/1 9/1 10/1 17/1**	Synthetic construct Homo sapiens clone ccsbBroadEn_00874 INS gene, encodes complete protein
		Select seq NM_001291897.1 **2/1 8/1 9/1 10/1 17/1**	Homo sapiens insulin (INS), transcript variant 4, mRNA
		Select seq JQ951950.1 **2/1 8/1 9/1 10/1 17/1**	Homo sapiens preproinsulin (INS) mRNA, complete cds
		Select seq JF909299.1 **2/1 8/1 9/1 10/1 17/1**	Homo sapiens insulin (INS) mRNA, partial cds
		Select seq AB587580.1 **2/1 8/1 9/1 10/1 17/1**	Synthetic construct DNA, clone: pF1KB8864, Homo sapiens INS gene for insulin, without stop codon, in Flexi system

Comparison between the alignments of Sequence 15/1 and Sequence of Insulin Chain A according to the "Species of Common Organisms":

Alignments Sequence 15/1	Description	Alignments Sequence Insulin Chain A	Description
		Select seq NM_001185098.1 **2/1 8/1 9/1 10/1 17/1**	Homo sapiens insulin (INS), transcript variant 3, mRNA
		Select seq NM_001185097.1 **2/1 8/1 9/1 10/1 17/1**	Homo sapiens insulin (INS), transcript variant 2, mRNA
		Select seq NG_007114.1 **2/1 8/1 9/1 10/1 17/1**	Homo sapiens insulin (INS), RefSeqGene on chromosome 11
		Select seq DQ778082.1 **2/1 8/1 9/1 10/1 17/1**	Homo sapiens clone BFC06103 insulin mRNA, complete cds
		Select seq DQ896283.2 **2/1 8/1 9/1 10/1 17/1**	Synthetic construct Homo sapiens clone IMAGE:100010743; FLH192918.01L; RZPDo839A1068D insulin (INS) gene, encodes complete protein
		Select seq NM_000207.2 **2/1 8/1 9/1 10/1 17/1**	Homo sapiens insulin (INS), transcript variant 1, mRNA
		Select seq BT007778.1 **2/1 8/1 9/1 10/1 17/1**	Synthetic construct Homo sapiens insulin mRNA, partial cds
		Select seq BT006808.1 **2/1 8/1 9/1 10/1 17/1**	Homo sapiens insulin mRNA, complete cds
		Select seq BC005255.1 **2/1 8/1 9/1 10/1 17/1**	Homo sapiens insulin, mRNA (cDNA clone MGC:12292 IMAGE:3950204), complete cds
		Select seq AC132217.15 **2/1 8/1 9/1 10/1 17/1**	Homo sapiens chromosome 11, clone RP11-889I17, complete sequence

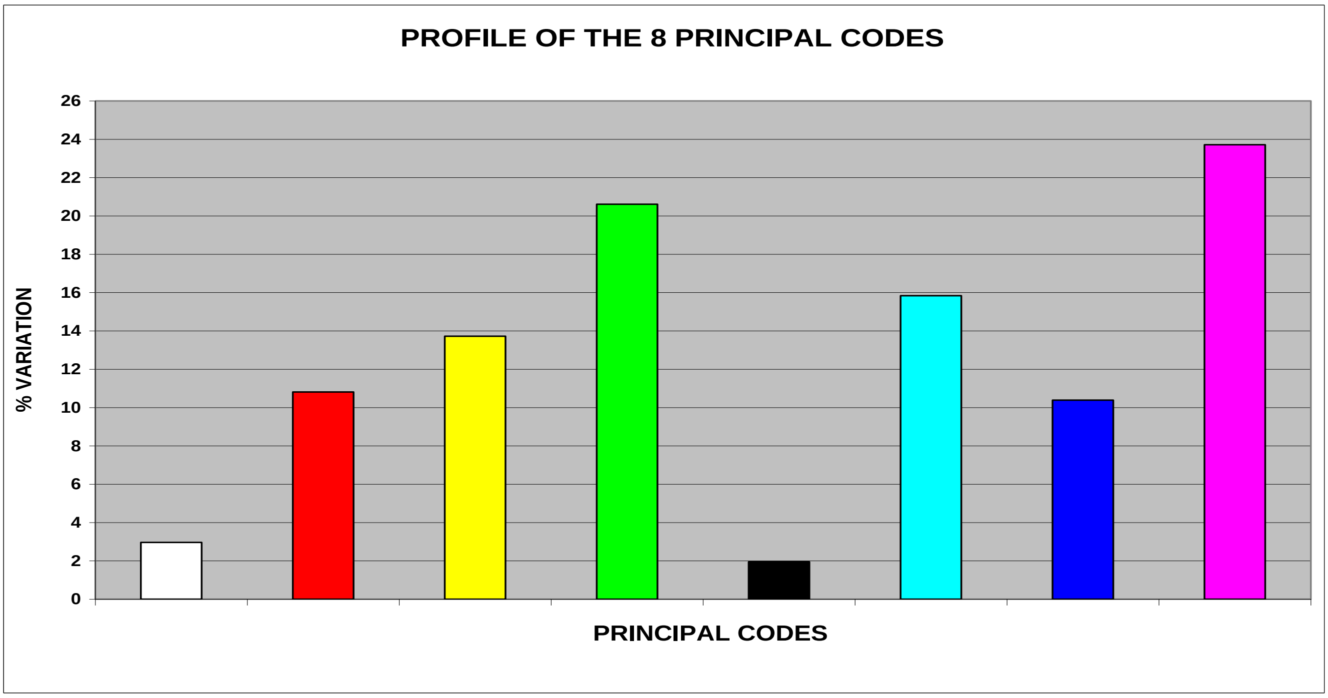
Comparison between the alignments of Sequence 15/1 and Sequence of Insulin Chain A according to the "Species of Common Organisms":			
Alignments Sequence 15/1	**Description**	**Alignments Sequence Insulin Chain A**	**Description**
		Select seq AC130303.8 **2/1 8/1 9/1 10/1 17/1**	Homo sapiens chromosome 11, clone RP4-539G11, complete sequence
		Select seq AY899304.1 **2/1 8/1 9/1 10/1 17/1**	Homo sapiens proinsulin mRNA, complete cds, alternatively spliced
		Select seq AJ009655.1 **2/1 8/1 9/1 10/1 17/1**	Homo sapiens ins gene, partial
		Select seq X70508.1 **2/1 8/1 9/1 10/1 17/1**	Homo sapiens mRNA for insulinoma pre-proinsulin
		Select seq L15440.1 **2/1 8/1 9/1 10/1 17/1**	Homo sapiens tyrosine hydroxylase (TH) gene, 3' end; insulin (INS) gene, complete cds; insulin-like growth factor 2 (IGF2) gene, 5' end
		Select seq KR710185.1 **2/1 8/1 9/1 10/1 17/1**	Synthetic construct Homo sapiens clone CCSBHm_00010262 INS (INS) mRNA, encodes complete protein
		Select seq AF050524.1 **2/1 8/1 9/1 10/1 17/1**	Synthetic Homo sapiens proinsulin-like protein BKRA gene, complete cds
		Select seq AC021233.9 **2/1 8/1 9/1 10/1 17/1**	Homo sapiens chromosome 11, clone RP11-215H22, complete sequence
		Select seq AK024581.1 **2/1 8/1 9/1 10/1 17/1**	Homo sapiens cDNA: FLJ20928 fis, clone ADSE01074

Analysis of
Sequence n° 16/1
of Insulin Chain A

1.32 GRAPHIC RESULTS OF THE “NON-OBVIOUS TREND” ANALYSIS OF SEQUENCE n° 16/1 OF INSULIN CHAIN A

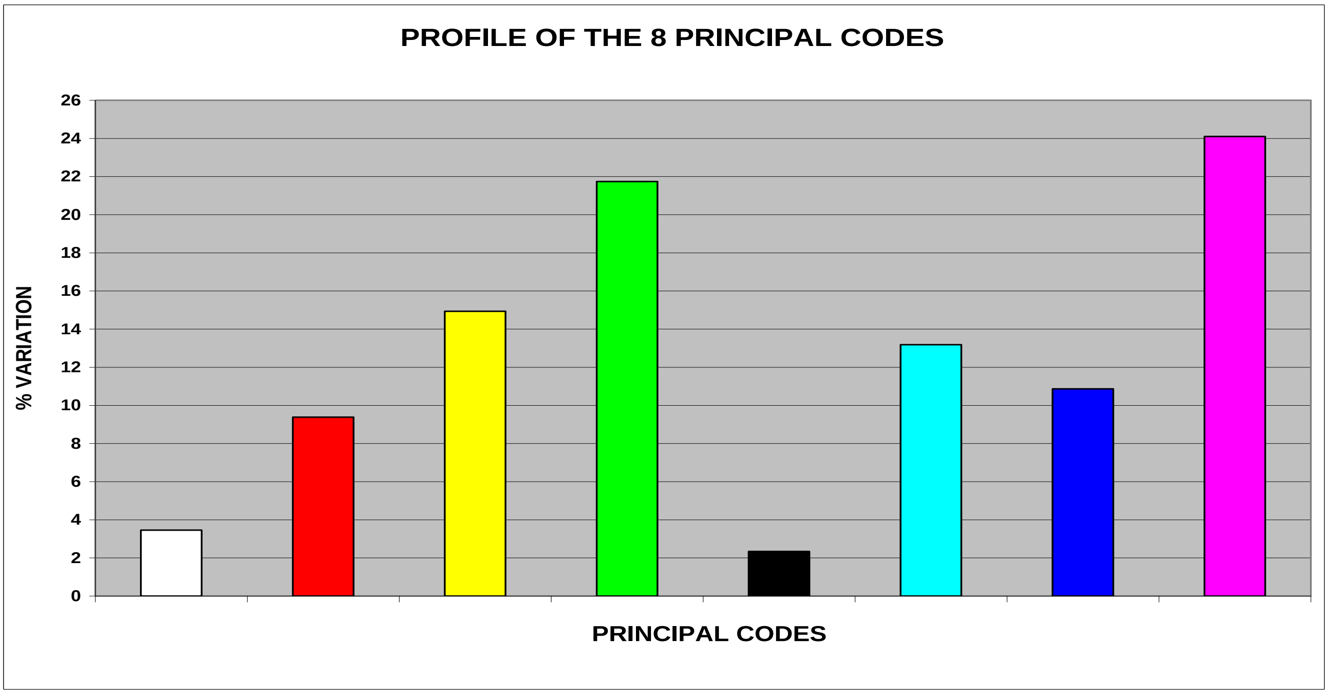
In the Pct. 61 (A e B) two **8 Principal Codes Profiles** are compared.

The chart in Pct. 61 (A) refers to the **original base sequence** of **Insulin Chain A**.



Pct. 61 (A)

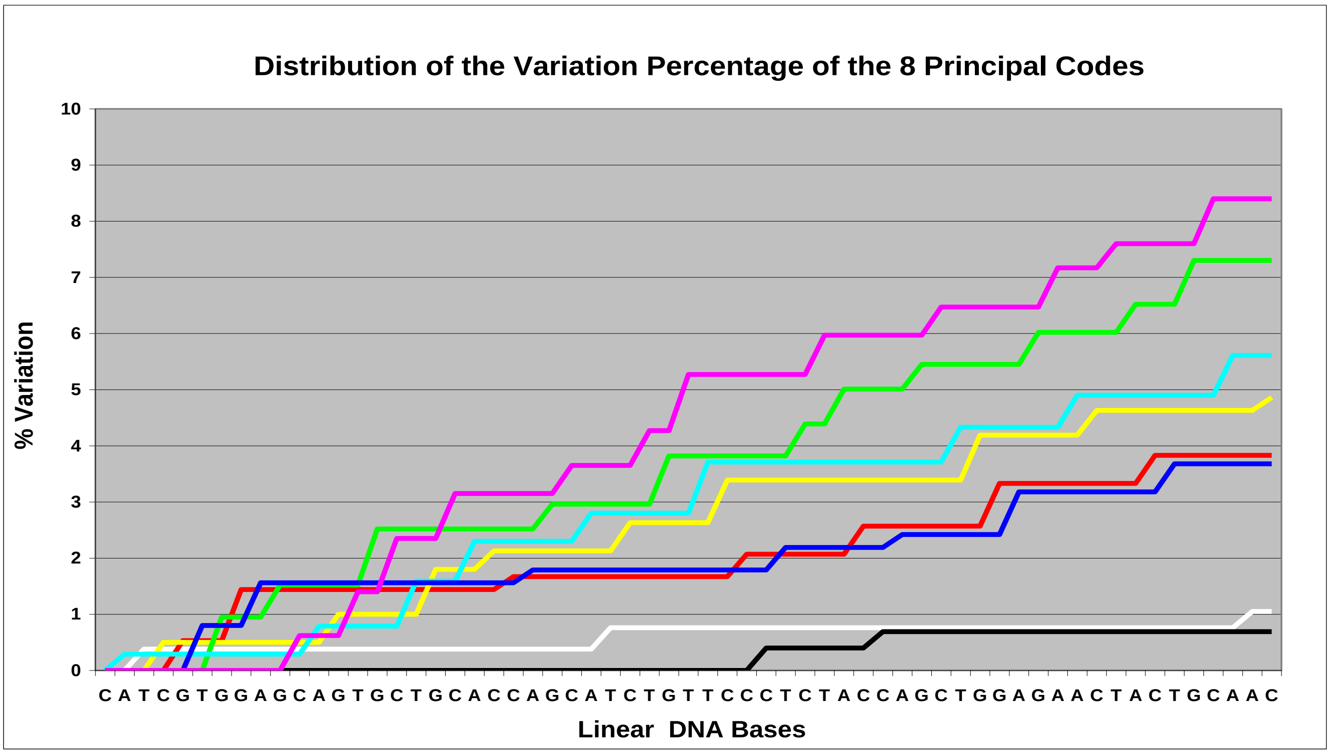
The chart in Pct. 61 (B) refers to the **sixteenth** **“new generated sequence”** (**Sequence n° 16/1**) that originates from the original one.



Pct. 61 (B)

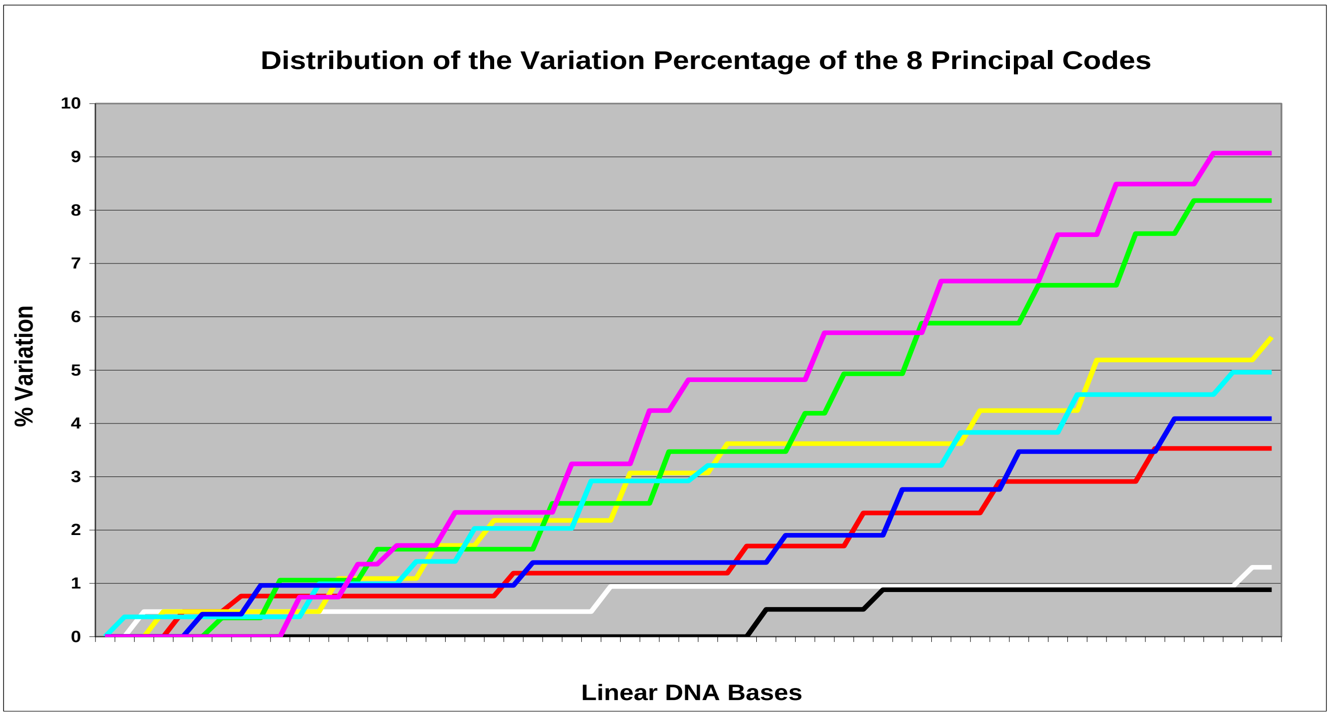
In Pct. 62 (A and B) two charts concerning the **Distribution of the Variation Percentage of the 8 Main Codes** are compared.

The charts in Pct. 62 (A) refers to the **original base sequence** analysed before.



Pct. 62 (A)

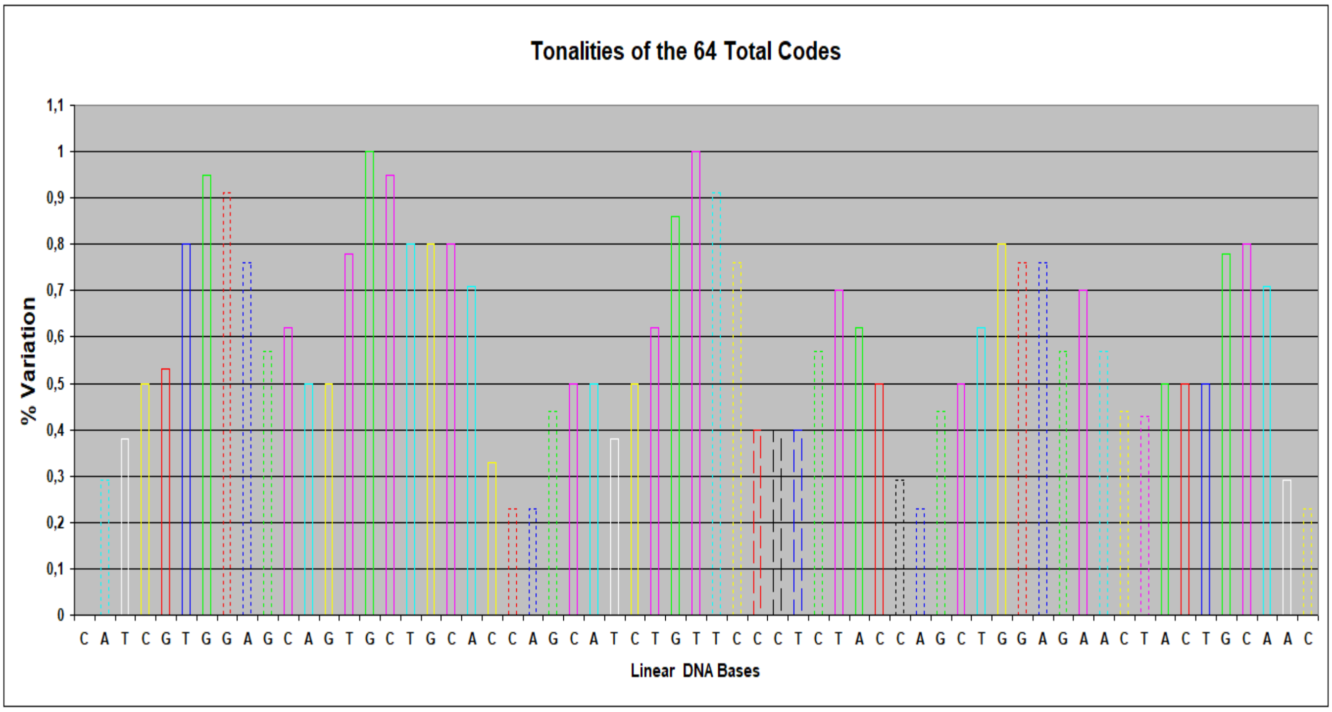
The chart in Pct. 62 (B) refers to the **“new generated sequence”** that originates from the original one.



Pct. 62 (B)

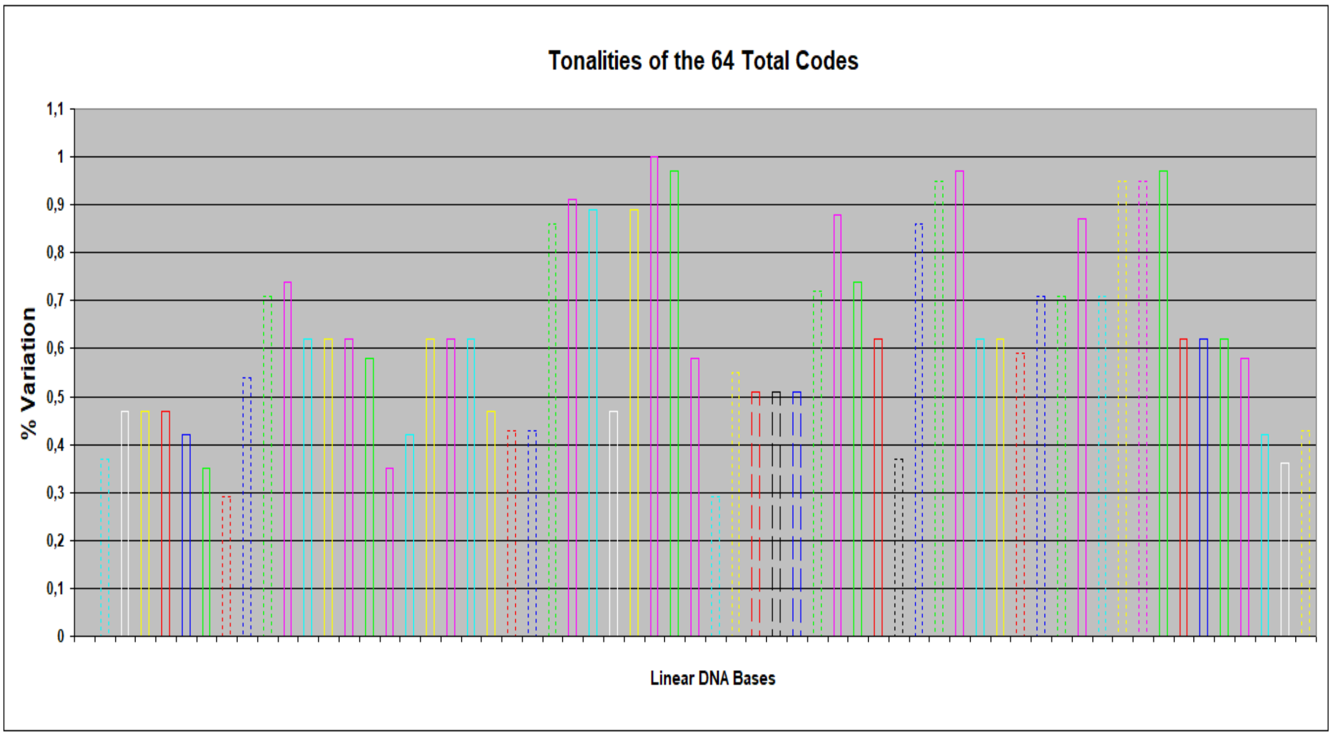
In Pct. 63 (A and B) two charts concerning the single **Tonalities of the 64 Total Codes** are compared.

The chart in Pct. 63 (A) refers to the **original base sequence** analysed before.



Pct. 63 (A)

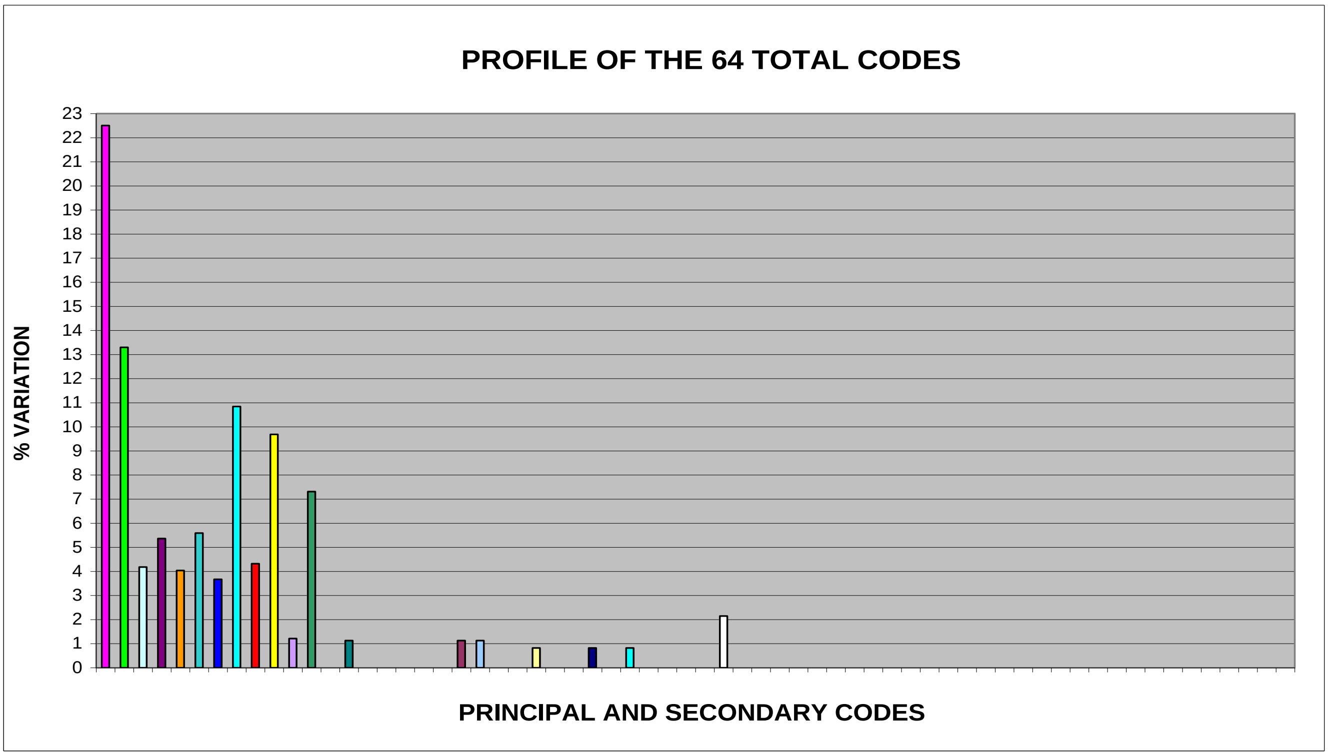
The chart in Pct. 63 (B) refers to the **"new generated sequence"** that originates from the original one.



Pct. 63 (B)

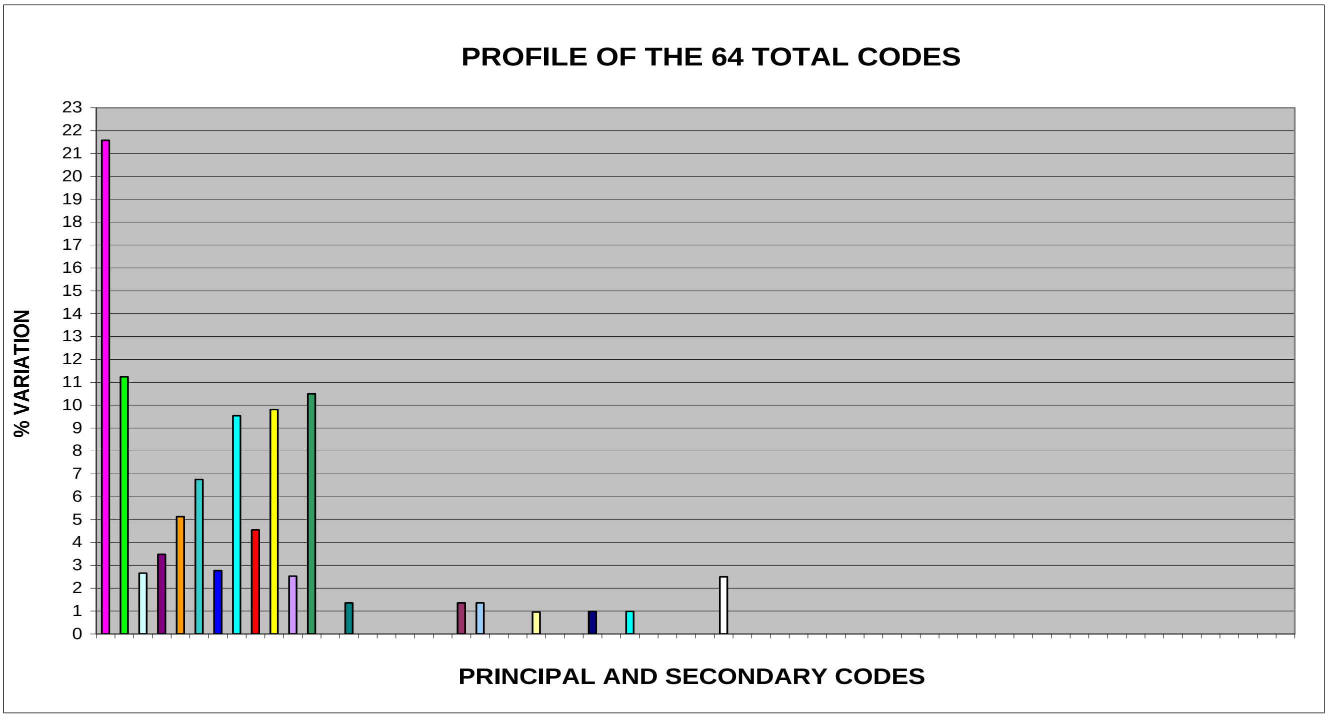
In Pct. 64 (A and B) two charts concerning the **Profile of the 64 Total Codes** are compared.

The chart in Pct. 64 (A) refers to the **original base sequence** analysed before.



Pct. 64 (A)

The chart in Pct. 64 (B) refers to the **"new generated sequence"** originated from the original one.



Pct. 64 (B)

The “non-obvious trend” analysis (obtained through the **T.T.E.S.**) of **Sequence n°16/1 of Insulin Chain A** results in **a comparison among different graphs** that are going to be interpreted in an analogous way to that in which the graphs related to the “non-obvious trend” of the **Sequences** analysed in the previous paragraphs **(n° 1/1, n° 2/1, etc.)** were. In order to avoid repetitions, here, the reader is deferred to the interpretation of the **comparisons among the different graphs** presented in the paragraph 1.2 .

Before concluding the paragraph, it is worth noting that, out of the **63** DNA bases of **Sequence n° 16/1**, ONLY **ELEVEN BASES** (the **17,46%**)**,** ARE EQUAL (by type and by position in sequence) TO THOSE OF THE ORIGINAL SEQUENCE (**Insulin Chain A**).

1.33 IMPLICATIONS RELATED TO THE GRAPHIC RESULTS OF THE "NON-OBVIOUS TREND" ANALYSIS OF SEQUENCE n° 16/1 OF INSULIN CHAIN A

The **63** DNA base sequence of the **new generated sequence** (**Sequence n° 16/1**) that arises from the **original** one has been subjected to **BLAST** research.

Please note:

nformation about the ***significant alignments*** produced by *BLAST research*, related to **Sequence n° 16/1,** and all the data acquired from *GenBank (3)* will be published in the **Appendix,** after the *General Conclusions.*

Query = NEW GENERATED SEQUENCE (Sequence n° 16/1)

Length = 63

Parameters of BLAST research:

Programme	*Blastn*
Word size	*11*
Expect value	*10*
Hitlist size	*100*
Match/Mismatch scores	*2,-3*
Gapcosts	*5,2*
Low Complexity Filter	*Yes*
Filter string	*L;m;*
Genetic Code	*1*

Please note:

Here, "**the organisms found to be in common**" between the results of BLAST research carried out on **Insulin Chain A** and results of BLAST research carried out on **Sequence n° 16/1**, were highlighted in **Red**.
As well, "**the organisms found to be in common**" between the results of BLAST research carried out on **Insulin Chain A**, results of BLAST research carried out on **Sequence n° 16/1** and results of BLAST research carried out on **at least one** of the *19 generated sequences*, were highlighted in **Green**.
Moreover, "**the denomination of the sequence**" (1/1, 2/1, ... 19/1) of the "**organism found to be in common**" between the results of BLAST research carried out on **Sequence n° 16/1** and results of BLAST research carried out on **at least one** of the *19 new generated sequences*, were highlighted in **Blue**.
Finally, "**the denomination of the sequence**" (1/1, 2/1, ... 19/1) of the "**organism found to be in common**" between the results of BLAST research carried out on **Insulin Chain A** and results of BLAST research carried out on *19 generated sequences*, were highlighted in **Yellow**.

Sequenza n° 16/1

Sequences producing significant alignments:

Selected seq		Description	Max score	Total score	Query cover	E value	Ident	Accession
1 XM_024211392.1		PREDICTED: Terrapene mexicana triunguis NRAS proto-oncogene, GTPase (NRAS), transcript variant X2, mRNA	43.7	43.7	49%	0.77	90%	XM_024211392.1
2 XM_024108278.1		PREDICTED: Chrysemys picta bellii NRAS proto-oncogene, GTPase (NRAS), transcript variant X2, mRNA	41.9	41.9	39%	2.7	96%	XM_024108278.1
3 XM_005294927.2		PREDICTED: Chrysemys picta bellii NRAS proto-oncogene, GTPase (NRAS), transcript variant X1, mRNA	41.9	41.9	39%	2.7	96%	XM_005294927.2
4 LR131938.1		Cottoperca gobio genome assembly, chromosome: 8	41.0	41.0	58%	2.7	84%	LR131938.1
5 CP029464.1	15/1	Bacillus pumilus strain ZB201701 chromosome, complete genome	41.0	41.0	46%	2.7	93%	CP029464.1
6 CP016784.1	15/1	Bacillus pumilus strain PDSLzg-1, complete genome	41.0	41.0	46%	2.7	93%	CP016784.1
7 XM_023472453.1		PREDICTED: Eurytemora affinis zinc finger protein 236-like (LOC111701258), mRNA	40.1	40.1	38%	9.4	96%	XM_023472453.1
8 LR134089.1		Staphylococcus saprophyticus subsp. saprophyticus strain NCTC7666 genome assembly, chromosome: 1	39.2	39.2	33%	9.4	100%	LR134089.1
9 CP032604.1		Lateolabrax maculatus linkage group 7 sequence	39.2	39.2	41%	9.4	92%	CP032604.1
10 CP027281.1		Lateolabrax maculatus chromosome Lm20	39.2	39.2	41%	9.4	92%	CP027281.1
11 LT963439.1		Staphylococcus xylosus isolate Staphylococcus xylosus ATCC 29971 genome assembly, chromosome: I	39.2	39.2	33%	9.4	100%	LT963439.1
12 LT963436.1		Staphylococcus saprophyticus isolate Staphylococcus saprophyticus 883 genome assembly, chromosome: I	39.2	39.2	33%	9.4	100%	LT963436.1
13 CP022093.2		Staphylococcus saprophyticus strain FDAARGOS_355 chromosome, complete genome	39.2	39.2	33%	9.4	100%	CP022093.2
14 CP022056.2		Staphylococcus saprophyticus strain FDAARGOS_336 chromosome, complete genome	39.2	39.2	33%	9.4	100%	CP022056.2

Sequences producing significant alignments:

Selected seq	Description	Max score	Total score	Query cover	E value	Ident	Accession
15 CP014113.2	Staphylococcus saprophyticus strain FDAARGOS_168 chromosome, complete genome	39.2	39.2	33%	9.4	100%	CP014113.2
16 CP014057.2	Staphylococcus saprophyticus strain FDAARGOS_137, complete genome	39.2	39.2	33%	9.4	100%	CP014057.2
17 CP013922.1	Staphylococcus xylosus strain S170, complete genome	39.2	39.2	33%	9.4	100%	CP013922.1
18 CP017786.1 15/1	Bacillus xiamenensis strain VV3, complete genome	39.2	39.2	52%	9.4	88%	CP017786.1
19 LN554884.1	Staphylococcus xylosus genome assembly Staphylococcus xylosus C2a, chromosome : Chr1	39.2	39.2	33%	9.4	100%	LN554884.1
20 CP008724.1	Staphylococcus xylosus strain SMQ-121, complete genome	39.2	39.2	33%	9.4	100%	CP008724.1
21 CP007208.1	Staphylococcus xylosus strain HKUOPL8, complete genome	39.2	39.2	33%	9.4	100%	CP007208.1
22 CP003949.1	Rhodococcus opacus PD630, complete genome	39.2	39.2	57%	9.4	83%	CP003949.1
23 EF456668.1	Staphylococcus xylosus DSM20267 C2a ATPase AAA family protein gene, complete cds	39.2	39.2	33%	9.4	100%	EF456668.1
24 XM_001437053.1	Paramecium tetraurelia hypothetical protein (GSPATT00038135001) partial mRNA	39.2	39.2	49%	9.4	87%	XM_001437053.1
25 AP008934.1	Staphylococcus saprophyticus subsp. saprophyticus ATCC 15305 DNA, complete genome	39.2	39.2	33%	9.4	100%	AP008934.1

Comparison between the alignments of Sequence 16/1 and Sequence of Insulin Chain A according to the "Species of Common Organisms":

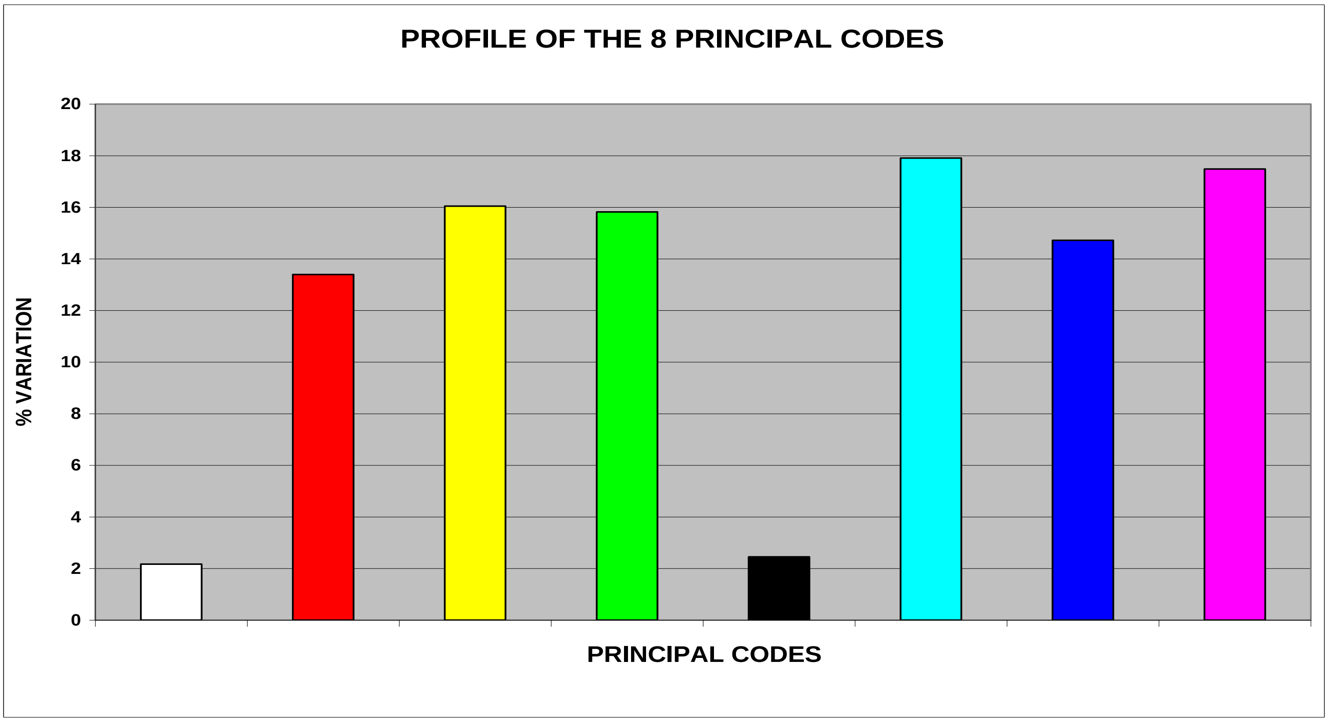
Alignments Sequence 16/1	**Description**	**Alignments Sequence Insulin Chain A**	**Description**
1 Select seq XM_024211392.1	PREDICTED: Terrapene mexicana triunguis NRAS proto-oncogene, GTPase (NRAS), transcript variant X2, mRNA	Select seq XM_024208870.1	PREDICTED: Terrapene mexicana triunguis insulin (INS), mRNA
2 Select seq XM_024108278.1	PREDICTED: Chrysemys picta bellii NRAS proto-oncogene, GTPase (NRAS), transcript variant X2, mRNA	Select seq XM_024102171.1	PREDICTED: Chrysemys picta bellii insulin (INS), transcript variant X2, mRNA
3 Select seq XM_005294927.2	PREDICTED: Chrysemys picta bellii NRAS proto-oncogene, GTPase (NRAS), transcript variant X1, mRNA	Select seq XM_005312381.2	PREDICTED: Chrysemys picta bellii insulin (INS), transcript variant X1, mRNA
4 Select seq LR131938.1	Cottoperca gobio genome assembly, chromosome: 8	Select seq LR131921.1 **4/1 6/1 7/1 18/1 19/1**	Cottoperca gobio genome assembly, chromosome: 14
		Select seq LR131917.1 **4/1 6/1 7/1 18/1 19/1**	Cottoperca gobio genome assembly, chromosome: 10
9 Select seq CP032604.1	Lateolabrax maculatus linkage group 7 sequence	Select seq CP032586.1 **14/1 17/1**	Lateolabrax maculatus linkage group 12 sequence
10 Select seq CP027281.1	Lateolabrax maculatus chromosome Lm20	Select seq CP027266.1 **14/1 17/1**	Lateolabrax maculatus chromosome Lm5

Analysis of
Sequence n° 17/1
of Insulin Chain A

1.34 GRAPHIC RESULTS OF THE "NON-OBVIOUS TREND" ANALYSIS OF SEQUENCE n° 17/1 OF INSULIN CHAIN A

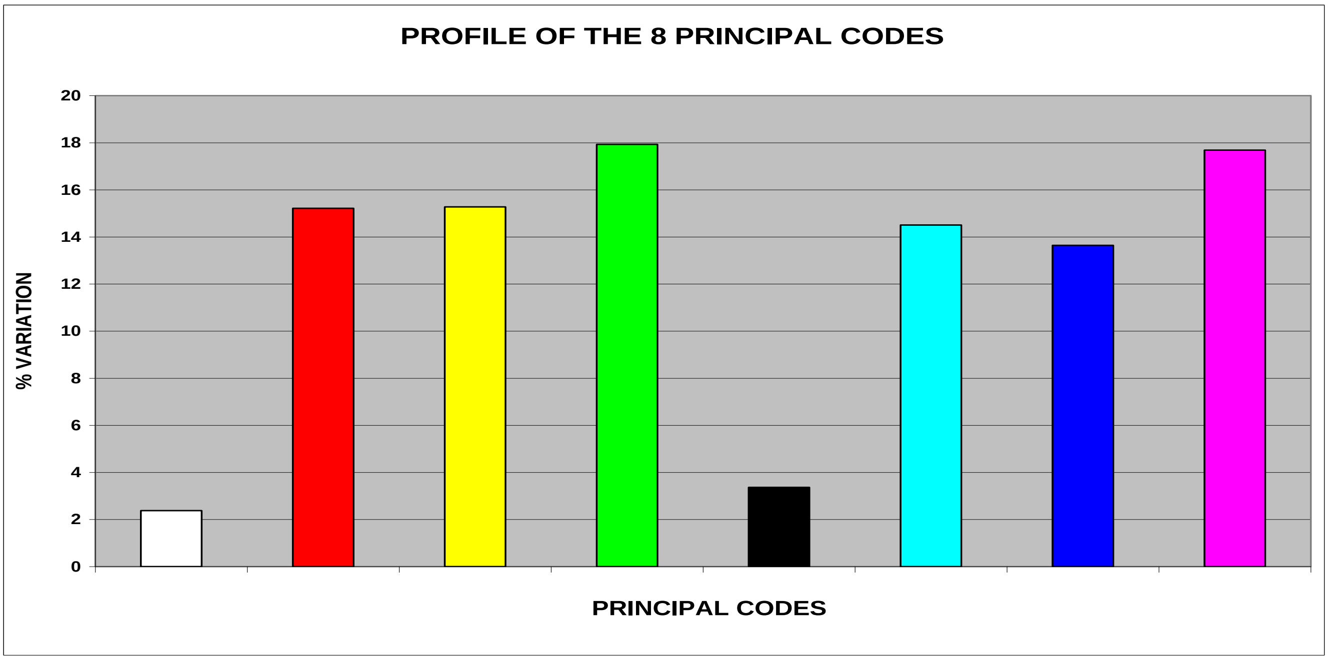
In the Pct. 65 (A e B) two **8 Principal Codes Profiles** are compared.

The chart in Pct. 65 (A) refers to the **original base sequence** of **Insulin Chain A**.



Pct. 65 (A)

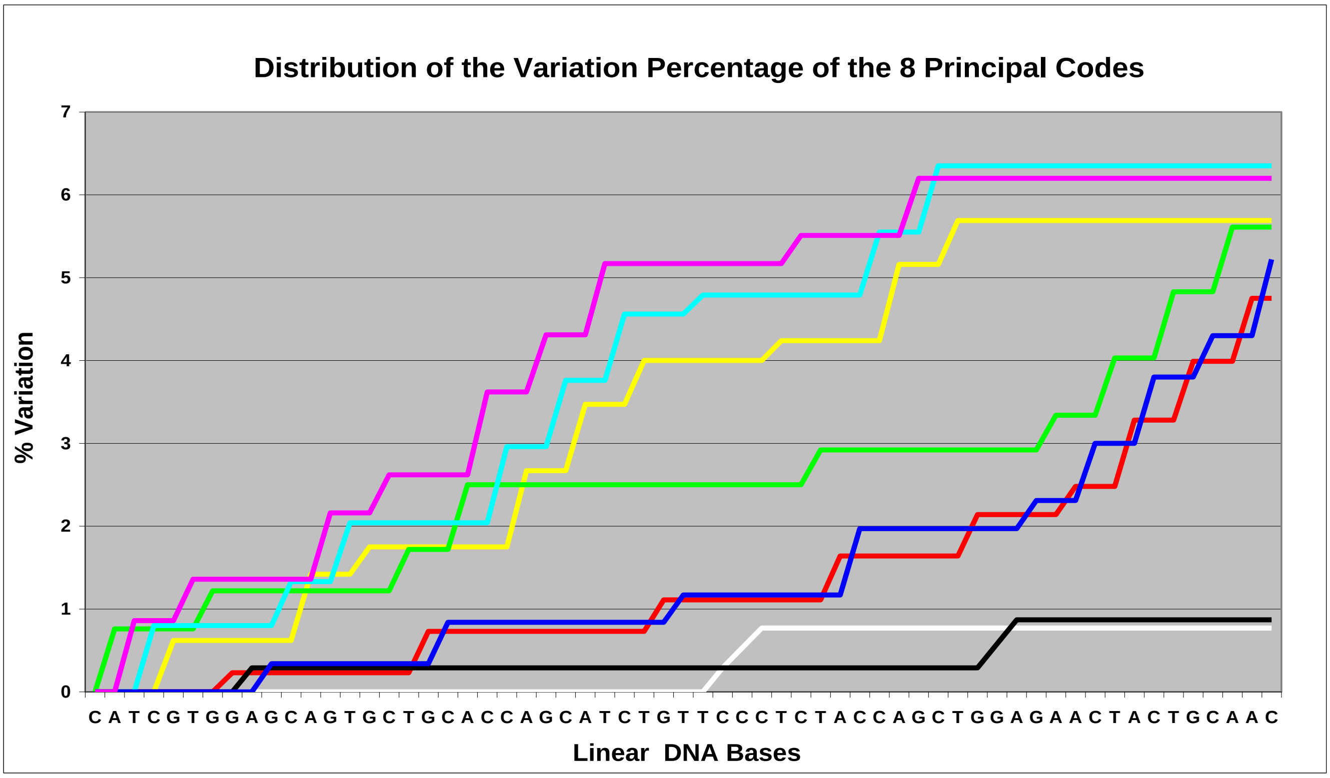
The chart in Pct. 65 (B) refers to the **seventeenth** **"new generated sequence"** (**Sequence n° 17/1**) that originates from the original one.



Pct. 65 (B)

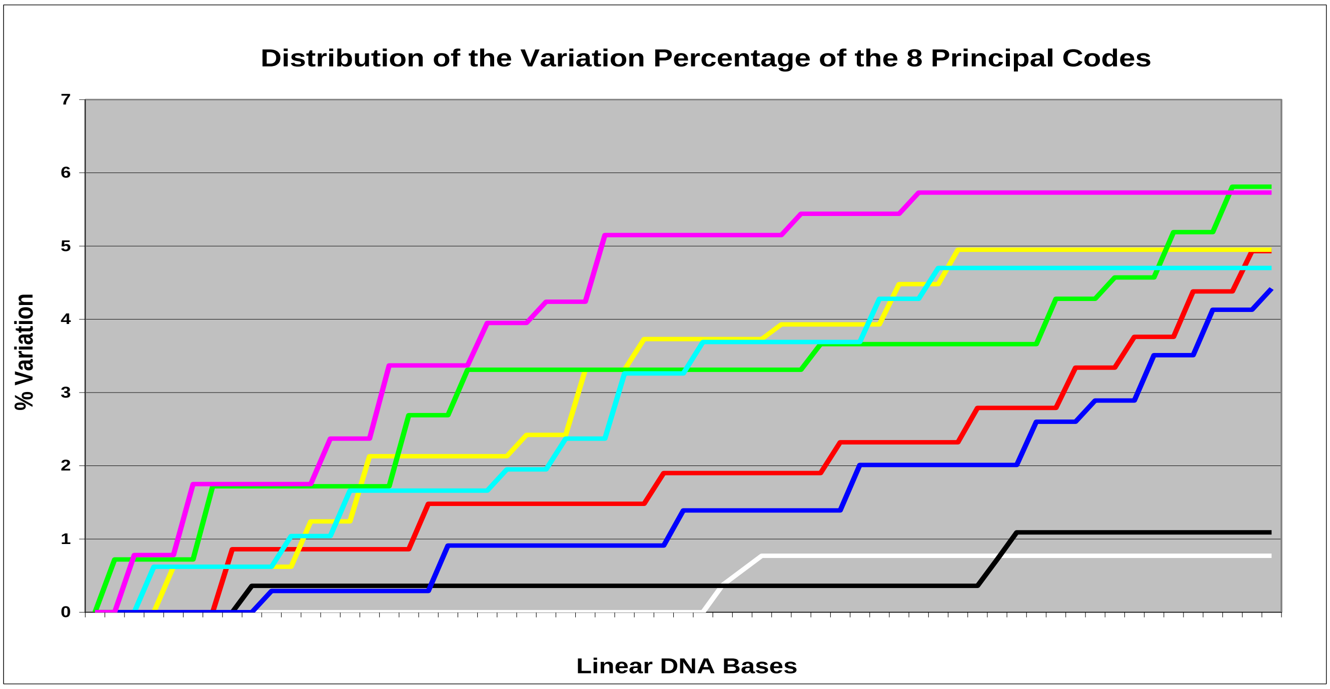
In Pct. 66 (A and B) two charts concerning the **Distribution of the Variation Percentage of the 8 Main Codes** are compared.

The charts in Pct. 66 (A) refers to the **original base sequence** analysed before.



Pct. 66 (A)

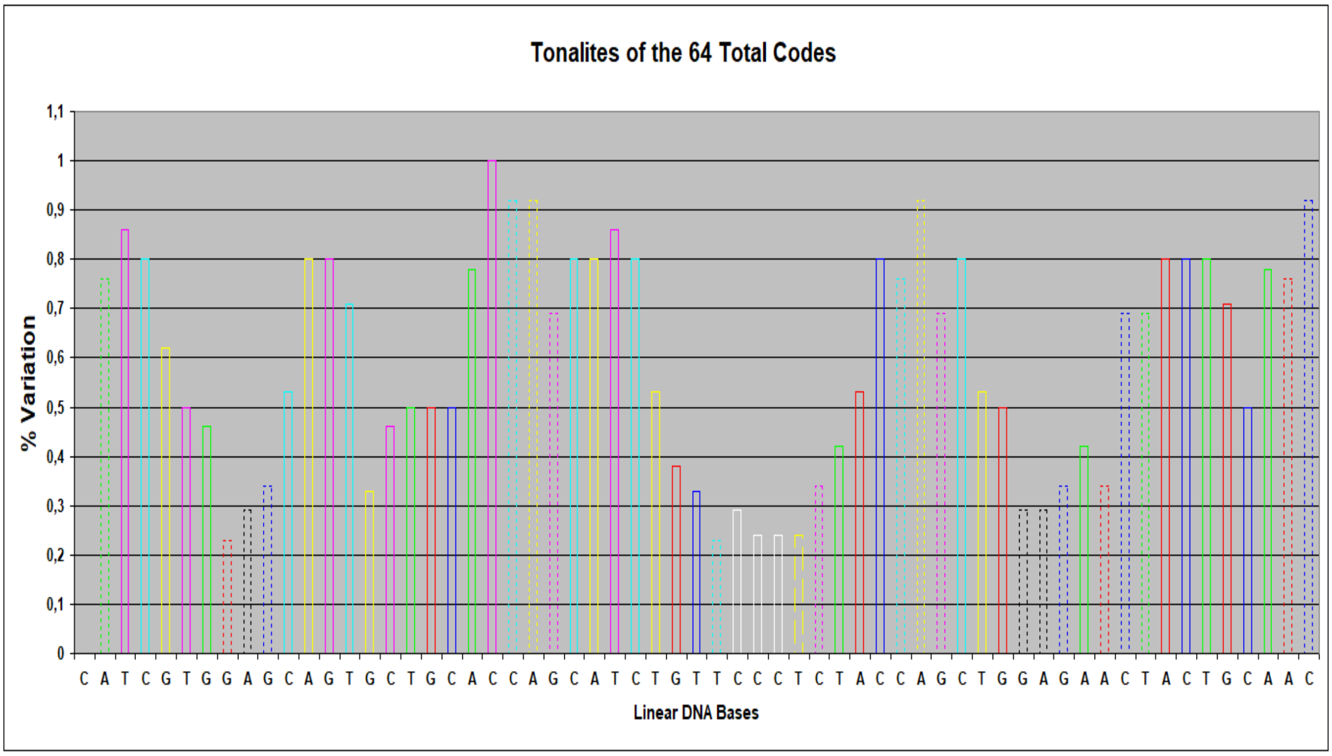
The chart in Pct. 66 (B) refers to the **"new generated sequence"** that originates from the original one.



Pct. 66 (B)

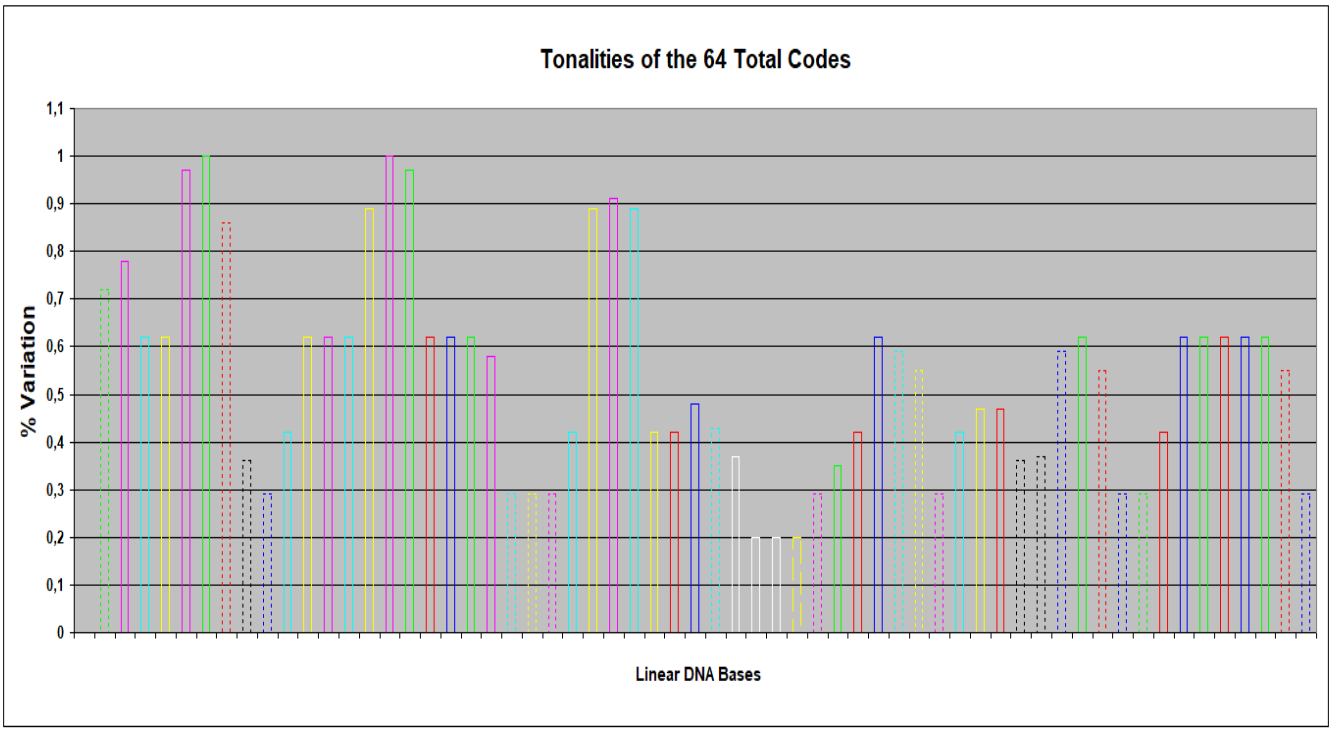
In Pct. 67 (A and B) two charts concerning the single **Tonalities of the 64 Total Codes** are compared.

The chart in Pct. 67 (A) refers to the **original base sequence** analysed before.



Pct. 67 (A)

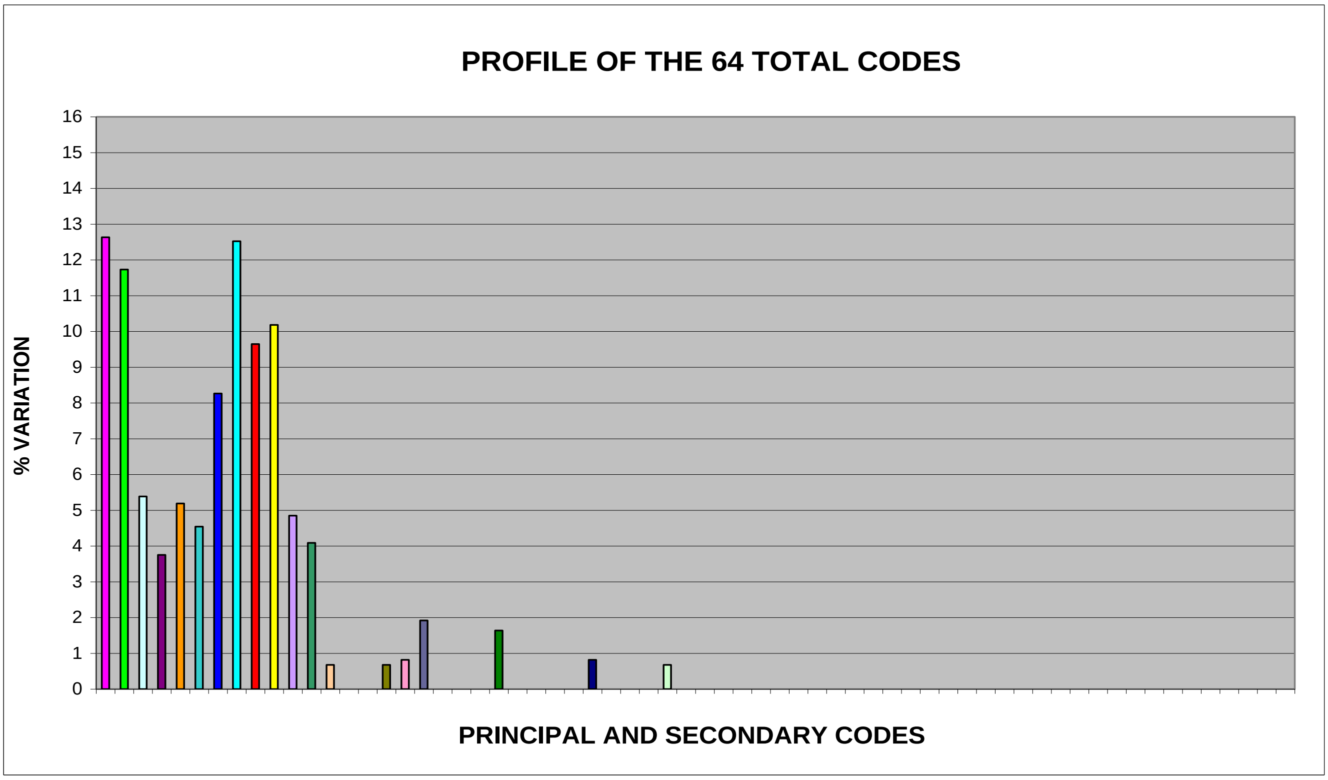
The chart in Pct. 67 (B) refers to the **"new generated sequence"** that originates from the original one.



Pct. 67 (B)

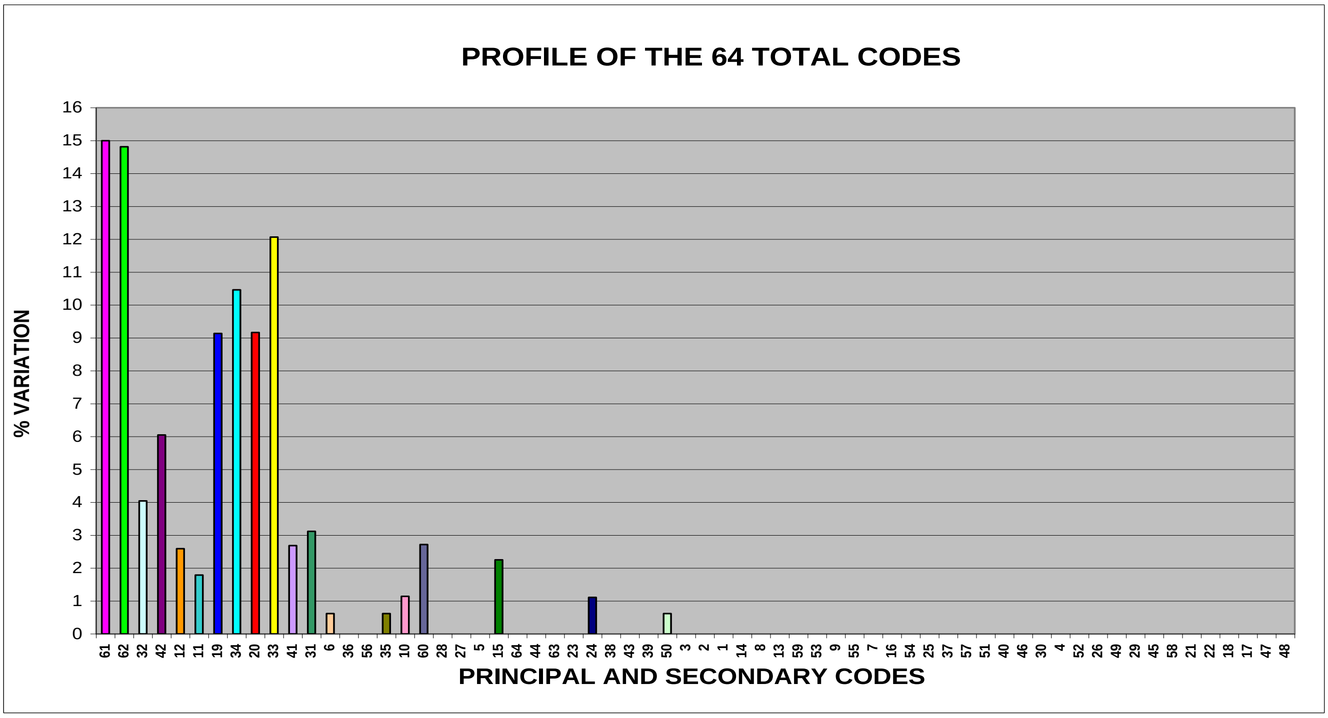
In Pct. 68 (A and B) two charts concerning the **Profile of the 64 Total Codes** are compared.

The chart in Pct. 68 (A) refers to the **original base sequence** analysed before.



Pct. 68 (A)

The chart in Pct. 68 (B) refers to the **“new generated sequence”** originated from the original one.



Pct. 68 (B)

The "non-obvious trend" analysis (obtained through the **T.T.E.S.**) of **Sequence n°17/1 of Insulin Chain A** results in **a comparison among different graphs** that are going to be interpreted in an analogous way to that in which the graphs related to the "non-obvious trend" of the **Sequences** analysed in the previous paragraphs **(n° 1/1, n° 2/1, etc.)** were. In order to avoid repetitions, here, the reader is deferred to the interpretation of the **comparisons among the different graphs** presented in the paragraph 1.2 .

Before concluding the paragraph, it is worth noting that, out of the **63** DNA bases of **Sequence n° 17/1**, ONLY **ELEVEN BASES** (the **17,46%**)**,** ARE EQUAL (by type and by position in sequence) TO THOSE OF THE ORIGINAL SEQUENCE (**Insulin Chain A**).

1.35 IMPLICATIONS RELATED TO THE GRAPHIC RESULTS OF THE “NON-OBVIOUS TREND” ANALYSIS OF SEQUENCE n° 17/1 OF INSULIN CHAIN A

The **63** DNA base sequence of the **new generated sequence** (**Sequence n° 17/1**) that arises from the **original** one has been subjected to **BLAST** research.

Please note:

Information about the ***significant alignments*** produced by *BLAST research*, related to **Sequence n° 17/1,** and all the data acquired from *GenBank (3)* will be published in the **Appendix,** after the *General Conclusions.*

Query = NEW GENERATED SEQUENCE (Sequence n° 17/1)

Length = 63

Parameters of BLAST research:

Programme	*Blastn*
Word size	*11*
Expect value	*10*
Hitlist size	*100*
Match/Mismatch scores	*2,-3*
Gapcosts	*5,2*
Low Complexity Filter	*Yes*
Filter string	*L;m;*
Genetic Code	*1*

Please note:

Here, “**the organisms found to be in common**” between the results of BLAST research carried out on **Insulin Chain A** and results of BLAST research carried out on **Sequence n° 17/1**, were highlighted in **Red**.
As well, “**the organisms found to be in common**” between the results of BLAST research carried out on **Insulin Chain A**, results of BLAST research carried out on **Sequence n° 17/1** and results of BLAST research carried out on **at least one** of the *19 generated sequences*, were highlighted in **Green**.
Moreover, “**the denomination of the sequence**” (1/1, 2/1, ... 19/1) of the “**organism found to be in common**” between the results of BLAST research carried out on **Sequence n° 17/1** and results of BLAST research carried out on **at least one** of the *19 new generated sequences*, were highlighted in **Blue**.
Finally, “**the denomination of the sequence**” (1/1, 2/1, ... 19/1) of the “**organism found to be in common**” between the results of BLAST research carried out on **Insulin Chain A** and results of BLAST research carried out on *19 generated sequences*, were highlighted in **Yellow**.

Sequenza n° 17/1

Sequences producing significant alignments:

Selected seq	Description	Max score	Total score	Query cover	E value	Ident	Accession
1 XM_023370401.1	PREDICTED: Centruroides sculpturatus prostatic spermine-binding protein-like (LOC111626878), mRNA	50.9	50.9	87%	0.005	80%	XM_023370401.1
2 NG_042811.1	Homo sapiens protein kinase cAMP-dependent type I regulatory subunit beta (PRKAR1B), RefSeqGene on chromosome 7	48.2	92.7	73%	0.018	83%	NG_042811.1
3 AC099731.5	Homo sapiens BAC clone RP11-1244M4 from 7, complete sequence	48.2	92.7	73%	0.018	83%	AC099731.5
4 AC144411.2	Homo sapiens BAC clone GS1-146C24 from 7, complete sequence	48.2	92.7	73%	0.018	83%	AC144411.2
5 **8/1** XM_636333.1	Dictyostelium discoideum AX4 GCN5-related N-acetyltransferase (eco1) mRNA, complete cds	44.6	44.6	69%	0.22	82%	XM_636333.1
6 **8/1** AF466307.2	Dictyostelium discoideum ABC transporter AbcB4 (abcB4) gene, complete cds	44.6	44.6	69%	0.22	82%	AF466307.2
7 XM_027632371.1	PREDICTED: Corapipo altera mucin-3B-like (LOC113941211), partial mRNA	43.7	43.7	80%	0.78	78%	XM_027632371.1
8 **6/1** CP017345.1	Talaromyces pinophilus strain 1-95 chromosome 2, complete sequence	43.7	43.7	80%	0.78	78%	CP017345.1
9 AC129018.4	Mus musculus BAC clone RP24-463L19 from chromosome 10, complete sequence	43.7	43.7	73%	0.78	80%	AC129018.4
10 CP034522.1	Eukaryotic synthetic construct chromosome 19	42.8	84.6	71%	0.78	81%	CP034522.1
11 CP034497.1	Eukaryotic synthetic construct chromosome 19	42.8	84.6	71%	0.78	81%	CP034497.1
12 CP034494.1	Eukaryotic synthetic construct chromosome 16	42.8	161	84%	0.78	81%	CP034494.1
13 NG_055257.1	Homo sapiens mucin 16, cell surface associated (MUC16), RefSeqGene on chromosome 19	42.8	84.6	71%	0.78	81%	NG_055257.1
14 AF429315.1	Homo sapiens junctophilin 3 (JPH3) gene, partial cds	42.8	42.8	79%	0.78	81%	AF429315.1
15 AC092720.4	Homo sapiens chromosome 16 clone RP11-482M8, complete sequence	42.8	42.8	79%	0.78	81%	AC092720.4

Sequences producing significant alignments:

Selected seq	Description	Max score	Total score	Query cover	E value	Ident	Accession
16 AC010536.8	Homo sapiens chromosome 16 clone RP11-278A23, complete sequence	42.8	42.8	79%	0.78	81%	AC010536.8
17 AC079437.2	Rattus norvegicus strain Brown Norway chromosome 4 clone RP31-275K4, complete sequence	42.8	42.8	84%	0.78	77%	AC079437.2
18 AC008734.7	Homo sapiens chromosome 19 clone CTD-2529P6, complete sequence	42.8	84.6	71%	0.78	81%	AC008734.7
19 LR535839.1	Mastacembelus armatus genome assembly, chromosome: 7	41.9	41.9	42%	2.7	96%	LR535839.1
20 LT629740.1	Mucilaginibacter mallensis strain MP1X4 genome assembly, chromosome: I	41.9	41.9	39%	2.7	96%	LT629740.1
21 **10/1** NM_128495.4	Arabidopsis thaliana metal tolerance protein B1 (MTPB1), mRNA	41.9	41.9	79%	2.7	78%	NM_128495.4
22 **6/1** **14/1** CP011906.1	Ovis canadensis canadensis isolate 43U chromosome 21 sequence	41.9	41.9	73%	2.7	80%	CP011906.1
23 LN591022.1	Cyprinus carpio genome assembly common carp genome, scaffold 000001171	41.9	41.9	61%	2.7	85%	LN591022.1
24 LK023368.1	Lichtheimia ramosa strain JMRC FSU:6197 genome assembly, scaffold: SCAF6	41.9	41.9	55%	2.7	86%	LK023368.1
25 **10/1** CP002685.1	Arabidopsis thaliana chromosome 2 sequence	41.9	41.9	79%	2.7	78%	CP002685.1
26 **10/1** BT015899.1	Arabidopsis thaliana At2g29410 gene, complete cds	41.9	41.9	79%	2.7	78%	BT015899.1
27 **10/1** BT014994.1	Arabidopsis thaliana At2g29410 gene, complete cds	41.9	41.9	79%	2.7	78%	BT014994.1
28 **10/1** AC004561.3	Arabidopsis thaliana chromosome 2 clone F16P2 map ve014, complete sequence	41.9	41.9	79%	2.7	78%	AC004561.3
29 **10/1** BX819615.1	Arabidopsis thaliana Full-length cDNA Complete sequence from clone GSLTFB94ZG01 of Flowers and buds of strain col-0 of Arabidopsis thaliana (thale cress)	41.9	41.9	79%	2.7	78%	BX819615.1
30 **6/1** **12/1** CP025669.1	Ipomoea triloba cultivar NCNSP0323 chromosome 10	41.0	41.0	46%	2.7	93%	CP025669.1
31 XM_011636383.2	PREDICTED: Pogonomyrmex barbatus prostatic acid phosphatase-like (LOC105425553), mRNA	41.0	41.0	53%	2.7	88%	XM_011636383.2

Sequences producing significant alignments:

Selected seq	Description	Max score	Total score	Query cover	E value	Ident	Accession
32 XM_016010635.2	PREDICTED: Ziziphus jujuba monocopper oxidase-like protein SKU5 (LOC107403720), mRNA	41.0	41.0	42%	2.7	93%	XM_016010635.2
33 XM_020589131.1	PREDICTED: Monopterus albus major histocompatibility complex class I-related gene protein-like (LOC109953661), partial mRNA	41.0	41.0	44%	2.7	93%	XM_020589131.1
34 XM_018139441.1	Phialophora attae Disintegrin and metalloproteinase domain-containing protein B (AB675_10653), partial mRNA	41.0	41.0	50%	2.7	88%	XM_018139441.1
35 NG_047001.1	Homo sapiens PHD finger protein 2 (PHF2), RefSeqGene on chromosome 9	41.0	41.0	79%	2.7	79%	NG_047001.1
36 KT384438.1	Pteropus alecto clone BAC22 genomic sequence	41.0	41.0	74%	2.7	79%	KT384438.1
37 LK065234.1	Apteryx australis mantelli genome assembly AptMant0, scaffold scaffold158	41.0	41.0	60%	2.7	85%	LK065234.1
38 XM_001536915.1	Histoplasma capsulatum NAm1 predicted protein partial mRNA	41.0	41.0	73%	2.7	83%	XM_001536915.1
39 CU372918.5	Mouse DNA sequence from clone DN-239C14 on chromosome 1, complete sequence	41.0	41.0	50%	2.7	88%	CU372918.5
40 AC133161.4	Mus musculus BAC clone RP24-534C7 from chromosome 1, complete sequence	41.0	41.0	50%	2.7	88%	AC133161.4
41 AC158580.3	Mus musculus chromosome 1, clone RP24-97G17, complete sequence	41.0	41.0	50%	2.7	88%	AC158580.3
42 AL353629.22	Human DNA sequence from clone RP11-30L4 on chromosome 9q22.1-22.33, complete sequence	41.0	41.0	79%	2.7	79%	AL353629.22
43 AC153369.4	Mus musculus 10 BAC RP23-103E4 (Roswell Park Cancer Institute (C57BL/6J Female) Mouse BAC Library) complete sequence	41.0	41.0	74%	2.7	79%	AC153369.4
44 XM_006567665.3	PREDICTED: Apis mellifera synaptosomal-associated protein 25 (LOC411114), transcript variant X13, mRNA	40.1	40.1	73%	9.5	80%	XM_006567665.3
45 XM_006567664.3	PREDICTED: Apis mellifera synaptosomal-associated protein 25 (LOC411114), transcript variant X12, mRNA	40.1	40.1	73%	9.5	80%	XM_006567664.3

Sequences producing significant alignments:

Selected seq	Description	Max score	Total score	Query cover	E value	Ident	Accession
46 XM_006567662.3	PREDICTED: Apis mellifera synaptosomal-associated protein 25 (LOC411114), transcript variant X11, mRNA	40.1	40.1	73%	9.5	80%	XM_006567662.3
47 XM_006567659.3	PREDICTED: Apis mellifera synaptosomal-associated protein 25 (LOC411114), transcript variant X10, mRNA	40.1	40.1	73%	9.5	80%	XM_006567659.3
48 XM_006567657.3	PREDICTED: Apis mellifera synaptosomal-associated protein 25 (LOC411114), transcript variant X9, mRNA	40.1	40.1	73%	9.5	80%	XM_006567657.3
49 XM_006567663.3	PREDICTED: Apis mellifera synaptosomal-associated protein 25 (LOC411114), transcript variant X8, mRNA	40.1	40.1	73%	9.5	80%	XM_006567663.3
50 XM_006567658.3	PREDICTED: Apis mellifera synaptosomal-associated protein 25 (LOC411114), transcript variant X7, mRNA	40.1	40.1	73%	9.5	80%	XM_006567658.3
51 XM_006567656.3	PREDICTED: Apis mellifera synaptosomal-associated protein 25 (LOC411114), transcript variant X6, mRNA	40.1	40.1	73%	9.5	80%	XM_006567656.3
52 XM_006567655.3	PREDICTED: Apis mellifera synaptosomal-associated protein 25 (LOC411114), transcript variant X5, mRNA	40.1	40.1	73%	9.5	80%	XM_006567655.3
53 XM_016912269.2	PREDICTED: Apis mellifera synaptosomal-associated protein 25 (LOC411114), transcript variant X4, mRNA	40.1	40.1	73%	9.5	80%	XM_016912269.2
54 XM_006567660.3	PREDICTED: Apis mellifera synaptosomal-associated protein 25 (LOC411114), transcript variant X3, mRNA	40.1	40.1	73%	9.5	80%	XM_006567660.3
55 XM_006567654.3	PREDICTED: Apis mellifera synaptosomal-associated protein 25 (LOC411114), transcript variant X2, mRNA	40.1	40.1	73%	9.5	80%	XM_006567654.3
56 XM_394588.7	PREDICTED: Apis mellifera synaptosomal-associated protein 25 (LOC411114), transcript variant X1, mRNA	40.1	40.1	73%	9.5	80%	XM_394588.7
57 CP032607.1	Lateolabrax maculatus linkage group 10 sequence	40.1	40.1	47%	9.5	90%	CP032607.1
58 CP027277.1	Lateolabrax maculatus chromosome Lm16	40.1	40.1	47%	9.5	90%	CP027277.1

Sequences producing significant alignments:

Selected seq	Description	Max score	Total score	Query cover	E value	Ident	Accession
59 CP034510.1	Eukaryotic synthetic construct chromosome Y	40.1	80.1	71%	9.5	80%	CP034510.1
60 CP034499.1	Eukaryotic synthetic construct chromosome 20	40.1	40.1	73%	9.5	75%	CP034499.1
61 XM_024327537.1	PREDICTED: Rosa chinensis uncharacterized LOC112188416 (LOC112188416), transcript variant X2, mRNA	40.1	40.1	69%	9.5	80%	XM_024327537.1
62 XM_024327529.1	PREDICTED: Rosa chinensis uncharacterized LOC112188416 (LOC112188416), transcript variant X1, mRNA	40.1	40.1	69%	9.5	80%	XM_024327529.1
63 XM_021559236.1	PREDICTED: Oncorhynchus mykiss zinc finger protein 2 homolog (LOC110487312), transcript variant X3, mRNA	40.1	40.1	57%	9.5	86%	XM_021559236.1
64 XM_021559235.1	PREDICTED: Oncorhynchus mykiss zinc finger protein 2 homolog (LOC110487312), transcript variant X2, mRNA	40.1	40.1	57%	9.5	86%	XM_021559235.1
65 XM_021559234.1	PREDICTED: Oncorhynchus mykiss zinc finger protein 2 homolog (LOC110487312), transcript variant X1, mRNA	40.1	40.1	57%	9.5	86%	XM_021559234.1
66 XM_007024827.2	PREDICTED: Theobroma cacao uncharacterized LOC18596393 (LOC18596393), mRNA	40.1	40.1	65%	9.5	81%	XM_007024827.2
67 LT594793.1	Theobroma cacao genome assembly, chromosome: VI	40.1	40.1	65%	9.5	81%	LT594793.1
68 KT731538.1	Lymphocytic choriomeningitis mammarenavirus isolate Comou segment S, complete sequence	40.1	40.1	38%	9.5	96%	KT731538.1
69 NG_030314.1	Homo sapiens ArfGAP with GTPase domain, ankyrin repeat and PH domain 1 (AGAP1), RefSeqGene on chromosome 2	40.1	40.1	79%	9.5	78%	NG_030314.1
70 6/1 BX927333.11	Zebrafish DNA sequence from clone CH211-69C15 in linkage group 10, complete sequence	40.1	40.1	46%	9.5	90%	BX927333.11
71 AC106739.5	Homo sapiens chromosome 16 clone CTD-3203P2, complete sequence	40.1	79.2	80%	9.5	80%	AC106739.5
72 AL050326.3	Human DNA sequence from clone RP5-836E13 on chromosome 20, complete sequence	40.1	40.1	73%	9.5	75%	AL050326.3

Sequences producing significant alignments:

Selected seq	Description	Max score	Total score	Query cover	E value	Ident	Accession
73 AC079176.15	Homo sapiens X BAC RP11-325D5 (Roswell Park Cancer Institute Human BAC Library) complete sequence	40.1	40.1	71%	9.5	80%	AC079176.15
74 AC064874.4	Homo sapiens BAC clone RP11-680O16 from 2, complete sequence	40.1	40.1	79%	9.5	78%	AC064874.4
75 LR132023.1	Betta splendens genome assembly, chromosome: 9	39.2	39.2	52%	9.5	88%	LR132023.1
76 LR132016.1	Betta splendens genome assembly, chromosome: 14	39.2	39.2	57%	9.5	83%	LR132016.1
77 CP026258.1	Scophthalmus maximus chromosome 16	39.2	39.2	84%	9.5	77%	CP026258.1
78 XM_020656039.1	PREDICTED: Labrus bergylta angiopoietin-related protein 2-like (LOC110000701), mRNA	39.2	39.2	41%	9.5	92%	XM_020656039.1
79 XM_011431523.2	PREDICTED: Crassostrea gigas histone deacetylase 8 (LOC105329992), transcript variant X3, mRNA	39.2	39.2	57%	9.5	83%	XM_011431523.2
80 XM_016435296.1	Kalmanozyma brasiliensis GHG001 hypothetical protein partial mRNA	39.2	39.2	65%	9.5	80%	XM_016435296.1
81 KU306397.1	Corynebacterium glutamicum plasmid pBL90, complete sequence	39.2	39.2	50%	9.5	88%	KU306397.1
82 **12/1** XM_951192.2	Neurospora crassa OR74A hypothetical protein (NCU05016), mRNA	39.2	39.2	65%	9.5	80%	XM_951192.2
83 LN597923.1	Cyprinus carpio genome assembly common carp genome, scaffold 000000423	39.2	39.2	49%	9.5	87%	LN597923.1
84 **6/1** XM_009014454.1	Helobdella robusta hypothetical protein mRNA	39.2	39.2	41%	9.5	92%	XM_009014454.1
85 XM_007415776.1	Melampsora larici-populina 98AG31 hypothetical protein (MELLADRAFT_73090), mRNA	39.2	39.2	60%	9.5	84%	XM_007415776.1
86 **8/1** XM_003289664.1	Dictyostelium purpureum hypothetical protein, mRNA	39.2	39.2	68%	9.5	81%	XM_003289664.1
87 FP067403.9	Pig DNA sequence from clone CH242-212L20 on chromosome X, complete sequence	39.2	39.2	73%	9.5	78%	FP067403.9
88 AC197615.4	Macaca Mulatta BAC clone CH250-38N17 from chromosome 10, complete sequence	39.2	39.2	73%	9.5	78%	AC197615.4

Sequences producing significant alignments:

Selected seq	Description	Max score	Total score	Query cover	E value	Ident	Accession
89 AC093519.3	Homo sapiens chromosome 16 clone RP11-107C10, complete sequence	39.2	39.2	73%	9.5	78%	AC093519.3
90 AC116612.5	Homo sapiens BAC clone RP13-582L3 from 4, complete sequence	39.2	39.2	57%	9.5	83%	AC116612.5

Comparison between the alignments of Sequence 17/1 and Sequence of Insulin Chain A according to the "Species of Common Organisms":

Alignments Sequence 17/1	**Description**	**Alignments Sequence Insulin Chain A**	**Description**
2 Select seq NG_042811.1	Homo sapiens protein kinase cAMP-dependent type I regulatory subunit beta (PRKAR1B), RefSeqGene on chromosome 7	Select seq AH002844.2 **2/1 8/1 9/1 10/1 15/1**	Homo sapiens insulin (INS) gene, complete cds
3 Select seq AC099731.5	Homo sapiens BAC clone RP11-1244M4 from 7, complete sequence	Select seq AH012037.2 **2/1 8/1 9/1 10/1 15/1**	Homo sapiens haplotype ICa tyrosine hydroxylase (TH) gene, partial sequence; insulin (INS) gene, complete cds; and insulin-like growth factor 2 (IGF2) gene, partial sequence
4 Select seq AC144411.2	Homo sapiens BAC clone GS1-146C24 from 7, complete sequence	Select seq NG_050578.1 **2/1 8/1 9/1 10/1 15/1**	Homo sapiens INS-IGF2 readthrough (INS-IGF2), RefSeqGene on chromosome 11
13 Select seq NG_055257.1	Homo sapiens mucin 16, cell surface associated (MUC16), RefSeqGene on chromosome 19	Select seq KR710184.1 **2/1 8/1 9/1 10/1 15/1**	Synthetic construct Homo sapiens clone CCSBHm_00010257 INS (INS) mRNA, encodes complete protein
14 Select seq AF429315.1	Homo sapiens junctophilin 3 (JPH3) gene, partial cds	Select seq KR710183.1 **2/1 8/1 9/1 10/1 15/1**	Synthetic construct Homo sapiens clone CCSBHm_00010256 INS (INS) mRNA, encodes complete protein
15 Select seq AC092720.4	Homo sapiens chromosome 16 clone RP11-482M8, complete sequence	Select seq KR710182.1 **2/1 8/1 9/1 10/1 15/1**	Synthetic construct Homo sapiens clone CCSBHm_00010255 INS (INS) mRNA, encodes complete protein
16 Select seq AC010536.8	Homo sapiens chromosome 16 clone RP11-278A23, complete sequence	Select seq KJ891480.1 **2/1 9/1 10/1 15/1 17/1**	Synthetic construct Homo sapiens clone ccsbBroadEn_00874 INS gene, encodes complete protein
18 Select seq AC008734.7	Homo sapiens chromosome 19 clone CTD-2529P6, complete sequence	Select seq NM_001291897.1 **2/1 8/1 9/1 10/1 15/1**	Homo sapiens insulin (INS), transcript variant 4, mRNA
35 Select seq NG_047001.1	Homo sapiens PHD finger protein 2 (PHF2), RefSeqGene on chromosome 9	Select seq JQ951950.1 **2/1 8/1 9/1 10/1 15/1**	Homo sapiens preproinsulin (INS) mRNA, complete cds

Comparison between the alignments of Sequence 17/1 and Sequence of Insulin Chain A according to the “Species of Common Organisms”:

Alignments Sequence 17/1	Description	Alignments Sequence Insulin Chain A	Description
69 Select seq NG_030314.1	Homo sapiens ArfGAP with GTPase domain, ankyrin repeat and PH domain 1 (AGAP1), RefSeqGene on chromosome 2	Select seq JF909299.1 **2/1** **8/1** **9/1** **10/1** **15/1**	Homo sapiens insulin (INS) mRNA, partial cds
71 Select seq AC106739.5	Homo sapiens chromosome 16 clone CTD-3203P2, complete sequence	Select seq AB587580.1 **2/1** **8/1** **9/1** **10/1** **15/1**	Synthetic construct DNA, clone: pF1KB8864, Homo sapiens INS gene for insulin, without stop codon, in Flexi system
73 Select seq AC079176.15	Homo sapiens X BAC RP11-325D5 (Roswell Park Cancer Institute Human BAC Library) complete sequence	Select seq NM_001185098.1 **2/1** **8/1** **9/1** **10/1** **15/1**	Homo sapiens insulin (INS), transcript variant 3, mRNA
74 Select seq AC064874.4	Homo sapiens BAC clone RP11-680O16 from 2, complete sequence	Select seq NM_001185097.1 **2/1** **8/1** **9/1** **10/1** **15/1**	Homo sapiens insulin (INS), transcript variant 2, mRNA
89 Select seq AC093519.3	Homo sapiens chromosome 16 clone RP11-107C10, complete sequence	Select seq NG_007114.1 **2/1** **8/1** **9/1** **10/1** **15/1**	Homo sapiens insulin (INS), RefSeqGene on chromosome 11
90 Select seq AC116612.5	Homo sapiens BAC clone RP13-582L3 from 4, complete sequence	Select seq DQ778082.1 **2/1** **8/1** **9/1** **10/1** **15/1**	Homo sapiens clone BFC06103 insulin mRNA, complete cds
		Select seq DQ896283.2 **2/1** **8/1** **9/1** **10/1** **15/1**	Synthetic construct Homo sapiens clone IMAGE:100010743; FLH192918.01L; RZPDo839A1068D insulin (INS) gene, encodes complete protein
		Select seq NM_000207.2 **2/1** **8/1** **9/1** **10/1** **15/1**	Homo sapiens insulin (INS), transcript variant 1, mRNA
		Select seq BT007778.1 **2/1** **8/1** **9/1** **10/1** **15/1**	Synthetic construct Homo sapiens insulin mRNA, partial cds
		Select seq BT006808.1 **2/1** **8/1** **9/1** **10/1** **15/1**	Homo sapiens insulin mRNA, complete cds

Comparison between the alignments of Sequence 17/1 and Sequence of Insulin Chain A according to the "Species of Common Organisms":

Alignments Sequence 17/1	**Description**	**Alignments Sequence Insulin Chain A**	**Description**
		Select seq BC005255.1 **2/1 8/1 9/1 10/1 15/1**	Homo sapiens insulin, mRNA (cDNA clone MGC:12292 IMAGE:3950204), complete cds
		Select seq AC132217.15 **2/1 8/1 9/1 10/1 15/1**	Homo sapiens chromosome 11, clone RP11-889I17, complete sequence
		Select seq AC130303.8 **2/1 8/1 9/1 10/1 15/1**	Homo sapiens chromosome 11, clone RP4-539G11, complete sequence
		Select seq AY899304.1 **2/1 8/1 9/1 10/1 15/1**	Homo sapiens proinsulin mRNA, complete cds, alternatively spliced
		Select seq AJ009655.1 **2/1 8/1 9/1 10/1 15/1**	Homo sapiens ins gene, partial
		Select seq X70508.1 **2/1 8/1 9/1 10/1 15/1**	Homo sapiens mRNA for insulinoma pre-proinsulin
		Select seq L15440.1 **2/1 8/1 9/1 10/1 15/1**	Homo sapiens tyrosine hydroxylase (TH) gene, 3' end; insulin (INS) gene, complete cds; insulin-like growth factor 2 (IGF2) gene, 5' end
		Select seq KR710185.1 **2/1 8/1 9/1 10/1 15/1**	Synthetic construct Homo sapiens clone CCSBHm_00010262 INS (INS) mRNA, encodes complete protein
		Select seq AF050524.1 **2/1 8/1 9/1 10/1 15/1**	Synthetic Homo sapiens proinsulin-like protein BKRA gene, complete cds
		Select seq AC021233.9 **2/1 8/1 9/1 10/1 15/1**	Homo sapiens chromosome 11, clone RP11-215H22, complete sequence

Comparison between the alignments of Sequence 17/1 and Sequence of Insulin Chain A according to the "Species of Common Organisms":

Alignments Sequence 17/1	**Description**	**Alignments Sequence Insulin Chain A**	**Description**
		Select seq AK024581.1 **2/1 8/1 9/1 10/1 15/1**	Homo sapiens cDNA: FLJ20928 fis, clone ADSE01074
7 Select seq XM_027632371.1	PREDICTED: Corapipo altera mucin-3B-like (LOC113941211), partial mRNA	Select seq XM_027651359.1	PREDICTED: Corapipo altera insulin (INS), transcript variant X3, mRNA
		Select seq XM_027651356.1	PREDICTED: Corapipo altera insulin (INS), transcript variant X2, mRNA
		Select seq XM_027651355.1	PREDICTED: Corapipo altera insulin (INS), transcript variant X1, mRNA
9 Select seq AC129018.4	Mus musculus BAC clone RP24-463L19 from chromosome 10, complete sequence	Select seq XM_021152514.1 **1/1 6/1 8/1 10/1 13/1 18/1**	PREDICTED: Mus caroli insulin-1 (LOC110286053), mRNA
40 Select seq AC133161.4	Mus musculus BAC clone RP24-534C7 from chromosome 1, complete sequence	Select seq DQ250565.1 **1/1 6/1 8/1 10/1 13/1 18/1**	Mus caroli preproinsulin 1 (Ins1) gene, complete cds
41 Select seq AC158580.3	Mus musculus chromosome 1, clone RP24-97G17, complete sequence	Select seq XM_021215010.1 **1/1 6/1 8/1 10/1 13/1 18/1**	PREDICTED: Mus pahari insulin-1 (LOC110333420), mRNA
43 Select seq AC153369.4	Mus musculus 10 BAC RP23-103E4 (Roswell Park Cancer Institute (C57BL/6J Female) Mouse BAC Library) complete sequence	Select seq NM_008386.4 **1/1 6/1 8/1 10/1 13/1 18/1**	Mus musculus insulin I (Ins1), mRNA
		Select seq BC145868.1 **1/1 6/1 8/1 10/1 13/1 18/1**	Mus musculus insulin I, mRNA (cDNA clone MGC:175755 IMAGE:40131171), complete cds

Comparison between the alignments of Sequence 17/1 and Sequence of Insulin Chain A according to the "Species of Common Organisms":

Alignments Sequence 17/1	**Description**	**Alignments Sequence Insulin Chain A**	**Description**
		Select seq DQ479923.1 **1/1 6/1 8/1 10/1 13/1 18/1**	Mus musculus strain BTBR T+ tf/J insulin 1 precursor, gene, complete cds
		Select seq AC163452.12 **1/1 6/1 8/1 10/1 13/1 18/1**	Mus musculus chromosome 19, clone RP23-405C7, complete sequence
		Select seq AC136710.8 **1/1 6/1 8/1 10/1 13/1 18/1**	Mus musculus chromosome 19, clone RP23-35B13, complete sequence
		Select seq AC140320.2 **1/1 6/1 8/1 10/1 13/1 18/1**	Mus musculus BAC clone RP23-401C13 from chromosome 19, complete sequence
		Select seq BC098468.1 **1/1 6/1 8/1 10/1 13/1 18/1**	Mus musculus insulin I, mRNA (cDNA clone MGC:107382 IMAGE:6432765), complete cds
		Select seq AK148541.1 **1/1 6/1 8/1 10/1 13/1 18/1**	Mus musculus adult pancreas islet cells cDNA, RIKEN full-length enriched library, clone:C820020F18 product:insulin I, full insert sequence
		Select seq AK007345.1 **1/1 6/1 8/1 10/1 13/1 18/1**	Mus musculus 10 day old male pancreas cDNA, RIKEN full-length enriched library, clone:1810005L03 product:INSULIN 1 PRECURSOR, full insert sequence
		Select seq XM_021168754.1 **1/1 6/1 8/1 10/1 13/1 18/1**	PREDICTED: Mus caroli insulin-2 (LOC110299132), transcript variant X2, mRNA
		Select seq XM_021168753.1 **1/1 6/1 8/1 10/1 13/1 18/1**	PREDICTED: Mus caroli insulin-2 (LOC110299132), transcript variant X1, mRNA
		Select seq NM_001185084.2 **1/1 6/1 8/1 10/1 13/1 18/1**	Mus musculus insulin II (Ins2), transcript variant 3, mRNA

Comparison between the alignments of Sequence 17/1 and Sequence of Insulin Chain A according to the "Species of Common Organisms":

Alignments Sequence 17/1	Description	Alignments Sequence Insulin Chain A	Description
		Select seq NM_001185083.2 **1/1 6/1 8/1 10/1 13/1 18/1**	Mus musculus insulin II (Ins2), transcript variant 1, mRNA
		Select seq NM_008387.5 **1/1 6/1 8/1 10/1 13/1 18/1**	Mus musculus insulin II (Ins2), transcript variant 2, mRNA
		Select seq JN959239.1 **1/1 6/1 8/1 10/1 13/1 18/1**	Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Ins2:tm1a(EUCOMM)Wtsi; transgenic
		Select seq JN951270.1 **1/1 6/1 8/1 10/1 13/1 18/1**	Mus musculus targeted non-conditional, lacZ-tagged mutant allele Ins2:tm1e(EUCOMM)Wtsi; transgenic
		Select seq BC145554.1 **1/1 6/1 8/1 10/1 13/1 18/1**	Mus musculus insulin II, mRNA (cDNA clone MGC:179126 IMAGE:9054118), complete cds
		Select seq BC099934.1 **1/1 6/1 8/1 10/1 13/1 18/1**	Mus musculus insulin II, mRNA (cDNA clone MGC:107381 IMAGE:6432976), complete cds
		Select seq BC132650.1 **1/1 6/1 8/1 10/1 13/1 18/1**	Mus musculus insulin II, mRNA (cDNA clone MGC:164281 IMAGE:40130927), complete cds
		Select seq DQ250569.1 **1/1 6/1 8/1 10/1 13/1 18/1**	Mus caroli preproinsulin 2 (Ins2) gene, complete cds
		Select seq AK007612.1 **1/1 6/1 8/1 10/1 13/1 18/1**	Mus musculus 10 day old male pancreas cDNA, RIKEN full-length enriched library, clone:1810027C14 product:INSULIN 2 PRECURSOR, full insert sequence
		Select seq AK007482.1 **1/1 6/1 8/1 10/1 13/1 18/1**	Mus musculus 10 day old male pancreas cDNA, RIKEN full-length enriched library, clone:1810013J24 product:INSULIN 1 PRECURSOR, full insert sequence

Comparison between the alignments of Sequence 17/1 and Sequence of Insulin Chain A according to the “Species of Common Organisms”:

Alignments Sequence 17/1	**Description**	**Alignments Sequence Insulin Chain A**	**Description**
		Select seq BC066208.1 **1/1 6/1 8/1 10/1 13/1 18/1**	Mus musculus insulin II, mRNA (cDNA clone IMAGE:6436276)
		Select seq AC012382.14 **1/1 6/1 8/1 10/1 13/1 18/1**	Mus musculus chromosome 7, clone RP23-92L23, complete sequence
		Select seq AY899305.1 **1/1 6/1 8/1 10/1 13/1 18/1**	Mus musculus proinsulin mRNA, complete cds, alternatively spliced
		Select seq AC013548.13 **1/1 6/1 8/1 10/1 13/1 18/1**	Mus musculus chromosome 7, clone RP23-209O22, complete sequence
		Select seq AP003182.2 **1/1 6/1 8/1 10/1 13/1 18/1**	Mus musculus genomic DNA, chromosome 7 clone:B189M11, complete sequences
		Select seq GQ915612.1 **1/1 6/1 8/1 10/1 13/1 18/1**	Mus musculus insulin-2 precursor (Ins2) mRNA, partial cds, alternatively spliced
		Select seq XM_021204833.1 **1/1 6/1 8/1 10/1 13/1 18/1**	PREDICTED: Mus pahari insulin-2 (LOC110326410), transcript variant X2, mRNA
		Select seq XM_021204825.1 **1/1 6/1 8/1 10/1 13/1 18/1**	PREDICTED: Mus pahari insulin-2 (LOC110326410), transcript variant X1, mRNA
10 Select seq CP034522.1	Eukaryotic synthetic construct chromosome 19	Select seq CP034516.1 **2/1**	Eukaryotic synthetic construct chromosome 13
11 Select seq CP034497.1	Eukaryotic synthetic construct chromosome 19	Select seq CP034491.1 **2/1**	Eukaryotic synthetic construct chromosome 13
12 Select seq CP034494.1	Eukaryotic synthetic construct chromosome 16		

Comparison between the alignments of Sequence 17/1 and Sequence of Insulin Chain A according to the “Species of Common Organisms”:

Alignments Sequence 17/1	Description	Alignments Sequence Insulin Chain A	Description
59 Select seq CP034510.1	Eukaryotic synthetic construct chromosome Y		
60 Select seq CP034499.1	Eukaryotic synthetic construct chromosome 20		
17 Select seq AC079437.2	Rattus norvegicus strain Brown Norway chromosome 4 clone RP31-275K4, complete sequence	Select seq DQ250563.1	Rattus losea preproinsulin 1 (Ins1) gene, complete cds
		Select seq AH002190.2	Rattus norvegicus insulin 2 (INS2) gene, complete cds
		Select seq FQ231224.1	Rattus norvegicus TL0AEA77YF17 mRNA sequence
		Select seq NM_019129.3	Rattus norvegicus insulin 1 (Ins1), mRNA
		Select seq NM_019130.2	Rattus norvegicus insulin 2 (Ins2), mRNA
		Select seq DQ250567.1	Rattus losea preproinsulin 2 (Ins2) gene, complete cds
		Select seq AC098563.6	Rattus norvegicus 1 BAC CH230-123A15 (Children's Hospital Oakland Research Institute) complete sequence
19 Select seq LR535839.1	Mastacembelus armatus genome assembly, chromosome: 7	Select seq LR535846.1	Mastacembelus armatus genome assembly, chromosome: 14
		Select seq XM_026329134.1	PREDICTED: Mastacembelus armatus insulin (LOC113143484), mRNA
		Select seq LR535851.1	Mastacembelus armatus genome assembly, chromosome: 19
		Select seq XM_026315125.1	PREDICTED: Mastacembelus armatus circularly permutated Ras protein 1-like (LOC113135260), transcript variant X2, mRNA

Comparison between the alignments of Sequence 17/1 and Sequence of Insulin Chain A according to the "Species of Common Organisms":

Alignments Sequence 17/1	**Description**	**Alignments Sequence Insulin Chain A**	**Description**
		Select seq XM_026315124.1	PREDICTED: Mastacembelus armatus circularly permutated Ras protein 1-like (LOC113135260), transcript variant X1, mRNA
22 Select seq CP011906.1 **14/1**	Ovis canadensis canadensis isolate 43U chromosome 21 sequence	Select seq XM_027959829.1 **6/1 14/1**	PREDICTED: Ovis aries insulin (INS), mRNA
		Select seq AH005355.3 **6/1 14/1**	Ovis aries insulin and insulin-like growth factor II (IGF-II) genes, complete cds
		Select seq XM_012167536.2 **6/1 14/1**	PREDICTED: Ovis aries musimon insulin (LOC105613195), mRNA
23 Select seq LN591022.1	Cyprinus carpio genome assembly common carp genome, scaffold 000001171	Select seq XM_019069183.1 **4/1 6/1**	PREDICTED: Cyprinus carpio insulin-like (LOC109051698), mRNA
83 Select seq LN597923.1	Cyprinus carpio genome assembly common carp genome, scaffold 000000423	Select seq LN590733.1 **4/1 6/1**	Cyprinus carpio genome assembly common carp genome, scaffold 000000053
33 Select seq XM_020589131.1	PREDICTED: Monopterus albus major histocompatibility complex class I-related gene protein-like (LOC109953661), partial mRNA	Select seq XM_020615193.1 **15/1**	PREDICTED: Monopterus albus insulin (LOC109968712), mRNA
		Select seq XM_020599783.1 **15/1**	PREDICTED: Monopterus albus insulin-like (LOC109959979), mRNA
		Select seq XM_020591214.1 **15/1**	PREDICTED: Monopterus albus insulin-like (LOC109955249), mRNA
36 Select seq KT384438.1	Pteropus alecto clone BAC22 genomic sequence	Select seq XM_006910977.1	PREDICTED: Pteropus alecto insulin (LOC102881117), mRNA
37 Select seq LK065234.1	Apteryx australis mantelli genome assembly AptMant0, scaffold scaffold158	Select seq XM_026079009.1 **5/1 6/1**	PREDICTED: Apteryx rowi insulin (INS), mRNA

Comparison between the alignments of Sequence 17/1 and Sequence of Insulin Chain A according to the “Species of Common Organisms”:

Alignments Sequence 17/1	**Description**	**Alignments Sequence Insulin Chain A**	**Description**
		Select seq XM_013957848.1 **5/1** **6/1**	PREDICTED: Apteryx australis mantelli insulin (INS), mRNA
		Select seq LK064676.1 **5/1** **6/1**	Apteryx australis mantelli genome assembly AptMant0, scaffold scaffold77
39 Select seq CU372918.5	Mouse DNA sequence from clone DN-239C14 on chromosome 1, complete sequence	Select seq X04725.1 **8/1** **10/1** **13/1**	Mouse preproinsulin gene I
		Select seq X04725.1 **8/1** **10/1** **13/1**	Mouse preproinsulin gene II
42 Select seq AL353629.22	Human DNA sequence from clone RP11-30L4 on chromosome 9q22.1-22.33, complete sequence	Select seq J02547.1 **8/1**	Human (synthetic) insulin gene, complete cds
		Select seq M31026.1 **8/1**	Synthetic human insulin B and mini-C chains using deactivated silica gel chromatography
		Select seq V00082.1 **8/1**	Artificial gene for human proinsulin
		Select seq M12913.1 **8/1**	Synthetic human proinsulin gene, complete cds
		Select seq LT733283.1 **8/1**	Human ORFeome Gateway entry vector pENTR223-INS, complete sequence
		Select seq M10039.1 **8/1**	Human alpha-type insulin gene and 5' flanking polymorphic region
		Select seq V00565.1 **8/1**	Human gene for preproinsulin, from chromosome 11. Includes a highly polymorphic region upstream from the insulin gene containing tandemly repeated sequences
		Select seq AB501190.1 **8/1**	Synthetic construct hpi gene for human M-proinsulin, complete cds

Comparison between the alignments of Sequence 17/1 and Sequence of Insulin Chain A according to the “Species of Common Organisms”:

Alignments Sequence 17/1	**Description**	**Alignments Sequence Insulin Chain A**	**Description**
		Select seq J02544.1 **8/1**	Human insulin A chain gene (synthetic)
		Select seq AL354999.17 **8/1**	Human DNA sequence from clone RP11-531B22 on chromosome 13, complete sequence
		Select seq AL354896.16 **8/1**	Human DNA sequence from clone RP11-512M17 on chromosome 13, complete sequence
57 Select seq CP032607.1	Lateolabrax maculatus linkage group 10 sequence	Select seq CP032586.1 **14/1 16/1**	Lateolabrax maculatus linkage group 12 sequence
58 Select seq CP027277.1	Lateolabrax maculatus chromosome Lm16	Select seq CP027266.1 **14/1 16/1**	Lateolabrax maculatus chromosome Lm5
63 Select seq XM_021559236.1	PREDICTED: Oncorhynchus mykiss zinc finger protein 2 homolog (LOC110487312), transcript variant X3, mRNA	Select seq XM_024402922.1 **6/1 10/1**	PREDICTED: Oncorhynchus tshawytscha insulin-like (LOC112234674), mRNA
64 Select seq XM_021559235.1	PREDICTED: Oncorhynchus mykiss zinc finger protein 2 homolog (LOC110487312), transcript variant X2, mRNA	Select seq XM_024402921.1 **6/1 10/1**	PREDICTED: Oncorhynchus tshawytscha insulin-like (LOC112234673), mRNA
65 Select seq XM_021559234.1	PREDICTED: Oncorhynchus mykiss zinc finger protein 2 homolog (LOC110487312), transcript variant X1, mRNA	Select seq XM_020464884.1 **6/1 10/1**	PREDICTED: Oncorhynchus kisutch insulin-like (LOC109873252), mRNA
		Select seq NM_001124670.1 **6/1 10/1**	Oncorhynchus mykiss preproinsulin 2 (LOC100136703), mRNA
		Select seq L11712.1 **6/1 10/1**	Oncorhynchus keta insulin gene, complete cds

Comparison between the alignments of Sequence 17/1 and Sequence of Insulin Chain A according to the "Species of Common Organisms":

Alignments Sequence 17/1	**Description**	**Alignments Sequence Insulin Chain A**	**Description**
66 Select seq XM_007024827.2	PREDICTED: Theobroma cacao uncharacterized LOC18596393 (LOC18596393), mRNA	Select seq LT594792.1 **9/1**	Theobroma cacao genome assembly, chromosome: V
67 Select seq LT594793.1	Theobroma cacao genome assembly, chromosome: VI		
75 Select seq LR132023.1	Betta splendens genome assembly, chromosome: 9	Select seq LR132016.1 **4/1 10/1**	Betta splendens genome assembly, chromosome: 14
76 Select seq LR132016.1	Betta splendens genome assembly, chromosome: 14	Select seq LR132007.1 **4/1 10/1**	Betta splendens genome assembly, chromosome: 10
77 Select seq CP026258.1	Scophthalmus maximus chromosome 16	Select seq CP026246.1 **10/1 13/1**	Scophthalmus maximus chromosome 4
		Select seq CP026255.1 **10/1 13/1**	Scophthalmus maximus chromosome 13
78 Select seq XM_020656039.1	PREDICTED: Labrus bergylta angiopoietin-related protein 2-like (LOC110000701), mRNA	Select seq XM_020661338.1	PREDICTED: Labrus bergylta insulin-like (LOC110006110), mRNA
		Select seq XM_020648941.1	PREDICTED: Labrus bergylta insulin-like (LOC109995271), mRNA
		Select seq XM_020629757.1	PREDICTED: Labrus bergylta insulin-like (LOC109981109), mRNA
		Select seq XM_020637557.1	PREDICTED: Labrus bergylta circularly permutated Ras protein 1-like (LOC109986768), transcript variant X2, mRNA
		Select seq XM_020637556.1	PREDICTED: Labrus bergylta circularly permutated Ras protein 1-like (LOC109986768), transcript variant X1, mRNA
88 Select seq AC197615.4	Macaca Mulatta BAC clone CH250-38N17 from chromosome 10, complete sequence	Select seq XM_015434180.1 **2/1 3/1 8/1**	PREDICTED: Macaca fascicularis insulin (INS), transcript variant X1, mRNA

Comparison between the alignments of Sequence 17/1 and Sequence of Insulin Chain A according to the "Species of Common Organisms":

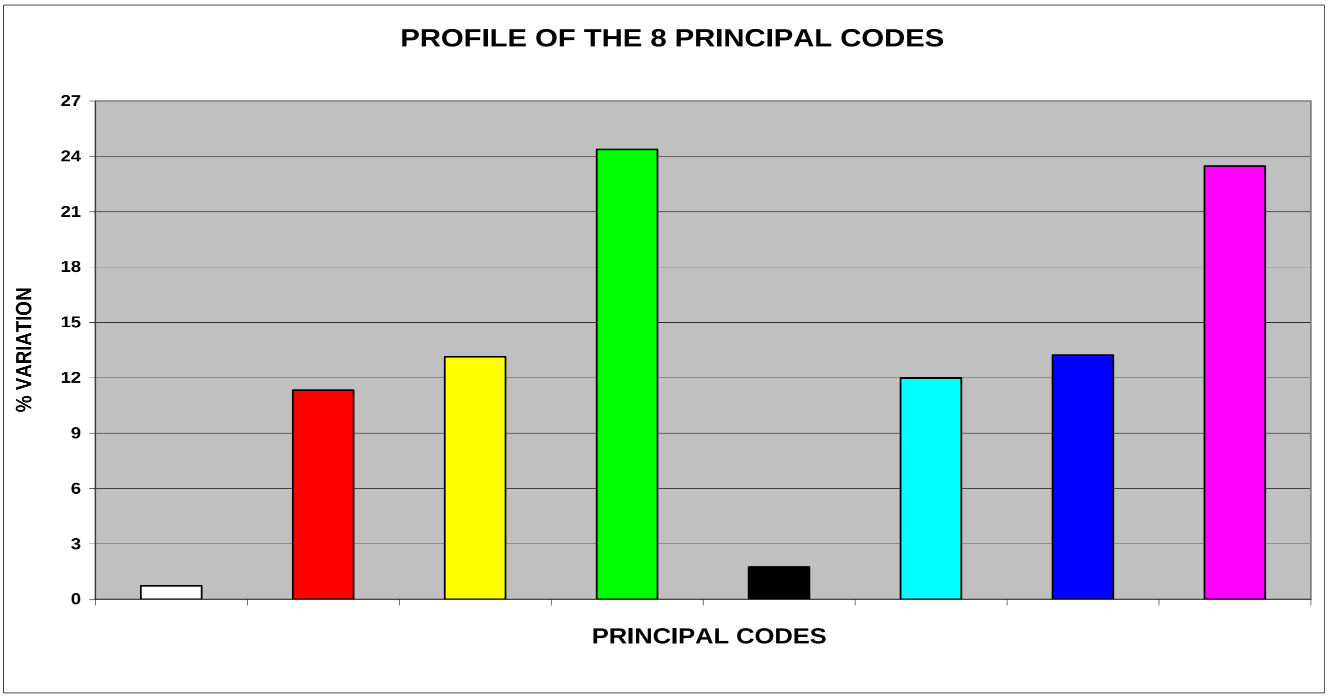
Alignments Sequence 17/1	Description	Alignments Sequence Insulin Chain A	Description
		Select seq XM_015113354.1 **2/1 3/1 8/1**	PREDICTED: Macaca mulatta insulin (INS), mRNA
		Select seq XM_011721319.1 **2/1 3/1 8/1**	PREDICTED: Macaca nemestrina insulin (INS), transcript variant X4, mRNA
		Select seq XM_011721318.1 **2/1 3/1 8/1**	PREDICTED: Macaca nemestrina insulin (INS), transcript variant X3, mRNA
		Select seq XM_011721317.1 **2/1 3/1 8/1**	PREDICTED: Macaca nemestrina insulin (INS), transcript variant X2, mRNA
		Select seq XM_011721316.1 **2/1 3/1 8/1**	PREDICTED: Macaca nemestrina insulin (INS), transcript variant X1, mRNA
		Select seq NM_001284919.1 **2/1 3/1 8/1**	Macaca fascicularis insulin (INS), mRNA

Analysis of
Sequence n° 18/1
of Insulin Chain A

1.36 GRAPHIC RESULTS OF THE "NON-OBVIOUS TREND" ANALYSIS OF SEQUENCE n° 18/1 OF INSULIN CHAIN A

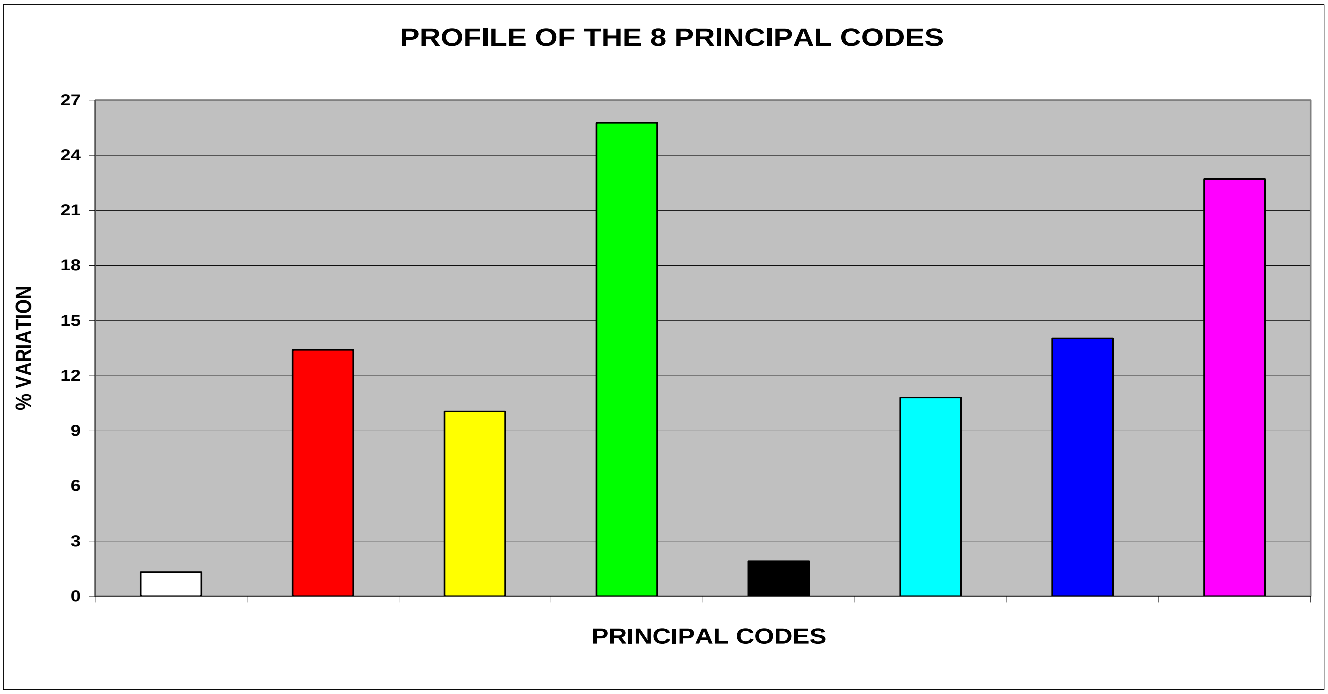
In the Pct. 69 (A e B) two **8 Principal Codes Profiles** are compared.

The chart in Pct. 69 (A) refers to the **original base sequence** of **Insulin Chain A**.



Pct. 69 (A)

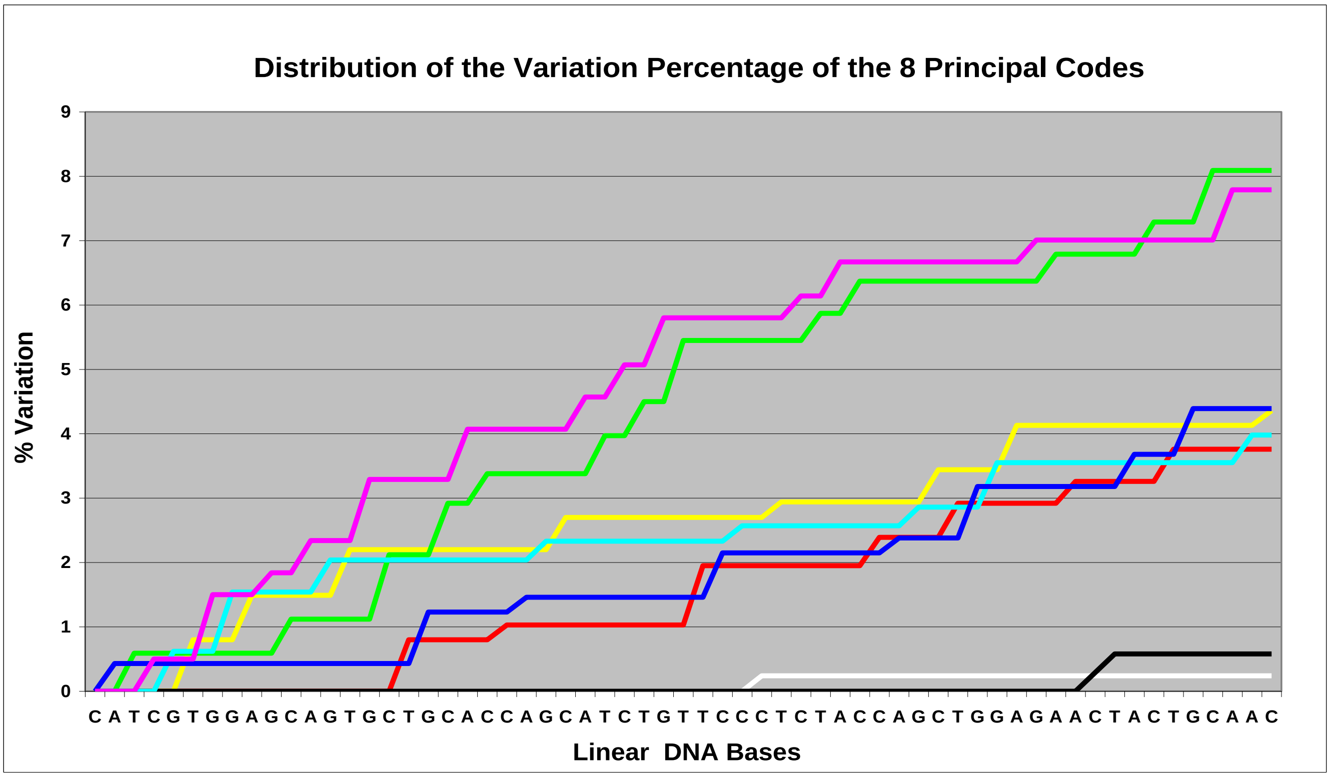
The chart in Pct. 69 (B) refers to the **eighteenth** **"new generated sequence"** (**Sequence n° 18/1**) that originates from the original one.



Pct. 69 (B)

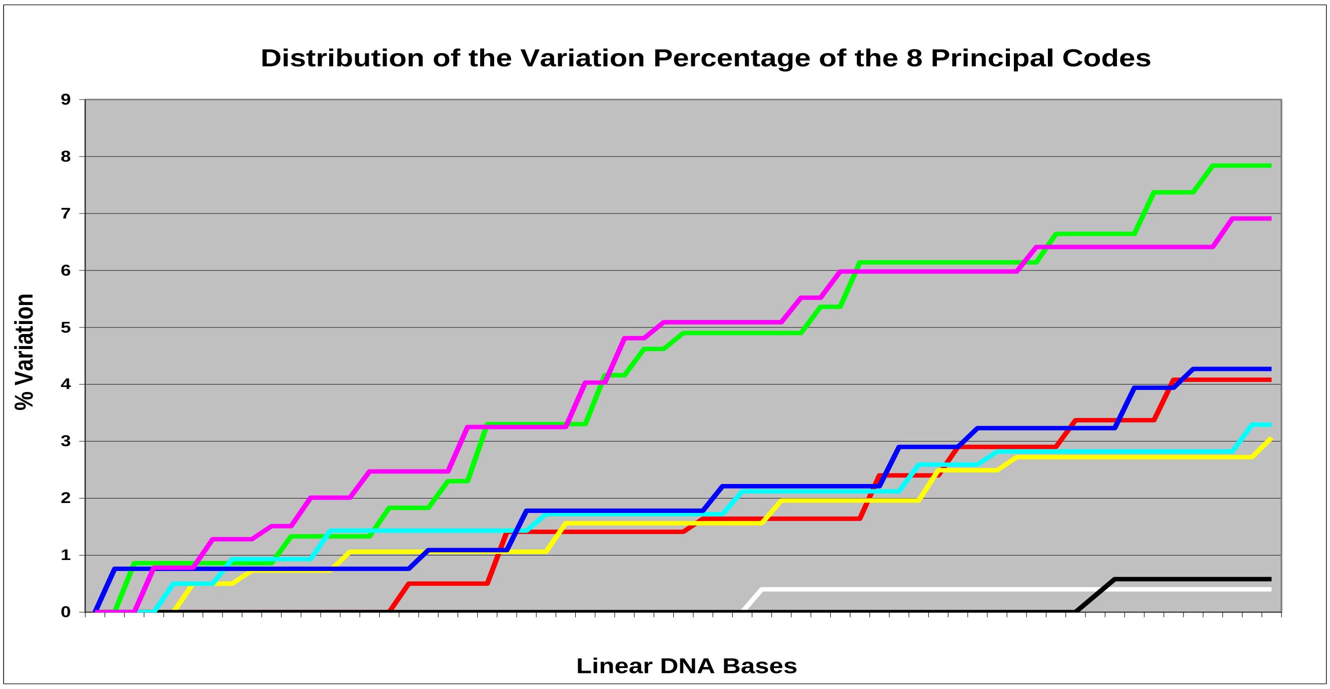
In Pct. 70 (A and B) two charts concerning the **Distribution of the Variation Percentage of the 8 Main Codes** are compared.

The charts in Pct. 70 (A) refers to the **original base sequence** analysed before.



Pct. 70 (A)

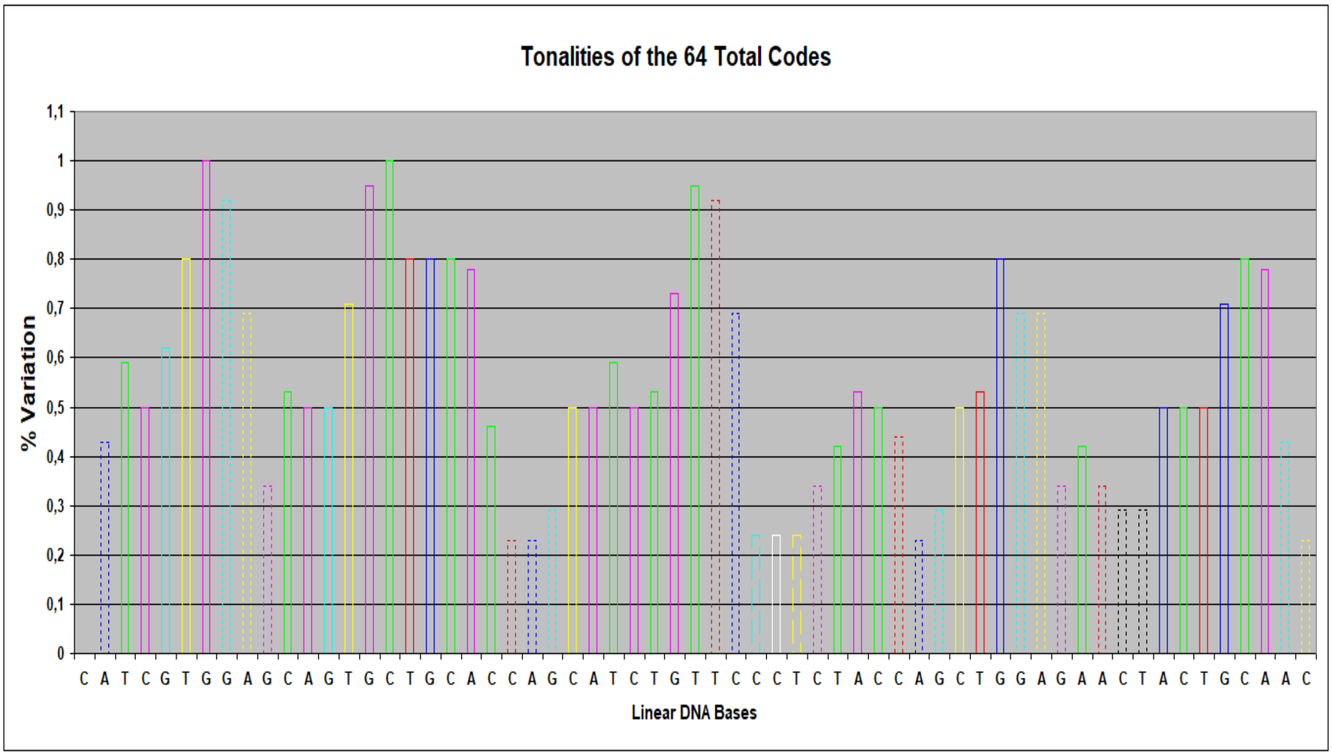
The chart in Pct. 70 (B) refers to the **"new generated sequence"** that originates from the original one.



Pct. 70 (B)

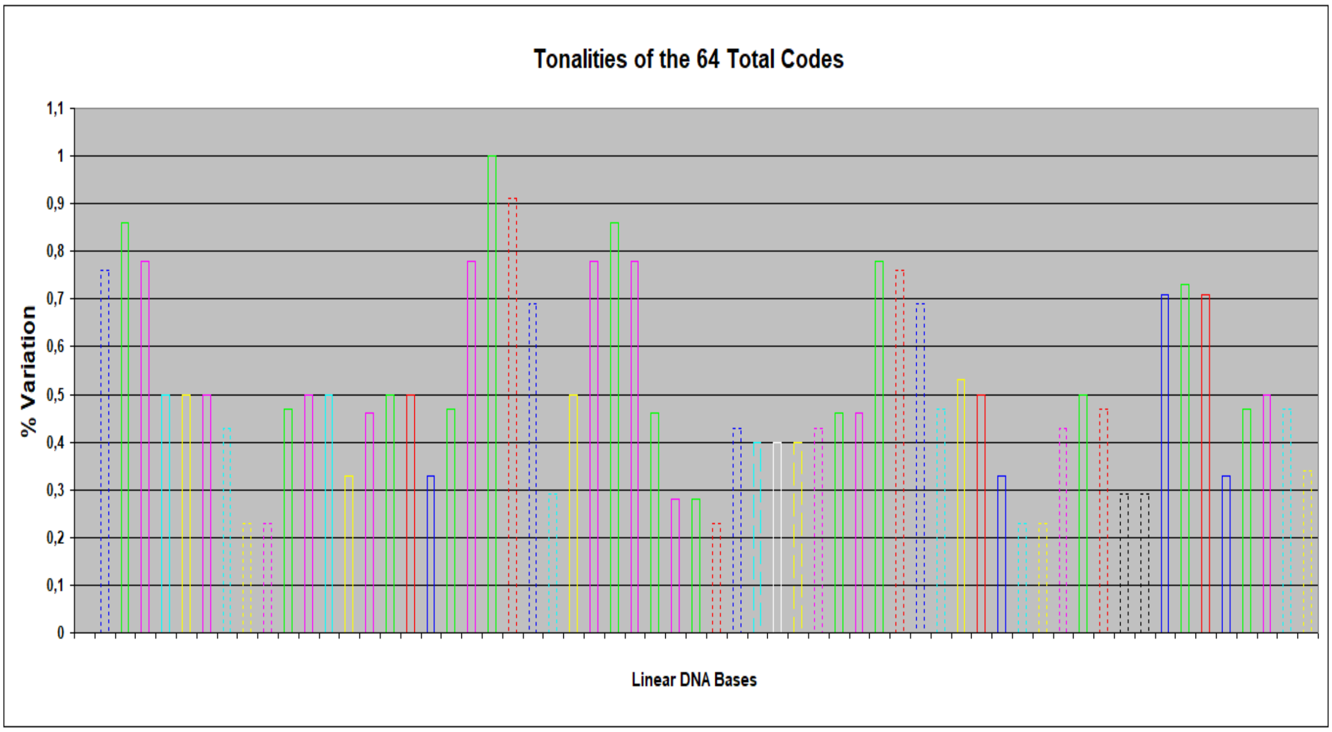
In Pct. 71 (A and B) two charts concerning the single **Tonalities of the 64 Total Codes** are compared.

The chart in Pct. 71 (A) refers to the **original base sequence** analysed before.



Pct. 71 (A)

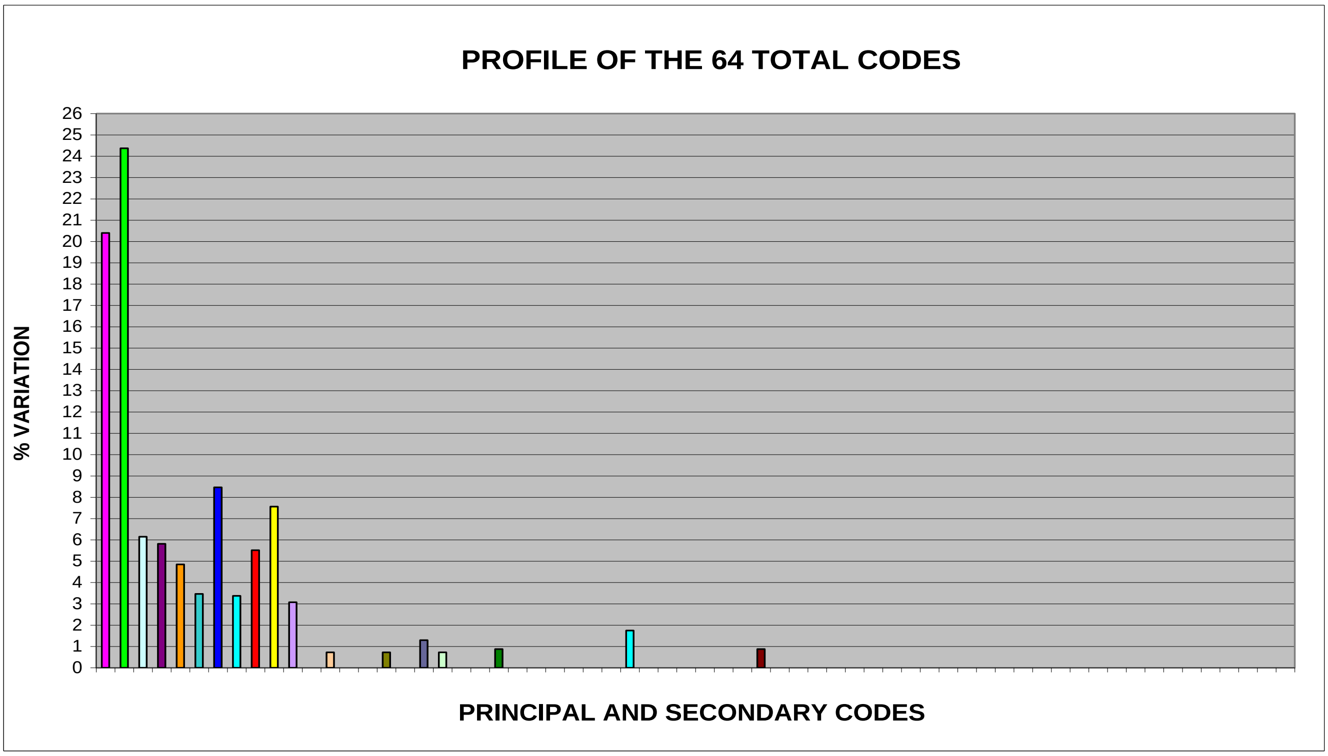
The chart in Pct. 71 (B) refers to the **"new generated sequence"** that originates from the original one.



Pct. 71 (B)

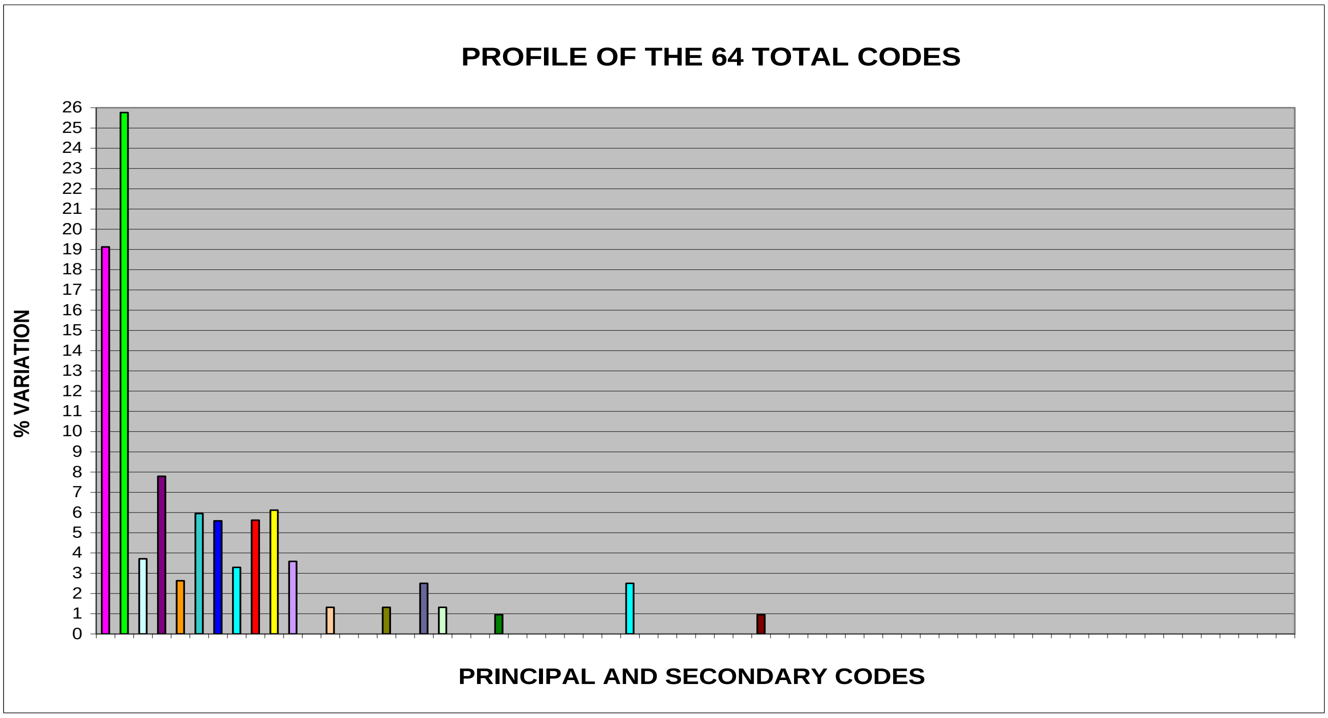
In Pct. 72 (A and B) two charts concerning the **Profile of the 64 Total Codes** are compared.

The chart in Pct. 72 (A) refers to the **original base sequence** analysed before.



Pct. 72 (A)

The chart in Pct. 72 (B) refers to the **"new generated sequence"** originated from the original one.



Pct. 72 (B)

The "non-obvious trend" analysis (obtained through the **T.T.E.S.**) of **Sequence n°18/1 of Insulin Chain A** results in **a comparison among different graphs** that are going to be interpreted in an analogous way to that in which the graphs related to the "non-obvious trend" of the **Sequences** analysed in the previous paragraphs **(n° 1/1, n° 2/1, etc.)** were. In order to avoid repetitions, here, the reader is deferred to the interpretation of the **comparisons among the different graphs** presented in the paragraph 1.2 .

Before concluding the paragraph, it is worth noting that, out of the **63** DNA bases of **Sequence n° 18/1**, ONLY **EIGHT BASES** (the **12,70%**)**,** ARE EQUAL (by type and by position in sequence) TO THOSE OF THE ORIGINAL SEQUENCE (**Insulin Chain A**).

1.37 IMPLICATIONS RELATED TO THE GRAPHIC RESULTS OF THE "NON-OBVIOUS TREND" ANALYSIS OF SEQUENCE n° 18/1 OF INSULIN CHAIN A

The **63** DNA base sequence of the **new generated sequence** (**Sequence n° 18/1**) that arises from the **original** one has been subjected to **BLAST** research.

Please note:

Information about the ***significant alignments*** produced by *BLAST research*, related to **Sequence n° 18/1,** and all the data acquired from *GenBank (3)* will be published in the **Appendix,** after the *General Conclusions.*

Query = NEW GENERATED SEQUENCE (Sequence n° 18/1)

Length = 63

Parameters of BLAST research:

Programme	*Blastn*
Word size	*11*
Expect value	*10*
Hitlist size	*100*
Match/Mismatch scores	*2,-3*
Gapcosts	*5,2*
Low Complexity Filter	*Yes*
Filter string	*L;m;*
Genetic Code	*1*

Please note:

Here, "**the organisms found to be in common**" between the results of BLAST research carried out on **Insulin Chain A** and results of BLAST research carried out on **Sequence n° 18/1**, were highlighted in **Red**.
As well, "**the organisms found to be in common**" between the results of BLAST research carried out on **Insulin Chain A**, results of BLAST research carried out on **Sequence n° 18/1** and results of BLAST research carried out on **at least one** of the *19 generated sequences*, were highlighted in **Green**.
Moreover, "**the denomination of the sequence**" (1/1, 2/1, ... 19/1) of the "**organism found to be in common**" between the results of BLAST research carried out on **Sequence n° 18/1** and results of BLAST research carried out on **at least one** of the *19 new generated sequences*, were highlighted in **Blue**.
Finally, "**the denomination of the sequence**" (1/1, 2/1, ... 19/1) of the "**organism found to be in common**" between the results of BLAST research carried out on **Insulin Chain A** and results of BLAST research carried out on *19 generated sequences*, were highlighted in **Yellow**.

Sequenza n° 18/1

Sequences producing significant alignments:

Selected seq	Description	Max score	Total score	Query cover	E value	Ident	Accession
1 **15/1** XM_024848591.1	Aspergillus steynii IBT 23096 hypothetical protein (P170DRAFT_433862), mRNA	41.0	41.0	42%	2.7	93%	XM_024848591.1
2 AC117994.12	Mus musculus chromosome 6, clone RP23-25K2, complete sequence	41.0	41.0	50%	2.7	88%	AC117994.12
3 AC156397.5	Mus musculus 6 BAC RP24-279P24 (Roswell Park Cancer Institute (C57BL/6J Male) Mouse BAC Library) complete sequence	41.0	41.0	50%	2.7	88%	AC156397.5
4 **5/1** CP036401.1	Massilia albidiflava strain DSM 17472 chromosome, complete genome	39.2	39.2	41%	9.5	92%	CP036401.1
5 LR131932.1	Cottoperca gobio genome assembly, chromosome: 24	39.2	39.2	42%	9.5	93%	LR131932.1
6 **3/1** LR214929.1	Schistosoma mansoni strain Puerto Rico genome assembly, chromosome: 1	39.2	39.2	33%	9.5	100%	LR214929.1
7 CP025263.1	Pseudomonas sp. S09G 359 chromosome	39.2	39.2	33%	9.5	100%	CP025263.1
8 XM_019705589.1	PREDICTED: Aedes albopictus uncharacterized LOC109429599 (LOC109429599), mRNA	39.2	39.2	33%	9.5	100%	XM_019705589.1
9 XM_019681863.1	PREDICTED: Aedes albopictus uncharacterized LOC109408541 (LOC109408541), mRNA	39.2	39.2	33%	9.5	100%	XM_019681863.1
10 LT629734.1	Agrococcus carbonis strain DSM 22965 genome assembly, chromosome: I	39.2	39.2	41%	9.5	92%	LT629734.1
11 **12/1** CP013398.1	Burkholderia seminalis strain FL-5-4-10-S1-D7 chromosome 1, complete sequence	39.2	39.2	41%	9.5	92%	CP013398.1
12 **12/1** CP013730.1	Burkholderia cepacia JBK9 chromosome 1, complete sequence	39.2	39.2	41%	9.5	92%	CP013730.1
13 **3/1** HE601624.1	Schistosoma mansoni strain Puerto Rico chromosome 1, complete genome	39.2	39.2	33%	9.5	100%	HE601624.1
14 **1/1** CP000712.1	Pseudomonas putida F1, complete genome	39.2	39.2	33%	9.5	100%	CP000712.1

Comparison between the alignments of Sequence 18/1 and Sequence of Insulin Chain A according to the “Species of Common Organisms”:

Alignments Sequence 18/1	**Description**	**Alignments Sequence Insulin Chain A**	**Description**
2 Select seq AC117994.12	Mus musculus chromosome 6, clone RP23-25K2, complete sequence	Select seq XM_021152514.1 **1/1 6/1 8/1 10/1** **13/1 17/1**	PREDICTED: Mus caroli insulin-1 (LOC110286053), mRNA
3 Select seq AC156397.5	Mus musculus 6 BAC RP24-279P24 (Roswell Park Cancer Institute (C57BL/6J Male) Mouse BAC Library) complete sequence	Select seq DQ250565.1 **1/1 6/1 8/1 10/1** **13/1 17/1**	Mus caroli preproinsulin 1 (Ins1) gene, complete cds
		Select seq XM_021215010.1 **1/1 6/1 8/1 10/1** **13/1 17/1**	PREDICTED: Mus pahari insulin-1 (LOC110333420), mRNA
		Select seq NM_008386.4 **1/1 6/1 8/1 10/1** **13/1 17/1**	Mus musculus insulin I (Ins1), mRNA
		Select seq BC145868.1 **1/1 6/1 8/1 10/1** **13/1 17/1**	Mus musculus insulin I, mRNA (cDNA clone MGC:175755 IMAGE:40131171), complete cds
		Select seq DQ479923.1 **1/1 6/1 8/1 10/1** **13/1 17/1**	Mus musculus strain BTBR T+ tf/J insulin 1 precursor, gene, complete cds
		Select seq AC163452.12 **1/1 6/1 8/1 10/1** **13/1 17/1**	Mus musculus chromosome 19, clone RP23-405C7, complete sequence
		Select seq AC136710.8 **1/1 6/1 8/1 10/1** **13/1 17/1**	Mus musculus chromosome 19, clone RP23-35B13, complete sequence
		Select seq AC140320.2 **1/1 6/1 8/1 10/1** **13/1 17/1**	Mus musculus BAC clone RP23-401C13 from chromosome 19, complete sequence
		Select seq BC098468.1 **1/1 6/1 8/1 10/1** **13/1 17/1**	Mus musculus insulin I, mRNA (cDNA clone MGC:107382 IMAGE:6432765), complete cds

Comparison between the alignments of Sequence 18/1 and Sequence of Insulin Chain A according to the "Species of Common Organisms":

Alignments Sequence 18/1	Description	Alignments Sequence Insulin Chain A	Description
		Select seq AK148541.1 **1/1 6/1 8/1 10/1 13/1 17/1**	Mus musculus adult pancreas islet cells cDNA, RIKEN full-length enriched library, clone:C820020F18 product:insulin I, full insert sequence
		Select seq AK007345.1 **1/1 6/1 8/1 10/1 13/1 17/1**	Mus musculus 10 day old male pancreas cDNA, RIKEN full-length enriched library, clone:1810005L03 product:INSULIN 1 PRECURSOR, full insert sequence
		Select seq XM_021168754.1 **1/1 6/1 8/1 10/1 13/1 17/1**	PREDICTED: Mus caroli insulin-2 (LOC110299132), transcript variant X2, mRNA
		Select seq XM_021168753.1 **1/1 6/1 8/1 10/1 13/1 17/1**	PREDICTED: Mus caroli insulin-2 (LOC110299132), transcript variant X1, mRNA
		Select seq NM_001185084.2 **1/1 6/1 8/1 10/1 13/1 17/1**	Mus musculus insulin II (Ins2), transcript variant 3, mRNA
		Select seq NM_001185083.2 **1/1 6/1 8/1 10/1 13/1 17/1**	Mus musculus insulin II (Ins2), transcript variant 1, mRNA
		Select seq NM_008387.5 **1/1 6/1 8/1 10/1 13/1 17/1**	Mus musculus insulin II (Ins2), transcript variant 2, mRNA
		Select seq JN959239.1 **1/1 6/1 8/1 10/1 13/1 17/1**	Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Ins2:tm1a(EUCOMM)Wtsi; transgenic
		Select seq JN951270.1 **1/1 6/1 8/1 10/1 13/1 17/1**	Mus musculus targeted non-conditional, lacZ-tagged mutant allele Ins2:tm1e(EUCOMM)Wtsi; transgenic
		Select seq BC145554.1 **1/1 6/1 8/1 10/1 13/1 17/1**	Mus musculus insulin II, mRNA (cDNA clone MGC:179126 IMAGE:9054118), complete cds

Comparison between the alignments of Sequence 18/1 and Sequence of Insulin Chain A according to the "Species of Common Organisms":

Alignments Sequence 18/1	Description	Alignments Sequence Insulin Chain A	Description
		Select seq BC099934.1 **1/1 6/1 8/1 10/1 13/1 17/1**	Mus musculus insulin II, mRNA (cDNA clone MGC:107381 IMAGE:6432976), complete cds
		Select seq BC132650.1 **1/1 6/1 8/1 10/1 13/1 17/1**	Mus musculus insulin II, mRNA (cDNA clone MGC:164281 IMAGE:40130927), complete cds
		Select seq DQ250569.1 **1/1 6/1 8/1 10/1 13/1 17/1**	Mus caroli preproinsulin 2 (Ins2) gene, complete cds
		Select seq AK007612.1 **1/1 6/1 8/1 10/1 13/1 17/1**	Mus musculus 10 day old male pancreas cDNA, RIKEN full-length enriched library, clone:1810027C14 product:INSULIN 2 PRECURSOR, full insert sequence
		Select seq AK007482.1 **1/1 6/1 8/1 10/1 13/1 17/1**	Mus musculus 10 day old male pancreas cDNA, RIKEN full-length enriched library, clone:1810013J24 product:INSULIN 1 PRECURSOR, full insert sequence
		Select seq BC066208.1 **1/1 6/1 8/1 10/1 13/1 17/1**	Mus musculus insulin II, mRNA (cDNA clone IMAGE:6436276)
		Select seq AC012382.14 **1/1 6/1 8/1 10/1 13/1 17/1**	Mus musculus chromosome 7, clone RP23-92L23, complete sequence
		Select seq AY899305.1 **1/1 6/1 8/1 10/1 13/1 17/1**	Mus musculus proinsulin mRNA, complete cds, alternatively spliced
		Select seq AC013548.13 **1/1 6/1 8/1 10/1 13/1 17/1**	Mus musculus chromosome 7, clone RP23-209O22, complete sequence
		Select seq AP003182.2 **1/1 6/1 8/1 10/1 13/1 17/1**	Mus musculus genomic DNA, chromosome 7 clone:B189M11, complete sequences

Comparison between the alignments of Sequence 18/1 and Sequence of Insulin Chain A according to the "Species of Common Organisms":

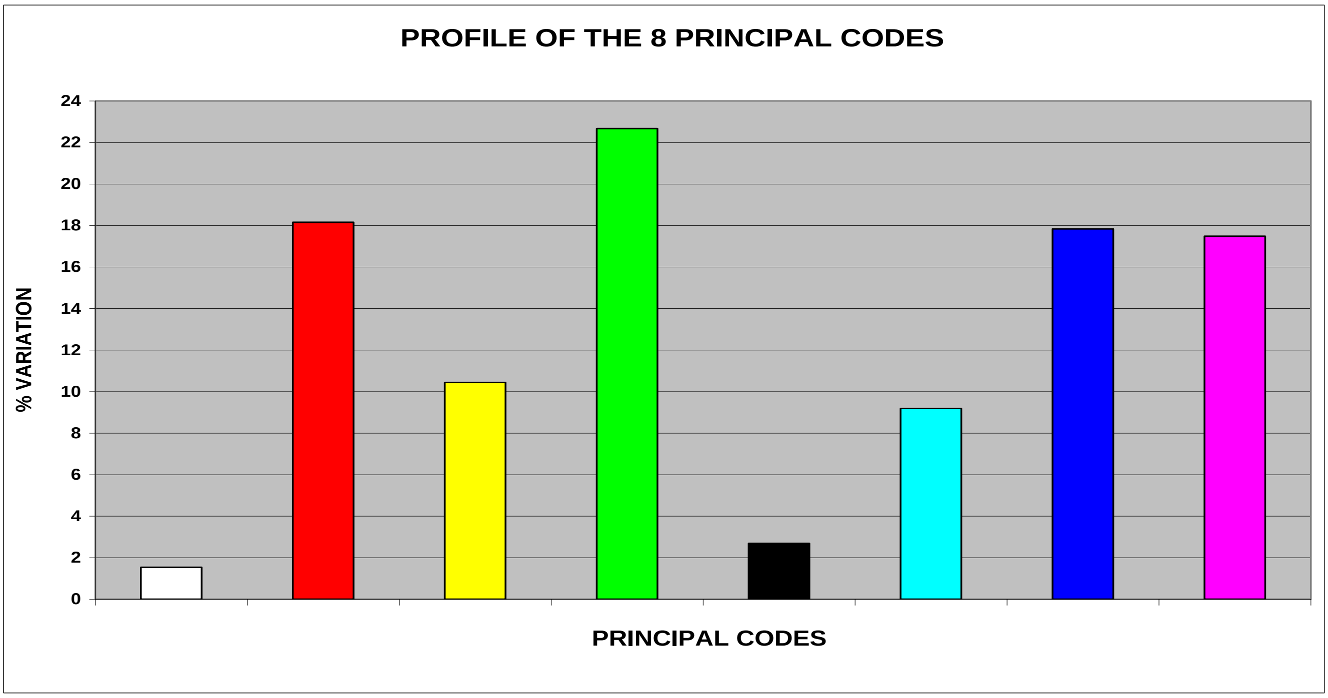
Alignments Sequence 18/1	**Description**	**Alignments Sequence Insulin Chain A**	**Description**
		Select seq GQ915612.1 **1/1 6/1 8/1 10/1 13/1 17/1**	Mus musculus insulin-2 precursor (Ins2) mRNA, partial cds, alternatively spliced
		Select seq XM_021204833.1 **1/1 6/1 8/1 10/1 13/1 17/1**	PREDICTED: Mus pahari insulin-2 (LOC110326410), transcript variant X2, mRNA
		Select seq XM_021204825.1 **1/1 6/1 8/1 10/1 13/1 17/1**	PREDICTED: Mus pahari insulin-2 (LOC110326410), transcript variant X1, mRNA
5 Select seq LR131932.1	Cottoperca gobio genome assembly, chromosome: 24	Select seq LR131921.1 **4/1 6/1 7/1 16/1 19/1**	Cottoperca gobio genome assembly, chromosome: 14
		Select seq LR131917.1 **4/1 6/1 7/1 16/1 19/1**	Cottoperca gobio genome assembly, chromosome: 10
7 Select seq CP025263.1	Pseudomonas sp. S09G 359 chromosome	Select seq CP026880.1 **1/1**	Pseudomonas sp. LH1G9 chromosome, complete genome
14 Select seq CP000712.1 1/1	Pseudomonas putida F1, complete genome	Select seq CP025263.1 **1/1**	Pseudomonas sp. S09G 359 chromosome
		Select seq CP018420.1 **1/1**	Pseudomonas veronii strain R02, complete genome
		Select seq LT599583.1 **1/1**	Pseudomonas veronii 1YdBTEX2 genome assembly, chromosome: PVE_r1

Analysis of
Sequence n° 19/1
of Insulin Chain A

1. 38 GRAPHIC RESULTS OF THE "NON-OBVIOUS TREND" ANALYSIS OF SEQUENCE n° 19/1 OF INSULIN CHAIN A

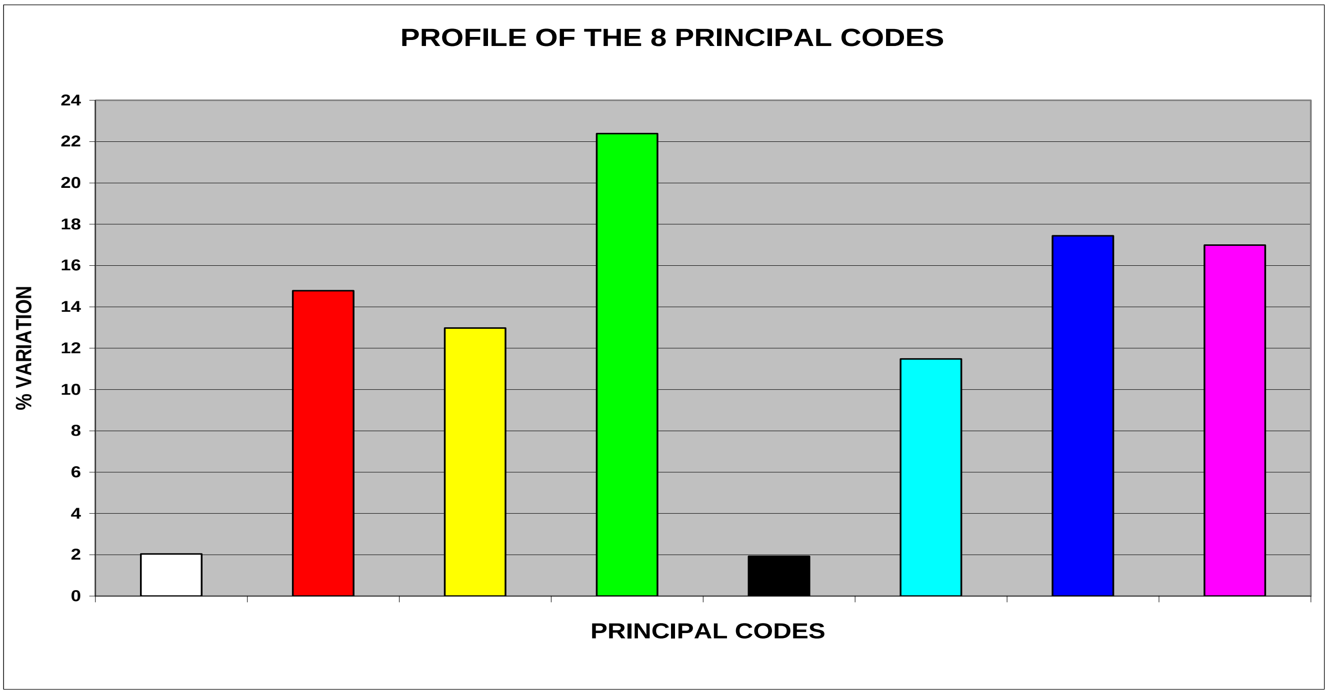
In the Pct. 73 (A e B) two **8 Principal Codes Profiles** are compared.

The chart in Pct. 73 (A) refers to the **original base sequence** of **Insulin Chain A**.



Pct. 73 (A)

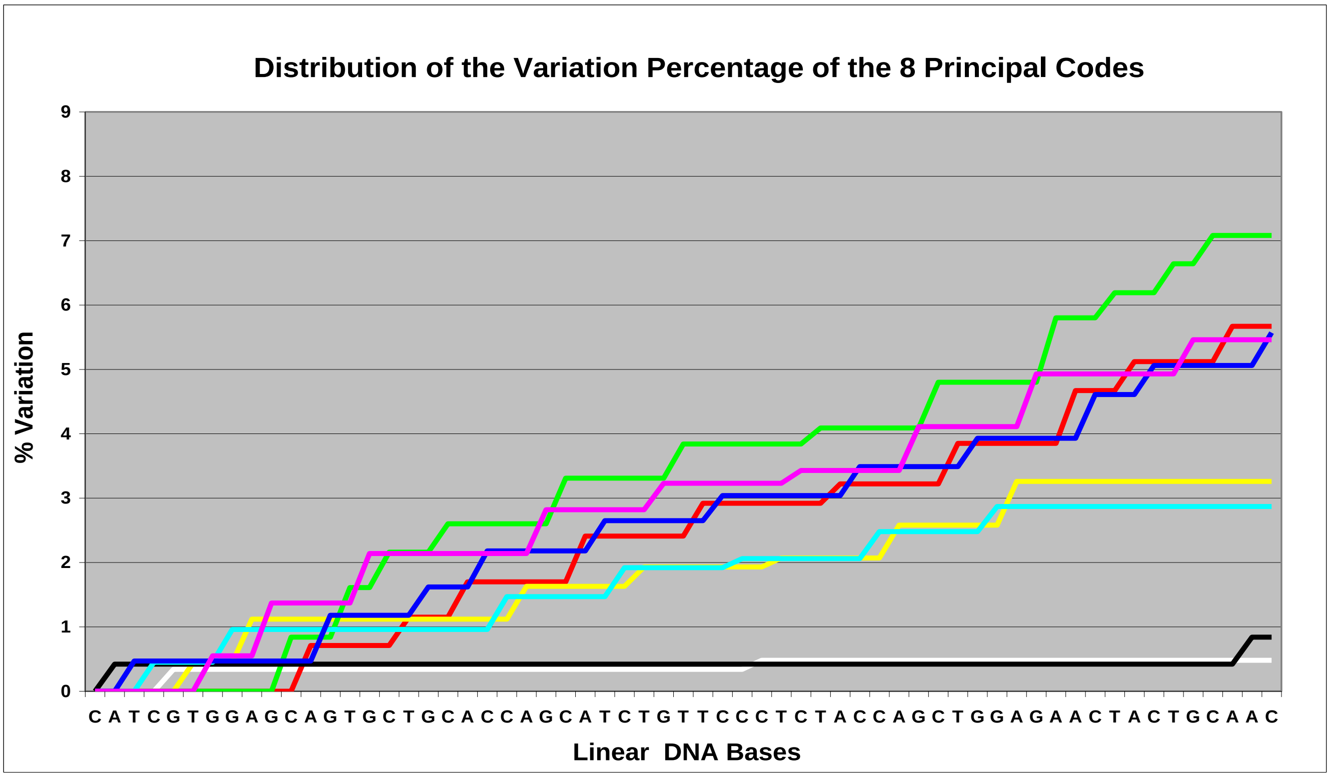
The chart in Pct. 73 (B) refers to the **nineteenth** **"new generated sequence"** (**Sequence n° 19/1**) that originates from the original one.



Pct. 73 (B)

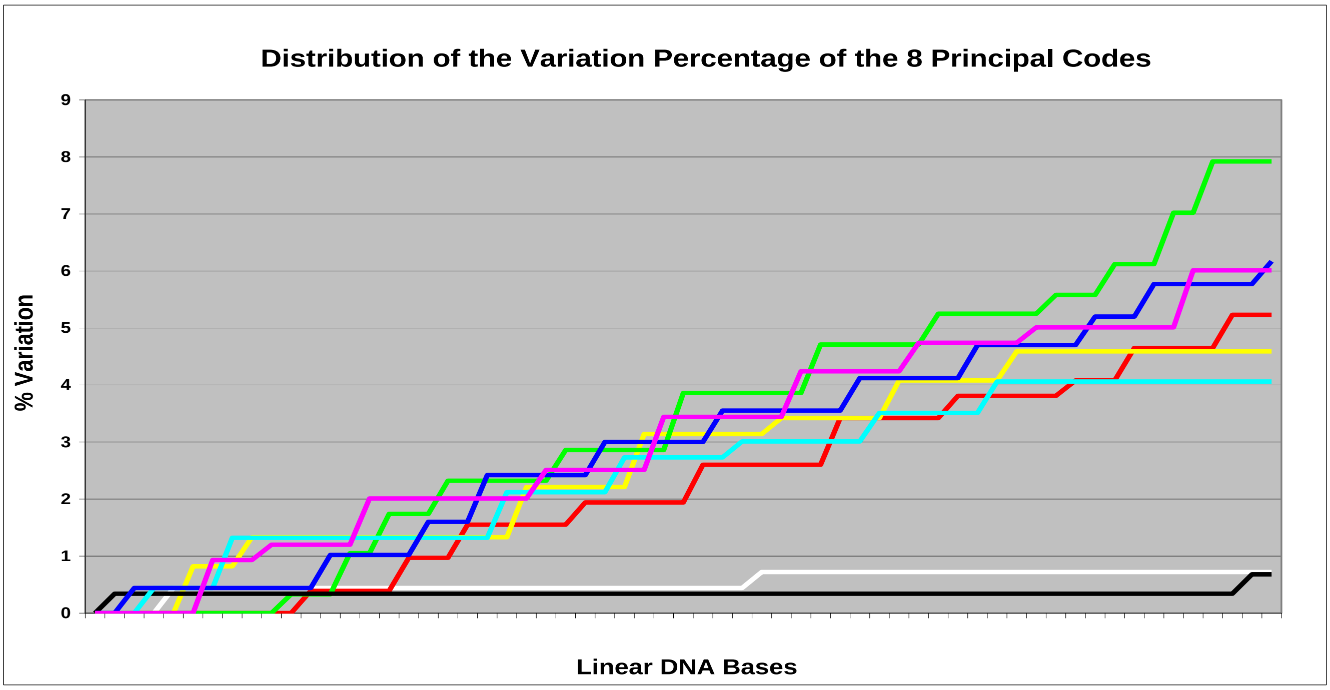
In Pct. 74 (A and B) two charts concerning the **Distribution of the Variation Percentage of the 8 Main Codes** are compared.

The charts in Pct. 74 (A) refers to the **original base sequence** analysed before.



Pct. 74 (A)

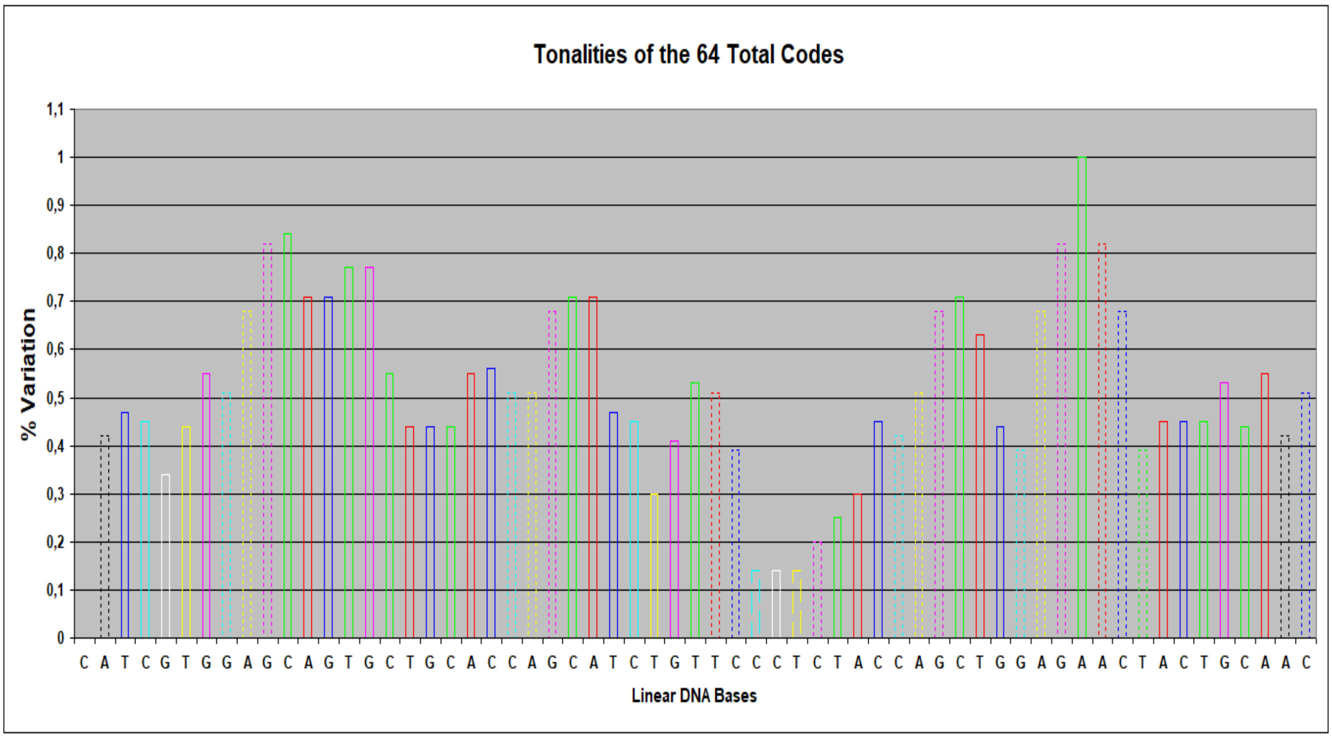
The chart in Pct. 74 (B) refers to the **“new generated sequence”** that originates from the original one.



Pct. 74 (B)

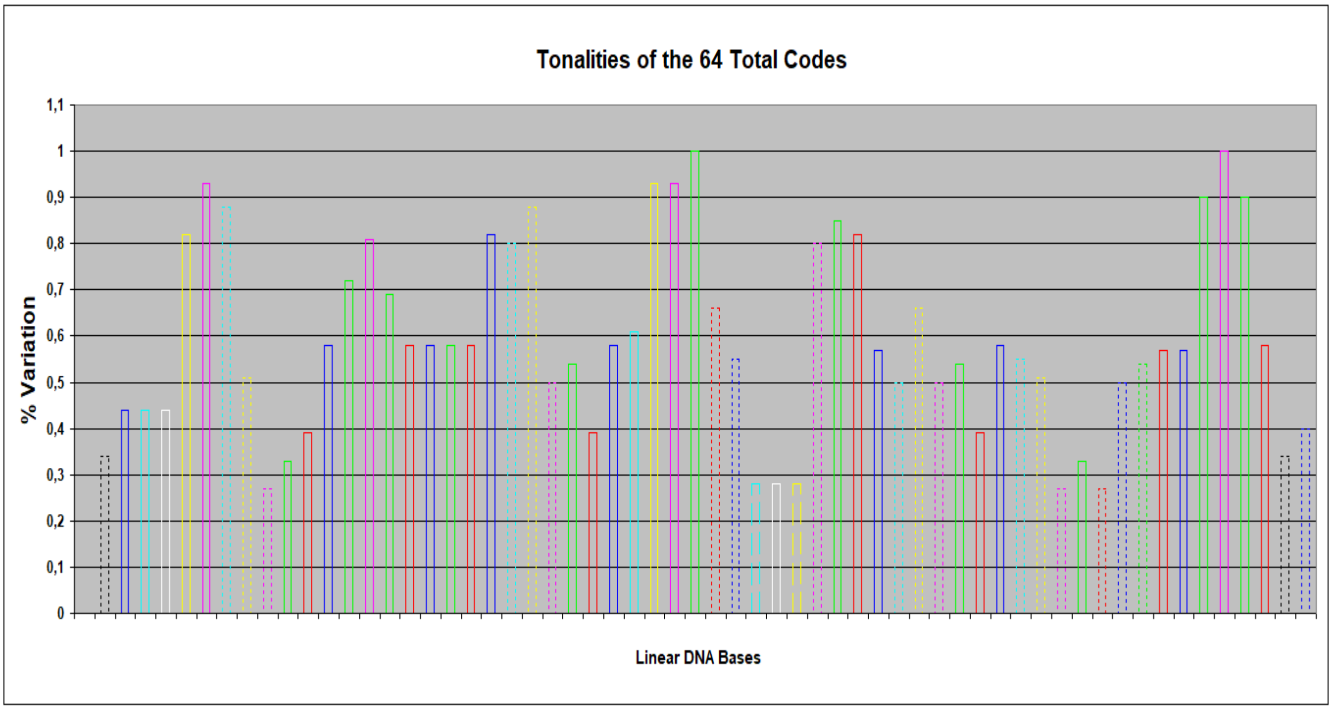
In Pct. 75 (A and B) two charts concerning the single **Tonalities of the 64 Total Codes** are compared.

The chart in Pct. 75 (A) refers to the **original base sequence** analysed before.



Pct. 75 (A)

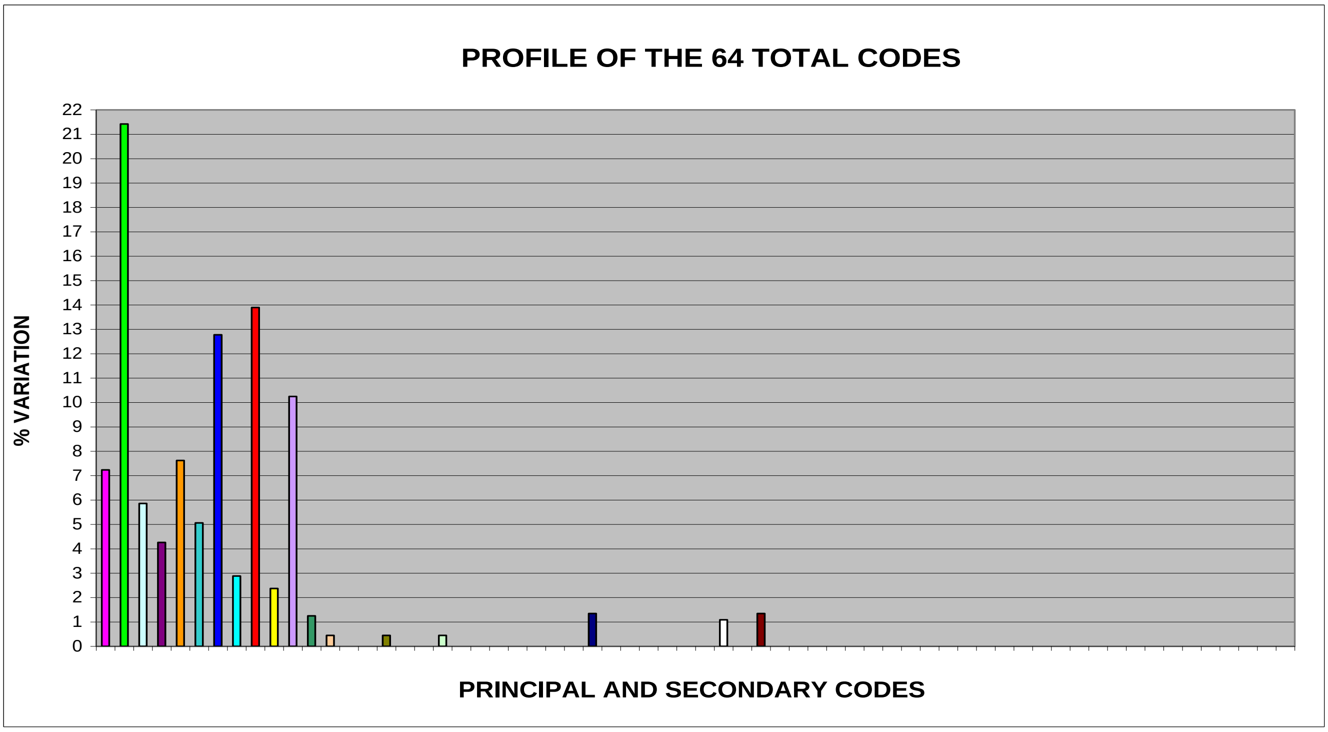
The chart in Pct. 75 (B) refers to the **"new generated sequence"** that originates from the original one.



Pct. 75 (B)

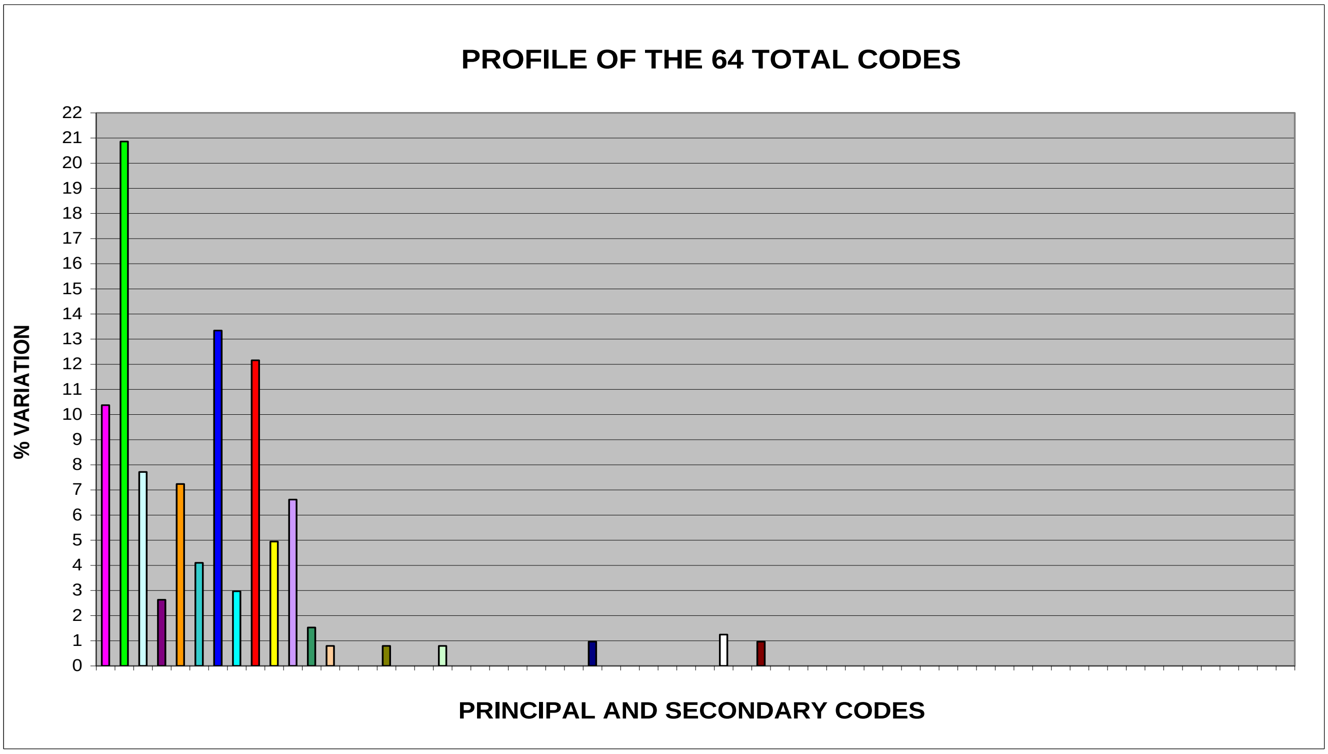
In Pct. 76 (A and B) two charts concerning the **Profile of the 64 Total Codes** are compared.

The chart in Pct. 76 (A) refers to the **original base sequence** analysed before.



Pct. 76 (A)

The chart in Pct. 76 (B) refers to the **“new generated sequence”** originated from the original one.



Pct. 76 (B)

The “non-obvious trend” analysis (obtained through the **T.T.E.S.**) of **Sequence n°19/1 of Insulin Chain A** results in **a comparison among different graphs** that are going to be interpreted in an analogous way to that in which the graphs related to the “non-obvious trend” of the **Sequences** analysed in the previous paragraphs **(n° 1/1, n° 2/1, etc.)** were. In order to avoid repetitions, here, the reader is deferred to the interpretation of the **comparisons among the different graphs** presented in the paragraph 1.2 .

Before concluding the paragraph, it is worth noting that, out of the **63** DNA bases of **Sequence n° 19/1**, ONLY **NINE BASES** (the **14,29%**)**,** ARE EQUAL (by type and by position in sequence) TO THOSE OF THE ORIGINAL SEQUENCE (**Insulin Chain A**).

1.39 IMPLICATIONS RELATED TO THE GRAPHIC RESULTS OF THE "NON-OBVIOUS TREND" ANALYSIS OF SEQUENCE n° 19/1 OF INSULIN CHAIN A

The **63** DNA base sequence of the **new generated sequence** (**Sequence n° 19/1**) that arises from the **original** one has been subjected to **BLAST** research.

Please note:

Information about the ***significant alignments*** produced by *BLAST research*, related to **Sequence n° 19/1,** and all the data acquired from *GenBank (3)* will be published in the **Appendix,** after the *General Conclusions.*

Query = NEW GENERATED SEQUENCE (Sequence n° 19/1)

Length = 63

Parameters of BLAST research:

Programme	*Blastn*
Word size	*11*
Expect value	*10*
Hitlist size	*100*
Match/Mismatch scores	*2,-3*
Gapcosts	*5,2*
Low Complexity Filter	*Yes*
Filter string	*L;m;*
Genetic Code	*1*

Please note:

Here, "**the organisms found to be in common**" between the results of BLAST research carried out on **Insulin Chain A** and results of BLAST research carried out on **Sequence n° 19/1**, were highlighted in **Red**.
As well, "**the organisms found to be in common**" between the results of BLAST research carried out on **Insulin Chain A**, results of BLAST research carried out on **Sequence n° 19/1** and results of BLAST research carried out on **at least one** of the *19 generated sequences*, were highlighted in **Green**.
Moreover, "**the denomination of the sequence**" (1/1, 2/1, ... 19/1) of the "**organism found to be in common**" between the results of BLAST research carried out on **Sequence n° 19/1** and results of BLAST research carried out on **at least one** of the *19 new generated sequences*, were highlighted in **Blue**.
Finally, "**the denomination of the sequence**" (1/1, 2/1, ... 19/1) of the "**organism found to be in common**" between the results of BLAST research carried out on **Insulin Chain A** and results of BLAST research carried out on *19 generated sequences*, were highlighted in **Yellow**.

Sequenza n° 19/1

Sequences producing significant alignments:

Selected seq	Description	Max score	Total score	Query cover	E value	Ident	Accession
1 LR131921.1	Cottoperca gobio genome assembly, chromosome: 14	39.2	39.2	41%	9.5	92%	LR131921.1
2 AC093141.2	Felis catus clone RP86-512F4, complete sequence	39.2	39.2	42%	9.5	93%	AC093141.2

Comparison between the alignments of Sequence 19/1 and Sequence of Insulin Chain A according to the "Species of Common Organisms":

Alignments Sequence 19/1	**Description**	**Alignments Sequence Insulin Chain A**	**Description**
1 Select seq LR131921.1 **7/1**	Cottoperca gobio genome assembly, chromosome: 14	Select seq LR131921.1 **4/1 6/1 7/1 16/1 18/1**	Cottoperca gobio genome assembly, chromosome: 14
		Select seq LR131917.1 **4/1 6/1 7/1 16/1 18/1**	Cottoperca gobio genome assembly, chromosome: 10
2 Select seq AC093141.2	Felis catus clone RP86-512F4, complete sequence	Select seq XM_019811180.2	PREDICTED: Felis catus insulin (INS), transcript variant X1, mRNA
		Select seq NM_001009272.1	Felis catus insulin (INS), mRNA
		Select seq AY986822.1	Felis catus preproinsulin mRNA, partial cds
		Select seq XM_023240193.1	PREDICTED: Felis catus insulin like growth factor 2 (IGF2), transcript variant X2, mRNA
		Select seq XM_023240192.1	PREDICTED: Felis catus insulin like growth factor 2 (IGF2), transcript variant X1, mRNA
		Select seq XM_019812848.1	PREDICTED: Felis catus insulin like growth factor 2 (IGF2), transcript variant X4, mRNA
		Select seq XM_019812847.1	PREDICTED: Felis catus insulin like growth factor 2 (IGF2), transcript variant X3, mRNA

Percentages and Number of Common Bases among all the Analyzed Sequences of Insulin Chain A

1.40 Percentages and Number of Common Bases (by type and by position in sequence) among all the Analyzed Sequences of Insulin Chain A

In the following **19 Tables** the **Percentages** and the **Number of Common Bases** (by type and by position in sequence) among all the Analyzed Sequences of Insulin Chain A are presented.

In the **First row in the Tables**, the names of the different base sequences are shown, from the Original (Orig., Insulin Chain A) to the nineteenth. The first name shown at the top left, the one highlighted in **Green**, corrisponds with the name of the sequence which is compared with the others.

In the **Second row in the Tables,** the **Percentages** and the **Number of Common Bases (% Bases)** between the sequence at the top left (in **Green**) and every other sequence are listed.

In the **Third row in the Tables,** the **Number of Common Bases (N° Bases)** between the top left sequence (in **Green**) and every other sequence is listed.

Finally, the numbers highlighted in **red** indicate, respectively, the **higher percentages of Bases** and the **the higher Number of Common Bases** between the top left sequence (in **Green**) and every other sequence; instead, the numbers highlighted in **blue** indicate, respectively, the **lower percentages** of **Bases** and the lower **Number of Common Bases** between the top left sequence (in **Green**) and every other sequence.

ORIG.	**1/1**	**2/1**	**3/1**	**4/1**	**5/1**	**6/1**	**7/1**	**8/1**	**9/1**	**10/1**	**11/1**	**12/1**	**13/1**	**14/1**	**15/1**	**16/1**	**17/1**	**18/1**	**19/1**
% Bases	**22,22**	**22,22**	**25,40**	**26,98**	**22,22**	**26,98**	**22,22**	**17,46**	**17,46**	**19,05**	**15,87**	**15,87**	**25,40**	**12,70**	**15,87**	**17,46**	**17,46**	**12,70**	**14,29**
N° Bases	**14**	**14**	**16**	**17**	**14**	**17**	**14**	**11**	**11**	**12**	**10**	**10**	**16**	**8**	**10**	**11**	**11**	**8**	**9**

Table 1

1/1	**2/1**	**3/1**	**4/1**	**5/1**	**6/1**	**7/1**	**8/1**	**9/1**	**10/1**	**11/1**	**12/1**	**13/1**	**14/1**	**15/1**	**16/1**	**17/1**	**18/1**	**19/1**
% Bases	**69,84**	**9,52**	**4,76**	**33,33**	**22,22**	**34,92**	**20,63**	**20,63**	**17,46**	**28,57**	**23,81**	**25,40**	**25,40**	**38,10**	**20,63**	**26,98**	**33,33**	**39,68**
N° Bases	**44**	**6**	**3**	**21**	**14**	**22**	**13**	**13**	**11**	**18**	**15**	**16**	**16**	**24**	**13**	**17**	**21**	**25**

Table 2

2/1	3/1	4/1	5/1	6/1	7/1	8/1	9/1	10/1	11/1	12/1	13/1	14/1	15/1	16/1	17/1	18/1	19/1
% Bases	7,94	4,76	30,16	25,40	31,75	26,98	25,40	23,81	28,57	22,22	30,16	33,33	36,51	19,05	31,75	36,51	34,92
N° Bases	5	3	19	16	20	17	16	15	18	14	19	21	23	12	20	23	22

Table 3

3/1	4/1	5/1	6/1	7/1	8/1	9/1	10/1	11/1	12/1	13/1	14/1	15/1	16/1	17/1	18/1	19/1
% Bases	71,43	19,05	15,87	19,05	19,05	41,27	31,75	22,22	30,16	34,92	36,51	15,87	28,57	17,46	15,87	17,46
N° Bases	45	12	10	12	12	26	20	14	19	22	23	10	18	11	10	11

Table 4

4/1	5/1	6/1	7/1	8/1	9/1	10/1	11/1	12/1	13/1	14/1	15/1	16/1	17/1	18/1	19/1
% Bases	19,05	25,40	22,22	23,81	39,68	22,22	20,63	30,16	28,57	33,33	17,46	42,86	19,05	12,70	17,46
N° Bases	12	16	14	15	25	14	13	19	18	21	11	27	12	8	11

Table 5

5/1	6/1	7/1	8/1	9/1	10/1	11/1	12/1	13/1	14/1	15/1	16/1	17/1	18/1	19/1
% Bases	6,35	25,40	4,76	31,75	36,51	22,22	36,51	33,33	30,16	17,46	26,98	20,63	12,70	26,98
N° Bases	4	16	3	20	23	14	23	21	19	11	17	13	8	17

Table 6

6/1	7/1	8/1	9/1	10/1	11/1	12/1	13/1	14/1	15/1	16/1	17/1	18/1	19/1
% Bases	47,62	85,71	25,40	22,22	30,16	28,57	20,63	23,81	34,92	23,81	36,51	33,33	41,27
N° Bases	30	54	16	14	19	18	13	15	22	15	23	21	26

Table 7

7/1	8/1	9/1	10/1	11/1	12/1	13/1	14/1	15/1	16/1	17/1	18/1	19/1
% Bases	34,92	41,27	15,87	30,16	20,63	6,35	41,27	17,46	52,38	17,46	15,87	88,89
N° Bases	22	26	10	19	13	4	26	11	33	11	10	56

Table 8

8/1	9/1	10/1	11/1	12/1	13/1	14/1	15/1	16/1	17/1	18/1	19/1
% Bases	20,63	19,05	33,33	25,40	20,63	25,40	31,75	19,05	46,03	38,10	31,75
N° Bases	13	12	21	16	13	16	20	12	29	24	20

Table 9

9/1	10/1	11/1	12/1	13/1	14/1	15/1	16/1	17/1	18/1	19/1
% Bases	12,70	42,86	14,29	6,35	88,89	4,76	46,03	11,11	6,35	41,27
N° Bases	8	27	9	4	56	3	29	7	4	26

Table 10

10/1	11/1	12/1	13/1	14/1	15/1	16/1	17/1	18/1	19/1
% Bases	7,94	84,13	25,40	12,70	49,21	11,11	30,16	44,44	9,52
N° Bases	5	53	16	8	31	7	19	28	6

Table 11

11/1	12/1	13/1	14/1	15/1	16/1	17/1	18/1	19/1
% Bases	3,17	14,29	50,79	14,29	49,21	12,70	22,22	36,51
N° Bases	2	9	32	9	31	8	14	23

Table 12

12/1	13/1	14/1	15/1	16/1	17/1	18/1	19/1
% Bases	20,63	11,11	53,97	11,11	34,92	46,03	9,52
N° Bases	13	7	34	7	22	29	6

Table 13

13/1	14/1	15/1	16/1	17/1	18/1	19/1
% Bases	6,35	34,92	11,11	31,75	30,16	4,76
N° Bases	4	22	7	20	19	3

Table 14

14/1	15/1	16/1	17/1	18/1	19/1
% Bases	1,59	44,44	15,87	11,11	44,44
N° Bases	1	28	10	7	28

Table 15

15/1	16/1	17/1	18/1	19/1
% Bases	7,94	19,05	88,89	12,70
N° Bases	5	12	56	8

Table 16

16/1	**17/1**	**18/1**	**19/1**
% Bases	**6,35**	**9,52**	**53,97**
N° Bases	**4**	**6**	**34**

Table 17

17/1	**18/1**	**19/1**
% Bases	**25,40**	**15,87**
N° Bases	**16**	**10**

Table 18

18/1	**19/1**
% Bases	**14,29**
N° Bases	**9**

Table 19

Discussion of Results, Clarifications and Conclusions

1.41 GENERAL DISCUSSION OF RESULTS

The aim of this Chapter was to present the results of the ***Analysis*** (carried out through the **TRICHROMATIC THEORY OF EQUILIBRIUM OF SYSTEMS**) of ***19 New Sequences*** of DNA bases generated by ***Insulin Chain A*** (*Original Sequence*).

These **19 new sequences** are constituted by almost totally different bases compared tp those of the **original sequence**.

The results show that the **19 new sequences** have **only a minimum** of 12,70 % and a maximum of 26,98 % of common bases with the **original sequence** (see the 19 Tables presented in paragraph 1.40 in this Chapter).

This first result clearly indicates that the DNA bases of the 19 new sequences differ (by type and position in sequence) by at least **73,02%** from those in the original sequence.

From this result it should then be concluded that the **19 new sequences** have very little or almost nothing to do with the characteristics of the **original sequence**.

Despite the blatant difference that was here ascertained, we hypothesized that the **19 new sequences**, as generated, in faithful observance of the **19** specific "non-obvious trends" of the original sequence, **have however a strong relationships with the characteristics of the original sequence**.

In this regard, **19** specific BLAST (*Basic Local Alignment Search Tool*) researches were carried out on ***19 new sequences*** and the results of ***all the significant alignments*** obtained were presented.

Therefore, from this paper’s standpoint, every *organism*, in which a significant alignment with the **19 new produced sequences** has been found, should be connected, indirectly or directly, with

1) the **original sequence** (**Insulin Chain A**);
2) those *organisms* that have been identified with Blast research carried out on **Insulin Chain A**;
3) as well as, partly, to those *organisms* in which significant alignments with the **19 new produced sequences** have been found.

The results obtained from the alignments analysis of the **original sequence** and those obtained from the **19 new generated sequences** show the presence of a significant number of **common** *organisms*. **Common** *organisms* were identified between those identified by **Insulin Chain A** and those organisms identified by the **19 new generated sequences**,. For a detailed analysis of these common *organisms* we defer the reader to the paragraphs that specifically deal with the alignments identified for the different sequences.

Here, we are interested in underlining that some *organisms*, identified by both the alignments of the sequence of **Insulin Chain A**, and by the **19 new generated sequences**, have also the same identical sequences in common.

We report below the **three** identified **organisms** and their **respective sequences**.

1) Cottoperca gobio. Sequence LR131921.1:

LR131921.1 **4/1 6/1 7/1** **16/1 18/1** **19/1**	Cottoperca gobio genome assembly, chromosome: 14	55.4	55.4	100%	1e-04	81%	LR131921.1
1 LR131921.1	Cottoperca gobio genome assembly, chromosome: 14	39.2	39.2	41%	9.5	92%	LR131921.1
1 LR131921.1	Cottoperca gobio genome assembly, chromosome: 14	39.2	39.2	41%	9.5	92%	LR131921.1

This Sequence was identified by Blast research carried out on Sequence of **Insulin Chain A**, on **Sequence n° 7/1** and on **Sequence n° 19/1**.
The **Insulin Chain A** has in common with the **Sequence n° 7/1** **22,22 %** of Bases (14 Bases), while it shares with **Sequence n° 19/1** only **14,29 %** of Bases (9 Bases).
On the other hand, **Sequence n° 7/1** and **Sequence n° 19/1**, have the highest percentage of Bases in common observed, i.e. **89,89 %** (56 Bases).

2) Anabas Testudineus. Sequence LR132049.1:

LR132049.1 **15/1**	Anabas testudineus genome assembly, chromosome: 19	42.8	42.8	69%	0.74	82%	LR132049.1
7 LR132049.1	Anabas testudineus genome assembly, chromosome: 19	40.1	40.1	38%	9.5	96%	LR132049.1

This Sequence was identified by Blast research carried out Sequence of **Insulin Chain A** and **Sequence n° 15/1**.
The **Insulin Chain A** has in common with the **Sequence n° 15/1** only **15,87 %** of Bases (10 Bases).

3) Pseudomonas sp. S09G 359. Sequence CP025263.1:

CP025263.1 **1/1** **18/1**	Pseudomonas sp. S09G 359 chromosome	41.9	41.9	41%	2.6	96%	CP025263.1
7 CP025263.1	Pseudomonas sp. S09G 359 chromosome	39.2	39.2	33%	9.5	100%	CP025263.1

This Sequence was identified by Blast research carried out Sequence of **Insulin Chain A** and **Sequence n° 18/1**.
The **Insulin Chain A** has in common with the **Sequence n° 18/1** the lowest percentage of Bases observed, i.e. **12,70 %** (8 Bases).

Even different *organisms*, identified by the alignments of the **19 new generated Sequences,** have the same identical Sequences in common.

The following are the **nine organisms** identified and their **respective Sequences**.

1) Bos mutus. Sequence CP027087.1:

8 **4/1** CP027087.1	Bos mutus isolate yakQH1 chromosome 19	39.2	39.2	33%	9.5	100%	CP027087.1
19 **3/1** CP027087.1	Bos mutus isolate yakQH1 chromosome 19	40.1	40.1	46%	9.0	90%	CP027087.1

This Sequence was identified by Blast research carried out on **Sequences n° 3/1** and **n° 4/1**.
The **Sequence n° 3/1** and **Sequence n° 4/1** have a considerable percentage of Bases in common, that is **71,43 %** (45 Bases).

2) Solanum lycopersicum. Sequence CP023759.1:

8 **8/1** CP023759.1	Solanum lycopersicum cultivar I-3 chromosome 3	41.0	41.0	52%	2.6	88%	CP023759.1
13 **4/1** CP023759.1	Solanum lycopersicum cultivar I-3 chromosome 3	40.1	40.1	53%	9.5	85%	CP023759.1

This Sequence was identified by Blast research carried out on **Sequences n° 4/1** and **n° 8/1**.
The **Sequence n° 4/1** and **Sequence n° 8/1** have only **23,81 %** of Bases in common (15 Bases).

3) Solanum lycopersicum. Sequence HG975515.1:

14 **8/1** HG975515.1	Solanum lycopersicum chromosome ch03, complete genome	41.0	41.0	52%	2.6	88%	HG975515.1
16 **4/1** HG975515.1	Solanum lycopersicum chromosome ch03, complete genome	40.1	40.1	53%	9.5	85%	HG975515.1

This Sequence was identified by Blast research carried out on **Sequences n° 4/1** and **n° 8/1**.
As already mentioned, these Sequences have in common only **23,81%** of Bases (15 Bases).

4) Cottoperca gobio. Sequence LR131937.1:

25 **6/1** LR131937.1	Cottoperca gobio genome assembly, chromosome: 7	39.2	39.2	41%	9.0	92%	LR131937.1
9 **4/1** LR131937.1	Cottoperca gobio genome assembly, chromosome: 7	42.8	42.8	52%	0.77	88%	LR131937.1

This Sequence was identified by Blast research carried out on **Sequences n° 4/1** and **n° 6/1**.
The **Sequence n° 4/1** and **Sequence n° 6/1** have only **25,40 %** of Bases in commun (16 Bases).

5) Dromaius novaehollandiae. Sequence XM_026120534.1:

8 **14/1** XM_026120534.1	PREDICTED: Dromaius novaehollandiae WD repeat domain 24 (WDR24), mRNA	39.2	39.2	60%	9.5	84%	XM_026120534.1
5 **9/1** XM_026120534.1	PREDICTED: Dromaius novaehollandiae WD repeat domain 24 (WDR24), mRNA	39.2	39.2	60%	9.5	84%	XM_026120534.1

This Sequence was identified by Blast research carried out on **Sequences n° 9/1** and **n° 14/1**.
The **Sequence n° 9/1** and **Sequence n° 14/1** have instead the highest percentage of Bases in common observed, that is **89,89 %** (56 Bases).

6) **Nothoprocta perdicaria**. Sequence XM_026048985.1:

9 **14/1** XM_026048985.1	PREDICTED: Nothoprocta perdicaria WD repeat domain 24 (WDR24), mRNA	39.2	39.2	60%	9.5	84%	XM_026048985.1
6 **9/1** XM_026048985.1	PREDICTED: Nothoprocta perdicaria WD repeat domain 24 (WDR24), mRNA	39.2	39.2	60%	9.5	84%	XM_026048985.1

This Sequence was identified by Blast research carried out on **Sequences n° 9/1** and **n° 14/1**.
As already mentioned, these Sequences have in common **89,89 %** of Bases (56 Bases).

7) **Leishmania mexicana**. Sequence XM_003878010.1:

18 **5/1** **14/1** XM_003878010.1	Leishmania mexicana MHOM/GT/2001/U1103 conserved hypothetical protein partial mRNA	39.2	39.2	49%	9.5	87%	XM_003878010.1
10 **5/1** **9/1** XM_003878010.1	Leishmania mexicana MHOM/GT/2001/U1103 conserved hypothetical protein partial mRNA	39.2	39.2	49%	9.5	87%	XM_003878010.1

This Sequence was identified by Blast research carried out on **Sequences n° 9/1** and **n° 14/1**.
As already mentioned, these Sequences have in common **89,89 %** of Bases (56 Bases).

8) **Spirochaeta thermophila**. Sequence CP002903.1:

19 **9/1** CP002903.1	Spirochaeta thermophila DSM 6578, complete genome	39.2	39.2	49%	9.5	87%	CP002903.1
11 **14/1** CP002903.1	Spirochaeta thermophila DSM 6578, complete genome	39.2	39.2	49%	9.5	87%	CP002903.1

This Sequence was identified by Blast research carried out on **Sequences n° 9/1** and **n° 14/1**.
As already mentioned, these Sequences have in common **89,89 %** of Bases (56 Bases).

9) Leishmania mexicana. Sequence FR799584.1:

20 **5/1** **14/1** FR799584.1	Leishmania mexicana MHOM/GT/2001/U1103 complete genome, chromosome 31	39.2	39.2	49%	9.5	87%	FR799584.1
12 5/1 9/1 FR799584.1	Leishmania mexicana MHOM/GT/2001/U1103 complete genome, chromosome 31	39.2	39.2	49%	9.5	87%	FR799584.1

This Sequence was identified by Blast research carried out on **Sequences n° 9/1** and **n° 14/1**.
As already mentioned, these Sequences have in common **89,89 %** of Bases (56 Bases).

10) Cercocebus atys. Sequence XR_001013343.1:

20 **12/1** XR_001013343.1	PREDICTED: Cercocebus atys pepsin A-like (LOC105581134), misc_RNA	39.2	39.2	33%	9.5	100%	XR_001013343.1
44 **10/1** XR_001013343.1	PREDICTED: Cercocebus atys pepsin A-like (LOC105581134), misc_RNA	39.2	39.2	33%	9.5	100%	XR_001013343.1

This Sequence was identified by Blast research carried out on **Sequences n° 10/1** and **n° 12/1**.
The **Sequence n° 10/1** and **Sequence n° 12/1** have a considerable percentage of Bases in common, that is **84,13 %** (53 Bases).

11) Ovis canadensis canadensis. Sequence CP011906.1:

4 **6/1** **17/1** CP011906.1	Ovis canadensis canadensis isolate 43U chromosome 21 sequence	40.1	40.1	39%	9.5	96%	CP011906.1
22 **6/1** **14/1** CP011906.1	Ovis canadensis canadensis isolate 43U chromosome 21 sequence	41.9	41.9	73%	2.7	80%	CP011906.1

This Sequence was identified by Blast research carried out on **Sequences n° 14/1** and **n° 17/1**.
The **Sequence n° 14/1** and **Sequence n° 17/1** have a very low percentage of Bases in common, i.e. **15,87%** (10 Bases).

Another interesting aspect that is worth noticing here is that for some *organisms*, the results obtained from the analysis of the alignments of the **19 new generated Sequences** show the involvement of several chromosomes.

We report below, just as examples, the *organisms* **Bos mutus** and **Cottoperca gobio**.

1) Bos Mutus:

The following *two Sequences* have been identified by Blast research carried out on Sequence of **Insulin Chain A**:

CP027097.1 **3/1** **4/1** **8/1**	Bos mutus isolate yakQH1 chromosome 29	87.8	87.8	100%	2e-14	90%	CP027097.1
XM_005903505.2 **3/1** **4/1** **8/1**	PREDICTED: Bos mutus insulin (LOC102274400), mRNA	87.8	87.8	100%	2e-14	90%	XM_005903505.2

The following *three Sequences* have been identified by Blast research carried out on **Sequence n° 3/1**:

8 **4/1** CP027087.1	Bos mutus isolate yakQH1 chromosome 19	39.2	39.2	33%	9.5	100%	CP027087.1
12 XM_014476435.1	PREDICTED: Bos mutus phospholipid scramblase 3 (PLSCR3), transcript variant X2, mRNA	39.2	39.2	33%	9.5	100%	XM_014476435.1
13 XM_005889943.2	PREDICTED: Bos mutus phospholipid scramblase 3 (PLSCR3), transcript variant X1, mRNA	39.2	39.2	33%	9.5	100%	XM_005889943.2

The following *two Sequences* have been identified by Blast research carried out on **Sequence n° 4/1**:

6 CP027084.1	Bos mutus isolate yakQH1 chromosome 16	41.0	41.0	42%	2.6	93%	CP027084.1
19 **3/1** CP027087.1	Bos mutus isolate yakQH1 chromosome 19	40.1	40.1	46%	9.0	90%	CP027087.1

This last *Sequence* was identified by Blast research carried out on **Sequence n ° 8/1**:

2 CP027081.1	Bos mutus isolate yakQH1 chromosome 13	41.9	41.9	39%	2.6	96%	CP027081.1

2) Cottoperca Gobio:

The following *two Sequences* have been identified by Blast research carried out on Sequence of **Insulin Chain A**:

LR131921.1 **4/1 6/1 7/1** **16/1 18/1 19/1**	Cottoperca gobio genome assembly, chromosome: 14	55.4	55.4	100%	1e-04	81%	LR131921.1
LR131917.1 **4/1 6/1 7/1** **16/1 18/1 19/1**	Cottoperca gobio genome assembly, chromosome: 10	46.4	46.4	100%	0.061	78%	LR131917.1

The following *Sequence* was identified by Blast research carried out on **Sequence n ° 4/1**:

25 **6/1** LR131937.1	Cottoperca gobio genome assembly, chromosome: 7	39.2	39.2	41%	9.0	92%	LR131937.1

The following *Sequence* was identified by Blast research carried out on **Sequence n ° 6/1**:

9 **4/1** LR131937.1	Cottoperca gobio genome assembly, chromosome: 7	42.8	42.8	52%	0.77	88%	LR131937.1

The following *Sequence* was identified by Blast research carried out on **Sequence n ° 7/1**:

1 LR131921.1	Cottoperca gobio genome assembly, chromosome: 14	39.2	39.2	41%	9.5	92%	LR131921.1

The following *Sequence* was identified by Blast research carried out on **Sequence n ° 16/1**:

4 LR131938.1	Cottoperca gobio genome assembly, chromosome: 8	41.0	41.0	58%	2.7	84%	LR131938.1

The following *Sequence* was identified by Blast research carried out on **Sequence n ° 18/1**:

5 LR131932.1	Cottoperca gobio genome assembly, chromosome: 24	39.2	39.2	42%	9.5	93%	LR131932.1

The following *Sequence* was identified by Blast research carried out on **Sequence n ° 19/1**:

1 LR131921.1	Cottoperca gobio genome assembly, chromosome: 14	39.2	39.2	41%	9.5	92%	LR131921.1

Before concluding, it is worth mentioning one last consideration.
From the observation of the **order of presentation** of the significant alignments identified by Blast research carried out on Sequence of **Insulin Chain A**, it is clear that this **order** often concerns the **same** ***organisms***. Furthermore, this **order** is also **similar to the order** of several significant alignments identified by Blast research carried out on **19 new generated Sequences**.
Here, we then report only an example, leaving to other researchers the onus to find other similar examples.

The following *five Sequences*, selected according to the **order of presentation**, have been identified by Blast research carried out on **Insulin Chain A**:

XM_005351571.2 **1/1**	PREDICTED: Microtus ochrogaster insulin (Ins), mRNA	96.9	96.9	100%	4e-17	94%	XM_005351571.2
XM_008160271.2	PREDICTED: Eptesicus fuscus insulin (LOC103303257), mRNA	96.9	96.9	100%	4e-17	94%	XM_008160271.2
XM_028118258.1 **1/1**	PREDICTED: Eumetopias jubatus insulin (LOC114220406), mRNA	96.9	96.9	100%	4e-17	94%	XM_028118258.1
XM_027579931.1 **1/1**	PREDICTED: Zalophus californianus insulin (INS), mRNA	96.9	96.9	100%	4e-17	94%	XM_027579931.1
XM_025879485.1 **1/1**	PREDICTED: Callorhinus ursinus insulin (LOC112829807), mRNA	96.9	96.9	100%	4e-17	94%	XM_025879485.1

The scheme presented below refers to the order of presentation of some alignments of **Sequence n ° 1/1**.

As it can be seen, **four** out of these **five** selected Sequences refer to the **same** *organisms* and are placed in the **same order of presentation** as those of **Insulin Chain A Sequence**:

6 XM_026789982.1	PREDICTED: Microtus ochrogaster pecanex 2 (Pcnx2), transcript variant X2, mRNA	40.1	40.1	49%	9.5	88%	XM_026789982.1
7 XM_013345975.2	PREDICTED: Microtus ochrogaster pecanex 2 (Pcnx2), transcript variant X1, mRNA	40.1	40.1	49%	9.5	88%	XM_013345975.2
8 XM_028095345.1	PREDICTED: Eumetopias jubatus TNFRSF1A associated via death domain (TRADD), mRNA	40.1	40.1	41%	9.5	93%	XM_028095345.1
9 XM_027618249.1	PREDICTED: Zalophus californianus UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 9 (LOC113935781), transcript variant X5, mRNA	40.1	40.1	41%	9.5	93%	XM_027618249.1
10 XM_027618248.1	PREDICTED: Zalophus californianus UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 9 (LOC113935781), transcript variant X4, mRNA	40.1	40.1	41%	9.5	93%	XM_027618248.1
11 XM_025888785.1	PREDICTED: Callorhinus ursinus TNFRSF1A associated via death domain (TRADD), mRNA	40.1	40.1	41%	9.5	93%	XM_025888785.1

The relevance of this observation is clear if we consider that **Insulin Chain A** has in common with **Sequence n° 1/1** a **very low** percentage of Bases, that is **22.22%** (14 Bases).

1.42 CLARIFICATIONS AND INTEGRATIONS RELATED TO THE ANALYSIS OF THE RESULTS DISCUSSES IN CHAPTER I° FIRST PART

Before completing this chapter, it is necessary to clarify some aspects related to the analysis of the results discusses in Chapter I° First Part, a chapter in which, out of the **19 new generated Sequences**, only **Sequence n ° 1/1** was analyzed.

The results of **BLAST** research on **Sequence n°1/1** have pointed out significant alignments with the DNA (or RNA) of different *organisms*, including some species of **Pseudomonas** bacteria and the nematode **Heligmosomoides polygyrus**.

It is beyond the current scope of the paper to put forward further speculations and other bibliographical research on the relationship between these **two** of organisms species and *insulin* (those interested in our conclusions are invited to read in full Chapter I° First Part); however, we believe that some clarificationsare necessary.

Regarding the nematode **Heligmosomoides polygyrus**, unfortunately, for reasons that are not known, researches related to its significant alignments were removed from the National Center for Biotechnology Information (NCBI) archive (see pages 40 and 191).

We can only add, to what has already been said in Chapter I° First Part, that also **Sequence n°12/1** underscores significant alignments with **Heligmosomoides polygyrus** (see page 191).

On the contrary, regarding the **Pseudomonas** bacterium, some additions to the conclusions of Chapter I° First Part appear to be useful.

In Chapter I° First Part, the parameters set for BLAST research, carried out on **Insulin Chain A sequence**, have considered only the first **100** (Hitlist size ***100***) significant alignments.

Differently, in new BLAST researches carried out in this Chapter, significant alignments have been extended to**1000** (Hitlist size ***1000***).

From new Blast researches, it has emerged that **849 sequences** highlight **significant alignments** with **Insulin Chain A**.

Among these significant alignments, **four** of them, refer to the **Pseudomonas bacterium**.

At the time of the writing of the Chapter I° First Part we were not aware of such information. Hence, we speculated on the possible relationships between **Pseudomonas** bacterium, the features of **Sequence n° 1/1** (from which were identified the significant alignments with **Pseudomonas**) and **Insulin**.

Today we know that, besides **Sequence n ° 1/1**, also **Sequence n ° 18/1** shows significant alignments with **Pseudomonas**.

Furthermore, one of the two significant alignments of **Sequence n ° 18/1** (Select seq CP025263.1, *Pseudomonas sp. S09G 359 chromosome*) is **identical** to the same Sequence of one out of the **four** significant alignments of **Insulin Chain A** with **Pseudomonas**.

In light of this new evidence, it appears pivotal to underscore that, out of the **four** significant alignments of **Insulin Chain A** with **Pseudomonas**, **two** of them (one of which is that in common with **Sequence n°18/1**) are referred to *bioprojects* which have the following goals:

1) to identify gene clusters among pseudomonads whose products inhibit human pathogens, not only for the treatment of **Cystic Fibrosis** patients but also for individuals infected with **MDR** (Select seq CP025263.1; BioProject: PRJNA419203);

2) to identify biosynthetic gene clusters within environmental bacteria whose products have been shown to inhibit the growth of these multi-drug resistant pathogens derived from **cystic fibrosis** (Select seq: CP026880.1; BioProject: PRJNA433821).

Here are reported **two** out of the **four** significant alignments of **Insulin Chain A** with **Pseudomonas**:

7 CP025263.1	Pseudomonas sp. S09G 359 chromosome	41.9	41.9	41%	2.6	96%	CP025263.1
CP026880.1 **1/1** **18/1**	Pseudomonas sp. LH1G9 chromosome, complete genome	41.9	41.9	41%	2.6	96%	CP026880.1

The following *Sequence* is instead referred to **one** of the **two** significant alignments of **Sequence n° 18/1** with **Pseudomonas**:

7 CP025263.1	Pseudomonas sp. S09G 359 chromosome	41.9	41.9	41%	2.6	96%	CP025263.1

It is also worth noting that **two** out of the **six** significant alignments of **Sequence n° 1/1** (see page 37 and following) with **Pseudomonas** are referred to *bioprojects* that have as objective that of using Pseudomonads to facilitate **antibiotic discovery** (Select seq: CP026674.1 - BioProject: PRJNA433544 ; Select seq: CP026676.1 - BioProject: PRJNA433544).

Here, **two** of the **six** significant alignments of **Sequence n° 1/1** with **Pseudomonas** are reported:

33 CP026674.1	Pseudomonas sp. SWI44 chromosome, complete genome	39.2	39.2	57%	9.5	83%	CP026674.1
34 CP026676.1	Pseudomonas sp. SWI6 chromosome, complete genome	39.2	39.2	57%	9.5	83%	CP026676.1

In conclusion, the new results obtained from the significant alignments related to **Pseudomonas** would seem to reinforce the hypothesis elaborated in Chapter I° First Part (that we were capable of deriving also thanks to an articulated **bibliographic research**): that is to say, the hypothesis according to which **Insulin** (and, therefore, also **Insulin Chain A**) is in involved in different ways with some characteristics of **Pseudomonas** bacteria (such a data was at the time discovered through Blast research carried out on **Sequence n°1/1** and it has later been corroborated by Blast research carried out on **Sequence n°18/1** and **Sequence of Insulin Chain A**).
In particolar, the reader is deferred to the considerations elaborated in Chapter I First Part, above all in regard to the possible implications of Insulin in the *Cystic Fibrosis* and in *Pseudomonas infections*.

1.43 CONCLUSIONS

Overall, the probability that such results can be ascribed to pure chances are extremely low (indeed, there was no need to carry out specific analyses for they would just be redundant and not necessary).

The results confirm the hypothesis of the presence of many *organisms* in common among the significant alignments of the **19 new Sequences** generated and those of **Insulin Chain A**.
Moreover, unexpectedly, as we saw in paragraph 1.41, the presence of **three identical Sequences** was also observed among the significant alignments of the **19 new Sequences generated** and those of **Insulin Chain A**.
It should be noted that the percentage of Bases in common between **Insulin Chain A** and the **identical identified Sequences** did not exceed **22.22%** (14 Bases). It is therefore a matter of Sequences with almost totally different Bases.

The results also confirm the hypothesis of the presence of many *organisms* in **common** among the significant alignments of the **19 new generated Sequences**.
The presence of **eleven identical Sequences** (corresponding to nine different organisms) were also observed among the significant alignments of the **19 new Sequences generated**.
Although the latter result could be partly predictable for those Sequences that have a considerable percentage (between **71.43** and **89.89%**) of Bases in common, it is certainly much less predictable when the percentage of Bases in common is very low (between **15.87** and **25.40%**).

Moreover, the hypothesis according to which, every *organism*, in which a significant alignment with the **19 new produced sequences** has been found, should be connected, indirectly or directly, with the **original sequence** (**Insulin Chain A**), should be delved into by interested researchers, and in particolar, by those researchers who have studied, to different extent, *organisms* e *Sequences* that significant alignments have identified.

In conclusion, the analysis (through the **T.T.E.S.**) of the *original Sequence* - based on **19** of its "non manifest trends" (the ***Trend n°1, n°2…n°19***) - and the creation of **19** *new DNA Sequences* (the **Sequences n°1/1, n°2/1,…n°19/1**) from the ***19 Trend*** of the *original Sequence*, deserves further *specific studies and bibliographical insights*.

The **comparative analysis** of all the *sequences* and "*organisms*" *identified by Blast research carried out on Insulin Chain A and by Blast research carried out on 19 new sequences* paves the way for a new perspective on genetic research and its uncountable applications.

END 1st CHAPTER (Second Part)

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