The Genetic code: Section I

A 24 codon table and the "exponent 2/3 series (ES)

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A 5-dimensional Numeral Series behind the Genetic Code

Introduction

DNA is built of 4 bases G-C-T-A. When DNA is copied to RNA, the T-base is replaced by the U-base. Different triplets as "codons" of these 4 bases G-C-U-A in RNA-chains encode for the 20 "classical" amino acids that united in long strings make up all proteins. The coding system is nearly universal throughout biological life.

Why this coding system? It's a fundamental question. A suggested view is presented in <u>file 0</u> (right column) to start with.

Since the construction of DNA was discovered in 1950th, one big, old question has been if the distribution of codons to amino acids are "a frozen hazard" or may reveal some hidden logic. Hundreds of articles have been published on the subject in **PubMed** during decades with different approaches and theories (one **review here** and a selection of such articles besides references in the text is found in **References**), but there is still no commonly accepted answer to the question.

The 5-dimensional model, <u>shortly **presented on the site here**</u>, led to the thought that if it had any relevance, it could appear in some form on superposed levels, not least in a "main stream" development towards life and the genetic code. Here results from this research.

As said above: In spite of an immense lot of research and new knowledge during last decades there is no consensus on how to interpret the genetic code and the system for protein synthesis but a lot of quite different hypothetical aspects and approaches. To really get the faintest idea or intuitive guess on the development of a cell - and life, it's proposed here as necessary to start from general assumptions as the following ones, some of them surely shared by many, others more controversial.

a. The enormous complexity of the cell and its metabolism must be understood as an **internal differentiation**, through opposite forces, which implies starting from some kind of (partly) enclosed "unit", defined by a centre and an substantiated "anti-center" as a partly penetrable circumference. (This could perhaps in a first stage be some kind of metal shell - analogous to later Me-skeletons of unicellular organisms; metals representing anticenter in relation to non-metals, the main structure-building elements of life.)

b. Next, about **forces**, it must be assumed that all forces recognized at the level of physics (probably redefined in the future) appear <u>on the biochemical level</u> too, in one or another form, not just the electromagnetic one. (Naturally also aspects from quantum mechanics.)

c. Further, about **dimensional conceptions** on the biochemical level: To get the slightest intuitive comprehension of the biochemical complexity, it seems quite necessary to extend the dimensional analysis to higher dimension degrees (d-degrees). It would imply that aspects on structure in simple 3D-terms were integrated with other biochemical gradients of differentkinds - binding and polarizing ones - as 4-dimensional vector fields, into some unified, multidimensional analysis.

It's surely also time to leave the concept of dimensions defined only in terms of "independent" variables (already questioned in physics) and adopt a view where dimensions are deeply integrated and interdependent in dynamical processes.

d. The character of the genetic code as **an information system** should be closer analysed: Is it a reference system between connected complementary forms, a memory system and / or a parallel development of the same structural kind on different levels, where underlying level becomes the "memory" ... or is seen as "representing" the superposed one - or the inverse. Perhaps it's only part in a more general system of references connected with concepts as inversions, resonances, conjugates, complementary units - and relations between different, dependent d-degrees?

e. Then, about **mass**, mostly disregarded when the genetic code is discussed. Mass is a property not yet understood by physicists. That shouldn't be taken as a reason for regarding mass as an unimportant property for the emergence of life. Sooner, it would be extremely astonishing if not all atomic properties played essential roles at the creation.

The *main objection* to reevaluate mass is surely such experiences which seem to show that some unusual isotopes don't change the studied metabolism in an established cell milieu of today.

Smaller changes of isotopes may be possible to neglect in properties as structures and volumes of molecules, (even if they theoretically should influence gradients in mass fields, if this term is allowed),

However, does such facts necessarily contradict a presumption that mass of common isotopes had a decisive importance at first configurations of elementary biomolecules?

It is reasonable to assume that mass is a property of higher d-degree, representing a deeper level, than charge. (The physicists' application of the gravity concept into microcosm and quantum mechanics could be mentioned here.) If so, it would agree with dimensional views that the deeper mass level was decisive for elementary structures, while the more superficial level of charge, expressed in electron shells, becomes the relevant level in processes, in metabolism as characterized by more of released kinetic energy.

Further, in research to find shortened ways to predict destinations and functions of proteins, mass is used as one factor besides polarity with obviously good results [1].

About counting on ordinary isotopes, the overwhelmingly most common ones, it could also be reason for reminding of the carbon-nitrogen cycle in the sun, where it is the 3 alpha carbon and 4 alpha oxygen that make up the start and end of the fusion: 4 protons (H) giving an alpha-particles (4 He).

Some more about this matter in concluding remarks.

f. Looking for an eventual **guiding principle** behind emergence of the code, where could it be found? If it isn't regarded as an invention from heaven, it's unavoidable to look for the guiding principle somewhere else, most naturally expressed in the singular atoms themselves.

Hence, we could suspect that the atoms themselves - with their underlying relations in the fusion processes - should serve as microcodes for cellular life and the principles guiding it. Those principles should probably be found in their internal configurations, also deeper in their nuclei and on a higher level in their spectral lines?

g. Finally, about **numbers** in general, it's hard to see why numeral series as such should be regarded as special exceptions when appearing in Nature. Different elements are regarded as characterized by numbers of units (u) and on a molecular level by protons equivalent with electrons and their relation to the "octet rule". Since all matter - as well as radiation - is quantified, it shouldn't be too strange to find underlying arithmetical relations behind the structuring principles in the genetic code.

Most scientists in the field may perhaps feel inconvenient with this idea, regarding it too abstract for any practical work. However, since pure mathematics has led to deeper understanding of nature on the level of physics and astronomy, why shouldn't it in biochemistry?

In fact, such number series could be compared with structure drawings for buildings, revealing mutual relations between later, stepwise materialized structures. Or perhaps more resemble the principal scheme for the working processes, the logistics? Just the way of Nature to organize itself.

After all, the numeral series behind the periodic system didn't "exist" - in any recognizable form - in the first materialized Universe after Big Bang.

Rather few contributions to interpretation of the genetic code have paid attention to number regularities as it seems (among references chiefly [2 and 3] but also in one aspect [4]). Recently, according to reference [5], it has been shown that the human genome as a whole single strand is of a fractal kind regarding frequency of codons.

Since long ago it's observed that features of Fibonacci number series and the golden section appear in Nature. (Below it's shown that such series show up also in mass analysis of the genetic code.)

There are more general and recognized numeral series: One very simple example is the valences of the central structuring elements in the genetic code: P - C - N - O - H with valences 5 - 4 - 3 - 2 - 1. (A suggestion here is that numbers also could refer to d-degrees or to dimensional steps, presumably as fractals, with the same patterns reappearing on different levels of evolution.)

Another essential example is the $2x^2$ -series (x = 5 - 0), 50 - 32 - 18 - 8 - 2, behind the <u>periodic system</u>, with intervals defining number of electrons in the different orbitals, the orbitals p, d, f also occupying increasing d-degrees in their orientation. It's natural to assume that the arrangement of electron shells have correspondences in the atomic nuclei, responsible for most of the atomic mass.

A third example is the formulas for spectral lines of hydrogen, where differences between inverted squares of integers as n = 1, 2, 3, 4 and m = 2,3,4, 3,4,5 etc. times a constant give the wavelengths.

Quotients between wavelengths (n = 2, m = 5, 4, 3) in the Balmer series times 10^2 happen to give the mass numbers of U- and A-bases too (112 and 135) and approximately the G-base (151,2), which could awake some suspicions...* (Quotients as a kind of phase waves? Alleged not to carry any information!)

Fig 1-1: From Balmer series for spectral lines of hydrogen:

a. 1/4 - 1/25 = 0.21. **b.** 1/4 - 1/16 = 0.1875 **c.** 1/4 - 1/9 = 0.13889.

a/b x 100 = 112 = U-base (mass number) b/c x 100 = 135 = A-base " a/c x 100 = 151,2. 151 = G-base "

(AUG = starting codon at protein synthesis. UAG = usually Stop-codon. C-base a secondary development from the U-base.)

(C-base eventually later developed to give two pairs? Last term in c. = 1/9, x 1000, = 111,1. C-base = 111)

A background model

The actual background behind this research was a very elementary 5-dimensional model or conceptual structure, suggested by the author for interpretations in theoretical physics.

(See <u>Physics.</u>)

Shortly: the model, with some redefinitions of the concept dimension and the 4th ddegree implies a development from a 5-dimnsional "entirety" through polarization steps towards lower degrees $5 \rightarrow 4 \rightarrow >3...$ with debranched degrees being translated to external motions or meeting "the other way around", see figure below. A reason to mention the background model, however primitive it may be, and include the figure, is that some of the found arithmetical patterns below reflect features of this model.

Fig 1.2 A dimension chain:



Each d-degree is supposed to be defined by the complementary poles or partial structures through polarization of the next higher one. First polarization into centre - anti-center (0 - 00) is regarded as defining d-degree 4 as vector fields, divergent / convergent, these fields through polarization transformed into 3D etc. Mass (with Space as complementary "pole"), is assumed to be defined in d-degree step 3-2, as a 3-dimensional property in its relation to Charge when this is analysed as 2-dimensional. (Level of analysis optional.) The 5th d-degree may ultimately be regarded as transformed into pure motions or kinetic energy through polarization of 1-dimensional structures in a step 1 @ 0/00, the "d-degree 0/00 of motions".

The thought was that such a model, if of any value, also should reveal itself in some form in sciences of superposed levels, not least in a "main stream" development towards life and the genetic code. This with the general hypothesis that similar patterns or principles reappear on all superposed levels of higher complexity.

0. Amino acids and codon bases. Why this coding system ?

A main question:

Why genes, why this coding system between RNA and proteins?

It's suggested here that the relation between codon triplets of bases and amino acids could be illustrated (note just illustrated) as in the table 0 below. Other classes of substances are marked as well in the pattern, i. e.. their main structural properties, showing on their close relationships.



Table 0: A hexagonal pattern as illustrating structural classes of substances

The hexagonal pattern - as in graphite - can be regarded either as a pattern of hexagons, sharing edges with one another - or as consisting of atomic points, centers with 3 radii.

Virtual 4th valence pointing upwards from the plane, as towards next layer in a crashed or sliced diamond.

In this illustration the relation **bases - amino acids** shows up to be only a question of complementary "aspects", a fundamental one on the whole pattern.

One property of these aspects is the polarity between circular and radial structures. Another is the center - anticenter polarity with regard to the carbon atoms: in amino acids a central C-atom of tetrahedrons, in hexagon rings decentralized, anti-centric atoms.

A third, also fundamental, aspect is the physical polarity between mass (atomic structure) versus space as antimatter, which may appear when regarding the whole pattern as structures of **fatty acids**. It means "semipermeable" membranes, another essential condition for life. At a certain temperature they also form hexagonal patterns (*Lindahl et al 1967*).

The mentioned polarities correspond to the complementary "poles" or "partial structures" in the proposed, dimensional background model and follows from polarizations of dimension degrees 5 - 4 - 3.

Codon bases - amino acids:

Each "3-radii-center" gets defined by 3 hexagons - as do amino acids through a codon triplet.

Each coding base gets synthesized to an essential degree of amino acids, the simplest one, Gly, being a kind of displaced center, an intermediate bridge between the two rings in purine bases G and A from Inosine (Hypoxantine). The amino acid Asp gives about half the rings of pyrimidine bases U and C.

(A hexagon ring of the bases include 4 C, 2 N, corresponding to 2 N-C-C-parts in bound backbone chains of amino acids.)

How could anything that only would be two different aspects, get translated to existing processes in a cell?

If departing from the illustration in the figure above, it seems necessary to imagine that the two opposite "aspects" on such a pattern - in some way* - get polarized into separate types of units, substantiated and saturated to structural classes of molecules in interaction with present substituents as N, O, H (nitrogen, oxygen and hydrogen). Further that the long range of intricate processes develops "the other way around" to recombine to the sense of a "reference system". This within - or on? - demarcating layers of fatty acids.

* The idea of a crashed diamond leads to the thought of different substances created from the different pathways and diffraction of light in the crystal.

Resevations:

The figure doesn't include pentagon rings, e.g. the extra three edges in purine bases or ribose molecules, not differences in angles of valences etc. With the figure above it's not the intention to assert that this was 'the way it happened'.

Yet, it may illustrate the close relations between substances and the underlying two aspects on the whole structure: a pattern of rings or a pattern of centers with 3 radii - and a virtual 4th for differentiated growth of side chains (R) of ams?

Abbreviations - ways of writing

Ams = amino acids (ama = amino acid) $00 = infinity sign(\infty).$

20 ams --> 24 codons: i.e. 4 ams with double codons: Arg 1, 2: codons CG + AG-A/G; Ser 1, 2: codons UC + AG-U/C; Leu 1, 2: codons CU + UU-A/G; and Ileu 1, 2: codons AU-A +AU-U/C, only differing in third base

3rd bases in the codons:

Codons with where A or G in 3rd place makes no difference, written A/G, where Uor C in 3rd position makes no difference = U/C.

Parts of an amino acid:

R = R-chain(s) = the "radical chain" of amino acids = "side" chains

= the differing part of ams not taking part in the peptide binding.

B = B-chain(s) = "ground chain" =

= the similar parts of ams which through condensation combines to peptide chains.

R | B: H2N-CH-COOH

Sums:

All sums refer to mass number A where not anything else is mentioned. They refer to R-chains where not anything else is denounced.

Codon groups, way of writing:

G1 - C1 - U1 - A1 = ams-groups coded by G-C-U-A respectively as first base. G2 - C2 - U2 - A2 = " " as second base.

Codon types, used denominations:

"Cross-codons" = GU-UG-AC-CA "Form-codons" = GA-UC-AG-CU "Pair-codons" = GG-UU-AA-CC "RNA-codons" = GC-UA-AU-CG 6 ams in each group.

 $\wedge =$ sign for inversion of numbers

A-numbers for the RNA-DNA-bases with +1 for the bond to ribose:

G = 151, A = 135, U = 112, C = 111...sum 509, + T 126 = 635.

Table 1: Codons and A-, N-, Z-numderzs of 20 + 4 amino acids

1st base	2nd base	Ans	N	z	A.	Å	z	N	Ans	lst base	2n d base
Gl	10 G 2	Gly	- -	\mathbf{T}	3 <u>1</u>	12	1	3. 2 3	Gþ	G	G1
	11 0 2	Ala.	6	9	15	101	563	45	årgl	$\mathbb{S}^{\mathbb{C}}$	
	U	Val	18	25	43	130	69	61	Trp	U	
	A.	٩٤k	28	31	39	47	25	22	Cys	U	
	A.	Glu	34	39	73	31	17	14	Ser2	Å	
						101	56	45	Are	Å	
Sum	5		86	105	191	411	224	187		6	Sum
C1	G	Arg l	45	56	101	15	9	6	ala.	G°	C2
	$ \mathbf{C} $	Рго	18	-24	42	42	24	18	Рго	\mathbf{C}	
	$\langle \mathbf{U} \rangle$	Leul	24	33	57	31	17	14	Serl	$\langle U \rangle$	
	$\mathbb{E}^{\mathbb{E}}$	Gfa	33	39	72	45	25	20	The	Å	
	$\mathbb{E}^{\mathbb{Z}}$	Ηø	38	-43	81						
Sum	ିରେ		158	195	353	133	7 5	- 58		4	
G1+C1	10		244	300	\$44	\$44	299	245		10	G2+C2
U 1	G	Qря	22	25	47	43	25	18	Yak	G	U2
	\boldsymbol{G}	Trp	61	69	130	S 7	33	24	Leul	C	
	C	Serl	14	17	31	T	33	24	Leu2	U	
	U	Leu2	24	33	57	91	49	42	Phe	U	
	IJ	Phe	42	49	91	ទា	33	24	Iel	A.	
	A .	Tyr	50	57	107	ទា	33	24	Ile2*	£*	
						75	41	34	Meth	Å	
Sum	6		213	250	463	437	247	190		7	
41	G	Ser2	14	17	31	Ð	31	28	جه	G	42
	G	Årg2	45	56	101	73	39	34	Glu	G	
	C	Thr	20	25	45	τ_2	39	33	Gln	\mathcal{C}	
	U	Ilel	24	33	57	81	43	38	His	C	
	U	Ile2*	24	33	57	107	57	50	Tyr	U	
	U	Meth	34	41	75	3	31	27	الك	¥	
	e de la	Å\$n	27	31	58	\mathcal{R}	42	31	Lys	Å	
	्रम	Lys	31	42	73	111100					
Sum	8		219	278	497	523	282	241		3	
01+A1	14		.432	528	960	960	529	431		14	U2+A2

*Ile, AU-codon, only differing in **type** of 3rd base

2. Table on amino acids and codons. - First observations

The investigation started in the 1980th - without prejudices - with a table of 20 + 4 codons (Table I) with and A-, N- and Z-numbers of side-chains (R) of the coded amino acids (ams), 4 ams having two different codons. Most common isotopes were used.

Hence, codons where the choice of purine bases U and C in 3rd position or of pyrimidine bases A and G in 3rd position makes no difference was counted as one and the same, as when 3rd base makes no difference at all (called "2-base-coded", generally in the literature called "degenerated"). The 4 ams with double codons are Arg CG + AG-A/G, Ser UC + AG-U/C, Leu CU + UU-A/G and Ileu AU-U/C + AUA, only differing in 3rd base *type*.

In these files all numbers will refer to atomic mass (nucleon number) and to side-chains (R) of ams where nothing else is mentioned.

First observations:

First to notice is that the mass sums of the two main groups with G+C-codons and U+A-codons become the same in 1st and 2nd base order, 544 and 960.

It implies that mass sums of ams with mixed codons changing position between the groups are the same, 385 (Table 2). These groups showed astonishing regularities, which seemed to support the hypothesis that mass distribution of ams on different codons wasn't a random one. Note the approximately equal sums horizontally and vertically, Table 2:

385			38	85		770		
17	5	2	10	2	08	1	77	6. D
GU	Val	CU	Leu	UC	Ser1	AC	Thr	$\rightarrow 176$
GA	Asp	CA	Gln	UG	Cys	AG	Ser2	$\rightarrow 209$
GA	Glu	CA	His	UG	Trp	AG	Arg	$\rightarrow 385$

 Table 2: Mixed codons 12 amino acids, sum 385:

The table is closer studied in file The two 12-groups of ams.

It led to a division of the 24 codons in 2 main groups of 12 ams, the other = 2 times 367, (Table 3), which doesn't show the same regularity as the other:

Table 3: Non-mixed codons. 12 amino acids, sum 734:

	414	320		
GG 1	CC 42	UU 148	AA 131	$\rightarrow 322$
GC 15	CG 101	UA 107	AU 189	$\rightarrow 412$
16	143	255	320	
1	59	575		734

This way of counting and organizing codons seems deviating from most other research. We get 4 subgroups of codons, here called Form-, Cross-, Pair- and RNA-codons:

Form-coded: GA, AG, UC, CU, 6 ams, sum 352

Cross-coded: GU, UG, CA, AC, 6 ams, sum $418...2 \times 385 = 770$ These two in Table 2.

Pair-coded: GG, CC, UU, AA, 6 ams, sum 322

RNA-coded: GC, CG, UA, AU, 6 ams, sum $412...2 \times 367 = 734$ These two in Table 4.

Note in Table 3: G1 + A1, 175 + 177 = 352, give the same mass as the Form-coded ams, U1 + C1, 208 + 210 = 418, give the same mass as the Cross-coded ams.

Before going on with the analysis, two annotations:

Survey of totals:

With mass in unbound backbone chains (B, B-chains) à 74 A, - 1 in the four ams Arg1 and 2, Lys and Pro. and mass 56 in bound ams, this gives following survey of totals:

24 ams: R: 1504, B unbound 1772, sum 3276 A, 24 ams: R: 1504, B bound 1344, sum 2848 A. N-Z: R: 828 Z, 676 N, R+B: 1516 N, 1760 Z, unbound ams.

Simple variations of the elementary number chain 5-4-3-2-1-0:

There are some simple variations of the elementary number chain (5-4-3-2-1-0), closer dealt with in files in section II, files 12-16, that more or less approximately give the division between some main codon groups of ams, G+C and U+A, but also other more detailed ones.

Hypothetically such simpler chains on integers $5 \rightarrow 0$ with exponents 4, 1, 3, 2 could underlie the more developed and differentiated chain in this section, precede this in a perhaps "inflationary" evolution of the code or represent underlying levels? Here only a couple of examples:

Reading the simple chain as triplets 543+432+321+210 gives 543 (G-C-group -1, U-A-group 960 +3,

Fig 2-1: The triplet series 543 - 432 etc.

1.4.94

$$= \frac{543}{G+C} - \frac{432 - 321 - 210}{963 = U + A},$$

-1 +3 Sum 1506 = total of 20 + 4 ams R, +2.

With exponent 4 the main division 544 - 960 (+2) derives from first three numbers 5^4 - 4^4 - 3^4 plus/minus 3rd number 81: G-C-group 544 = 625 - 81, U-A-group 960 (+2) = 625 + 256 + 81.

With exponent 2 in the $2x^2$ -chain behind the periodic system, times a factor 16, several different codon-groups of ams appear (+/-1), the main division showed in figure. 2-2:

Fig. 2-2: Relations to $2x^2$ -series, 34-26-60 times a factor 16:

$$50 - 32 - 18 - 8 - 2 - 0$$

$$\uparrow 26 \uparrow 26 \times 16 = 960 = U+A-coded ams R$$

$$\uparrow 26 \uparrow 26 \times 16 = 416 = difference$$

$$\uparrow 34 \qquad 34 \times 16 = 544 = G+C-coded ams R$$

Total sum of the chain, 110, times 16 = 1760, the total Z of the 24 ams (R+B). See further file "Simpler number chains" about the $2x^2$ -chain.

3. The exponent 2/3 number series (ES)

Mass of codon grouped amino acids

ES-chain and main codon domains of ams:

The elementary number series 5 to 0 with exponent 2/3 times 10^2 shows up to highly correlate with mass distribution on codon domains of ams, both the division on codons G+C — U+A (544 and 960), the 12-grouos of ams from tables 2 and 3 (770 and 734), codon type pairs as G+A — C+U and individual codon groups, especially the G- and C-groups.

<u>1. Total mass and codon groups G+C and U+A:</u>

The series $5^{2/3} - 4^{2/3} - 3^{2/3} - 2^{2/3} - 1^{2/3} - 0$, times 100, gives the abbreviated numbers 292 - 252 - 208 - 159 - 100 - 0. Marking these numbers 5' - 4' etc. we have that 2 times 5' + 4' + 3' give mass sum of the 24 ams R = 2 x 752.

Fig 3-1: The ES-chain:

	52/3	$-4^{2/3}$	$-3^{2/3}$	$-2^{2/3}$	-12/3 -	- 0	$x 10^{2}$
=	292,4.	252,0.	208,0.	158,7.	100		
abridged:	292	252	208	159	100		
Sum:		752		259)		
	54	14	$x_2 = 416$				

2 x 752 = 1504, total sum of 24 ams R.

544 = G+C-coded ams = 752 - 208 544 + 416 = 960 = U+A-coded ams = 752 + 208

To repeat the way of writing:

G1, C2, etc. refer to mass sums of side-chains (R) of ams coded by G as 1st base and those coded by C as 2nd base respectively etc.

G+C or U+A refers to the sums of coded ams (R), equal in 1st and 2nd base order.

G + C = 292 + 252 = 544 U + A = 292 + 252 + 2 x 208 = 960

<u>2. Number of ams</u>, correlating with the elementary numbers 5 - 4 - 3:

Fig 3-2: Number of ams:

Note: the relation with ams-groups: 5' - 4' = 292 - 252 = 40: $2 \times 5' = 584, -40 = 544 = G + C, 2 \times 5 \text{ ams}$ $2 \times (4' + 3') = 920, +40 = 960 = U + A, 2 \times 7 \text{ ams}$ The individual and pairs of codon groups are given through minus/plus lower numbers or intervals in the series, reminding of the principle view of debranched degrees meeting "the other way around" in <u>the background model</u>:

Fig 3-3: A dimension chain, the loop version of the model:



(For a very short description of the model, see <u>here</u>.)

3. Mixed and not-mixed codons, 12-groups 770 and 734:

The two 12-groups of ams presented in <u>tables 2 and 3</u> are given directly in a simple way, groups 544 and 208, -/+ 159 times 2:

Fig 3-4: The two 12-groups 770 and 734:



2 (544 - 159) = 770, Cross- and Formcoded ams 2 (208 + 159) = 734, Pair- and RNA-coded ams

U- and A-groups in 734-group = 2 x 208 + 159 = 575, G- and C-groups in 734-group = 159

(575 also = 3' + 2' + 1' = 467, + interval 3' - 1' = 108. UU + AU + AA = 467 + 1, Tyr UA = 108 - 1.)

GG + GC + CC (Gly + Ala + Pro) = interval 59, -1,CG (Arg) = end interval 100, +1.

Arg can transform to Pro leaving its end-group CN3H5 = 59.

[In the background model the last step $1 \rightarrow 0$ is interpreted as a step from d-degree 1 into motions. It has been told that Arginine is especially rich in the tails of sperms. However, number 101 appears also in other contexts.]

See further details in file The two 12-groups of ams.

It may be added already here (see further file Mass division on atom kinds...)

Mass of C-atoms in 770-group = 444 = 544 - 100 Mass of C-atoms in 734-group = 516 = 416 + 100,

Cross- + RNA-codons: $ams = 418 + 412 = 830 = 2 \times 416$, -2 Form- + Pair-codons: ams = 352 + 322 = 674 = 2(544 - 208), +2 Adding bound B-chains to these codon *type* groups, we get sums approximately equivalent (~) with the division in R- and B-chains:

Cross	s RNA	Form	Pair	
418	412	352	322 R	
+ <u>336</u>	336	336	336 B	
754	748	688	658	
= 1	502	1346		
~ R	-2	$\sim B$	+2	

[In the sum of cross- plus pair-coded ams with R = 740, the close to equal division between U+G-codons and C+A-codons (the keto-/amino polarity) should be noted::

UU + GG + UG + GU = 370 - 1

CC + AA + CA + AC = 370 + 1 See Short files, 17.9, 3.

370 equivalent with 5 B-chins unbound à 74 A.

370 = 367 + 3, the other 2 codon-groups 2 x $382 = 2 \times 385 - 3$]

4. Purine - pyrimidine base pair groups, G+A and C+U:

Base pair group divided in purine and pyrimidine kinds are shown below. It should be noted that we can regard the whole chain included through number 934 as 2×467 :

Fig 3-5: *Base pair groups* C+U, G + A:

$$\frac{259}{2 \times 252} - \frac{208}{467} - \frac{159}{100} - \frac{100}{0}$$

A division of 5', number 544, gives the purine and pyrimidine codon pairs from G+C, U+A:

Or: G1 + A1 = **960 - 272** = 688 C1 + U1 = **544** + **272** = 816

Halving of 3', number 208, distributed inwards - "backwards" to 292 and 252 gives both a division on codon groups and on atom kinds, see **file 04**.

4b. Parents of he codon bases with mass 292 distributed to following numbers:

Number 292 $(5^{2/3} \times 10^2)$ is the sum of Orotate (156) and Hypoxanthine (136), the parents to the pyrimidine and purine bases U, C and G, A. Just a coincidence?

Transferred to following two numbers in the ES-chain, times 2, happen to give the codon domain sums of ams in 1st base order, curiously enough:

Fig 3-6:

$$292 - 252 - 208$$

$$\downarrow \rightarrow + 156 + 136
= 408 = 344$$

$$2 \times 408 = 816 = U1 + C1,$$

$$2 \times 344 = 688 = G1 + A1$$

Remains to explain how this rather remarkable, simple derivations of mass numbers could be interpreted in terms of biological processes.

5. Single code base groups:

G- and C-groups illustrate remarkably a similar -/+ operation of lower numbers in the chain:

Fig 3-7: *G-C-groups and numbers 100 - 159:*

$$5^{2/3} - 4^{2/3} - 5^{2/3} - 2^{2/3} - 1^{2/3} - 0 \times 10^{2}$$

$$\sim 292 \quad 252 \quad 208 \quad 159 \quad 100 \quad 0$$

$$|\langle -1 = 107, \text{Tyr UA} + 1 = 101, \text{Arg CG} \quad G1 = 292 - 101 = 101, \text{C21} = 292 - 159 = 133$$

$$C1 = 252 + 101 = 353. \quad G21 = 252 + 159 = 411$$
1) Note the changed order from 1st to 2nd base.

$$U22 = 544 - 107 = 437 \quad U1 = 252 + 208, +3$$

$$A22 = 416 + 107 = 523 \quad A1 = 208 + 292, -3$$
2) Or:
$$U2 = 544 - 208 = 336, +101, A2 = 416 + 208 = 624, -101$$

U1 and A1 groups are less clear in derivations from the ES-chain than the G-C-groups; an alternative view with "polarization" of 544 in +/- 272:

U1 = G1 (191) 1 + 272 = 463 A1 = C1 (353) + 416 - 272 = 497

U1 and A1 mass sums of ams may naturally be indirectly derived exactly though operations from G1+A-group 688, - G1, U1+C1-group 816, - C1.

Another way to write the derivations:

A1 = (5' + 4') - (3' - 2'), +2 = 497
U1 = (2 x 3') + (3' - 2'), -2 = 463
U2 = (5' + 4') - (3' - 1'), +1 = 437
A2 = $(2 \times 3') + (3' - 1'), -1 = 523$

About Tyr 107 and Arg 101: Since Tyr derives from Phe, UU-coded, we could eventually regard Tyr as an expression for the step U2 \rightarrow .A2. Arg, which gets its end-group from the G-base, eventually from an G1-code?)

In the same way A1 = 544 - 47, U1 = 416 + 47: 47 = mass of Cys R with UG-codon, as if from Meth AUG-codon - but Cys generally is regarded as derived from Ser.

With interval 3' - 1' -1 = 107 and 2' - 1' = 59 +1 (see below), the difference become 47.

(In the background model last step 1 to 0 represent the step to the d-degree of motions. Cf. that Arginine is said to be especially rich in the tails of sperms! However, number 101 appears also in other contexts.)

Interval 59 in step $2 \rightarrow 1$, -/+ 1 = 58 and 60, gives the difference between code-base groups in 1st and 2nd base order:

$$C2 = G1 - 58G2 = C1 + 58U1 = A2 - 60A1 = U2 + 60$$

(Interval 59 in step 2' —1' may be associated with main contributions from outside into the citrate cycle: acetyl(-Coa) + OH, 59 (60) in the step from oxaloacetate 132 to citrate 192. Corresponding step 4' \rightarrow > 3' in the ES-chain = 44 ~ CO2, the preceding contribution in the cycle, with pyruvate giving malate.

Notes.

Notes 1.Number 544

Number 544 may be regarded as divided in three ways: 292 - 252, 336 - 208 and in interval 544 - 367 = 177 and 367.

C2 = 177 - 44 (the 2nd interval 4' - 3', G2 = 367 + 44

All four 2nd base groups (-/+1) from the interval 44:

544 - 367, - 44 = 133 = C2-coded ams 208 + 159, + 44 = 411 = G2-coded ams 272 + 208, - 44 = 436 = U2-coded ams - 1 272 + 208, + 44 = 524 = A2-coded ams +1

Note 2. -/+ Tyr from C1 to U1 ?

 $C1 = 252 + 208 (= 460), -107 (\sim Tyr) = 353.$ $U1 = 252 + \frac{1}{2} \times 208 + \frac{107}{2} (\sim Tyr) = 463$

Note 3: G1-group 191 divided after 2nd base:

GG + GA = **133** = 5' - 2'; GU + GC = **58** = 2' - 1', -1.

Divisions within single base groups in 2nd base order:

In G2 + C2: 1st base G or A: sum of ams = 193, \sim G1 +2 (GG + AG = 133; GC + AC = 60.). 1st base U or C: sum of ams = 351, \sim C1 - 2 (CG + UG = 278; CC + UC = 73)

In U2 + A2:

1st base G2 or A2: sum of ams = **495**, ~ A**1** + **2**. (GU + AU = 232; GA + AA = 263.) 1st base C2 or U2: sum of ams = **465**, ~ U**1** + **2** (CU + CA = 210; UU + UA = 255.)

Number of ams in single base groups with odd number of ams:: Odd numbers of ams Even numbers of ams G1, 5 ams 2nd base G, A: 3 ams, 2nd base C, U: 2 ams. C1: 5 ams. 2nd base G, A: 3 ams, 2nd base C, U: 2 ams... division 3 -/2

U2: 7 ams: 1st base G, A: 4 ams, 1st base C, U: 3 ams

A2: 7 ams: 1st base G, A: 4 ams, 1st base C, U: 3 ams... division 4 - 3. (*Thanks to Tyr without partner*)

Two sets of the single base groups in 1st and 2nd base order:

5' 2 x 292 = 584 ,	-100 = 484 = C1 + C2 - 2
4' 2 x 252 = 504	+100 = 604 = G1 + G2 + 2
3' 2 x 208 = 416 + 584	-100 = 900 = U1 + U2 (U1+U2 from the C-groups)
3' 2 x 208 = 416 + 504	+100 = 1020 = A1 + A2 (A1+A2 from the G-groups)

6. 3rd base groups:

Number 292 as the sum of Hypoxanthine and Orotate, the parents to the code-bases from which these bases get synthesized, are connected with differentiation of codons in 3rd base: A/G (+A or G) or U/C, implying a connection too with 1st base in the anti-codons in tRNAs.

Mass sum of ams with differentiated codons in 3rd base = $1169 = 4 \times 292 + 1$. It shows up to be divided nearly equal. (Also a coincidence!?)

G1 + A1: **584** = 2 x 292 C1 + U1: **584** +**1**. = 2 x 292 +1

All ams with indifferent 3rd base = 335 = 544 - 208 = 336, -1 (336 if Pro CC before ring closed.)

ES-chain with intervals in steps 5' - 4' - 3':

292 --- (40) --- 252 --(44) -- 208

 $4 \times 292 + 1 =$ sum of ams with differentiating 3rds base in codons.

4 x 40 = 160, - 1 = 159 = "2-base-coded" ams among non-mixed codon group 4 x 44 = 176 = "2-base-coded" ams in the group with mixed-codons.

4 x 208 = 832 = G2 + A2 with differencing 3rd base: G2: 1 x 208 + 101, A2: 3 x 208 - 101. 4 x 84 = 336, +1 = C2 + U2C2: 0 + U2: 337 We get 8 ams in each group 8 ams with 3rd base A/G or A or G = 638 (3 ams only one choice: AUG, AUA, UGG), 8 ams with 3rd base U/C = 531 8 ams with indifferent 3rd base = 335

Numbers 638 and 531 may eventually be derived in this way: A/G-coded ams: $272 + 367 = 639, -1 = (\frac{1}{2} \times 5' + 3' + 2') - 1$ U/C-coded ams: $272 + 259 = 531 = (\frac{1}{2} \times 5' + 2' + 1')$

7. Individual codons and amino acid mass numbers:, See file 05.

8. Some extra annotations to base pair groups:

a) 84 - interval 292 - 208 = "5 - 3":

U+A: 960, - 84 = 876 = C1 + A2 G+C: 544, + 84 = 628 = G1 + U2. (C1 + 84 = U2)

C2 + U2 = 570, + **84** = **654** = G1 + U1 = C2 + A2 - 2 G2 + A2 = 934, - **84** = **850** = C1 + A1 = G2 + U2 + 2

In general terms these number operations as +/-84 (5' \leftrightarrow 3') could express a process outwards - inwards: "5 \rightarrow 4 \rightarrow 3 \rightarrow \leftarrow 3 \leftarrow 4 \leftarrow 5".

b) Examples of similarities in N and Z between base pair groups:

N-number:	G1 + U1 = 299	= 299 = A2 + C2
	G2 + U2 = 377	= 377 = A1 + C1
Z-number:	G1 + U1 = 355 + 2	= 357 = A2 + C2
	G2 + U2 = 471 + 2	=473 = A1 + C1

Crosswise addition N-Z between G2-C2-groups, U2-A2-groups gives the same numbers as Cross- plus Form-coded ams = 770, RNA- plus Pair-coded ams = 734:

G2: N + C2: Z = 262, \rightarrow 734 \leftarrow 472 = U2: N + A2: Z. Interval 208 +2. G2: Z + C2: N = 282. \rightarrow 770 \leftarrow 488 = U2: Z + A2: N. Interval 208 - 2.

c) Displacements 220 and 26 between groups in 1st and 2nd position:

G1 to G2 and C1 to C2: +/- 220 = 2 x 110 and A1 to A2: -/+ 26 (See further file 7 and file **13** about N-Z-division.) U1 to U2 It may be noted here that G+C = 544, + 26 = 570 = C2 + U2,(G2 411 + 26 = U2 437. C2 133 + 26 ~ 159, - 26 = 107.) U+A = 960, - 26 = 934 = A2 + G2.

U+A = 960, - 110 = **850** = C1 + A1 (~ U --> C); 960 - 220 = 740 = Cross + Pair coded ams G+C = 544, + 110 = **654** = G1 + U1 (~ C --> U); 544 + 220 = 764 = Form + RNA-coded ams.

9. Some general annotations:

a) Half the number 292 = 146 is the mass of α -ketoglutarate, from which Glu (147 A) derives directly with a central role for amination of the amino acids

b) 146* happens also to be the number of base-pairs in DNA winded around the **histones** in chromosomes. Why this curiously exact number? *(*Later in Wikipedia changed to 147.*)

c) 292 is also the mass of **P-P-ribose** part of bases in the form of coenzymes. (Ribose 150 + two H3PO4 (98, x 2), - 3 x H2O).

d) Another feature is that G- and C-coded ams "come first" in the ES-chain as connected with the numbers 5'- 4'. This agrees with what scientist have found in experiments where ams appear in liquids. There are also indications of a pressure towards more A-T-rich DNA during evolution according to the scientists, as in agreement with steps $5' \rightarrow 4' \rightarrow 3'$ in the ES-chain, ams with A-U-codons including number 2 x 3'.

e) P-ribose groups in nucleotides:

e1) The P-ribose-groups in chain binding = 195 uncharged, 194 charged (64 or 63 + 131):

584, 2 x 292 in the ES-chain \rightarrow 3 x 195 (-1).

Could this number from the ES-chain perhaps be one aspect on the cause for triplets of the bases in codons?

e2) A suggestion by Copley et al (2005) is that ams could have been synthesized at the inner OH-group of ribose in a string of nucleotides. In the illustration to this hypothesis a P-P-"ribose group binds to two nucleotides.(P-ribose + bases). The whole ES-chain could somehow illustrate the mass numbers where the synthesis of ams should appear in the middle step :

Fig. 3-8: Copley-figure numbers in ES:

292	→ 252 → 208 —	-> < 159 < 100 < 0
<u>292</u>	<u>_460 /</u>	<u>\~259 /</u>
P-P~ribose	2 x P-ribose	Base pair DNA ,bound (-1)
	à 230	~ 259 (260)

(P-P-ribose: 2 x 98 + 150, - 3 x 18 = 292, P-ribose: 98 + 150, - 18)

Yet, here is counted with ribose in RNA, not deoxyribose, but with base pairs in DNA with the T-base instead of the U-base. Bonds (-18) to the bases also neglected or somehow occurring in the middle step. (Cf. 385 - 367 = 18.544 - 159, 208 + 159).

Testing of the ES-chain?

-

- 1) Only e.g. heavy water or other deviating isotope of C, N or O in the type of Miller experiment. Does it change the reactions in any way?
- 2) Construct a peptide with atomic masses in accordance with the ES-chain, e. g.: Glu,Glu,Lys,Glu His,Gln,Leu,Pro Trp,Cys,Ser Ala,Gly,Pro Arg ?

(In a liquid of Miller type, with small variations in pH. Does it have any effect?

4. Mass division on atom kinds and on other bases than codons

<u>1. Mass division on kinds of atoms:</u>

First to observe is the fact the mass division on C-atoms versus other atoms is the same as between U+A-coded ams and G+C-coded ones:

C-atoms, 80 = 960N + O + S + H = 544

The division on codon grouped ams of the "substituents", N, O, S, H = 544:

G1 + A1: **292** C1 + U1: **252**

Mass of C-atoms in 12-group 770 = 444 = **544 - 100** Mass of C-atoms in 12-group 734 = 516 = **416 + 100**,

H-atoms: 252 - 100 = 152 = 4' - 1' N+O+S-atoms: 292 + 100 = 392 = 5' + 1'

The division between N-atoms and S+O+H-atoms could perhaps be noted too:

Atoms in R: $C + N = 3 \times 376$, $\frac{1}{2} (5' + 4' + 3')$. O + S + H = 376

10 O + 2 S + 152 H = $376 = 1/2 \times 752$ |- 2 x 208 12 N = $168 = 1/2 \times 336 (544 - 208)$. 80 C + 12 N = $1128 = 3 \times 376$

<u>2. The division of C-atoms on codon groups Purine - Pyrimidine pairs:</u> and simultaneously on codon groups: s

G1 + A1: 33 C = 292 + ½ x 208 = 396 C1 + U1: 47 C = 460 + ½ x 208 = 564

When one of the two 208-groups is divided on first numbers 292 - 252, we get the relations between mass division on **atom kinds** and on **codon groups of ams** shown below:

Fig 4-1: Division of atom kinds and ams groups, halving 208

1	04	104	C-atoms in $G1+A1 = 396 = 292 + 104$
. ↓î	. ↓	10.	C-atoms in U1+C1 = $564 = 460 + 104$
+292	2-252	208	
= 396	5 356	+ 208	→ 960 = C- atoms:
+ 292	2 + 252		\rightarrow 544 = H+O+S+N atoms
688	3	816	
G1+4	A1 🛉 U	J1 + C1	
	356	= UG+U	C+UU, $208 = UA + CG$
*	252	= CA+CU	J+CC
396	= GA + A	G+AA+G	G, 2 nd base also G or A
292	= GC+G	U+AC+A	U, 2 nd base U or C
396	292	252	356 + 208
+101	- 101	+101	- 101
= A1	= G1	= C1	= U1

In table 4 below we find number 104 as the difference between groups G1 + C1 and U1 + A1. With number 416 uncounted, the sums get equally divided vertically and horizontally.

The arrangement could perhaps reveal a symmetric phase in step 5'- 4' along two axes (544) in opposite directions: C-atoms to/from "substitutes", before a stage 3' (416).

1st base order	C-atoms	N+O+S+H	2 nd base order	C-atoms	N+O+S+H
G1 + C1	324	220	G2 + C2	312	232
U1 + A1	220 + 416	<u>32</u> 4	U2 + A2	232 + 416	312

Table 4: Mass of C-atoms in G+C = mass of other atoms in U+A

The domain groups of ams along the third polarity between bases, the keto-/amino types, shows in 2nd base order a mass division on atom kinds with strong regularity:

C-atoms: $G2 + U2 = 576 = 3 \times 192 (292 - 100)$. Other atoms = 272 $C2 + A2 = 384 = 2 \times 192 (292 - 100)$. Other atoms = 272

Cf. in B-chains unbound: C = 576, O = 2 x 384; N = 336 (544 - 208), H 96 - 4.

This number 192 appears in many sums in the genetic code. Why? In the ES-chain = 5' - 1', the interval 292 -- 100. (I's the mass of citrate, isocitrate, however not an explanation. It's 3 times 64, 6 times 2^5 .).

1536 - 1344 - 1152 - 960 - 768 - 576 - 384 - 1928 7 6 5 4 3 2 1 x 192 1536 = sum of all C-atoms in 24 ams, R + B. 1344 = sum of 24 bound B-chains (24 x 56) 960 = U+A-coded ams 768 + 2 = ams with mixed codons, 2 x 384 576 - 1 = U+A-group in non-mixed codons192 - 1 = G1-coded ams This division doesn't concern codon distribution but seems related to the ES-series and number 584, 2 x 292, with certain assumptions. (Here C for carbon.)

Phe and Tyr are synthesized as 3C- plus 4C-molecules, Trp as 3C + 4C + 5C - 1C. Trp gets its B-chain from Ser, shares codon with Cys and can brake down to Ala, hence here regarded as "meeting the other way around", added to the 1 C group.

Fig 4-2: *Cn: 4C*, *7C*, *3C* +*0C*, *2C*, *1C* + *9C*

4 C	7C + 3C, + 0C	2 C	1 C	+ 9 C, Trp
584	504		416	
8 ams	8 ams		8 ams	
G1 + A1: 292 - 4	G2 + A2: 252+1		G1 + A1:	208
U1 + C1: 292 +4	U2 + C2: 252 -1		C1 + U1:	208

(4 C: Arg1, Arg2, Lys, His = 356, + Leu1, Leu2, Ile1, Ile2 = 228. 7 C: Phe + Tyr = 198; 3 C: Glu, Gln, Val, Meth, Pro = 305; 0 C = Gly = 1; 2 C = Asp, Asn, Thr = 162; 1 C: Ala, Ser1, Ser 2, Cys = 124; 9 C: Trp = 130.)

4. Number of C-atoms in codon groups of ams as halvings:

We may also note that number of C-atoms are approximately distributed on codon groups as 2/3 - 1/3 in two steps

53 C in U1+A1-coded ams (+1 in A2 + U2), ~ 2/3 x 81 27 C in G1+C1-coded ams (-1 in G2 + C2), ~ 1/3 x 81 ↓→18 in C1, 19 in G2, ~ 2/3 x 27 9 in G1, 7 in C2, ~ 1/3 x 27

5. End atoms of R-chains as basis for mass division:

- Ams with end atoms CHx plus Gly(H) = 420.
- Ams with end atoms O, OH, S and no N = sum 468
- N in end-groups or in rings (Trp and His), including Gln and Asn = 616.

420 + 468 = 2 (544 - 100) = 888616 = 2 (208 + 100) = 616*

*(2 Arg charged = 200 + 2, rest 416 - 2)

Note that all N-contenting ams but Trp derive from the citrate cycle. (Another division: ams more or less polar: $468 + 616 = 2 \times 544 - 4$. Non polar ams, the CHx-group = $2 \times 208 + 4$.)

6. 81 - 47, a division of number 128 and number of atoms:

There are 128 C-atoms in the R-+B-chains of the 24 ams 128 = 544 - 416.

His 81 and Cys 47 (mass of R-chains) cooperate in an enzyme to break fructose at the start of the glycolysis.

The number of atoms in R-chains are exactly twice the total number of C-atoms in R+B-chains in groups G + C and U + A:

G1+C1: \mathbf{R} + \mathbf{B} = 47 \mathbf{C} \rightarrow all atoms in \mathbf{R} = 94; (G2 + C2 46 and 91) U1+A1: \mathbf{R} + \mathbf{B} = 81 \mathbf{C} \rightarrow all atoms in \mathbf{R} = 162; (U2 + A2 82 and 165)

Fig. 04-3, 81-47

R-chains, number of atoms:					<u>coms:</u> <u>C</u>	<u>C-atoms, number in R+B-chains:</u>			
AI + U1=	162	#	2	x	81	81	$(81 \text{ A} = \text{His}, R)^*$		
GI + C1 =	94	-	2	х	47	47	$(47 \text{ A} = \text{Cys}, \text{ R})^*$		
A2 + U2=	165	=	2	x	82 +1	82			
G2 + C2 =	91	=	2	х	46 - 1	46			

Which skeleton doubles its projection in its radical part? The human body in the brain!?

U1 + A1-coded ams: 81 C = entire number of C-atoms in R-chains +1 G1 + C1-coded ams: 47 = entire number of C-atoms in B-chains - 1

Minus / plus 81 and 47 gives also from the codon groups of ams from 544 and 416: $\frac{1}{2} \times 544 - 81 = G1, 191$ $\frac{1}{2} \times 544 + 81 = C1, 353$ 544 - 81 = U1, 463. 544 - 47 = A1, 497416 + 81 = A1, 497 416 + 47 = U1, 463....difference 34 = 81 - 47.

Why this division of number 128?

Fig. 4-4, 60-26-34, cf. 13-2 in file 13

$$50 - \frac{60}{32 - 18 - 8} - 2 - 0 \qquad 60 \ge 16 = 960 = U + A - coded ams R$$

$$\uparrow 26 \uparrow 26 \ge 16 = 416 = difference$$

$$\uparrow 34 \qquad 34 \ge 16 = 544 = G + C - coded ams R$$

94 + 34 = 128, 47 + 34 = 81

7. A similar "perpendicular" relation between number of C and H in the same codon groups:

C + H: total in U+A-coded ams R = 152, ~ number of H in all R-chains C + H: total in G+C-coded ams R = 80, ~ number of C in all R-chains. (See <u>figure here</u>.)

This division doesn't concern codon distribution but seems related to the ES-series and number 584, 2 x 292, with certain assumptions. (Here C for carbon.)

Phe and Tyr are synthesized as 3C- plus 4C-molecules, Trp as 3C + 4C + 5C - 1C. Trp gets its B-chain from Ser, shares codon with Cys and can brake down to Ala, hence here regarded as "meeting the other way around", added to the 1 C group.

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8 ams	8 ams		8 ams	
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Fig. 04-3, 81-47

<u>R-chains</u> , number of atoms:					<u>coms:</u> <u>C</u>	C-atoms, number in R+B-chains:			
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5. The two 12-groups of amino acids - details

I. 12-group 770:

Table 2: 12-group 770:

385				38	85		770	
175 210		10	208		177		6 0	
GU	Val	CU	Leu	UC	Ser1	AC	Thr	$\rightarrow 176$
GA	Asp	CA	Gln	UG	Cys	AG	Ser2	$\rightarrow 209$
GA	Glu	CA	His	UG	Trp	AG	Arg	$\rightarrow 385$

Division of **385** in **176** -/+**1** and **209** -/+**1** in table 2 appears in the ES-chain as interval 177 and number 208 = 3', the sums of columns U1 and A1. (-/+2 gives G1 + C1.)

a) Individual codon groups are closely related to intervals in the chain:

Fig 5-1: Mass of ams on individual codons in the ES-chain:

385 = !77 + 208 = 544 - 159. 544 - 467 = 77. 177 = UG., 208 - 177 = 31 = UC, Serin 133 - 1 = GA = AG. 152 + 1 = CA. $44 - !+1 = GU, AC. 2 \times 44 = UC + CU$

UG: Trp + Cys, GA Glu + Asp, AG Arg + Ser, GU Val, AC Thr, CA His + Gln, UC Ser, CU Leu.

Note: 544 divided in a third way, 177 and 367:

C2 = 133 = **177 - 44**, G2 = 411 = **367 + 44**.

b) Factor 77 times 5 divided 3-2 is a remarkable feature in the 770-group of ams, table
5. In the ES-chain 77 is the interval 544 - 467, i. e.,. the whole chain divided in step 4' - 3'.

Table 5: Factor 77:

G1 + C1	U1 + A1	
$154 \rightarrow 2 \times 77$ Glu + His	$\begin{array}{c} 231 \rightarrow 3 \times 77 \\ Trp + Arg \end{array}$	→ 385
$231 \rightarrow 3 \times 77$	$154 \rightarrow 2 \times 77$	
Asp + Gln	Cys + Ser2	$\rightarrow 209$
Val + Leu	Ser1 + Thr	$\rightarrow 176$
175 + 210	208 + 177	770

Factor 11: It's suggested here that this factor 77 and factor 11 characterizing this group is derived from a deeper, more elementary level, a double-directed chain:

Mirror-codons, 1st and 2nd bases, code for masses of ams that all are dividable by factor 11:

UG + GU = 11 x 20, CA + AC = 11 x 18, GA + AG = 11 x 24, UC + CU = 11 x 8.

A support for the suggestion of a two-way direction of the chain on this level is also that $4 \rightarrow 3$ gives 43 + 34 = 77: the division of sums 231 in the table: $3 \times 43 = 129$, $3 \times 34 = 102$, +/-1 gives Trp (130) and Arg (101). +/-2 gives Asp + Gln (131) and Val + Leu (100). (Cf. perhaps in 734-group: $2 \times 54 = 108 = Tyr + 1$, $2 \times 45 = 90 =$ Phe -1.)

Factor 11 appears in the individual sums (-/+1), sum 132 in several pairs, GA, AG, also AU as Meth + one Ileu, besides in 88 -/+1 and UG 176 +1, CA 154 -1. (Biochemically it's perhaps natural to search for it's root in the CO2-molecule, 44A?)

(It may be mentioned that halved numbers in the ES-chain x 10, with the inverted exponent 3/2, as $14,6^{3/2}$, $12,6^{3/2}$ etc. if abbreviated downwards to integers, give the chain 55 - 44 - 33 - 22 - 11.

Such a chain with increasing factor 1 to 5 as the following one gives the sum 385:

 $1 \times 55 + 2 \times 44 + 3 \times 33 + 4 \times 22 + 5 \times 11 = 55 - 88 - 99 - 88 - 55 = 385$:

Odd steps = $209 = 11 \times 19$, even steps $176 = 11 \times 2 \times 8$. (55 + 99 = 154, 2 x 88 + 55 = 231.).

Factors 5 and 7 in 385 as 11 x 35 appear as the elementary numbers 5 and 4 + 3 in the basic series, also the numbers of ams in Gl, C1 and U2, A2 groups. (More about number 35 in the file <u>here</u>.)

Factors 27 and 8: We observe that the sum of ams with differentiating 3rd base is 385 + 209 = 594, 2 x 11 x 27. The last row = 2 x 1 x 8.

For mor about these factors 3^3 and 2^3 , see <u>file 14</u>.

c) 3rd bases are with one exception A or G in the row 1 of tables above with heavier ams, U or C in the lighter row 2. Exception is the CA-pair His - Gln, possibly connected with the fact that His is the only ams not derived from stations in Glycolysis - Citrate cycle but from the A-base. His can brake down to the end station α -ketoglutarate, origin for Glu and Gln. It may express a turn of direction regarding 3rd base, since U/C-coded ams generally derives from an earlier station than the A/G-coded, sharing first two bases - as along an axis Orotate <--> Hypoxanthine. Cf. U-base from Orotate and all U1-U2-coded ams from glycolysis. d) The equivalence between groups G1 + A1 with Form-coded ams and U1 + C1 with the Cross-coded ams follows from the one between pairs in row 3, both 88: Val +Thr and Leu + Ser. If the CU-codon sometimes gets translated as Ser as it's said, it could perhaps depend on this UC-CU-group as decided by number 88 and reflect the suggested underlying two-way direction in an elementary chain.

e) N-Z-division in 770-group shows up to be the same -/+1 as between Form- and Cross-coded ams: $2 \times 176 - 1 = 351$ and $2 \times 209 + 1 = 419$.

In the the other 12-group 734 the same concerns the A-U-group: N = U1-coded +1, Z = A1-coded -1. This is one among several examples of similar number divisions within different basis of mass divisions as along different coordinate axes. It makes the table of mixed codons almost 3-dimensional.

For another example of an "orthogonal" table, see for instance <u>file 10</u> about number of atoms in codon bases.

Fig. from "17 short files", 02-12

G1:	Val GU	AC Thr Al:
	Asp GA - 175	177 - AG Ser,
	Glu GA	AG Arg
C1:	Leu CU	UC Ser, U1:
	His CA - 210	208 - UG Cys
	Gln CA	UG Trp
	= 385	= 385
	7 N	$I = \Lambda$
	<u>Z</u> <u>N</u>	ΝZ
	210 175	176 209

Also:

N, total sum = **351** ~ Form-coded ams, A, -1 Z, total sum = **419** ~ Cross-coded ams, A, +1

R+B-chains:	B-chains	= 12 x 74 A, -1	= 887 A
	R-chains	1 1	= 770A
	N total R+B	= 351 + 12 x 35	= 771N
	Z-total R+B	$= 419 + 12 \times 39, -1$	= 886 Z

f) There are three main divisions of number 752, 5' + 4' + 3':

752 = 292 - 460 in step 5'-4', 752 = 544 - 208 in step 4'-3', and 752 = 336 - 416, (544 - 208) - (2 x 208).

The third division (+/-1) combines codon type groups in pairs across the two groups 770 and 734:

336 +1, x 2 = **674** = Form- + Pair-coded ams, 352 + 322 416 - 1, x 2 = **830** = Cross + RNA-coded ams, 418 + 412

Table 3: 12-group 734

	414	320		
GG 1	CC 42	UU 148	AA 131	$\rightarrow 322$
GC 15	CG 101	UA 107	AU 189	$\rightarrow 412$
16	143	255	320	
1	59	5	75	734

In this more irregular group it's the G+C-group versus U+A-group that appears as the main division, shown below. (The division in RNA- and Pair-coded deviates with -/+ 4 from 2 x 208 and 2 x 159.)

Fig 5-2: Twelve-group 734:

G1 + C1 = 159 $U1 + A1 = 575 = 2 \times 208 + 159$

N-Z-division in the U+A-group:

 $N = 256 \sim U1 \text{-coded ams } +1$ Z = 319 = A1-coded ams -1.

(The similar scheme as among mixed codon groups

U1 = **255** = 208 + 49 - 2, A1 = **320** = 2 x 159 + 2.

Cf. an eventual displacement of **Cys 47** from an A1-codon (Meth AUG?) to an U1-codon:

A1 = 497 = 544 - 47,U1 = 463 = 416 + 47.

It could support the thought of a displacement of Cys that we simultaneously, in the 12group 734 A+U-coded ams = 575 have:

U1 = 255 = 208 + 47A1 = 320 = 367 - 47

[Regarding the two 12-groups of ams 770 and 734 as 752 ± 18 , we can the division of the 734-group in G1 + A1 = 752 - 416 = **336**, C1 + U1 = **416 - 18**.(One reason perhaps why Pro, CC, has a tendency to get hydroxylated, yet only + O, 16 A?. Adding 2 H2O gives the sum 770 as in the other 12-group. Lys, AA-coded, in this 734-group has the same tendency.]

Some individual mass numbers of ams approximately connected with the 12-group of non-mixed codons 734:

133 - 59 = 74, +/-1 Meth 75, Lys 73 59 -1, -2 = Asn 58, Ile1, Ile2, Leu2 = 57 252 - 159 = 93, -2 = Phe 208 - 100, -1 = Tyr 44, - 2 = Pro. 44 - 59 = 15 = Ala. 100 +1 = Arg. + Gly 1.]

Asp and Ala are often regarded as typical for ams (a figure shown in file 06)...

Asp, R+B unbound = 133 = 5' - 2' in the ES-chain. R = 2' - 1'.

The difference as secondary interval defines the normal value 74 of B-chains. Ala 15 becomes the secondary interval between intervals 4' - 3' and 2' - 1' = 44 - 59,

bridging over the middle step 3' - 2'. Cf. that Ala may derive from Pyruvate or from oxaloacetate.

[Of the 24 individual mass numbers of ams R, at lest 16 gather around number or intervals in the ES-chain:

4 around 73 with sum 292 +1, 4 around interval 44 with sum 177 (544 - 367), 6 at interval 59 -1,-2 with the two sets of Ile and Leu, 2 at 100 (+1) with two Arg.]

III. A special operation, amino acid masses with exponent 2/3:

If the mass numbers of R-chains of ams separately are "compressed" through exponent 2/3 (e.g. Trp $130^{2/3} = 25,66$,), their codon grouped sums give approximate numbers at the middle of the ES-chain as shown in figure 5-3 below.

If not haphazard, it could hypothetically imply that the individualization of ams, if not occur, at least is connected with the middle of the chain. (Cf. an added dimensional aspect in end discussion.)

Fig 5-3: Individually 'compressed' ams with exponent 2/3

R-chains:

$\Sigma [ams^{2/3}]$:	C1	: 84,6	106,1:	U1
	Al	: 124,1	52,0:	Gl
	Σ	208,7	158,1	
		~ 3'	~ 2'	

R+B-chains bound:

$$\Sigma \text{ [ams}^{2/3}\text{]:} \quad \begin{array}{rrrr} C1: 125,7 & 155,3: \ U1 \\ \underline{A1: 192,0} & 102,5: \ G1 \\ \Sigma & \textbf{317,7} & \textbf{257,8} \\ & & & & \\ & & & & \\ & & & & \\ & & & & \\ & & & & \\ & & & & & \\ & &$$

Note the keto-amino polarity: C1 plus A1- groups 208,7., U1- plus G1-groups 158,2. Sum $366,8. \sim 367 = 3' + 2'$.

IV. Transformations between number-base systems (nb-x):

To forestall later files:

 $\frac{\text{nb-10}}{\text{G-base } 151 = 227}$ G-base 111 = 157...Sum **384**. Transformed together = **386**. U-base 112 = 160

A-base 135 = 207... Sum **367**

Here we have the central numbers of the two 12-groups. And two times the 4 bases transformed together (1018) gives 1772, exactly the sum of the unbound backbone chains (B-chains). These curious facts led to the investigations in files "**Transformations**", such transformations eventually part of the reference system.

See also about these numbers file "<u>Geometries and special arithmetic operations</u>" and file "<u>Halved orbitals numbers</u>" in section II.

V. The weightt series of ams:

Mass in ordder of heavines: A division $\sim 2/3$ around the middle = 600 — 904. Gly \rightarrow Asp = 14 aa, 1-15-31-31-42-43-45-47-57-57-57-57-58-59, sum 600 Gln \rightarrow Trp = 10 aa, 72-73-73-75-81-91-101-107-130, sum 904

6. Backbone chains

 $\sqrt{\pi}$, x 10^3 = 1772.45 ~ 24 B-chains unbound $\sqrt{\pi} \times 10^3$ = 56.05 ~ one B-chain bound $\sqrt{56} \times 56 \times 56$ = 752.101 ~ half the R-chains

If these operations have sense, it remains for more advanced mathematicians to explain. What kind of geometry could correspond to the square root of π ?

The similar parts of ams, the backbone (B) part, make up a separate coordinate axis, not governed by codons. It gives a good reason not to include them when studying differentiation of R-chains. The B-chains appear in the ES-chain in groups of 6 (cf. the 4 codon type groups?).

R | B-chains: (H)NH2—CH—COO(H) = 74 A. Times 6 = 444.

Minus 1 H in the 4 ams Arg1,2 and Lys (charged), plus Pro gives 443. Total sum 1776 - 4H = 1772.

Groups and condensations to bound B-chains are shown in figure 6-1:

Fig 6-1: Condensation of B-chains in groups of six

$$\begin{array}{rl} \underline{292 - 252} - 208 - 159 - 100 \\ 544 < & \longrightarrow 100 = 444 = 6 \text{ B-chains à 74 A. (More correct 443*.)} \\ 208 < & \longrightarrow 100 = 108 = \text{minus 6 x 18 (H_2O), condensation} \\ 544 < & \longrightarrow 208 & = 336 = 6 \text{ x 56, the B-chains bound.} \end{array}$$

The division of the 6 unbound B-chains (444) in two intervals around the middle of the ES-chain supports the recognition of B-chains in this chain and connects R-chains with the middle step

Interval 544 to $367 = 177 = 6 \times 29,5$, the NH2(+H)-CH-part of a B-chain, and 367 to $100 = 267 = 6 \times 44,5$, the COO(H)-part of this chain as illustrated below. The decimal 0,5 may illustrate the displacement of H in COOH to N-group, charging both ends of B-chains. After condensation there is balance 28-28 between the groups, times 6 = 168 - 168.

Fig 6-2: Division of interval 444 as 6 B-chains



(Interval 292 to 208, 5' - 3', = $84 = 1,5 \times 56$, the bound B-chain. 111, 1/4 of 444 = 1,5 x 74, the unbound B-chain. Perhaps an aspect on why peptide bonds go on as if always a half was lacking?)

The number of B-chains from the exponent series was grouped in 6: Two of the number series giving the R-chains with the operation below are not enough for the B-chains: 544 + 208, x 2 = 1504 = 24 R-chains 544 - 208, x 2 = 672 = 12 B-chains bound

Should the first three steps in the exponent series eventually be read both forward and backwards, (as in the "triplet series 5-4-3 + 3-4-5 = 888, x 2 = 24 unbound B-chains à 74 A)? Eventually connected in some way with the opposite directions of R-chains in proteins? More about this triplet series in <u>file II: 15.</u>

It's often said that Asp - or Ala - constitute the elementary form of an ams.

Whole mass of Asp R+B = 133 = interval 292 <-->159 in the ES-chain, its R-chain 59 is following interval, 159 - 100, figure 6-3.

Number 74 for B-chains becomes a secondary interval as Ala, R 15, the secondary interval 44 - 59. (Cf. that origin of Ala can be both Pyruvate in glycolysis (2 x 44) and Oxaloacetate (132) in citrate cycle.

Fig 6-3: Asp-Ala, R-chains 59, 15



A-base 135, \land = 740740740x10 ^x : (Sign \land here for inversion.)
At the protein synthesis it is the A-base as AMP that binds to B-chains of ams and
transports them to tRNAs. Square of this number 1/135 gives the "factor chain"

1 x 54 = 54	$>\sqrt{54-86-96-84-50}=74074,074074074$
$2 \ge 43 = 86$	
$3 \ge 32 = 96$	370 / 5 = 74. Corresponding "factor chain" inwards = 235
4 x 21 = 84	= 5 x 47: 47 = R-chain of Cys which binds protein strings to more
$5 \ge 10 = 50$	complex structures.
Sum <u>370</u>	
~ 5 x 74	

Two times the **inverted number of the C-base 111** A gives $18 (\sim H2O)$ as periodic number, <u>180180180</u>...and with one 10-power of displacement it gives the difference* to inverted A-base <u>560560560</u>..., the bound B-chains à 56.

It looks like a connection with the common **A-C-C-ends of tRNAs** at which the ams get attached, an intricate relation between mass of codon bases and ams where inversions appear as resonances in a complementary field? Only random associations?

*(Inversion of the G-base as bound (150A) to the period $66666..x10^{x}$ gives a difference to the inverted A-base that only is a displacement of one 10-power in the period 740740... as if guiding the move of tRNAs between positions on ribosomes?)

Another association about ACC-ends of tRNAs:

Sums of ams (R) with A- and C-contenting codons in 1st and/or 2nd position:

A = 888+1 = AA + AU + AG + AC + GA + CA + UAC = 444 = CC + CG + CA + CU + GC + AC + UC,

These sums happen to approximate numbers for groups of B-chains. A- plus two Cgroups gives about the sum of 24 B-chains à 74 A. If the ACC-ends of tRNAs eventually should be part of a reference system, it seems surely very intricate.

Keto-/amino polarity between bases:

Peptide bonds when O- and N-groups meet from two ams remind of the keto-/amino polarity between the bases U + G versus A + C. Two groups of codons divided by this polarity give sums of ams $R = 370, 5 \times 74, -/+1$ (Pair- + Cross-coded):

UU + GG + UG + GU = 370 - 1AA + CC + AC + CA = 370 + 1.

370, corresponding to 5 B-chains à 74 A

Number of different atoms in the B-chains unbound:

C 48 = 576 = 3 x 192 O 48 = 768 = 4 x 192 ...(Note C+ O ~1344, sum of bound B-chains.) N 24 = 336 H = 96 -4 H (in Arg1, Arg2, Lys (charged) and in Pro)

7. N-Z-divisions and H-atoms

Number 26 and total N and Z derived from the ES-chain:

Number of H-atoms is of course an essential result of and expression for structures of ams. Total N- and Z-sums without $H = 2 \times 676 = 2 \times 26^2$. (Cf. <u>file 13</u>, about the 2x^2-chain behind the periodic system: 26 as 18 + 8 in the middle of this chain and 26 as factor in total sum R+B of ams, $3276 = 26 \times 126$.)

N-Z-sums derived from the ES-chain (?):

 $Z = 2 \times 544 - 259 = 829, -1 = 828,$ N = 2 x 208 + 259 = 675, +1 = 676.

N-Z-division similar to division between codon groups of ams:

In <u>Table 1</u> it could be noted that N- and Z-sums didn't change more than one single unit (u) between main groups G+C and U+A from 1st to 2nd base order (as if only through a change $n \rightarrow p$!), indicting that also N-Z-divisions may be guided by the numeral series. We had the same similarity among mixed and non-mixed codons:

N-Z-division in 770-group shows up to be the same -/+1 as between Form- and Cross-coded ams: $N = 2 \times 176 - 1 = 351$ and $Z = 2 \times 209 + 1 = 419$.

In the the other 12-group 734 the same concerns the A-U-group: N = U1-coded ams +1, Z = A1-coded ams -1.

This is one among several examples of similar number divisions within different basis of mass divisions as along different coordinate axes.

(Another example is e.g. the number of atoms in 48 codon bases, 1st and 2nd position, = 674 (2/3 x sum of the ES-chain 1011): See <u>file 10</u> about the bases.

Displacements in N-Z from 1st to 2nd base order:

Dividing the differences - as "displacements" - between codon base groups in 1st and 2nd base order in N and Z gives as a border numbers of the ES-chain (+1 in C- and A- groups), shown in figure 7-1. A-groups = 500 = 3' + 5', U-groups = 460 = 4' + 3'. Cf. R- chains: A1 = 500 - 3, U1 = 460 + 3.

Fig	7-1:	N-Z-l	border	between	1st and	2nd	base a	order:
-----	------	-------	--------	---------	---------	-----	--------	--------

	500 .		
Ť	460 1		
292 -	- 252 - 208		
GI:	$191 \longrightarrow + 101 \text{ N} \longrightarrow 292 \longrightarrow +119 \text{ Z} \longrightarrow$	411	G2
C1	$353 \longrightarrow -100 \text{ N} \longrightarrow 253 \longrightarrow -120 \text{ Z} \longrightarrow$	133	C2
U2:	$437 \longrightarrow + 23 \text{ N} \longrightarrow 460 \longrightarrow + 3 \text{ Z} \longrightarrow$	463	U1
A2:	$523 \longrightarrow -22 \text{ N} \longrightarrow 501 \longrightarrow -4 \text{ Z} \longrightarrow$	497	A1

Note that the order U+A in the figure have been reversed, 2nd to 1st base order.

U1 463 - 3 Z = 460, - 23 N = 437 = U2 A1 497 + 4 Z = 501, + 22 N = 523 = A2

Adding displacements of pyrimidine and purine bases respectively, we find that they are exactly the same in N and Z = 123:

 $C1 + U1 \rightarrow C2 + U2 = -123 \text{ N}, -123 \text{ Z}.$ $G1 + A1 \rightarrow G2 + A2 = +123 \text{ N}, +123 \text{ Z}.$ U-C-pair is divided in step 1 - 2: 100 - 23 (+/-1): 1 ---- 3 A-G-pair is divided in step 2 - 3: 120 - 3 (-/+1): 1 ----2 ---- 3

Displacements 220 and 26,:in G-C-groups 220, in A-U-groups 26.

Cf. a series $10^2 - 8^2 - 6^2 - 4^2 - 2^2$:

$$\frac{100}{N} - \frac{64 - 36 - 16 - 4}{Z}$$

Another way to get these numbers, abbreviated:

G-C: $5^{4/3} - 4^{4/3}$, x 100 = 220. A-U: $(5+3)^{4/3} - (4+3)^{4/3}$, x 10 = 26.

Could the exponent 4/3 represent an underlying level?

√3/2:

 $\sqrt{3}/2$ gives the total relation Z - N = 828/676 very closely, as it does in the separate G+C- and U+A-groups.

The number of H in these main groups is circa 1/10 of totals 544 and 960, 55+/-1 in G+C-groups, 97 -/+1 in U+A-groups.

Interval 49 in the middle step: 3' - 2'

The interval in step 3' - 2' (208 - 159) at the middle of the ES-chain = 49. Divisions of sums 544 and 960 -/+ 49 (+/-1) give approximately the N-Z-division between main codon groups G+C, A+U:

Fig 7-2: *N-Z-division approximately from -/+ middle interval 49:*

			15	st base order	2nd base	order
292	- interval 49	= 243 = N	- 1,	G+C-groups	- 2	G+C
252	+ interval 49	= 301 = Z	+1,	- " -	+2	G+C
272 + 208	- interval 49	= 431 = N	- 1,	A+U-groups	+ 0	A+U
272 + 208	+ interval 49	= 529 = Z	+1,	_ " _	+ 0	A+U

Here we could associate to a d-degree step 3 - 2 as a relation mass versus charge: neutrons n polarized by weak interaction into charges, protons and electrons:

 $n \rightarrow p++e-+$ antineutrino.

H-atoms:

Total number of H-atoms in 24 ams R-chains = $152 = 8 \times 19$. It is rather precisely distributed on the individual codon groups as 1/8 - 2/8 in G-C-groups, 2/8 - 3/8 in U-A-groups with exchange of the numbers from 1st to 2nd base sums:

G1 1/8, C1 2/8, G2 2/8, C1 1/8. U1 2/8, A1 3/8, U2 3/8, A2 2/8.

This makes it possible to derive the N- and Z-numbers of the individual codon base groups -/+ 1-2 units. Examples:

G1 = 191 A, - 19 = 172, x $\frac{1}{2}$ = 86 = N, + 19 = 105 = Z A1 = 497 A, - 57 = 440, x $\frac{1}{2}$ = 220 = N+1, + 57 = 277 = Z -1.

A special observation regarding 3rd base groups:

The figure shows ams with differentiating 3rd base, to the left from glycolysis, to the right from the citrate cycle.

Fig. 17 files, 02-10 a, b: A/G (A or G): ams R = 638 A, = Z total of both groups U/C: ams R = 531 A. = N total of both groups 3^{rd} base A/G(A,G); Trp+Leu+Ile₂+Meth + Glu +Gln+Lys+Arg₂ 7. 176 176 352 286 Ζ 164 122 3rd base U/C: Tyr+Phe+Cys+lle1 Asp+Asn+Ser2+His Sum: 638 ~ A/G-(A,G)-coded ams, A. $2x^2$ -chain x 11: 550 -352 -198 - 88 - 22 (x = 5 - 4 - 3 - 2 - 1)286 352 A/G U/C 7.

This is still another example of equal number divisions along different "property axes". (In numbers of the ES-chain:

272 + 367 = 638 + 1.272 + 259 = 531or 584 +/- 54, half the interval 3'- 1' 108 = 531 - 1 and 638.)

8. Geometries

- Golden section - Special arithmetical operations, e.g.

 $\pi + \sqrt{2}$, - ES-series and Cheops pyramid - $\sqrt{1/3}$ and $\sqrt{2/3}$

Hopefully some advanced mathematicians will find this file on the web and get provoked enough to search for explanations!

Geometrical relations in the two 12-groups:

385 x $\sqrt{2}$ is ~ 544. Through this factor $\sqrt{2}$ and inversions (\wedge) the codon groups 385 and 367 in the ES-series become related, figure 8-1 below.. How to interpret such relations? They are very likely only one example among many similar dimensional relations on a deeper underlying level that remains to investigate. ($\sqrt{2}$ should probably not be regarded as a relation diagonal/side in a square, sooner in its serial development?)

Fig 8-1: *Geometrical relations through* $\sqrt{2}$ *:*

$$\begin{array}{r} \underline{367} \\ \underline{292} \quad \underline{252} \quad \underline{208} \quad \underline{159} \quad \underline{100} \\ \underline{544} < \underline{385} \quad \underline{} \\ 2 \times 272 \end{array} > \begin{vmatrix} \underline{367} \\ \underline{159} \quad \underline{100} \\ \underline{259} \end{vmatrix}$$

385 x $\sqrt{2}$ = 544,5 ≈ 2 x 272,2.→ Then 272 \land 367. x 10⁻⁵ 367 x $\sqrt{2}$ = 519,0.≈ 2 x 259.5. → Then 259 \land 386. x 10⁻⁵ (259,5 \land 385,3. x 10⁻⁵)

The diagonals halved, refer to each other through inversions.

Two notes:

1) A right-angled triangle with the sides 176 and 209 (the number division of 385 within mixed codon groups) gives the hypotenuse 273.23.; 273 the mean number of two ams R + B unbound.

2) Cf. perhaps the relations between Z-numbers of ATP and NADPH(+H) around 258-387, a 2/3-relation, 6 x 43 — 9 x 43, see <u>Biochemistry</u>.

Intervals in the ES-chain with exponents 3/2 and 4/3:

Intervals 40-44-84 in the ES-chain with exponent 3/2 gives numbers 253 292, and 770, as a kind of feed back (?) or mutual references, re-establishing the ES-numbers 5' and 4' (+1):

 $40^{3/2} = 252.98. = 253.$ $44^{3/2} = 291.86. = 292.$ Sum 544 +1.

(Third number 208?: 84 - 49 = 35, $\rightarrow 353/2 = 207.06 = 208 - 1$)

 $84^{3/2} = [292 - 208]3/2 = 770. =$ Cross- plus Form-coded ams.

Compare with 42, 1/2 times the interval 84, divided and whole number:

Fig. 8-1-b

$$2 \ge (20^{3/2} + 22^{3/2}) = 385,26.$$

 $159.$
 $2 \ge 42^{3/2} = 544,38.$

Intervals in the three middle steps of the ES-chain, sum 152:

$$44^{3/2} = 291.9. \quad 49^{3/2} = 343 \quad 59^{3/2} = 453.2....sum \ 1088.15. \approx 2 \ x \ 544.$$

Exponent 4/3?

Testing this exponent - as related to a higher d-degree step 4 - 3 (?) - shows up to be another way to re-establish the starting number 292:

 $40^{4/3} + 44^{4/3} \rightarrow 292.13$. (Cf. $5^{2/3} = 2.924$.)

Note that 404/3 is about 136 +1 and 444/3 about 156 -1: 136 mass of Inosine, 156 mass of Orotate, the parents of the bases in the codons

$$84^{4/3} = 367.9 = 208 + 159, +1;$$
 x 2 = 736. = RNA- + Pair-coded ams +2.

The golden section:

....

The golden section (gs) as Fibonacci series appears also in this ES-chain and mass relations within groups of ams. Following series, figure 8-2, leads from 2' in the ES-series to total sum R + B of the 24 bound ams through steps as times gs:

The ES-numbers 208 and 367 gives for instance the groups G+C 544 and U+A 960 approximately.

Fig 8-2: Golden section (gs) steps in the ES-series:

208 x gs = 336,5 x gs = 544,5.
+ 367 x gs = 593,8, x gs = 960,8. (367 =
$$\frac{1}{2}$$
 x 734-group, 3' + 2')
= 575 x gs² = 1505. 1504 +1 575 → Pure A-U-codons in group 734.

2' = 158,74...x gs = 256,8 $\approx 208 + 49$ x gs = 416. 24 B-chains x gs = 672. (2 x 336) B-chains x gs = 1088, (2 x 544), bound x gs = 1760. (total Z of 24 ams unbound, R+B) x gs = 8 x 24²

Higher numbers abridged. Number 257. = 208 + middle interval 49. In 7th step we get 2848, x gs = 2 x $2304 = 2 \times 48^2$.(24 = number of codons, ams.)

Forms of R-chains:

Elementary structure of R-chains as basis for grouping of ams may give three elementary groups: vary roughly ring-formed, "straight" and "branched":

<u>Ring-formed</u> ams 292 + 159 (a loop 5' - 2'.) = **451**, three aromatic ams 328, + His + Pro 123.

<u>"Straight"</u> ams = $2 \times 159 (2') = 318$, Ala, 2 Ser, Thr, Cys, Lys, Meth = 317, + Gly 1.

Ring-formed + "straight" = 770 - 1.

 $\underline{\text{Branched}} = 734 + 1$ (as at middle of the ES-chain): CHx-groups = 271; O-OH + O-NHx = 262; 2 Arg NHx-NHx = 202.

<u> π and $\sqrt{2}$, an arithmetical curiosity:</u>

Reading and adding 2 x 5 two-figure-numbers (31 + 41 + 59..., 14 + 15 + 92...) from first eleven figures in these transcendent celebrities gives both whole and partial sums of the codon grouped amino acids as well as vertically numbers from the exponent series, see the figure below.

No motivation for the operation is offered here. Should there exist any sense in the operation, it's left to more advanced mathematicians to find it.

Fig 8-3: π and $\sqrt{2}$:

* 160 = 159 + 1, $271 = \frac{1}{2} \times 544$, -1. 132 = 292 - 159, -1. $189 = \frac{1}{2} \times 960 - 292$, +1. = 292 = 460

In ES-numbers: $431 = \frac{1}{2} \times 544 + 159$ $321 = \frac{1}{2} \times 960 - 159$

$$221 + 175 = 396 = 292 + 104; 210 + 146 = 356 = 252 + 104$$

*Cf. fig. 4-1.

Sums of numbers from $\pi = 431$ and from $\sqrt{2} = 321$; cf. triplet numbers 432-321. If $\sqrt{2}$ is seen connected to d-degree step 2-1 and π to step 3-2, the number 321 from $\sqrt{2}$ could be thought of as displaced, here one 10-power step:

Fig. 8-3-x. *Sum 431 + 321 with displaced 321 number*

$$\pi : 4 3 2$$

$$\sqrt{2}: 3 2 1$$

$$4 6 4 1 \dots \approx 10^{2/3},$$

4641, \rightarrow lg. \rightarrow x 100 = 366,7. sum "3 + 2" (366,75.) in the exponent series.

[Cheops pyramid:

 $\frac{1}{2} \ge 292 = 146 \sim$ the height of this pyramid - in meters!

 $\frac{1}{2} \times 460 = 230 \sim \text{side of this pyramid - in meters!}$

If the old Egyptians were acquainted with cubic roots and exponents 2/3 is probably uncertain. The Pharaoh measure "ell" is said to have been about half a meter.

That the circumference of the base is approximately 2π times its height is a well-known fact.]

 π and $\sqrt{2}$ in figure 8-3: the 2-figure numbers summed in another way:

One example:

$$\pi \qquad 31\ 14\ 41\ 15 \qquad 59\ 92\ 26\ 65 \qquad 53\ 35 \\ \sqrt{2} \qquad \underline{14\ 41\ 14\ 42} \qquad \underline{21\ 13\ 35\ 56} \qquad \underline{62\ 23} \\ \underline{210+2} \qquad \underline{367} \qquad 175-2 \\ \underline{385} \qquad \underline{385}$$

 $[212 \times 173 = 366, 76 \times 10^{2}.3' + 2' = 366, 74.)$

What kind of relation could exist, which closely couples π and $\sqrt{2}$? π represents 1/2 of a unity circle, but $\sqrt{2}$ only 1/4, if illustrated as in the figure below? Could we interpret it in terms of a step or displacement in dimension degree 3 to 2: (4-3-1 \rightarrow 3-2-1 as sums of the 2-figure numbers above)? π related to a 3dimensional world, $\sqrt{2}$ to a 2-dimensional one.

Fig. 8-4 Bell's theorem



Assuming the definition of a dimension as characterized by two complementary "endpoles" (0 - 00 in figure a), the shortest step between the poles in an 1-dimensional world would be 2 r and the shortest step in a 2-dimensional world could be only $\sqrt{2}$. In a 3-dimensional world, the shortest way could be the circular one (with reference to Einstein)?

(There is an association here to Bell's theorem and Aspect's experiments with photons in quantum physics: measurements in two dimensions (directions) as φ a branched way for two possible outcomes. If there were no coupling between the photons, the maximum result of Bell's formula should be +/- 2. But the experiments showed on a maximum of +/- $2\sqrt{2}$ showing that the photons were entangled.

The question arises: what would be the result if such measurements were carried out in three dimensions?)

Arc tan $\sqrt{2} = \varphi$ 54.736. Sin $\varphi = \sqrt{2/3}$, Cos $\varphi = \sqrt{1/3}$

Treating these numbers sin - cos in the same way as π and $\sqrt{2}$ above gives these results:

Fig. 8-5. Sin - Cos for arc tan $\sqrt{2}$



Taking each other 2-figure number from the cosine series and each other from sine numbers, the upper ten first, gives sums of the ES-chain:

Fig. 8-6. Sin-Cos-series with sum 1011 of the ES-series

Sum:	192	352	367	100
	292-100 	252+100 	208 + 159 	100
x100:	₅ 2/3	42/3	3 ^{2/3} 2 ^{2/3}	1 ^{2/3}
	G-coded ams +1 7 numbers	C-coded ams —1 5 numbers	½x RNA+Pair- coded ams 3+3 numbers	2 numbers

05 08 77 16 35 49 02 65 69 80 | 57 81 73 64 50 96 26 58 91 09

9. Glycolysis - Citrate cycle Codon grouped amino acids on the basis of their origin.

1. Sum of ams with **U-base** in 1st and/or 2nd position of codons is **752**, exactly half the total = 292 + 252 + 208 in the ES-series. It's division between the two 12-groups 770 and 734:

Group 770: Cross- and Form-coded: **208** + **100** = **308** Group 734: RNA- and Pair-coded: **544** - **100** = **444**

All these ams derive from stations in glycolysis, no one from citrate cycle.

(It's suggested here that this is connected with the fact that U as coenzyme UTP-UMP is the one engaged in bonds and breaking of glycogen.)

Hence, we could imagine that the two groups or number chains à 752 also represent the two sides outside/inside mitochondria membranes. This under following conditions:

Ala is regarded as derived from oxaloacetate (may also derive from pyruvate). Ser2, AG-coded, likewise, as along the outer loop from oxaloacetate via homoserine back to 3-P-glycerate. Gly (one unit) from Ser1 or 2? Meth as connected with Cys (?).

With these assumptions we get ams derived from the different stations in the processes as shown in table 6: Note the approximate ES-number divisions

	Glycolysis	R-chains, mass			
3-P-glycerate	Ser1, Gly, Cys, Meth	154			
P-enolpyruvate	Trp, Phe, Tyr	328	1/2 x 960 +2	753	
Pyruvate	Val, Ile1,2, Leu1,2	271	1/2 x 544 -1		
С	itrate cycle				
Oxaloacetate	Ala, Asp,Asn, Thr,Ser2	208	208		
α-ketoglutarate	Glu, Gln, Lys, Arg1, Arg2, Pro, His	543	543	751	

Table 6: Amino acids from stations in glycolysis - citrate cycle

2. The divisions in codon type groups 770 and 734 on the both sides of mitochondria membrane is shown in figure 9-1 below. Included in the figure is an observation from files about number-base systems that these groups -/+1 seem to refer to each other through transformations between nb-10 and nb-8 and in opposite directions:

Fig 9-1: *Codon type groups, division on Glycolysis and Citrate cycle:* (The codon type groups defined in file 2.)



222	>	544, -100 = 444, U in codons	The rest 292 -2
252			and the second
208	>	208, $+100 = 308$, U in codons	** 252+208, +2

Differences, cf. interpretation of number 77:

 $308 - 444 = 136 = 4 \times 34$ $462 - 290 = 172 = 4 \times 43$ (Cf. A1 - U1 = 1 x 34, A2 - U2 = 2 x 43)

43 to 34: 9 ~ OH- Z

Also the rest, not U-contenting codon groups, are divided +/-2 in numbers of the ESchain, a division in step 5 - 4, while U-groups represent a number division in step 4 - 3.

In the figure above we have for instance 18 as differences 308-290, 444-462 and ± -2 in the transformations. We have perhaps (?) here a correlation among ams to the general theme in the processes, secretion of 2H and processing of H2O (18). If so, what about ± -154 ? Could it eventually express the same as the loop, outside the main steps, from oxaloacetate via homoserine (and homocysteine) back to 3-P-glycerate where sum of ams = 154?

Codons and ams in the four groups are shown below:

Fig 9-2: Amino acids in the 4 codon type groups:

 $\frac{\text{Mirror-codons (factor 11), 770-group:}}{308 = UG + GU = 220, UC + CU = 88}$ 462 = CA + AC = 198, GA + AG = 264 $\frac{\text{RNA- and Pair-codons, 734-group:}}{444 = UU+UA+AU, \quad U\text{-contenting codons}}$ $290 = CC+CG+GC+GG, +AA, \quad \text{The rest}$ \downarrow CC+CG (143) + UU (148) = 291 $\frac{GG+GC+AA (147)}{290} + \frac{UA+AU (296)}{444 (3 \times 148)} = 443$

3. Division in G+C- and A+U-coded ams between the two parts of the process shows notable agreement with divisions in the ES-chain (+/-1).

Fig 9-3: Division on groups G+C, A + U from stations in Glycolysis - Citrate cycle:

		1 st base	grouping	2 nd base	grouping
		G+C	A+U	$\underline{G+C}$	A+U
Glycolysis:	753: <	100 + 1	752 - 100	208 +1	544
		1	\downarrow	↑	\downarrow
Citrate cycle:	751: →>	<u>544 - 100 - 1</u>	208 +100	336 - 1	416

Mass number distribution above: displacements from 1^{st} to 2^{nd} base order:

G1+C1	\rightarrow	G2+C2:	Glycolysis + 108
- " -	\rightarrow	- " -	Citrate cycle - 108
A1+ U	$1 \rightarrow$	A2+U2	Glycolysis - 108
- " -	\rightarrow	- " -	Citrate cycle + 108
(108 =	208 -	100 = inter	val 3' - 1'.)
100 - /	- 10	(II O) /	U.O on accontial acreat on these proc

 $108 = 6 \times 18 (H_2O)$. -/+ H₂O an essential aspect on these processes.

4. Atom divisions on ams from Glycolysis and from Citrate cycle become the same for C-atoms as between U1+C1-coded and G1+A1-coded ams (cf. file 4, figure 4-1):

Glycolysis 47 C = 564 = 460 + 104, other atoms 292 - 104 +1. Citrate cycle 33 C = 396 = 292 + 104, other atoms 252 + 104 -1.

Fig. 9-4: Division on atom kinds

$$= \frac{\underline{Glycolysis,}}{47 \text{ C} = 564} \qquad \qquad \underline{S+0+N+H} \\ = \underline{\frac{S+0+N+H}{188+1}} = 292 \cdot 104, +1 \qquad \underline{S+0+N+H} \\ \text{diff. 168} \qquad \underline{S+0+N+H} \\ = \underline{292 \cdot 104, +1} \qquad \underline{S+0+N+H} \\ \text{diff. 168,-2} \qquad \underline{S+0+N+H} \\ = 252 + 104, -1 \\ \text{diff. 168,-2} \qquad \underline{S+0+N+H} \\ \underline{356 \cdot 1} \\ = 252 + 104, -1 \\ \underline{S+0+N+H} \\ \underline{356 \cdot 1} \\ \underline{S+0+N+H} \\ \underline{356 \cdot 1} \\ \underline{S+0+N+H} \\ \underline{356 \cdot 1} \\ \underline{S+0+N+H} \\ \underline{556 \cdot 1} \\ \underline{S+0+N+H} \\ \underline{556 \cdot 1} \\ \underline{556 \cdot 1$$

5. Sums of stations in the two processes, compared with groups of ams, a) bound, b) with +1 for charge and bonds to S- or P-enzymes:

Glycolysis, 8 C3-stations: a) 736, b) 750. Citrate cycle, 10 stations*: a) 2 x 736, b) 2 x 748

*Malate, Oxaloacetate, Citrate, Cisaconitate, Isocitrate, Oxalosuccinate, α-ketoglutarate, Succinyl(~Coa), Succinate, Fumarate.

That the sums approximate numbers as 752 and 734 among ams in the ES-series is not so natural as it perhaps may seem.

Molecules	C	0	H, incl. 1 for charg e s + 1 bond	Bond (1), charges 23	
a-ketoglutarate	$5 \ge 12 = 60$	$5 \times 16 = 80$	6	2	146
Succynyl(~CoA)	$4 \ge 12 = 48$	$3 \times 16 = 48$	5 + 1~	2	102
Succinate	$4 \times 12 = 48$	$4 \times 16 = 64$	6	2	118
Fumarate	$4 \ge 12 = 48$	$4 \times 16 = 64$	4	2	116
Malate	$4 \ge 12 = 48$	$5 \times 16 = 80$	6	2	134
Oxaloacetate	$4 \ge 12 = 48$	$5 \times 16 = 80$	4	2	132748
Citrate	$6 \times 12 = 72$	$7 \times 16 = 112$	8	3	192
Cis-aconitate	$6 \times 12 = 72$	6x16=96	6	3	174
Isocitrate	$6 \times 12 = 72$	$7 \times 16 = 112$	8	3	192
Oxalosuccinate	$6 \times 12 = 72$	7 x 16=112	6	3	190748
Sum	49 C = 588	53 O = 848	60 = 59 H + 1 ~	24	
				60-24 = 36 H	1496

 Table 7: Molecules in the citrate cycle

 $1496 = 11 \text{ x } 136 (\sim \text{Inosine}) = 44 \text{ x } 34.$

Molecules with 5 C and 4 C = 748 - 12 (6 x 2) for charges, bond = 736; molecules with 6 C =: 748, - 12 (4 x 3) = 736.

 $736 = 32 \times 23$.

Sum of substances = 1496, x 2 (turns) = $2992 = 11 \times 272$ (half the number 544)

Eight of the stations in Citrate cycle as uncharged, compared with the ES-chain:

 $101 = Succinyl \rightarrow$ $\rightarrow 2 \ge 59 = Succinate \rightarrow$ $\rightarrow \rightarrow 2 \ge 58 = Fumarate \rightarrow$ $\rightarrow \rightarrow 2 \ge 133 \pm 1/-1 (= 292 \pm 159)$ Malate $\pm Oxaloacetate \rightarrow$ $\rightarrow \rightarrow \rightarrow 2 \ge 133 \pm 1/-1 (= 292 \pm 159)$ Malate $\pm Oxaloacetate \rightarrow$ $\rightarrow \rightarrow \rightarrow \rightarrow 2 \ge 192 (292 \pm 100) = Citrate \pm Isocitrate \rightarrow$ $\rightarrow \rightarrow \rightarrow \rightarrow \rightarrow 146 (\frac{1}{2} \ge 292) = \alpha$ -ketoglutarate, $\rightarrow (\rightarrow Succinyl...101)$ (Two substances excluded here, Cisaconitate 174 and Oxalosuccinate 190.)

6. 44 - 59, intervals in the E-chain:

It is worth noting the intervals 44 (4' \rightarrow >3') and 59 (2' \leftarrow 1') in the ES-chain, steps that correspond to each other in the background model. See figure 9-4. It is numbers equivalent with main molecules incorporated into the citrate cycle: CO2 in step from Pyruvate (88) to Malate (133+1) and of acetyl-(CoA) + O(H) = 59 (60) in step from Oxaloacetate (133 -1) to Citrate 192 (132 + 60 (~ 133 -1 and 59 +1):

Fig 9-5: Intervals 44 and 59 in ES-chain as additions into Citrate cycle:

$$252 - 208 - 159 - 100$$

 $44 - 15 - 59$
COO⁻ CH3

7. Orotate <----> Inosine; codons U/C \rightarrow A/G in 3rd position:

There is a trend from ams with 3rd base U/C to ams with 3rd base A/G like a coordinate axis through the processes, in ams codons from first stations in the glycolysis to Glu in the citrate cycle, illustrated by following examples:

Fig 9-6: Orotate - Inosine, a coordinate axes through the processes

Examples: Cys	Phe	Asp	Asn	Ser2 - 3 rd base U/C
1	T	1	1	
Trp	Leu	Glu	Lys	Arg2 - 3 ^{#1} base and A/G

8. Anti-codons:

Most codons of ams from Glycolysis have anti-codons that are codons for ams from the Citrate cycle - as a kind of "complementary poles". Is it perhaps possible to imagine that the two series of codons once originated from opposite strands of DNA (via tRNAs)? One such variant is shown in table 7:

$Glycolysis \rightarrow$	codons		anticodons	\leftarrow Citrate cycle		Mass, R
Ser	UC-		CGA	Arg1, 2		G2↔C2
Gly	GG-		GCC	Ala		
Cys	UG-U/C		ACA	Thr ACU	\rightarrow Ser2	
Trp	UGG		CCA	Pro		
209		+		335		$\rightarrow 544$
Tyr	UA-U/C		AUA,GUA	1 .		
Phe	UU-U/C		GAA	Glu		U2→A2
Leu2	UU-A/G		AAA	Lys		
Leul	CU-		CAG	Gln		
Val	GU-		GAC	Asp		
Ile1	AU-U/C		AAU	Asn		
Ile2	AUA		UAU, Tyr	-		
Meth	AUG		CAU	His		
544	544			416		→ 960
753				751		

Table 8: Anti-codons:

Among ams from Citrate cycle the AG-codons of double-coded Ser and Arg can only be derived in a second step through a change between optional U and C in 3rd base as from Thr and Pro.

Exchanges within group 416 in the table are possible

10. The bases - some annotations

Codon bases G, C, U, A in RNA; T instead of U in DNA: Some material from file Biochemistry 04:

1. Complementarities and inversions:

At least in actual cells of today the bases are synthesized in complementary ways: the purine type from the amino acid Gly as centre, the pyrimidine type from the amino acid Asp together with carbamoyl phosphate.

In both cases circa molecules of circa 60 A are added: Gly 75 + 60 = A-base 135, Asp 133 + carbamyl ~ 60 A to Asp 133 (- 2 x 18 at condensation to Orotate); cf. interval 159 - 100 in the ES-chain.

Both mass numbers of Gly and Asp are found in the ES-chain as intervals:

Gly 75 A = 292 - 367 Asp 133 A = 292 - 159...Sum **208** = 3'

It could also be observed that these numbers are inversions of each other:

75 \wedge **133**... x 10^x, = 3/4 - 4/3 x 100

Approximate inversions are also the mass sums of purine versus pyrimidine bases:

G 151+ A 135 = **286**. U 112 + C 111 + T 126 = **349**:

286 ∧ **349**.65 x 10⁻⁵

2. Exponent 2/3:

Pairs of the RNA-bases - with exponent 2/3 appear to be inversions of their complementary ones:

Fig 10-1: Pairs of bases as each other's inversions through exponent 2/3

2 x G-base 151 = 302. $302^{2/3} \wedge x 10^4 = 2 \times 111,08. \approx C$ -base 111 x 2 2 x U-base 112 = 224. $224^{2/3} \wedge x 10^4 = 2 \times 135,56. \approx A$ -base 135 x 2

Another relation to the ES-chain:

The single bases as bound (= -1) with exponent 2/3, (figure 10-2 below), times 10, give the sums G + A \approx 544, U + C \approx 460, sums 5'+4' and 4+3' in the ES-chain. With exponent 2/3 applied again on the four obtained numbers the sum becomes \approx 159 = 2' in the ESchain. First obtained four numbers without times 10 are \approx 100 = 1': Fig 10-2: Bases bound with exponent 2/3:

G: $150^{2/3} \ge 10 = 282,31$. A: $134^{2/3} \ge 10 = 261,86$...\$um 544,17 = 544. = 292+252 = "5 + 4"U: $111^{2/3} \ge 10 = 230,97$. C: $110^{2/3} \ge 10 = 229,58$...\$um 460,55 = 460. = 252+208 = "4 + 3"T: $125^{2/3} \ge 10 = 250$ C: $110^{2/3} \ge 10 = 229,58$...\$um 479,58 = 480. $= 960 \ge \frac{1}{2} \ge \frac{1}{2} \ge \frac{1}{2} \le \frac{1}{2}$

G + A give together the A-number sum for amino acids coded G or C, (first and second base ordering).

T + C give half the sum of amino acids coded A and U.

Number 100 and 159 in the Exponent series::

 $\begin{array}{l} 150^{2/3}+134^{2/3}+111^{2/3}+110^{2/3}=100,5.\approx 100.\ ("1").\\ 282,31^{2/3}+261,86^{2/3}+230,97^{2/3}+229,58^{2/3}=159,10\approx 159.\ ("2") \end{array}$

3. ES-numbers, a few first notes:

Parents of the bases (inosine 136 and orotate 156) = 292 = 5'

N-Z-division in 4 DNA-bases:

4 DNA-bases, sum 523 A: N-Z compared with numbers in the ES-chain:

Z: $272 = 544 \text{ x}^{1/2}$. G + C: 136, A + T 136 (- 8 in RNA with U-base = 128) N: 251 = 252, -1: G + C: 126, A + T 125 (- 6 in RNA = 119)

Mean value of a base pair of DNA:

Mean value of a base pair of DNA happens to be a quotient from the ES-series:

544 / 208, x 100 = 261,5.

Five bases. including T = 635, circa 292/460 x 10^3 (634,7)

A step of polarization outwards can be recognized from G + C-bases to U + A-bases, reminding of order of dominating groups in the ES-chain:

The bonds $G \equiv C$ are 3 versus 2 in U=A-pair and G + C include both N and O in the Hbridges, while these are "polarized" to only N in A-base, only O in U/T-bases.

4. Atoms in the bases - a 2-dimensional table

Number of atoms in 24 codons, 1st and 2nd bases:

Fig. 10-3: Atoms in the bases - a 2-	-dimensional table
--------------------------------------	--------------------

	С	N	Ο.	Н.,				
A	75	75		75 =	210+15	=	225	
G	55	55	11	55=	176		176	> 401
U	52	26	26	52 =	144+12	=	156	> 151
C	36	27	9	45 =	117	-	117	>2/3
	209+9	176+7	44+2	218+9				
-	218	183	46	227				
	\ 40	1 /	\ 27.	3 /				

A+G-bases: atom numbers \sim C + N U+C-bases: atom numbers \sim O + H

Number of atoms in 24 codons, 1st and 2nd bases:

For 23 ams, without AUA-codon for Ile2, the sums become

horizontally 401 - 15 = **386**, 273 - 12 = **261**, vertically 401 - 16 = **385**, 273 - 11 = **262**

(The division of 385 on N and C vertically in 209 - 176, the same as in the table of mixed codons.)

Sum of atoms in 24 ams = 674, 2 x 337. Assuming an equal distribution of bases in 3rd position we get the sum 1011 = sum of the whole ES- series:

 $\frac{292 - 252}{544} - \frac{208 - 159 - 100 - 0}{467}$ Sum 1011

Number of atoms in the bases and adding equal number in 3rd base:

13 U with 12 atoms = 156, + 6 x 12 = 228 15 A with 15 atoms = 225, + 6 x 15 = 315...**Sum 544 -1** 11 G with 16 atoms = 176, + 6 x 16 = 272 9 C with 13 atoms = 117, + 6 x 13 = 195...**Sum 467**

The equivalences could be connected with the function that the bases have as coenzymes in relation to the different classes of substances. Roughly:

U-base (UTP) with carbohydrates (with dominating atom O), C-base (CTP)- with lipids (characterizing atom may be said to be H) G-base (GTP) with proteins (with typical atom N). A-base: (ATP), main energy storage and with transporting function ? (C-skeleton?)

5. Bases U, A, G from "phase waves":

(From index file, figure 01-1..) Quotients between wavelengths (n = 2, m = 5, 4, 3) in the Balmer series times 10^2 happen to give the mass numbers of U- and A-bases too (112 and 135) and approximately the G-base (151,2), which could awake some suspicions...* (Quotients as a kind of phase waves? Alleged not to carry any information!) Fig. 10-4: From Balmer series for spectral lines of hydrogen:

a. 1/4 - 1/25 = 0.21. **b.** 1/4 - 1/16 = 0.1875 **c.** 1/4 - 1/9 = 0.13889.

a/b x 100 = 112 = U-base (mass number) b/c x 100 = 135 = A-base " a/c x 100 = 151,2. 151 = G-base "

(AUG = starting codon at protein synthesis. UAG = usually Stop-codon. C-base a secondary development from the U-base.)

(C-base eventually later developed to give two pairs? Eventually from a quotient between a spectral line of hydrogen and oxygen.

Or cf. last term in c. = 1/9, x 1000, = 111,1. C-base = 111)

6. Just some numbers. a selection of operations

a) Sum of 1st and 2nd bases in 24 codons = 6141. Quotient to sum of 24 ams R + B unbound 3276:

 $6141 / 3276 = 1..8745 \sim 1.875$. = $15/8 = 5 \times 3 \times 1 / 4 \times 2$, odd/even d-degrees.

(Cf. 0.1875, 2nd spectral line of hydrogen.

For number 6141 = number 1357 transformed to number base system (nb-x) 6, see file 19, fig. 19-3.

b) DNA-bases with +2 for double-bonds in the rings:

A = +8, G = +6, C = +4, T = +2 = **543**.

c) - 14 (A+T = 261), \land , x 10⁷ = 2736.7 <u>- 10 (G+C = 262), \land , x 10⁷ = 3816.8</u> Sum = 6553.5 = 2 x 3276.76. ~ 2 x 24 ams R + B unbound

 $[6 \times 509 (24 \text{ baser RNA}) = 3054, \land, \times 10^7 = 3274.4]$

d) 4 RNA-bases = 509 and number 32

 $25/2\pi$, x 100 = 509 (509.3) (4th root of 32, x 100 ~ 752.12 x10^-2, 752 half the sum of 24 ams R)

e) G/5 + A/4 + T/3 + U/2 + C/1 = 273 (272.95), 273 the mean value of two ams R+B unbound

f) 4 DNA-bases = 523 A: $5232 = 2735.29 \times 10^{2}$ 2735 = sum of 20 amino acids, R+B-chains, without the extra set of 4 ams with two codons.

g) G-base, mass number from the simple dimension chain:

1 / 543 + 1 / 210, $\land = 151.43$. ~ G-base 151

More material may be found in files about biochemistry: The protein synthesis, Synthesis of the bases, Numbers DNA/RNA

11. Transmitters and the ES-chain

Transmitters

Several transmitters show up to have halved mass numbers of the ES-series (-/+1):

Fig 11-1: Some transmitters:

The expo	nent series	Transmitters			
"5"	$= 292 = 2 \times 146$	146 = Acetylcholine			
"4 + 1"	= 352 $=$ 2 x 176	176 = Serotonin			
"3"	= 208 $=$ 2 x 104	104 = Choline			
"3"	= 208 = 2 x 104	$104 - 1 = \gamma$ -Aminobuturate			
"4"	= 252 = 2 x 126	126 - 1 = Taurine			
"5"	= 292 = 2 x 146	146 + 1 = Glu			
"5 + 3 + 2"	$= 659 = 2 \times 329 (+1)$	329 = Cyclic AMP			
"3 + 2"	= 367 $=$ 2 x 183 (+1)	183 = Adrenaline			
"5 + 4 - 3"	= 336 = 2 x 168	168 + 1 = Noradrenaline			
"3 + 1"	= 308 $=$ 2 x 154	154 - 1 = Dopamine			

(Cf. opposite forces that cancel each other and only halved or polarized become active.)

Fig 11-2: Example Acetylcholine:



*To Section II: Simpler chains - comparisons.

A survey of sums of amino acids derived from the ES-chain on next page.

The chain 5-4-3-2-1-0 with exponent 2/3, x 100, abbreviated numbers:										
292 - 252 - 208 - 159 - 100 - 0										
	<u>،</u>	"5" -	"4" - "	·3" - "2	2 " - "1"	" –	0			
20 + 4 ams		1504	2(5+4+	3) * (See no	ote)		in E	xponent series =		
Pairs of codon groups										
G1 + C1 =	G2 + C2	544	= 5 + 4				752	2 - 208		
U1 + A1 =	U2 + A2	960	= 5 + 4 + 3	3 + 3			752	2 + 208		
C1 + U1		816	= 5 + 4, +	$\frac{1}{2}(5+4) =$	2(4+3) - 1/2	2 x 3	544	$+272 (\frac{1}{2} \times 544)$		
G1 + A1		688	$= 2 \times 3, + \frac{1}{2}(5+4) = 2 \times 5 + \frac{1}{2} \times 3$				416 + 272 "			
C2 + U2		570	=2(5+4-2-1)				2(544 - ,259)			
G2 + A2 934 $= 2(3 + 2 + 1)$ $2(208 + 259)$								08 + 259)		
			Individu	ial codon g	roups (-/+	one	unit)			
G1		191	= 5 - 1			- 1	292	-101 (CG = 101)		
C1		353	= 4 + 1			+ 1	252	+101 (CG = Arg)		
C2		133	= 5 - 2				292	- 159		
G2		411	= 4 + 2				252	+159		
U2		437	= 5 + 4 - ((3 - 1)		+1	544	- 107 (UA = 107)		
A2		523	$= 2 \times 3 +$	(3 - 1)		- 1	416	+107 (UA =Tyr)		
U1		463	=4+3+	½ x 3 - 1		- 1	460	+104 - 101		
A1		497	$= 5 + \frac{1}{2} x$	3 + 1		+1	292	+104 +101		
	A1	497	= C1 + 2 x	$3 - \frac{1}{2}(5 +$	4)		353	+ 416 - 272		
	U1	463	= G1	$+\frac{1}{2}(5+$	4)		191	+272		
		r	Co	don types			•			
Cross plus	Form:	770	= 2(5+4)	- 2)			2(54)	$44 - 159) = 2 \times 385$		
RNA plus I	Pair:	734	= 2 (3 + 2))			2(20	$(2+159) = 2 \times 367$		
Pure	G-C-codons	s, pure A-l	J -codons in	1^{st} and 2^{nd}	position (o	f RN	A-+	Pair-groups)		
GG+GC+C	G + CC	159	= 2				159			
UU+UA+A	$JU+UA+AU+AA \qquad 575 = 2 \times 3 + 2$					416 + 159				
		r	3 rd bas	se grouping	g (-/+ one)	unit)	•			
"2-base-coo	led" ams	335	= 5 + 4,	- 3		- 1	544	- 208, - 1		
A/G (A or 0	G) + U/C	1169	= 5 + 4 + 2	$2 \times 3, +3 =$	4 x 5	+1	960	+208, +1		
G1+A1 wi	thout	688-104	$= 2 \times 5$	"2-base-co	ded"		584	= 2 x 292		
"2-base-coo	led"			GG+GC+	GU+AC					
C1 + U1 wi	thout	816-231	$= 2 \times 5$	"2-base-co	ded"	+1	585	$= 2 \times 292, +1$		
"2-base-coo	led"			CG+CC+	CU+UC					
G2 + A2 w	ithout	934-102	$= 4 \times 3$				4 x 1	208 = 832		
"2-base-coo	led"									
C2 + U2 wi	thout	570-233	= 5 + 4 - 3			+1	544	- 208, +1		
"2-base-coo	led"									
Mass division on atoms in the 24 ams R-chains										
C-atoms 80)	960	= 5 + 4 + 3	3 + 3, - A +	U-coded a	ms	80 0	2		
S+O+N+H 544			$= 5 + 4$, \sim G+C-coded ams							
Н		152	= 4 - 1			152 H				
S+O+N 392			= 5 + 1				2 S, 10 O, 12 N			
Ams, R-chains, grouped according to end atoms in R-chains										
a) R with only CHx, H 420		420				including Gly				
b) R with S, O, no N		468	a)+b) = 888 = 2 (544 - 100)							
c) R with N	616	$= 2\ 208 + 100)$			including Gln,Asn					
Ams (mass) divided in groups according to number of C-atoms in R-chains										
4 C	7 C	3 C	0 C	2 C	1 C	9	С	See page 21 on		
584	198	305	1	162	124	1.	30	7C (Phe. Tyr)		
2 x 5		2 x 4	2 x 3			9 C (Trp)				

Table 9: Survey of mass sums of amino acids derived from the exponent series

* Reference numbers 5-4-3-2-1 written without quotation marks.