

**Earlier findings and operation:  
16 files from homepage u5d.net in one pdf-file**

**Sub titles:**

- 00 Survey of codon grouped totals of 24 amino acids
- 01 Square root out of 6-figure numbers in a 5-dimensional chain
- 02 Similarities of number divisions along different "axes of polarizations"
- 03 Atoms in 24 amino acids  
- mass division on atom types related to codon groups-
- 04 Z - L - p-numbers  
generating mass numbers of codon groups in R-chains
- 05 Triplet chains as approximation of sums of amino acids  
- two other formations -
- 06 Inversions of numbers  
generating sums among amino acids
- 07 Pyramids of numbers
- 08 3276 - 1504 - 544 - 960...  
Some other derivations of masses for codon groups
- 09 Chemical aspects on the distribution of codons
- 10  $385 \times 2$ , the "exchanged" amino acids,  
number 11 and number 7 etc.
- 11 B-chains — some more aspects
- 12 "Quark numbers"
- 13 Particle physics - some number connections?
- 14 3rd base grouping of codons
- 15 Numbers of amino acids generating mass numbers
- 16 "A-Z"-numbers of elements  
plus various other odds and ends

**Table:**

Codons and N-Z-A-sums for 24 amino acids: R-chains, 1<sup>st</sup> and 2<sup>nd</sup> base grouping:  
(Gln = Glu-NH<sub>2</sub>, Asn = Asp-NH<sub>2</sub>)

1 <sup>st</sup> base	2 <sup>nd</sup> base	Ams	N	Z	A	A	Z	N	Ams	1 <sup>st</sup> base	2 <sup>nd</sup> base
<b>G1</b>	G	Gly	-	1	1	1	1	-	Gly	G	<b>G2</b>
	C	Ala	6	9	15	101	56	45	Arg <sub>1</sub>	C	
	U	Val	18	25	43	130	69	61	Trp	U	
	A	Asp	28	31	59	47	25	22	Cys	U	
	A	Glu	34	39	73	31	17	14	Ser <sub>2</sub>	A	
<b>Σ 5</b>			86	105	<b>191</b>	<b>411</b>	224	187		<b>6 Σ</b>	
<b>C1</b>	G	Arg <sub>1</sub>	45	56	101	15	9	6	Ala	G	<b>C2</b>
	C	Pro	18	24	42	42	24	18	Pro	C	
	U	Leu <sub>1</sub>	24	33	57	31	17	14	Ser <sub>1</sub>	U	
	A	Gln	33	39	72	45	25	20	Thr	A	
	A	His	38	43	81						
<b>Σ 5</b>			158	195	<b>353</b>	<b>133</b>	75	58		<b>4 Σ</b>	
<b>U1</b>	G	Cys	22	25	47	43	25	18	Val	G	<b>U2</b>
	G	Trp	61	69	130	57	33	24	Leu <sub>1</sub>	C	
	C	Ser <sub>1</sub>	14	17	31	57	33	24	Leu <sub>2</sub>	U	
	U	Leu <sub>2</sub>	24	33	57	91	49	42	Phe	U	
	U	Phe	42	49	91	57	33	24	Ileu <sub>1</sub>	A*	
	A	Tyr	50	57	107	57	33	24	Ileu <sub>2</sub>	A*	
<b>Σ 6</b>			213	250	<b>463</b>	<b>437</b>	247	190		<b>7 Σ</b>	
<b>A1</b>	G	Ser <sub>2</sub>	14	17	31	73	39	34	Glu	G	<b>A2</b>
	G	Arg <sub>2</sub>	45	56	101	59	31	28	Asp	G	
	C	Thr	20	25	45	72	39	33	Gln	C	
	U	Ileu <sub>1</sub>	24	33	57	81	43	38	His	C	
	U	Ileu <sub>2</sub>	24	33	57	107	57	50	Tyr	U	
	U	Meth	34	41	75	58	31	27	Asn	A	
	A	Lys	31	42	73	73	42	31	Lys	A	
	A	Asn	27	31	58						
<b>Σ 8</b>			219	278	<b>497</b>	<b>523</b>	282	241		<b>7 Σ</b>	

\* Ileu 1: AU-U/C, Ileu 2: AU-A, codon differing only in 3<sup>rd</sup> base type.

**Abbreviations and ways of writing:**

Ams = amino acids (ama = amino acid)

20 ams --> 24 codons: i.e. 4 ams with double codons:

Arg1, 2: codons CG + AG-A/G;

Ser1, 2: codons UC + AG-U/C;

Leu1, 2: codons CU + UU-A/G; and

Ileu1, 2: codons AU-A +AU-U/C, only differing in third base

Codons where A or G in 3<sup>rd</sup> position makes no difference are counted as one and the same, as codons where U or C in 3<sup>rd</sup> position makes no difference.

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

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.

G1 - C1 - U1 - A1 = groups of ams coded by G-C-U-A respectively as first base.

G2 - C2 - U2 - A2 = " " as second base.

Types of codons, with respect to 1<sup>st</sup> and 2<sup>nd</sup> base, used denominations:

"Cross-codons" = GU-UG-AC-CA Val - Cys, Trp - Thr - Gln, His

"Form-codons" = GA-UC-AG-CU Asp, Glu - Ser1 - Arg2, Ser2- Leu1

"Pair-codons" = GG-UU-AA-CC Gly -Phe, Leu2 - Asn, Lys - Pro

"RNA-codons" = GC-UA-AU-CG Ala - Tyr - - Meth, Ile1, Ile2 -Arg1

6 ams in each group.

"The exponent series", the 5-4-3-2-1-0-chain of numbers with exponent 2/3, x 100:  
=  $5^{2/3} \times 100$ ,  $4^{2/3} \times 100$  etc.

In some places a shortened way of writing is used: "5", "4" etc.

^ = sign for inversion of numbers

~ = sign for "equivalent with" or "the same number as" or "circa".

3<sup>rd</sup> base:

8 ams with G or A in 3<sup>rd</sup> place: A/G, or either A or G, for instance Glu GA-A/G, and Meth AUG

8 ams with U or C in 3<sup>rd</sup> place: U/C, for instance Asp GA-U/C

8 ams with indifferent base (G-C-U-or A) in 3<sup>rd</sup> place = "2-base-coded"

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

G = 151

A = 135

U = 112

C = 111.

"0-bases" = U, C (T)

"00-bases" = G, A, referring to the forms: single or double rings.

# 1. Survey of codon grouped totals of 24 amino acids

24 ams: R-chains, 1504 A  
 B-chains, 1772 A,.....sum **3276 A**

24 B-chains = 1772 A = 24 x 74 A (1776)  
 - 1 H in B-chains of Arg 1, Arg 2, Lys, Pro.

## R-chains:

G1 = 191 A	411 A = G2
<u>C1 = 353 A</u>	<u>133 A = C2</u>
544	544

U1 = 463 A	437 A = U2
<u>A1 = 497 A</u>	<u>523 A = A2</u>
960	960

N-sum of 24 ams, R: 676 N  
 |-- 152 H  
 Z-sum of 24 ams, R: 828 Z

## 3276, total sum of R+B-chains of 24 free ams, divided 1282-1994:

	<u>N</u>	<u>Z</u>	<u>A</u>	<u>A</u>	<u>Z</u>	<u>N</u>	
G1:	261	300	561	853	456	397	:G2
C1:	333	388	721	428	230	198	:C2
	<u>594</u>	<u>688</u>	<u>1282</u>	<u>1281</u>	<u>686</u>	<u>595</u>	
U1:	423	484	907	955	520	435	:U2
A1:	499	588	1087	1040	554	486	:A2
	<u>922</u>	<u>1072</u>	<u>1994</u>	<u>1995</u>	<u>1074</u>	<u>921</u>	

Something to note perhaps:

G1+C1: **1282** = 4 RNA-nucleotides, charged<sup>-3</sup>

A1+U1: **1994** = 4 RNA-bases' coenzymes -TP, charged<sup>-3</sup>

G1 + C1 = 1282 <-----712-----> 1994 = U1 + A1  
 G2 + C2 = 1281 <-----714-----> 1995 = U2 + A2

Triplet series from a dimension chain:

Outwards 543 - 432 - 321 - 210; Inwards: 012 - 123 - 234 - 345  
           **543**          **963**                          **714**  
 R-chains: = G+C -1 = A+U +3

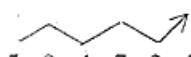
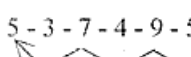
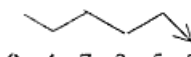
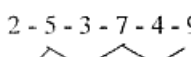
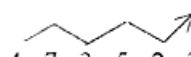
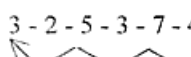
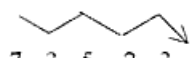
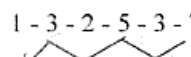
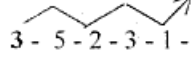
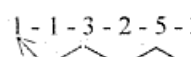
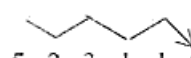
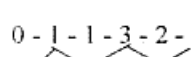
**A-N-Z sums of 24 ams:**

R+B-chains: 3276 A, 1516 N, 1760 Z  
 R-chains: 1504 A, 676 N, 828 Z

	R-chains:			R+B-chains		
	A	N	Z	A	N	Z
G1+C1:	<b>544</b>	244	300	1282	594	688
G2+C2	544	245	299	1281	595	686
A1+U1:	<b>960</b>	<b>432</b>	<b>528</b>	1994	922	1072
A2+U2	960	431	529	1995	921	1074

Displacements of only 1 unit (1-2 in R+B-chains) from 1st to 2nd base grouping.  
 Compare the similar equivalence in "cross-pairing" G+U / A+C

## Square roots out of 6-figure numbers in a 5-dimensional chain

$\begin{array}{cccccc} & 9 & 7 & 5 & 3 & 1 \\ / & \backslash & / & \backslash & / & \backslash \\ 5 & 4 & 3 & 2 & 1 & 0 \end{array}$	
 5-9-4-7-3-5	$\text{Cross- plus Form-coded ams +1}$ $\text{---> } \sqrt{\quad} = 771,19$ $> 1504,33 - 24 \text{ ams R-chains}$
 5-3-7-4-9-5	$\text{---> } \sqrt{\quad} = 733,14$ $\text{RNA- plus Pair-coded ams -1}$
 9-4-7-3-5-2	$\text{---> } \sqrt{\quad} = 973,32$ $> 1477,05 \quad 20 \text{ ams B-chains}$
 2-5-3-7-4-9	$\text{---> } \sqrt{\quad} = 503,74$
 4-7-3-5-2-3	$\text{---> } \sqrt{\quad} = 688,13$ $/ Z-1$ $> 1258, 55 \quad 20 \text{ ams R-chains}$
 3-2-5-3-7-4	$\text{---> } \sqrt{\quad} = 570,42$ $\backslash N+1$
 7-3-5-2-3-1	$\text{---> } \sqrt{\quad} = 857,46.$ $> 1221,5 (?) \sim 11 \times 111, \Lambda = 819 \times 10^6,$ $819 = 1/4 \times 3276, \text{ the whole sum } 24 \text{ ams}$
 1-3-2-5-3-7	$\text{---> } \sqrt{\quad} = 364,06$
 3-5-2-3-1-1	$\text{---> } \sqrt{\quad} = 593,56.$ $> 930,09 \quad 24 \text{ ams B-chains } Z-1 (2)$
 1-1-3-2-5-3	$\text{---> } \sqrt{\quad} = 336,53$ $> 1759,77 \sim 24 \text{ ams } Z = 1760$
 5-2-3-1-1-0	$\text{---> } \sqrt{\quad} = 723,26$ $> 829,68 \quad 24 \text{ ams, R-chains, +1 (2)}$
 0-1-1-3-2-5	$\text{---> } \sqrt{\quad} = 106,42$
$\downarrow$	
$2-3-1-1-0 \text{ ---> } \sqrt{\quad} = 152$ $= \text{number of H i } 24 \text{ ams R. } 828 - 152 = 676 = N\text{-number}$	

$$[4-7-3-5-2-3] - [3-2-5-3-7-4] \text{ ---> } \sqrt{\quad} = 384,9 \sim 385, 1/2 \times 770:$$

Number 385: sum of ams exchanged from G-C-groups to A-U-groups and inversely between 1<sup>st</sup> base order and 2<sup>nd</sup> base order = Cross- plus Form-coded ams:

<b>385</b>	GA Glu	CA His		UG Trp	AG Arg
<b>209</b>	GA Asp	CA Gln		UG Cys	AG Ser
<b>176</b>	GU Val	CU Leu		UC Ser	AC Thr
<b>Σ 770</b>	175	210		208	177
	<b>385</b>			<b>385</b>	

## 2. Similarities of number divisions along different " axes of polarizations":

### 2-1. A-N-Z: Summary 24 ams, different codon pair groups:

	R-chains: "RNA"-pairing			R-chains: "Cross"-pairing			
	A	N	Z		A	N	Z
G1+C1:	544	244	300	G1+U1:	654	299	355
G2+C2:	544	245	299	A2+C2:	656	299	357
A1+U1:	960	432	528	G2+U2:	848	377	471
A2+U2:	960	431	529	A1+C1:	850	377	473

### 2-2. "Pair"-pairing. A-numbers:

$$\begin{array}{l}
 A1 + A2 = 2 \times 510 \\
 U1 + U2 = 2 \times 450 \\
 \hline
 > 751 \qquad 753 \qquad \times 2: \sim \text{a halving of the sum } 1504. \\
 G1 + G2 = 2 \times 301 \\
 C1 + C2 = 2 \times 243
 \end{array}$$

Compare the amino acids derived from the citrate cycle.

### 2-3. Note:

$$\begin{array}{l}
 G: 301 \sim Z \ G1 + C1 + 1 \\
 C: 243 \sim N \ G1 + C1 - 1
 \end{array}$$

### 2-4. "Form"-pairing, ~ same intervals:

	A	N	Z		A	N	Z
G1 + A1:	688	305	383	A1 - G1:	306	133	173
	<246	<123	<123	U2 - C2:	304	132	172
G2 + A2:	934	428	506				
C1 + U1:	816	371	445	A2 - G2:	112	54	58
	<246	<123	<123	U1 - C1:	110	55	55
C2 + U2:	570	248	322				

Note:

688 = Z-number for 20 ams, without the double-coded ams, Arg, Ser, Ile, Leu.

570 = N-number for 20 ams, "

Sum: 1258.

246 also = sum of the 4 double-coded ams, R-chains.

### 2-5. N- plus Z-numbers from opposite groups, R-chains:

$$G1 + G2: N, + C1 + C2: Z = 543$$

$$G1 + G2: Z, + C1 + C2: N = 545 \dots 544 \text{ } -/+ 1, \sim G+C$$

$$U1 + U2: N, + A1 + A2: Z = 963$$

$$U1 + U2, Z, + A1 + A2: N = 957 \dots 960 \text{ } +/- 3, \sim A+U$$

**2-6. G + A and U + C: A-numbers divided as R - B-chains, 24 ams:**

$$\begin{array}{l}
 \text{Total A-numbers} \\
 G1 + G2 = 561 + 853 = 1414 = 2 \times 707 \\
 C1 + C2 = 721 + 428 = 1149 = 2 \times 575, -1 \\
 U1 + U2 = 907 + 955 = 1862 = 2 \times 931 \\
 A1 + A2 = 1087 + 1040 = 2127 = 2 \times 1063, +1 \\
 \hline
 C+U\text{-groups, mean value} = 1505 = \text{sum of R-chains} + 1, \\
 G+A\text{-groups, mean value} = 1771 = \text{sum of B-chains} - 1 *
 \end{array}$$

$\left. \begin{array}{l} \leftarrow \\ \leftarrow \end{array} \right\} 1771^*$   
 $\left. \begin{array}{l} \leftarrow \\ \leftarrow \end{array} \right\} 1505$

\*Compare perhaps the role of A- and G-bases as coenzymes in the protein synthesis.?

**2-7. A-numbers R+B-chains divided as N - Z:**

$$G1 + U2 = 1516 = \text{the total number N of 24 ams. R+B}$$

$$G2 + U1 = 1760 = \text{the total number Z of 24 ams "}$$

$$C2 + A1 = 1515 = N - 1.$$

$$C1 + A2 = 1761 = Z + 1,$$

**2-8. 1468-1808, same A-sums and divisions N-Z, R+B-chains:**

$$G1 + U1: \begin{array}{ccc} \underline{N} & \underline{Z} & \underline{A} \\ 684 & 784 & 1468 \end{array} = \begin{array}{ccc} \underline{A} & \underline{Z} & \underline{N} \\ 1468 & 784 & 684 \end{array} : C2 + A2$$

$$C1 + A1: \begin{array}{ccc} \underline{N} & \underline{Z} & \underline{A} \\ 832 & 976 & 1808 \end{array} = \begin{array}{ccc} \underline{A} & \underline{Z} & \underline{N} \\ 1808 & 976 & 832 \end{array} : G2 + U2$$

$$G1 + G2 + U1 + U2: N = 684 + 832 = 1516 = \text{total sum N}$$

$$C1 + A1 + C2 + A2: Z = 976 + 784 = 1760 = \text{total sum Z}$$

**2-9. Grouping after 1st base type equivalent with 1st code base groups +/-2:**

"00"-bases = G, A. "0"-bases = C, U:

R-chains 24 ams:

$$\begin{array}{l}
 G2 \\
 00_1 \leftarrow = GG, GC, AG, AG, AC = 193 \sim G1\text{-coded ams} + 2 \\
 C2
 \end{array}$$

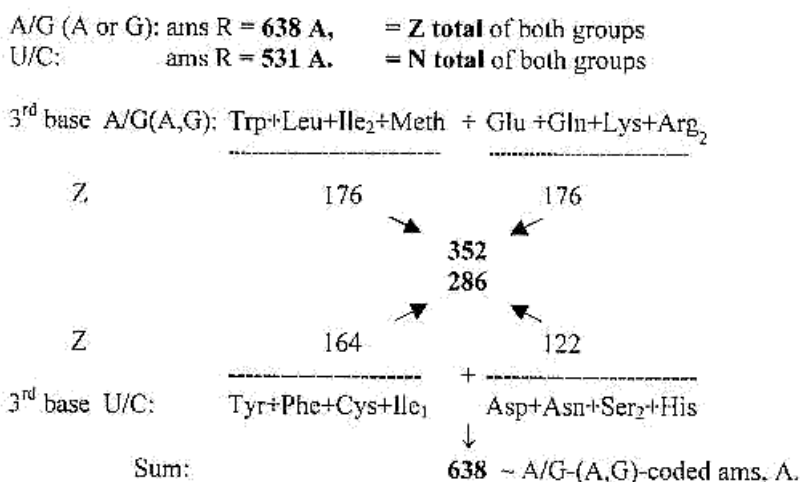
$$\begin{array}{l}
 G2 \\
 0_1 \leftarrow = UG, UG, UC, CG, CC = 351 \sim C1\text{-coded ams} - 2 \\
 C2
 \end{array}$$

$$\begin{array}{l}
 A2 \\
 0_1 \leftarrow = CA, CA, CU, UA, UU, UU = 465 \sim U1\text{-coded ams} + 2 \\
 U2
 \end{array}$$

$$\begin{array}{l}
 A2 \\
 00_1 \leftarrow = GA, GA, GU, AA, AA, AU, AU, AU = 495 \sim A1\text{-coded ams} - 2 \\
 U2
 \end{array}$$



## 2-10 Division between 3rd bases in types and N-Z:



To the left: ams with U1 or U2 in their codons,  
 all derived from stations before the citrate cycle.  
 To the right the other.

Number 638 divided 352-286:

$$\begin{array}{r}
 2x^2\text{-chain} \times 11: \\
 (x = 5-4-3-2-1)
 \end{array}
 \begin{array}{r}
 550 - 352 = 198 = 88 \cdot 22 \\
 \hline
 352 \quad 286 \\
 \text{A/G} \quad \text{U/C} \quad \text{Z}
 \end{array}$$

## 2-11. Basic and acidic ams: N-Z-numbers divided as on the 2 ams in each pair:

R+B-chains, Glu and Asp non ionized:

Acidic:

Asp:	$\frac{Z}{70}$		$\frac{N}{63}$
	$> \frac{148}{= \text{Glu}+1}$		$\frac{132}{= \text{Asp} - 1} <$
Glu:		A-numbers	

Basic:

Lys:	$\frac{80}{80}$		$\frac{66}{66}$
	$> \frac{174}{= \text{Arg}}$		$\frac{146}{= \text{Lys}} <$
Arg:		A-numbers	

Asp: 133 A ~ N, acidic +1      Lys: 146 A ~ N, basic  
 Glu: 147 A ~ Z, acidic - 1      Arg: 174 A ~ Z, basic

## 2-12. Cross- plus Form-coded ams, A-numbers, R-chains: same division between G and C, A and U as between N and Z (+/-1 in A1-U1-groups):

$$\begin{array}{r} \text{G1:} \\ \text{Val GU} \\ \text{Asp GA} \\ \text{Glu GA} \end{array} \bigg| - 175 \quad 177 - \begin{array}{r} \text{AC Thr A1:} \\ \text{AG Ser}_2 \\ \text{AG Arg}_2 \end{array}$$
  

$$\begin{array}{r} \text{C1:} \\ \text{Leu CU} \\ \text{His CA} \\ \text{Gln CA} \end{array} \bigg| - 210 \quad 208 - \begin{array}{r} \text{UC Ser}_1 \text{ U1:} \\ \text{UG Cys} \\ \text{UG Trp} \end{array}$$


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$$\begin{array}{r} = 385 \\ / \quad \backslash \\ \underline{Z} \quad \underline{N} \\ 210 \quad 175 \end{array} \quad \begin{array}{r} = 385 \\ / \quad \backslash \\ \underline{N} \quad \underline{Z} \\ 176 \quad 209 \end{array}$$

Also:

N, total sum = 351 ~ Form-coded ams, A, -1

Z, total sum = 419 ~ Cross-coded ams, A, +1

$$\begin{array}{r} \text{R+B-chains:} \\ \text{B-chains} = 12 \times 74 \text{ A, -1} = 887 \text{A} \\ \text{R-chains} = \phantom{12 \times 74 \text{ A, -1}} = 770 \text{A} \end{array}$$

$$\text{N total R+B} = 351 + 12 \times 35 = 771 \text{N}$$

$$\text{Z-total R+B} = 419 + 12 \times 39, -1 = 886 \text{Z}$$

We have a connection N-number ~ Form-coded ~ R-chains, and  
Z-number ~ Cross-coded ~ B-chains.

## 2-13. Numbers 714-792 from the triplet series:

$$\begin{array}{r} \text{Triplets in the chain:} \\ \underline{543} \quad - \quad \underline{432} \quad - \quad \underline{321} \quad - \quad \underline{210} \\ 543 \qquad \qquad \qquad 963 \\ \text{G+C -1} \qquad \qquad \text{A+U +3} \end{array}$$

$$\begin{array}{r} 543 + 432 + 321 + 210 = 1506 \\ | \text{-----792} \\ 345 + 234 + 123 + 012 = 714^* \end{array}$$

$$5 \text{ G1} + 7 \text{ A2} = 191 + 523 = 714^*$$

$$5 \text{ C1} + 7 \text{ U2} = 353 + 437 = 790$$

$$\text{Sum of intervals in the triplet chain} = 3 \times 111 = 543 - 210 = 333$$

$$543 + 333 = 876 \quad 876 = \text{C1} + \text{A2}, \quad \text{U1} + \text{G2} = 874$$

$$963 - 333 = 630 \quad 630 = \text{A1} + \text{C2} \quad \text{G1} + \text{U2} = 628$$

\* 1258: sum of 20 ams R, without double-coded ams:

Triplet chain outwards - inwards:

$$\begin{array}{r} 543 \\ \phantom{5} \\ \phantom{5} \\ \phantom{5} \\ \phantom{5} \\ \phantom{5} \\ + 012 \\ \hline 543 \quad + \quad 714 \quad = 1257 \\ \text{G1+C1-} \quad \text{A1+U1-} \quad \text{(UU-codon of Leu deducted.)} \\ \text{coded ams -1} \quad \text{-coded ams} \end{array}$$

**2-14. Compare codon bases and nucleotides:**

RNA:	A	N	Z
G-base	151	73	78
C-base	111	53	58
G+C	<u>262</u>	<u>126</u>	<u>136</u>
A-base	135	65	70
U-base	<u>112</u>	<u>54</u>	<u>58</u>
A+U	<u>247</u>	<u>119</u>	<u>128</u>
4 bases	509	245	264

N total = 245 = A-number sum of A + C 246, -1

Z total = 264 = A-number sum of G +U 263, +1

### 3. Atoms in 24 amino acids, mass division on atom types related to codon groups:

#### 3-1. Distribution of the total mass on different atoms, R-chains:

C-atoms = 960 A

Other atoms = 544 A

	Quantity	Mass (u)		
C-atoms:	80	$\dot{a}$ 12 = 960	- 960	~ A+U-coded ams
O-atoms:	10	$\dot{a}$ 16 = 160		
N-atoms:	12	$\dot{a}$ 14 = 168	- 544	~ G+C-coded ams
S-atoms:	2	$\dot{a}$ 16 = 64		
H-atoms:	152	$\dot{a}$ 1 = 152		

Hence, we have the same partition of the mass on atoms, divided in these two groups, as in the main codon groups.

Atom types and their distribution on individual codon base groups of ams in 1st and 2nd base ordering, R-chains:

- Also an example of similar number divisions along different "dimensions of polarities".

1<sup>st</sup> base grouping:

Base	C	H	C+H		N	O	S	N+O+S
A	24	59	83	149	5	3	1	9
U	29	37	66		1	2	1	4
G	9	19	28	83	-	4	-	4
C	18	37	55		6	1	-	7
Sum:	80	152	$\leftarrow$		12	10	2	

2<sup>nd</sup> base grouping:

Bas	C	H	C+H		N	O	S	N+O+S
A	25	41	66	152	5	7	-	12
U	29	57	86		-	-	1	1
G	19	37	56	80	7	1	1	9
C	7	17	24		-	2	-	2
Sum:	80	152	$\leftarrow$		12	10	2	

Quantity of C+H in ams with A+U-codons corresponds to total number of H: 152  
 " C+H in ams with G+C-codons corresponds to total number of C: 80

### 3-2. A comparison of the total number of atoms in the R-chains with number of C-atoms in R+B-chains:

Total of atoms in R-chains = 256:

Total of C-atoms in R+B-chains: 128. Quotient 2/1.

<u>R-chains, number of atoms:</u>	<u>C-atoms, number in R+B-chains:</u>	
A1 + U1 = 162 = 2 x 81 -----	81	(81 A = His, R)*
G1 + C1 = 94 = 2 x 47 -----	47	(47 A = Cys, R)*
A2 + U2 = 165 = 2 x 82 + 1 -----	82	
G2 + C2 = 91 = 2 x 46 - 1 -----	46	

Can this halving above in the codon groups be more than a coincidence?

How to express the "law" behind this, if any?

Which skeleton as the C-skeleton doubles its nuclear positions in its active reactive or "radical" part ? One example could be the doubled projection of the body in the brain?

\* Footnote:

a) His + Cys co-operate in the active centre of the enzyme which breaks P-fructose-P into two halves, the start of the glycolyse.

$$\begin{aligned}
 &81 \times 47 \\
 &= 3807 \\
 &\quad |----- \underline{3276} = 24 \text{ ams R+B, A-number} \\
 &\quad 7083 \\
 &(\text{Mirrored numbers})
 \end{aligned}$$

#### Survey:

C-atoms: 24 ams: 128 R+B 1  
 All atoms: 24 ams: 256 R 2 quotient  
 All atoms: 20 ams: 384 R+B 3  
                   |- 84  
 All atoms, 24 ams: 468 R+B

Note: number 384 of 20 ams, without double-coded, is divided  
 - 207 in R-chains  
 - 177 in B-chains, approximately the same division as of number 385.

Note: A2 + C2: 104 atoms ~ number of C+N+O+S in all, R-chains  
> 24 ams

G2 + U2: 152 atoms ~ number of H in all, R-chains

Number of C-atoms in R+B-chains, 24 ams, = 128:

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

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

\*

#### 4. Z - L - p-numbers generating mass numbers of codon groups in R-chains:

##### 4-1. First, for comparison;

Triplet numbers in a dimension chain giving circa A @ N @Z-numbers:

$$\begin{array}{r}
 \text{"Triplet chain"} \quad 543 \quad | \text{-- } 543, + 1 = 544 = \text{G+C-coded ams, R} \\
 \quad \quad \quad \quad 432 \quad | \quad \quad \quad \quad \quad \quad \quad \quad \quad > 1504 \text{ A} \\
 \quad \quad \quad \quad 321 \quad | \text{-- } 963, - 3 = 960 = \text{U+A-coded ams, R} \\
 \quad \quad \quad \quad + \quad 210 \quad | \\
 \quad \quad \quad \quad = \quad 1506
 \end{array}$$

$$\begin{array}{r}
 210 = \text{Z-number } \underline{\text{UG-UC-AC-AG}}, +1 \quad \leftarrow = \text{G2-C2-codons of} \\
 321 = \text{Z-number } \text{UU-UA-AU-AA}, +2 \quad \quad \quad \uparrow \quad \text{A1-U1-codons} \\
 432 = \text{N-number } \text{A1+U1}^* \quad \quad \quad \uparrow \\
 543 = \text{A-number } \text{G+C}, -1 \quad \quad \quad \uparrow
 \end{array}$$

\*431 in A2+U2.

Reduction or addition of 2 (H?) in relation to the triplet series, from 1506 to 1504?  
 It could perhaps be interpreted in several ways. A potential possibility for some ams (His or Trp ?) to bind another 2 H ?

Generally, +/- 2H is a main theme in biochemistry; -2H in the citrate cycle for instance.

##### 4-2. Z-L-p-numbers generating A-numbers of R-chains:

Starting with a conclusion: Original mass numbers in atoms are expressed in the electron shells and steps between levels in these shells.

The hypothesis here was that electron shells of atoms in molecules, when these get activated or "excited", step by step are raised towards the surface, towards higher levels (corresponding to later steps in a dimension chain), with a simultaneous suppression of inner, deeper shells, towards the Z-level, @ the level of L-shell @ the level of the p-orbital in atoms as C, N, O, S.

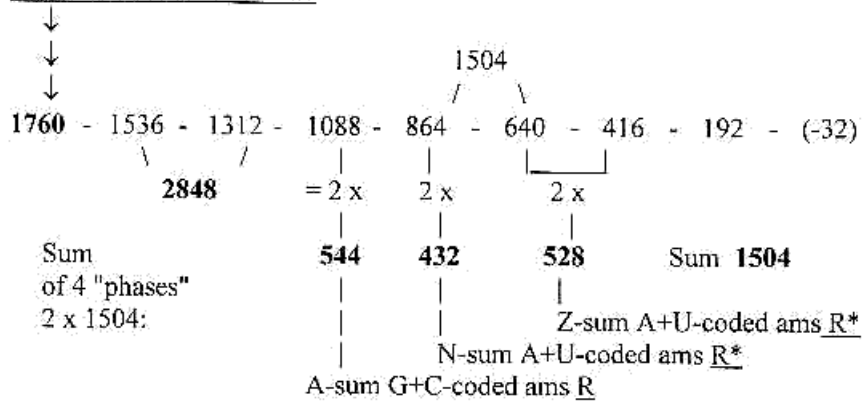
$$\begin{array}{r}
 5 \text{ -- } 4 \text{ -- } 3 \text{ -- } 2 \text{ -- } 1 \text{ -- } 0/00 \\
 \quad \quad \quad \text{A} \quad \quad \quad \text{Z}
 \end{array}$$

24 ams, R+B-chains:

Number of atoms C+O+N+S = 224. (H = 244)

With only 1 electron of the deeper levels suppressed in each step, from atoms C-N-O-S, we get the step by step reduction with 224 from the Z-number, giving following result:

Z-sum 24 ams R+B-chains:



\*(In 1st base grouping, +/-1 in 2nd base grouping.)

The presumed excitation in Z-numbers generates - reflects - reveals (?)  
the mass numbers doubled in different stages.

The L-shells in the atoms seem to be responsible for the R-chains of ams.

Note:

- In the 6th step, at number 416, the value of charge of the C-atom is Zero.

- 416 is the difference between mass sums of the A+U-group and the G+C-group,  
R-chains, 960 - 544.

- Sum of "phases" 2 and 3 1536 + 1312 = 2848.

2848 = A-number for 24 ams R+B-chains in peptide binding

Interval 224 in each step = 4 x 56: 56 A = B-chain in peptide binding.

1760 - 416 = 1344 = 24 B-chains in peptide binding.

Sum of all stages from 1536 to 416 = 24 x 244, the sum of H-atoms.

Compare the numbers of the "triplets" in point 1 from the dimension chain:

$$543 \times 2 = 1086 + 2 = 1088$$

$$432 \times 2 = 864 - 0 = 864$$

$$321 \times 2 = 642 - 2 = 640$$

$$210 \times 2 = 420 - 4 = 416$$

#### 4-3. Series of "phases" for R- and B-chains taken separately:

(Electron reduction as activation towards the surface.)

24 ams:

R-chains: 104 atoms C-N-O-S (+ 152 H-atoms). = - 104 per step

B-chains: 120 atoms C-N-O (+ 92 H-atoms). = - 120 per step

Z-sum B-chains = 932

Z-sum R-chains = 828. Difference 104 Z

$$\begin{array}{cccccccc}
 & / & 1504 & \backslash & & & & \\
 & / & \mathbf{1504} & \backslash & & 784 & 544 & \\
 | & / & \backslash & | & / & \backslash & / & \backslash \quad \underline{2 \times 152} \\
 \text{B: } \mathbf{932} & - & 812 & - & 692 & - & 572 & - & 452 & - & 332 & - & 212 & - & 92 & - & (-28) \\
 \\
 \text{R: } \mathbf{828} & - & 724 & - & 620 & - & 516 & - & 412 & - & 308 & - & \underline{204} & - & \underline{100} & - & (-4) \\
 | & \backslash & / & | & \backslash & / & & & & & & & & & & & & & & \mathbf{2 \times 152} \\
 & \backslash & \mathbf{1344} & / & & & & & & & & & & & & & & & & 720 \\
 & & \backslash & & / & & & & & & & & & & & & & & & \mathbf{1344} & /
 \end{array}$$

B-chains give in first 4 phases the A-sum of 2 x 1504, the sum of R-chains.  
2 x 1504 A

R-chains give in first 4 phases the A-sum of 2 x 24 B-chains in binding:  
2 x 1344 A.

H-atoms, sum 92 in B-chains, become the rest in the 7th step in the B-chain series.  
The last two steps, 6th and 7th, give 2x 152, the sum of H-atoms in R-chains,  
in both B- and R-chains.

[And how if we count with only 20 amino acids? That means minus 1 x 187 per  
step:

Z-sum of 20 ams = 1466:

Z-sum of 20 ams = 1466:

$$\begin{array}{cccccccc}
 1466 & - & 1279 & - & 1092 & - & 905 & - & 718 & - & 531 & - & 344 & - & 157 \\
 | & & \underbrace{\hspace{10em}} & & & & & & & & & & & & \\
 \mathbf{20 \text{ ams}} & & & & \mathbf{3276} & & & & & & & & & & \\
 \text{Z} & & & & \mathbf{24 \text{ ams R+B, A-number}} & & & & & & & & & & & & & & & & & ]
 \end{array}$$

\*



## 5. Triplet chains as approximation of sums of amino acids, two other formations:-

### 5-1. Triplet chain expanded:

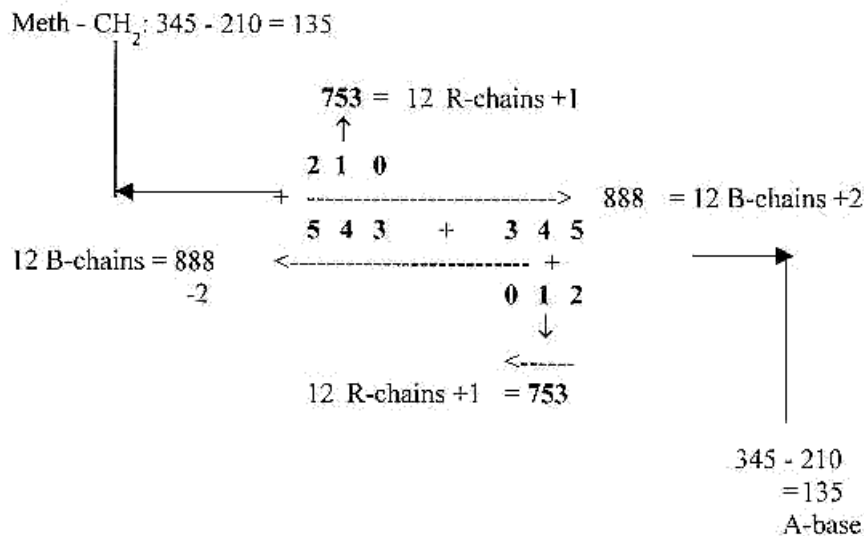
$$\begin{array}{r}
 \underline{987 + 876 + 765 + 654} \quad - \quad | \quad - \quad \underline{543 + 432 + 321 + 210} \\
 \qquad \qquad \qquad \downarrow \qquad \qquad \qquad \downarrow \qquad \qquad \qquad \downarrow \\
 \qquad \qquad \qquad 3282 \qquad \qquad \qquad 1776 \qquad \qquad \qquad 1506 \\
 \qquad \qquad \qquad \downarrow \qquad \qquad \qquad \downarrow \qquad \qquad \qquad \downarrow \\
 3282 = 24 \text{ ams R+B} \qquad \qquad \qquad \downarrow \qquad \qquad \qquad 1506 = 24 \text{ ams R} \\
 + 2\text{H in R-chains,} \qquad \qquad \qquad \downarrow \qquad \qquad \qquad + 2\text{H in R-chains} \\
 \text{and with + 4 H in B-chains.*} \qquad \qquad \qquad \downarrow \\
 \qquad \qquad \qquad \text{difference } 1776 \\
 \qquad \qquad \qquad = 24 \text{ B-chains } \dot{\text{a}} 74 \text{ A} \\
 \qquad \qquad \qquad \text{Each interval in the triplet series} \\
 \qquad \qquad \qquad = 111 = \frac{3}{2} \times 74.
 \end{array}$$

\* Cf. 4 ams, Arg1,2, Lys, Pro have -1 H in the B-chain.

Compare 3282: the difference between doubled products of base pairs:

$$\begin{array}{r}
 \text{G-base: } 151 \text{ A} \\
 \text{C-base: } 111 \text{ A} \\
 \text{A-base: } 135 \text{ A} \\
 \text{U-base: } 112 \text{ A} \\
 \downarrow \\
 \text{(A-numbers of bases with +1 for the bond to ribose.)}
 \end{array}
 \begin{array}{r}
 > 2 \times 151 \times 111 = 33522 \\
 \uparrow \\
 \text{-----} \rightarrow 3282 \\
 \downarrow \\
 > 2 \times 135 \times 112 = 30240
 \end{array}$$

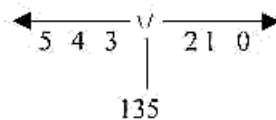
**5-2. Triplet chains, 543-210, x 2: a big survey with Meth and A-base: 24 amino acids from two simple dimension chains as triplet numbers:**



Arrows in reading directions:

24 B-chains = 2 x 888 A, 24 x 74 A, - 4 H in Arg<sub>1,2</sub>, Lys, Pro\*

24 R-chains = 2 x 753 A = 1506, - 2 H



135 A 74 0 74 0 74 0 74 0 ... (x10<sup>x</sup>) = series of B-chains before bindings.

135 = A-base, A-number. As coenzyme transporting ams to the t-RNA end at protein synthesis: AMP<sup>2-</sup> = 345 A.

135 = Meth 149 A without its utmost CH<sub>2</sub>-group (14 A), deducted when Meth is activated.  
Meth starts the RNA-synthesis, and is activated by the A-base (as coenzyme),

$$3282 / 2 = 1641, +/- 135 = <$$

$$1776 = 24 \text{ B-chains à } 74 \text{ A}$$

$$1506 = 24 \text{ R-chains, } +2\text{H}$$

A-base, A-number

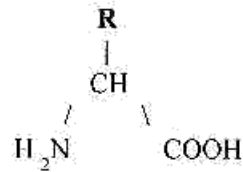
$$3282 = 6 \times 547$$

$$5 \times 547 = 2735 = 20 \text{ ams, without the 4 double-coded ams.}$$

\* At the protein synthesis 4 H must reasonably be added at Arg<sub>1,2</sub>, Lys and Pro for condensation

5-3. How is then the B-chains divided if according to the triplets "outwards" 543 and "inwards" 345?

B-chains in the amino acids:

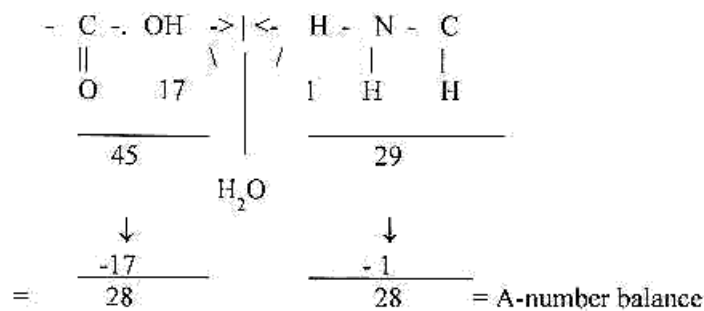


$$543 + 345 = 888 = 12 \text{ B-chains à } 74 \text{ A}$$

$$543 / 12 = 45,25 \sim 45 \text{ A} = \text{COOH}$$

$$345 / 12 = 28,75 \sim 29 \text{ A} = \text{H}_2\text{N-CH}$$

Peptide bonds = condensation =  $-\text{H}_2\text{O} = -12 \times \text{OH}_2 - 12 \times \text{H}$ .



$$\begin{aligned} \text{Cf. R-chains: mean value } 62,67.: \quad 543 / 12 &= 45,25 \text{ (} \sim \text{COOH)} \\ &+ \\ 210 / 12 &= 17,5 \text{ (} \sim \text{NH}_2 \text{ or OH-group)} \\ &| \\ &62,75 \\ &= \text{mean value if } +2\text{H in one phase, } 1506 \text{ A. } ] \end{aligned}$$

B-chain with +1 for the R-chain

$$\begin{array}{ccc} \text{H}_2\text{N} - \text{CH}_2 - \text{COOH} \\ \hline 30 \quad \quad 45 \quad \text{A: } 30 \times 45 = 1350, \wedge 74 \text{ } 0 \text{ } 74 \text{ } 0 \text{ } 74 \text{ } 0 \end{array}$$

74 = the A-number of B-chains without +1 for the R-chain.

\*

## 6. Inversions of numbers generating sums among amino acids:

### 6-1. 3276, total sum of 24 ams, R+B chains, as a periodic number:

$$\begin{aligned}
 & \frac{3276}{=} \\
 & \frac{555 \times 55 \wedge \times 10^8}{5 \times 111 \times 11 \times 5 \wedge \times 10^8} \\
 & 2 \times \left[ \frac{1}{55} - \frac{1}{555} \right] \times 10^5
 \end{aligned}$$

We get the sum 3276 as a periodic number from the inversions of numbers 555 and 55.

$$1 / [555 \times 55] = 3276 \ 00 \ 3276 \ 00 \ 3276 \ 00 \dots \times 10^x.$$

Note Number Five in a set of 5, in some sense corresponding to a dimension chain Divided 3 - 2 in quantity of fives - or ones.

1/55 = 181818181818.... as period = H<sub>2</sub>O, the A-number of water

1/555 = 180180180180.... as period = Glucose (fructose), A-number

Out of the difference - or product - we can derive the total A-number of the amino acids.

All ams but His has their origin from stations in the break down of glucose-fructose in the glycolysis and the following citrate cycle. (His is said to derive from A-base which is constructed mostly by amino acids.

### 6-2. Fructose in P --- P-bonds at the start of the glycolysis = 180 - 2H = 178 A:

$$178 / 543 \ 345 \ 543 \ 345 \dots = 3276 \quad (\times 10^x)$$

(Cf. The Triplet chain: 543 + 345 = 888 = 12 B-chains à 74 A.)

Another way to look at it: as a relation between H<sub>2</sub>O-molecules (?):

$$\begin{array}{r}
 \text{H}_2\text{O} \quad \quad \quad \text{H}_2\text{O} \\
 \diagdown \quad \quad \quad \diagup \\
 18 \ 0 \ 18 \\
 \hline
 55
 \end{array} = 3276 \times 10^{-1}$$

**6-3. A-numbers for B-chains periodically (cf. The big triplet chain):**

$$\begin{array}{r}
 \begin{array}{ccc}
 \xrightarrow{\quad} & \xrightarrow{\quad} & \begin{array}{ccc} 5 & 4 & 3 \end{array} & \begin{array}{ccc} 2 & 1 & 0 \end{array} \\
 \begin{array}{ccc} 5 & 4 & 3 \end{array} & \begin{array}{ccc} 3 & 4 & 5 \end{array} & \begin{array}{ccc} \text{-----} & \text{-----} & \text{-----} \\ \text{-----} & \text{-----} & \text{-----} \end{array} \\
 + \begin{array}{ccc} 0 & 1 & 2 \end{array} & - \begin{array}{ccc} 2 & 1 & 0 \end{array} & & & \\
 \hline
 = \begin{array}{ccc} 5 & 5 & 5 \end{array} & \begin{array}{ccc} 1 & 3 & 5 \end{array} & & & \\
 \begin{array}{c} | \\ \Lambda \end{array} & \begin{array}{c} | \\ \Lambda \end{array} & & & \\
 1/555 & 1/135 & & & \\
 | & | & & & \\
 | & \xrightarrow{\quad} & 74,0\ 74\ 0\ 74\ 0\ 74\dots \times 10^{-4}, \text{ B-chains} & & \\
 | & \xrightarrow{\quad} & 18,0\ 18\ 0\ 18\ 0\ 18\dots \times 10^{-4}, \text{ H}_2\text{O} & & 
 \end{array}$$

Difference: 56, 0 56 0 56 0 56... B-chains in peptide binding.

Cf.  $0,56\ 56\ 56\ 56\dots$ :  $543-345 = 210-012 = 198, \times \frac{1}{2} = 99$ ;  
 $1,8\ \Lambda = 0,55555555 + 99\ \Lambda = 0,0101010101 = 0,565656\dots$

G-base: the role of GTP at the protein synthesis?

$$\begin{array}{r}
 \text{Inversions: A-base } 135: \Lambda = 74,0\ 74\ 0\ 74\ 0\dots \times 10^{-4} \\
 \text{G-base bound: } 150\ \Lambda = 66,666666\dots \times 10^{-4} \\
 \hline
 \text{Difference: } 74,0\ 74\ 0\ 74\ 0\ 74\dots \times 10^{-5}
 \end{array}$$

This relation implies a 10-power displacement one step:  
 Could possibly the role of the G-base be to displace the amino acids towards nodes for condensation? Some more about B-chains here.

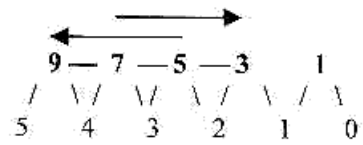
**6-4. Inversions of numbers on the superposed level of a dimension chain:**

$$\begin{array}{ccccccc}
 & & \xleftarrow{\quad} & & & & \\
 & 9 & 7 & 5 & 3 & 1 & \\
 / & \backslash & / & \backslash & / & \backslash & / & \backslash \\
 5 & 4 & 3 & 2 & 1 & 0 & 
 \end{array}$$

1-3-5-7:

$$\begin{array}{r}
 1 \quad 3 \quad 5 \quad 7 \\
 2 - 2 - 2 - 2 : \\
 = [1/2 + 1/8 + 1/32 + 1/128], \Lambda, \times 10^3 = \mathbf{1506}. (1505,9) \\
 = 24 \text{ ams R-chains} + 2 \text{ (Cf the sum of the simple Triplet chain} = 1506.)
 \end{array}$$

**6-5. Numbers with their inverted triplets added (!) - on the other side of the unity number 1: As "resonances" in the field of opposite direction ?**

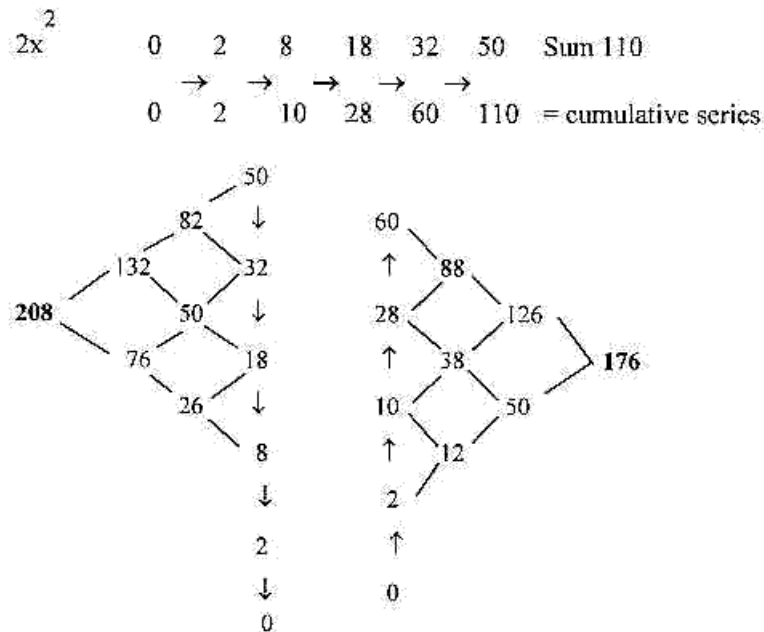


$$\begin{array}{r}
 \overline{579} \wedge \overline{173} \cdot 10^{-5} \\
 \backslash + / \\
 752 \quad \times 2 = 1504 = 24 \text{ ams R-chains} \\
 \overline{753} \wedge \overline{133} \cdot 10^{-5} \\
 \backslash + / \\
 886 \quad \times 2 = 1772 = 24 \text{ ams B-chains}
 \end{array}$$

\*

## 7. Pyramids of numbers:

### 7-1. An elementary chain: 0 - 1 - 2 - 3 - 4 - 5:



Sums of pyramids  $208 + 176 = 384$ .

Compare number 385, the amino acids changing position from G+C-group to A+U-group and the reverse from 1st base order to 2nd base order:

	<u>G1</u>	<u>U1</u>	<u>A1</u>	<u>C1</u>
209	G A Asp	U G Cys	Ser A G	Gln C A
385	G A Glu	U G Trp	Arg A G	His C A
176	G U Val	U C Ser	Thr A C	Leu C U

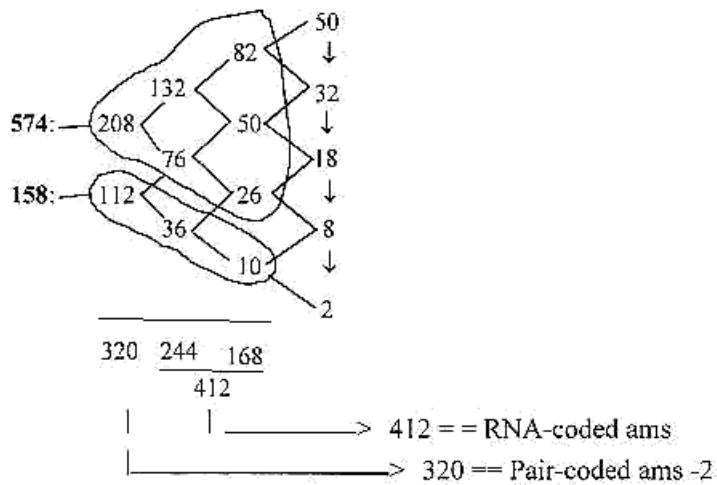
  

175	208	177	210
$\swarrow$ $\nwarrow$ $\swarrow$ $\nwarrow$ 385 385			

Note: Pyramids not complete, last step  $2 \rightarrow 1 \rightarrow 0$  (8-2-0) not included in number 208.

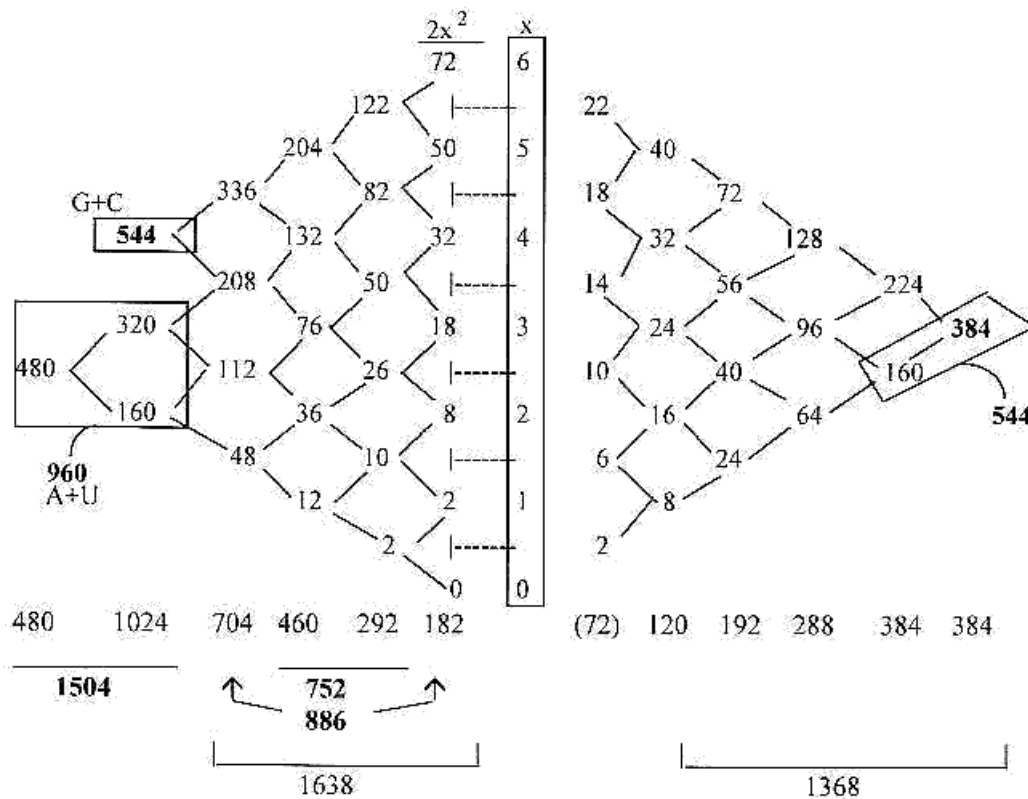
See subsets 132, 88:  $GA = AG = 132$ .  $GU + AC = 88 = UC + CU$

**7-2. If the number pyramid for 208 is developed with step 2-->1:**



158 + 1 = pure G-C-codons: GG+GC+CC+CG  
 574 + 1 = pure A-U-codons: AA+AU+UU+UA

**7-3. Expanded pyramid on the chain 2x2 including a step 5-6 and the "orbital series" as intervals (instead of the cumulative series above):**



- 1504 = 24 ams R



- $886 = 704 + 182 = \frac{1}{2} \times 24$  ams, B-chains
- $752 = 460 + 292 = \frac{1}{2} \times 24$  ams, R-chains (Cf. numbers of the Exponent series.)

- $1638 = \frac{1}{2} \times 3276$ , 24 ams R+G
- $1368 = \frac{1}{2} \times 2736 = 20$  ams R+B, +1

- $544 = \text{G+C-coded ams R}$
- $960, 2 \times 480, = \text{A+U-coded ams R}$

- If the left pyramid is completed, we get  $864 + 480 = 1344$ :  
 $1344 = 24$  ams B-chains in peptide binding à 56 A.

- Inner part of the left pyramid:  
 $208 \ 320 + 208 = 528 = \text{Z-number A+U-coded ams}$   
320  
 $112 \ 320 + 112 = 432 = \text{N-number A+U-coded ams.}$

How then derive a 6th step as expression for a 6th dimension, if we keep to the fundamental hypothesis or conceptual structure of 5 elementary ones?

We could presume the triplet of the superposed level, 9-7-5, divided in triplets  $654 + 321$  e.g.?

#### 7-4. 1234 as another kind of pyramids:

a)

$$1506 \leftarrow \begin{array}{r|l} 4 & \\ 34 & \text{--- } 272, \quad + \ 272 = \mathbf{544} = \text{G+C-coded ams} \\ \hline 234 & \\ 1234 & \text{--- } 1234, \quad - \ 272 = \mathbf{962} = \text{A+U-coded ams} +2 \end{array}$$

b) 20 ams, R-chains:

$$\begin{array}{r|l} 34 & + \ 01234 = \mathbf{1268} = 20 \text{ ams N, } -1 \\ 2736 \leftarrow & 234 \\ \hline & 1234 \quad - \quad = \mathbf{1468} = 20 \text{ ams Z, } +2 \\ & 01234 \end{array}$$

= 20 ams +1  
R+B-chains

c)

$$\begin{array}{r} 3 \\ 23 \\ \hline 123 \\ = 149 = \text{Meth's A-number R+B} \end{array}$$

Starting ams at the protein synthesis

d)

$$\begin{array}{r} 2 \\ 12 \\ \hline = 14 = \text{CH}_2\text{-group in Meth's R-chain} \\ \text{also} = \text{difference T-base in DNA - U-base in RNA} \end{array}$$

\*

## 8. 3276 - 1504 - 544 - 960...Some other derivations of masses for codon groups:

### 8-1. A chain $2x^2$ , ( $x = 5-1$ ) : 50 - 32 - 18 - 8 - 2, x lg 2:

Compare with the triplet series,  
And - on other pages - with the "Exponent series":

Abbreviated numbers:

$$2 \times 5^2, \quad \times \lg 2, \quad \times 100 = 1505. \quad 1504 = \text{sum of 24 R-chains}$$

$$2 \times 4^2, \quad \times \lg 2, \quad \times 100 = 963. \quad 960 = \text{U+A-coded ams R}$$

$$2 \times 3^2, \quad \times \lg 2, \quad \times 100 = 542. \quad 544 = \text{G+C-coded ams R}$$

### 8-2. Dimension steps as products of the type Force x Distance:

$$\begin{array}{ccccccc}
 5 & \longrightarrow & 4 & \longrightarrow & 3 & \longrightarrow & 2 & \longrightarrow & 1 & \longrightarrow & 0 \\
 = & & \frac{5 \times 4}{20} & & \frac{4 \times 3}{12} & & \frac{3 \times 2}{6} & & \frac{2 \times 1}{2} & & \\
 & & \backslash & & / & & \backslash & & / & & \\
 & & & & 32 & & & & 8 & & \\
 & & 20^2 & + & 12^2 & = & 544 & & & & \\
 & & & & & & & & & & > 1504 \\
 & & 32^2 & - & 8^2 & = & 960 & & & & (\text{A-U-level as superposed})
 \end{array}$$

(Sum of squares:  $20^2 + 12^2 + 6^2 + 2^2 = 584$ , = 2 x the number 292, cf. the "Exponent series".)

### 8-3. 1504 as product sums from 2-figure reading in "two--level chain":

$$\begin{array}{cccccccc}
 94 \times 47 & + & 73 \times 35 & + & 52 \times 23 & + & 31 \times 11 & = & 851 & \times & 10 \\
 & & & & & & & & & & \\
 9 & & 7 & & 5 & & 3 & & 1 & & \\
 / & \backslash & / & \backslash & / & \backslash & / & \backslash & / & \backslash & \\
 5 & & 4 & & 3 & & 2 & & 1 & & 0 \\
 & & & & & & & & & & \\
 49 \times 74 & + & 37 \times 53 & + & 25 \times 32 & + & 13 \times 11 & = & 653 & \times & 10 \\
 & & & & & & & & & & \\
 & & & & & & & & \text{Sum} & & 1504 \times 10
 \end{array}$$

C1 + A1-coded ams = 850 (U2 + G2-coded = 848) R-chains  
U1 + G1-coded ams = 654 (C2 + A2-coded = 656) "

(Cf. on menu Biochemistry "Numbers: DNA-RNA", point 1:  
In a corresponding way one gets the mass sums for DNA- and RNA-bases.)

Footnote:

Compare the square with numbers 1-9 placed to give the sum 15 in each row, vertically, horizontally and diagonally: - Diagonals rightwards = 654 / 852.

6	7	2	↗
1	5	9	→
8	3	4	↘

- Middle vertical row = 753,  $\frac{1}{2} \times 24$  ams R-chains +1.
- Middle horizontal row = 159 = ams with pure G-C-codon, R: GG+GC+CG+CC.

Cf. also Uranium, N-Z-numbers from such a square.

#### 8-4. $2^x$ -series and the number for the total sum, 3276:

$2^1$	$2^3$	$2^5$	$2^7$	$2^9$	$2^{11}$	Odd exponents	
2	+	32	+	512		= 546	
		8	+	128	+	2048	= 2184
							< 1638
							> 3276
4	+	64	+	1024		= 1092	
		16	+	256	+	4096	= 4368
							< 3276
$2^2$	$2^4$	$2^6$	$2^8$	$2^{10}$	$2^{12}$	Even exponents	

The whole sum:  $2^1 \rightarrow 2^{12} = 8190 = 5/2 \times 3276$

$$546 = 1/6 \times 3276$$

$$2184 = 2/3 \times 3276$$

$$1092 = 1/3 \times 3276$$

$$4368 = 4/3 \times 3276$$

$$\begin{array}{r}
 3276 \\
 / \quad / \quad \backslash \quad \backslash \\
 2^3 + 2^2 + 2^7 + 2^6, + 2^{10} + 2^{11} = 3276 \\
 \hline
 204 \qquad \qquad \qquad 3072 \\
 = \text{Trp, heaviest ams}
 \end{array}$$

#### 8-5. One suspect hypothesis in background papers:

The sum of outer poles in d-degree 4 = 10, eventually appearing as log base in outward direction, the sum of poles in d-degree 0/00 = 2 appearing as log-base in inward direction: 2 the principle number for divisions, polarizations.

Sum of a dimension chain:  $5+4+3+2+1 = 15$ :

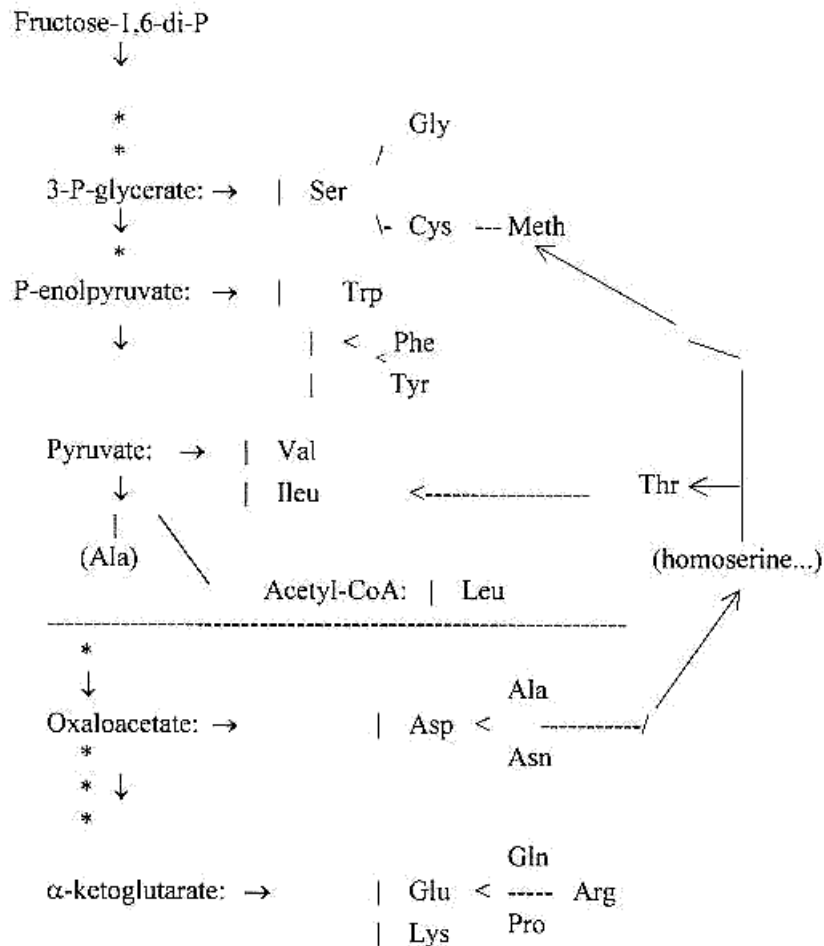
$$2^{15} = 3^{23} = 3276, 8 \times 10$$

## 9. Chemical aspects on the distribution of codons:

### 9-1. Glycolysis and Citrate cycle: derivation of the amino acids:

References: P.O.Karlson: "Biokemi", 1976. D.E.Nicholson: "Metabolic Pathways", 1976.

Amino acids from the different stations:

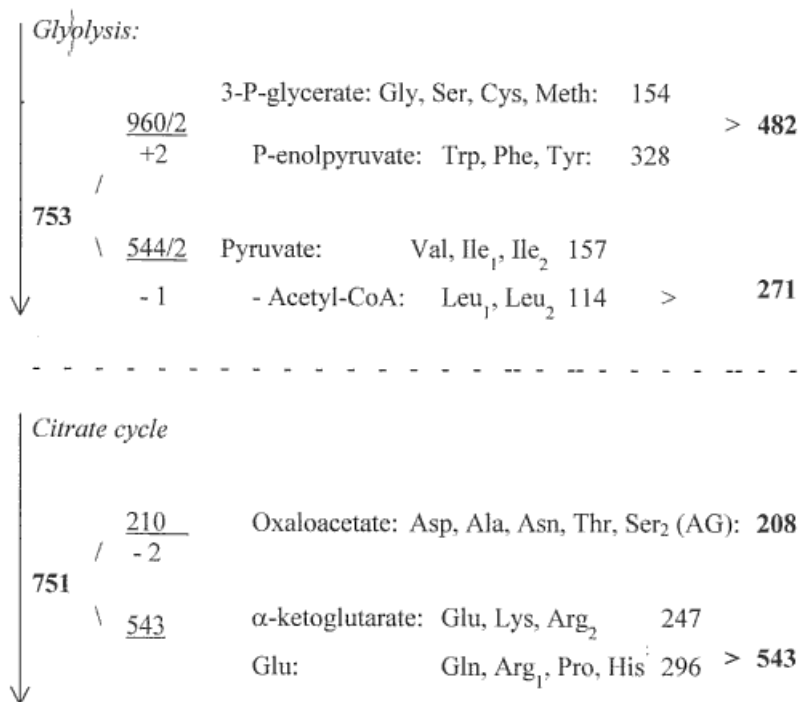


Not from these stations: His, from ATP->AMP, but breaks down to Glu.

There are obviously two simple ways to Ala, from Pyruvate and from Oxaloacetate

There is a bit unsure too, from which stations one ought to refer Thr and Meth along the "side way" via homoserine from Oxaloacetate.

**9-2. A-number distribution for R-chains of the 24 amino acids, 6 stations: Triplet numbers of a dimension chain: : 543 + 210 = 753:**

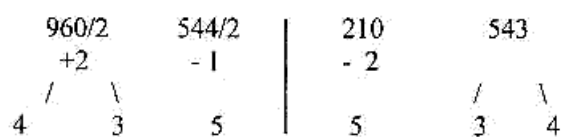


From the loop back from Oxaloacetate via Homoserine Thr is derived which can transform into Ileu.

This same loop connects Meth: Meth  $\rightleftharpoons$  Cys  $\rightarrow$  Ser  $\rightarrow$  Gly.  
That is why Ser<sub>2</sub> has been seen as derived from Oxaloacetate here.

With these options we have a halving (+/-1) of the total mass of ams, one half from glycolysis, one half from the citrate cycle inside the mitochondrias.

Number of amino acids and A-sums in the groups above:



According to the numbers we could probably also see the derivation way of ams in the opposite direction: from the key substance a-ketoglutarate, the C5-substance responsible for aminating the amino acids, towards oxaloacetate and outwards, to C4 and C3 substances.

Another key substance in the citrate cycle is Succinyl-Coa, which follows directly after a-ketoglutarate and leads to porphyrin rings: it could be said to mark the crossing point between the vegetable kingdom and the animal kingdom, between the Photosynthesis and the Glycolysis. We could presume that it marks a central point in a bigger loop or dimension chain.

We can also see the way from Pyruvate to a-ketoglutarate as a way of synthesis, that is directed inwards (as into the mitochondrias too), also meaning inwards higher dimension degrees in a chain.

### 9-3. Codons with U-base in 1st and/or 2nd position:

We should notice that all ams but Gly derived from stations in the glycolysis have the U-base in 1st or 2nd position of their codons, if we disregard the possibility of Ala deriving from Pyruvate; no ams from stations in the citrate cycle.

This circumstance could possibly have connection with the fact that U (and T) as coenzymes (-TP, -DP-, MP-forms) are the active ones in syntheses or break down of carbohydrates.

Cross- + Pair-coded, 370* -1		A-numbers, R-chains 370* +1		Form- + RNA-coded: 382 +2		382 -2	
Cys	UG	His	CA	Ser	UC	Arg	AG
Gly	GG	Pro	CC	Meth	AU	Glu	GA
Trp	UG	Gln	CA	Tyr	UA	Arg	CG
Phe	UU	Lys	AA	Ileu	AU	Ser	AG
Val	GU	Thr	AC	Ileu	AU	Asp	GA
Leu	UU	Asn	AA	Leu	CU	Ala	GC
	↓		↑		↓		↑
<i>Glycolysis</i>		<i>Citrate cycle</i>		<i>Glycolysis</i>		<i>Citrate cycle</i>	

\*Cf. "factor chains" 370:

$$\begin{array}{l}
 1 \times 54 = 54 \\
 2 \times 43 = 86 \\
 3 \times 32 = 96 \\
 4 \times 21 = 84 \\
 5 \times 10 = 50 \dots \text{sum } 370
 \end{array}$$

$$\sqrt{54-86-96-84-50} = 74,074+74074\dots \times 10^3$$

↓

B-chains as periodic number  
= 1 / 135, 135 = A-base.

$$2 \times \sqrt[4]{54-86-96-84-50} = \underline{544},331\dots$$

G+C-coded ams

#### 9-4. Functional groups / "endings" in R-chains of the the amino acids:

(Or typical atom groups.) Besides the list above and the comment on the U-base codons, there hasn't been possible to find anything indicating a connection between chemical aspects of the individual amino acids and the distribution of codons. (This according to the scientists.) Collective mass numbers seem more governing, according to the papers here.

	CHx	SH	OH COOH	H	NHx-CHx NHx-O
	Phe	Cys	Ser1	Gly	Trp
	Val	Meth	Ser2		Lys
	Ile <sub>1</sub>		Tyr		Arg1
	Ile <sub>2</sub>		Thr		Arg2
	Leu <sub>1</sub>		Asp		His
	Leu <sub>2</sub>		Glu		Asn
	Ala				Gln
	Pro				
A-sum R:	419	122	346	1	616
	\	/	\		/
	<b>541</b>			<b>963*</b>	
	~ G+C-coded -3			~U+A-coded +3	
	<b>2 x 210</b>			<b>2 x 543</b>	
	-1			-1	

This grouping, differentiating only the nonpolar group CHx from the other ones, connects to the triplet series 2 x (543 + 210) It could eventually reveal one figuration in the fairy dance of the amino acids ? (Cf. the position of C in relation to N and O on the page about "A-Z-"numbers.)

$$*543 = \frac{432 + 321 + 210}{963}$$

(If Gly is put together with the nonpolar group we get 2 x 210, 2 x 543, -2.)

\*

## 10. 385 x 2, "exchanged" amino acids, number 11 and number 7 etc.:

### 10-1. The "Cross"- and "Form"-coded amino acids:

Counting on 24 amino acids we get the same sums for G+C-coded and A+U-coded ams in 1st and 2nd base ordering. This implies that the ams changing position to the other group in both directions have the same mass or A-number sums, 385.

Amino acids with these codons are here named Cross-coded and Form-coded ams.

385:

	G1	U1	A1	C1
209	G A Asp	U G Cys	Ser A G	Gln C A
385	G A Glu	U G Trp	Arg A G	His C A
176	G U Val	U C Ser	Thr A C	Leu C U
	175	208	177	210
			385	
			385	

Row sums shows the same number partition as the columns:  
385 - 209 / 176.

In this arrangement we have the lighter ams in each pair of codons (differing only in 3rd base) on the first row, the heavier ones on the middle row.

About the 3rd base in the codons, note that

Row 1 has 3rd base = U / C, except Gln.

X a "pole exchange" in last step.\*

Row 2 has 3rd base = A / G, except His.

Row 3 has only "2-base coded" ams, i. e. 3rd base indifferent.

\*Cf. His the only ams not derived from stations in the glycolysis.



Number 11 - and factor 7 - dominates these groups:

$$\begin{array}{lcl}
 \text{Column 2 and 3:} & \text{Trp + Arg} & = 231 = 3 \times 77 & \text{UG + AG} \\
 & \text{Cys + Ser} & & \text{UG + AG} \\
 & & > = 154 = 2 \times 77 & \\
 & \text{Ser + Thr} & & \text{UC + AC}
 \end{array}$$

$$\begin{array}{lcl}
 \text{Column 1 and 4:} & \text{Glu + His} & = 154 = 2 \times 77 & \text{GA + CA} \\
 & \text{Asp + Gln} & & \text{GA + CA} \\
 & & > = 231 = 3 \times 77 & \\
 & \text{Val + Leu} & & \text{GU + CU}
 \end{array}$$

$$\begin{array}{l}
 231 \text{ divided: } 130 - 101 = \text{Trp} - \text{Arg} \\
 \quad \quad \quad 131 - 100 = \text{Asp+Gln} - \text{Val + Leu}
 \end{array}$$

$$\begin{array}{l}
 154 \text{ divided: } 78 - 76 = \text{Cys+Ser} - \text{Ser+Thr} \\
 \quad \quad \quad \underline{81 - 73} = \text{His} - \text{Glu} \\
 \quad \quad \quad = \frac{420}{2 \times 210} - \frac{350}{2 \times 175} \longrightarrow \text{Note: N} = 420 - 1, \text{ Z} = 350 + 1..
 \end{array}$$

Compare similarities of different number divisions:

$$\begin{array}{l}
 \text{B-chains} = 12 \times 74 - 1 = 887 \text{ A} \\
 \text{R-chains} = \quad \quad \quad = 770 \text{ A}
 \end{array}$$

$$\begin{array}{l}
 \text{N-sum R+B-chains} = 771 \text{ N} \\
 \text{Z-sum R+B-chains} = 886 \text{ Z}
 \end{array}$$

Numer 35 is the N-number of the unbound B-chains.

### 10-2. Number 385 a random one?

$$\begin{array}{l}
 \text{a. } 385 = 11 \times 35 = 11 \times [3^3 + 2^3] = 297 + 88 \\
 \quad \quad \quad \quad \quad \quad \quad \downarrow \quad \downarrow \\
 \quad \quad \quad \quad \quad \quad \quad 27 - 8 = 19, \times 11 = 209
 \end{array}$$

Cf. the human hand: 27 bones, divided 8 in the wrist, + 19 fingerbones.

**b. 385 = the side in a square with the diagonal 544 (the A-number for G+C-coded ams, R):**

$$544 / \sqrt{2} = 384,66.$$

**c. From a chapter named "Factor chains":**

$$\begin{array}{r}
 1 \times 55 = 55 \\
 2 \times 44 = 88 \\
 3 \times 33 = 99 \\
 4 \times 22 = 88 \\
 5 \times 11 = 55 \\
 \hline
 209 + 176 = 385
 \end{array}
 \quad
 \begin{array}{r}
 110 \\
 \times 2 = 198 \\
 \hline
 220 \quad 198 \quad 352
 \end{array}$$

Cross-coded ams:  $UG+UG+GU = 220$   
 $CA+CA+AC = 198$

Form-coded:  $GA+AG: 3 \times 88, UC+CU = 1 \times 88$

**d. Sums in the "2-figure-reading" of numbers in a dimension chain with superposed level:**

$$\begin{array}{r}
 94 + 73 + 52 + 31 + 10 = 260, \quad -52 = 208 \\
 \begin{array}{ccccccc}
 & 9 & & 7 & & 5 & & 3 & & 1 \\
 & \swarrow & \searrow & \swarrow & \searrow & \swarrow & \searrow & \swarrow & \searrow & \\
 5 & & 4 & & 3 & & 2 & & 1 & & 0
 \end{array} > 260 + 125 = 385 \\
 49 + 37 + 25 + 13 + 01 = 125, \quad +52 = 177
 \end{array}$$

$[543/210]$   
 e. 10 = 385,2. Quotient between triplet numbers as exponent

f. Numbers of ams: 5 + 5 in G1-C1-groups, 7+7 in A2+U2-groups:

$$385 = 5 \times 77 = 7 \times 55$$

See about numbers of ams giving mass numbers.

\*

## 11: B-chains — some more aspects:

### 11-1. A-number of unbound B-chain 74, in bonds 56:

a. Inversion of the A-base mass number 135:  $\Lambda = 74\ 0\ 74\ 0\ 74\ 0\ \dots \times 10^x$

b. Sum of B-chains of 24 ams: 1772:

$$1772 = \sqrt{\pi} \times 10^3 \quad (1772,45)$$

$$\sqrt{\pi \times 10^3} = 56,05. \quad 56 = \text{the B-chain bound.}$$

Factor chain" 370:

$$\begin{array}{r} 1 \times 54 = 54 \\ 2 \times 43 = 86 \\ 3 \times 32 = 96 \\ 4 \times 21 = 84 \\ 5 \times 10 = 50 \\ \hline \text{Sum} \quad 370 \end{array} \quad \begin{array}{l} \text{--->} \sqrt{54-86-96-84-50} = 74074,074074074\dots \\ \underline{370 = 5 \times 74.} \end{array}$$

Corresponding factor chain in inward direction (1 x 45, 2 x 34 etc.) gives the sum  $235 = 5 \times 47$ .

47 = Cys, R-chain: Cys-Cys-bonds in proteins are responsible for much of their more entangled structures

c. Number "quarks" (more on "quark numbers" on another page):

B-chain 74 A before peptide binding. Condensation - 18 = 56 A.

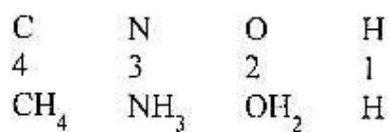
"Quark" 74 plus 2 "anti-quarks" 47, divided by 3, gives a new number as "quark" etc.:

$$\frac{74 + 2 \times 47}{3} = 56$$

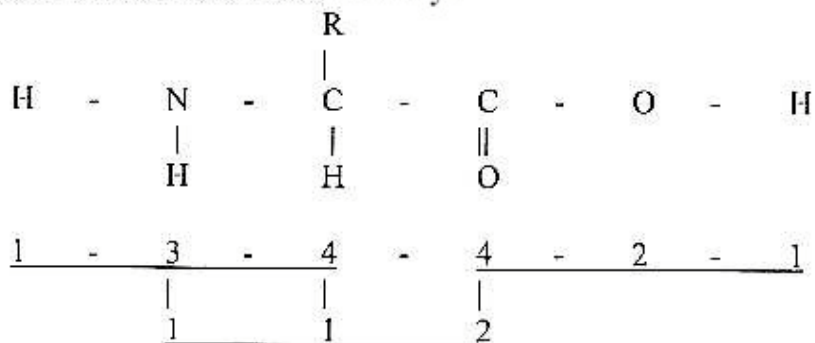
e. 3 B-chains à 56 A in peptide binding:

$56\ 56\ 56 \text{ --->} \sqrt{\phantom{x}} = 752,101, \times 2 = 1504,2. \sim 24 \text{ ams R}$

### 11-2. Valences for the atoms in the B-chains of ams:

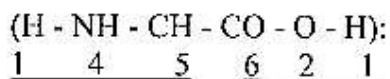


Valences in the B-chain seen linearly:



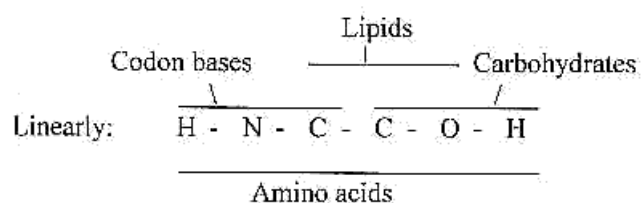
Read as  
3-figure  
numbers:  $\rightarrow 134 + 421 = 555$ , or  $344 + 211 = 555$ ,  
 $+ 112 = 667 = Z\text{-numbers of C-C-N.}$

Summed valences:



$\rightarrow 1-4-5 + 6-2-1 = 766 = Z\text{-numbers of N-C-C}$

### 11-3. Atoms of a B-chain and dominating atoms in main classes of substances:



\*

## 12. "Quark numbers" - a new invention, all rights reserved !

### 12-1. The charge unit in physics is supposed to be distributed on thirds in the so called "quarks", one anti-quark (-1/3) and two quarks (2 x +2/3) in protons.

A similar, simplified principle is here applied to numbers as mass units: a number (as mass units u) attracting two anti-numbers (mirrored ones; opposite direction) in a kind of "quark-anti-quark-relation". The addition of these then divided by three (3), giving a new number which in its turn can attract two new anti-numbers as "quarks" etc.

Formula for generating more and more complex "quarks":  
One-figure numbers become their own anti-quarks, generates only themselves again. So to "mirror numbers" as e.g. 101.

$$\frac{\bar{n} + 2n}{3}$$

Other numbers lead to chains of numbers - and after a certain amount of steps back to some earlier number in the chain, i. e. lead into a loop. - or to an one figure number (we could call it a "point loop").

The number in the loop which directly leads to the first starting number is named "loop number". For instance, number 36 is the "loop number" for number 54:

$$[36 + 2 \times 63] / 3 = 54.$$

### NADP generating the sum of amino acids:

Starting with 744 = NADP, mass number A:

$$744 + 2 \times 447, \times 1/3 = 546 = 1/6 \times 3276, + 2 \times 645, \times 1/3$$

	<u>1836 ~ p/e-quotient</u>											
744	-	546	-	612	-	348	-	678	-	810	-	282
		<u>546</u>		<u>960</u>								
		↓		↓						↓		
		G+C, +2		A+U								
Sums:		<b>1506</b>				<b>1770</b>						
		= R-chains +2				= B-chains -2						
		<hr/>										
		<b>3276</b>										

Mean value for 2 amino acids unbound is 273, x 2 = 546.

Note: 546 + 282 (= 612 + 1 x 216) = 828 = Z total for 24 ams R.

678 = N total + 2 for 24 ams R

	546	-	612	-	348	-	678	-	810	-	282
↑	<u>1638</u>				<u>1092</u>						
	= 1/2 x 3276				1/3 x 3276						
	<hr/>										
	<b>1638</b>										

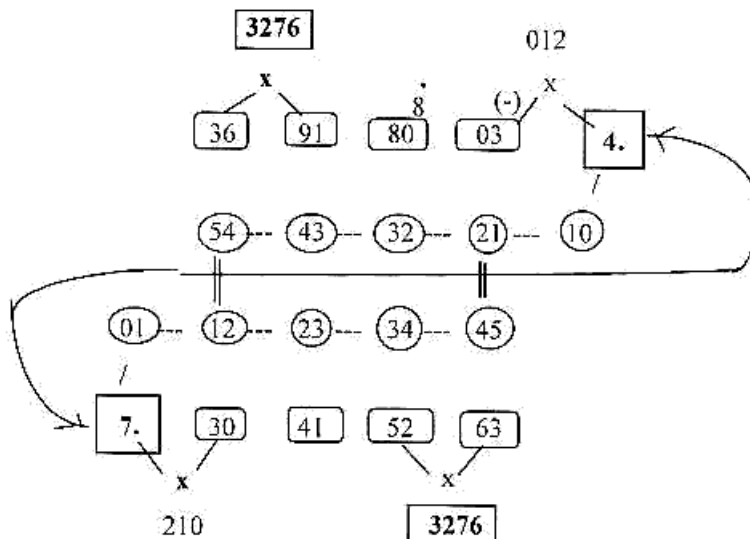
= 612, (= 1/3 x 1836, ~ the quotient p/e), + 2 x 216, x 1/3 etc., gives the number chain:

**12-2. The steps in a dimension chain as numbers 54 - 43 - 32 etc. developed in such quark loops: One example: 54 gives the chain :**

$$54 \rightarrow 48 \rightarrow 72 \rightarrow 42 \rightarrow 30 \rightarrow 12 \rightarrow 18 \rightarrow 60 \rightarrow 24 \rightarrow 36$$

$\uparrow$ 
—————
 $\downarrow$

**In the figure below the numbers for dimension degree steps are encircled, the "loop numbers" written above//below in squares.**



We get the total sum of 24 amino acids, 3276, as products of the loop numbers in steps 5@4, and 4@3 and inwards: 4@5, 3@4. (Cf. L-D-forms of ams?)

Note the "point loop numbers" in steps 1@0 and 0@1: 4 and 7, reminding of the 11 dimensions of the String theory: 4 said to be developed outwards, 7 "undeveloped", surely meaning inwards.

Footnotes:

a) Step 32 leads to a point loop 8, if we don't read 08,  $+ 2 \times 80, \times 1/3 = 32$ . Step 21 is the only step which doesn't lead back to itself, nor to a point loop but back to an earlier stage in its own chain. We have to read 03 to get 21 as a "quark".

b) In all step numbers 54, 45, 34 and 32, 23 (but not 43) partial sums of quark + 2 anti-quarks give partial sums of the type 612, 918 1224, i. e.  $1/3, 1/2$  or  $2/3$  of 1836, the approximated p/e quotient.

**12-3. Amino acids grouped according to the 3rd base: R-chains, mass numbers:**

3rd base grouping:

A/G (or A,G) coded ams:  $638, + 2 \text{ aq } (2 \times 836) = 2310$

U/C-coded:ams  $531, + 2 \text{ aq } (2 \times 135) = 801$

"2-base-coded" ams  $335, + 2 \text{ aq} (2 \times 533) = 1401... = 3 \times 1504$

$2310 = 3 \times 770 = 3 \times \text{Cross-plus Form-coded ams}$

$801 = 3 \times 267$

$> = 3 \times 734 = 3 \times \text{RNA- plus Pair-coded ams, } 2[3(367 -/+ 100)]$

$1401 = 3 \times 467$

#### 12-4. "Quark"-chains and 2-figure readings in the dimension chain, - a comparison:

$$\begin{array}{cccccccc}
 9 & 7 & 5 & 3 & 1 & & & \\
 \swarrow & \searrow & \swarrow & \searrow & \swarrow & \searrow & \swarrow & \searrow \\
 5 & 4 & 3 & 2 & 1 & 0 & & \\
 & & & \downarrow & & & & \\
 & & & \downarrow & & & & \\
 & & & \underline{207} & = & 47 + 73 + 35 + 52 & & \\
 & & & \underline{273} & = & 59 + 94 + 47 + 73 & & 
 \end{array}$$

Numbers on superposed level;

Quark 79 gives the number 273, as  $q + 2 \text{ aq}$ . (Cf. the  $\pi$ -meson,  $\pi/e$ -quotient)

quark 57 gives the number 207. (Cf. the  $\mu$ -lepton.)

(The  $\text{aq } 97 = \text{HPO}_3$ .  $75 = \text{Meth}$ , R-chain.)

273 also the mean value of two amino acids unbound, R+B.

Quark 147 is given from number 73:  $\text{Glu}$ , R, = 73, R+B = 147:

$$\begin{array}{cccccccc}
 & 9 & 7 & 5 & 3 & 1 & & \\
 & \swarrow & \searrow & \swarrow & \searrow & \swarrow & \searrow & \\
 5 & 4 & 3 & 2 & 1 & 0 & & \\
 & & & \downarrow & & & & \\
 & & & \downarrow & & & & \\
 & & & \underline{147} & = & 32 + 25 + 53 + 37 & & 
 \end{array}$$

**Cf. Glu, from a-ketoglutarate, ammoniating all amino acids,  
and compare "A-Z"-numbers and the atom N.**

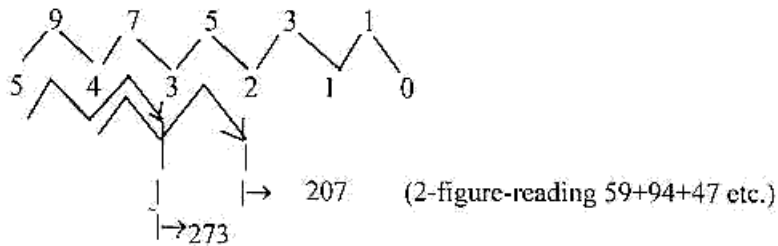
\*

### 13. Particle physics - some number connections?

- The  $\pi$ -meson and  $\mu$ -lepton
- Numbers for relative strength of the 4 known forces
- The numbers 27 - 8

#### 13-1. Numbers 546 + 960 out of numbers 207 and 273:

273 = quotient charged p/e. 207 = quotient m/e.



$$\begin{array}{r} 2 \times 273 = 546 = \text{G+C-coded ams R, } +2 \\ + 207 \\ \hline = 480 \end{array}$$

$$2 \times 480 = 960 = \text{A+U-coded ams R.}$$

→ 1506

#### 13-2. Ten-power relations between the strength of the 4 forces (old data):

**3276 = 24 ams, R+B.**

2 alternatives:

		a	b	
e.g.	$F_G$ :	-26	-39	a. $26 \times 12 \times 14 = 4368$
				$= 4/3 \times 3276$
	$F_{sv}$ :	0	-14	
	$F_{EM}$ :	+12	-2	b. $39 \times 14 \times 2 = 1092$
				$= 1/3 \times 3276$
	$F_K$ :	+14	0	



**13-3. Numbers 8 / 27, related to "The eightfold way" (Gell-Man) and such things and matrices among elementary particles:**

$$\frac{3^3}{27} \text{ --- } \frac{2^3}{8}$$

a) 1.  $\sqrt[3]{27/8} \times 10^3 = 1837,12 \sim \text{p/e-quotient} + 1$

2.  $\sqrt{8/27} \times 10^3 = 544,3. \sim \text{G+C-coded ams R}$

---

3.  $1/\sqrt{8} \times 10^3 = 353,55. \quad 353 = \text{C1-coded ams R}$

4.  $1/\sqrt{27} \times 10^3 = \underline{+ 192,45} \quad 191 = \text{G1-coded ams R}$

Sum  $\quad 546. = 2 \times 273.$

$\times 6 = 3276 = 24 \text{ ams R+G}$

b)  $[8/27]^4 \times 10^5 = \underline{770,734} \text{ 66}$

|  $\xrightarrow{\quad} \text{RNA- plus Pair-coded ams}$

|  $\xrightarrow{\quad} \text{Cross- plus Form-coded ams}$

**13-4. B-chains of ams:**

B-chains bound, linearly: N - C - C - O,  
 Z-value on L-shell level: 5 4 4 6

$$5446, \Lambda \text{ (inverted)} = \underline{1836,21} \times 10^{-7},$$

↓  
 circa the p/e-quotient.

\*

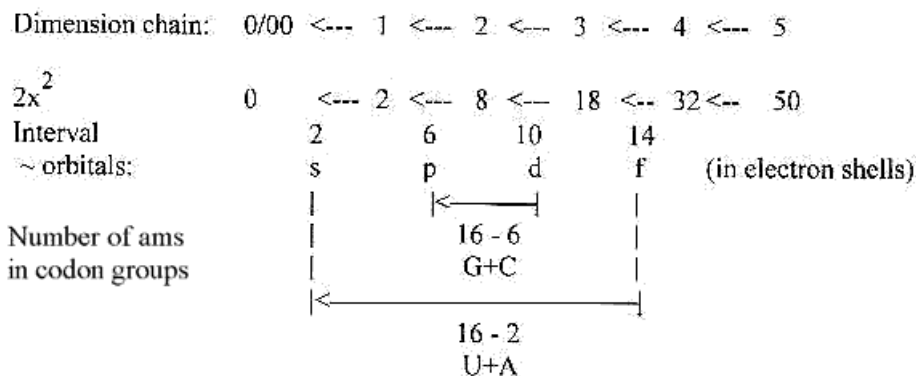
## 14. 3rd base grouping of codons:

### 14-1. For 24 amino acids we have an 8-8-8- division:

A-number, R-chains:

$$\begin{array}{rcl}
 8 \text{ "2-base"-coded (3}^{\text{rd}} \text{ base indifferent)} & = & 335 \\
 8 \text{ "2,5-base"-coded with 3}^{\text{rd}} \text{ base U/C} & = & 531 \\
 5 \text{ "2,5-base"-coded with 3}^{\text{rd}} \text{ base A/G} & = & 376 \\
 3 \text{ "3-base"-coded with 3}^{\text{rd}} \text{ base A or G} & = & 262 \\
 & & > \mathbf{638} \\
 2\text{-base-coded + A/G(+A or G)-coded} & = & 335 + 638 = \mathbf{973} \\
 \text{U/C-coded} & & = \mathbf{531} \\
 \\ 
 \text{Triplet chain: } & 543 + 432 & = \mathbf{975} \\
 & & > 1506 \cdot -2 = 1504. \\
 & 321 + 210 & = \mathbf{531}
 \end{array}$$

### 14-2. Number of ams seen in an orbital series:



In G+C-groups, 10 ams: 6 of them 2-base-coded\* ~ d --> p-orbitals

In U+A-groups, 14 ams: 2 of them 2-base-coded \*~ f --> s-orbitals

\*GG+CC+GC+CG, + GU+CU (R total 159 + 100 = 259)

\*AC+UC (R total = 76)

A doubling of the "2-base"-coded ams gives 32 ams, as disintegrated into steps  
 $\rightarrow 14 \rightarrow 10 \rightarrow 6 \rightarrow 2$ .

"2-base"-coded as separated off outwards in the chain (as the higher f-orbital in heavy atoms could be thought of as disintegrating into s- and p-electrons before the f2-orbital gets any electrons in the periodic system).

### 14-3. Z-N-numbers of the 2,5-3-base-coded ams:

The division on Z and N in the groups with 3rd base U/C and A/G(A,G) is the same as between the codon types: 638 Z - 531 N, see about Similarities in number divisions along different "polarities".

\*

## 15. Numbers of amino acids generating mass numbers:

### 15-1. Quantity of ams as mass (or A-) numbers, R-chains:

Number of ams:	5 G1	6 G2
	5 C1	4 C2
	6 U1	7 U2
	8 A1	7 A2

Number readings:

$$\begin{aligned}
 5 \times 77 \quad ("G1 \times U2-A2") &= 385 \\
 7 \times 55 \quad ("U2 \times G1-C1") &= 385 > 770 \text{ A Cross- and Form-coded ams} \\
 6 \times 64 \quad ("U1 \times G2-C2")_1 &= 384 \\
 8 \times 46 \quad ("A1 \times C2-G2") &= 368 > 752 \text{ A} = \frac{1}{2} \times 24 \text{ ams}
 \end{aligned}$$

2 x 384, +2 = Cross- plus Form-coded ams

2 x 368, - 2 = RNA- plus Pair-coded ams

etc.

### 15-2. Numbers 5, 7:

5	4	3	3	4	5	
-----	-----		-----	-----		
5	7		7	5		Sum of 24 ams
G1	U2		A2	C1		

Quotient A+U-coded / G+C-coded ams = 1,4 =  
said to be the observed one of bases in RNA.

Cf. Glycolyse - Citrate cycle,  
4 - 3 - 5 / 5 - 3 + 4 in one formation  
= number of ams derived from the different stations.

### 15-3. Is then the A2-U2-group divided in numbers 4 + 3 in some specific way?

After type of base: G,A = "00-bases", C,U = "0-bases":

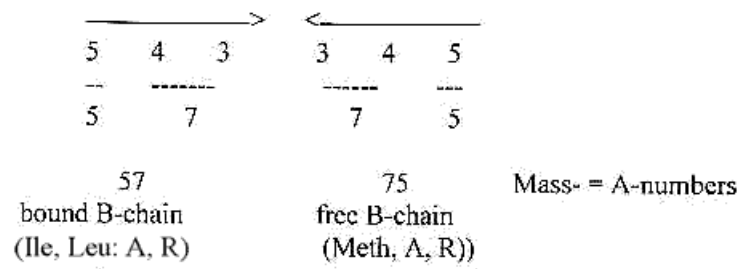
A2-group: 4 00<sub>1</sub>-bases, 3 0<sub>1</sub>-bases GA-GA-AA-AA / UA-CA-CA

U2-group: 4 00<sub>1</sub>-bases, 3 0<sub>1</sub>-bases AU-AU-AU-GU / UU-UU-CU

-----  
Sums ams: 495            465    A-numbers R  
          |                |  
          ~ A1-coded -2    ~ U1-coded +2

Cf. Similarities in number divisions  
along different dimensional "polarities".

**15-4. B-chains before / after peptide bindings, with +1 for the R-chain, as in Gly:**



\*

## 16. "A-Z"-numbers of elements - plus various other odds and ends:

### 16-1. "A-Z"-numbers for elements:

The relation Mass - Charge in the papers about physics presumed to be a relation 3 to 2 in dimension degrees.

Writing the A- and Z-numbers together as 3-figure numbers, read as sums in a 2-figure reading in the dimension chain with superposed odd-figure level:

A -Z

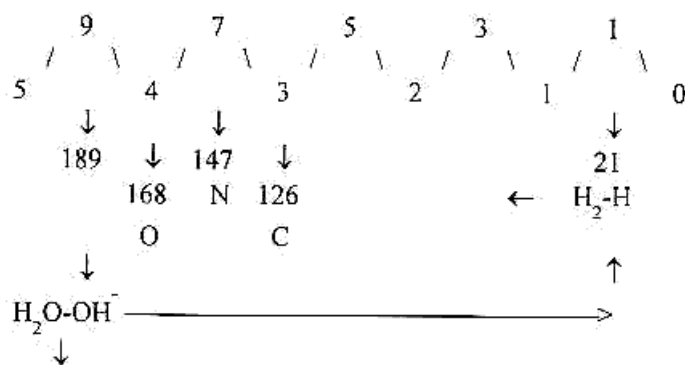
C-atom:  $12-6 = 73 + 53$

N-atom:  $14-7 = 74 + 73$

O-atom:  $16-8 = 94 + 74$

Additions in the chain:

$95+94 = 189$ ,  $94+74 = 168$ ,  $74 + 73 = 147$  etc.



- ionization of water equivalent with a d-degree step  $1 \rightarrow 0/00$   
branched off at the step  $5 \rightarrow 4$ .

$N + C = 147 + 126 = 273$ , the mean value of two ams,  $\times 12 = 3276$

If such a wild but nice "deriving" of the atom numbers should reveal something, there should be some difference in the inner split of the masses in O and C (not an equal division), but an inner split in the Z-number of N (as in water). (Cf. perhaps the capacity of N to attract an extra H as if it had valence 4??)

Completing the number derivation, we get  $105 - 84 - 63 - 42 - 21$ :  
that is

Bohr - (2 alpha) - 6Li - 4He - D (if not H2-H)

seen from the last step inwards a way of fusion.

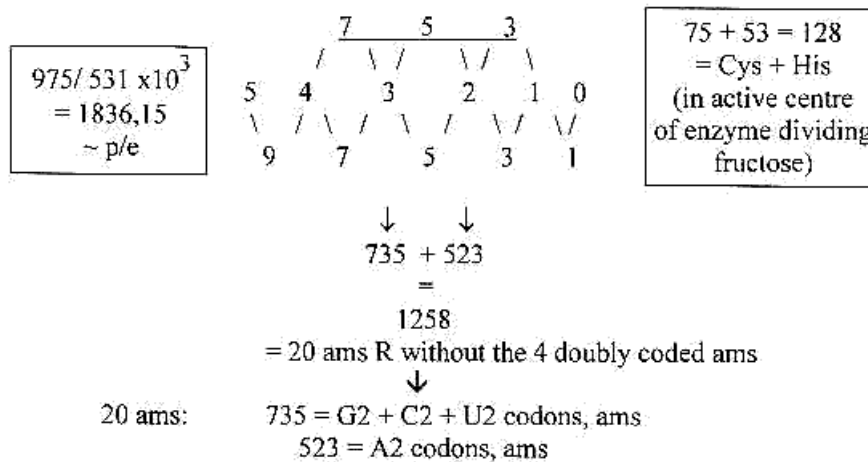
Why not try to use Bohr too, perhaps as a kind of "coenzymes" in fusion experiments?

**16-2. Mass number 79, PO<sub>3</sub> generating number 1504 (24 ams, R):**

$$\begin{array}{r}
 79 \\
 / \quad \backslash \\
 O_2 \quad x \quad P=O \\
 32 \quad x \quad 47 \quad = 1504
 \end{array}$$

**16-3. A simple way of reading in a dimension chain:**

$$753 \times 2 = 1506 = 24 \text{ ams R} + 2H = 975 + 531$$



Sum of 3-figure reading  $947 + 735 + 523 + 311 = 2 \times 1258$

Note:

Sum of  $594 + 473 + 352 + 231 + 110 = 1760 =$  total sum of Z in 24 free ams.  
(Cf. Z-sum generating A-numbers of codon grouped ams.)

**16-4. Another way of reading the sum of A+U and G+C groups of ams  
960 - 544+2H:**

$  \begin{array}{cccccc}  9 & 7 & 5 & 3 & 1 & \\  / & \backslash & \backslash & \backslash & \backslash & \backslash \\  5 & 4 & 3 & 2 & 1 & 0  \end{array}  $	$975 - 15 = 960 = \text{A+U-group}$
$  \begin{array}{ccc}  9 & 7 & 5 \\  \uparrow \downarrow & \uparrow - & 15 = \text{Ala}  \end{array}  $	$531 + 15 = 546 = \text{G+C-group} + 2H$
$  \begin{array}{ccc}  5 & 3 & 1 \\    & & \\    \longrightarrow & 73 = \text{Glu} \\    \longrightarrow & 59 = \text{Asp}  \end{array}  $	

Ala can derive from Pyruvate outside mitochondrias as well as from Oxaloacetate inside these. Could perhaps be viewed as representing the "other way around" in a dimension chain  $5 \leftarrow 1$ .

### 16-5. Miscellaneous:

#### a) B-chains from 8th root of the superposed chain of odd numbers:

$$\sqrt[8]{97,531 \times 10^3} = 1772,73 \quad 1772 = 24 \text{ unbound B-chains}$$

#### b) Connecting to the square root of 6-figure numbers in a chain:

$$5-4-3-2-1-0 \rightarrow \sqrt{\quad} = 737,03$$

|- 386.

$$0-1-2-3-4-5 \rightarrow \sqrt{\quad} = 351,35$$

$$\text{Sum } 1088,38 = 2 \times 544.$$

<p>c) <math>97 \times 75 \times 53 = \underline{385} \cdot \underline{575}</math></p> <p style="margin-left: 40px;">exchanged groups <u>385</u></p>	<p style="margin-left: 40px;">pure A+U codon group AA, AU, UU, UA</p>	<p><math>75 \times 53 = 5^2 \times \underline{159}</math></p> <p style="margin-left: 40px;">pure G+C codon group GG, CC, GC, CG</p>
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### 16-6. "Computer language":

A dimension chain as triplets:

543	←	
432	>	975
321	←	
210	>	531
579		
+ 135	↑	

$2^9 + 2^7 + 2^5$
$+ 2^5 + 2^3 + 2^1$
↓
$= 714 = 012+123+234+345$

(Cf. the hypothesis about number 2 as a natural log base in inward direction:  
2 as the "E"-number = sum of poles in dimension degree 0/00.)

714:  $27 + 21 + 24 = 146$  (A-number for a-ketoglutarate)

=  $1/2 \times 292$ , see the Exponent series.

146 also number of base pairs of DNA on histones.

$$\begin{aligned}
 2^5 + 2^4 + 2^3 &= 56 \\
 + 2^2 + 2^1 + 2^0 &= 7 \dots \text{sum } 63 \\
 &\text{(63} \sim \text{circa mean value of } 1 \text{ ams R)}
 \end{aligned}$$

$2^5 + 2^4 + 2^3$	= 56	— 56 = Serine*, Z-number, R+B
$2^4 + 2^3 + 2^2$	= 28	— 28 > 105 A
$2^3 + 2^2 + 2^1$	= 14	— 49 = Serine, N-number, R+B
$2^2 + 2^1 + 2^0$	= 7	
↓ → 56 28 14 7 A = $\underline{1776,8} \cdot 10^x$		
(24 B-chains à 74 A)		

$5 / 7 = 7 / 14 = 14 / 28 = 28 / 56$  (Cf. menu Biochemistry about  $1/7$  etc.)

$14 \rightarrow 28 \rightarrow 56$  is also a way of fusion in the stars: Si - Ni - Fe.

\* Serine is a special amino acid in having two diametrical codons:  
UC and AG(U/C).

### 16-7. $\pi$ - approximately out of a dimension chain:

$$5 - 4 - 3 - 2 - 1 - 0/00$$

↓  
equivalent with  $5'$

$$5/4 + 4/3 + 3/2 + 2/1 + 1/5' =$$

$$= 2 \times 3,141\ 666 \sim 2\pi \rightarrow \text{one revolution.}$$

↓  
 $377 / 60$  as a used approximation to the  $\pi$ -number.

\*