창조과학스쿨

생명체와 수학적 설계 증거

제네시스 연구소

- 양승원 -

생명체의 수학적 질서 한글hwp강의안.pdf

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  2.3. 신성한 서문 속에 숨겨진 생명의 수(數)

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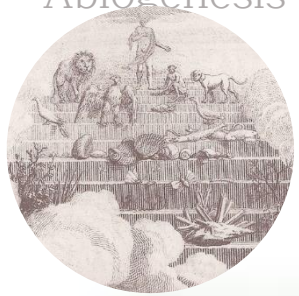
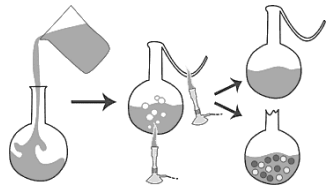
5. 나눔을 위한 질문

서론 Introduction

자연발생설
Abiogenesis

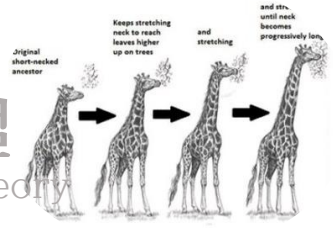




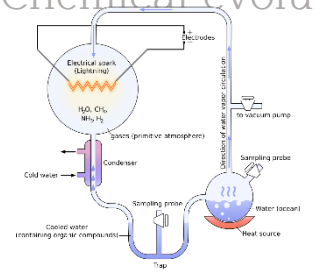
생물속생설
Biogenesis

생물정보학
Bioinformatics

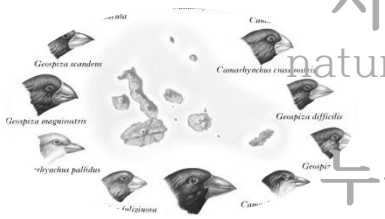
용불용설
use & disuse theory



화학진화
Chemical evolution



자연선택
natural selection

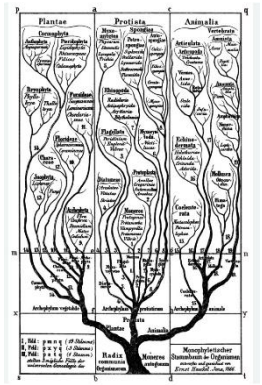


누적선택
cumulative selection

진화론?
Evolution theory

생명체의 기원
Origin of Life

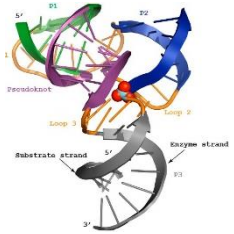
창조론?
Creationism



진화계통나무
Evolutionary tree

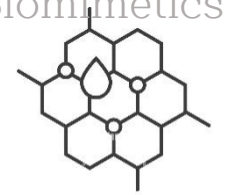
돌연변이
mutation

후성유전학
Epigenetics



RNA세계
RNA world theory

생체모방공학
Biomimetics



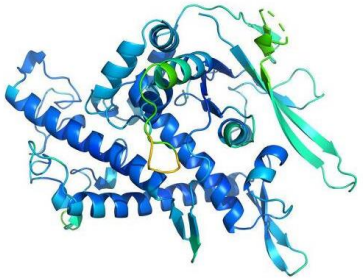
지적설계
Intelligent Design

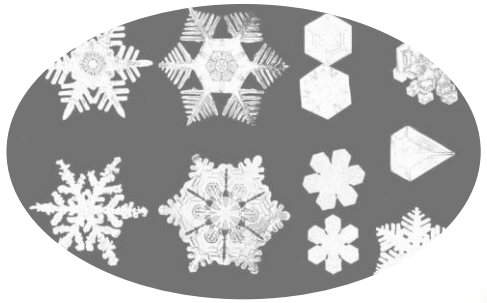
서론 Introduction

규칙, 법칙-진화의 도구?

Denton, M. J. (2003)

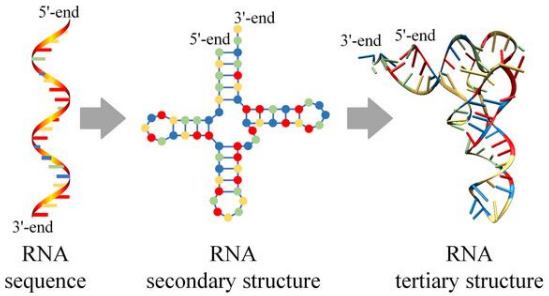
단백질 접힘
Protein folding





기하학 구조
Geometric structure

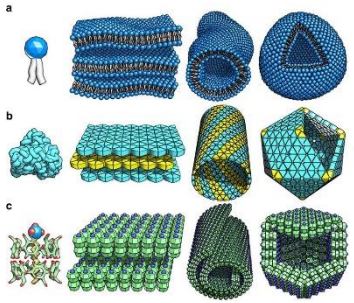
RNA 접힘
RNA folding



진화론?
Evolution theory

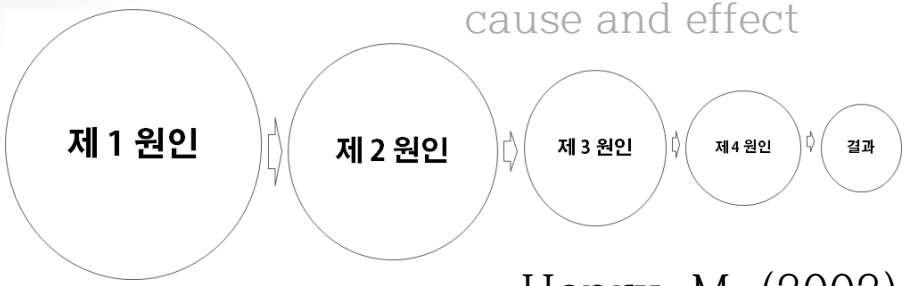
생명체의 기원
Origin of Life

창조론?
Creationism



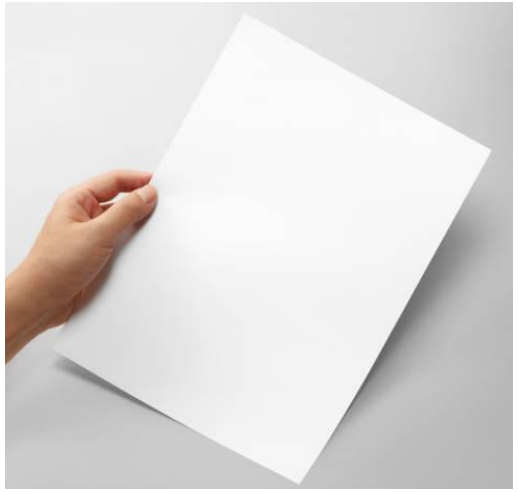
나노물질조립
Self assembly

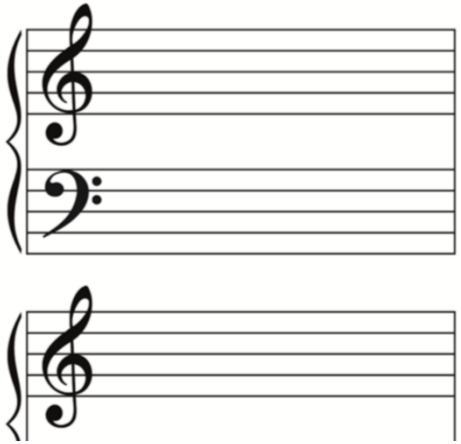
인과율법칙
cause and effect

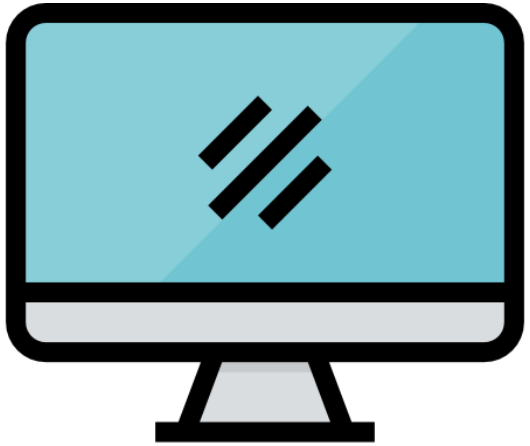


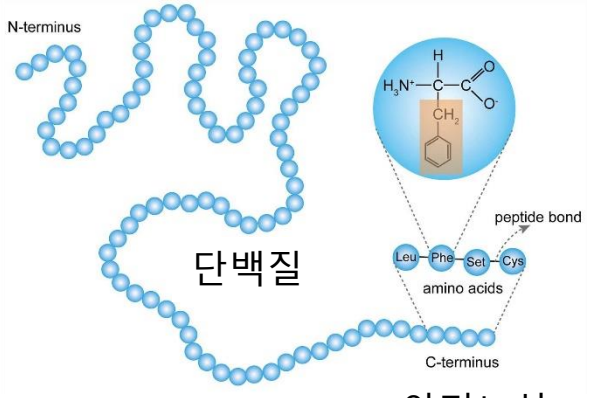
Henry, M. (2002)

생명체의 설계 증거?…

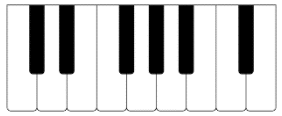


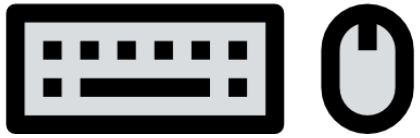




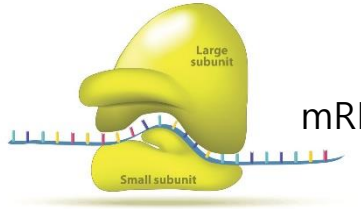


아미노산





RIBOSOME



mRNA

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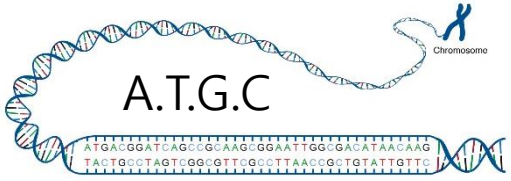
0001000010001000



정보이론

정보의 생산자

(발신자)

전송 및 수신된 신호의 존재

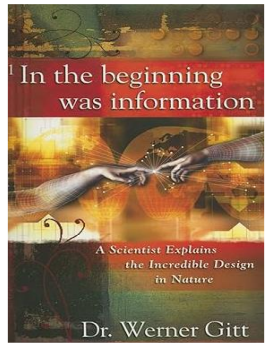
사용된 암호(언어체계)

의도된 목적과 달성된 결과

의식의 존재

정보의 소비자

(수신자)

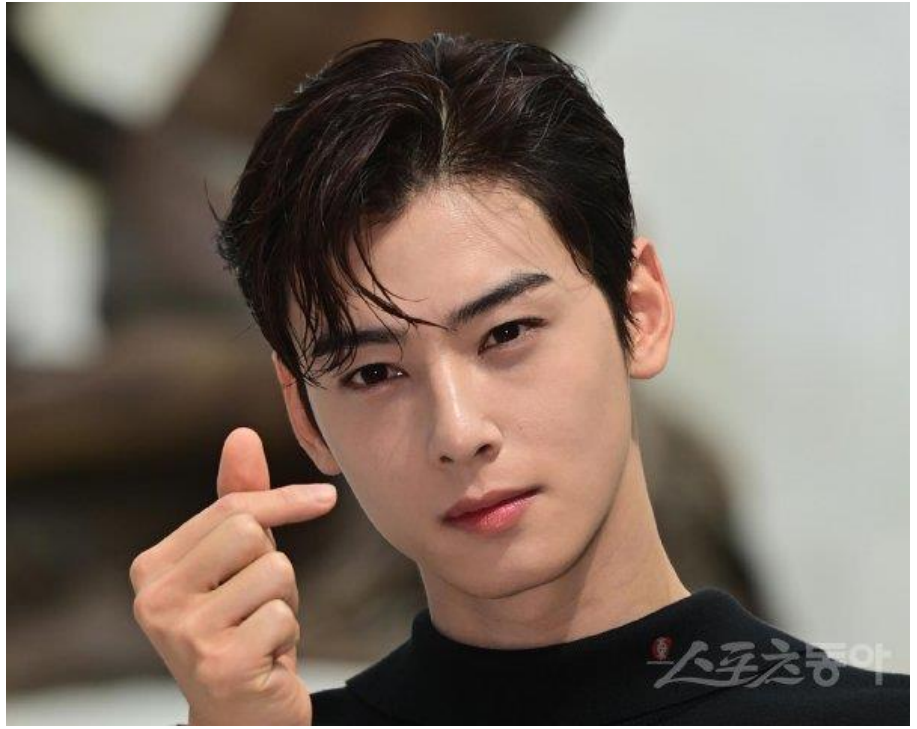


Gitt, W. (2006). In the beginning was information.

생명체의 아름다움(美)은 어디에서 오는가?

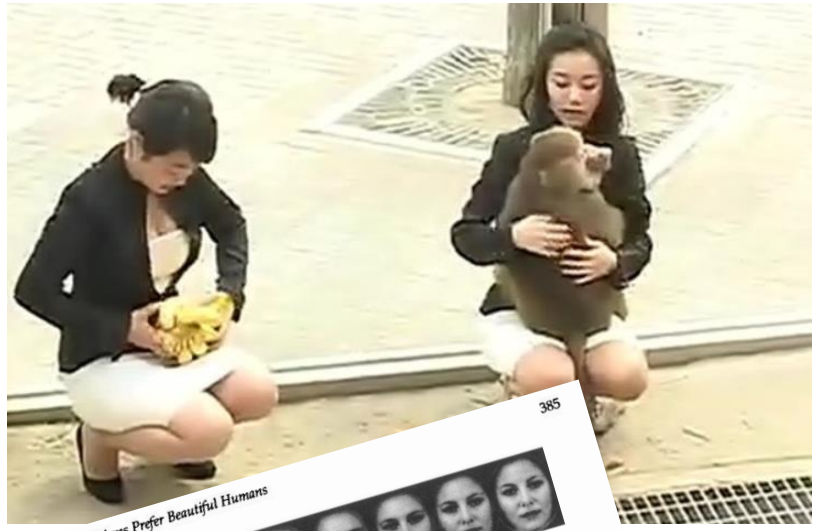
생명체의 아름다움(美)과 황금비

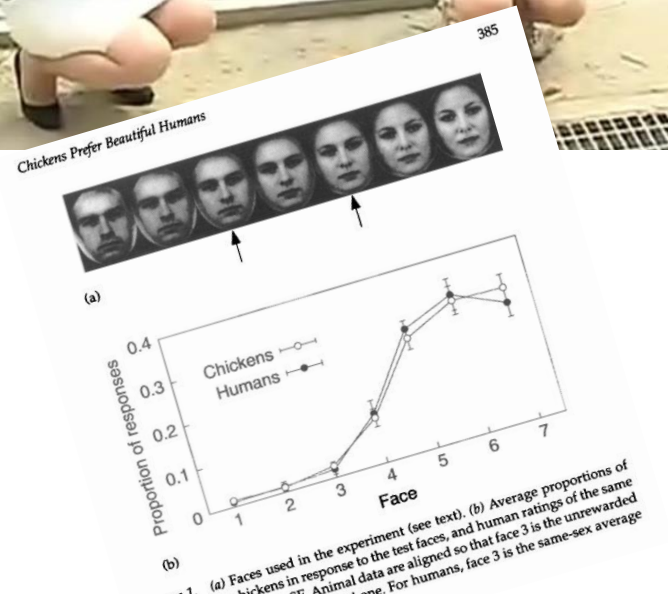

ELLE COKR




su:m37°

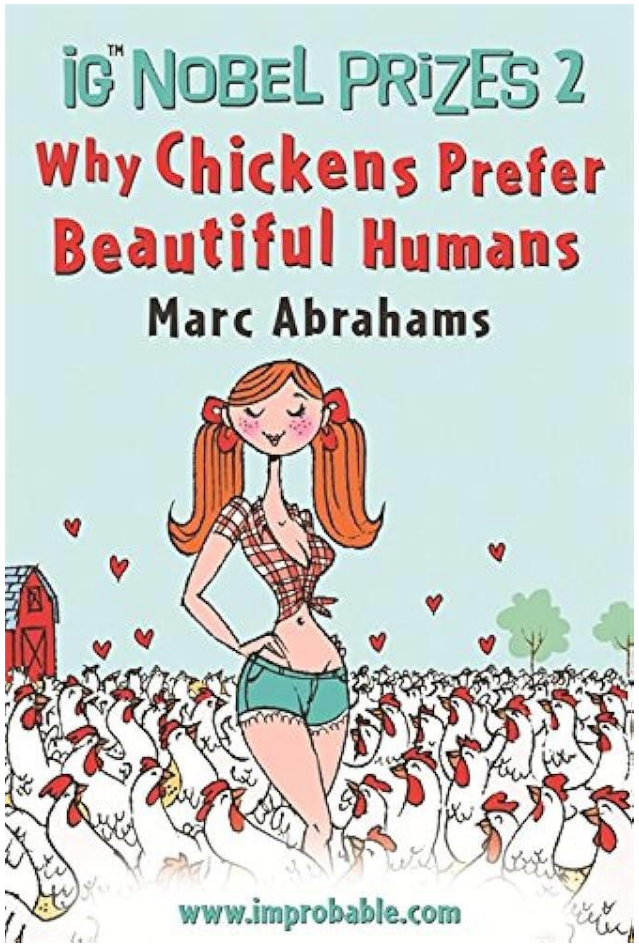
동물들도 선호하는 외모가 있다?





Ghirlanda, S., Jansson, L., & Enquist, M. (2002). Chickens prefer beautiful humans. Human Nature, 13, 383-389.

닭도 아름다운 인간을 더 좋아한다



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Chickens prefer beautiful humans

Published: September 2002 | 13, 383–389 (2002)

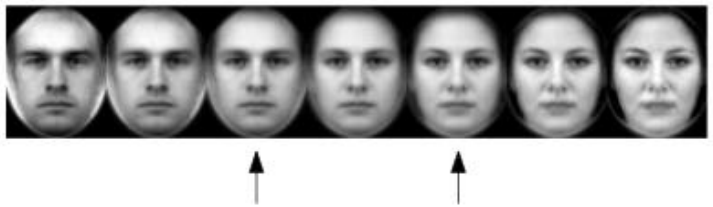
Stefano Ghirlanda, Liselotte Jansson & Magnus Enquist

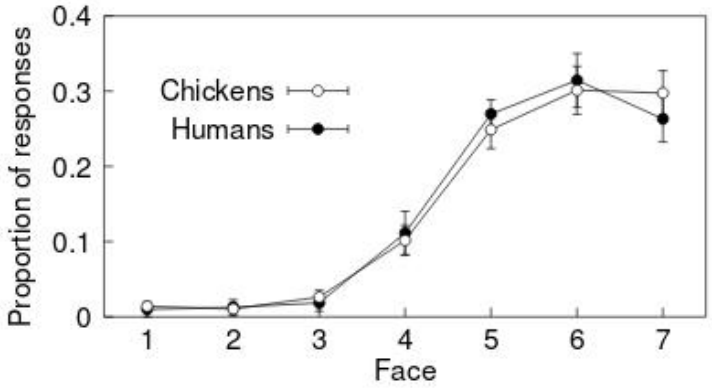
3389 Accesses 26 Citations 274 Altmetric 8 Mentions Explore all metrics →

Cite this article

Abstract

We trained chickens to react to an average human female face but not to an average male face (or vice versa). In a subsequent test, the animals showed preferences for faces consistent with human sexual preferences (obtained from university students). This suggests that human preferences arise from general properties of nervous systems, rather





Ghirlanda, S., Jansson, L., & Enquist, M. (2002). Chickens prefer beautiful humans. *Human Nature*, *13*, 383-389.

Ghirlanda et al (2002)

어떤 얼굴이 더 매력적인가?

British Journal of Psychology (2000), **91**, 125–140 *Printed in Great Britain*

Sex-typicality and attractiveness: Are supermale and superfemale faces super-attractive?

Gillian Rhodes*
University of Western Australia and University of Canterbury, New Zealand

Catherine Hickford
University of Canterbury, New Zealand

Linda Jeffery
University of Western Australia, Australia

Many animals find extreme versions of secondary sexual characteristics attractive, and such preferences can enhance reproductive success (Andersson, 1994). We hypothesized, therefore, that extreme versions of sex-typical traits may be attractive in human faces. We created supermale and superfemale faces by exaggerating all spatial differences between an average male and an average female face. In Expt 1 the male average was preferred to a supermale (50% exaggeration of differences from the female average). There was no clear preference for the female average or the superfemale (50% exaggeration). In Expt 2, participants chose the most attractive face from sets of images containing feminized as well as masculinized images for each sex, and spanning a wider range of exaggeration levels than in Expt 1. Chinese sets were also shown, to see whether similar preferences would occur for a less familiar race (participants were Caucasian). The most attractive female image was significantly feminized for faces of both races. However, the most attractive male image for both races was also significantly feminized. These results indicate that feminization, rather than sex exaggeration *per se*, is attractive in human faces, and they corroborate similar findings by Perrett *et al*. (1998).

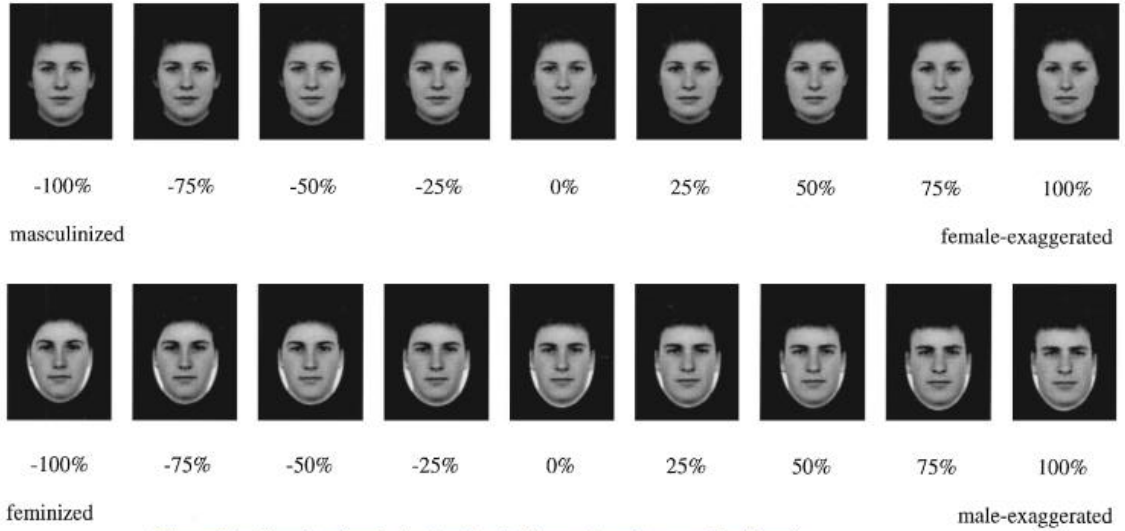
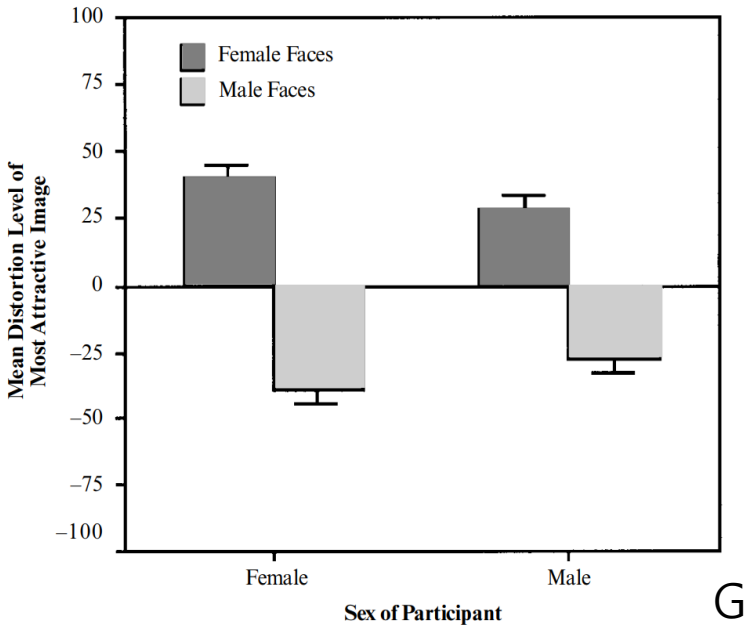


Figure 2 A. Caucasian female (top) and male (bottom) continua used in Expt 2.



Gillian et al (2000)

본론1 Body1

아름다움(美)이란?

안정감

조화

만족

쾌감

선호

아름다움(美)이란?

황금비

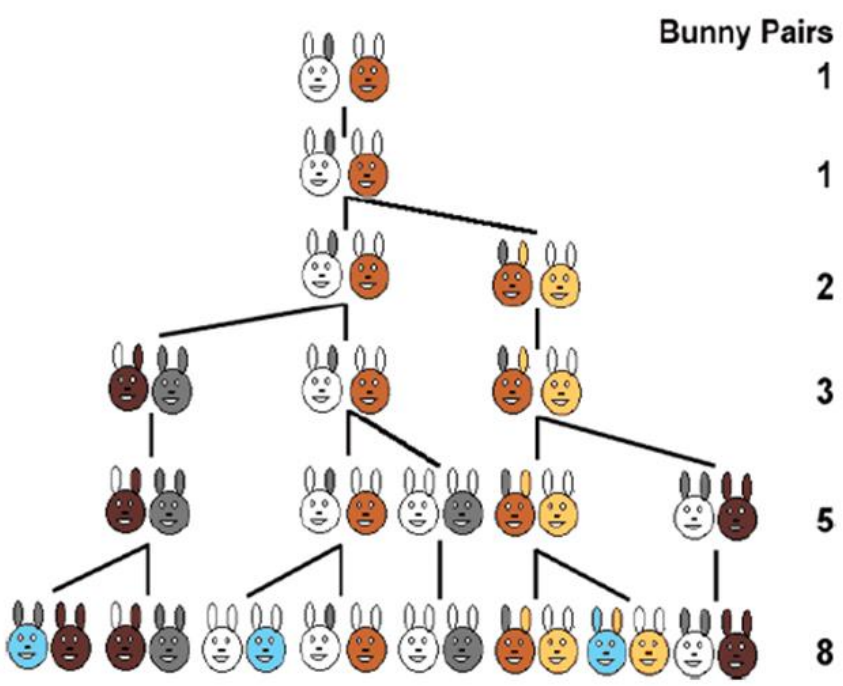
매력

질서

균형

생명

피보나치 수열과 황금비



Month	Baby Rabbit	Mature Rabbit	Total
January 1	1	0	1
February 1	0	1	1
March 1	1	1	2
April 1	1	2	3
May 1	2	3	5
June 1	3	5	8
July 1	5	8	13
August 1	8	13	21
September 1	13	21	34
October 1	21	34	55
November 1	34	55	89
December 1	55	89	144

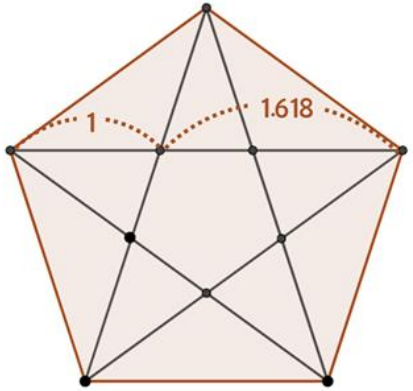
피보나치 수열: 1, 1, 2, 3, 5, 8, 13, 21, 34, 55, 89, 144…

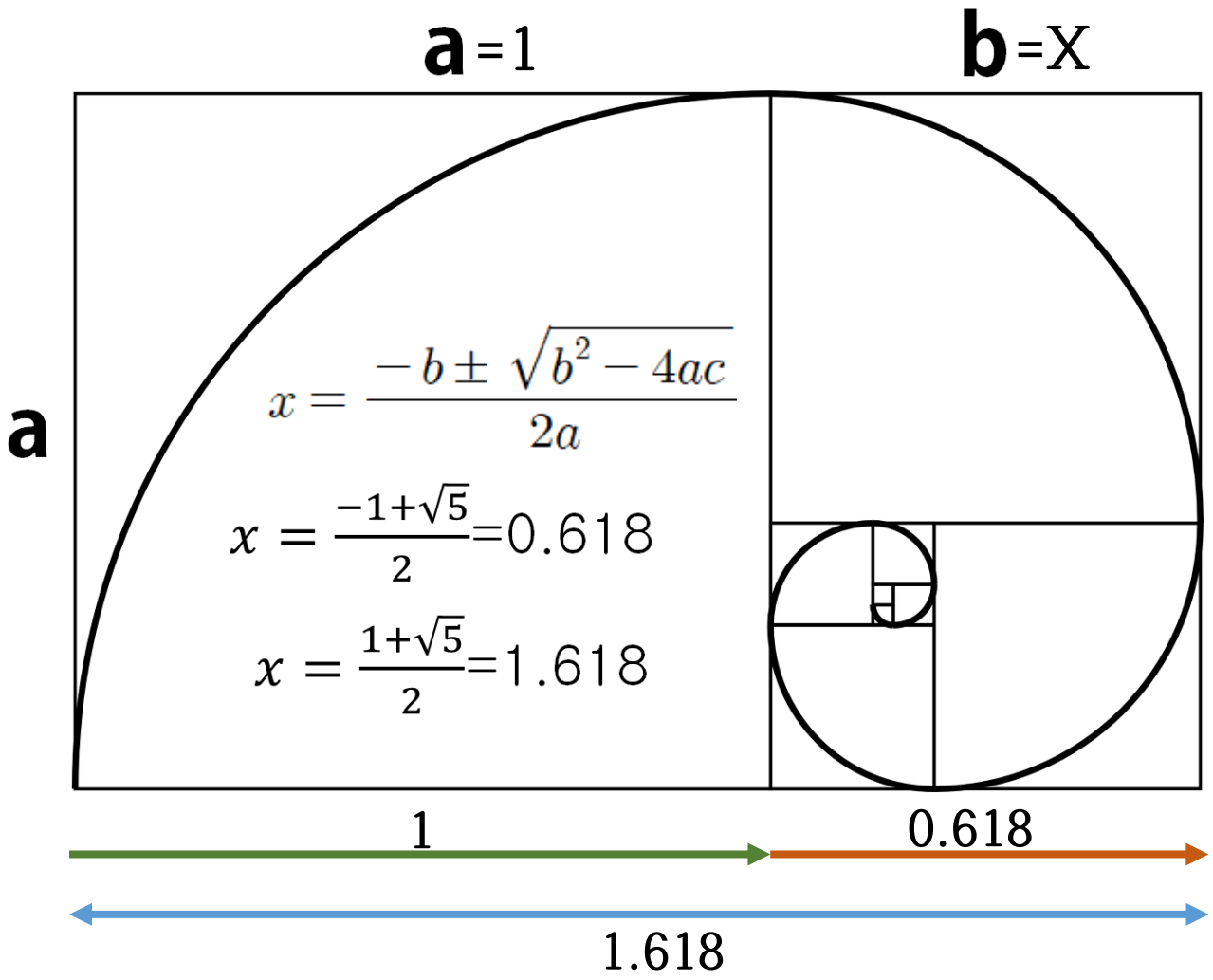
비율a: 1/2, 1/3, 2/5, 3/8, 5/13… = 0.382

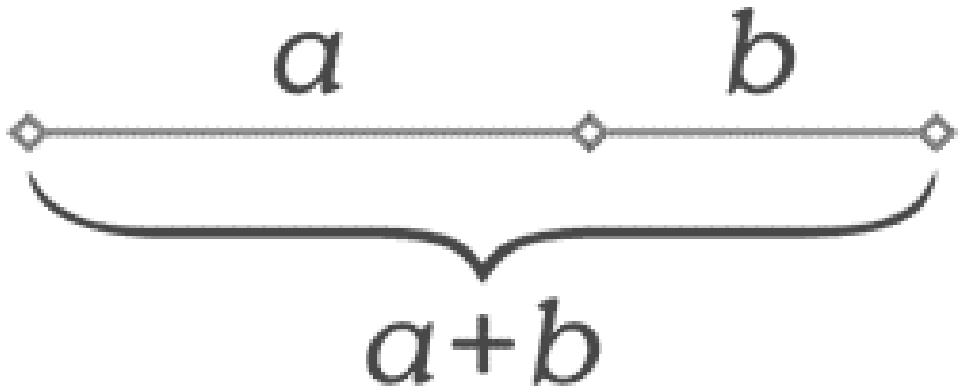
비율b: 1/1, 1/2, 2/3, 3/5, 5/8, 8/13… = 0.618

비율c: 2/1, 3/2, 5/3, 8/5, 13/8 … =1.618 -> 황금비율

황금비 구하는 방법



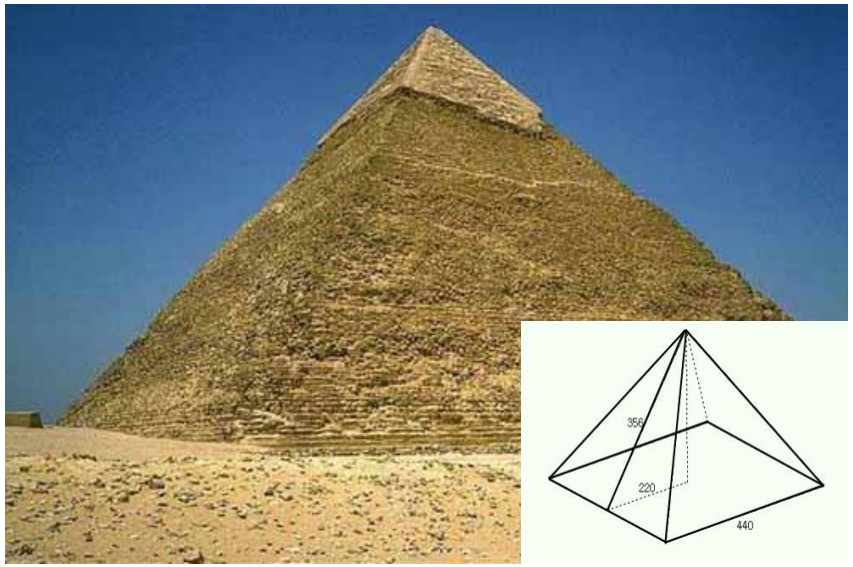




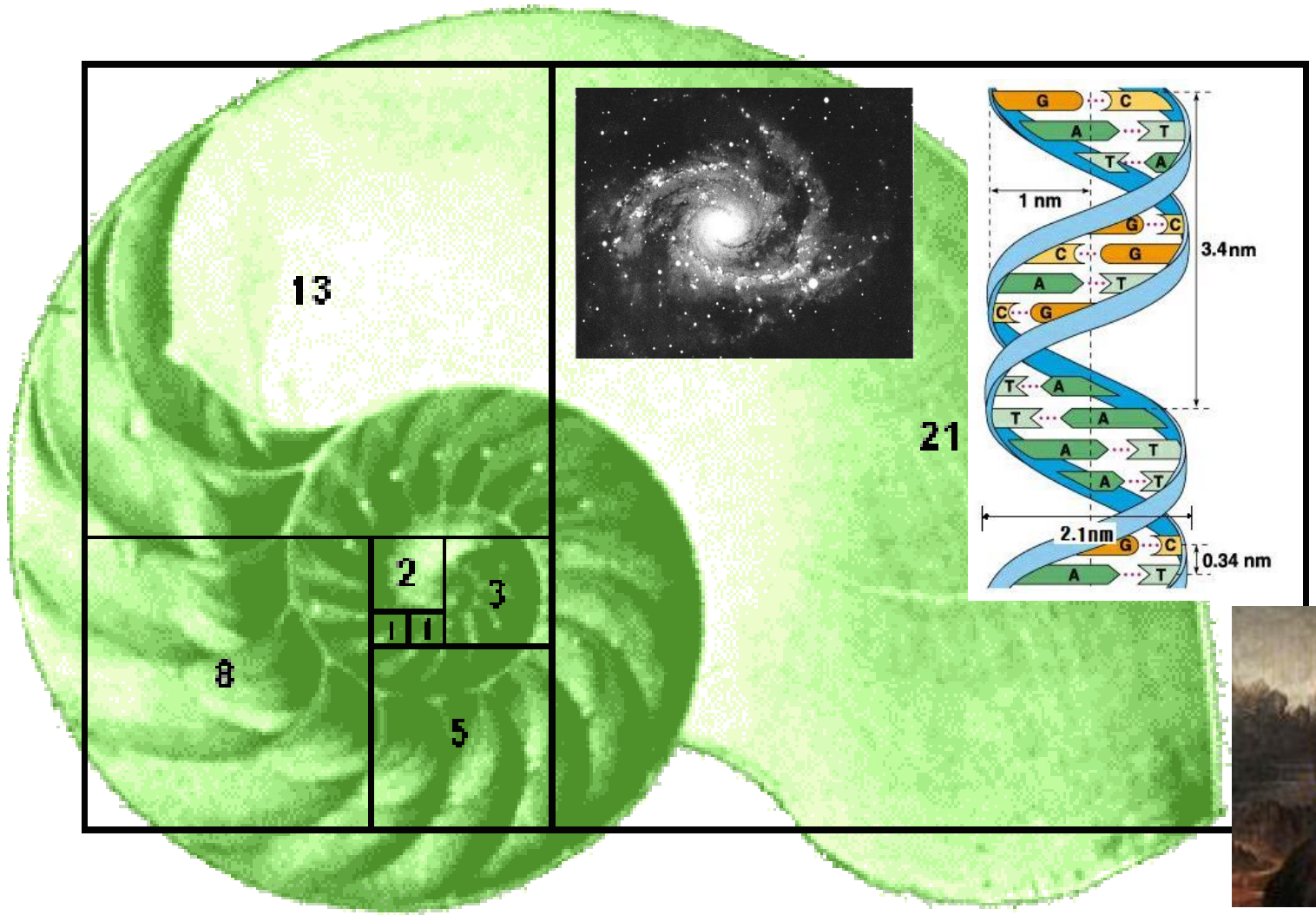
$a : a+b = b : a$

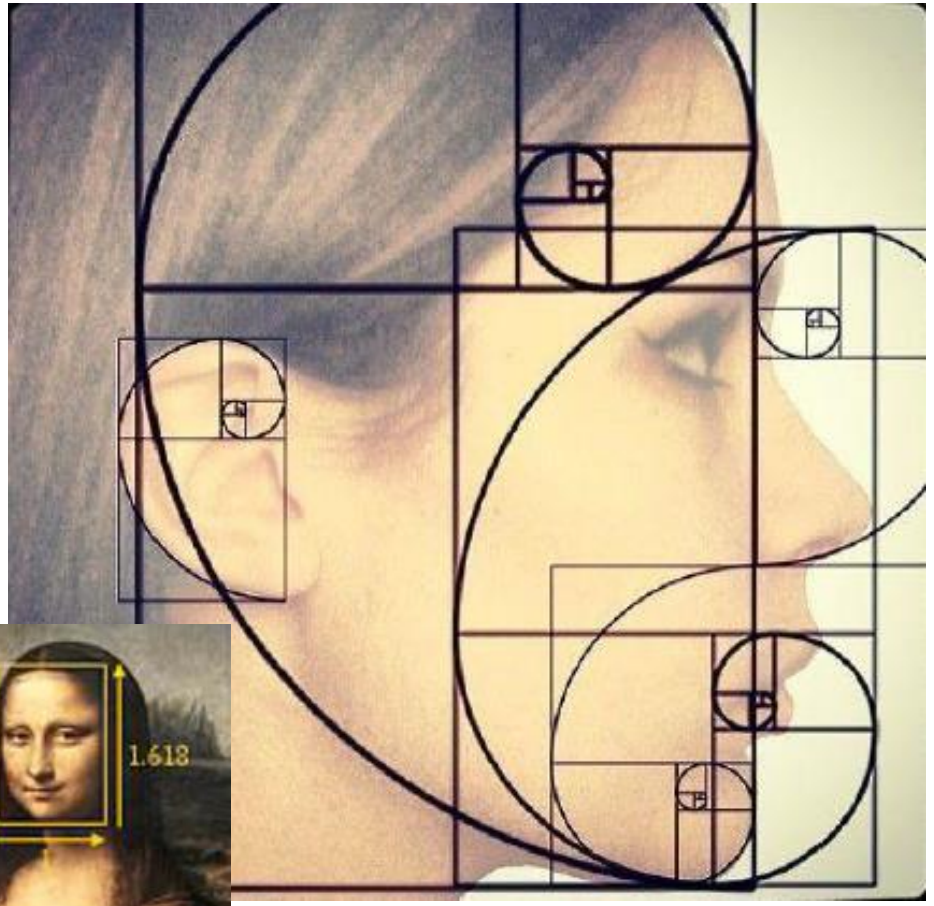
$1 : 1+x = x : 1$ ➡ $x^2 + x^1 - 1 = 0$

황금비율-안정감



생명체 나타난 황금비





피보나치 수열: 1, 1, 2, 3, 5, 8, 13, 21, 34, 55, 89, 144…

생명체 나타난 황금비

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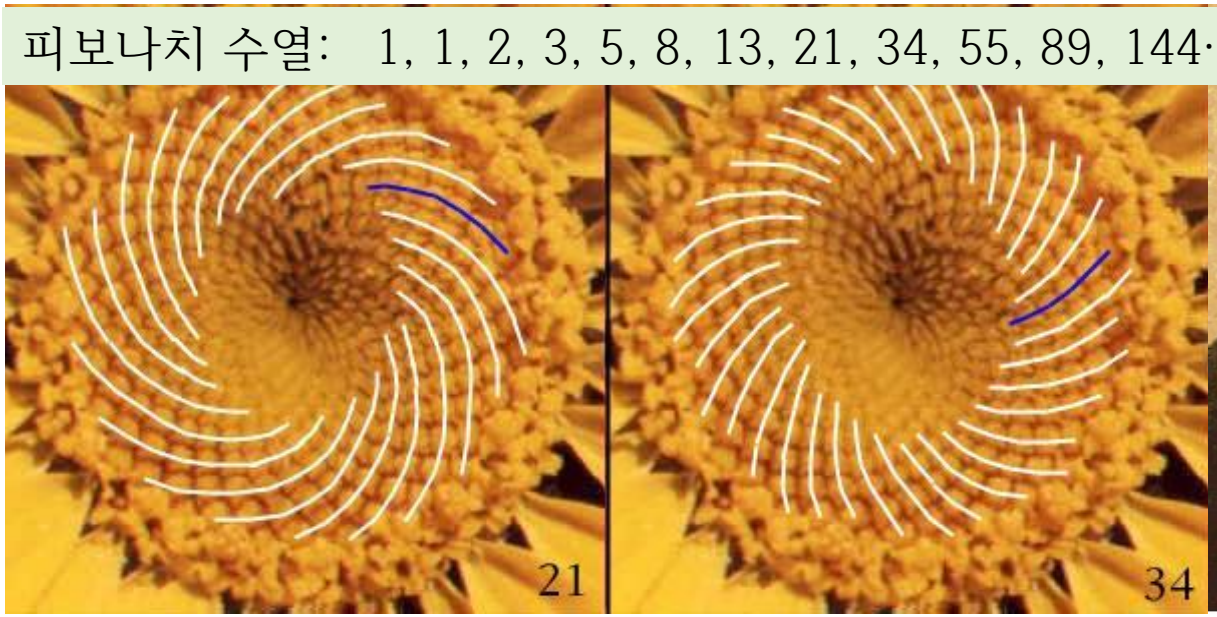
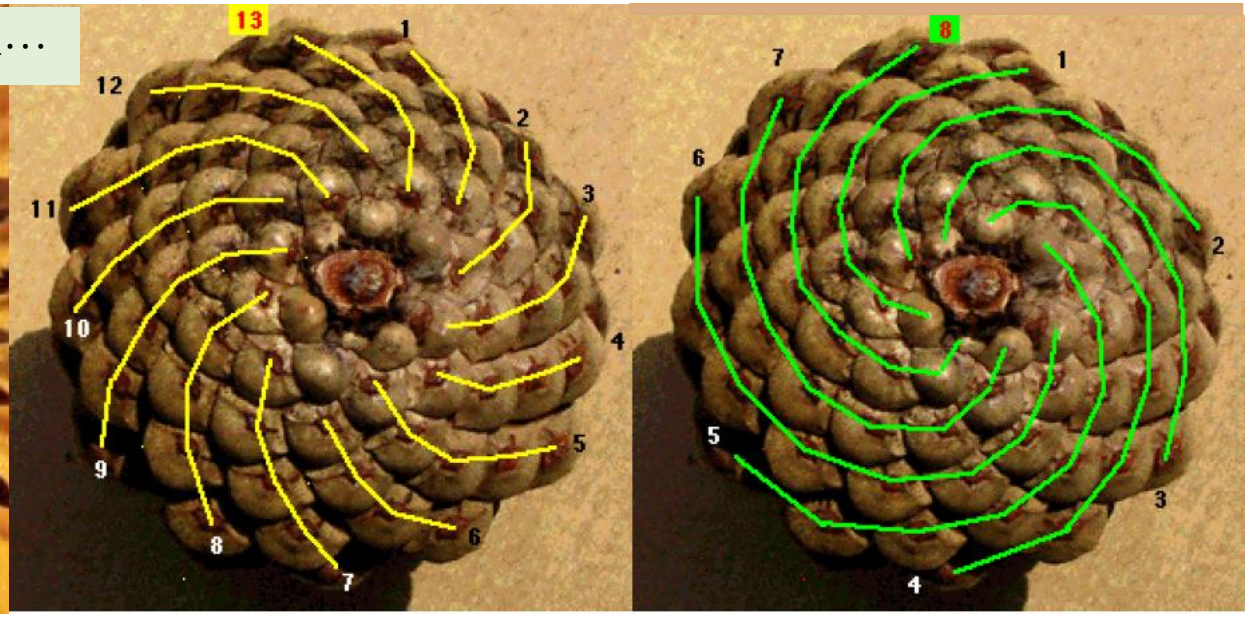
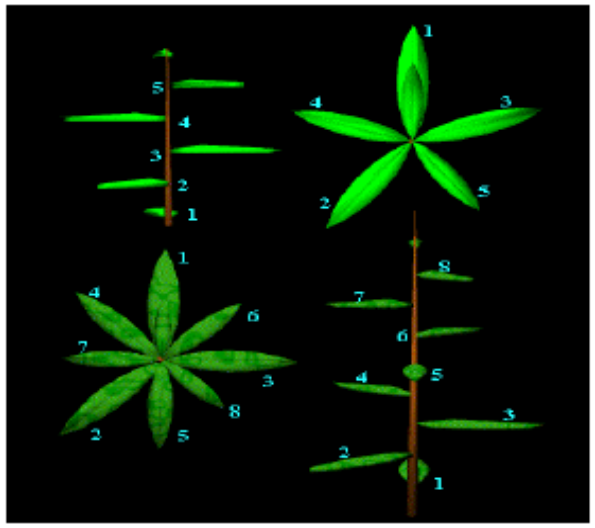
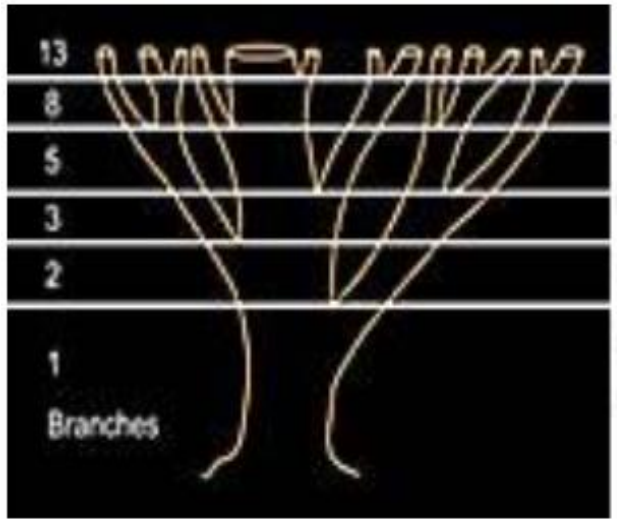
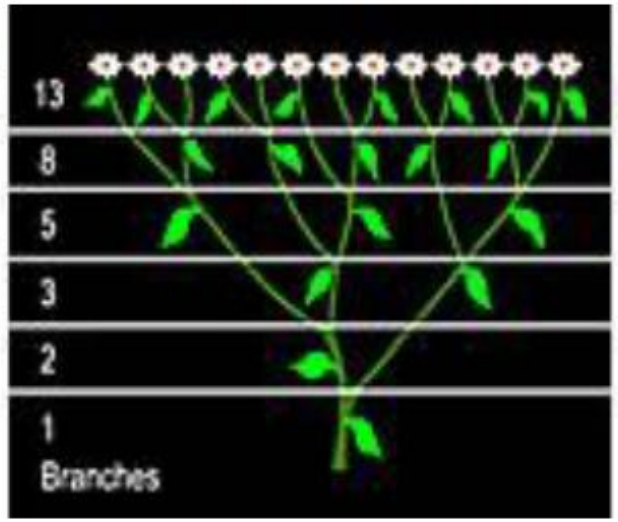
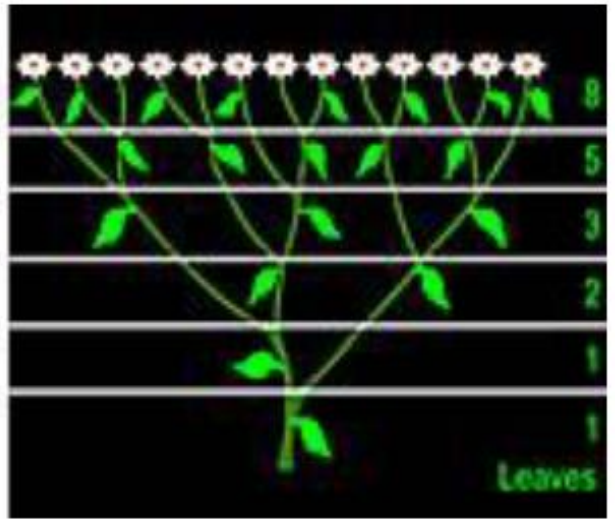




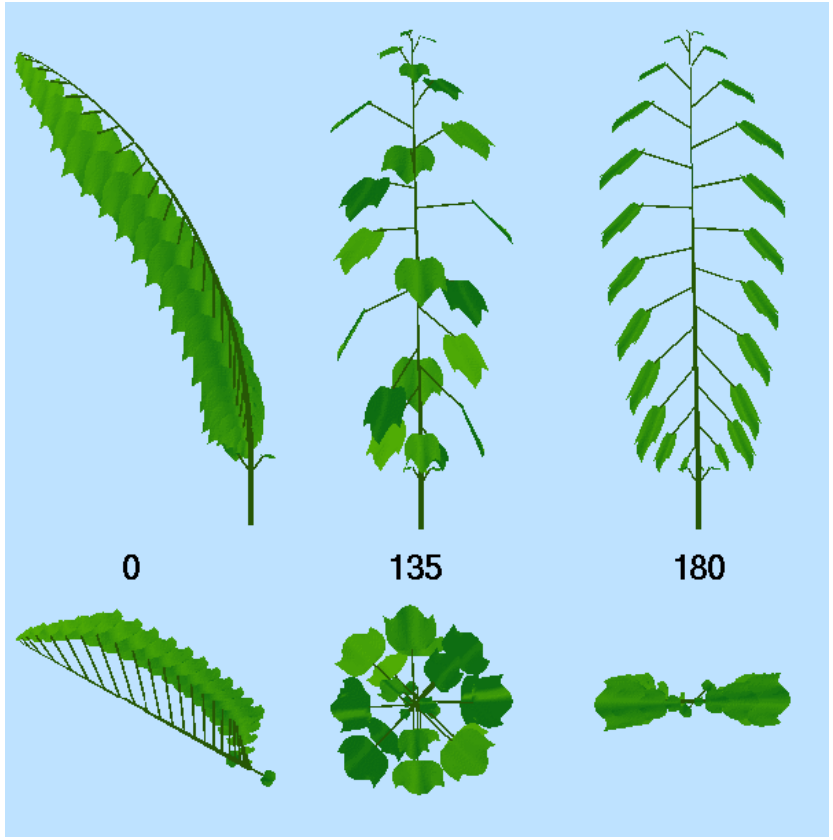


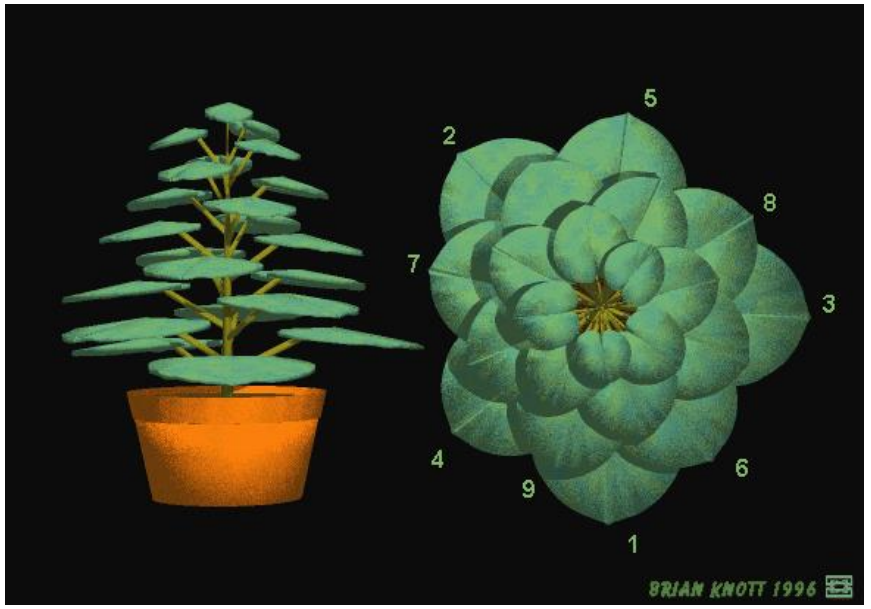


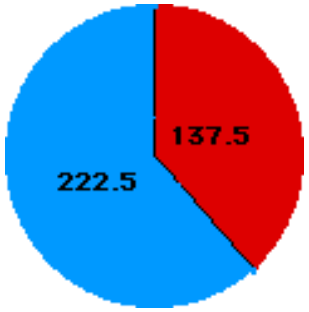




생명체 나타난 황금비







0.618034를 각도로 나타내면

시계반대방향 0.618034×360=222.92

시계방향 각 137.0776(360-222.92)

222.5 ÷ 137.5 = 1.618…

행성 공전주기 및 식물의 나선잎 정렬과 피보나치 수와의 관계				
	관측치(일)	이론치	비율	식물
명왕성	90,000		(2:3 해왕성)	
해왕성	60,193	62,000		
천왕성	30,688	31,000	1:2	느릎나무
토성	10,670	10,333	1:3	너도밤나무
목성	4,332	4,133	2:5	살구
소행성들	1200~2000	1,550	3:8	배
화성	687	596	5:13	아몬드
지구	365	**366(8:13)**	8:21	
금성	225	**277(13:21)**	8:21	소나무
수성	88	87	13:34	소나무

안정감

조화

만족

쾌감

선호

아름다움(美)이란?

황금비

매력

질서

균형

생명

안정감

조화

만족

쾌감

선호

어떻게?아름다움(美)

황금비

매력

질서

균형

생명

안정감

조화

만족

쾌감

선호

왜? 아름다움(美)

매력

황금비

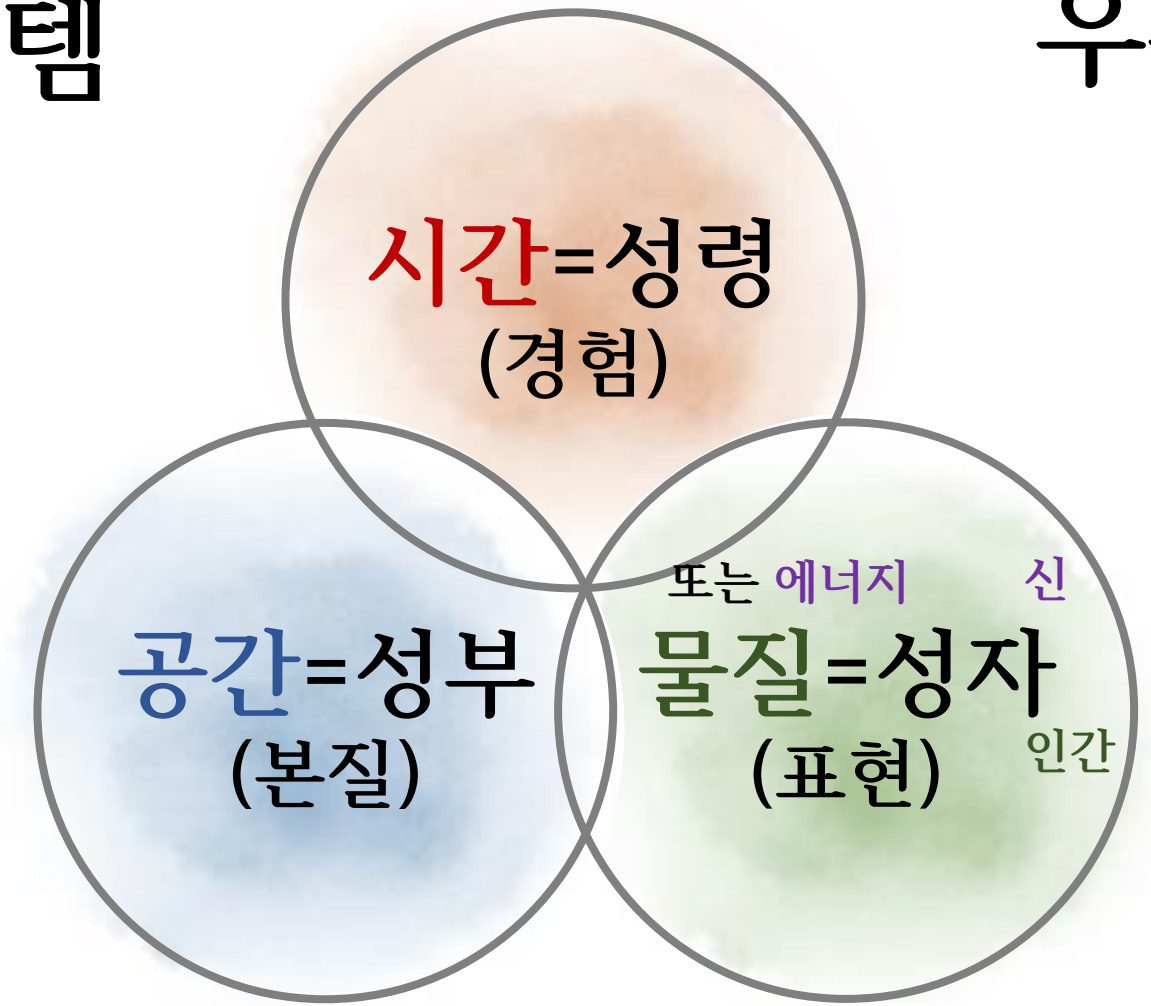
질서

균형

생명

우주의 시스템

우주의 설계자

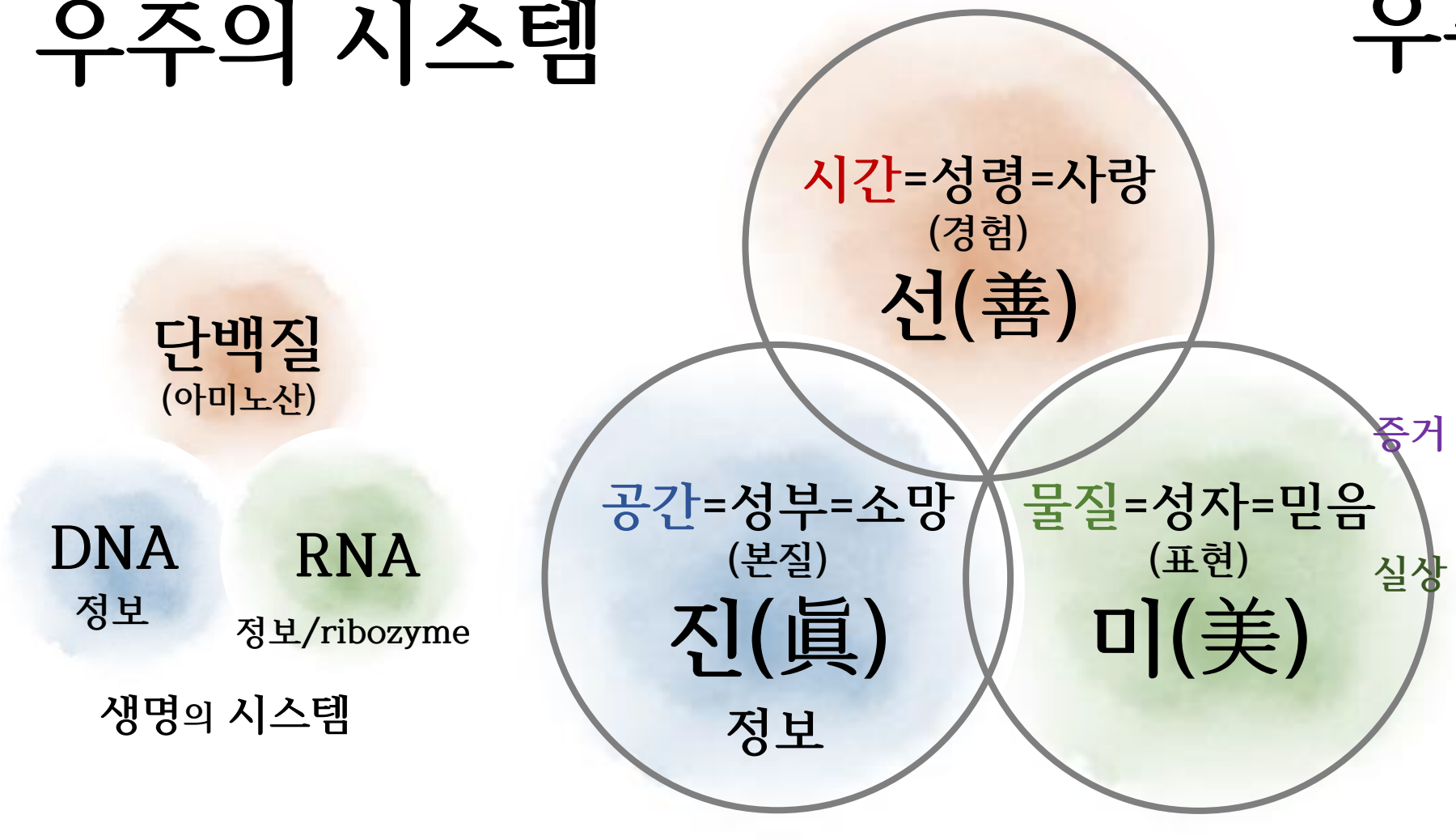


우주의 삼 요소 vs 삼위일체 하나님 vs 질서와 조화

헨리모리스.『현대과학의 성서적 기초』이현모 역

우주의 시스템

우주의 설계자



우주의 삼 요소 vs 삼위일체 vs 진선미 vs 질서와 조화

정보이론과 아름다움(美)의 본체?

정보의 생산자

(발신자)

전송된 신호(황금비.질서)의 존재

사용된 암호 數 (언어.말 체계)

의도된 목적(생명)과 달성된 결과(美)

의식(설계자.로고스)의 존재

정보의 소비자

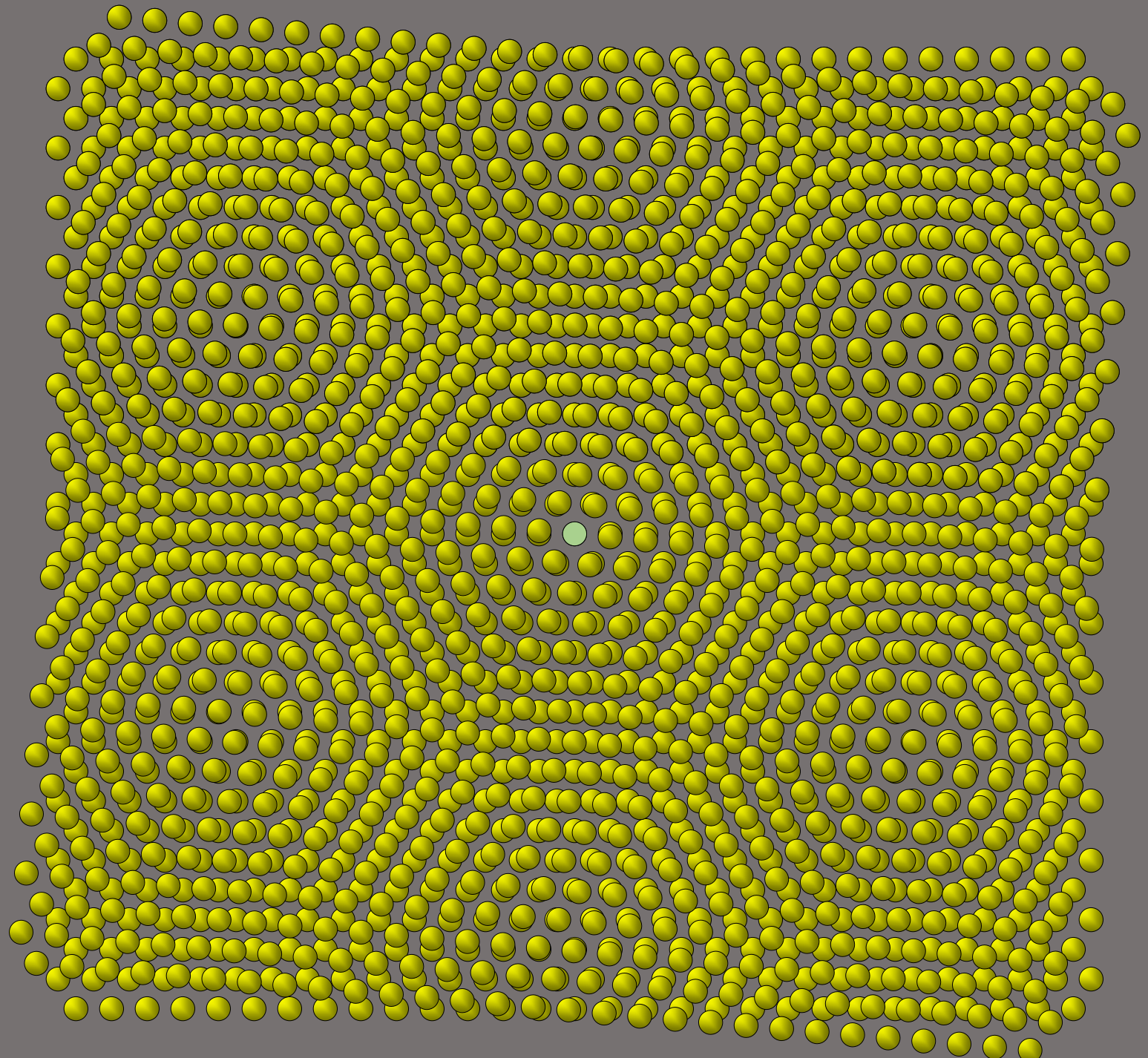
(수신자)

Gitt, W. (2006). In the beginning was information.

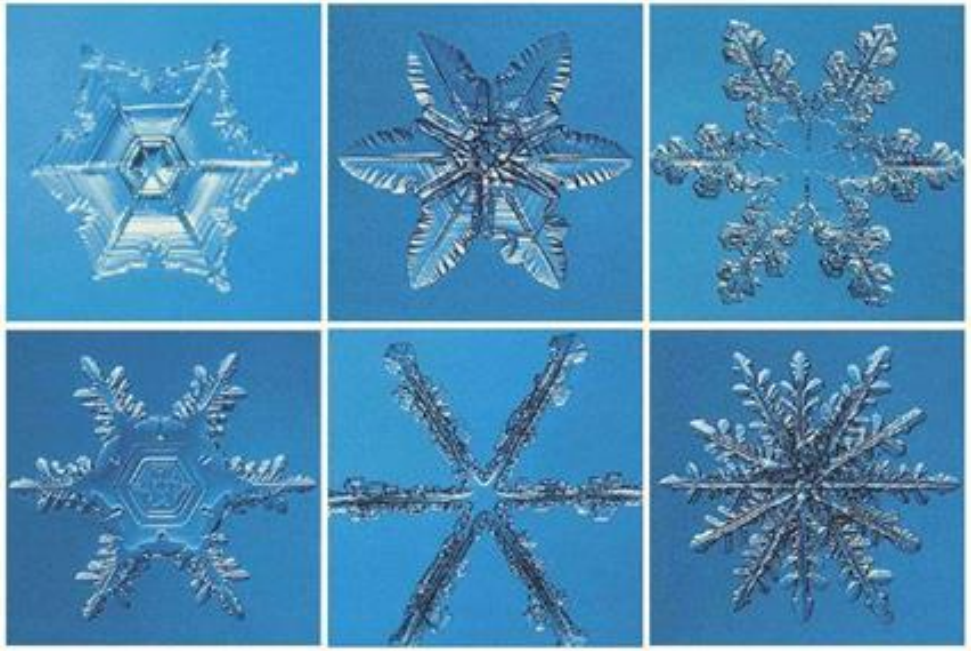
본론2 Body2

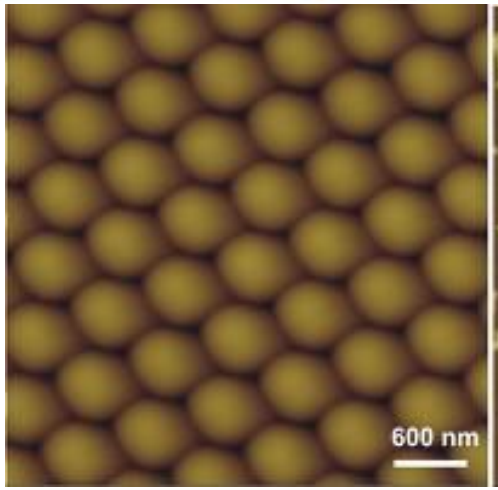
생명체에 나타나는 수학적 질서에는 무엇이 있을까?

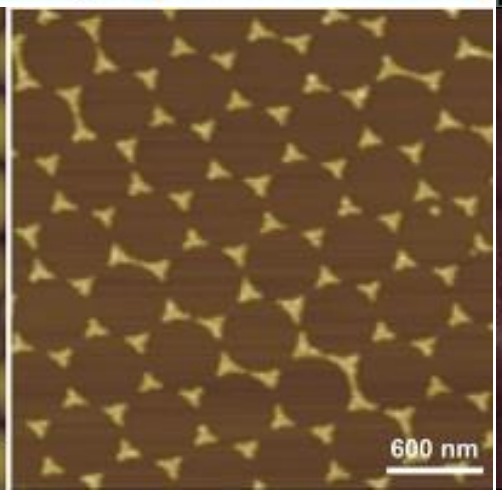
기하학적 구조와 생명체의 수(數)

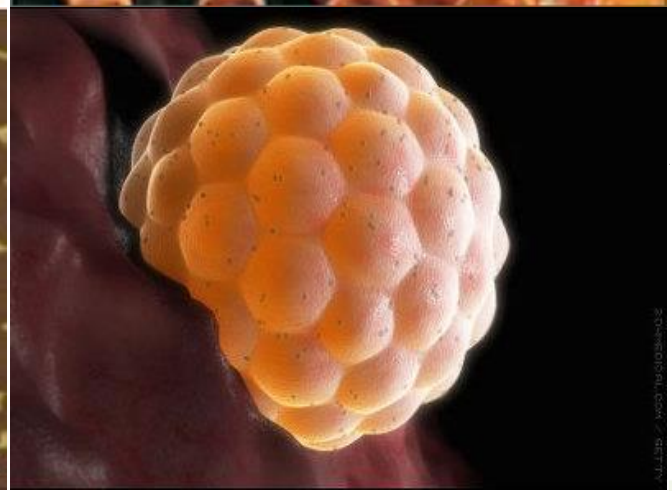


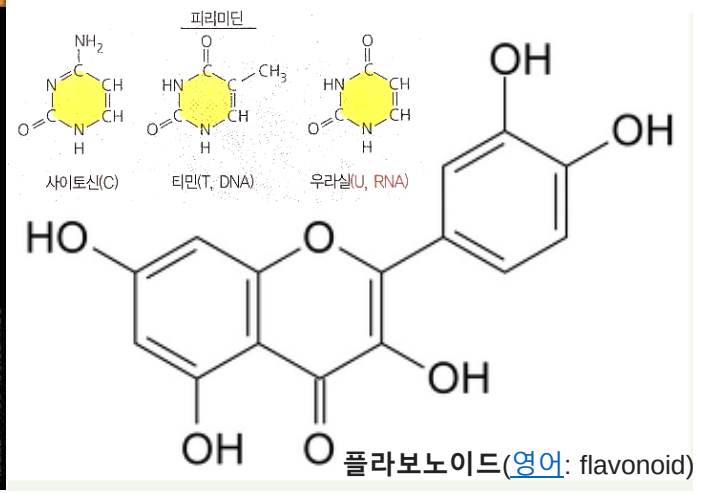
육각형(육각별)과 생명체



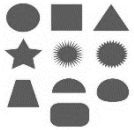






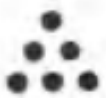


플라보노이드(영어: flavonoid)



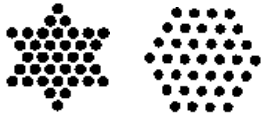
생명체의 수(數)? 기하학?

3-균형: 삼원색



6-불완전: 피조세계

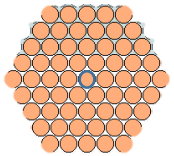
7-완전: 분류, 생식주기



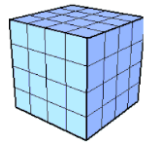
37-생명체 체온, 배란

Ἀδάμ
1+4+1+40

46-염색체 수(數)



61-아미노산 매칭 유전암호



64-3자리 유전암호 가지 수

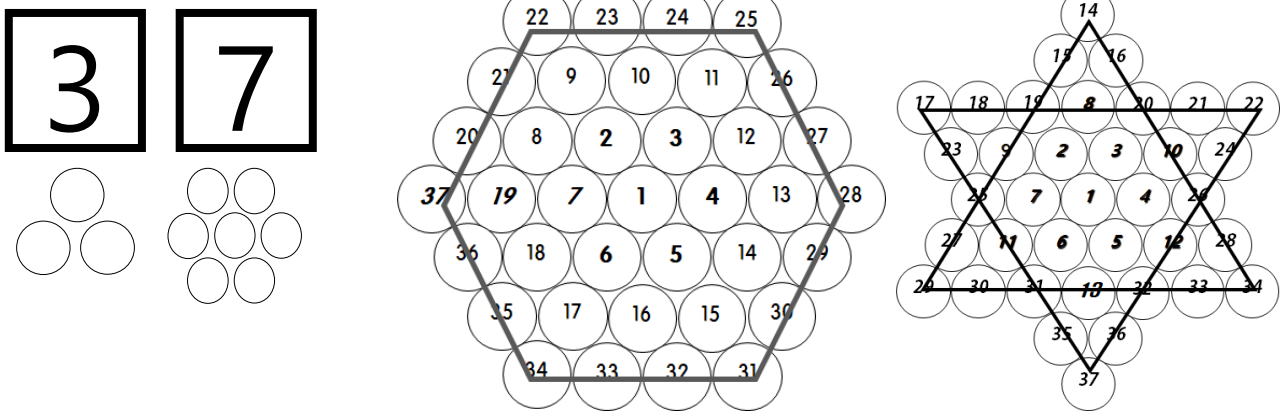
73-보온, 합성, 프롤린

74-아미노산 블록 질량수

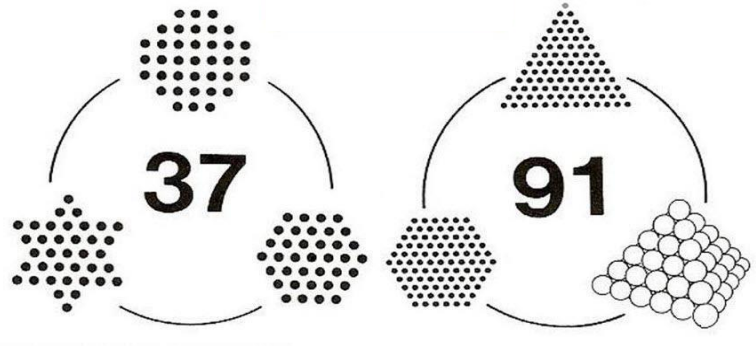
* 육각별 수(數) 식: $6n^2-6n+1$, 1, 13, 37, 73, 121…

** 육각형 수(數) 식: $3n^2-3n+1$, 1, 7, 19, 37, 61, 91…

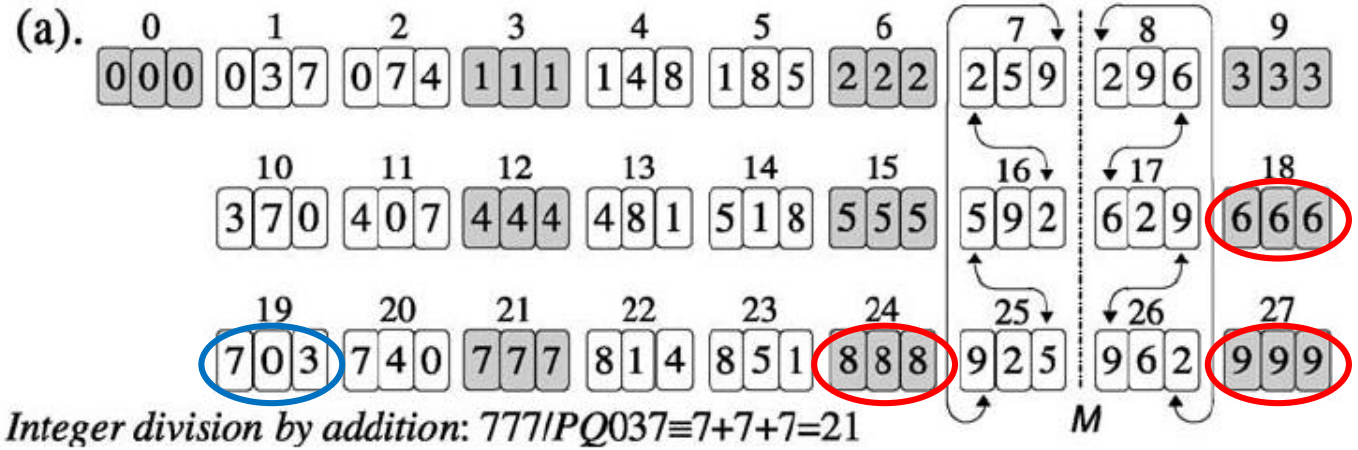
37은 육각형과 육각별 모두 표현가능한 수



삼형수: 3가지 도형으로 표현



Vernon et al (1993)



37의 배수들과 반복되는 수:
111, 222, 333…999

shcherbak, V. I. (2003)

유전암호(64)와 아미노산(20)

DNA

FIRST BASE	SECOND BASE T	SECOND BASE C	SECOND BASE A	SECOND BASE G	THIRD BASE
T	TTT Phe	TCT Ser	TAT Tyr	TGT Cys	T
	TTC Phe	TCC Ser	TAC Tyr	TGC Cys	C
	TTA Leu	TCA Ser	TAA Stop	TGA Stop	A
	TTG Leu	TCG Ser	TAG Stop	TGG Trp	G
C	CTT Leu	CCT Pro	CAT His	CGT Arg	T
	CTC Leu	CCC Pro	CAC His	CGC Arg	C
	CTA Leu	CCA Pro	CAA Gln	CGA Arg	A
	CTG Leu	CCG Pro	CAG Gln	CGG Arg	G
A	ATT Ile	ACT Thr	AAT Asn	AGT Ser	T
	ATC Ile	ACC Thr	AAC Asn	AGC Ser	C
	ATA Ile	ACA Thr	AAA Lys	AGA Arg	A
	ATG Met	ACG Thr	AAG Lys	AGG Arg	G
G	GTT Val	GCT Ala	GAT Asp	GGT Gly	T
	GTC Val	GCC Ala	GAC Asp	GGC Gly	C
	GTA Val	GCA Ala	GAA Glu	GGA Gly	A
	GTG Val	GCG Ala	GAG Glu	GGG Gly	G

시작암호

RNA

FIRST BASE	SECOND BASE U	SECOND BASE C	SECOND BASE A	SECOND BASE G	THIRD BASE
U	UUU Phe	UCU Ser	UAU Tyr	UGU Cys	U
	UUC Phe	UCC Ser	UAC Tyr	UGC Cys	C
	UUA Leu	UCA Ser	UAA Stop	UGA Stop	A
	UUG Leu	UCG Ser	UAG Stop	UGG Trp	G
C	CUU Leu	CCU Pro	CAU His	CGU Arg	U
	CUC Leu	CCC Pro	CAC His	CGC Arg	C
	CUA Leu	CCA Pro	CAA Gln	CGA Arg	A
	CUG Leu	CCG Pro	CAG Gln	CGG Arg	G
A	AUU Ile	ACU Thr	AAU Asn	AGU Ser	U
	AUC Ile	ACC Thr	AAC Asn	AGC Ser	C
	AUA Ile	ACA Thr	AAA Lys	AGA Arg	A
	AUG Met	ACG Thr	AAG Lys	AGG Arg	G
G	GUU Val	GCU Ala	GAU Asp	GGU Gly	U
	GUC Val	GCC Ala	GAC Asp	GGC Gly	C
	GUA Val	GCA Ala	GAA Glu	GGA Gly	A
	GUG Val	GCG Ala	GAG Glu	GGG Gly	G

Universal genetic code

TCAG (4^3=64)

Amino Acid	
Name	Abb'n
Alanine	Ala
Arginine	Arg
Asparagine	Asn
Aspartic acid	Asp
Cysteine	Cys
Glutamic acid	Glu
Glutamine	Gln
Glycine	Gly
Histidine	His
Isoleucine	Ile
Leucine	Leu
Lysine	Lys
Methionine	Met
Phenylalanine	Phe
Proline	Pro
Serine	Ser
Threonine	Thr
Tryptophan	Trp
Tyrosine	Tyr
Valine	Val

A
R
N
D
C
E
Q
G
H
I
L
K
M
F
P
S
T
W
Y
V

생명의 시스템

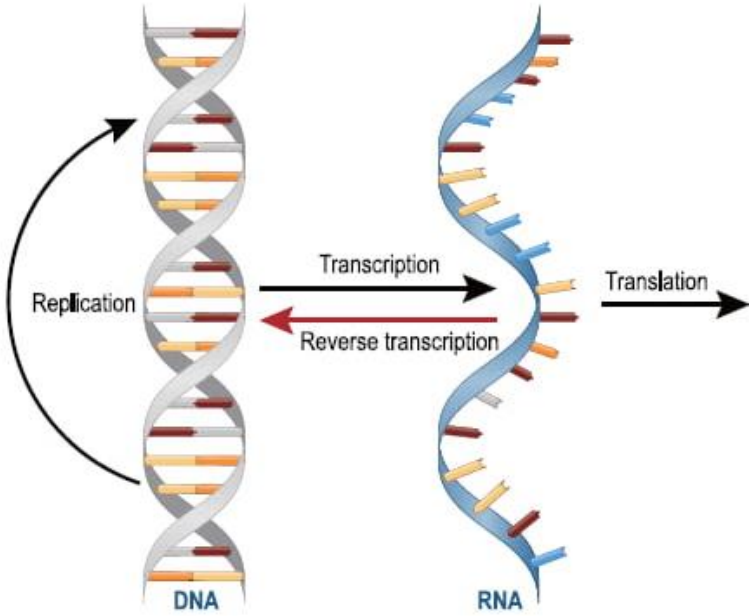
누가 조율하는가?

중심원리-Central Dogma

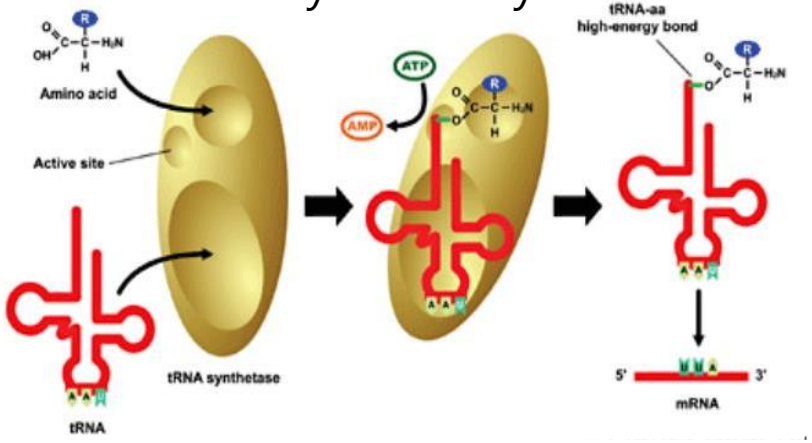
DNA->RNA->단백질(아미노산)

DNA polymerase

RNA polymerase



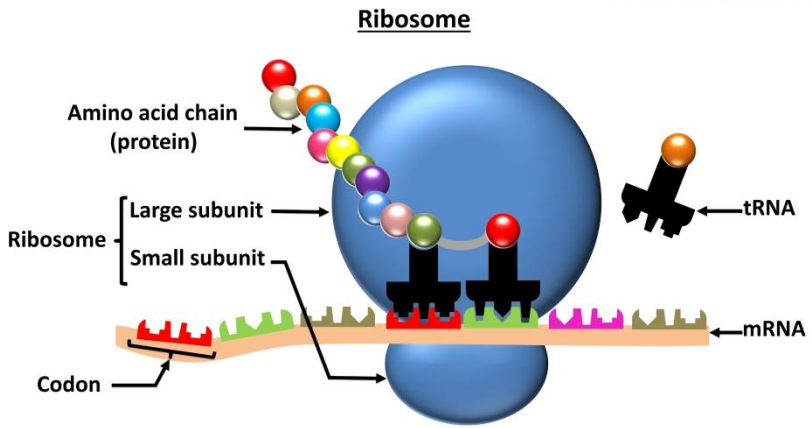
Aminoacyl-tRNA synthetase

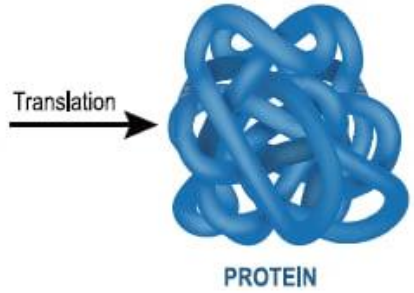


단백질
(아미노산)

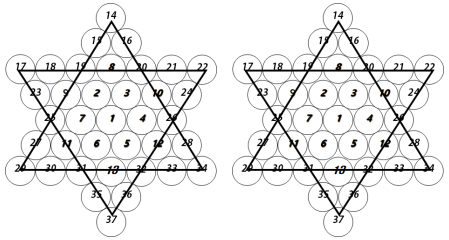
DNA
정보

RNA
정보/ribozyme

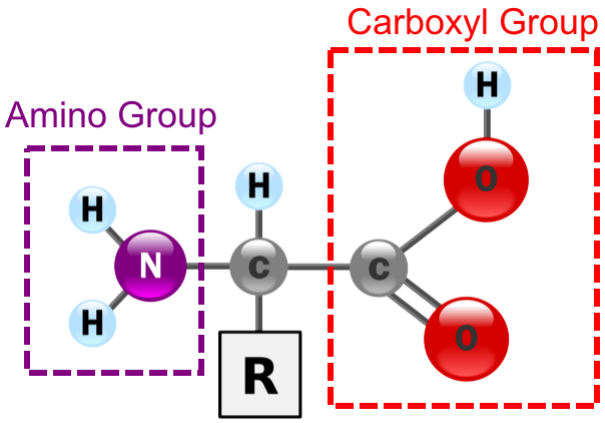




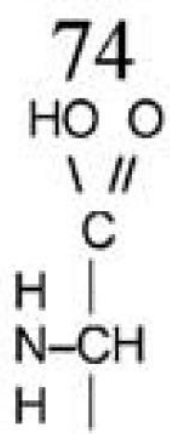
아미노산 질량수: 74



74=37 x 2



B: 74



중성자수	양성자수	핵자수
35	39	74
5*7	3*13	2*37

아미노산

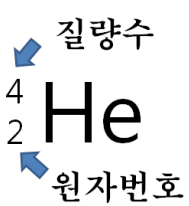
R

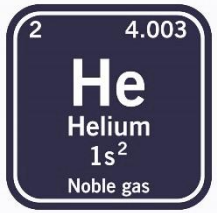
H_2NCHCO_2H

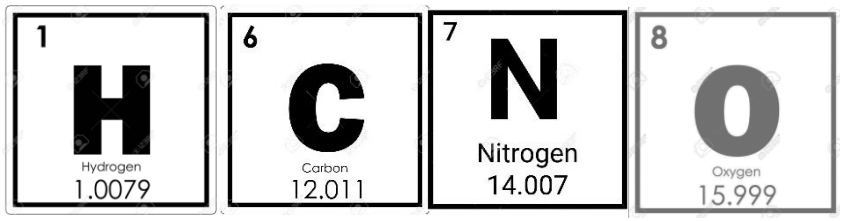
R: 측쇄

B: 블록

B: 74 ($H_2$2+N14+C12+H1+C12+$O_2$32+H1)







Element		Nucleons		
Name	Symbol	Protons	Neutrons	Total
Hydrogen	H	1	0	1
Carbon	C	6	6	12
Nitrogen	N	7	7	14
Oxygen	O	8	8	16
Sulphur	S	16	16	32

Element	Approx Atomic Mass of most common isotope	Atomic Mass natural isotope mixture
H	1	1.008
C	12	12.011
N	14	14.007
O	16	15.999
S	32	32.066

Rakočević, M. M. (2004)

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A harmonic structure of the genetic code

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Department of Chemistry, Faculty of Science, University of Niš, Ćirila i Metodija 2, Serbia & Montenegro, Yugoslavia

Received 7 October 2003; received in revised form 19 March 2004; accepted 26 March 2004

Abstract

In this paper is presented a new, very harmonic structure of the genetic code (GC) within a system of "4 × 5" (and/or of "5 × 4") of amino acids (AAs) in two variants. In first variant, the five rows within the system start with one polar charged amino acid (AA) each, making first column, consisting from five polar charged AAs (D, R, K, H, E). Five polar non-charged AAs (N, P, Y, W, Q) follow, then five non-polar AAs as last column (A, L, F, V, I) and, finally, five polar or non-polar AAs, in a combination, as first to last column (A as non-polar; S, T as polar, and G, P as ambivalent AAs). A second variant is subsequent to this one—"4 × 5" system with five nitrogen AAs (K, R, P, H, W), five oxygen (D, E, Y, S, T), five solely carbon (A, L, F, V, I) and five "combined" AAs (G with hydrogen as side chain; C and M with carbon and sulfur; N and Q with carbon, oxygen and nitrogen). A strict balance of atom and nucleon number as well as molecule mass follows the classification in both system variants.

Keywords: Genetic code; Siemion–Siemion's rule; Davidov's rule; Damjanović's spiral model; Atom-number; Nucleon number; System theory

1. Introduction

In a previous paper (Rakočević, 1998a), we presented a system of "2 × 10" (10 pairs) of canonical amino acids (AAs), with firmly determined positions in pairs, within two classes, handled by class I and class II of enzymes aminoacyl-tRNA synthetases (Fig. 1, in relation to Fig. 2). However, in this paper we will present a system of "4 × 5" (four quintets and five quartets at the same time) of AAs, with characteristics of a harmonic structure, "hidden" i.e. integrated within the system of "2 × 10" (Table 1). The system is being generated in

D–R–K–H–E
N–F–Y–W–Q

A – P – T – S – G
L – I – M – C – V

Starting from aspart
polar charged AAs
linear and continual
AAs are being added
Finally, the cycle is b
derivatives to their
stand within the syst
of D–E within step
pair D–N remains in
in the last row. This way, the first and second column
within the system of "4 × 5" are being realized, shown in Table 1. Finally, step (3) presents the manner on which

shcherbak, V. I. (2003)

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Arithmetic inside the universal genetic code

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Department of Applied Mathematics, al-Faraby Kazakh National University, 71 al-Faraby Avenue, Almaty 480078, Kazakhstan, CIS

Received 28 October 2001; received in revised form 23 April 2002; accepted 10 December 2002

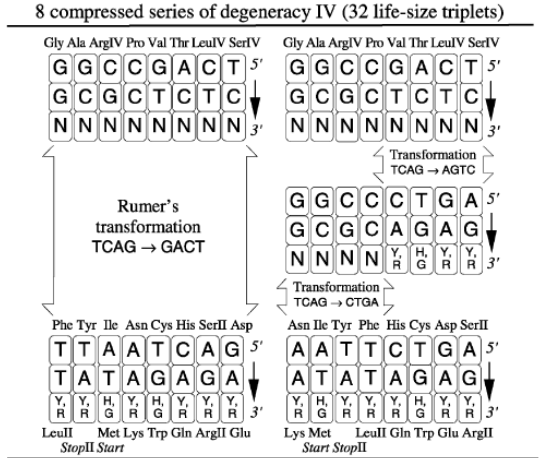
Abstract

The first information system emerged on the earth as primo
appearance of arithmetic power in such a linguistic milieu is
systems of extremely high efficiency. In this case, the arithmetic
code. A number is the fundamental arithmetic symbol produce
detected inside the genetic code, it would be natural to expec
control, safety, and precise alteration of the genetic texts. The n
suitable for embodiments of digits. These assumptions were us

The compressed, life-size, and split representation of the *E*
considered simultaneously. An exact equilibration of the nucl
was found repeatedly within specified sets of the genetic code.
decimal representation, the unique form 111, 222, . . . , 999. This
criterion could simplify some computing mechanism of a cell i
symmetry of the genetic code demonstrates that possibly a zero
the genetic code could be explained by activities of some hypot
digital genetic texts.

It is well known that if mutation replaces an amino acid, the
strong. The antisymmetrical correlation between the amino aci
that these and some other familiar properties may be a physico

The "frozen accident" model, giving unlimited freedom to t
both arithmetic symbols and physicochemical protection inside



모든 아미노산의 질량수의 합: 37의 배수

AMINO ACID	SYMBOL	MOLAR MASS
Alanine	Ala /A	89.09
Arginine	Arg/R	174.20
Asparagine	Asn/N	132.12
Aspartic acid	Asp/D	133.10
Cysteine	Cys/C	121.16
Glutamic acid	Glu/E	147.13
Glutamine	Gln/Q	146.14
Glysine	Gly/G	75.07
Histidine	His /H	155.15
Isoleucine	Ile /I	131.17
Leucine	Leu/L	131.17
Lysine	Lys/K	146.19
Methionine	Met/M	149.21
Phenylalanine	Phe/F	165.19
Proline	Pro /P	115.13
Serine	Ser/S	105.09
Threonine	Thr/T	119.12
Tryptophan	Trp/W	204.23
Tyrosine	Tyr/Y	181.19
Valine	Val /V	117.15

	1	2	3	4	ROW TOTALS
1	Asp/D	Asn/N	Ala /A	Leu/L	
	133.10	132.12	89.09	131.17	485.48
2	Arg/R	Phe/F	Pro /P	Ile /I	
	174.20	165.19	115.13	131.17	585.69
3	Lys /K	Tyr/Y	Thr/T	Met/M	
	146.19	181.19	119.12	149.21	595.71
4	His /H	Trp/W	Ser/S	Cys/C	
	155.15	204.23	105.09	121.16	585.63
5	Glu/E	Gln/Q	Gly/G	Val /V	
	147.13	146.14	75.07	117.15	485.49
COLUMN TOTALS	755.77	828.87	503.50	649.86	2738.00

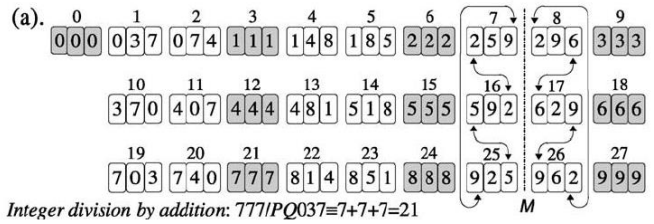
=

=

1332.37
= 2x666+0.37

1405.63
= 2x703-0.37

= 37 x 74
= 2 x 37^2



Rakočević, M. M. (2004)

모든 아미노산의 질량수의 합: 37의 배수

AMINO ACID	SYMBOL	MOLAR MASS
Alanine	Ala /A	89.09
Arginine	Arg/R	174.20
Asparagine	Asn/N	132.12
Aspartic acid	Asp/D	133.10
Cysteine	Cys/C	121.16
Glutamic acid	Glu/E	147.13
Glutamine	Gln/Q	146.14
Glysine	Gly /G	75.07
Histidine	His /H	155.15
Isoleucine	Ile /I	131.17
Leucine	Leu/L	131.17
Lysine	Lys /K	146.19
Methionine	Met/M	149.21
Phenylalanine	Phe/F	165.19
Proline	Pro /P	115.13
Serine	Ser/S	105.09
Threonine	Thr/T	119.12
Tryptophan	Trp/W	204.23
Tyrosine	Tyr/Y	181.19
Valine	Val /V	117.15

	1	2	3	4	ROW TOTALS
1	Asp/D	Asn/N	Ala /A	Leu/L	
	133.10	132.12	89.09	131.17	485.48
2	Arg/R	Phe/F	Pro /P	Ile /I	
	174.20	165.19	115.13	131.17	585.69
3	Lys /K	Tyr/Y	Thr/T	Met/M	297.855
	~~146.19~~	~~181.19~~	~~119.12~~	~~149.21~~	
					297.855
4	His /H	Trp/W	Ser/S	Cys/C	
	155.15	204.23	105.09	121.16	585.63
5	Glu/E	Gln/Q	Gly /G	Val /V	
	147.13	146.14	75.07	117.15	485.49
COLUMN TOTALS	755.77	828.87	503.50	649.86	2738.00

1369.025 = 37^2 + 0.025

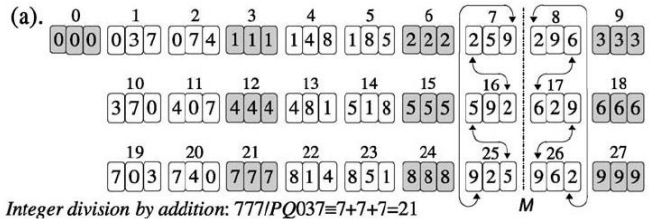
1368.975 = 37^2 − 0.025

1332.37 = 2x666+0.37

1405.63 = 2x703-0.37

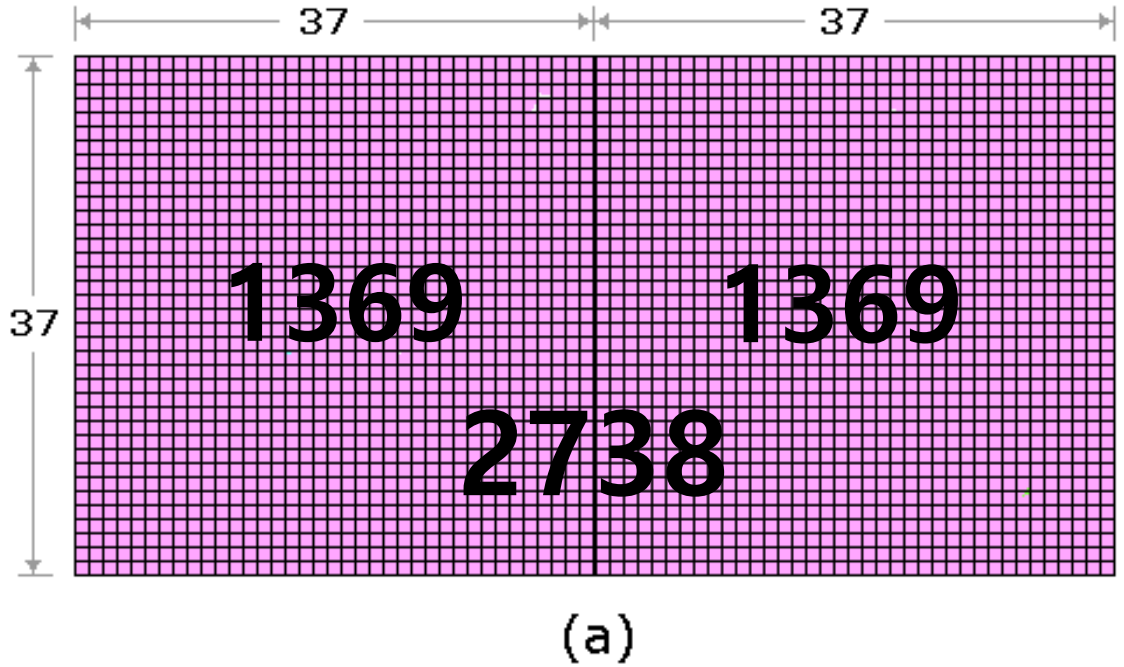
= 37 x 74

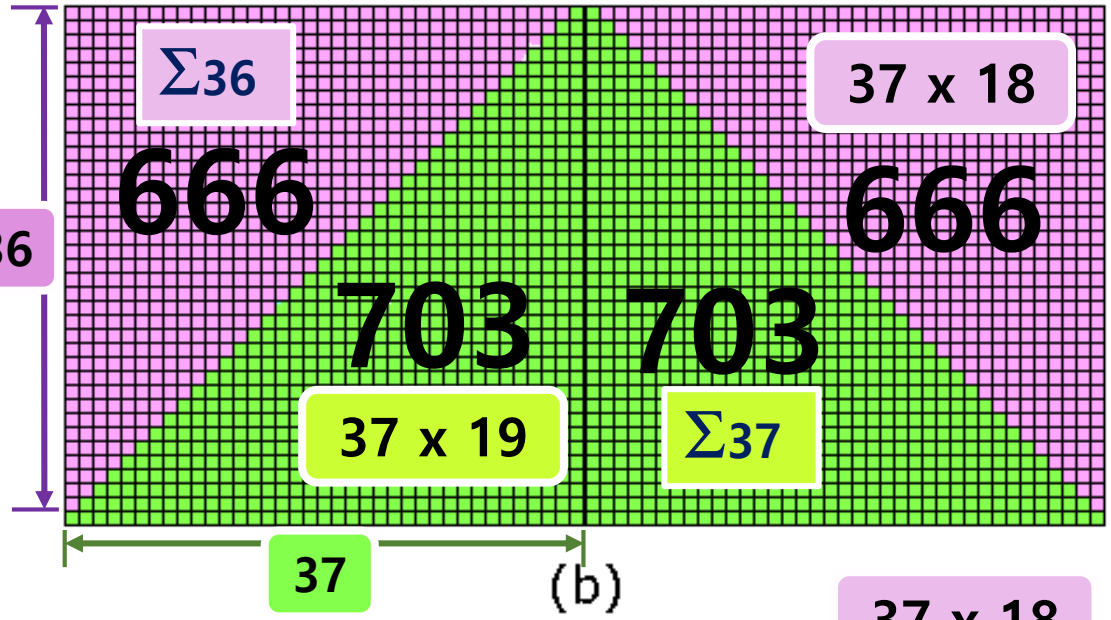
= 2 x 37^2

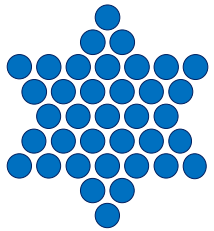


Rakočević, M. M. (2004)

모든 아미노산의 질량수의 합: 37의 배수







37 x 74 ⇨ 2738

1+2+3+.. ..+35+36 = Σ36

$$\sum_{k=1}^{n} k = \frac{n(n+1)}{2}$$

1+2+3+.. ..+36+37 = Σ37

37 x 18

666

703

37 x 19

shCherbak의 RNA 암호패턴

RNA

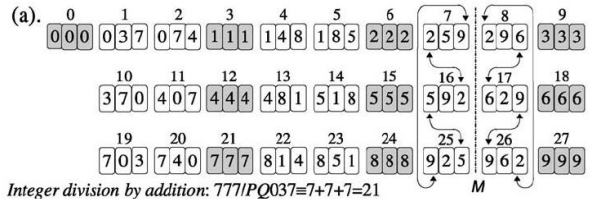
FIRST BASE	SECOND BASE U	SECOND BASE C	SECOND BASE A	SECOND BASE G	THIRD BASE
U	UUU UUC UUA UUG	UCU UCC UCA UCG	UAU UAC UAA UAG	UGU UGC UGA UGG	U C A G
C	CUU CUC CUA CUG	CCU CCC CCA CCG	CAU CAC CAA CAG	CGU CGC CGA CGG	U C A G
A	AUU AUC AUA AUG	ACU ACC ACA ACG	AAU AAC AAA AAG	AGU AGC AGA AGG	U C A G
G	GUU GUC GUA GUG	GCU GCC GCA GCG	GAU GAC GAA GAG	GGU GGC GGA GGG	U C A G

Universal genetic code
UCAG (4^3=64)

SECOND BASE	FIRST BASE A	FIRST BASE G	FIRST BASE U	FIRST BASE C
A	AAU Asn AAC Asn AAA Lys AAG Lys	GAU Asp GAC Asp GAA Glu GAG Glu	UAU Tyr UAC Tyr UAA Stop UAG Stop	CAU His CAC His CAA Gln CAG Gln
G	AGU Ser AGC Ser AGA Arg AGG Arg	GGU Gly GGC Gly GGA Gly GGG Gly	UGU Cys UGC Cys UGA Stop UGG Trp	CGU Arg CGC Arg CGA Arg CGG Arg
U	AUU Ile AUC Ile AUA Ile AUG Met	GUU Val GUC Val GUA Val GUG Val	UUU Phe UUC Phe UUA Leu UUG Leu	CUU Leu CUC Leu CUA Leu CUG Leu
C	ACU Thr ACC Thr ACA Thr ACG Thr	GCU Ala GCC Ala GCA Ala GCG Ala	UCU Ser UCC Ser UCA Ser UCG Ser	CCU Pro CCC Pro CCA Pro CCG Pro

shCherbak의 암호패턴
AGUC (4^3=64)

Shcherbak의 유전암호 1st 패턴과 핵자 수 37



(a). The amino acids of degeneracy IV series

	Gly	Ala	SerIV	Pro	Val	Thr	LeuIV	ArgIV	Σ_{Total}	Σ_{Total} / PQ 037
Nucleon number of whole molecule, N:	75	89	105	115	117	119	131	174	925	$25=5^2$
standard box, B:	74	74	74	73+1	74	74	74	74	592	$16=4^2$
side chain, R:	1	15	31	42–1	43	45	57	100	333	$9=3^2$

PQD feature

Squares of first three Pythagorean numbers

(b). The amino acids and syntactic signs of degeneracy III, II, I series

	Cys	Ile	StopII	SerII	LeuII	Asn	Asp	Gln	Lys	Glu	His	Phe	ArgII	Tyr	Start Met	Trp	Σ_{Total}
B:	74	74	0	74	74	74	74	74	74	74	74	74	74	74	74	74	111 +999
R:	47	57	0	31	57	58	59	72	72	73	81	91	100	107	75	130	111 +999

Balance

PQD feature

Shcherbak의 첫 번째 패턴

		FIRST BASE			
		A	G	U	C
SECOND BASE	A	AAU Asn AAC Asn AAA Lys AAG Lys	GAU Asp GAC Asp GAA Glu GAG Glu	UAU Tyr UAC Tyr UAA Stop UAG Stop	CAU His CAC His CAA Gln CAG Gln
	G	AGU Ser AGC Ser AGA Arg AGG Arg	GGU Gly GGC Gly GGA Gly GGG Gly	UGU Cys UGC Cys UGA Stop UGG Trp	CGU Arg CGC Arg CGA Arg CGG Arg
	U	AUU Ile AUC Ile AUA Ile AUG Met	GUU Val GUC Val GUA Val GUG Val	UUU Phe UUC Phe UUA Leu UUG Leu	CUU Leu CUC Leu CUA Leu CUG Leu
	C	ACU Thr ACC Thr ACA Thr ACG Thr	GCU Ala GCC Ala GCA Ala GCG Ala	UCU Ser UCC Ser UCA Ser UCG Ser	CCU Pro CCC Pro CCA Pro CCG Pro

(a) Ⅳ그룹 아미노산 핵자수 (b) Ⅰ~Ⅲ그룹 아미노산 핵자수

R	B	합	R	B	합
333	592	925	1110	1110	2220
3*3*37	4*4*37	5*5*37	3*10*37	3*10*37	3*4*5*37

shcherbak, V. I. (2003)

Shcherbak의 유전암호 2nd 패턴과 핵자 수 37

(a). The amino acids and syntactic signs of the series with the 5′ pyrimidine bases (the first 5′ bisection)

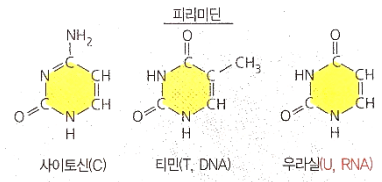
	5′T: Phe	LeuII	SerIV	Tyr	StopII	Cys	Trp	5′C: LeuIV	Pro	His	Gln	ArgIV	Σ_{Total}
B:	74	74	74	74	0	74	74	74	73+1	74	74	74	814
R:	91	57	31	107	0	47	130	57	42–1	81	72	100	814

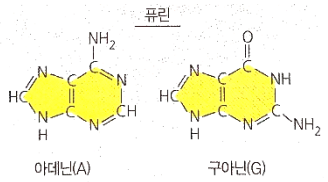
Balance

(b). The amino acids and syntactic signs of the series with the 5′ purine bases

	5′A: Ile	Met	Thr	Asn	Lys	SerII	ArgII	5′G: Val	Ala	Asp	Glu	Gly	Σ_{Total}
	Start												
N:	131	149	119	132	146	105	174	117	89	133	147	75	925 + 2Δ
B:	74	74	74	74	74	74	74	74	74	74	74	74	592 + Δ
R:	57	75	45	58	72	31	100	43	15	59	73	1	333 + Δ

Δ=1110–814





Shcherbak의 두 번째 패턴

		FIRST BASE A	FIRST BASE G	FIRST BASE U	FIRST BASE C
SECOND BASE	A	AAU Asn AAC Asn AAA Lys AAG Lys	GAU Asp GAC Asp GAA Glu GAG Glu	UAU Tyr UAC Tyr UAA Stop UAG Stop	CAU His CAC His CAA Gln CAG Gln
	G	AGU Ser AGC Ser AGA Arg AGG Arg	GGU Gly GGC Gly GGA Gly GGG Gly	UGU Cys UGC Cys UGA Stop UGG Trp	CGU Arg CGC Arg CGA Arg CGG Arg
	U	AUU Ile AUC Ile AUA Ile AUG Met	GUU Val GUC Val GUA Val GUG Val	UUU Phe UUC Phe UUA Leu UUG Leu	CUU Leu CUC Leu CUA Leu CUG Leu
	C	ACU Thr ACC Thr ACA Thr ACG Thr	GCU Ala GCC Ala GCA Ala GCG Ala	UCU Ser UCC Ser UCA Ser UCG Ser	CCU Pro CCC Pro CCA Pro CCG Pro

(a) 피리미딘 아미노산 핵자수

R	B	합
814	814	1628
2*11*37	2*11*37	4*11*37

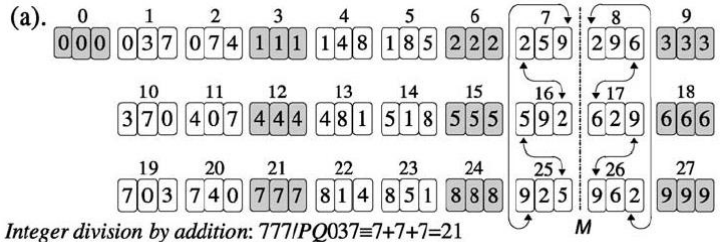
(b) 퓨린 아미노산 핵자수

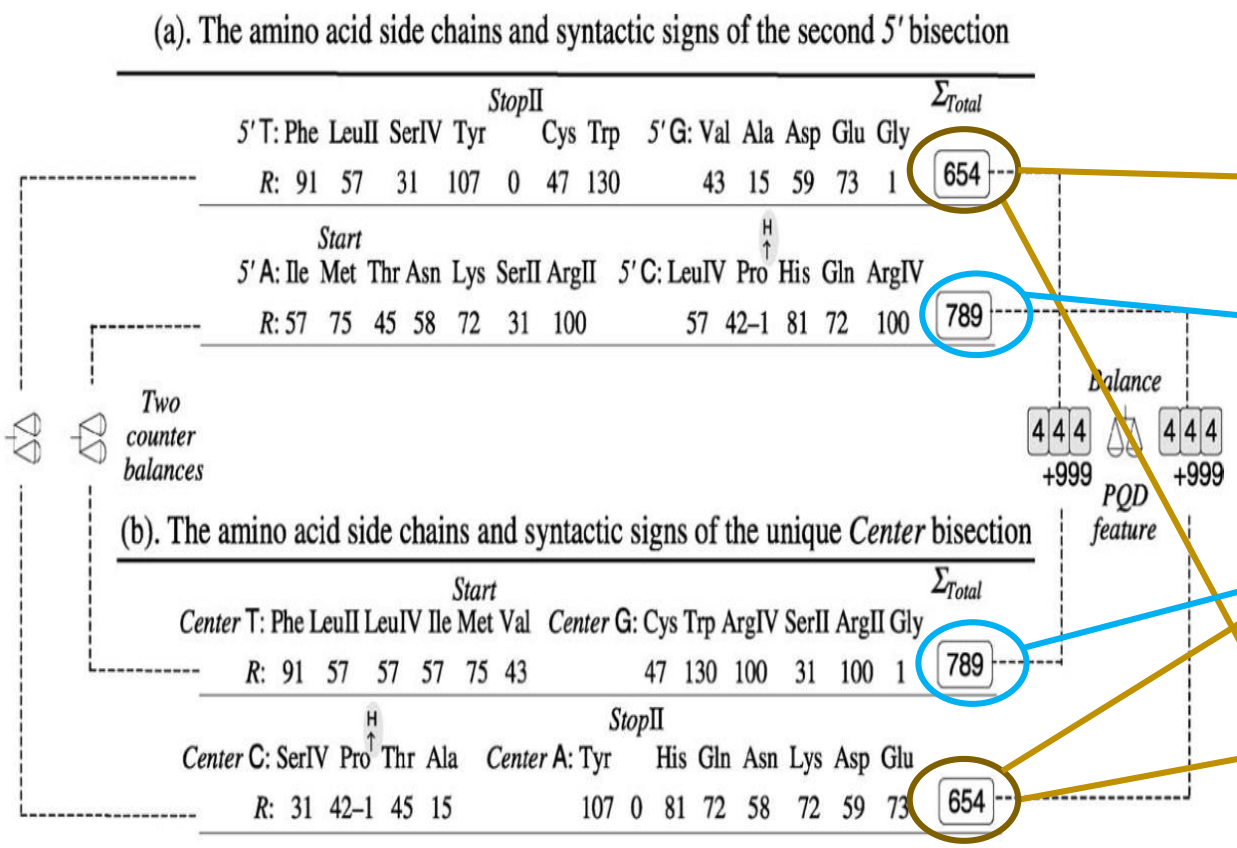
R	B	합
629	888	1517
17*37	24*37	41*37
333+Δ	592+Δ	925+2Δ

*** Δ = 1110-814=296**

shcherbak, V. I. (2003)

Shcherbak의 유전암호 3rd 패턴과 핵자 수 37





(ㄱ) 세로형

Shcherbak의 세 번째 패턴

(ㄴ) 가로형

SECOND BASE	FIRST BASE A	FIRST BASE G	FIRST BASE U	FIRST BASE C
A	AAU Asn AAC Asn AAA Lys AAG Lys	GAU Asp GAC Asp GAA Glu GAG Glu	UAU Tyr UAC Tyr UAA Stop UAG Stop	CAU His CAC His CAA Gln CAG Gln
G	AGU Ser AGC Ser AGA Arg AGG Arg	GGU Gly GGC Gly GGA Gly GGG Gly	UGU Cys UGC Cys UGA Stop UGG Trp	CGU Arg CGC Arg CGA Arg CGG Arg
U	AUU Ile AUC Ile AUA Ile AUG Met	GUU Val GUC Val GUA Val GUG Val	UUU Phe UUC Phe UUA Leu UUG Leu	CUU Leu CUC Leu CUA Leu CUG Leu
C	ACU Thr ACC Thr ACA Thr ACG Thr	GCU Ala GCC Ala GCA Ala GCG Ala	UCU Ser UCC Ser UCA Ser UCG Ser	CCU Pro CCC Pro CCA Pro CCG Pro

(1) 주황 아미노산 핵자수

R	B	합
654	814	1468
A	2*11*37	

(2) 파랑 아미노산 핵자수

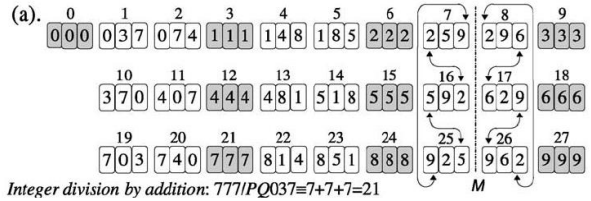
R	B	합
789	888	1677
B	24*37	

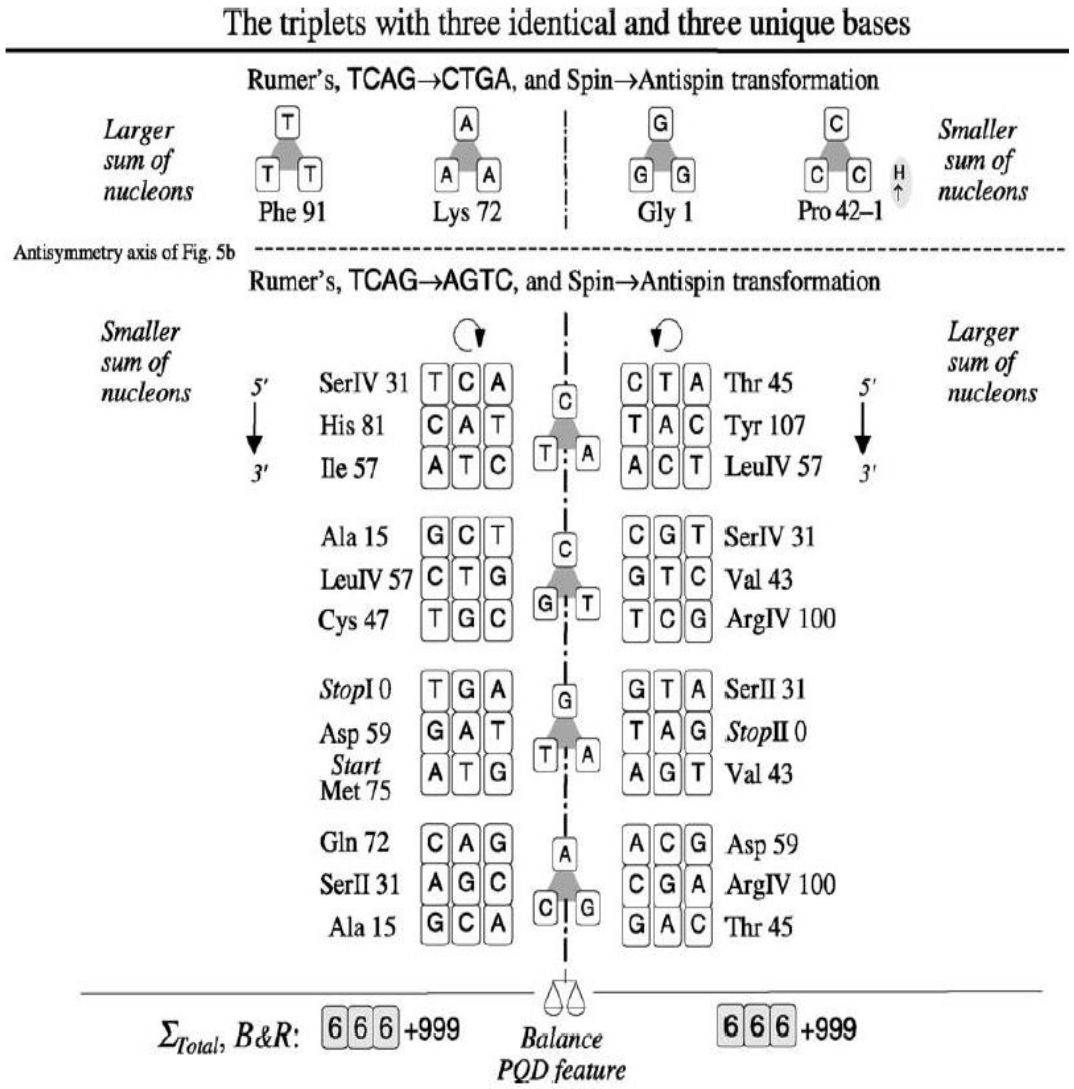
*** A+B = 1443 = 444 + 999**

3*13*37

shcherbak, V. I. (2003)

Shcherbak의 유전암호 4th 패턴과 핵자 수 37





Triplets of Identical Bases			
TTT Phe	R = 91 ; B = 74	GGG Gly	R = 1; B = 74
AAA Lys	R = 72 ; B = 74	CCC Pro	R = 41; B = 74

Clockwise Codons		Triplets of Unique Bases	AntiClockwise Codons	
TCA Ser	R = 31; B = 74	T A C	CTA Leu	R = 57; B = 74
CAT His	R = 81; B = 74		TAC Tyr	R = 107; B = 74
ATC Ile	R = 57; B = 74		ACT Thr	R = 45; B = 74
GCT Ala	R = 15; B = 74	G T C	CGT Arg	R = 100; B = 74
CTG Leu	R = 57; B = 74		GTC Val	R = 43; B = 74
TGC Cys	R = 47; B = 74		TCG Ser	R = 31; B = 74
TGA Stop	R = 0 ; B = 0	T A G	GTA Val	R = 43; B = 74
GAT Asp	R = 59; B = 74		TAG Stop	R = 0 ; B = 0
ATG Met	R = 75; B = 74		AGT Ser	R = 31; B = 74
CAG Gln	R = 72; B = 74	C G A	ACG Thr	R = 45; B = 74
AGC Ser	R = 31; B = 74		CGA Arg	R = 100; B = 74
GCA Ala	R = 15; B = 74		GAC Asp	R = 59; B = 74

(a) 시계방향코돈 핵자수

R	B	합
703	962	1665
666 + 999		45*37

(b) 시계반대방향 아미노산 핵자수

R	B	합
703	962	1665
666+999		45*37

shcherbak, V. I. (2003)

유전암호에 따른 아미노산의 블록B 및 측쇄R의 원자수, 질량수 총합

AMINO ACID	Particles in the Individual Amino Acids				DNA/RNA PF*	Particles in the Products of the Genetic Code			
	Atoms	Protons	Neutrons	Total		Atoms	Protons	Neutrons	Total
Std Blk	9	39	35	74	61	549	2379	2135	4514
Ala /A	13	48	41	89	4	52	192	164	356
Arg/R	26	94	80	174	6	156	564	480	1044
Asn/N	17	70	62	132	2	34	140	124	264
Asp/D	16	70	63	133	2	32	140	126	266
Cys/C	14	64	57	121	2	28	128	114	242
Glu/E	19	78	69	147	2	38	156	138	294
Gln/Q	20	78	68	146	2	40	156	136	292
Gly/G	10	40	35	75	4	40	160	140	300
His /H	20	82	73	155	2	40	164	146	310
Ile /I	22	72	59	131	3	22/44	72/144	59/118	131/262
Leu/L	22	72	59	131	6	132	432	354	786
Lys/K	24	80	66	146	2	48	160	132	292
Met/M	20	80	69	149	1	20	80	69	149
Phe/F	23	88	77	165	2	46	176	154	330
Pro /P	18	63	52	115	4	72	252	208	460
Ser/S	14	56	49	105	6	84	336	294	630
Thr/T	17	64	55	119	4	68	256	220	476
Trp/W	27	108	96	204	1	27	108	96	204
Tyr/Y	24	96	85	181	2	48	192	170	362
Val /V	19	64	53	117	4	76	256	212	468

Totals	'rebels' included	1147	4264	3654	7918
	'rebels' excluded	1078	4004	3430	7434

AMINO ACID	TOTAL NUCLEONS	RELATED CODONS	NUCLEON GRAND TOTAL
Gly/G	75	2+2	300
Ala /A	89	2+2	356
Ser/S	105	2+2	420
Pro /P	115	2+2	460
Val /V	117	2+2	468
Thr/T	119	2+2	476
Leu/L	131	2+2	524
Arg/R	174	2+2	696
8	925 [5x5x37]	32 [4x8]	3700 [10x10x37]

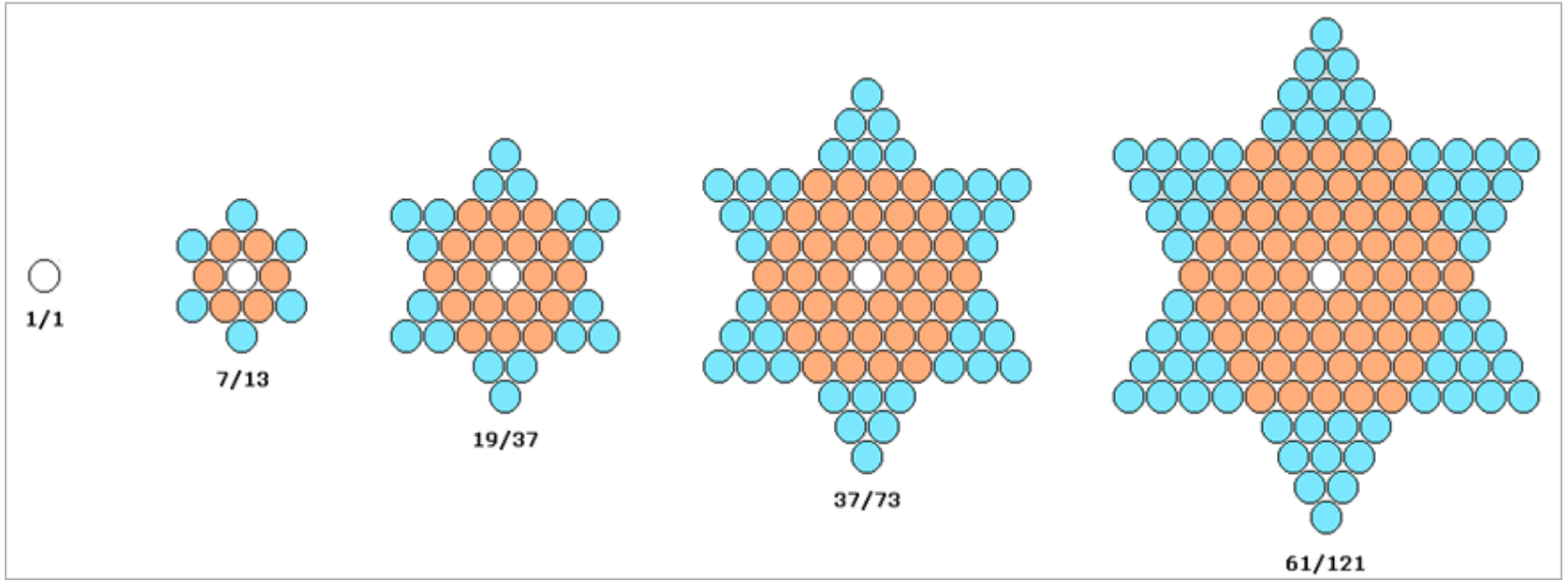
AMINO ACID	TOTAL NUCLEONS	RELATED CODONS	NUCLEON GRAND TOTAL
(STOP)	(0)	(2+1)	(0)
Ser/S	105	2	210
Cys/C	121	2	242
Leu/L	131	2	262
Ile /I	131	2+1	393
Asn/N	132	2	264
Asp/D	133	2	266
Gln/Q	146	2	292
Lys/K	146	2	292
Glu/E	147	2	294
Met/M	149	2-1	149
His /H	155	2	310
Phe/F	165	2	330
Arg/R	174	2	348
Tyr/Y	181	2	362
Trp/W	204	2-1	204
16	2220 [3x4x5x37]	32 [2x16+2-2]	4218 [6x19x37]

4그룹	1-3그룹	합
3700	4218	7918
100*37	6*19*37	214*37

shcherbak, V. I. (2003)

유전암호에 따른 아미노산의 각각 질량수의 합과 도형수 비교

Particles	In the base of each amino acid	In all amino acids	In the 'rebel group'	In all amino acids without the 'rebel group'
NUCLEONS	**74** [= 37x2]	**7918** [=37x214]	**484** [= 121x4]	**7434** [= 7x1062]
PROTONS	**39** [= 13x3]	**4264** [= 13x328]	**260** [= 13x20]	**4004** [= 13x7x44]
NEUTRONS	**35** [= 7x5]	**3654** [= 7x522]	**224** [= 7x32]	**3430** [= 7x7x7x10]



정보이론과 생명체의 수(數) 37?

정보의 생산자

(발신자)

전송된 신호(육각형.질서)의 존재

사용된 암호 數 37 (언어.말 체계)

의도된 목적(생명)과 달성된 결과

의식(설계자.로고스)의 존재

정보의 소비자

(수신자)

본론3 Body3

성경말씀에도 수학적 질서(수, 기하학)가 존재하는 곳이 있을까?

신성한 서문에 숨겨진 생명의 수

CEN Tech. J., vol. 7(2), 1993, pp. 184–196

The Ultimate Assertion:

בראשית ברא אלהים את השמים ואת הארץ׃ והארץ

Evidence of Supernatural Design in the Divine Prologue

VERNON JENKINS

ABSTRACT

Some alternative views of Genesis 1:1 that explain why this first verse of the Hebrew Scriptures must be regarded as the most remarkable combination of words ever written.

SOME PRELIMINARIES

(1) The term **characteristic value** will be found to occur frequently in the following pages. It refers to a numerical attribute of **every** Hebrew word, or group of words, that has its origin in **the alphabetic scheme of numeration** introduced into Jewish society circa 200 BC. This is given in Table 1 where the Hebrew alphabet of 22 letters — five with **end-forms** — is presented as a set of numerals.

The practice then was to record numbers on **an additive basis**, that is, letter-values were simply added together to obtain the number represented by a group of characters. It is in this manner that the **characteristic values** are calculated.

(2) In an appropriate example of this procedure the derivation of the characteristic values of **the eight opening words** of the Bible is explained in Table 2. Reading from **right to left**, the eight numbers bracketed beneath the text are obtained by adding together

Position in alphabet	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22
Letter	א	ב	ג	ד	ה	ו	ז	ח	ט	י	כ ך	ל	מ ם	נ ן	ס	ע	פ ף	צ ץ	ק	ר	ש	ת
Numerical Value	1	2	3	4	5	6	7	8	9	10	20	30	40	50	60	70	80	90	100	200	300	400

Table 1. The basis of the Hebrew alphabetic scheme of numeration.

(90)(200)(1)(5)(6)	(90)(200)(1)(5)	(400)(1)(6)	(40)(10)(40)(300)(5)	(400)(1)	(40)(10)(5)(30)(1)	(1)(200)(2)	(400)(10)(300)(1)(200)(2)
והארץ׃	הארץ	ואת	השמים	את	אלהים	ברא	בראשית
EARTH THE AND	EARTH THE	AND	HEAVEN THE	-	GOD	CREATED	BEGINNING THE IN
(302)	(296)	(407)	(395)	(401)	(86)	(203)	(913)

Table 2. Derivation of the characteristic values of the eight opening words of the Bible, the first seven words making up Genesis 1:1.

Ἀδάμ
1+4+1+40

수-문자 체계(Alpha numeric system)

(히브리어)

Place:	1	2	3	4	5	6	7	8
Letter:	א	ב	ג	ד	ה	ו	ז	ח
Name:	aleph	beyt	gimel	dalet	hey	vav	zayin	hhet
Numeral:	1	2	3	4	5	6	7	8
Place:	9	10	11	12	13	14	15	
Letter:	ט	י	כ ך	ל	מ ם	נ ן	ס	
Name:	tet	yud	kaph	lamed	mem	nun	samech	
Numeral:	9	10	20	30	40	50	60	
Place:	16	17	18	19	20	21	22	
Letter:	ע	פ ף	צ ץ	ק	ר	ש	ת	
Name:	ayin	pey	tsadey	quph	resh	shin	tav	
Numeral:	70	80	90	100	200	300	400	

(헬라어)

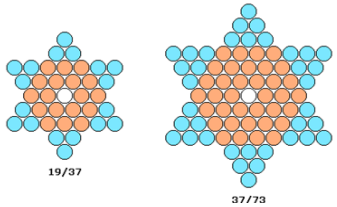
Place:	1	2	3	4	5	6	7	8
Letter:	Αα	Ββ	Γγ	Δδ	Εε	Ζζ	Ηη	Θθ
Name:	Alpha	Beta	Gamma	Delta	Epsilon	Zeta	Eta	Theta
Numeral:	1	2	3	4	5	7	8	9
Place:	9	10	11	12	13	14	15	16
Letter:	Ιι	Κκ	Λλ	Μμ	Νν	Ξξ	Οο	Ππ
Name:	Iota	Kappa	Lambda	Mu	Nu	Xi	Omicron	Pi
Numeral:	10	20	30	40	50	60	70	80
Place:	17	18	19	20	21	22	23	24
Letter:	Ρρ	Σσς	Ττ	Υυ	Φφ	Χχ	Ψψ	Ωω
Name:	Rho	Sigma	Tau	Upsilon	Phi	Chi	Psi	Omega
Numeral:	100	200	300	400	500	600	700	800

(5+13+11+8) 서수 값=37

חָכְמָה 지혜(호크마)

(5+40+20+8) 숫자 값=73

73



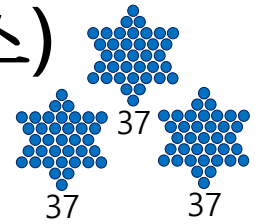
(9+7+18+15+20+18) 서수 값=87

Ι η σ ο ύ ς 예수(이에수스)

(10+8+200+70+400+200) 숫자 값=888

888=8 x 3 x 37=111*8

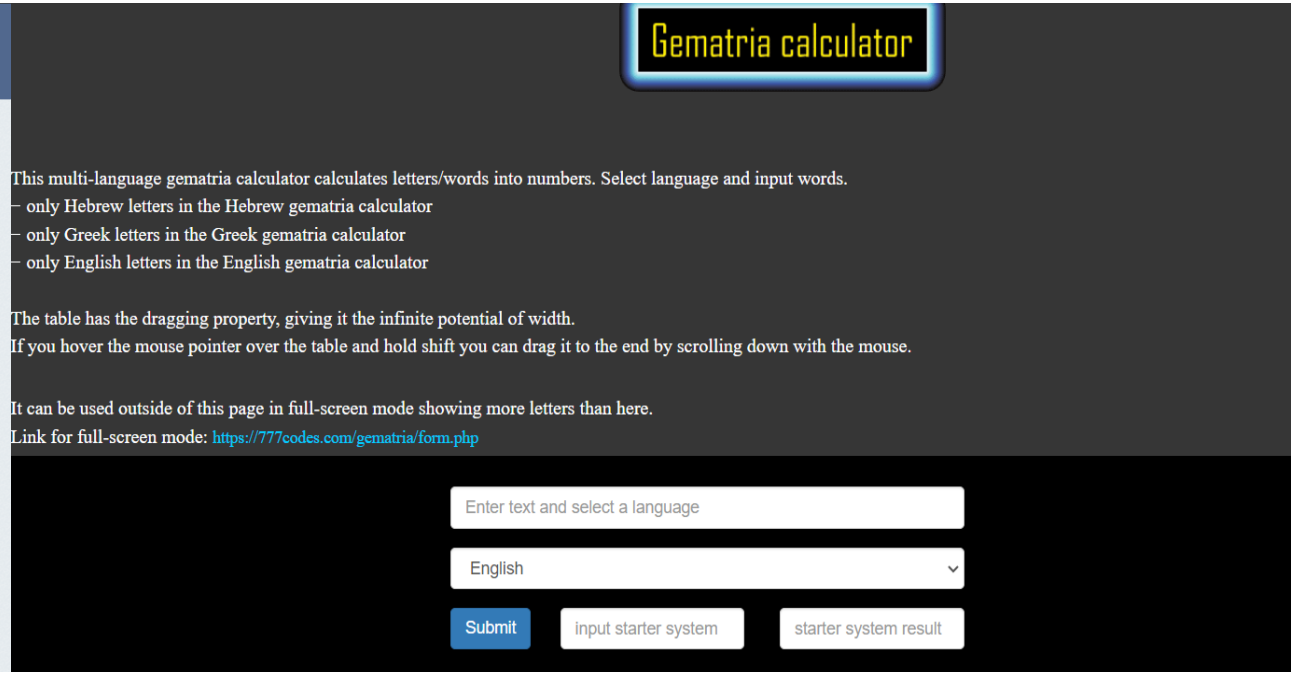
111=3*37



Vernon et al (1993)

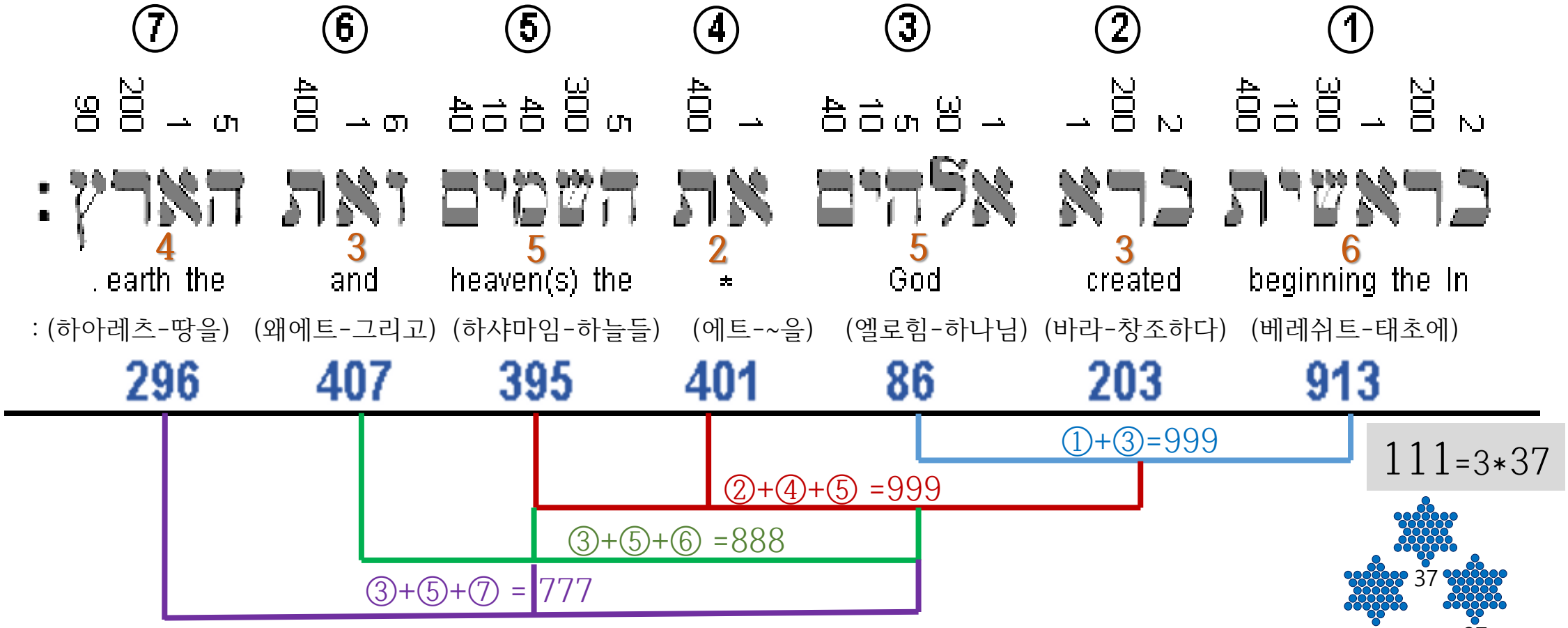
참고사이트: Blue Letter(원어연구)

참고사이트: Gematria calculator



창세기1장1절의 숫자 값(2701)과 특별한 질서들

GENESIS 1:1



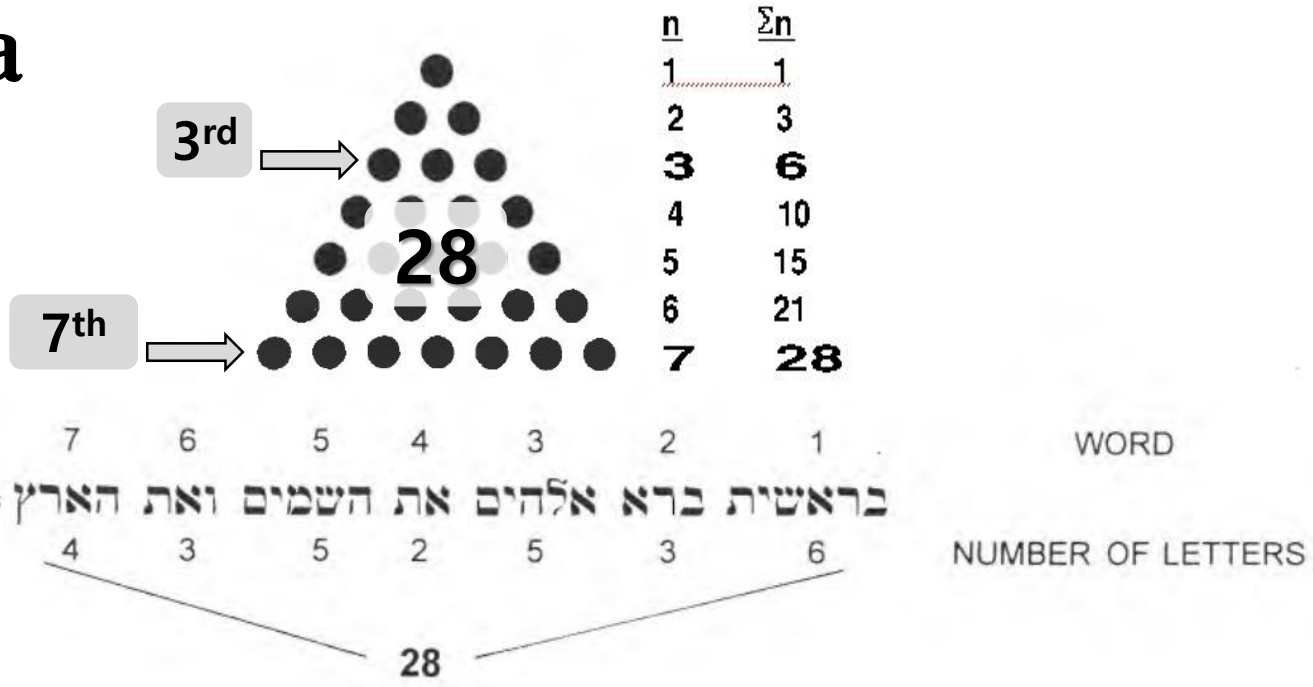
7개의 단어, 28의 문자, 1절 전체 숫자 값: 2701(913+203+86+401+395+407+296)

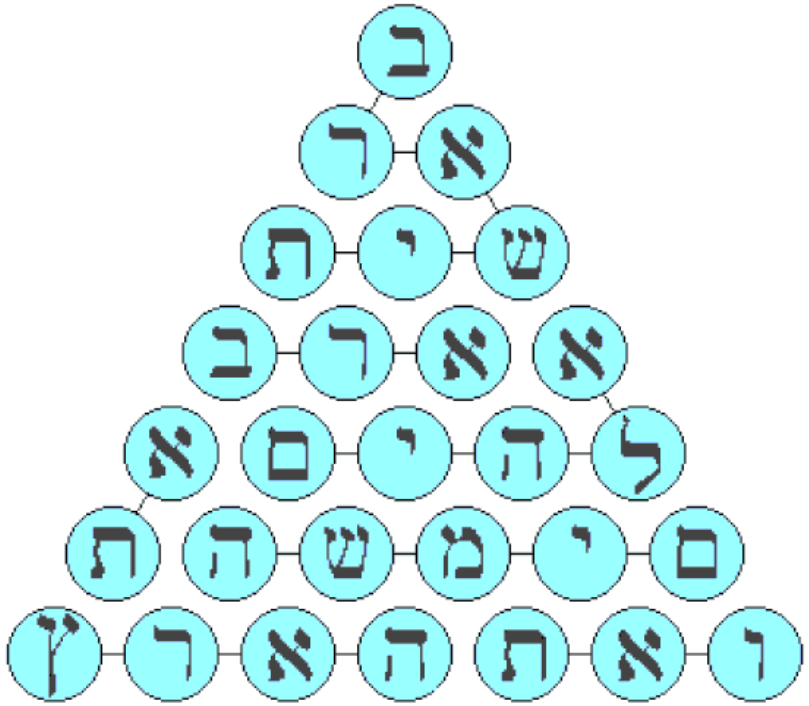
①+③=999, ②+④+⑤=999, ③+⑤+⑥=888, ③+⑤+⑦=777, 111=3*37

Vernon et al (1993)

창세기 1장 1절 = 7개의 단어, 28의 문자, 7th 삼각형 수

a

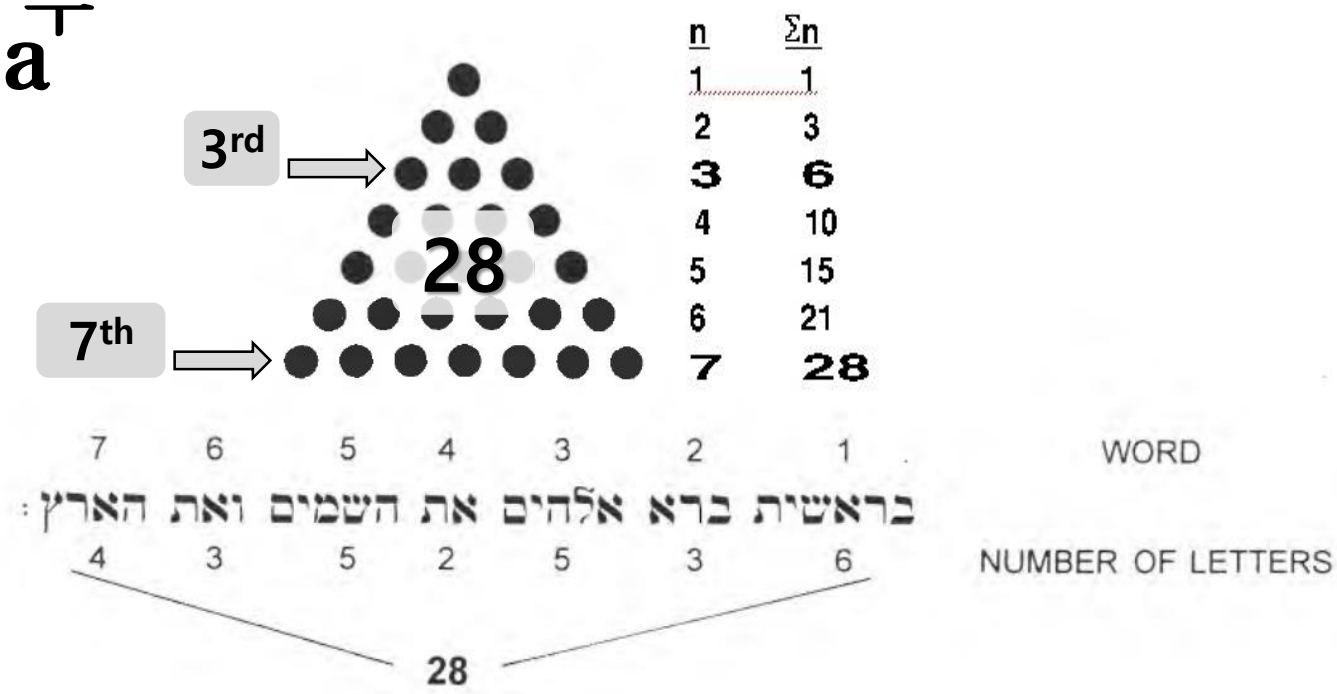




בְּרֵאשִׁית בָּרָא אֱלֹהִים אֵת הַשָּׁמַיִם וְאֵת הָאָרֶץ׃

창세기 1장 1절 = 2701, 73rd 삼각형 수

a



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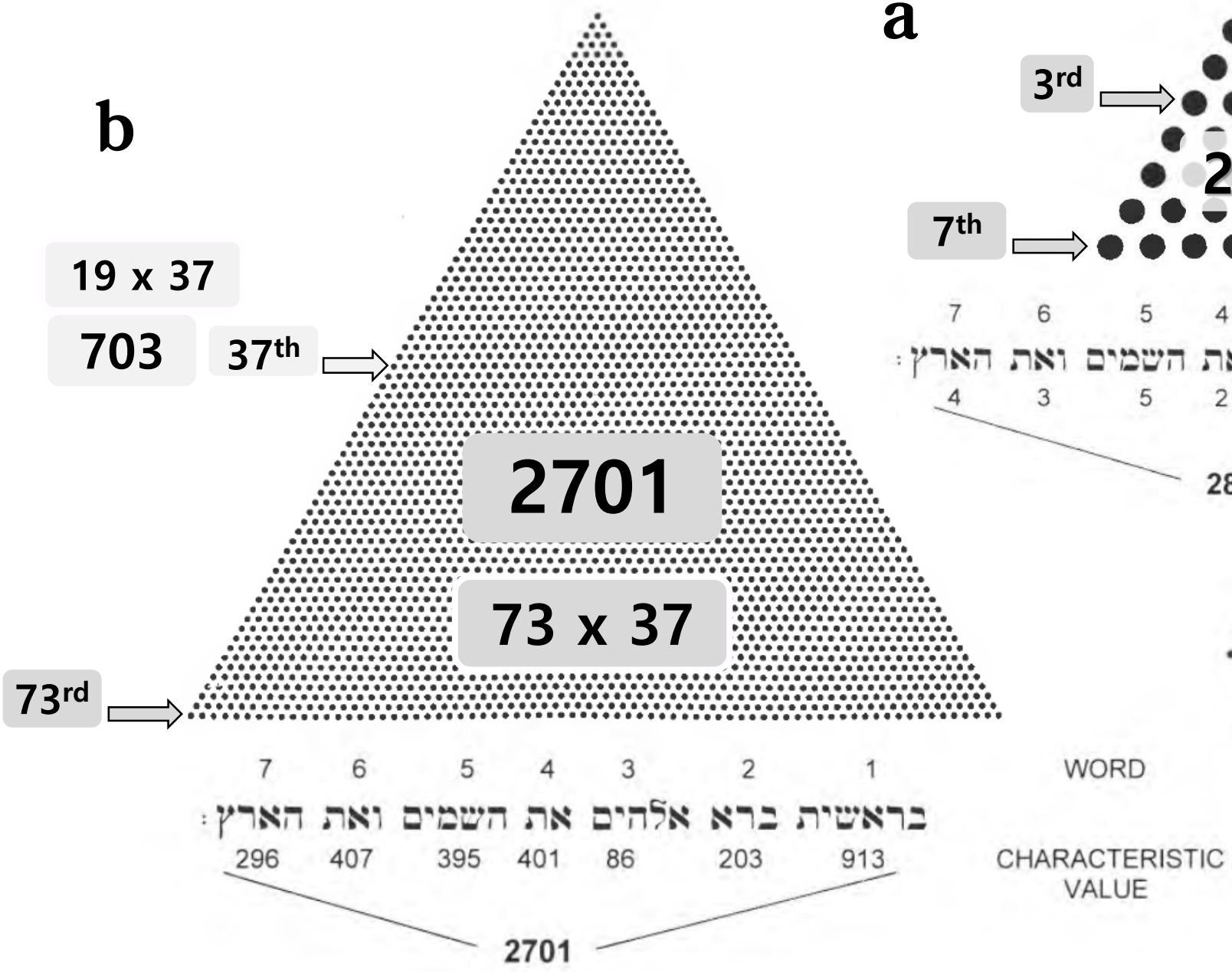

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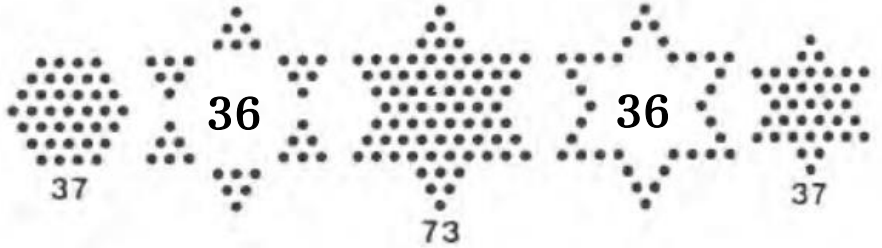
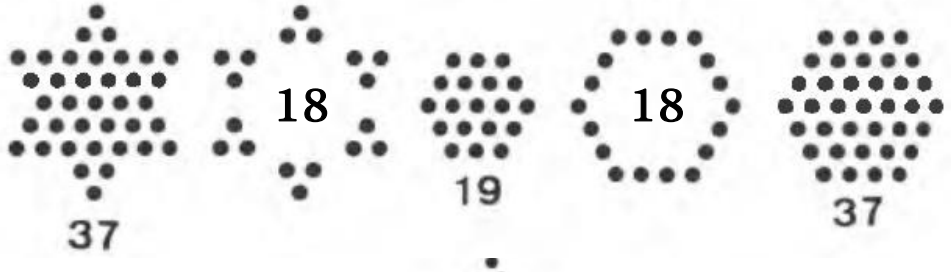


Vernon et al (1993)

a



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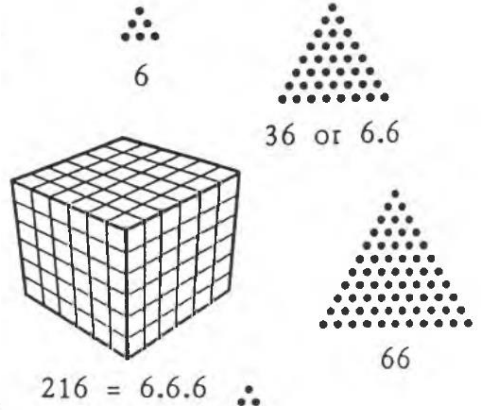
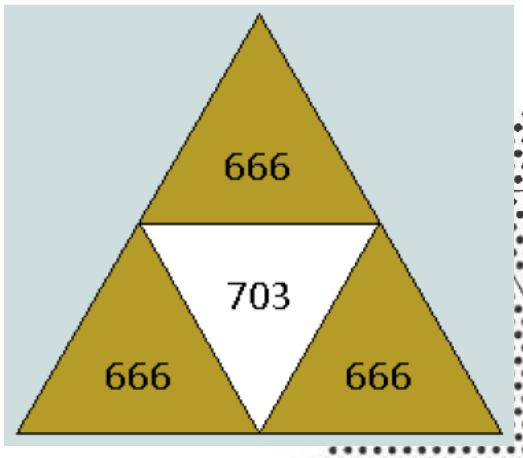
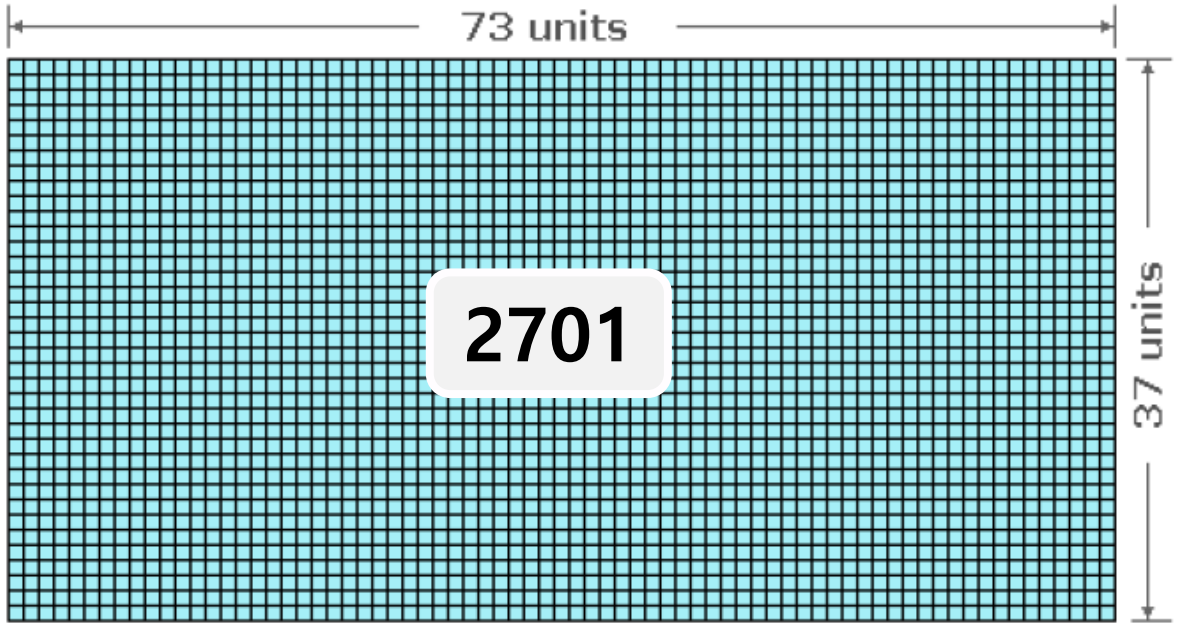


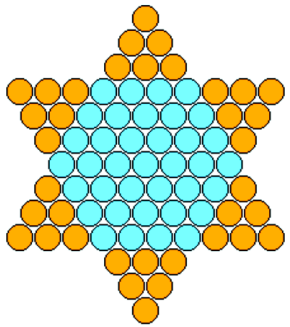


그리고, 땅을 = 703, 37th 삼각형 수

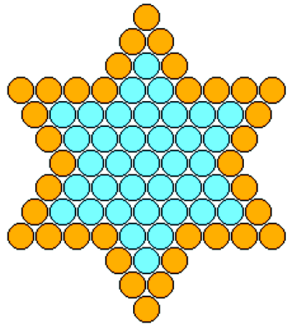
Vernon et al (1993)

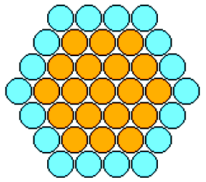
창세기 1장 1절 = 2701, 73*37, 직사각형

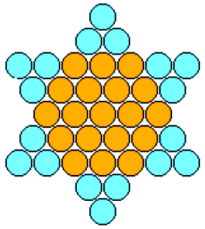



73-as-hexagram with
37-as-hexagon inset

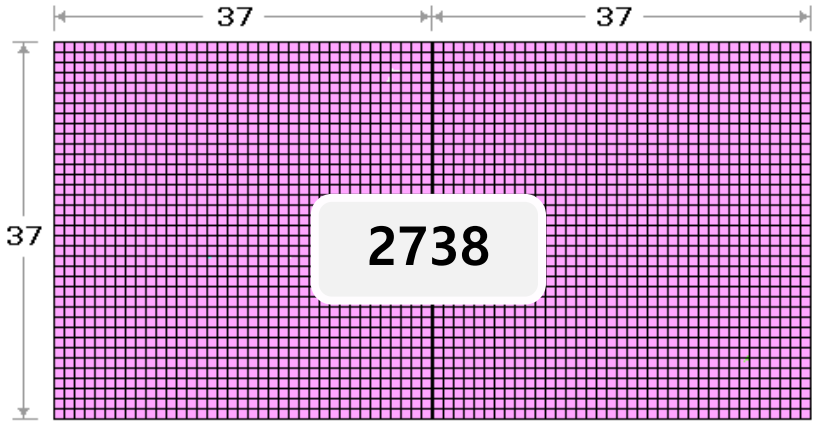

A snow crystal displays the same underlying design


73-as-hexagram with
37-as-hexagon inset


37-as-hexagon with
19-as-hexagon inset

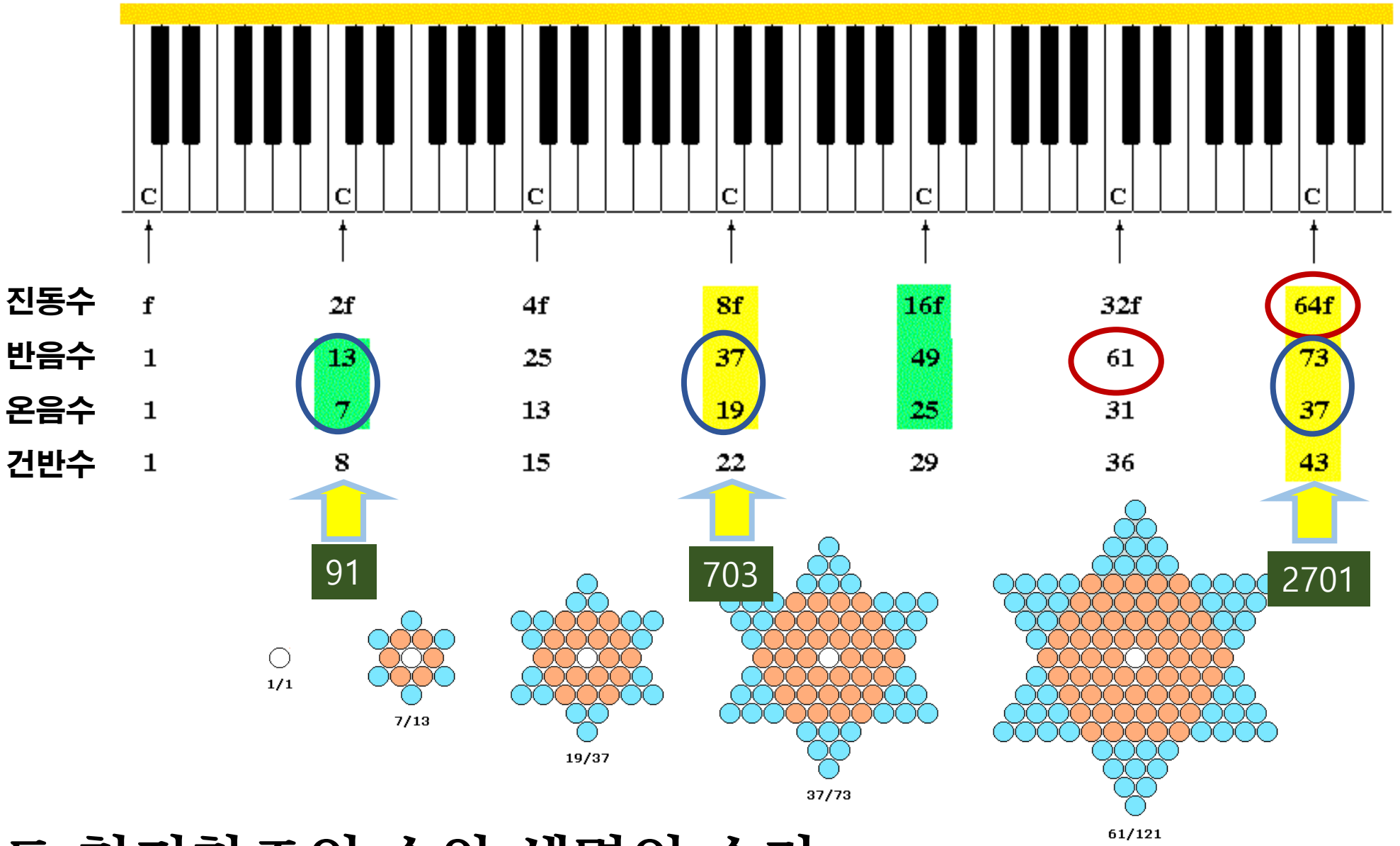

37-as-hexagram with
19-as-hexagon inset

2738 = 2701 + 37



모든 아미노산의 질량수의 합

Vernon et al (1993)



음악에도 천지창조의 수와 생명의 수가…

Vernon et al (1993)

Ἰησοῦς Χριστός

Word

λογος **(Logos)**

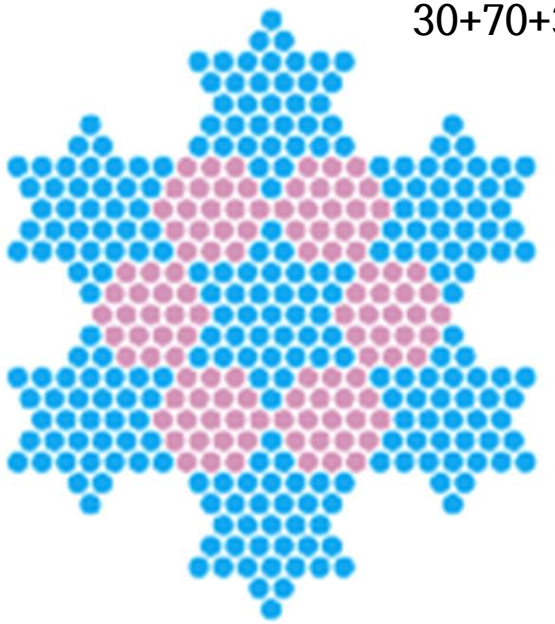
30+70+3+70+200

200 70 3 70 30

λογος

Word,

373



373 = 7 x 37 + 6 x 19

259 114

19 as Hexagon | 37 as Star | 37 as star with 19 as Hexagon

Ἰησοῦς

(10) (8) (200) (70) (400) (200)

Ιησους

888

= 24 x 37

= 3 x 296

Χριστός

(600) (100) (10) (200) (300) (70) (200)

Χριστος

1480

= 40 x 37

= 5 x 296

37

5 13 11 8

חכמה

5 40 20 8

73

2368

= 64 x 37

= 8 x 296

⑦

200 90 1 5

הארץ

4

. earth the

: (하아레츠-땅을)

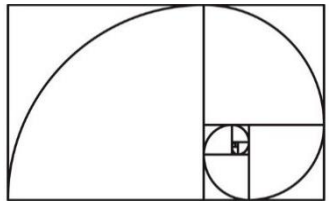
296

예수께서 대답하시되 진실로 진실로 네게 이르노니 사람이 물과 **성령**으로 나지 아니하면 하나님의 나라에 들어갈 수 없느니라(요3:5)

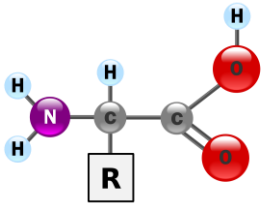
Vernon et al (1993)

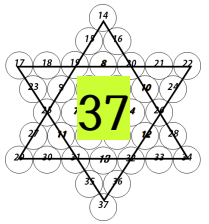
결론 Conclusion

생명체가 나타내는 아름다움(조화)에는 질서가 있으며 황금비율과 같은 수학적 질서가 존재한다.



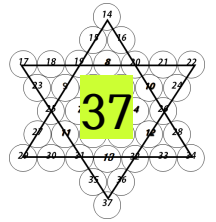
생명체 관련 수들 중에 유전자와 아미노산 속의 규칙 가운데 나타나는 37이 생명의 수에 가장 가깝다.





신성한 서문과 음악 속에 숨겨진 수학적 질서들 속에도 생명의 수(數) 37이 존재하는 것을 보아 생명수 되시는 창조주는 지혜이자 진리이시다.

בְּרֵאשִׁית בָּרָא אֱלֹהִים אֵת הַשָּׁמַיִם וְאֵת הָאָרֶץ׃



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(https://c2c809b8-35c8-4f15-887e-f137df902d3e.usrfiles.com/ugd/c2c809_396bdebd880249dd9b764dcf6e911e11.pdf)

shCherbak, V. (2008). The arithmetical origin of the genetic code. In The codes of life: the rules of macroevolution (pp. 153-185). Dordrecht: Springer Netherlands.

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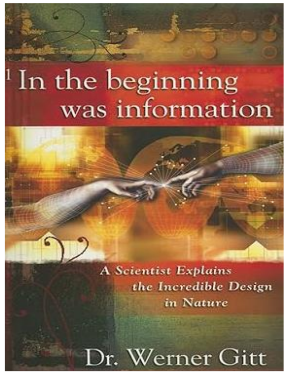
Vernon, J. (1993). The Ultimate Assertion : Evidence of Supernatural Design in the Divine Prologue, CEN Technical Journal.,vol.7(2), pp.184-196. (https://dl0.creation.com/articles/p028/c02814/j07_2_184-196.pdf)



인터넷 사이트

성경 원어와 영어번역본 비교 사이트: https://www.blueletterbible.org/kjv/gen/1/1/ss0/rl0/t_conc_1001

성경 말씀의 숫자 값 계산 사이트: https://777codes.com/index.php/gematria-calculator/

나눔을 위한 질문 Questions for Sharing

1. 아름다움의 기준이 황금비와 관련이 있다는데 내적인(영적인) 아름다움의 기준은 무엇인가요?

2. 왜 수학적 질서와 규칙(37의 배수)이 유전자 암호와 아미노산의 질량수에 반복해서 나타날까요?

3. 생명의 수(천지창조의 수.창조자 예수)가 나타나는 다른 곳이 또 있을까요?

4. 7일 창조(안식일 포함)를 기하학으로 표현할 수 있을까요?