



Linux与生物信息数据处理

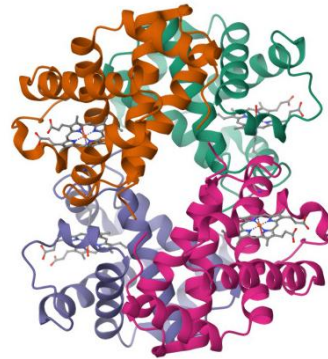
解增言

生命健康信息科学与工程学院





斑头雁 (*Anser indicus*)



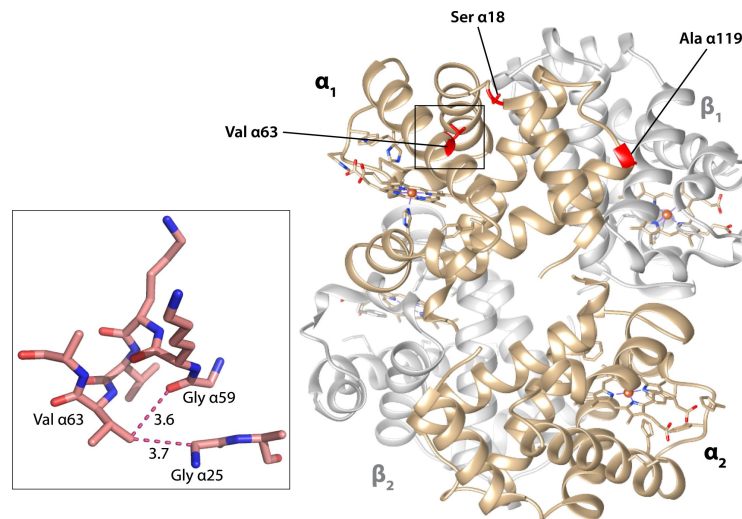
灰雁 (*Anser anser*)

>ACT80359.1 hemoglobin alpha A subunit [Anser indicus]

MVLSAADKTNVKGVF^{SKIS}GHAEYGAETLERMFTAYPQTKTYFP^{PHDL}QH^{GS}AIKAHGKKV^VAALVEA
VNHIDDIAGALSKLSDLHAQKL^RVD^PVNF^KFLGHCFLV^VVVAIH^HPSAL^TAEVHASL^DKFLCAVGT^VLTA^K
YR

>ACT80855.1 hemoglobin alpha A subunit [Anser anser]

MVLSAADKTNVKGVF^{SKI}G^HAEYGAETLERMFTAYPQTKTYFP^{PHDL}QH^{GS}AIKAHGKKV^AAALVEA
VNHIDDIAGALSKLSDLHAQKL^RVD^PVNF^KFLGHCFLV^VVVAIH^HPSAL^TPEVHASL^DKFLCAVGT^VLTA^K
YR



教材与参考书



教材:

解增言,
Linux与生物信息学数据处理.
自编讲义

参考书1:

鸟哥,
**鸟哥的Linux私房菜
基础学习篇 (第四版) .**
人民邮电出版社, 2018

参考书2:

刘遑,
Linux就该这么学 (第2版) .
人民邮电出版社, 2021





- 请到雨课堂课件查看

考核方式



○ 平时成绩（100分×60%）：

雨课堂（课前预习、课堂练习）：20分

课堂作业：20分（每次2分，共10次）

课后作业：20分（每次2分，共10次）

随堂测试：20分（每次5分，共4次）

课程网站学习情况：10分

学银慕课学习情况：10分

缺课：每次-2分

附加任务：教材找错（每处错误确认后+1分，第一个找到的同学有效，最高至平时成绩满分）

○ 期末考试（100分×40%）：

单选、多选、填空、简答（题目来自课程网站www.linuxstudio.cn题库）



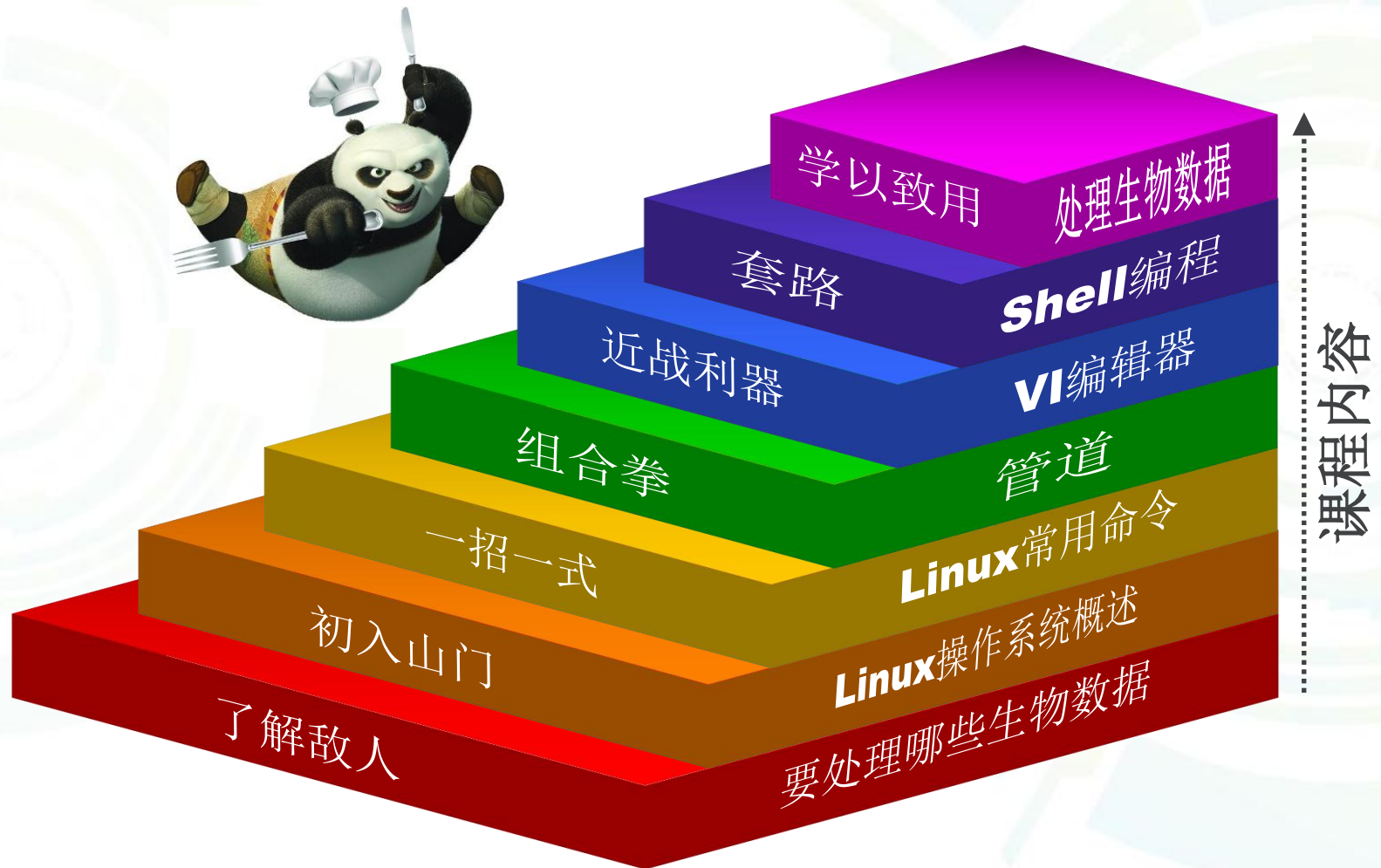
课程简介



- Linux与生物信息数据处理课程主要内容是学习利用Linux命令、管道及Shell编程，处理生物学数据（主要是分子生物学数据）。



课程内容



课时安排



8学时

应用实例

10学时

Shell编程基础

6学时

VI编辑器

16学时

Linux常用命令

2学时

Linux文件系统

2学时

Linux系统概述

2学时

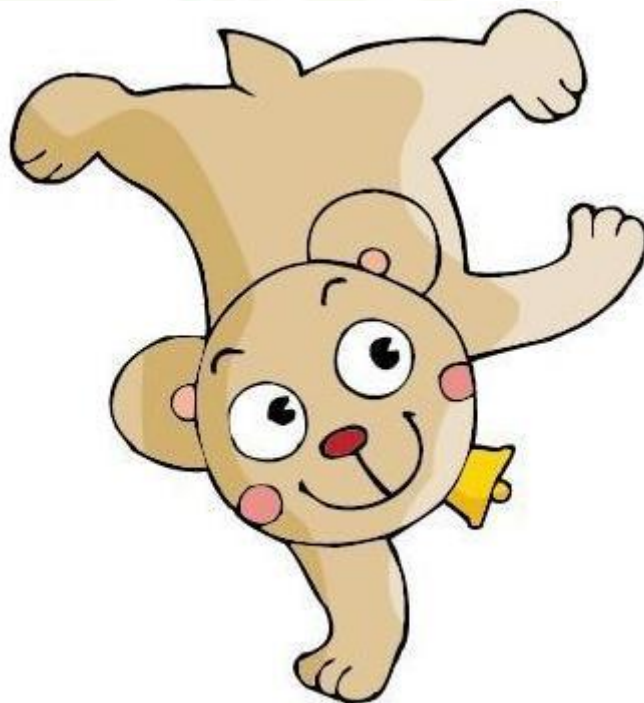
课程简介、生物中的信息（数据）

上课形式



○ 翻转课堂

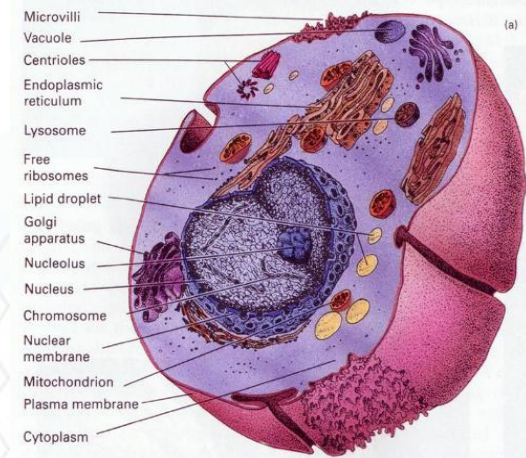
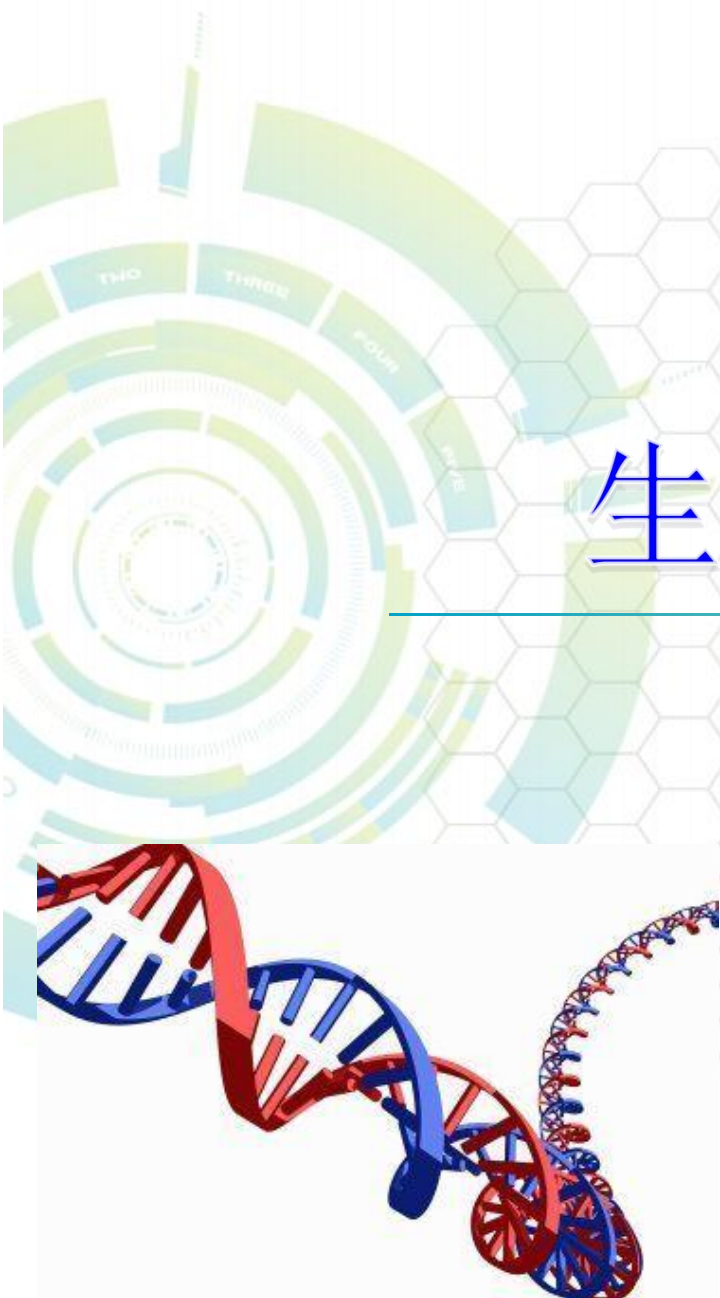
- ✓ 课前：观看教学视频，预习教材文字内容及课件，提前练习命令
- ✓ 课内：练习、作业、测试、解答问题、重点讲解、总结
- ✓ 课后：作业、复习、练习、测试



怎样获得一个好成绩



- 按时**预习**：上课前完成指定的内容，完成雨课堂推送的课件预习；
- 完成**课堂任务**：上课时专心听讲，及时完成课堂练习和课堂作业；
- 按时完成**课后作业**：根据要求，按时完成服务器上的课后作业；
- **学银慕课**：按时完成慕课教学视频学习及测试，积极参加慕课平台的讨论；
- **课程网站**：按时完成课程网站的文字材料学习及练习，多做自主测试，参加课程阶段测试；按时上课：按时签到，不迟到，不旷课。
- **最重要的一点：多练习、理解Linux命令，并用来解决实际问题。**

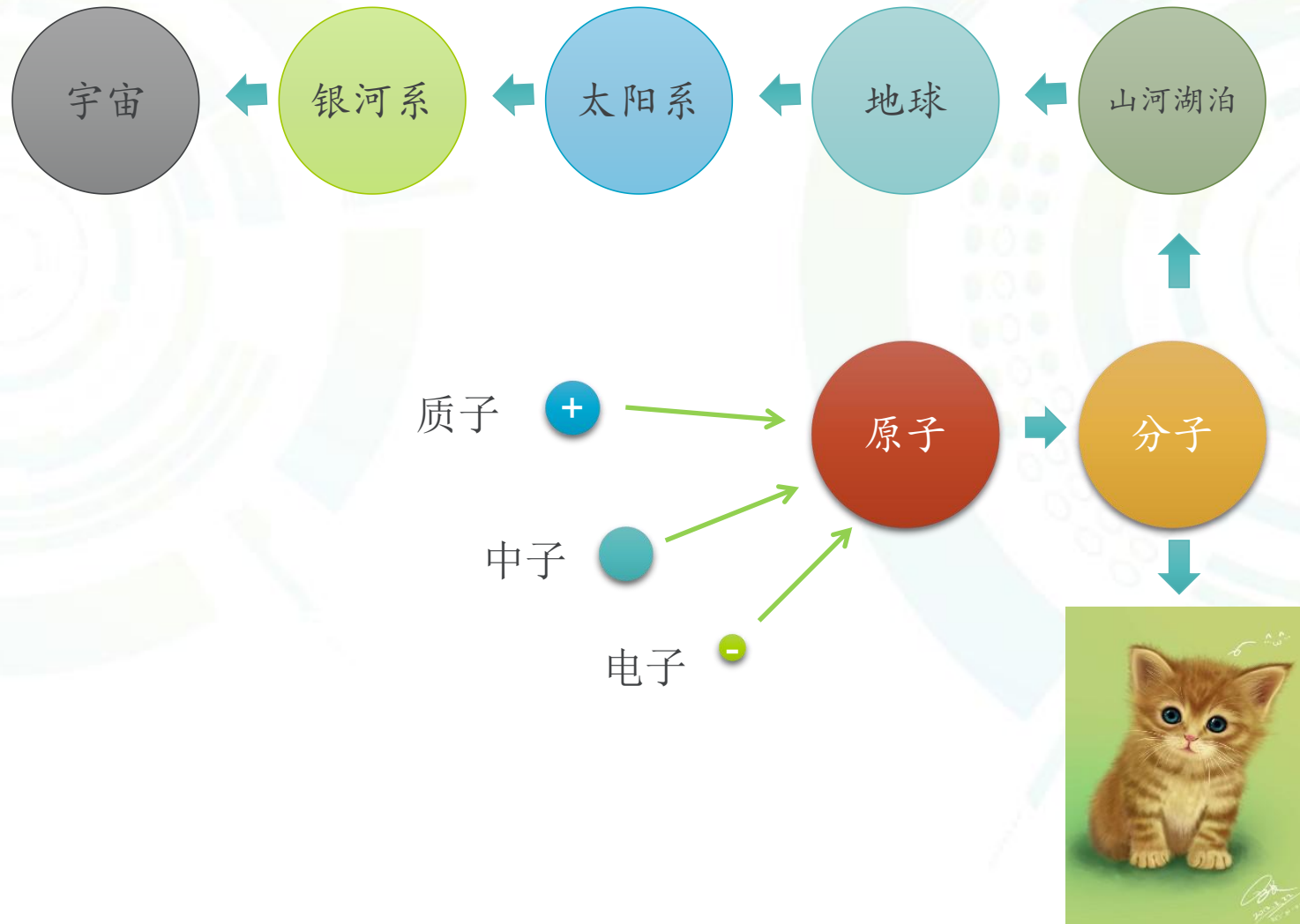


生物学中的数据

解增言

生命健康信息科学与工程学院

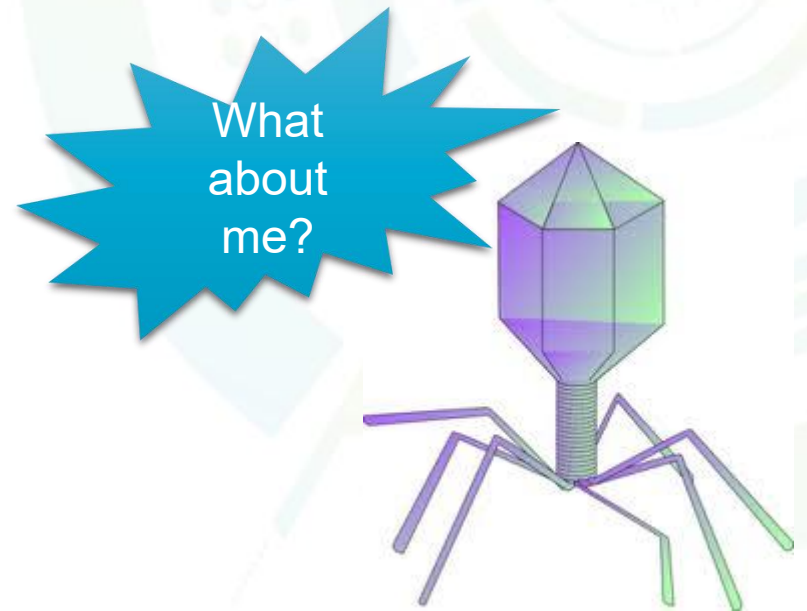
从宇宙到生物



生物的特征（与非生物的区别）



- 细胞是结构和功能的基本单位
- 新陈代谢
- 生长与发育
- 应激性
- 繁殖
- 遗传和变异
- 适应与进化
- 与外界进行物质交换
- 呼吸



生物类群



- 原核生物

真细菌

古细菌

- 真核生物

原生生物

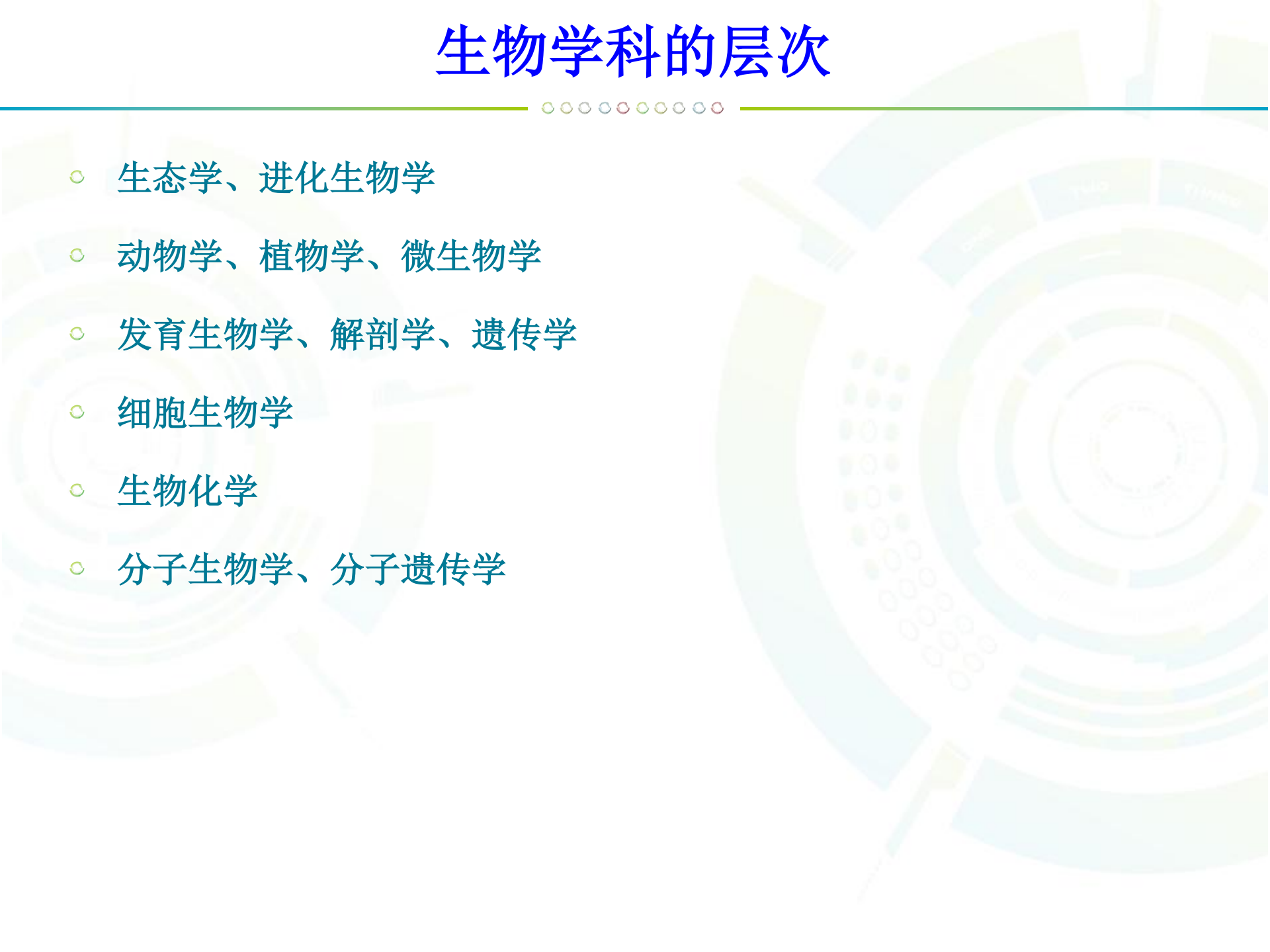
真菌

动物

植物



生物学科层次



- 生态学、进化生物学
- 动物学、植物学、微生物学
- 发育生物学、解剖学、遗传学
- 细胞生物学
- 生物化学
- 分子生物学、分子遗传学

生物学数据的类型



- 生态学和生物多样性数据
- 分子生物学数据
- 生理生化数据
-

生物大分子



- 核酸

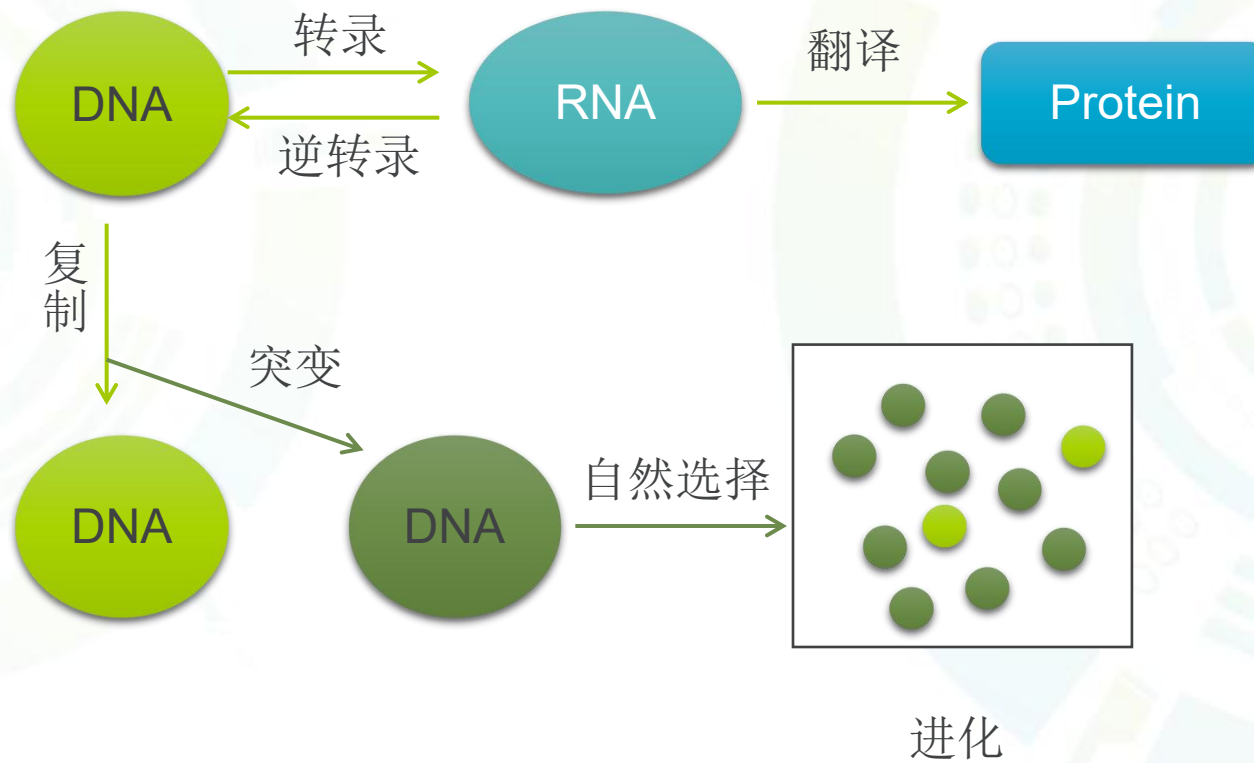
DNA（脱氧核糖核酸）

RNA（核糖核酸）

- 蛋白质

- 多糖

生物信息传递



分子生物学数据的类型



- 核酸一二三级结构
- 蛋白质一二三四级结构
- 基因表达数据
- 基因组数据
- 基因/蛋白质相互作用数据
- 基因/蛋白质修饰（甲基化等）数据

组成生物大分子的单位：生物单分子



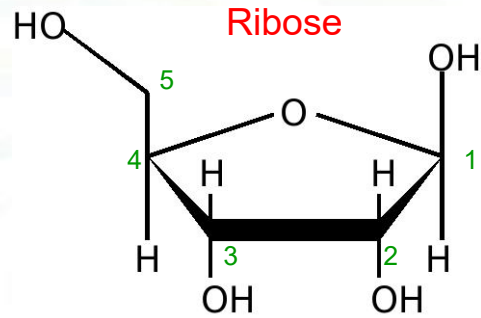
- 主要生物单分子：

核糖核苷酸

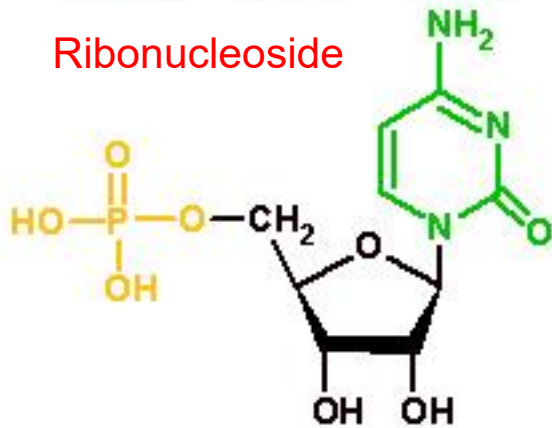
脱氧核糖核苷酸

氨基酸

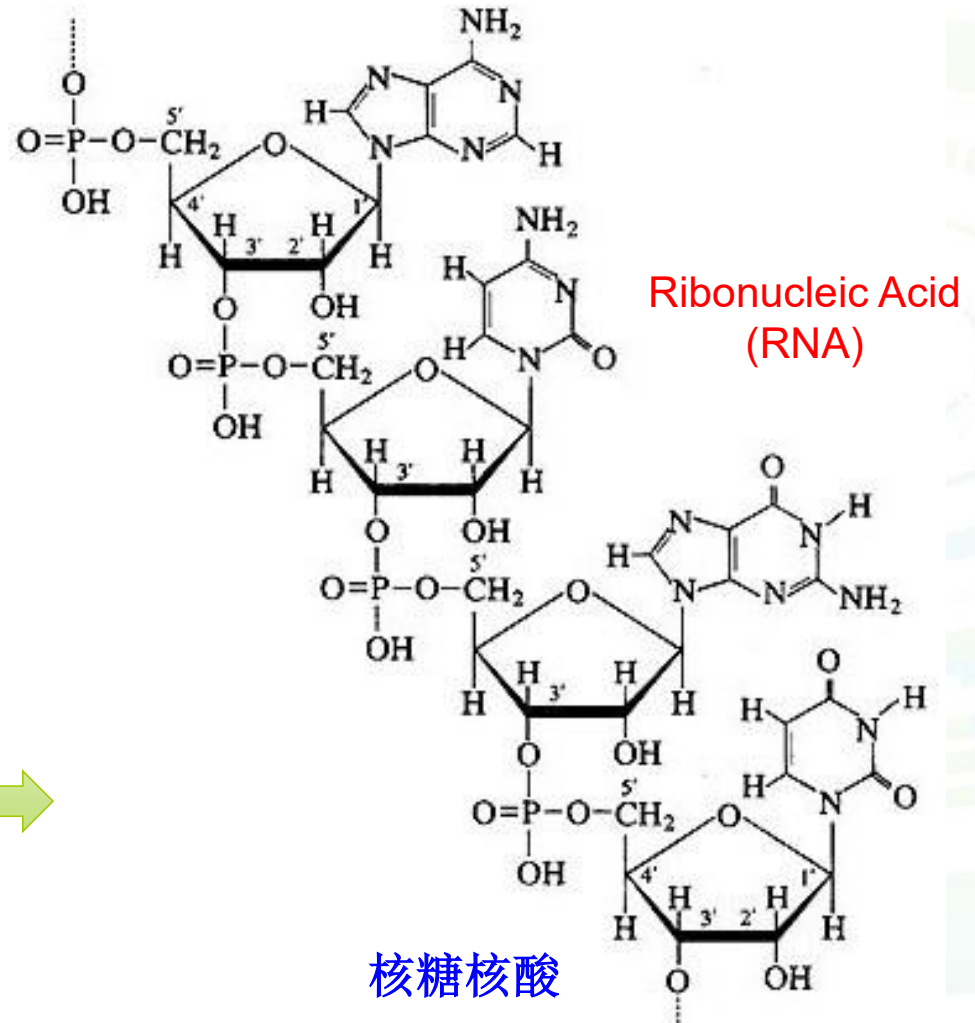
RNA构成



核糖

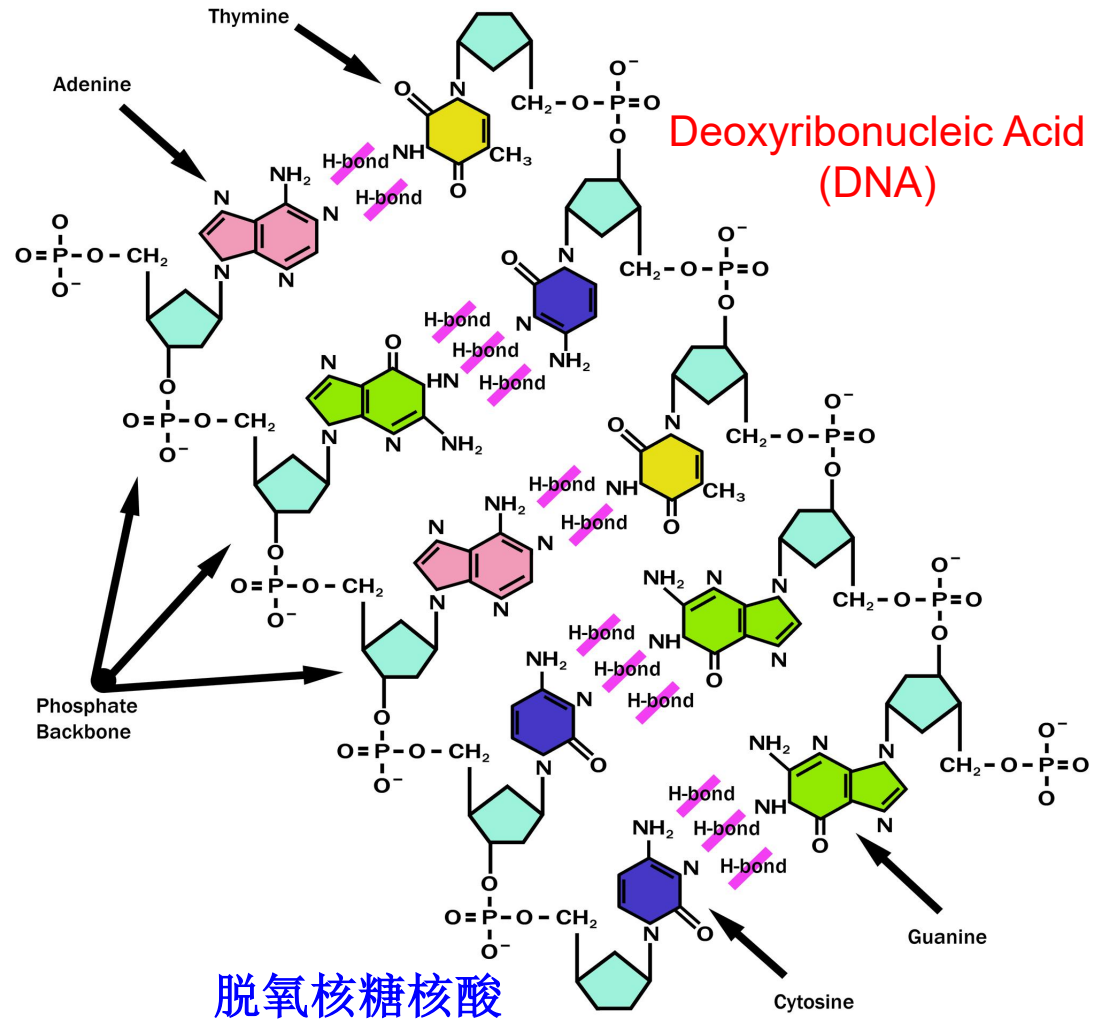
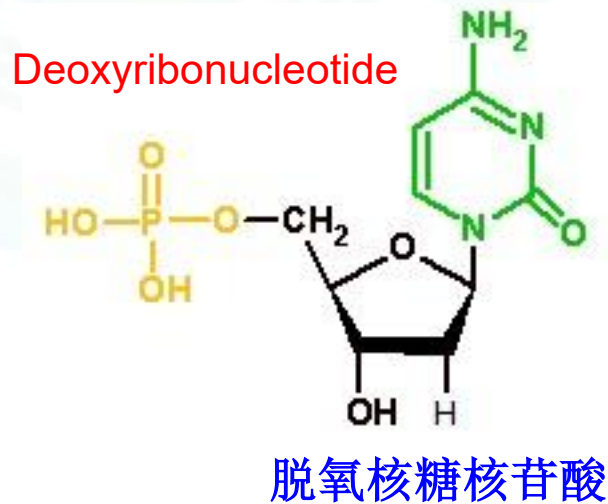
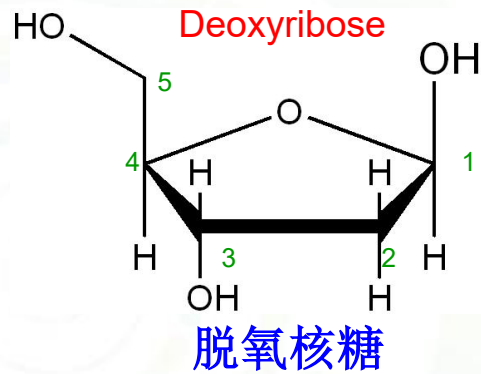


核糖核苷酸



核糖核酸

DNA构成



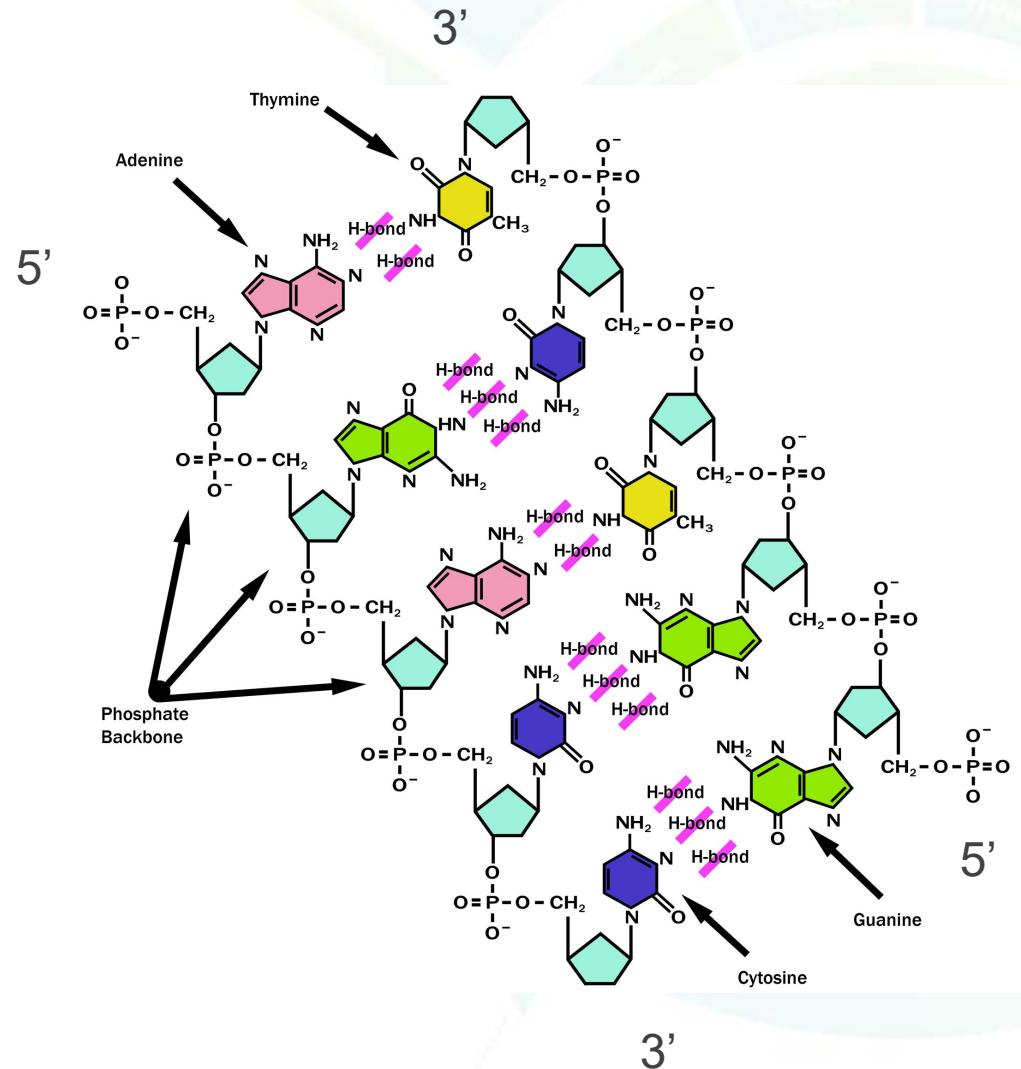
DNA简写



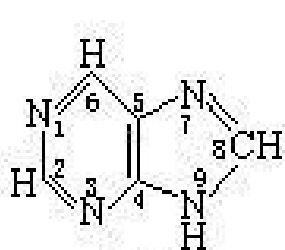
5' AGACC 3'

3' TCTGG 5'

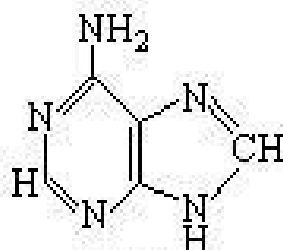
5' ATGGCCAGGTAA 3'



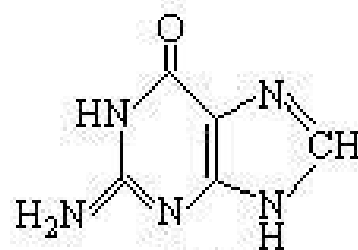
常见碱基



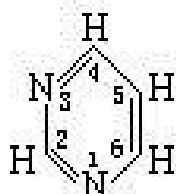
嘌呤



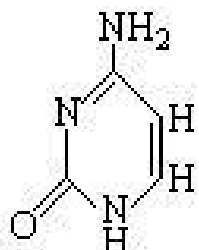
腺嘌呤 **A**



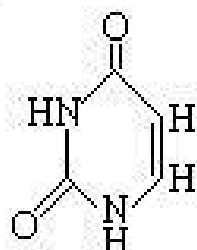
鸟嘌呤 **G**



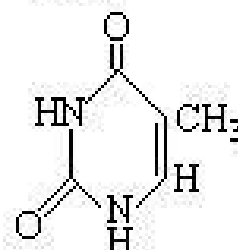
嘧啶



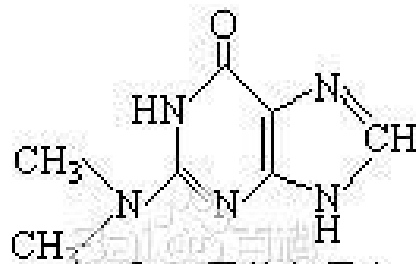
胞嘧啶 **C**



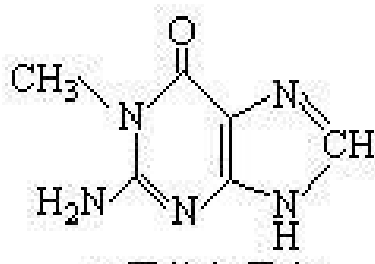
尿嘧啶 **U**



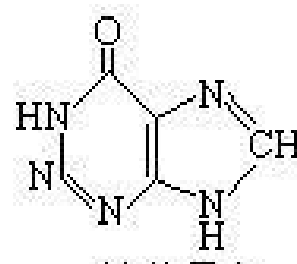
胸腺嘧啶 **T**



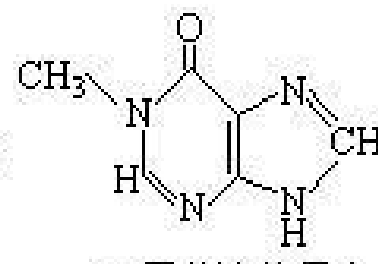
N²-二甲基鸟嘌呤



1-甲基鸟嘌呤



次黄嘌呤



1-甲基次黄嘌呤

关于DNA和RNA，下面说法正确的是：

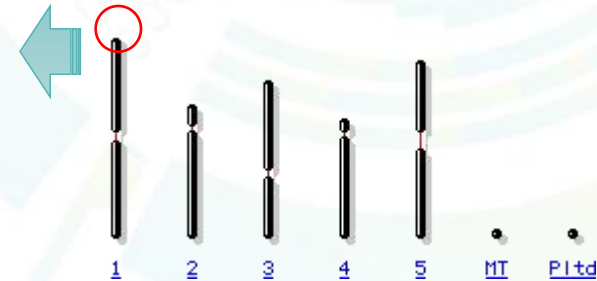
- ☐ A 尿嘧啶只存在于DNA中
- ☒ B RNA中没有胸腺嘧啶
- ☐ C 组成RNA的碱基只有4种
- ☐ D RNA比DNA稳定

提交

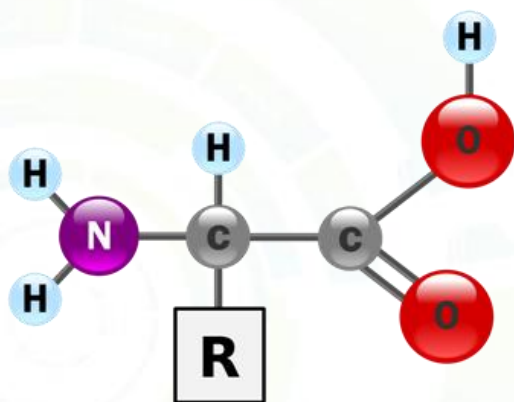
拟南芥第一条染色体部分序列

- >Chr1 CHROMOSOME dumped from ADB: Feb/3/09 16:9;
last updated: 2007-12-20

```
CCCTAAACCCTAAACCCTAAACCCTAAACCTCTGAATCCTTAATCCC  
TAAATCCCTAAATCTTTAAATCCTACATCCATGAATCCCTAAATACC  
TAATTCCCTAAACCCGAAACCGGTTTCTCTGGTTGAAAATCATTGTG  
TATATAATGATAATTTTATCGTTTTTATGTAATTGCTTATTGTTGTG  
TG TAGATTTTTTAAAAATATCATTTGAGGTCAATACAAATCCTATTT  
CTTGTGGTTTTTCTTTCCTTCACTTAGCTATGGATGGTTTATCTTCAT  
TTGTTATATTGGATACAAGCTTTGCTACGATCTACATTTGGGAA
```

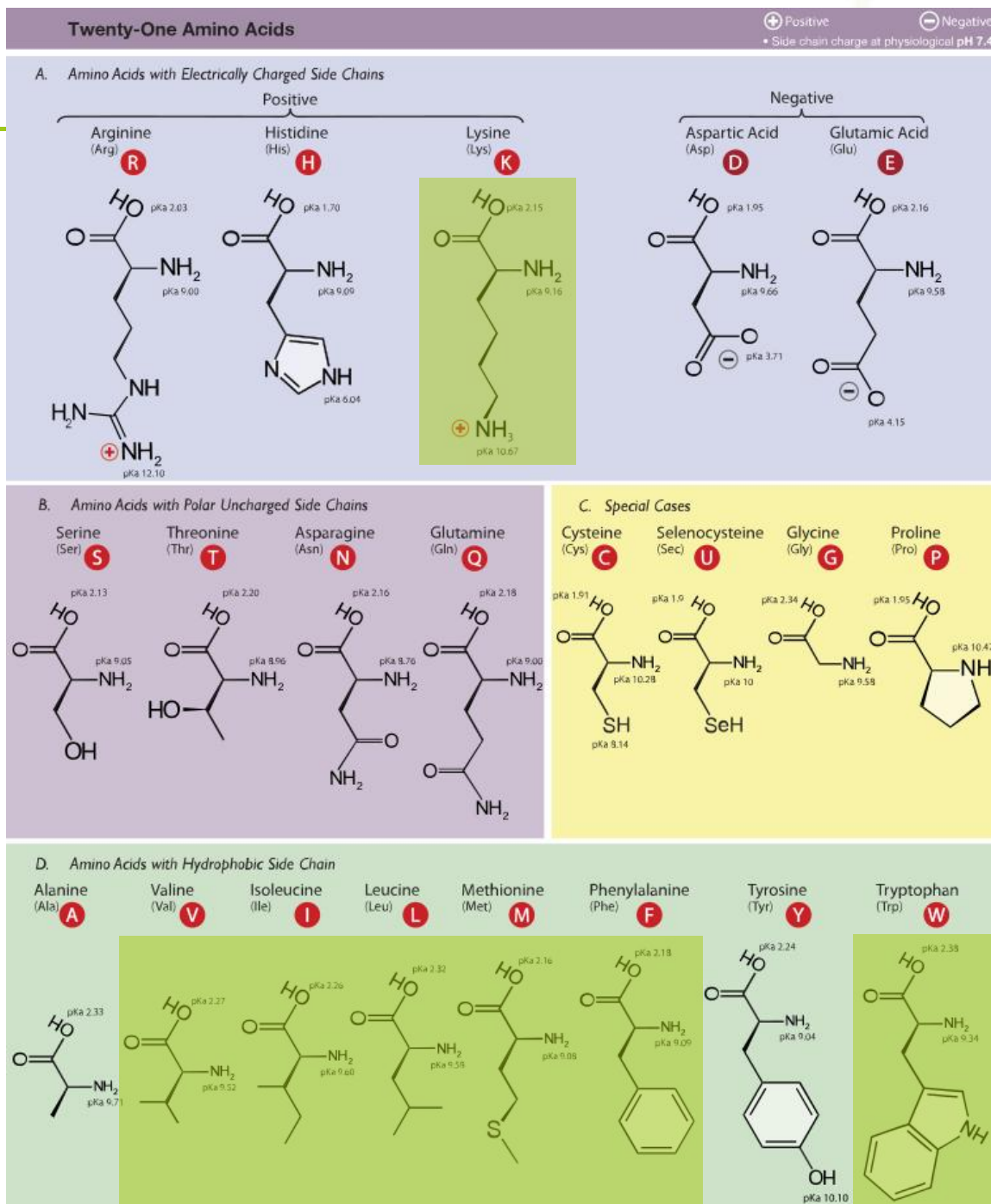


蛋白质构成



氨基酸结构

21种氨基酸



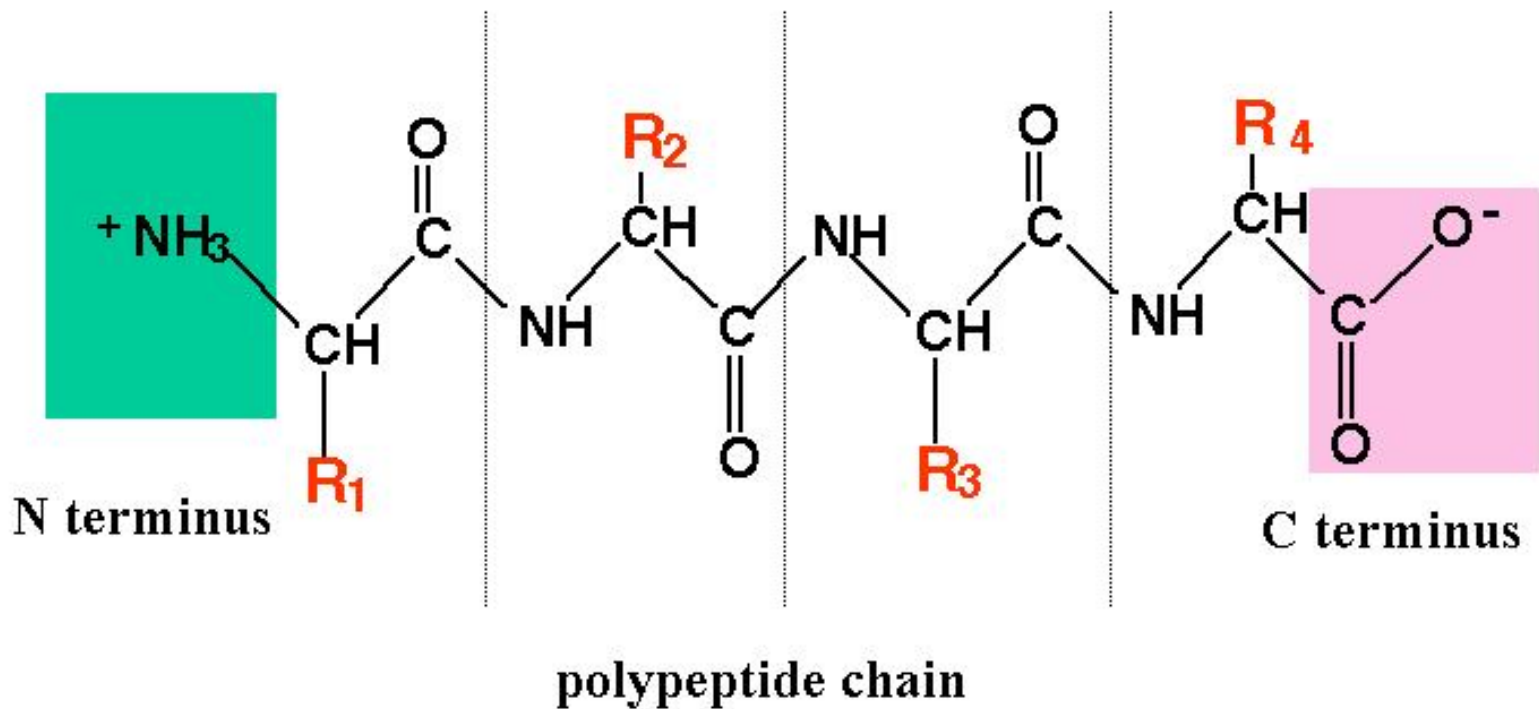
NONPOLAR, HYDROPHOBIC
POLAR, UNCHARGED
R GROUPS

Alanine Ala A MW = 89	$\begin{array}{c} ^- \text{OOC} \\ \\ \text{H}_3\text{N}^+ - \text{CH} - \text{CH}_3 \end{array}$		$\begin{array}{c} \text{H} - \text{CH} - \text{COO}^- \\ \\ \text{N}^+ \text{H}_3 \end{array}$	Glycine Gly G MW = 75
Valine Val V MW = 117	$\begin{array}{c} ^- \text{OOC} \\ \\ \text{H}_3\text{N}^+ - \text{CH} - \text{CH}(\text{CH}_3)_2 \end{array}$		$\begin{array}{c} \text{HO} - \text{CH}_2 - \text{CH} - \text{COO}^- \\ \\ \text{N}^+ \text{H}_3 \end{array}$	Serine Ser S MW = 105
Leucine Leu L MW = 131	$\begin{array}{c} ^- \text{OOC} \\ \\ \text{H}_3\text{N}^+ - \text{CH} - \text{CH}_2 - \text{CH}(\text{CH}_3)_2 \end{array}$		$\begin{array}{c} \text{OH} \\ \\ \text{CH}_3 - \text{CH} - \text{CH} - \text{COO}^- \\ \\ \text{N}^+ \text{H}_3 \end{array}$	Threonine Thr T MW = 119
Isoleucine Ile I MW = 131	$\begin{array}{c} ^- \text{OOC} \\ \\ \text{H}_3\text{N}^+ - \text{CH} - \text{CH}(\text{CH}_3) - \text{CH}_2 - \text{CH}_3 \end{array}$		$\begin{array}{c} \text{HS} - \text{CH}_2 - \text{CH} - \text{COO}^- \\ \\ \text{N}^+ \text{H}_3 \end{array}$	Cysteine Cys C MW = 121
Phenylalanine Phe F MW = 131	$\begin{array}{c} ^- \text{OOC} \\ \\ \text{H}_3\text{N}^+ - \text{CH} - \text{CH}_2 - \text{C}_6\text{H}_5 \end{array}$		$\begin{array}{c} \text{HO} - \text{C}_6\text{H}_4 - \text{CH}_2 - \text{CH} - \text{COO}^- \\ \\ \text{N}^+ \text{H}_3 \end{array}$	Tyrosine Tyr Y MW = 181
Tryptophan Trp W MW = 204	$\begin{array}{c} ^- \text{OOC} \\ \\ \text{H}_3\text{N}^+ - \text{CH} - \text{CH}_2 - \text{C}_8\text{H}_6\text{N}_2 \end{array}$		$\begin{array}{c} \text{NH}_2 \\ \\ \text{O}=\text{C} - \text{CH}_2 - \text{CH} - \text{COO}^- \\ \\ \text{N}^+ \text{H}_3 \end{array}$	Asparagine Asn N MW = 132
Methionine Met M MW = 149	$\begin{array}{c} ^- \text{OOC} \\ \\ \text{H}_3\text{N}^+ - \text{CH} - \text{CH}_2 - \text{CH}_2 - \text{S} - \text{CH}_3 \end{array}$		$\begin{array}{c} \text{NH}_2 \\ \\ \text{O}=\text{C} - \text{CH}_2 - \text{CH}_2 - \text{CH} - \text{COO}^- \\ \\ \text{N}^+ \text{H}_3 \end{array}$	Glutamine Gln Q MW = 146
Proline Pro P MW = 115	$\begin{array}{c} ^- \text{OOC} \\ \\ \text{CH} - \text{CH}_2 - \text{CH}_2 - \text{CH}_2 \\ \\ \text{HN} \end{array}$		POLAR BASIC $\begin{array}{c} ^+ \text{NH}_3 - \text{CH}_2 - (\text{CH}_2)_3 - \text{CH} - \text{COO}^- \\ \\ \text{N}^+ \text{H}_3 \end{array}$	Lysine Lys K MW = 146
Aspartic acid Asp D MW = 133	$\begin{array}{c} ^- \text{OOC} \\ \\ \text{H}_3\text{N}^+ - \text{CH} - \text{CH}_2 - \text{C}(=\text{O})\text{O}^- \end{array}$		$\begin{array}{c} \text{NH}_2 \\ \\ \text{N}^+ \text{H}_2 = \text{C} - \text{NH} - (\text{CH}_2)_3 - \text{CH} - \text{COO}^- \\ \\ \text{N}^+ \text{H}_3 \end{array}$	Arginine Arg R MW = 174
Glutamic acid Glu E MW = 147	$\begin{array}{c} ^- \text{OOC} \\ \\ \text{H}_3\text{N}^+ - \text{CH} - \text{CH}_2 - \text{CH}_2 - \text{C}(=\text{O})\text{O}^- \end{array}$		$\begin{array}{c} \text{HN} = \text{C} - \text{CH}_2 - \text{CH} - \text{COO}^- \\ \\ \text{N}^+ \end{array}$	Histidine His H MW = 155

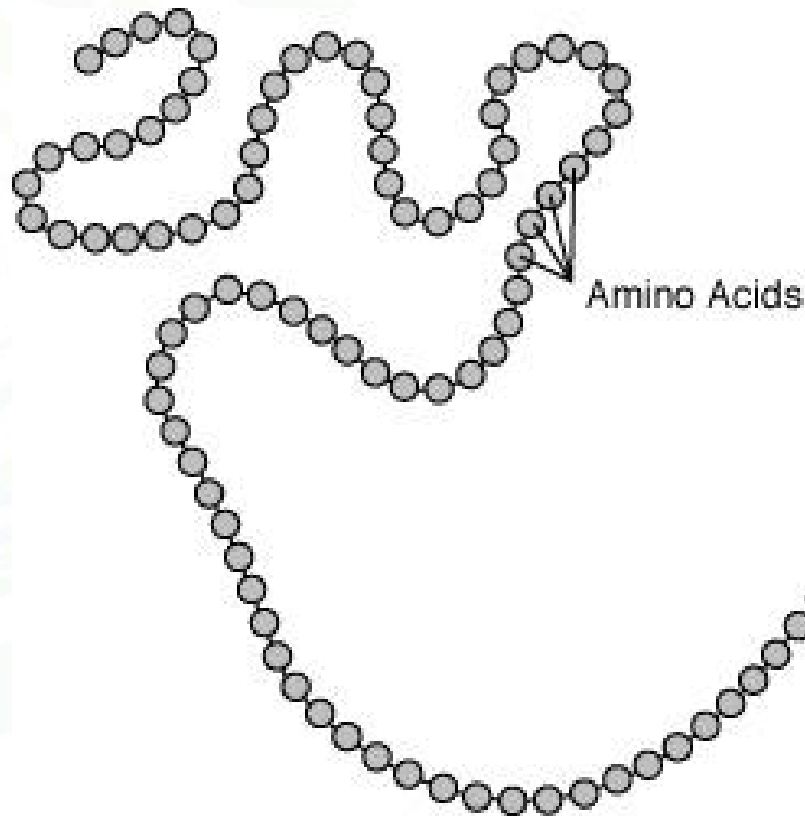
多肽结构



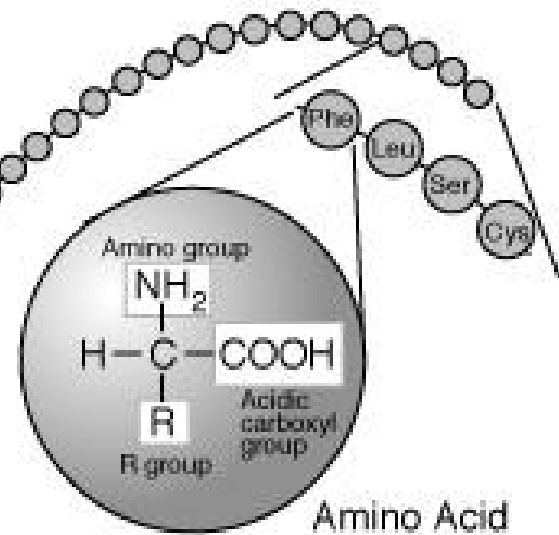
Peptide = chain of amino acids



蛋白质一级结构



Primary protein structure
is sequence of a chain of amino acids





Asp	D	Aspartic acid	Ile	I	Isoleucine
Thr	T	Threonine	Leu	L	Leucine
Ser	S	Serine	Tyr	Y	Tyrosine
Glu	E	Glutamic acid	Phe	F	Phenylalanine
Pro	P	Proline	His	H	Histidine
Gly	G	Glycine	Lys	K	Lysine
Ala	A	Alanine	Arg	R	Arginine
Cys	C	Cysteine	Trp	W	Tryptophan
Val	V	Valine	Gln	Q	Glutamine
Met	M	Methionine	ASN	N	Asparagine

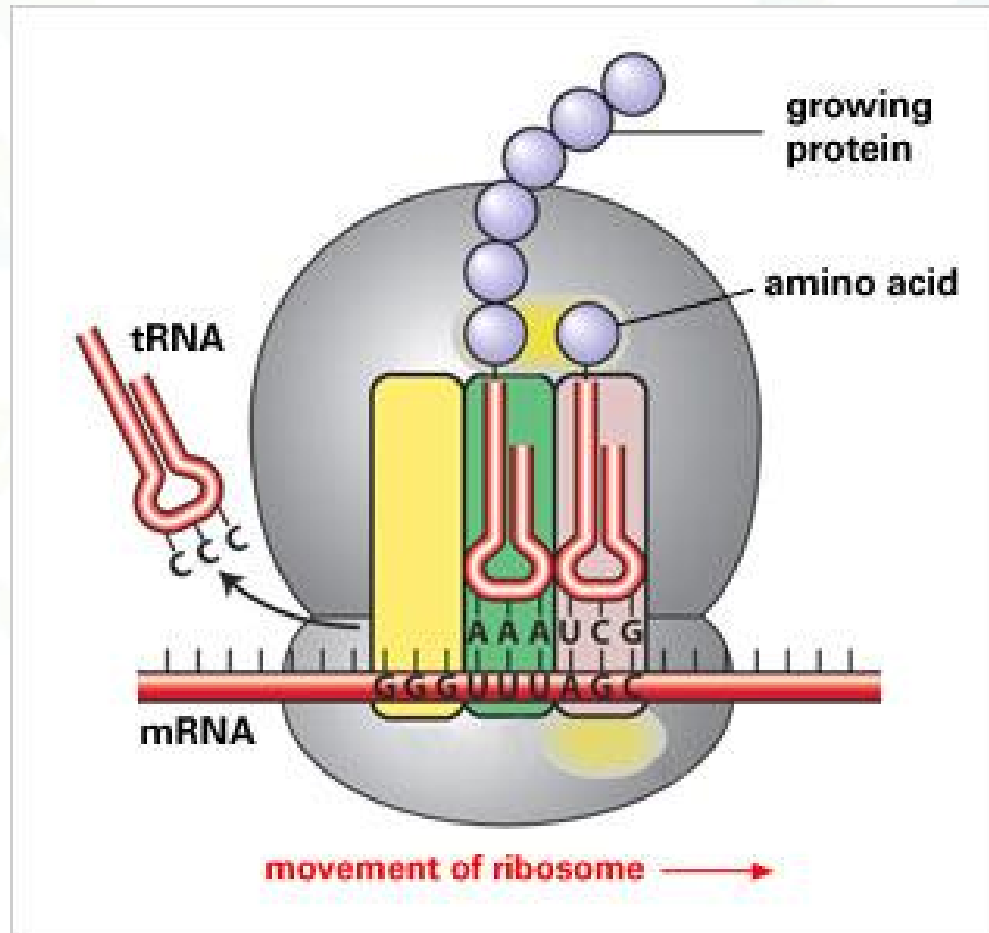
氨基酸编码

●●●●●●●●●●

Seconed Position											
U		C		A		G					
code	Amino Acid	code	Amino Acid	code	Amino Acid	code	Amino Acid	code	Amino Acid		
U	UUU	phe	UCU	ser	UAU	tyr	UGU	cys	U		
	UUC		UCC		UAC		UGC		C		
	UUA		UCA		UAA		STOP		UGA	STOP	A
	UUG		UCG		UAG		STOP		UGG	trp	G
C	CUU	leu	CCU	pro	CAU	his	CGU	arg	U		
	CUC		CCC		CAC		CGC		C		
	CUA		CCA		CAA	gln	CGA		A		
	CUG		CCG		CAG		CGG		G		
A	AUU	ile	ACU	thr	AAU	asn	AGU	ser	U		
	AUC		ACC		AAC		AGC		C		
	AUA		ACA		AAA	lys	AGA	arg	A		
	AUG	met	ACG		AAG		AGG		G		
G	GUU	val	GCU	ala	GAU	asp	GGU	gly	U		
	GUC		GCC		GAC		GGC		C		
	GUA		GCA		GAA	glu	GGA		A		
	GUG		GCG		GAG		GGG		G		

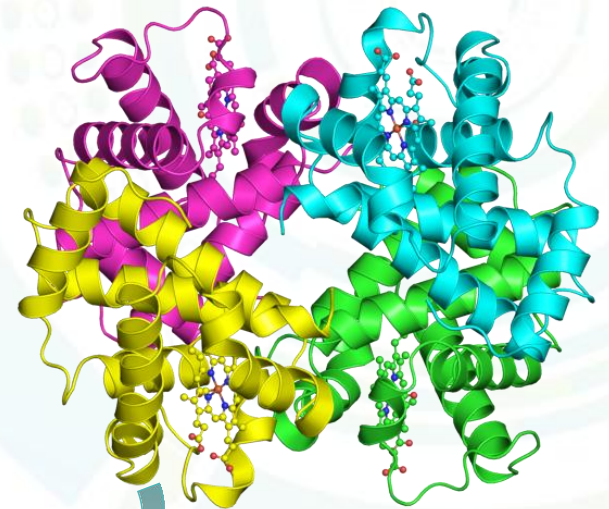
概念：密码子简并性

蛋白质合成

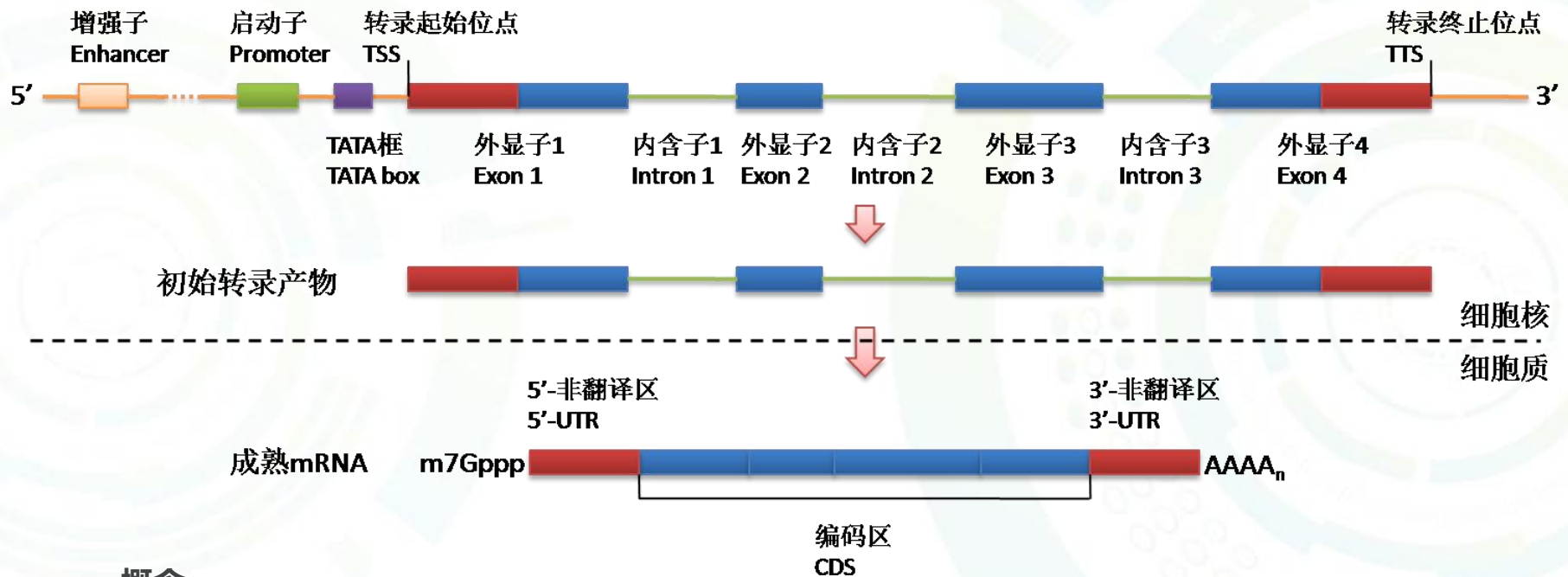


人类血红蛋白 α 亚基序列

- `>gi|4504345|ref|NP_000508.1| hemoglobin
subunit alpha [Homo sapiens]
MVLSPADKTNVKAAWGKVGAGHAGEYGAEALERMFLSFPT
TKTYFPHFDLSHGSAQVKGHGKKVADALTNAVAHVDDMP
NALSALSDLHAHKLRVDPVNFKLLSHCLLVTLAAHLPAE
FTPAVHASLDKFLASVSTVLTSKYR`



基因结构（真核生物）



概念:

TSS (转录起始位点)

TTS (转录终止位点)

CDS (编码区)

UTR (非翻译区)

Exon (外显子)

Intron (内含子)

基因结构示例



- >NC_003076.8:19315061-19315975 Arabidopsis thaliana chromosome 5 sequence
- ATGGAACGTGGAGGCTTCCATGGCTACCGCAAGCTGTCCGTGAACAACACCACTCCTTCTCCACCAG~~gta~~
- ~~gtgccattctctataccccctcttttcacaggctctcttcatttcagttgcatgcgaaaccattctctgc~~
- ~~aatccctccattgtcatgtctgtactcttttcatgacgaacagttaatgaaatagcttttcaatcttata~~
- ~~aaccgcgcatgcagacgtcatcgaagccattatgcactaaaacttccatttttcttatttttgtttag~~GAT
- TAGCAGCGAATTTTCTGATGGCAGAGGGCAGTATGCGTCCTCCAGAATTCAACCAGCCTAACAAAACCAG
- TAATGGTGGTGAGGAGGAGTGCACGGTGAGGGAGCAAGACAGGTTCATGCCTATTGCCAACGTGATACGG
- ATCATGCGGAGGATCTTACCTGCTCACGCCAAGATCTCAGATGACTCCAAGGAGACGATCCAAGAGTGTG
- TTTCGGAGTACATCAGCTTCATAACAGGGGAGGCTAATGAGCGGTGCCAGCGGGAACAGCGCAAGACCAT
- CACTGCTGAGGACGTCTTGTGGGCAATGAGCAAGCTCGGTTTTGATGACTACATCGAACCCCTCACGTTG
- TACCTCCACCGCTACAGAGAGTTGGAAGGTGAAAGAGGGGTTAGCTGCAGTGCTGGGTCCGTTAGTATGA
- CCAACGGCTTGGTGGTCAAGAGGCCTAATGGGACCATGACCGAGTATGGAGCCTACGGGCCTGTGCCAGG
- GATTCACATGGCGCAGTACCATTATCGTCATCAGAACGGGTTTGTTCAGTGGTAACGAACCTAATTCT
- AAGATGAGTGGTTCATCTTCAGGAGCAAGTGGCGCCAGAGTTGAAGTATTTCCGACTCAACAACATAAGT
- ACTGA

拟南芥*LEAFY COTYLEDON 1*基因的编码区（CDS）包含一个内含子，上面序列部分小写字母为内含子，内含子一般以**GT**开始，以**AG**结束

TAIR数据库拟南芥基因组序列



Download - Araport11 blastsets

☐	Araport11_3_utr_20220505.gz	3,812 KB	2022-05-05
☐	Araport11_5_utr_20220505.gz	3,157 KB	2022-05-05
☐	Araport11_cdna_20220505.gz	19,275 KB	2022-05-05
☐	Araport11_cdna_20220505_representative_gene_model.gz	15,491 KB	2022-05-05
☐	Araport11_cds_20220505.gz	13,208 KB	2022-05-05
☐	Araport11_cds_20220505_representative_gene_model.gz	11,918 KB	2022-05-05
☐	Araport11_downstream_1000_20220505.gz	10,891 KB	2022-05-05
☐	Araport11_downstream_1000_translation_end_20220505.gz	10,606 KB	2022-05-05
☐	Araport11_downstream_3000_20220505.gz	28,985 KB	2022-05-05
☐	Araport11_downstream_3000_translation_end_20220505.gz	27,605 KB	2022-05-05
☐	Araport11_downstream_500_20220505.gz	5,812 KB	2022-05-05
☐	Araport11_downstream_500_translation_end_20220505.gz	5,820 KB	2022-05-05
☐	Araport11_intergenic_20220505.gz	16,834 KB	2022-05-05
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☐	Araport11_pep_20220505.gz	8,441 KB	2022-05-05
☐	Araport11_pep_20220505_representative_gene_model.gz	8,009 KB	2022-05-05
☐	Araport11_seq_20220505.gz	29,101 KB	2022-05-05
☐	Araport11_seq_20220505_representative_gene_model.gz	24,593 KB	2022-05-05
☐	Araport11_upstream_1000_20220505.gz	10,882 KB	2022-05-05
☐	Araport11_upstream_1000_translation_start_20220505.gz	10,511 KB	2022-05-05
☐	Araport11_upstream_3000_20220505.gz	29,215 KB	2022-05-05
☐	Araport11_upstream_3000_translation_start_20220505.gz	27,591 KB	2022-05-05
☐	Araport11_upstream_500_20220505.gz	5,786 KB	2022-05-05
☐	Araport11_upstream_500_translation_start_20220505.gz	5,742 KB	2022-05-05

TAIR数据库

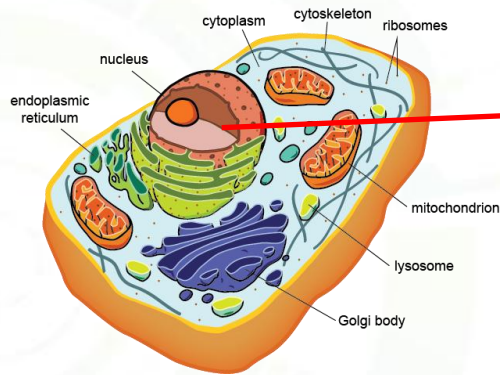
(<https://www.arabidopsis.org>)

的拟南芥基因组数据下载界面，
注意其中的

UTR (非翻译区)、**cDNA**
(即mRNA)、**CDS** (编码
区)、**InterGenic** (基因间序
列)、**intron** (内含子)、
pep (蛋白质, peptide)、
seq (基因组核酸序列) 的含
义。

基因组结构

真核生物



原核生物

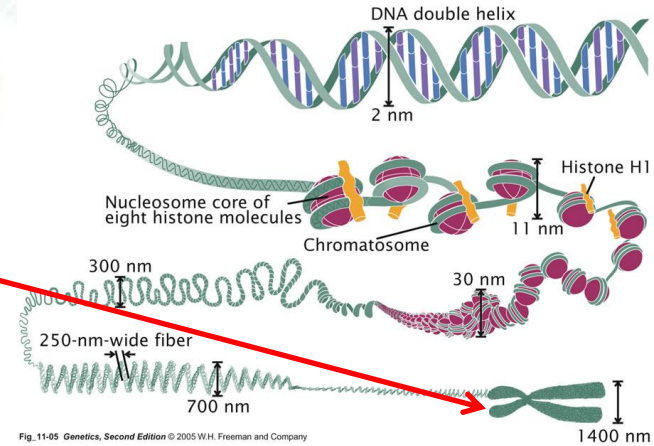
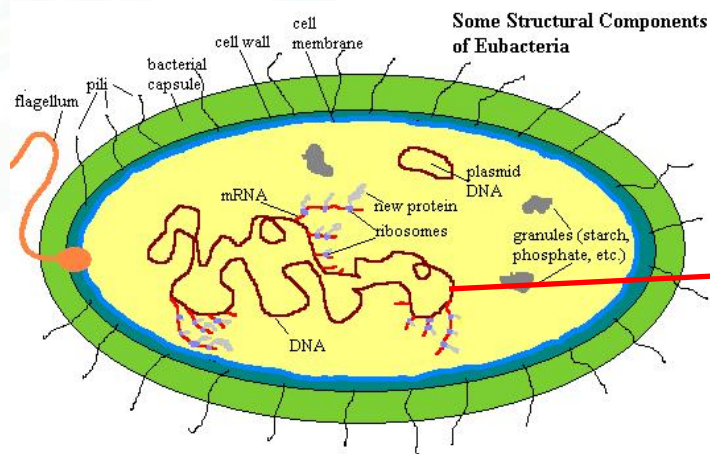


Fig. 11-05 Genetics, Second Edition © 2005 W.H. Freeman and Company

常见生物数据格式



- **FASTA**: 最常用的蛋白质/核酸序列格式
- **FASTQ**: 新一代测序数据格式
- **GenBank (GenPept)**: GenBank数据库的核酸和蛋白质序列格式
- **EMBL**: 欧洲分子生物学实验室定义的核酸和蛋白质序列格式
- **GFF/GTF**: 描述基因组测序数据中的序列特征的数据格式
- **PDB**: 描述大分子空间结构的数据格式
- **NEXUS**: 系统发育与分子进化数据格式
- **NWK**: 描述进化树的数据格式

FASTA



- >gi|13810245|emb|CAC37410.1| globin [Sabella spallanzanii]
MFRFALLCAFVADASAEGCCSMEDRQEVLNAWEALWSAEYTGRRVMIAQA
AFQKLFKAPDSKALFTRVNVDNIGSPQFRAHCIRVTNGFDTIINMAFDTDV
LEELLTHLGNQHTKYQGMRAAYLTHFRESFAEILPQAIPCFNTAAWNRCITA
MQDKIGASLAA

FASTQ



```
@SRR001666.1 071112_SLXA length=36
GGGTGATGGCCGCTGCCGATGGCGTCAAATCCCACC
+SRR001666.1 071112_SLXA length=36
|||||9|G9|C
```

GenBank/GenPept

LOCUS CAC37410 165 aa linear INV 20-JUL-2001
DEFINITION globin [Sabella spallanzanii].
ACCESSION CAC37410
VERSION CAC37410.1 GI:13810245
DBSOURCE embl accession [AJ131283.1](#)
KEYWORDS .
SOURCE Sabella spallanzanii
ORGANISM [Sabella spallanzanii](#)
Eukaryota; Metazoa; Lophotrochozoa; Annelida; Polychaeta; Palpata;
Canalipalpata; Sabellida; Sabellidae; Sabella.
REFERENCE 1
AUTHORS Pallavicini, A., Negrisol, E., Barbato, R., Dewilde, S.,
Ghiretti-Magaldi, A., Moens, L. and Lanfranchi, G.
TITLE The primary structure of globin and linker chains from the
chlorocruorin of the polychaete Sabella spallanzanii
JOURNAL J. Biol. Chem. 276 (28), 26384-26390 (2001)
PUBMED [11294828](#)

FEATURES

Location/Qualifiers

source

1..165

/organism="Sabella spallanzanii"

/db_xref="taxon:[85702](#)"

/tissue_type="haematopoietic"

/dev_stage="adult"

/note="Gmelin, 1791"

Protein

1..165

/product="globin"

/function="respiratory pigment"

Region

28..159

/region_name="Mb_like"

/note="myoglobin_like; M family globin domain; cd01040"

/db_xref="CDD:[271266](#)"Site

order(65..66, 82, 85..86, 89, 110, 113..114, 120, 124..125, 128)

/site_type="other"

/note="heme binding site [chemical binding]"

/db_xref="CDD:[271266](#)"CDS

1..165

/gene="globin"

/coded_by="AJ131283.1:54..551"

/experiment="experimental evidence, no additional details recorded"

/db_xref="GOA:[Q9BHK3](#)"/db_xref="InterPro:[IPR000971](#)"/db_xref="InterPro:[IPR009050](#)"/db_xref="InterPro:[IPR012292](#)"/db_xref="InterPro:[IPR014610](#)"/db_xref="UniProtKB/TrEMBL:[Q9BHK3](#)"

ORIGIN

```
1 mfrfallcaf vadasaegcc smedrquevlñ awealwsaey tgrrvmiaqa afqklfekap
61 dskalftrvn vdnigspqfr ahcirvtngf dtiinmafdt dvleellthl gnqhtkyqgm
121 raaylthfre sfaeilpqai pcfntaawnr citamqdkig aslaa
```

//



ID SC10H5 standard; DNA; PR0; 4870 BP.

XX

AC AL031232;

XX

DE *Streptomyces coelicolor* cosmid 10H5.

XX

KW integral membrane protein.

XX

OS *Streptomyces coelicolor*

OC Eubacteria; Firmicutes; Actinomycetes; Streptomycetes;

OC Streptomycetaceae; *Streptomyces*.

XX

RN [1]

RP 1-4870

RA Oliver K., Harris D.;

RT ;

RL Unpublished.

FT misc_feature 4769..4870
FT /note="overlap with cosmid 3A7 from 1 to 102"
XX

SQ Sequence 4870 BP; 769 A; 1717 C; 1693 G; 691 T; 0 other;

gatcagtaga	cccagcgaca	gcagggcggg	gcccagcagg	ccggccgttg	cgtagagcgc	60
gaggacggcg	accggcgttg	ccaccgacag	gatggctgcg	gcgacgcgga	cgacaccgga	120
gtgtgccagg	gcccaccaca	cgccgatggc	cgcgagcgcg	agtcccgcgc	tgccgaacag	180
ggcccacagc	acactgcgca	gaccggcggc	cacgagtggc	gccaggacgg	tgcccagcag	240
gagcagcagg	gtgacgtggg	cgcgcgctgc	actgtggccg	ccccgtccgc	ccgacgcgcg	300
cggctcgtca	tctcgcggtc	ccaccaccgg	tcggccccat	tactcgtcct	caaccctgtg	360
gcgactgacg	ttccccggac	aggtcgtacc	gattgccgcc	acgccccacc	acgcacaggg	420
cccagacgac	gaagcctgac	atggtgatca	tgacgacgga	ccacaccggg	tagtacggca	480
gcgagaggaa	gttggcgatg	atcaccagcc	cggcgatggc	gaccccgggtg	acacgtgccc	540
acatcgccgt	tttgagcagc	ccggcgctga	cgaccatggc	gagcgcgcgc	agcgcgagat	600
ggatccaccc	ccacccggtg	agatcgaact	ggaaaacgta	gttgggcgtg	gtgacgaaga	660
cgtcgtcctc	ggcgatggcc	atgatgcccc	ggaagaggct	gagcagcccc	gcgaggaaga	720
gcatcaccgc	cgcgaaggcg	gtaaggcccc	tcgccatttc	ctgcctcgcg	gtgtgtgccg	780
ggtggtgggt	atgtgacgtg	gtcatctcgg	acctcgtttc	gtggaatgcg	gatgcttcag	840
cgagcggagg	cgccgggtgcc	cgccgcgccc	gtgtgccctg	ccgggcccgtg	accggacagg	900
accaattcct	tcgccttgcg	gaactcctcg	tccgtgatgg	caccccggtc	tcggatctcg	960
gagagccggg	ccagctcgtc	gacgtctgctg	gacccgcgcg	ccacgggtctt	cctgatgtag	1020

GFF/GTF

■ GFF格式包括以下字段（制表符分割）：

- **seqname** - name of the chromosome or scaffold;
- **source** - name of the program that generated this feature, or the data source
- **feature** - feature type name, e.g. Gene, Variation, Similarity
- **start** - Start position of the feature, with sequence numbering starting at 1.
- **end** - End position of the feature, with sequence numbering starting at 1.
- **score** - A floating point value.
- **strand** - defined as + (forward) or - (reverse).
- **frame** - One of '0', '1' or '2'.
- **attribute** - A semicolon-separated list of tag-value pairs

如：

```
pseudogene Ensembl gene 11869 14409 . + . ENSG00000223972
```

```
p_transcript Ensembl transcript 11869 14409 . + . ENSG00000223972
```

NWK (Newick)



○ ((A,B),(C,D))

