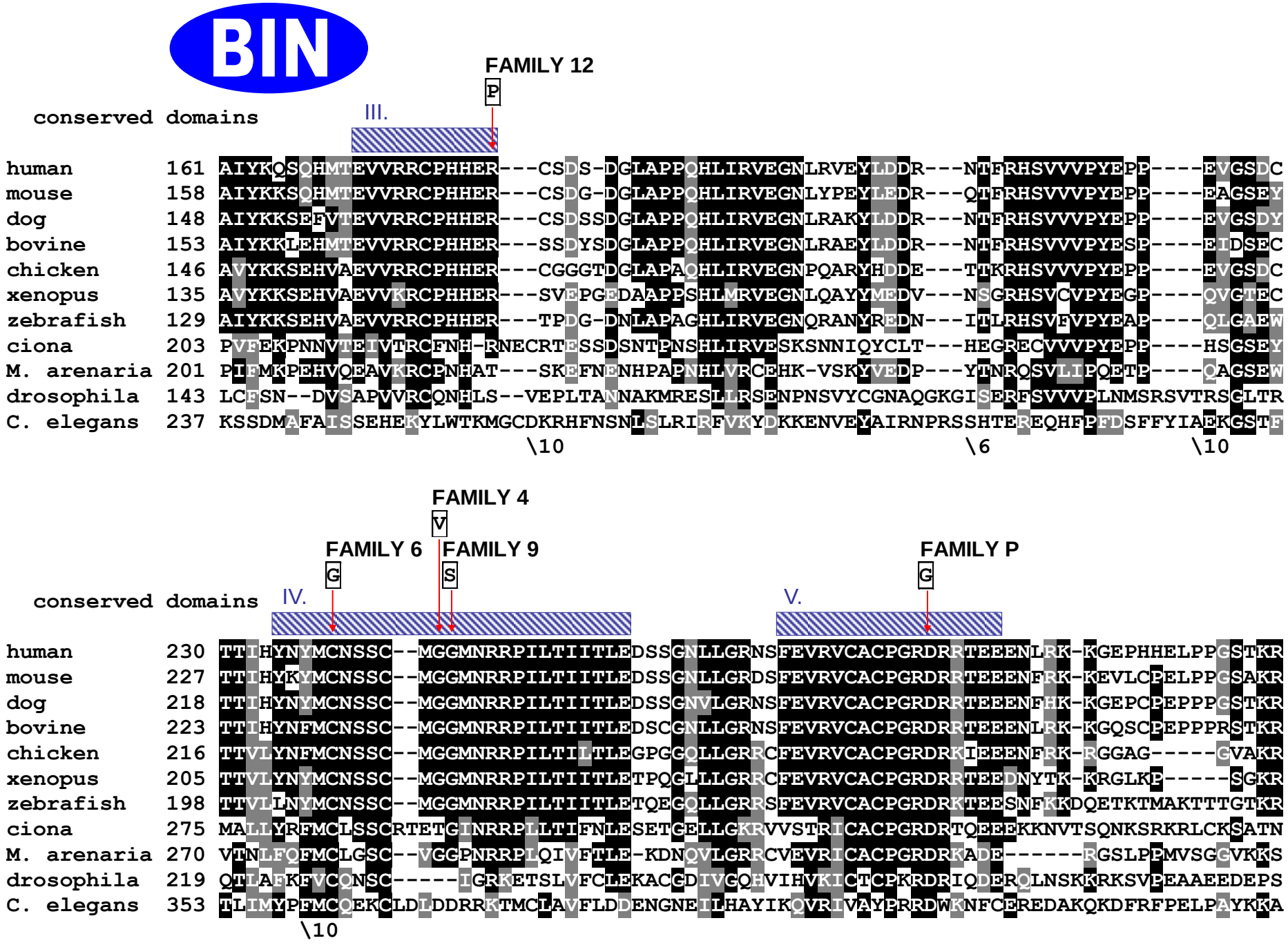
BIN
FAMILY 12
P
conserved domains
III.
human 161 AIYKQSQHMTEVVRRCPHHER---CSDS-DGLAPPQHLIRVEGNLRVEYLDDR---NTFRHSVVVPYEPP----EVGSDC
mouse 158 AIYKKSQHMTEVVRRCPHHER---CSDG-DGLAPPQHLIRVEGNLYPEYLEDR---QTFRHSVVVPYEPP----EAGSEY
dog 148 AIYKKSEFVTEVVRRCPHHER---CSDSSDGLAPPQHLIRVEGNLRAKYLDDR---NTFRHSVVVPYEPP----EVGSDY
bovine 153 AIYKKLEHMTEVVRRCPHHER---SSDYSDGLAPPQHLIRVEGNLRAEYLDDR---NTFRHSVVVPYESP----EIDSEC
chicken 146 AVYKKSEHVAEVVRRCPHHER---CGGGTDGLAPAQHLIRVEGNPQARYHDDE---TTKRHSVVVPYEPP----EVGSDC
xenopus 135 AVYKKSEHVAEVVKRCPHHER---SVEPGEDAAPPSHLMRVEGNLQAYYMEDV---NSGRHSVCVPYEGP----QVGTEC
zebrafish 129 AIYKKSEHVAEVVRRCPHHER---TPDG-DNLAPAGHLIRVEGNQRANYREDN---ITLRHSVEVPYEAP----QLGAEW
ciona 203 PVEEKPNNVTEIVTRCFNH-RNECRTESSDSNTPNSHLIRVESKSNNIQYCLT---HEGRECVVVPYEPP----HSGSEY
M. arenaria 201 PIEMKPEHVQEAVKRCPNHAT---SKEFNENHPAPNHLVRCEHK-VSKYVEDP---YTNRQSVLIPQETP----QAGSEW
drosophila 143 LCESN--DVSAPVVRCQNHLS--VEPLTANNAKMRESLLRSENPNSVYCGNAQGKGISERFSVVVPLNMSRSVTRSGLTR
C. elegans 237 KSSDMAFAISSEHEKYLWTKMGCDKRHFNSNLSLRIRFVKYDKKENVEYAIRNPRSSHTEREQHFPFDSFFYIAEKGSTF
\10
\6
\10
FAMILY 4
V
FAMILY 6
G
FAMILY 9
S
FAMILY P
G
conserved domains
IV.
V.
human 230 TTIHYNYMCNSSC--MGGMNRRPILTIITLEDSSGNLLGRNSFEVRVCACPGRDRRTEEENLRK-KGEPHHELPPGSTKR
mouse 227 TTIHYKYMCNSSC--MGGMNRRPILTIITLEDSSGNLLGRDSFEVRVCACPGRDRRTEEENFRK-KEVLCPELPPGSAKR
dog 218 TTIHYNYMCNSSC--MGGMNRRPILTIITLEDSSGNVLGRNSFEVRVCACPGRDRRTEEENFHK-KGEPCPEPPPGSTKR
bovine 223 TTIHYNFMCNSSC--MGGMNRRPILTIITLEDSCGNLLGRNSFEVRVCACPGRDRRTEEENLRK-KGQSCPEPPPRSTKR
chicken 216 TTVLYNFMCNSSC--MGGMNRRPILTILTLEGPGGQLLGRRCFEVRVCACPGRDRKIEEENFRK-RGGAG-----GVAKR
xenopus 205 TTVLYNYMCNSSC--MGGMNRRPILTIITLETPQGLLLGRRCFEVRVCACPGRDRRTEEDNYTK-KRGLKP-----SGKR
zebrafish 198 TTVLLNYMCNSSC--MGGMNRRPILTIITLETQEGQLLGRRSFEVRVCACPGRDRKTEESNFKKDQETKTMAKTTTGTKR
ciona 275 MALLYRFMCLSSCRTETGINRRPLLTIFNLESETGELLGKRVVSTRICACPGRDRTQEEEKKNVTSQNKSRKRLCKSATN
M. arenaria 270 VTNLFQFMCLGSC--VGGPNRRPLQIVFTLE-KDNQVLGRRCVEVRICACPGRDRKADE------RGSLPPMVSGGVKKS
drosophila 219 QTLAFKFVCQNSC-----IGRKETSLVFCLEKACGDIVGQHVIHVKICTCPKRDRIQDERQLNSKKRKSVPEAAEEDEPS
C. elegans 353 TLIMYPFMCQEKCLDLDDRRKTMCLAVFLDDENGNEILHAYIKQVRIVAYPRRDWKNFCEREDAKQKDFRFPELPAYKKA
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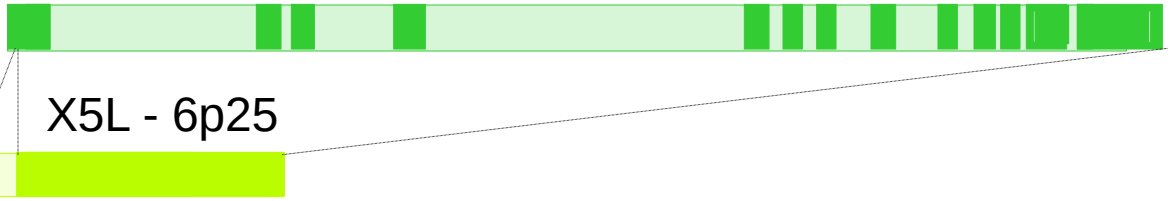
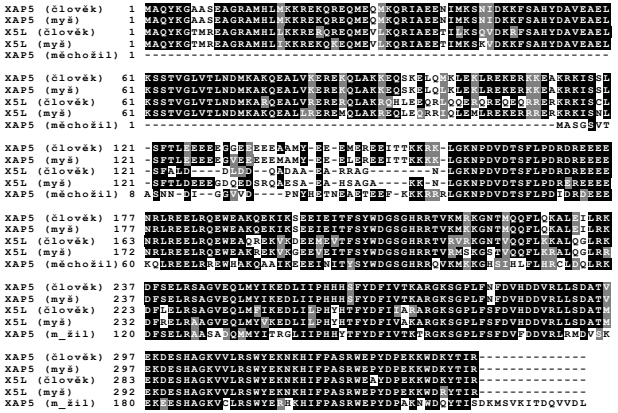
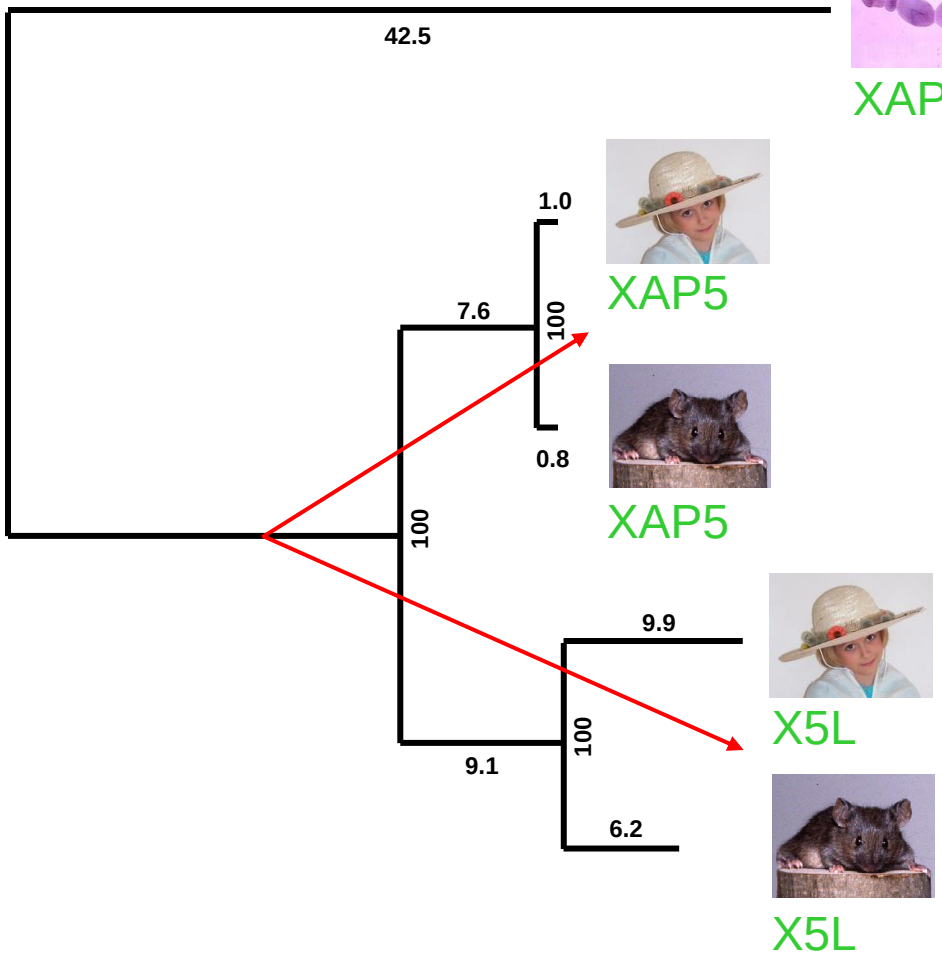
BIN

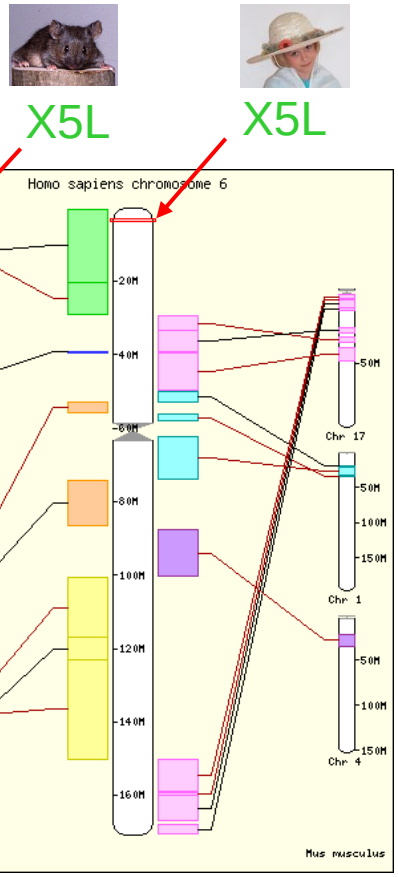
XAP5 - Xq28

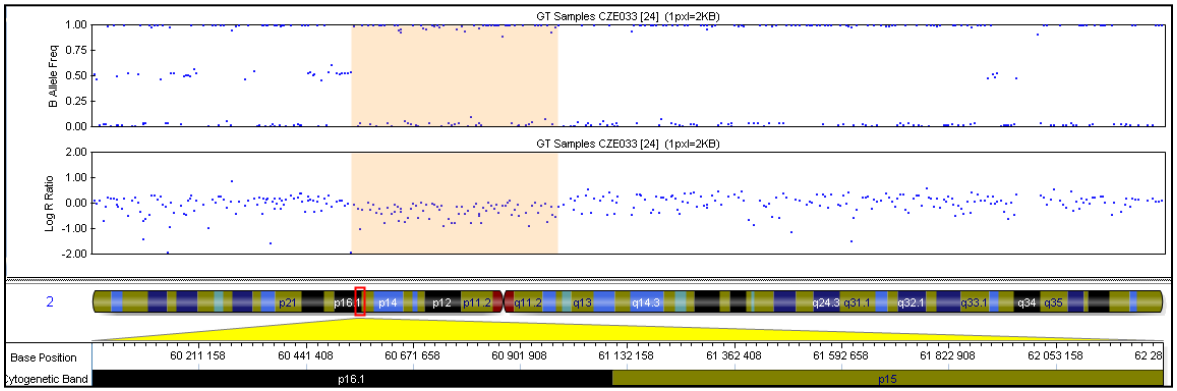
X5L - 6p25

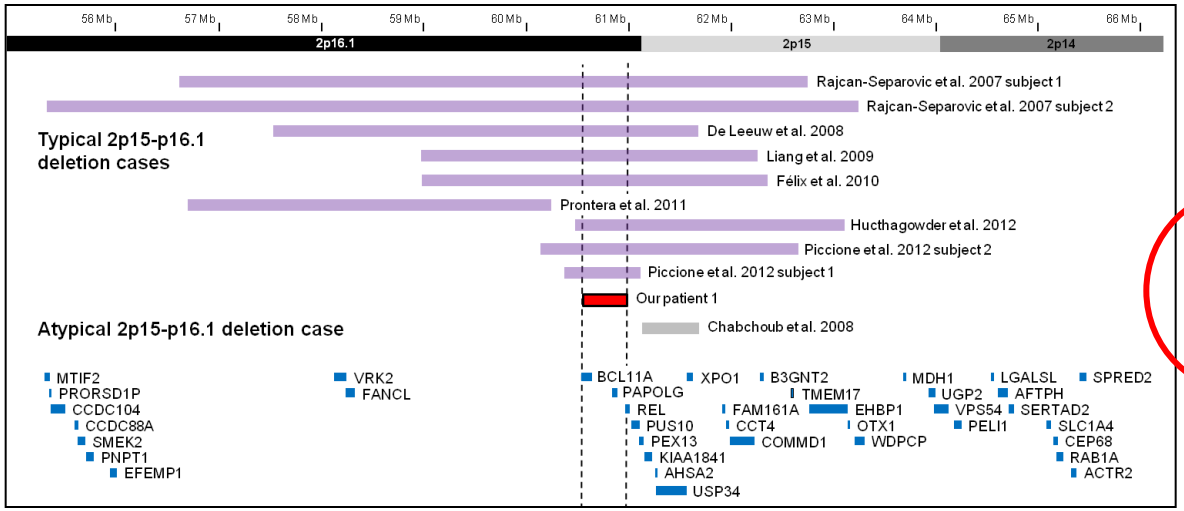


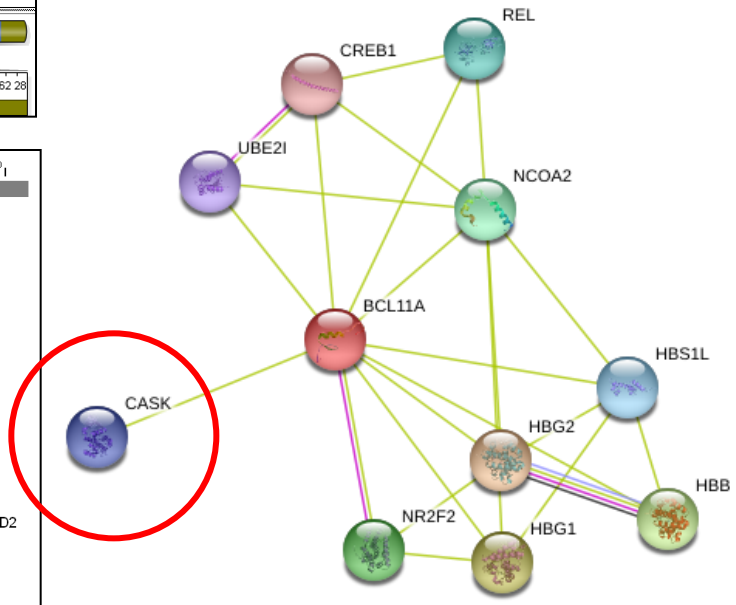












Journal of Neuroscience Research

Journal of Neuroscience Research 88:2364–2373 (2010)

X-Linked Mental Retardation Gene CASK Interacts With Bcl11A/CTIP1 and Regulates Axon Branching and Outgrowth

Ting-Yu Kuo, Chen-Jei Hong, Hsu-Ling Chien, and Yi-Ping Hsueh*

The Institute of Molecular Biology, Academia Sinica, Taipei, Taiwan, Republic of China

definice života

živý organismus je
přirozeně se vyskytující
sám sebe reprodukující systém,
který vykonává řízené manipulace
s hmotou, energií a informací

složitá organizace a řád

regulace a udržování vnitřní homeostázy
získávání a využití energie,
    výměna látek a energie s prostředím
schopnost reagovat na vnější podněty
reprodukce,
    dědičnost a proměnlivost (variabilita)
vývoj a růst
adaptace na prostředí

život v prostoru: prostorová hierarchie živých systémů

biosféra
ekosystém
společenstva
populace
organismus
orgány a orgánové systémy
tkáně
buňky
organely
molekuly

kontinuita života je zajištěna předáváním genetické informace

život v čase 1: evoluce živých systémů (evolution)

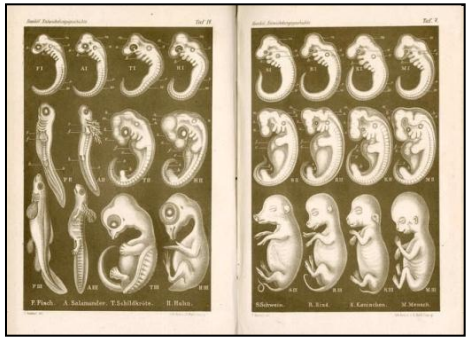
časové měřítko cca 3.8 mld let od vzniku života na planetě

http://rainbow.ldeo.columbia.edu/courses/v1001/arch.berl.gif

život v čase 2: vývoj živých systémů (development)

časové měřítko mezi vznikem a zánikem jedince

http://www.wellcome.ac.uk/stellent/groups/corporatesite/@msh_publishing_group/documents/image/wtx054619.jpg



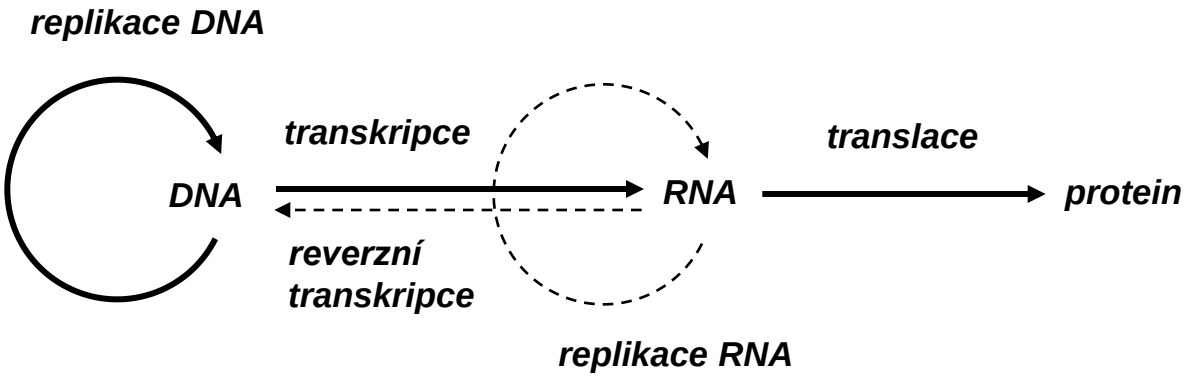
kontinuita života je zajištěna předáváním genetické informace

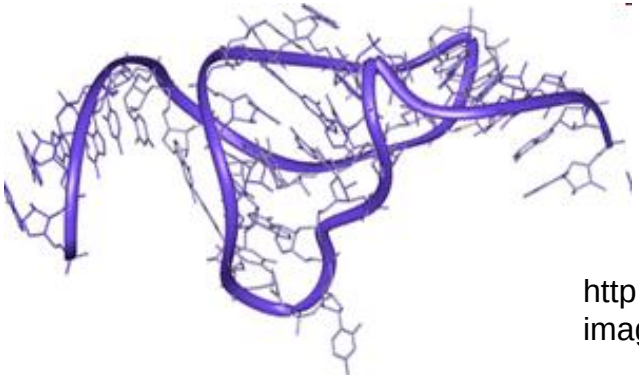
BIN

- organizace a fungování živé hmoty
- tok genetické informace: molekuly, procesy, kód
- struktura genetické informace (člověka)
  velikost, obsah, evoluce, metody, HGP
- variabilita genetické informace
  typy variability, evoluce, důsledky pro fenotyp, metody
- exprese genetické informace
  regulace, evoluce, důsledky pro fenotyp, metody

T. Dobzhansky:
"Nothing in biology makes sense
except in the light of evolution."

tok genetické informace: centrální dogma



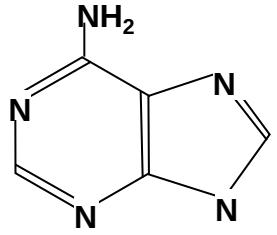


http://evolution.berkeley.edu/evolibrary/images/interviews/rnastructure.gif

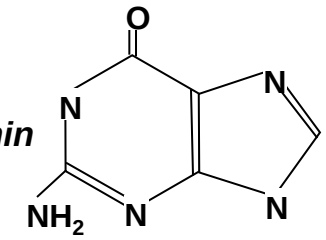
tok genetické informace - informační makromolekuly: DNA

purinové báze

adenin

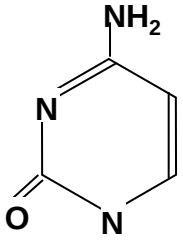


guanin

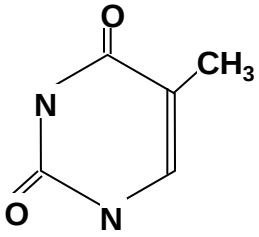


pyrimidinové báze

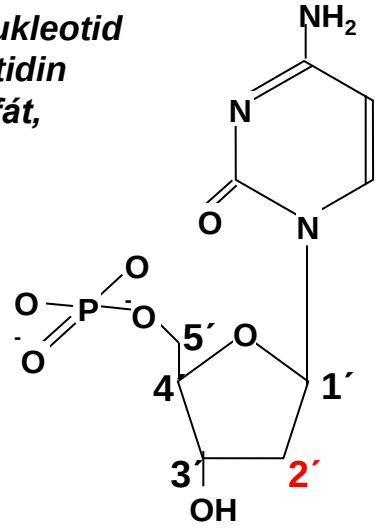
cytosin



thymin

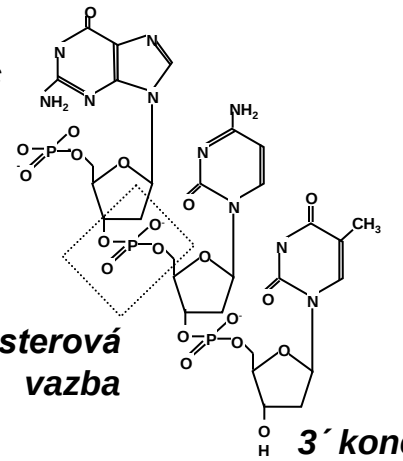


deoxyribonukleotid (2´ deoxycytidin 5´ monofosfát, dCMP)

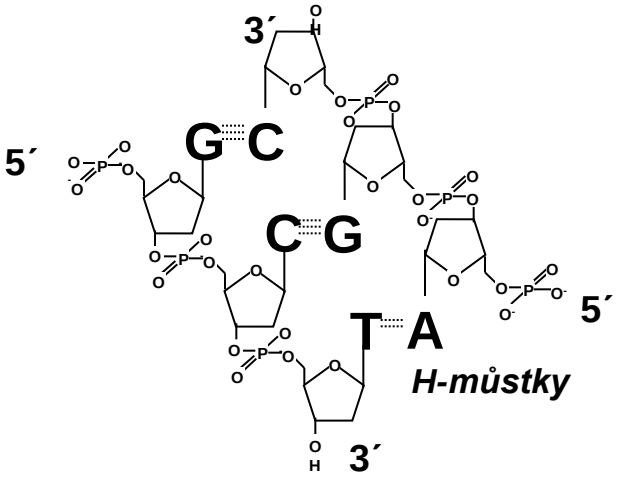


tok genetické informace - informační makromolekuly: DNA

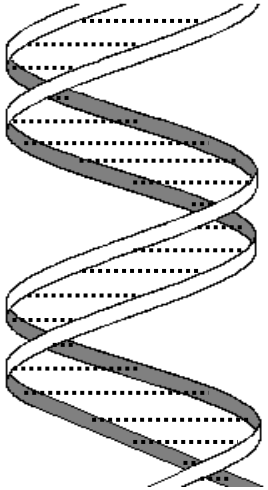
jednořetězec DNA
(sekvence 5´ GCT 3´)



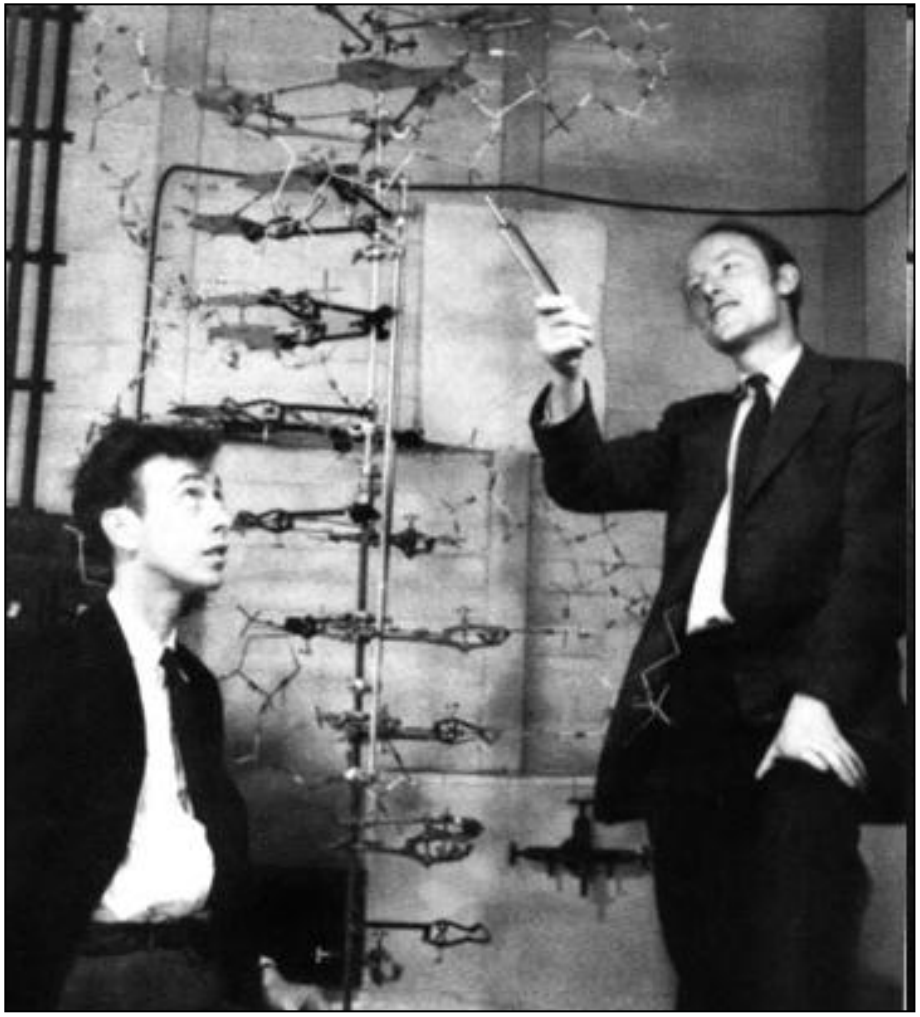
dvouřetězec DNA



dvojitá spirála



tok genetické informace - informační makromolekuly: DNA



April 25, 1953 NATURE 737

MOLECULAR STRUCTURE OF NUCLEIC ACIDS

A Structure for Deoxyribose Nucleic Acid

WE wish to suggest a structure for the salt of deoxyribose nucleic acid (D.N.A.). This structure has novel features which are of considerable biological interest.

A structure for nucleic acid has already been proposed by Pauling and Corey[1]. They kindly made their manuscript available to us in advance of publication. Their model consists of three intertwined chains, with the phosphates near the fibre axis, and the bases on the outside. In our opinion, this structure is unsatisfactory for two reasons: (1) We believe that the material which gives the X-ray diagrams is the salt, not the free acid. Without the acidic hydrogen atoms it is not clear what forces would hold the structure together, especially as the negatively charged phosphates near the axis will repel each other. (2) Some of the van der Waals distances appear to be too small.

Another three-chain structure has also been suggested by Fraser (in the press). In his model the phosphates are on the outside and the bases on the inside, linked together by hydrogen bonds. This structure as described is rather ill-defined, and for this reason we shall not comment on it.

We wish to put forward a radically different structure for the salt of deoxyribose nucleic acid. This structure has two helical chains each coiled round the same axis (see diagram). We have made the usual chemical assumptions, namely, that each chain consists of phosphate diester groups joining β-D-deoxyribofuranose residues with 3',5' linkages. The two chains (but not their bases) are related by a dyad perpendicular to the fibre axis. Both chains follow right-handed helices, but owing to the dyad the sequences of the atoms in the two chains run in opposite directions. Each chain loosely resembles Furberg's[2] model No. 1; that is, the bases are on the inside of the helix and the phosphates on the outside. The configuration of the sugar and the atoms near it is close to Furberg's 'standard configuration', the sugar being nearly perpendicular to the attached base. There is a residue on each chain every 3·4 A. in the z-direction. We have assumed an angle of 36° between adjacent residues in the same chain, so that the structure repeats after 10 residues on each chain, that is, after 34 A. The distance of a phosphorus atom from the fibre axis is 10 A. As the phosphates are on the outside, cations have easy access to them.

The structure is an open one, and its water content is rather high. At lower water contents we would expect the bases to tilt so that the structure could become more compact.

The novel feature of the structure is the manner in which the two chains are held together by the purine and pyrimidine bases. The planes of the bases are perpendicular to the fibre axis. They are joined together in pairs, a single base from one chain being hydrogen-bonded to a single base from the other chain, so that the two lie side by side with identical z-co-ordinates. One of the pair must be a purine and the other a pyrimidine for bonding to occur. The hydrogen bonds are made as follows: purine position 1 to pyrimidine position 1; purine position 6 to pyrimidine position 6.

If it is assumed that the bases only occur in the structure in the most plausible tautomeric forms (that is, with the keto rather than the enol configurations) it is found that only specific pairs of bases can bond together. These pairs are: adenine (purine) with thymine (pyrimidine), and guanine (purine) with cytosine (pyrimidine).

In other words, if an adenine forms one member of a pair, on either chain, then on these assumptions the other member must be thymine; similarly for guanine and cytosine. The sequence of bases on a single chain does not appear to be restricted in any way. However, if only specific pairs of bases can be formed, it follows that if the sequence of bases on one chain is given, then the sequence on the other chain is automatically determined.

It has been found experimentally[3,4] that the ratio of the amounts of adenine to thymine, and the ratio of guanine to cytosine, are always very close to unity for deoxyribose nucleic acid.

It is probably impossible to build this structure with a ribose sugar in place of the deoxyribose, as the extra oxygen atom would make too close a van der Waals contact.

The previously published X-ray data[5,6] on deoxyribose nucleic acid are insufficient for a rigorous test of our structure. So far as we can tell, it is roughly compatible with the experimental data, but it must be regarded as unproved until it has been checked against more exact results. Some of these are given in the following communications. We were not aware of the details of the results presented there when we devised our structure, which rests mainly though not entirely on published experimental data and stereochemical arguments.

It has not escaped our notice that the specific pairing we have postulated immediately suggests a possible copying mechanism for the genetic material.

Full details of the structure, including the conditions assumed in building it, together with a set of co-ordinates for the atoms, will be published elsewhere.

We are much indebted to Dr. Jerry Donohue for constant advice and criticism, especially on interatomic distances. We have also been stimulated by a knowledge of the general nature of the unpublished experimental results and ideas of Dr. M. H. F. Wilkins, Dr. R. E. Franklin and their co-workers at King's College, London. One of us (J. D. W.) has been aided by a fellowship from the National Foundation for Infantile Paralysis.

J. D. WATSON
F. H. C. CRICK

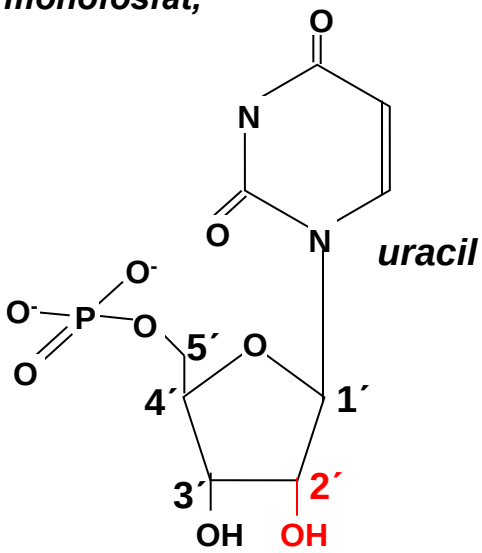
Medical Research Council Unit for the Study of the Molecular Structure of Biological Systems,
Cavendish Laboratory, Cambridge.
April 2

[1] Pauling, L., and Corey, R. B., *Nature*, this issue, p. 346; *Proc. U.S.*, *39*, 84 (1953).
[2] Furberg, S., *Acta Chem. Scand.*, *6*, 634 (1952).
[3] Chargaff, E., *Experientia*, *6*, 201 (1950).
[4] Chargaff, E., Lipshitz, R., and Green, C., *J. Biol. Chem.*, *195*, 155 (1952).
[5] Wilkins, M. H. F., Gosling, R. G., and Seeds, W. E., *Nature*, this issue, p. 334; *J. Applied Phys.* (in the press).
[6] Wilkins, M. H. F., and Randall, J. T., *Biochim. et Biophys. Acta*, *10*, 192 (1953).

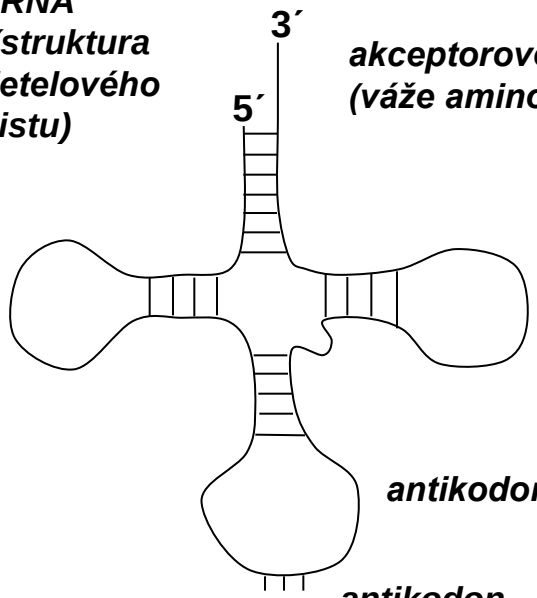
http://web.virginia.edu/Heidi/chapter30/Images/30_01.jpg

tok genetické informace - informační makromolekuly: RNA

ribonukleotid (uridin 5´ monofosfát, UMP)

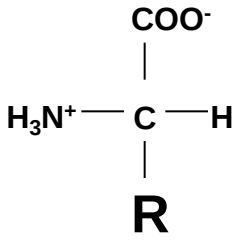


tRNA (struktura jetelového listu)



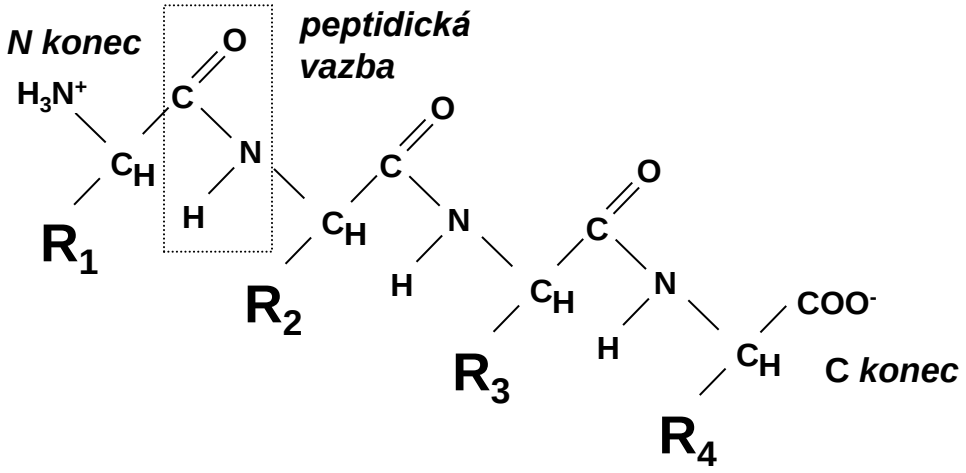
tok genetické informace - informační makromolekuly: proteiny

aminokyselina



postranní řetězec

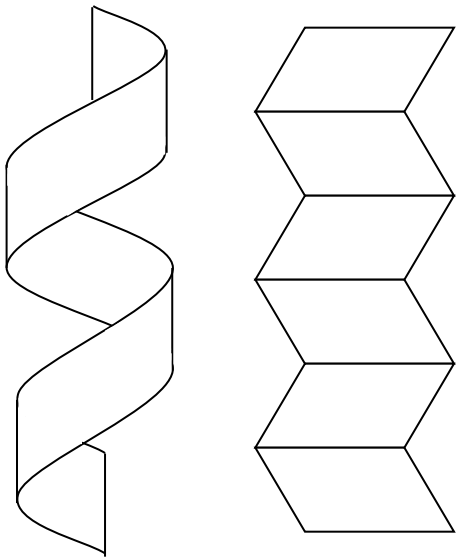
polypeptidický řetězec



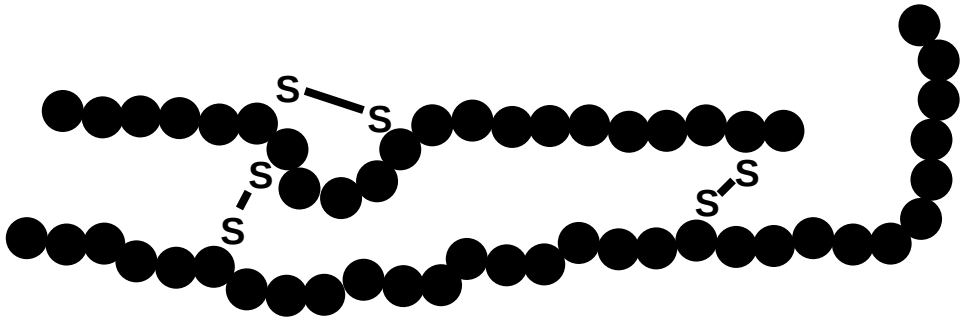
tok genetické informace - informační makromolekuly: proteiny

sekundární struktura proteinů

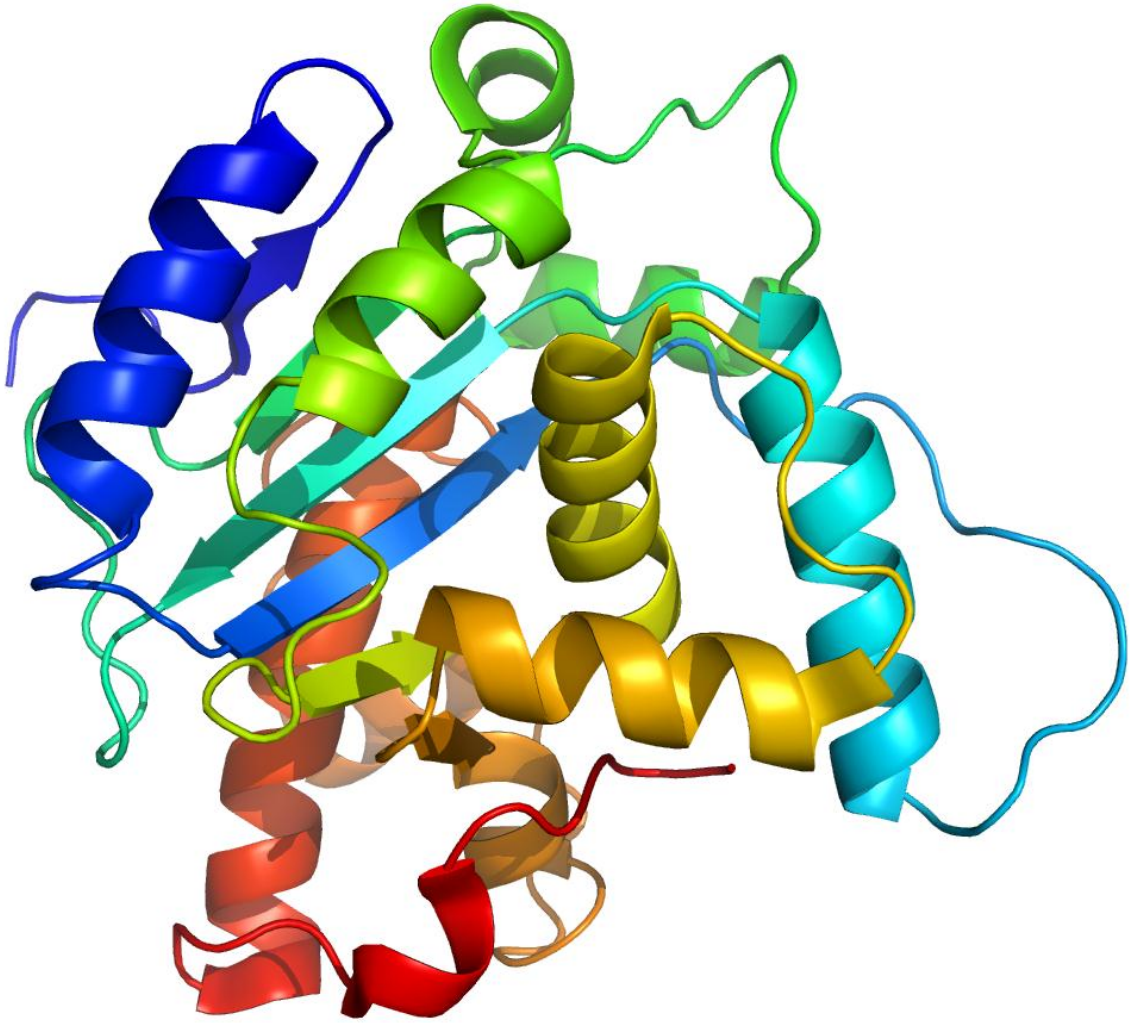
α-helix ***β-skládaný list***



disulfidické můstky v řetězcích A a B lidského inzulínu

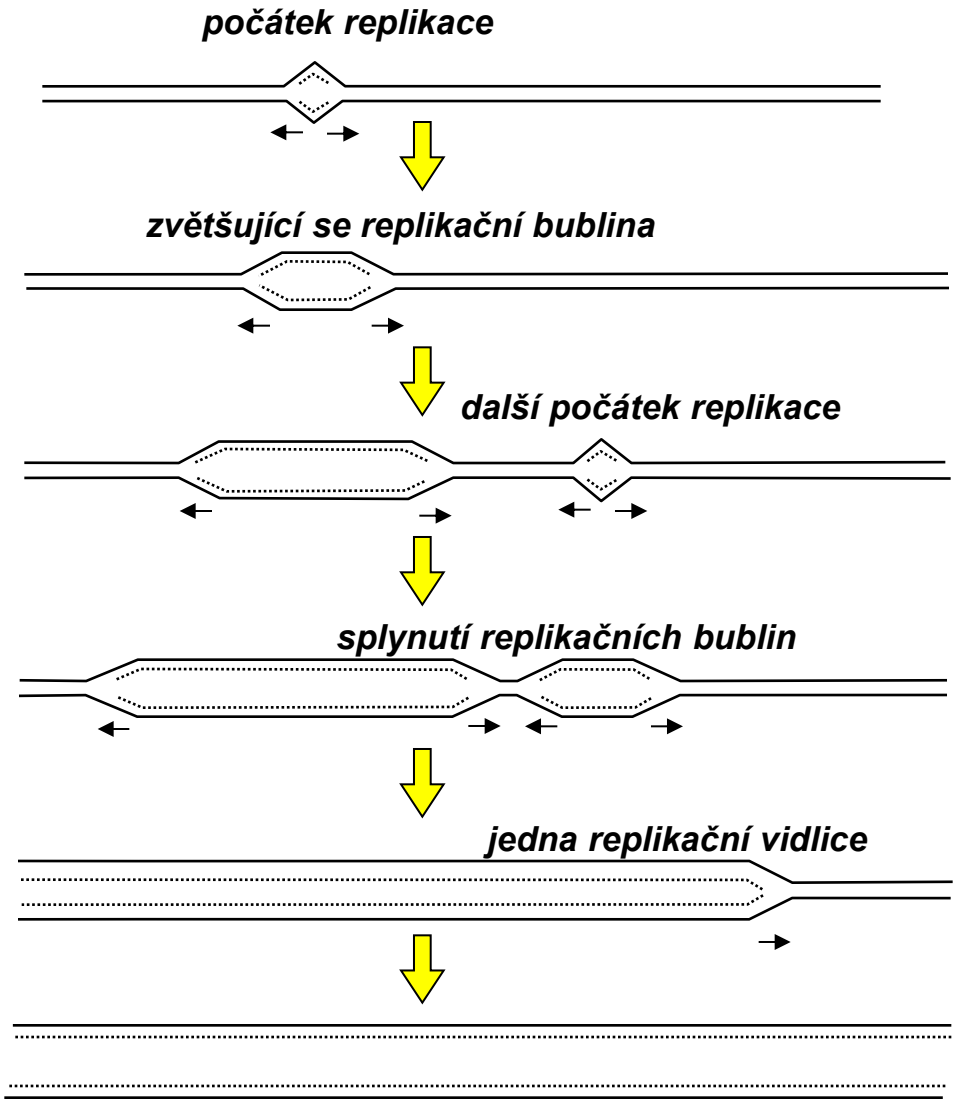


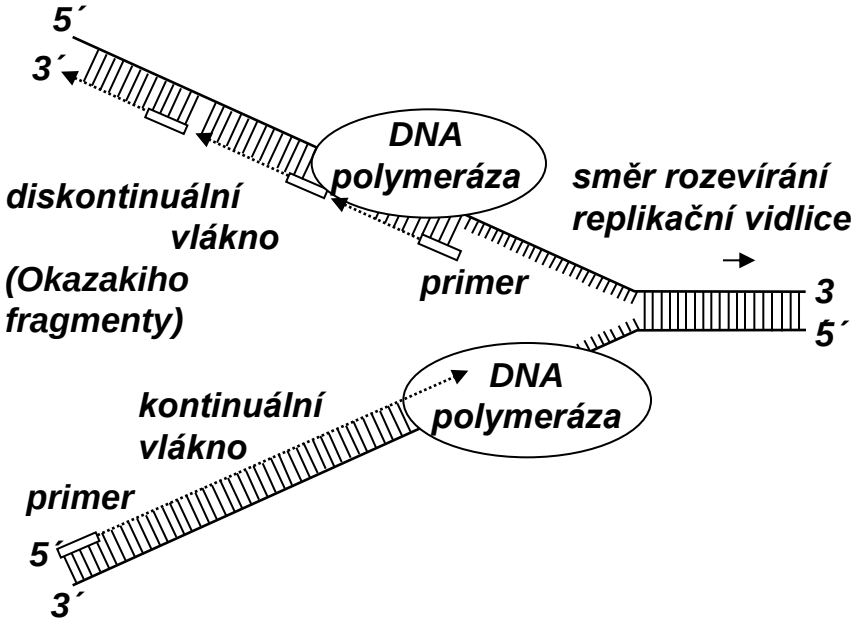
tok genetické informace - informační makromolekuly: proteiny



http://upload.wikimedia.org/wikipedia/commons/e/e6/Spombe_Pop2p_protein_structure_rainbow.png

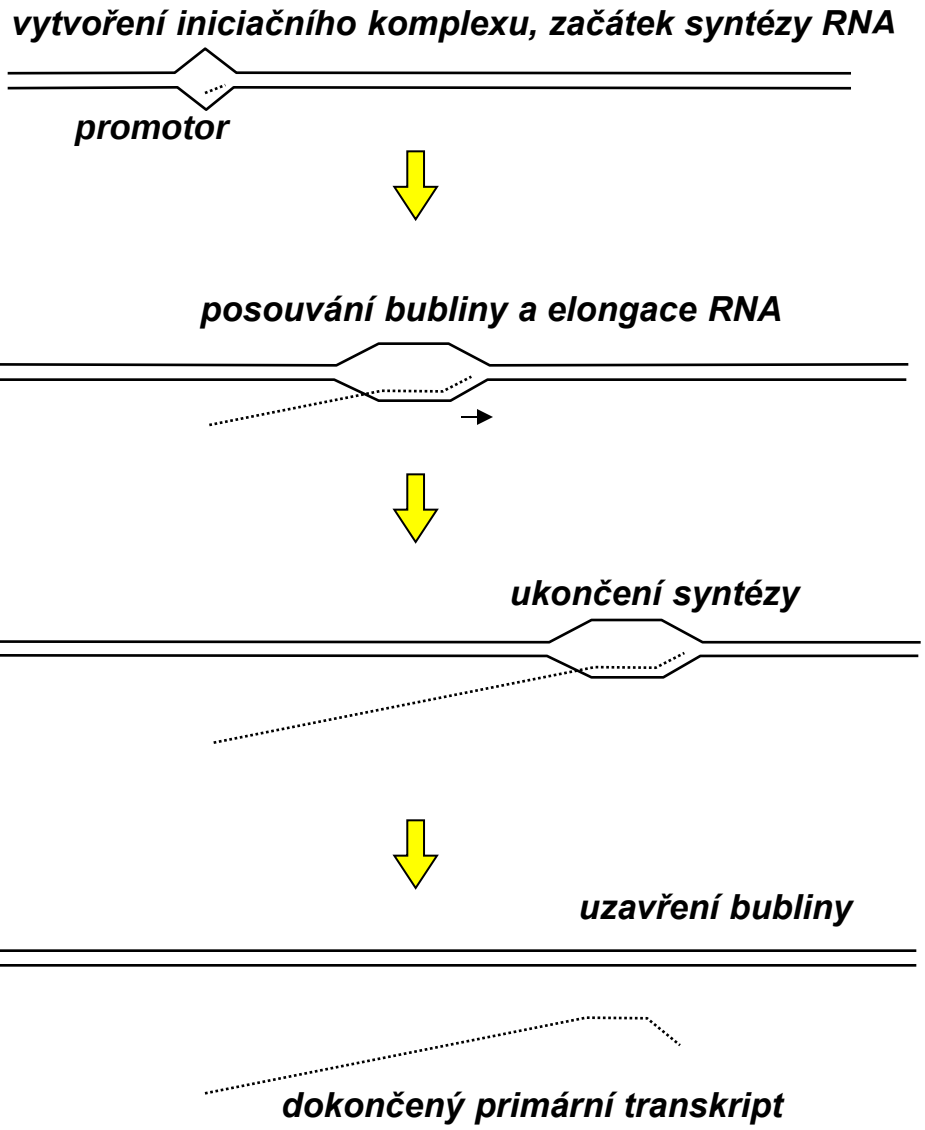
tok genetické informace - procesy: replikace DNA

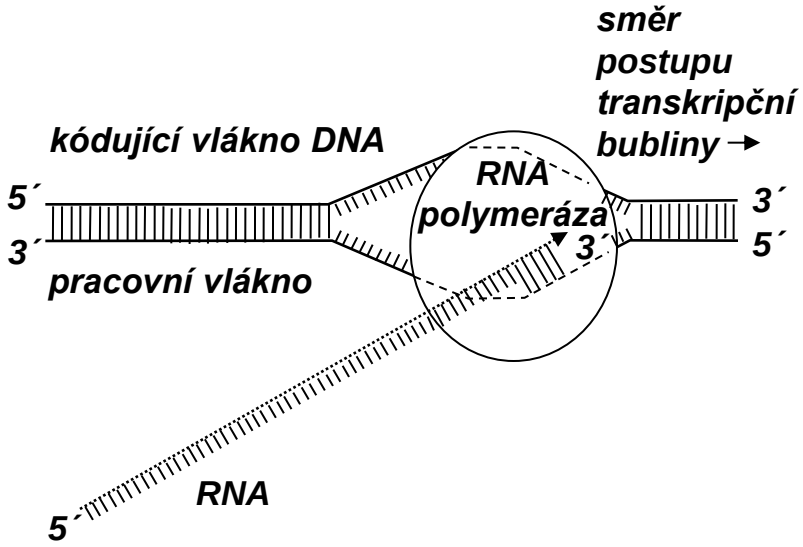




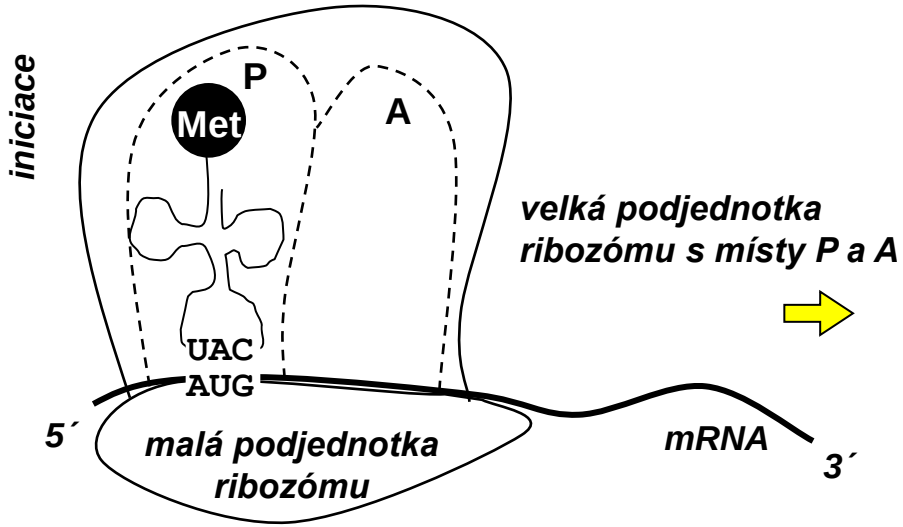
dceřinné molekuly DNA - jeden starý a jeden nový řetězec

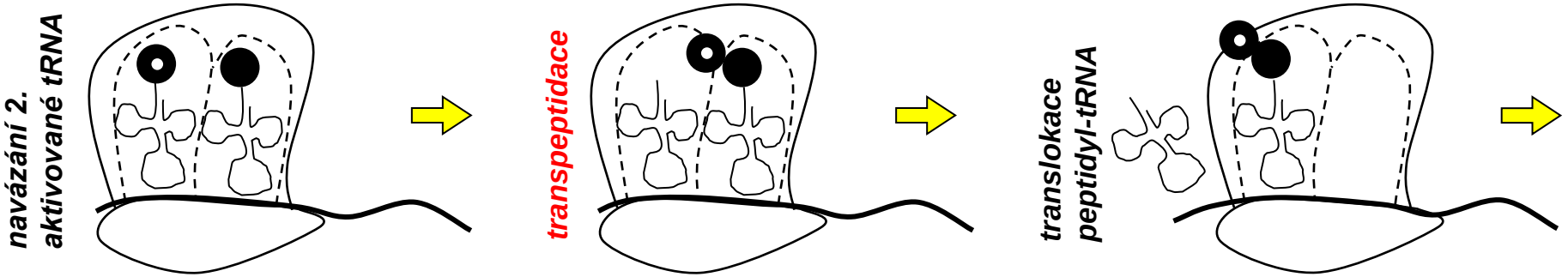
tok genetické informace - procesy: transkripce RNA

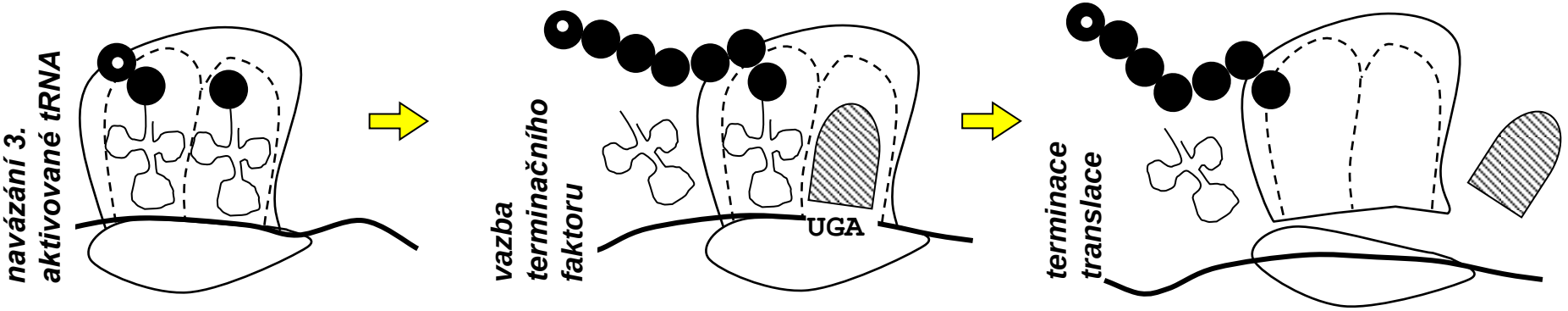




translace


iniciace
P
Met
A
UAC
AUG
5´
malá podjednotka ribozómu
mRNA
3´
velká podjednotka ribozómu s místy P a A


navázání 2. aktivované tRNA
transpeptidace
translokace peptidyl-tRNA


navázání 3. aktivované tRNA
vazba terminačního faktoru
UGA
terminace translace

tok genetické informace: genetický kód

1. pozice kodonu	2. pozice kodonu				3. pozice kodonu
	U	C	A	G	
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

aminoacyl-tRNA syntetázy