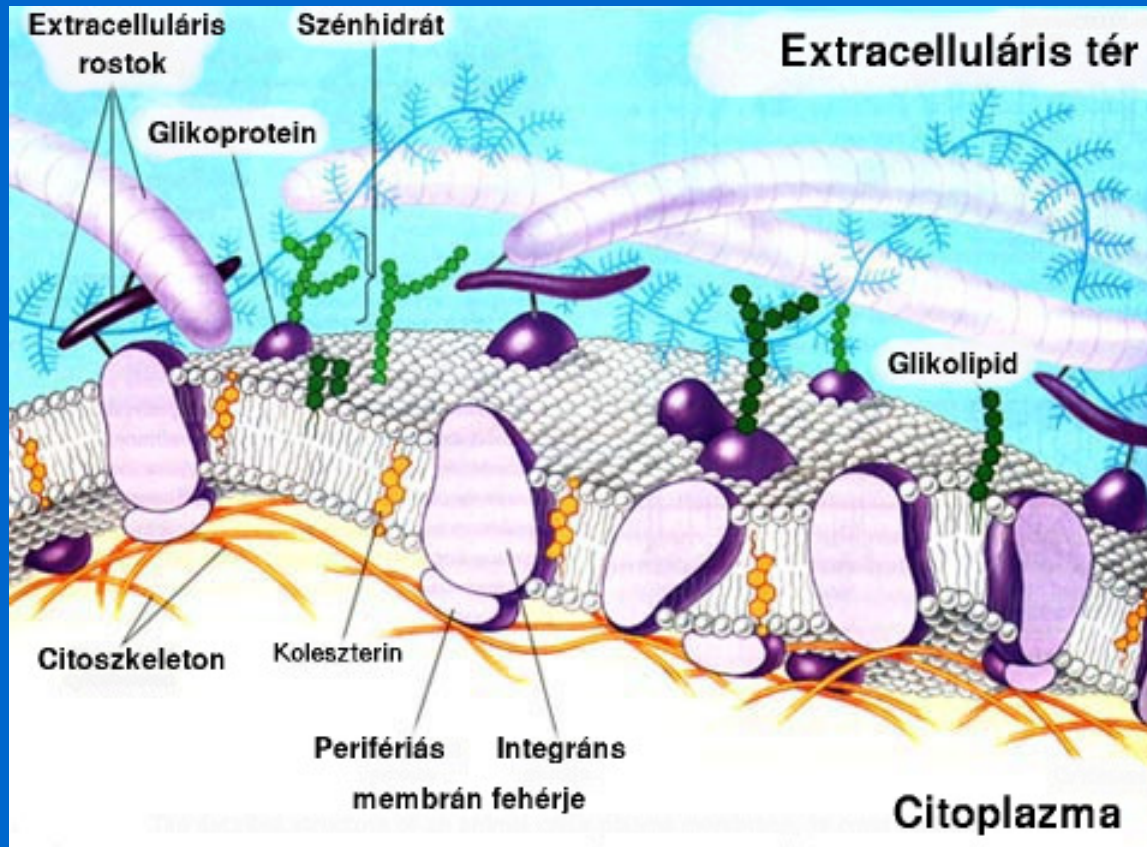


Makromolekulák

Simon István

Transzmembrán fehérjék



Anyagcsere folyamatok

Transzporterek

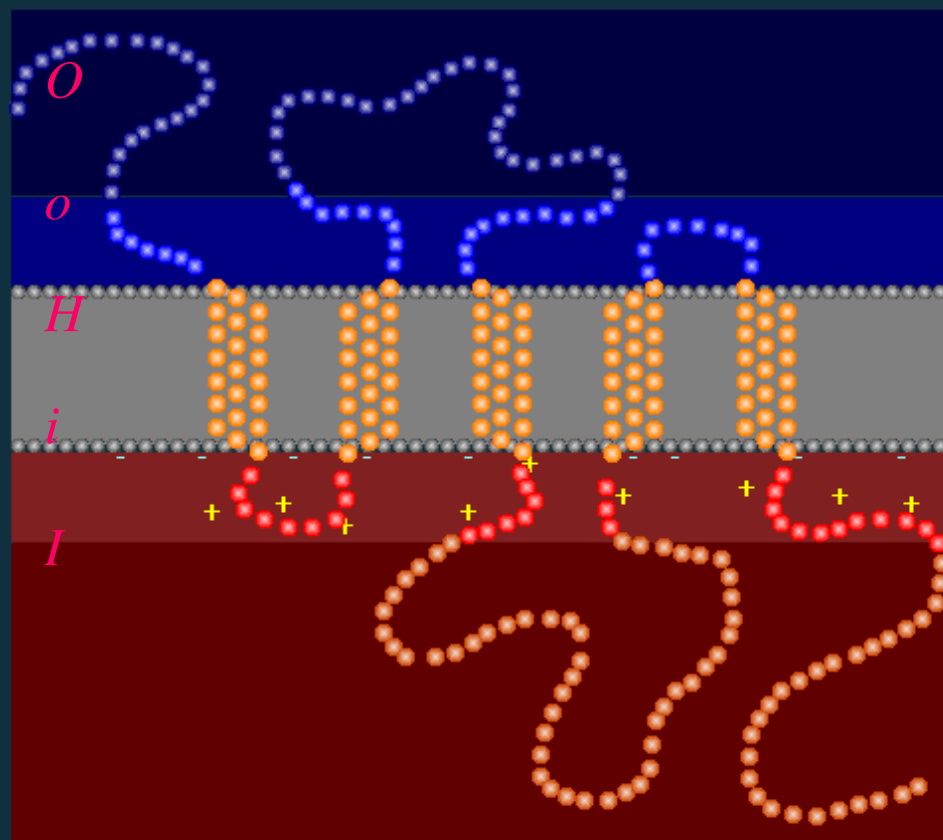
Ion csatornák

Hordozók

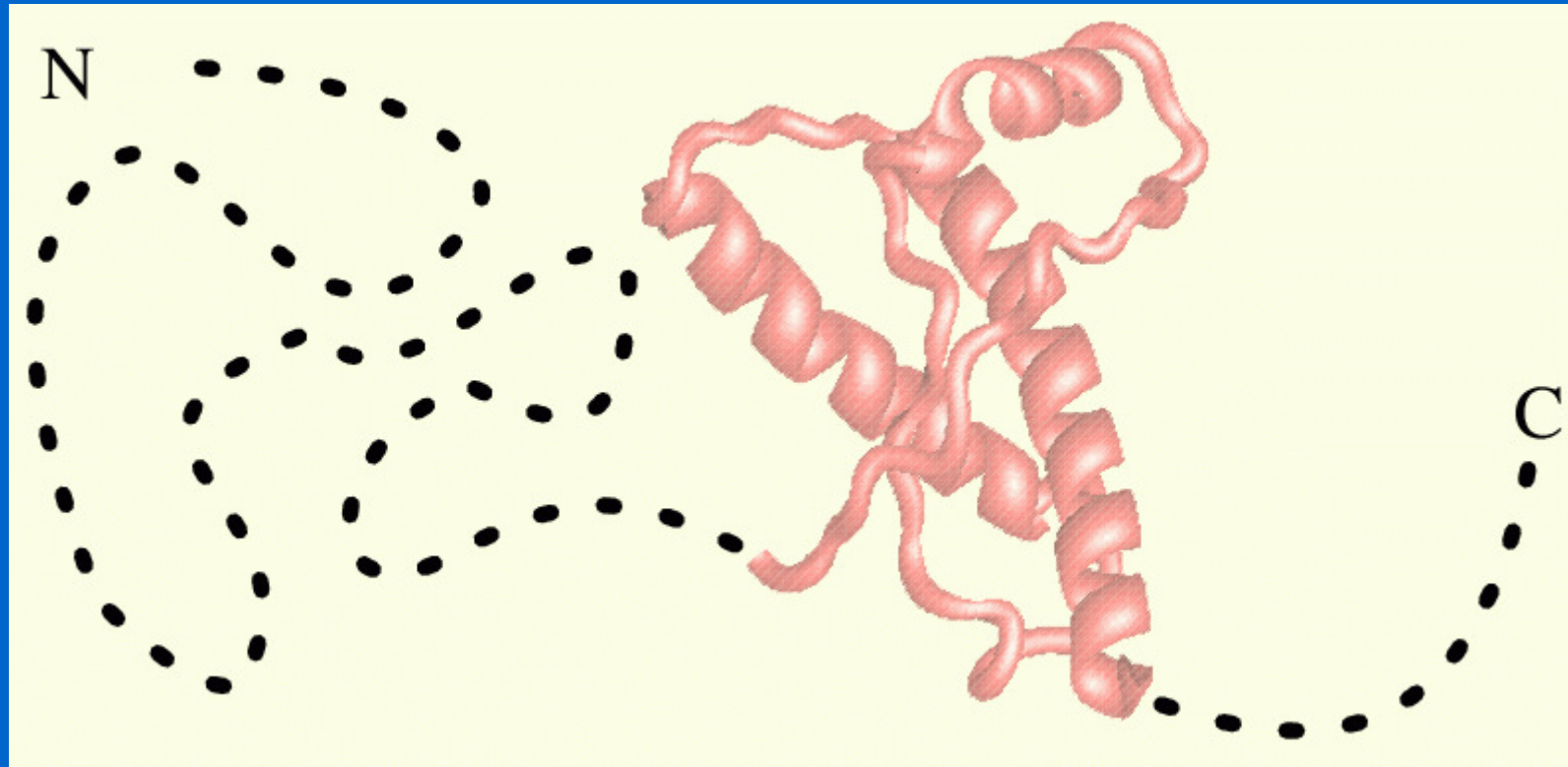
Információ csere

Receptorok

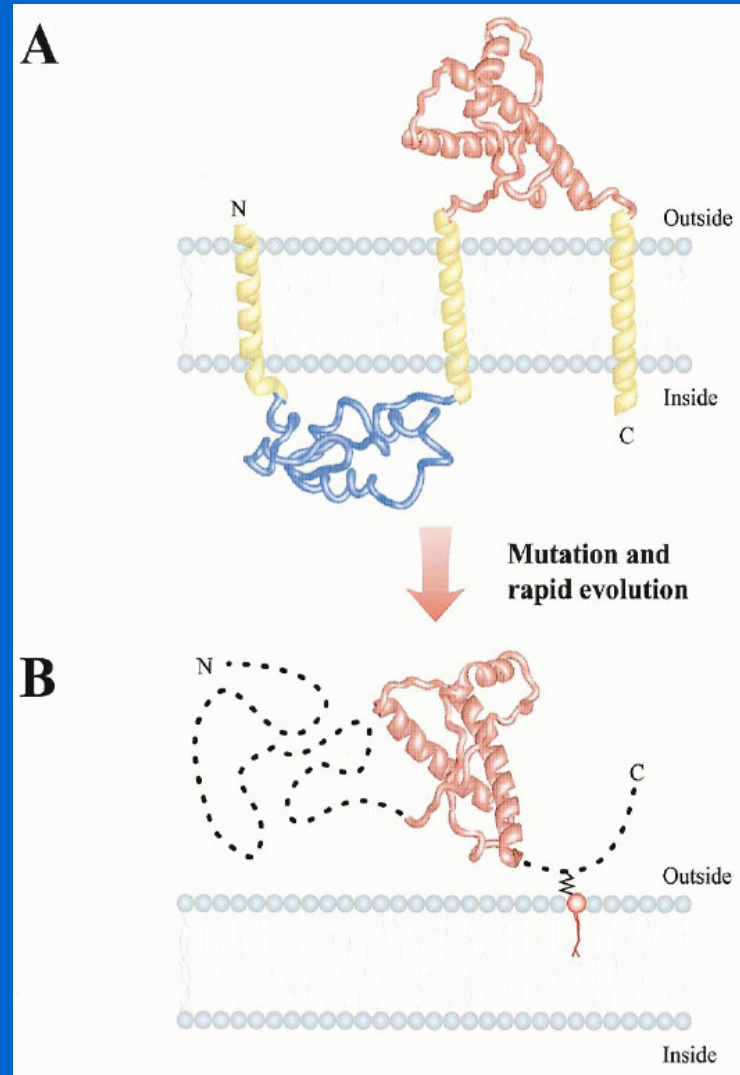
A HMMTOP eljárás



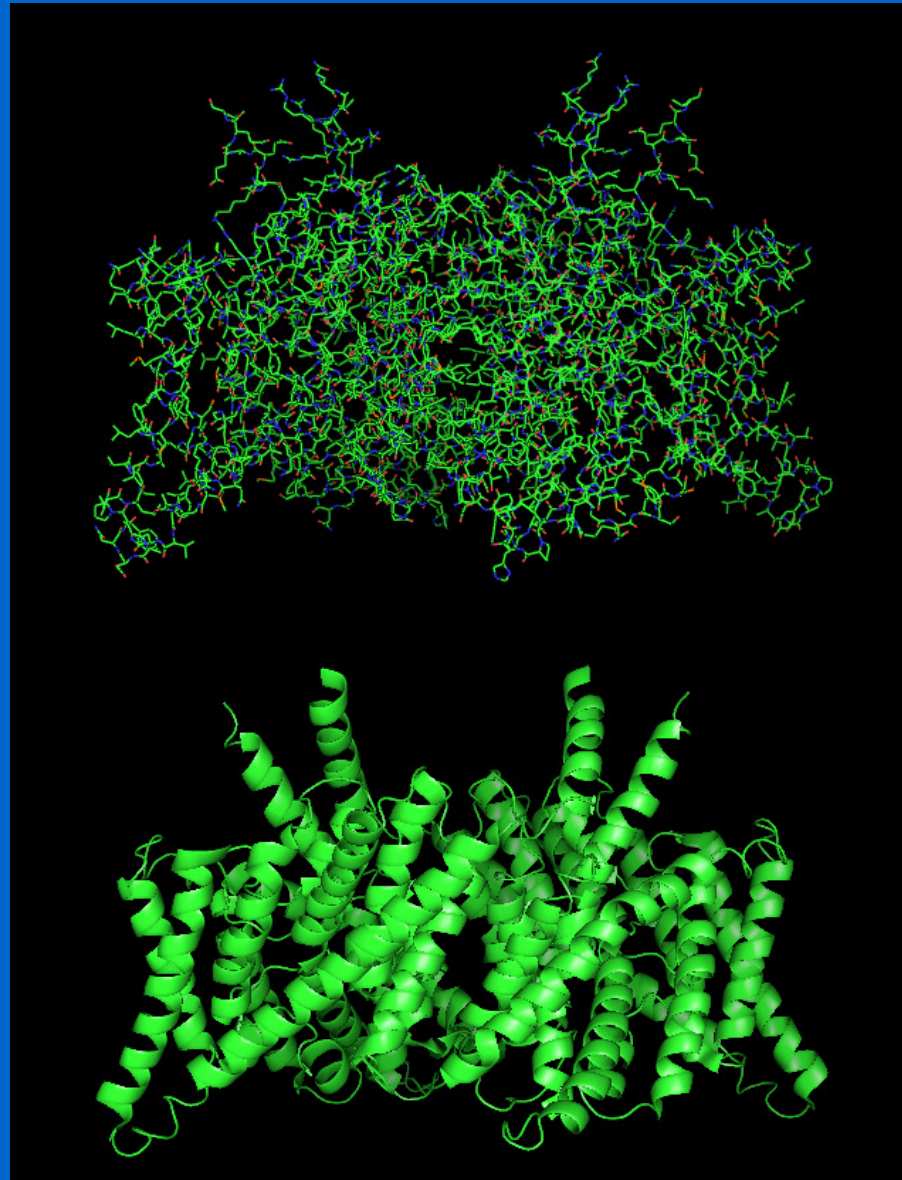
Prion protein



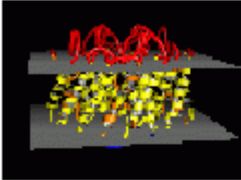
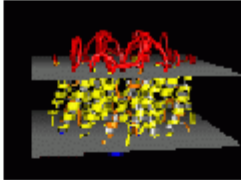
Prion fehérje



E. Coli klorid csatorna fehérje



Membrán pozíció lokalizálása transzmembrán fehérjékben

<u>1fqy</u>	Alpha helical protein
	
Chain 'A' has 6 transmembrane segments:	
Unknown	1-7 (MASEFKK)
Side 2	8-10 (KLF)
Transmembrane	11-31 (WRAVVAEFL..LFVFISIGS)
Side 1	32-49 (ALGFKYPVGNQTAVDN)
Transmembrane	50-69 (VKVSLAFGLSIATLAQSVGH)
Side 2	70-70 (I)
Membrane loop	71-85 (SGAHLNPAVTLGLLL)
Side 2	86-91 (SCQISI)
Transmembrane	92-112 (FRALMYIA..GAIVATAIL)
Side 1	113-137 (SGITSSLTG..LADGVNSGQ)
Transmembrane	138-156 (GLGIEIIGTLQLVLCVLAT)
Side 2	157-165 (TDRRRDLG)
Transmembrane	166-184 (GSAPLAIGLSVALGHLLAI)
Side 1	185-187 (DYT)
Membrane loop	188-201 (GCGINPARSEFGSAV)
Side 1	202-207 (ITHNES)
Transmembrane	208-230 (NHWIFWVGP..LAVLIYDFI)
Side 2	231-233 (LAP)
Unknown	234-269 (RSSDLTDRV..NSRVEMKPK)

A PDB_TM adatbázis



Protein Data Bank of Transmembrane Proteins

Welcome to the PDB_TM, the first comprehensive and up-to-date transmembrane protein selection of the [Protein Data Bank \(PDB\)](#).

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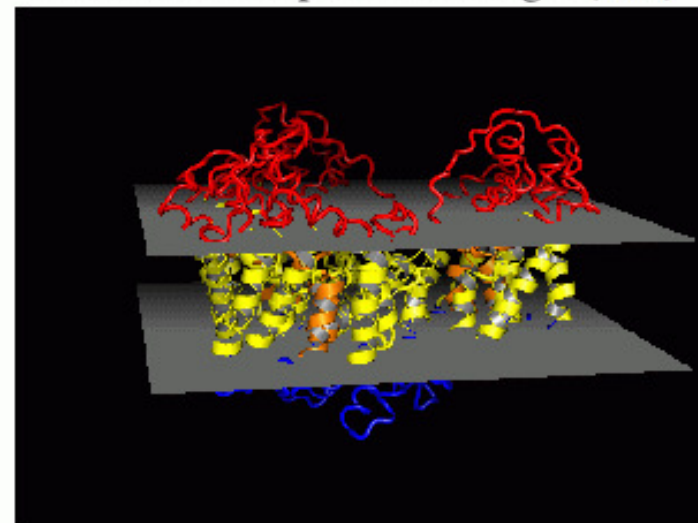
- 28957 structures,
- 459 transmembrane structures,
 - 339 alpha helical,
 - 92 beta barrel.

Last update: 18 Nov, 2004 .

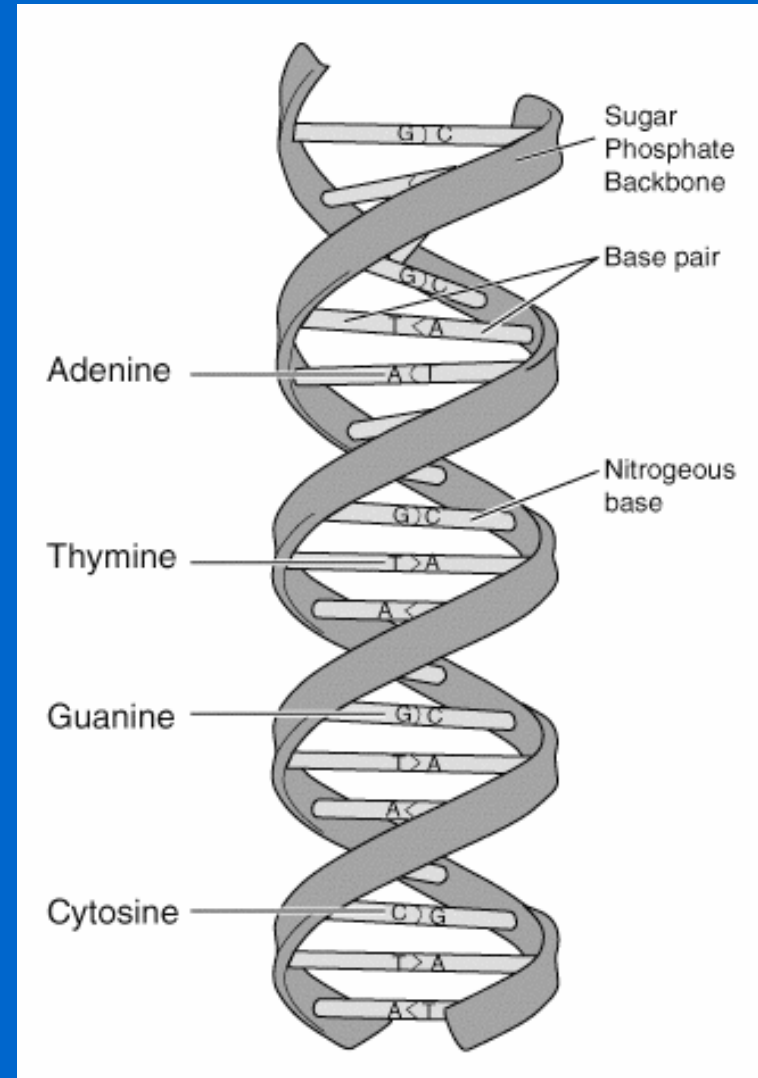
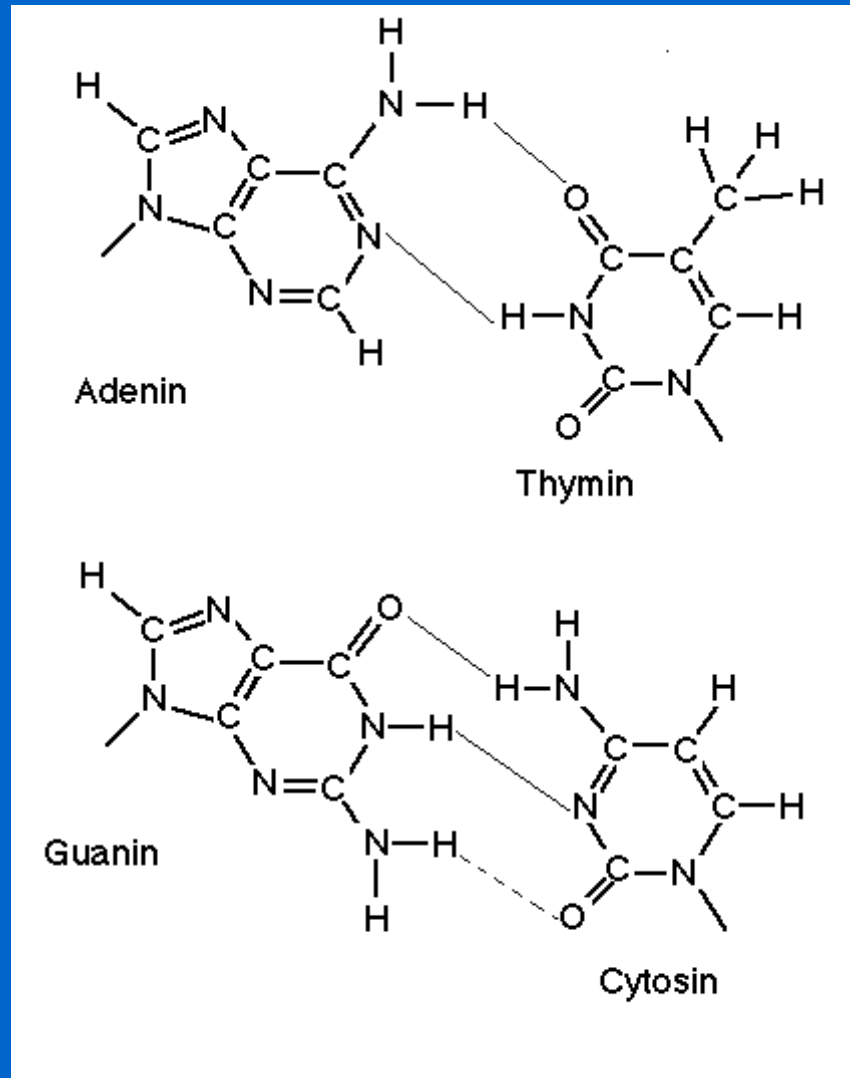
More [statistics](#).

Molecule of the month:

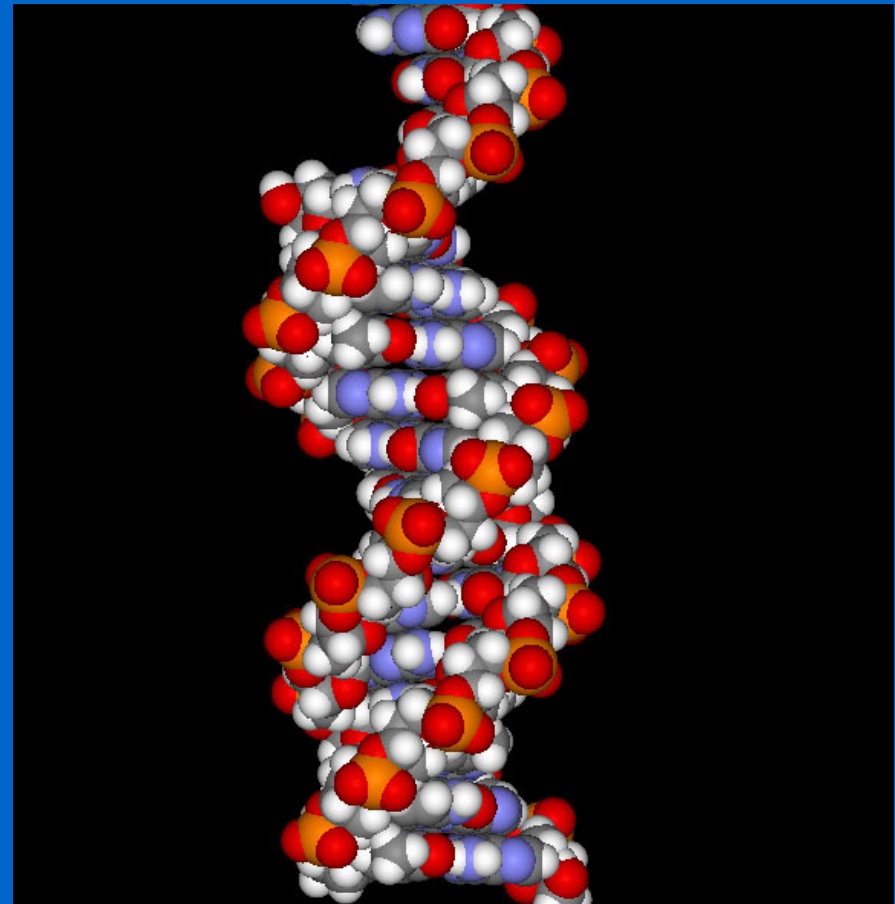
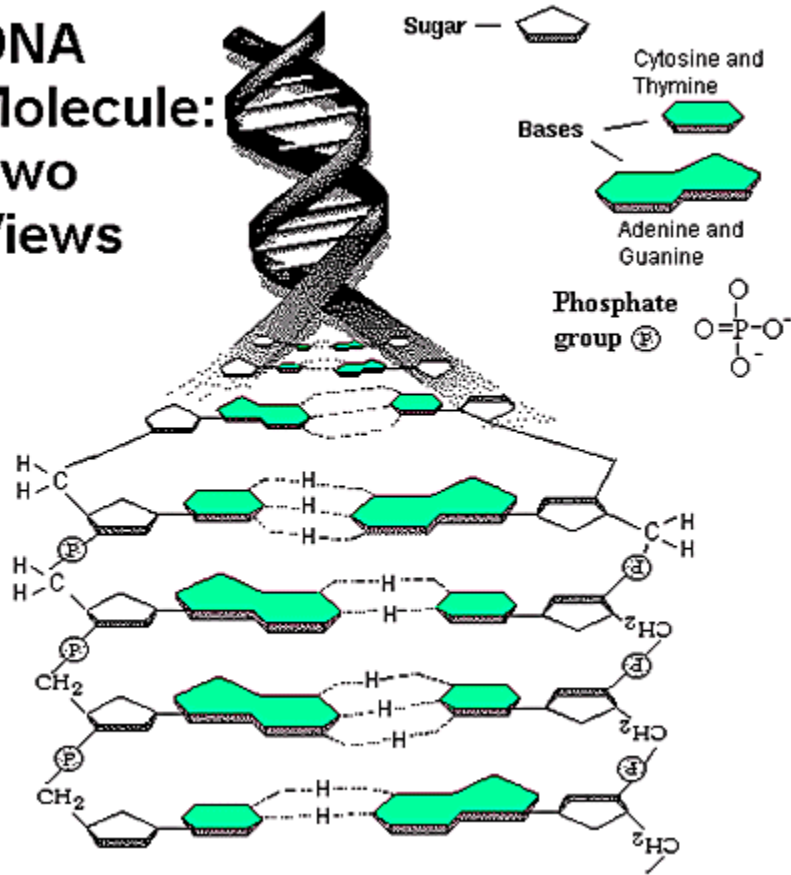
Glutamate transporter homologue ([1xfh](#))



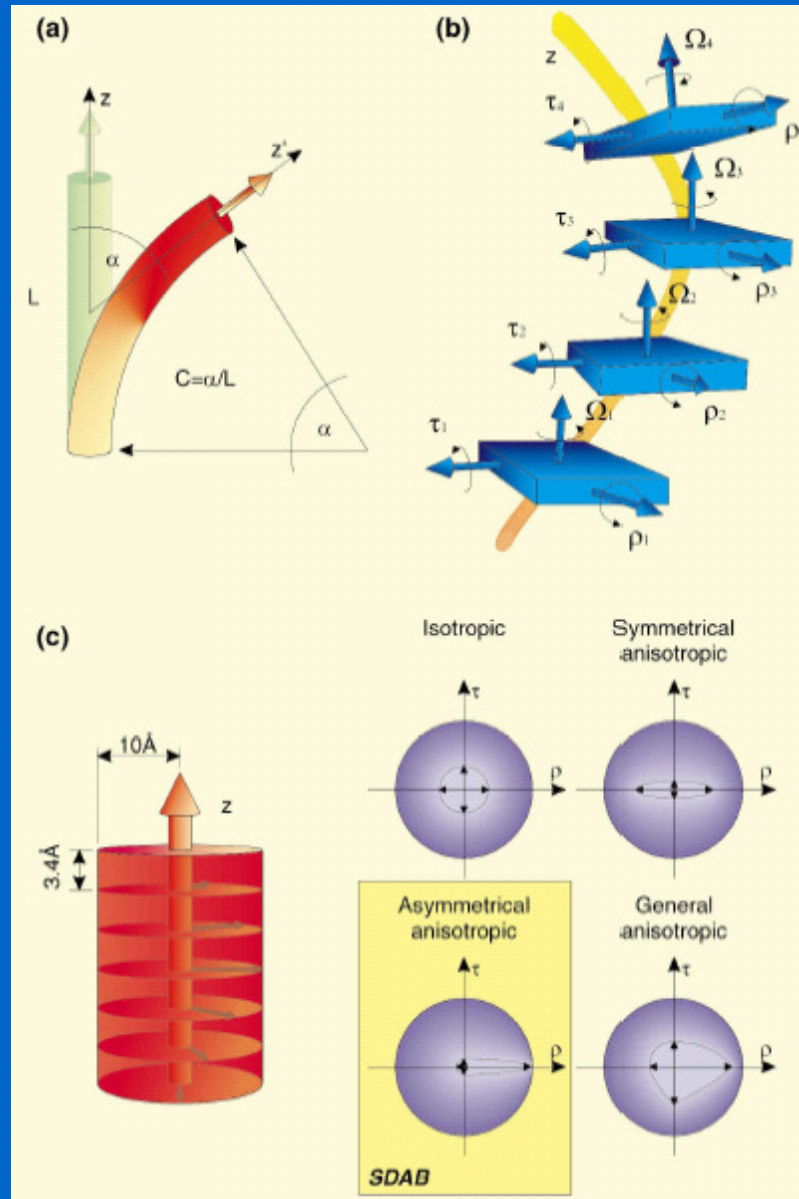
DNS



DNA Molecule: Two Views

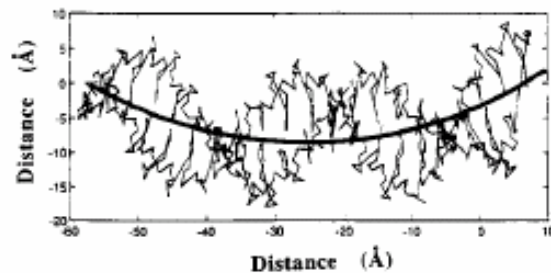
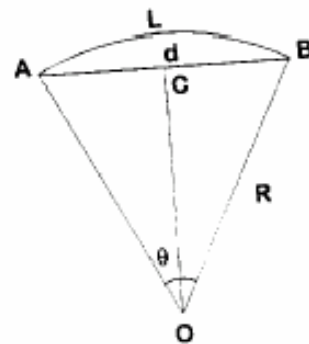
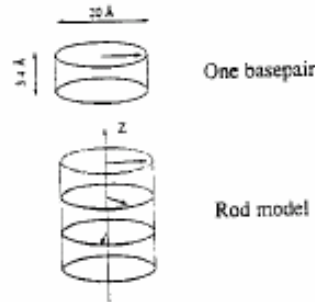


Inhomogén anizotróp rúd hajlítása



DNS hajlítás

A sequence-dependent anisotropic bending (SDAB) model of DNA



DNA stiffness (Young's modulus) scale for the trinucleotides in DNA [5]

Trinucleotide	Young's modulus, E (10^8 N/m ²)	Trinucleotide	Young's modulus, E (10^8 N/m ²)
AAA/TTT	7.176	CAG/CTG	1.668
AAC/GTT	6.272	CCA/TGG	6.813
AAG/CTT	4.736	CCC/GGG	3.868
AAT/ATT	7.237	CCG/CGG	5.440
ACA/TGT	3.810	CGA/TCG	3.810
ACC/GGT	4.156	CGC/GCG	4.678
ACG/CGT	4.156	CTA/TAG	2.673
ACT/AGT	6.033	CTC/GAG	3.353
AGA/TCT	3.410	GAA/TTC	4.214
AGC/GCT	3.524	GAC/GTC	3.925
AGG/CCT	4.445	GCA/TGC	2.842
ATA/TAT	1.613	GCC/GGC	2.448
ATC/GAT	5.087	GGA/TCC	3.581
ATG/CAT	2.169	GTA/TAC	3.467
CAA/TTG	3.581	TAA/TTA	2.955
CAC/GTG	3.239	TCA/TGA	1.447

Computed Young's modulus for Cro operators, mutants and non-operators

No.	Code	Sequences	E (10^8 N/m ²)	ΔG (kcal/mole)
<i>Operators</i>				
1	OR1	TACCTCTGGCGGTGATA	3.45	-15.4
2	OR2	CAACACGCACGGTGTTA	4.07	-14.1
3	OR3	TATCCCTTGGCGGTGATA	3.45	-16.1
4	OL1	TACCACTGGCGGTGATA	3.74	-15.5
5	OL2	TATCTCTGGCGGTGTTG	3.90	-14.9
6	OL3	AACCATCTGCGGTGATA	4.01	-14.4
<i>Operator mutants</i>				
7	OM1	TTTACCTCTGGCGGTGATAAT	4.30	-13.33
8	OM2	TTTACCTCTGGCGGTATTAAT	4.48	-13.11
9	OM3	TTTACCTCTGGCGGAGTTAAT	4.61	-13.26
<i>Non-operators</i>				
10	N1	TAAAACACCTCACGAGTTAAT	4.49	-13.40
11	N2	TAAATCACTCCCGGTATATT	4.22	-12.90
12	N3	TATATCAGTGGCAGTGTGAAT	3.60	-10.97
13	N4	TAGATCACCGCAGCGGTTGCT	3.88	-11.76
14	N5	TTCAGCACCGCTGATGCTGCT	3.40	-9.97

DNS-Cro fehérje kölcsönhatás

