

PERSONALIZED THERAPY – CHALLENGE FOR THE MEDICINE IN XXI CENTURY

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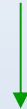
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DISEASES

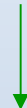


**N
A
T
U
R
E**

DNA



RNA



AA



3D



**BIOLOGICAL
ACTIVITY**



**DRUG
DESIGN**

MUTATIONS

MISFOLDING

MALFUNCTION

GENOMICS

Probability calculus
Gene identification
Comparative analysis
SNP identification

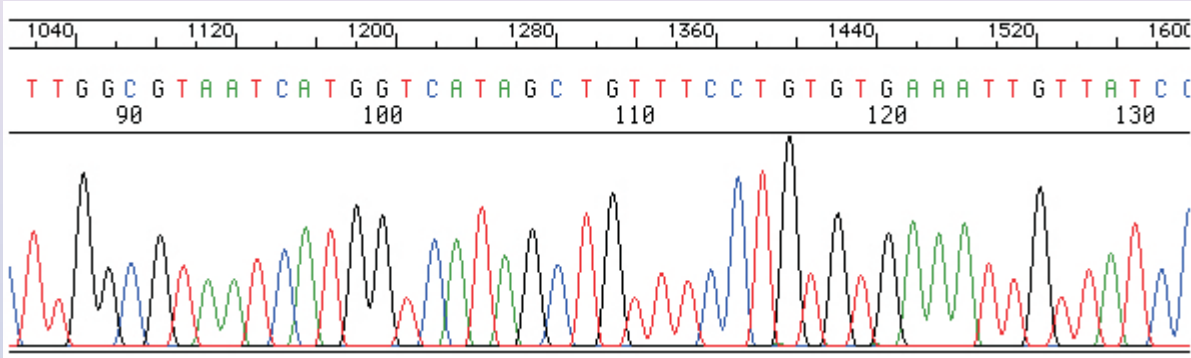
PROTEOMICS

Optimization procedures
Differential equations
Matrix theory

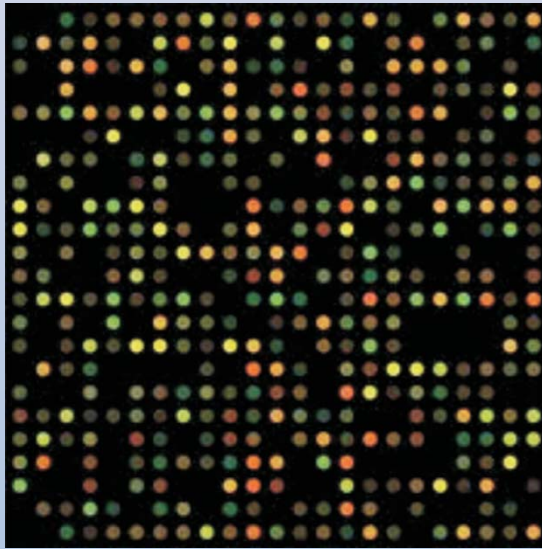
Protein structure prediction
3-D comparative analysis
Misfolding disease – Alzheimer
disease – improperly folded protein
is deprived of its natural biological
function

**THERAPY
DESIGN**

HUMAN



GENOMICS



DRUG DESIGN



PROTEOMICS

Chain 6 (691 residues)
 UniProt code: [P02788](#) (TRFL_HUMAN) [Plan] [Ensembl:gene]

CATH structural classification (4 domains):

Domain	Links	CATH no.	Class	Architecture
1		3.40.190.10	Alpha Beta 3-Layer (aba)	Sandwich
2		3.40.190.10	Alpha Beta 3-Layer (aba)	Sandwich
3		3.40.190.10	Alpha Beta 3-Layer (aba)	Sandwich
4		3.40.190.10	Alpha Beta 3-Layer (aba)	Sandwich

Sequence:
 1 5 10 15 20 25 30 35 40 45 50 55 60
 GRRRSVQCTVSQPEATKCPQWRMRKVRGFPVSCIKRDSPIQCIGATAENRQAVTLQ
 61 65 70 75 80 85 90 95 100 105 110 115 120
 QGFTYENGIAPIPKLRFVAAEYVGERQPRTHYAVAVVHKGSFQLNELGQLKSGHGLR
 121 125 130 135 140 145 150 155 160 165 170 175 180
 FFFY
 FKGNNPIGTLRPFPLNWTGPEPEIENAVRFPSSASVKGADKQFPNLCRLGAGTGENK
 181 185 190 195 200 205 210 215 220 225 230 235 240
 CAPSSQEPYPSYSGAFKCLRDGAGVAFIRSTVFEDLSDDAERDVEYLICPQNRKQVD
 241 245 250 255 260 265 270 275 280 285 290 295 300
 KFKDCHLAVPSHVVAVRSVNGKEDAIDNLLRQAQEKFGDKSKPKPOLFSQPSQKQLLF
 301 305 310 315 320 325 330 335 340 345 350 355 360
 KDGATGFSRVPPRIIDGLYLGGVYPTAIQNLRKSEEDVAARRARVVCAGVQDELKCNQ