

Nové léčebné terapie a jejich analytika

Jak pandemie urychlila vývoj genových terapií

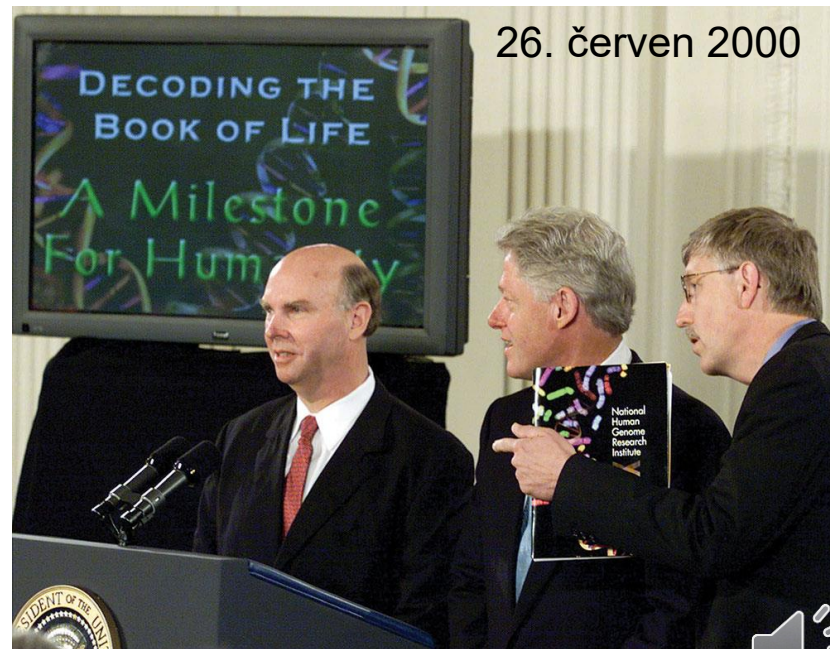
Martin Gilar

23. 11. 2021, Vize 2021



Příslib genových terapií

- Známe generický kód - můžeme léčit jakoukoliv nemoc
- Obecný mechanismus - specifický DNA cíl
- Nejen léčit – vyléčit!
 - Oligonukleotidy (AON, siRNA)
 - mRNA
 - Virové vektory
 - Crisper/Cas 9
 - Modifikované T buňky (CAR-T)
- Individuální terapie
- Vzácné nemoci
- Běžné nemoci



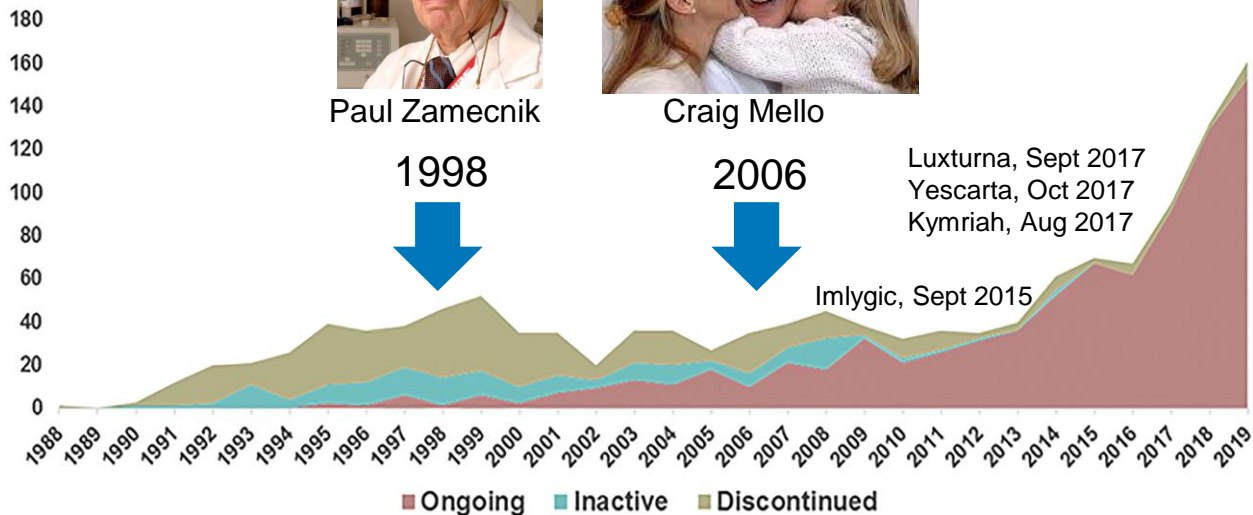
Nové genové terapie



Paul Zamecnik



Craig Mello

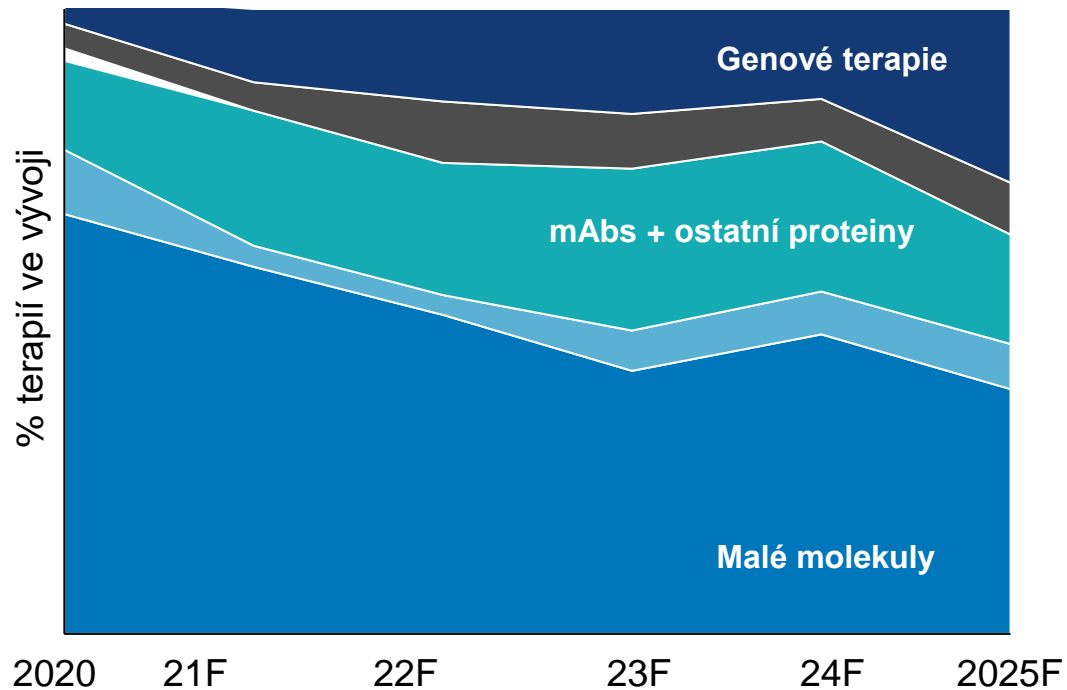


- **Vyřešené problémy:**
- **Syntéza a biosyntéza**
- **Doprava do buněk a orgánů**
- **Stabilita**
- **Vedlejší účinky a toxicita**
- **Analytické metody**

“Clinical Development of Gene Therapies: The First Three Decades and Counting” Lapteva, et al. 2020.



Nové terapie vstupují na scénu



- Genové terapie
- Buněčné terapie
- mAbs + ostatní proteiny
- Jiné
- Malé molekuly



Co jsou to Nové Modality?

Traditional Biotherapeutics



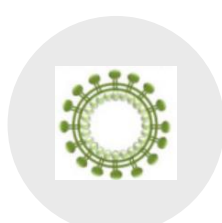
mAb & mAb fragments

150 kD, <150kD



Antibody-Drug Conjugates

~152 kD



Virus Like Particles

No viral genome



Proteins & Peptides

Peptides < 6 kDa



Bispecific & Trispecific mAb, Fusion proteins

Bi & Tri mAb > 150 kDa

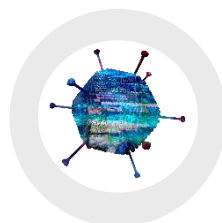


pDNA

607 kDa (1000 bp)

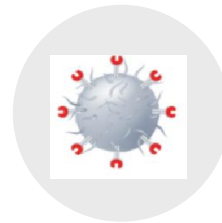
Foundation of biosynthesis; emerging therapeutic/vaccine

Emerging New Modalities / Advanced Therapies



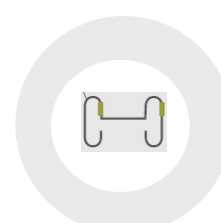
Viral Vectors

Gene Therapy
AAV(ø20nm): 3700 kDa
Adenovirus & Lentivirus (ø90 nm)



Cell Therapy

Most common, CAR-T autologous or allogeneic cells



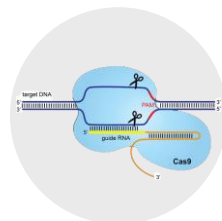
Transgene

Genetic material delivered for CGT



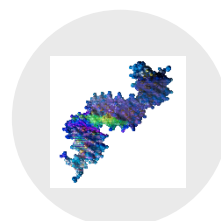
mRNA

960-1600 kDa (300-5000 nt)
cell-free bioprocess



CRISPR Cas

Gene Editing,
gRNA, 100 nt, 32.2kDa
Cas protein 163 kDa



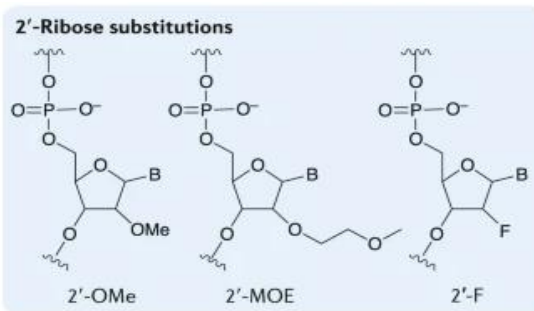
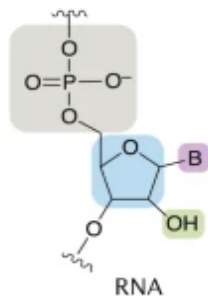
Oligos

Gene Silencing
siRNA, RNAi, ASO
21-23nt; 6.9-7.5kDa

Antisense oligonukleotidy, siRNA, miRNA



[Frontiers in Bioengineering and Biotechnology](#)



Zdroj: [Nature. 2020](#)



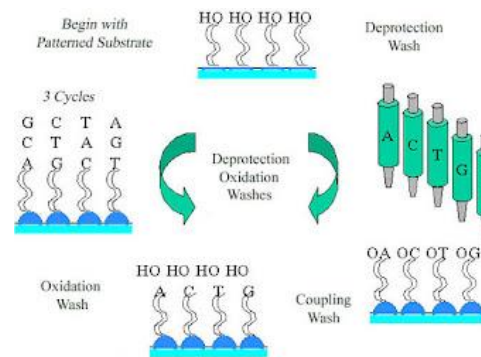
www.youtube.com/watch?v=uiObPBeof5s

Richard Jorgensen
Craig Mello, Andrew Fire

Umíme selektivně zapnout a
vypnout geny



Syntéza oligonukleotidů – revoluce v biotechnologii



5' 3'

UUC UGU AAU CUC UUG UCU ATT (N)

UUC UGU AAU CUC UUG UCU ATT (N-1)

UUC UGU AAU CUC UUG UCU ATT (N-2)

UUC UGU AAU CUC UUG UCU ATT (N-3)

UUC UGU AAU CUC UUG UCU ATT (N-4)

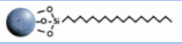
UUC UGU AAU CUC UUG UCU ATT (N-5)

UUC UGU AAU CUC UUG UCU ATT (N-6)


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Chromatografické metody analýzy oligonukleotidů



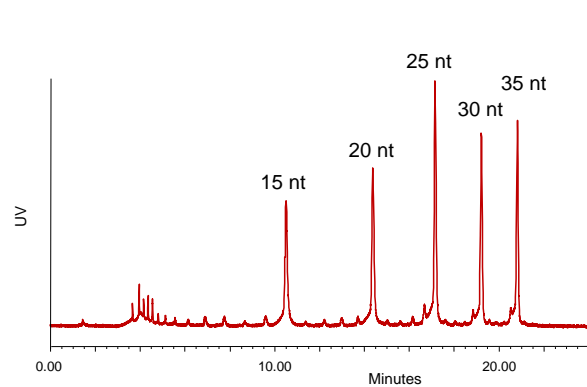
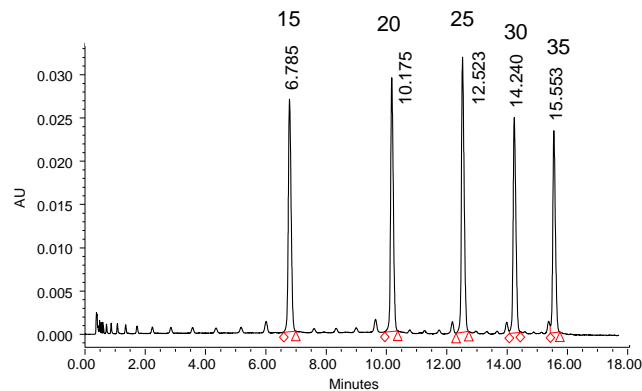
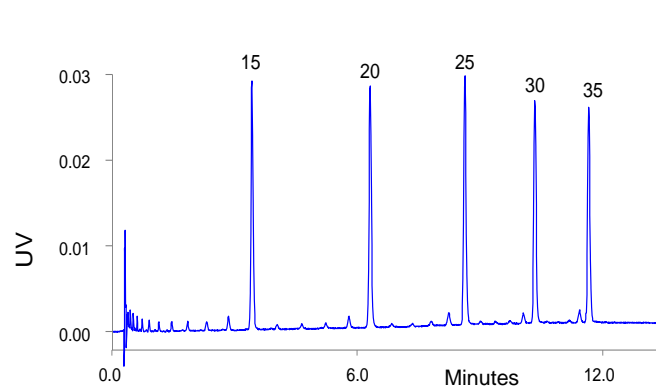
Reversed Phase
Ion Pairing



HILIC

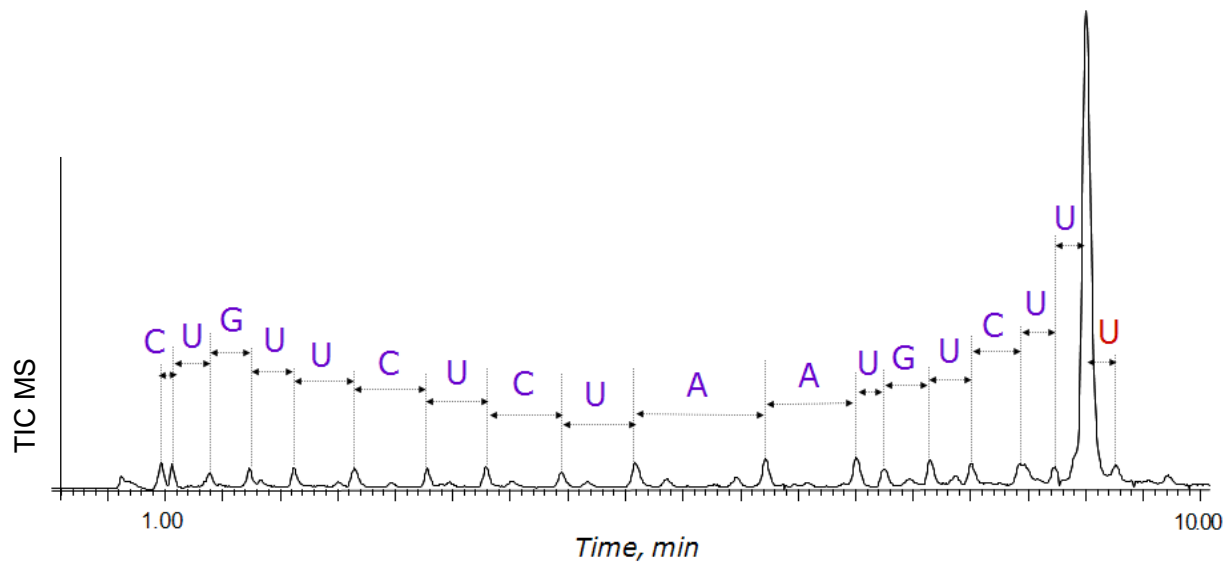


Anion Exchange



5' UUC UGU AAU CUC UUG UCU ATT 3'

RNAi
21-mer

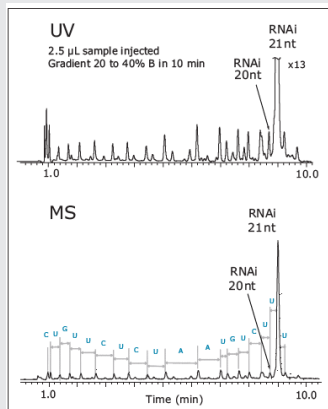


V. Ivleva, Y.Q. Yu, M. Gilar, RCM 2010, 24, 2631

Examples of Application Notes for Oligonucleotides

Additional Application notes in the Waters' *"Application Solutions for Oligonucleotides"*

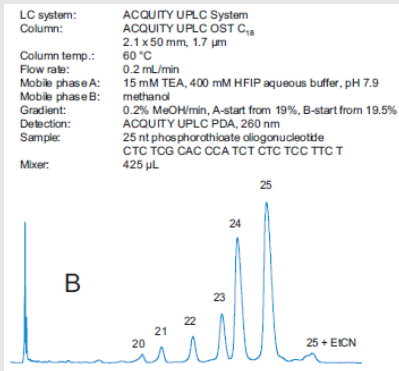
UPLC-MS Analysis of Interfering RNA Oligonucleotides



Detection and quantitation of process-related impurities from synthesis as well as modification or truncations of the oligonucleotide.

<https://www.waters.com/webassets/cms/library/docs/720002873en.pdf>

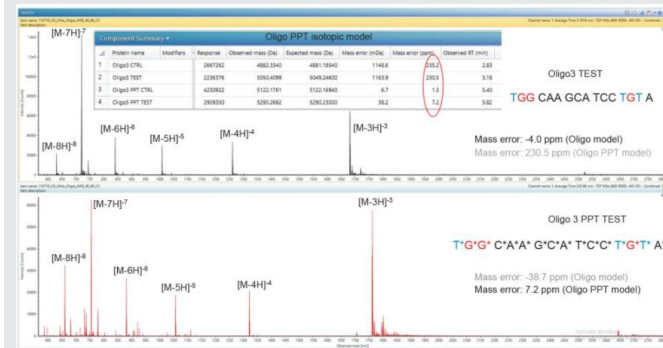
UPLC Analysis of Phosphorothioate Oligonucleotides: Method Development



A single analysis method applied to antisense oligonucleotides that replaces the need for multi-step post purification methods.

<https://www.waters.com/webassets/cms/library/docs/720002873en.pdf>

Modified Oligonucleotides – intact analysis



Compliance Ready LC-MS workflow for mass confirmation for unmodified and extensively modified oligonucleotides using the BioAccord.

[Intact Mass Confirmation Analysis on the BioAccord LC-MS System for a Variety of Extensively Modified Oligonucleotides](#)



Technologie CRISPR-Cas9 – permanentní editace genů

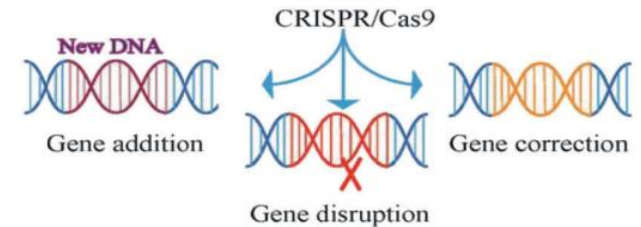
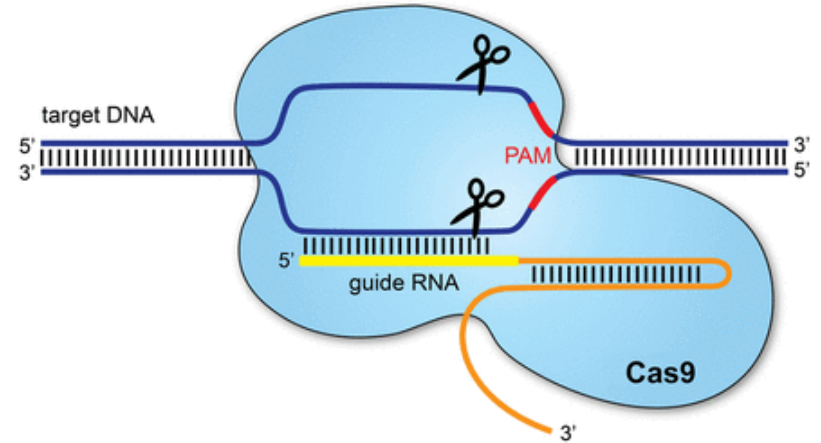
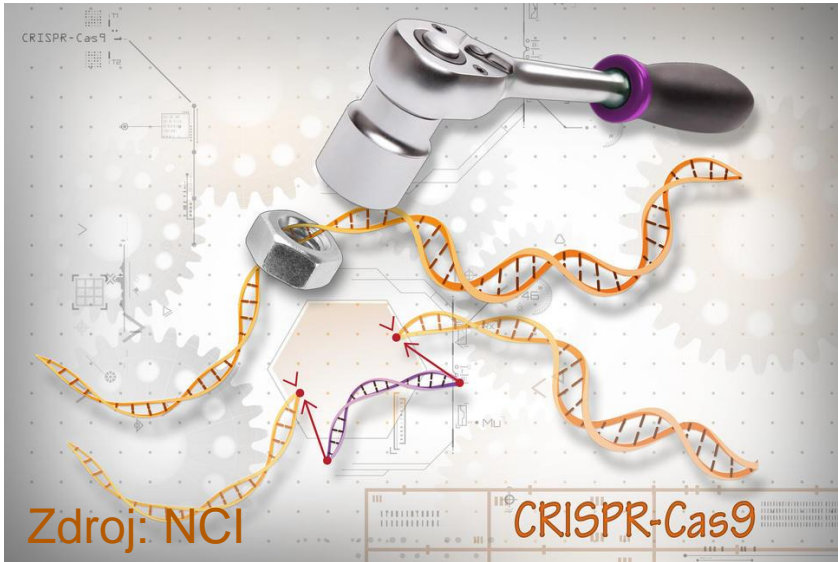
Clustered Regularly Interspaced Short Palindromic Repeats

Bakteriální obranný mechanismus – „genetická paměť“

Cas9 – nukleáza, štípe dsDNA

100 mer guideRNA (gRNA) – určí štěpné místo

Jennifer Doudna 2020 Nobel prize



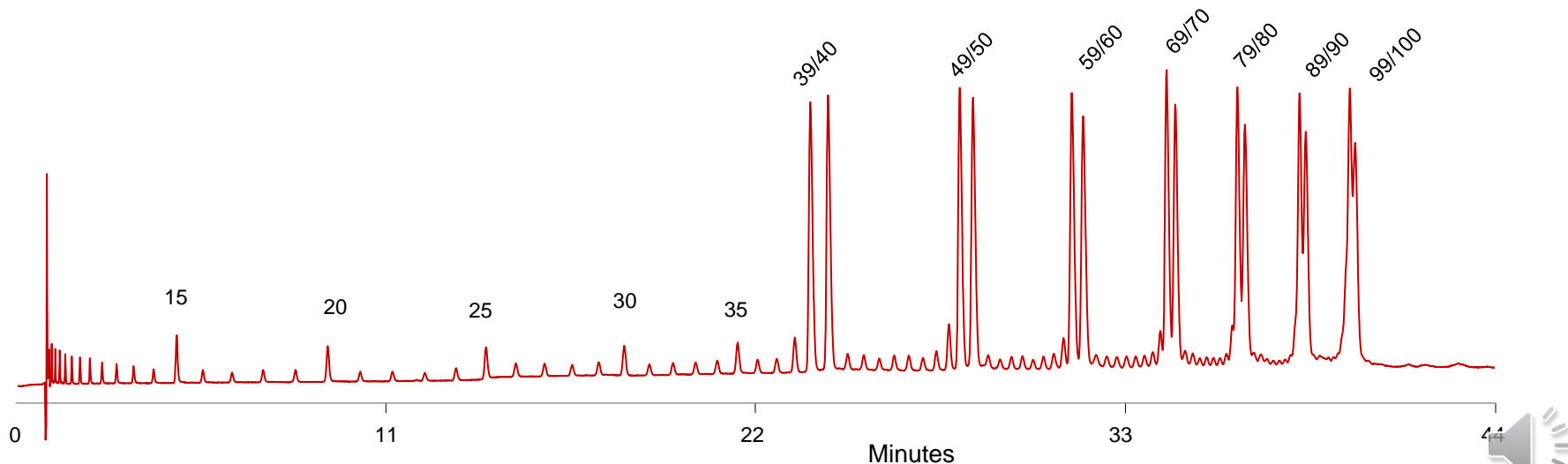
Separace 5-100 dT oligonukleotidů

ACQUITY PREMIER Oligonucleotide BEH C18, 130 Å, 1.7 µm, 2.1 x 150 mm column

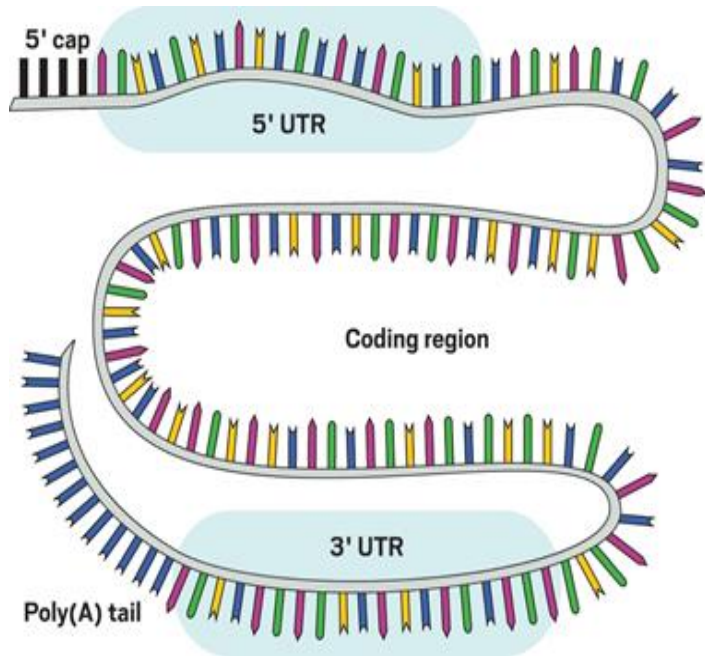
Mobile phase A: 100 mM Hexylammonium acetate pH 8 (HAA) : MeCN, 75 : 25 (v:v)

Mobile phase B: 100 mM HAA : MeCN, 25 : 75 (v:v)

Conditions: 60 °C, 0.4 mL/min, UV 260 nm, gradient 15-50% B in 60 minutes



Anatomie mRNA - principy mRNA technologie

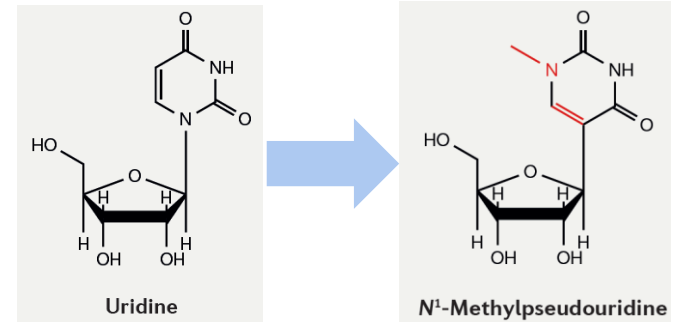
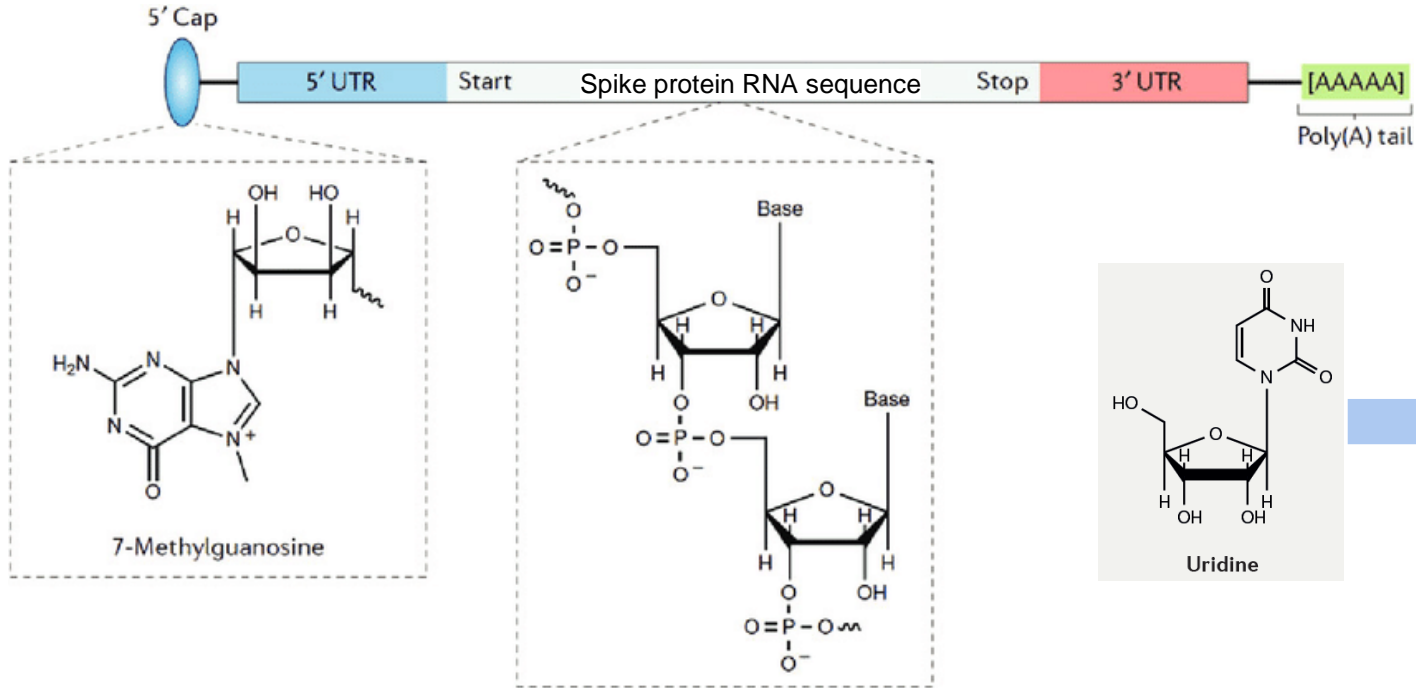


- 1970' – struktura a funkce 3' polyA konce
- 1970' – struktura a funkce 5' “čepice”
- 1985 – biosyntéza mRNA (T7-RNA polymeráza)
- 1987 – komercializace PCR a Taq polymerázy
- 1980-2010' – vývoj lipidových nanočástic
- 2005 – modifikovaná mRNA - minimálně imunogenní
- 2014 – mRNA technologie funguje



Katalin Karikó (BioNtech)

Struktura Covid 19 mRNA – mRNA syntetizuje Spike protein

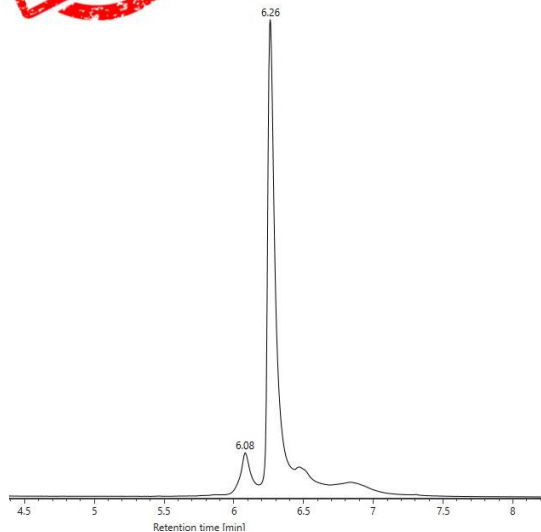


LC-UV Chromatograms of mRNA using IP-RPLC

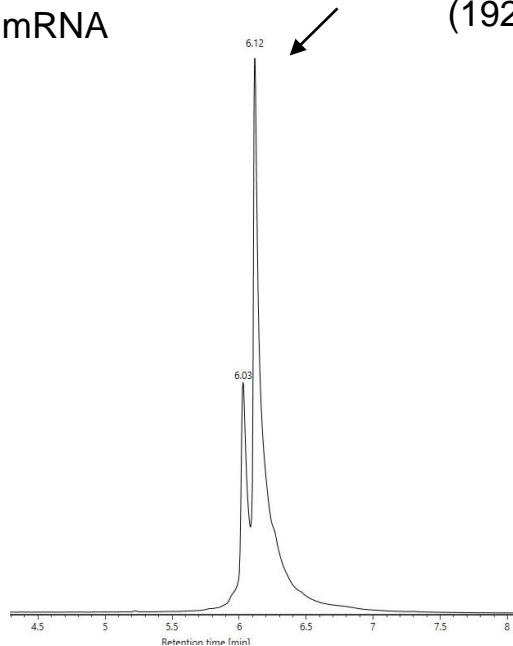
ACQUITY Premier Oligonucleotide Column, 2.1 x 50 mm, 1.7 μ m, 130 Å, DIPEA/HFIP Mobile Phase System



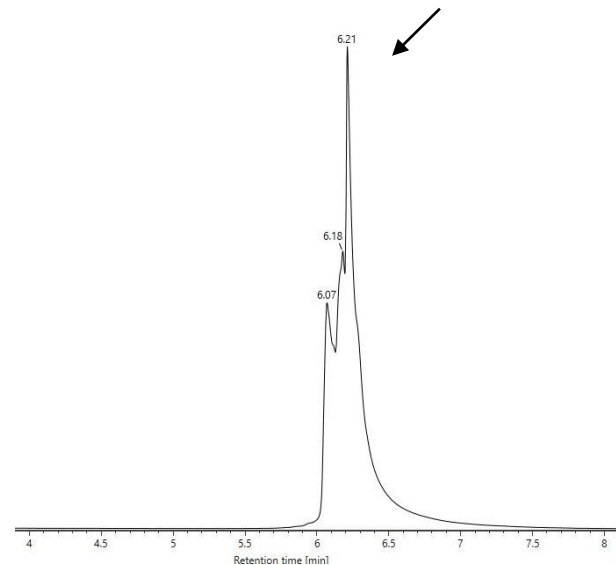
TriLink EPO (human erythropoietin) mRNA (858 nt)



TriLink Luc (firefly luciferase) mRNA (1929 nt)



TriLink Cas-9 (CRISPR associated protein 9) mRNA (~ 4,521 nt)

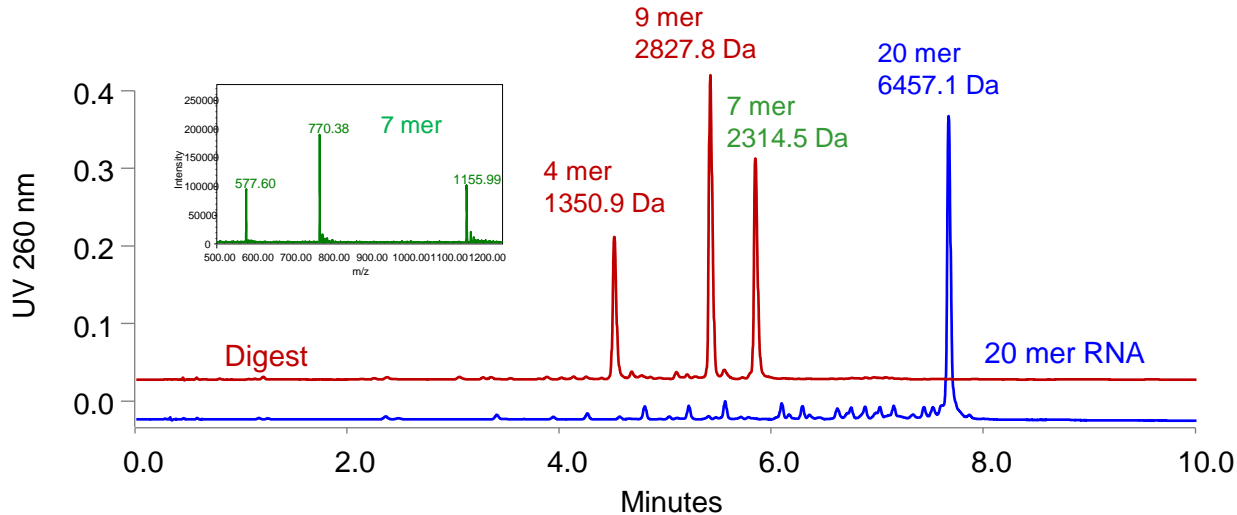


Data: Catalin Doneanu

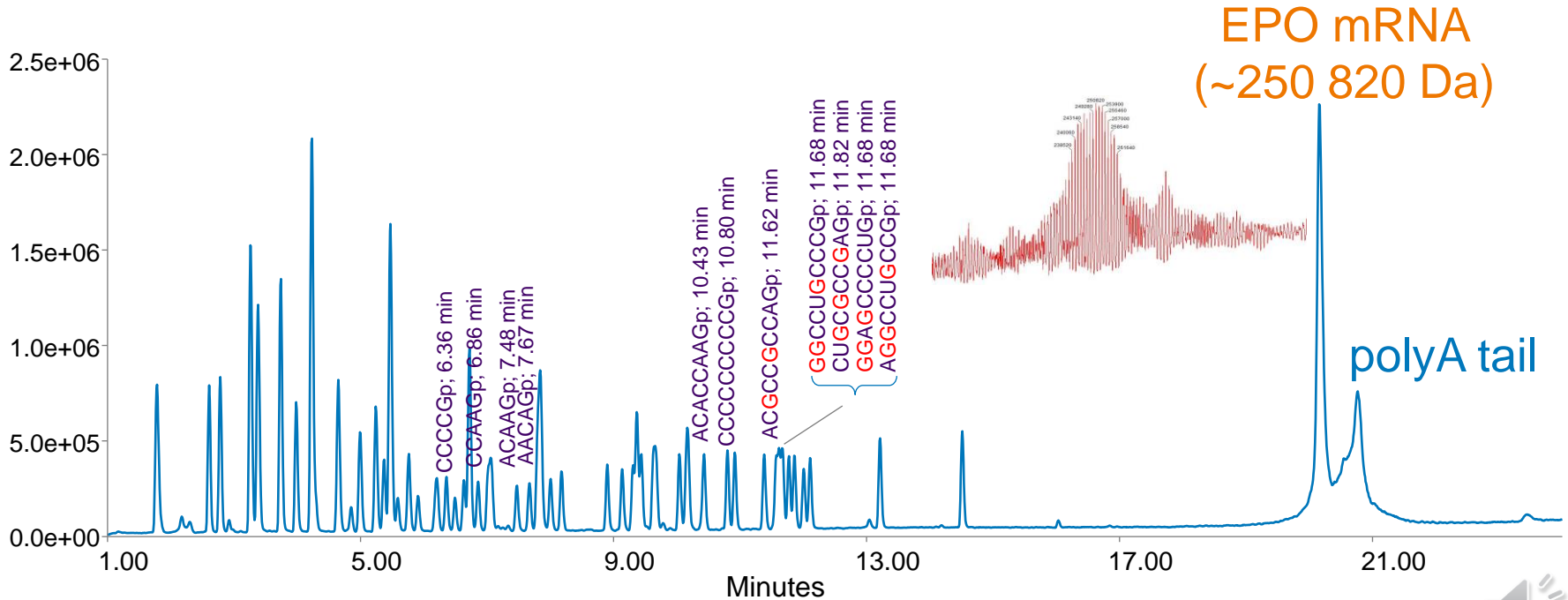


HILIC analysis of RNase T1 digest

rArArArGrArArArArCrArGrArArArUrArArATT	20 mer, 6457.1 Da
rArArArG-PO ₃ H	4 mer, 1350.9 Da
rArArArArCrArG-PO ₃ H	7 mer, 2314.5 Da
ArArArUrArArATT	9 mer, 2827.8 Da

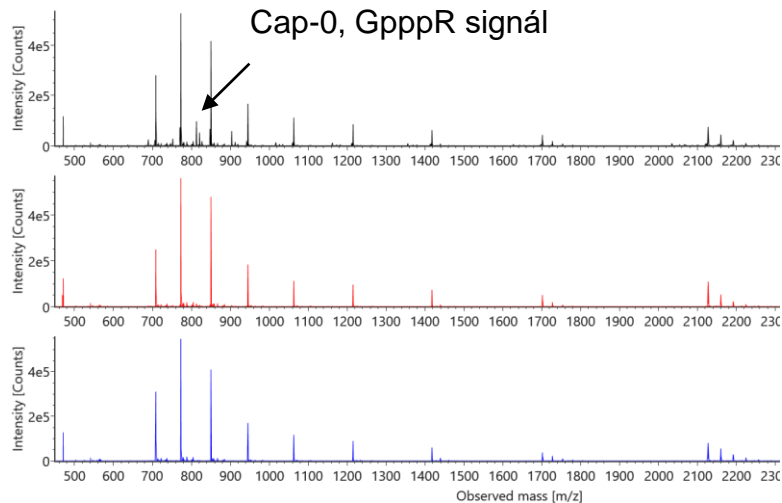
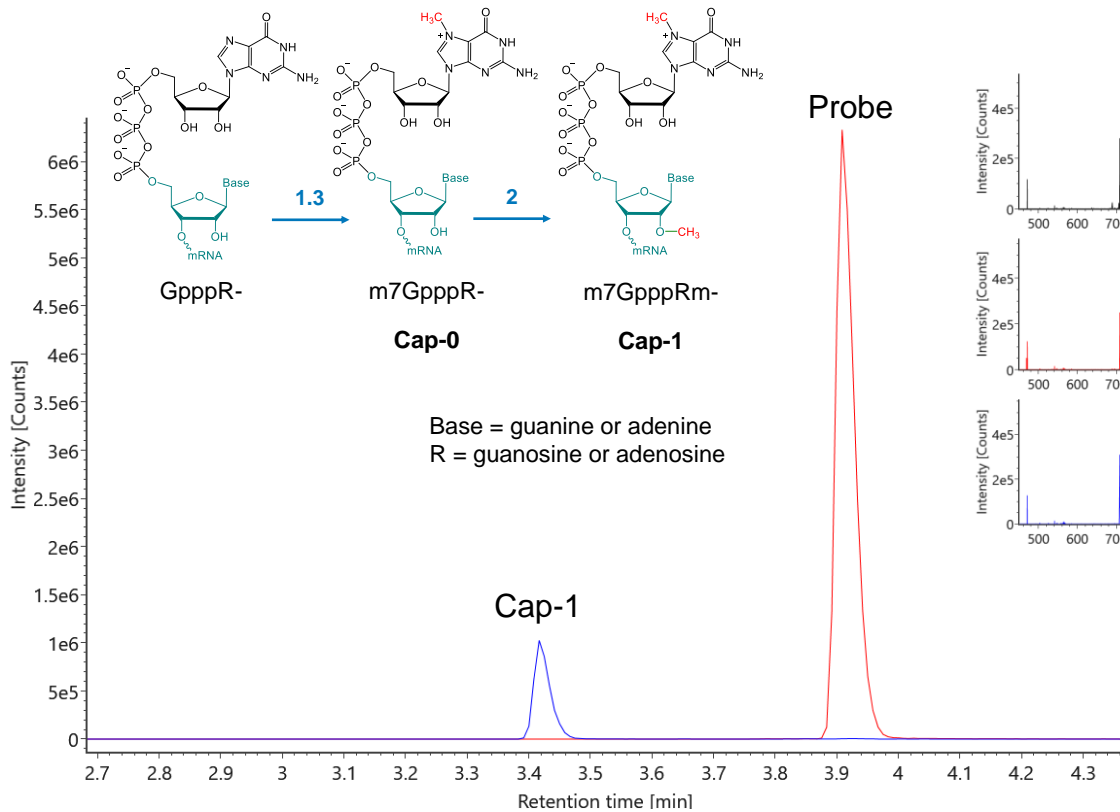


EPO mRNA mapping – RNase T1 digest

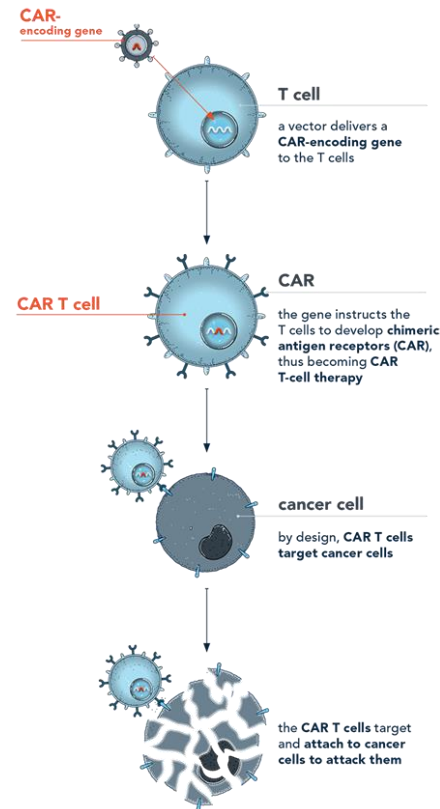
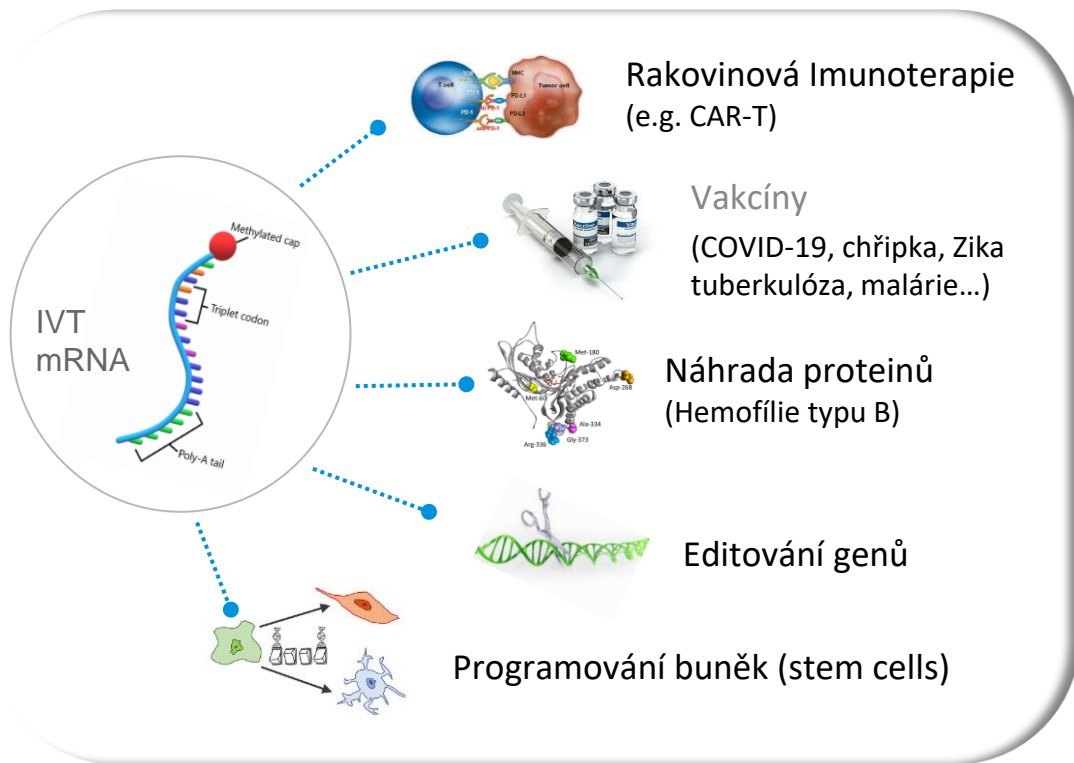


LC MS data: Catalin Doneanu

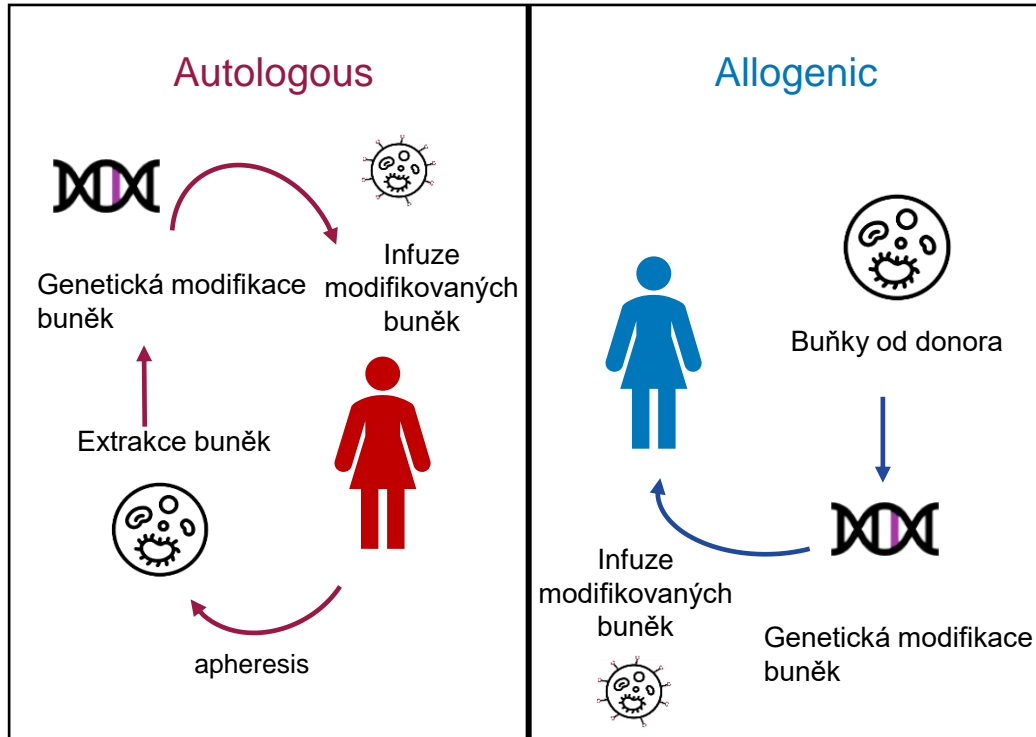
RNase H digest, 5'Cap LC-MS analysis



mRNA vakcíny: Úspěch otevírá dveře dalším terapiím



CAR-T: Chimeric antigen receptor T-cell

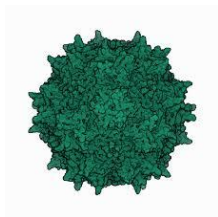


- Ex-vivo modifikace
- Pouze T-buňky (T-lymfocyty) jsou modifikovány; mRNA vyprodukuje CAR protein
- mRNA je meziprodukt pro ssDNA kódující Crispr-Cas9 komplex. ssDNA je vložena do T-lymfocytů. Crispr-Cas9 přeprogramuje buňku na CAR T-cell
- Ex-vivo postup minimalizuje možnost nežádoucí genové změny „mimo cíl“ - v jiných typech buněk
- 5 komerčních Car-T terapií

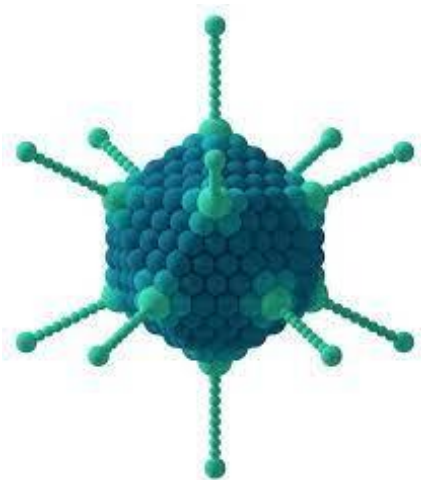


Anatomie virových vektorů

DNA je vložena do buněčného jádra



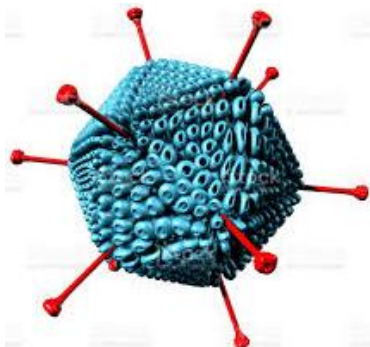
- **Adeno Associated Viry (AAV)**
- Malé nepatogenní viry, hmotnost 4.8 MDa (ekvivalent 32 mAb)
- AAV se skládá z 60 proteinů
- VP1:VP2:VP3 ~ 5:5:50
- VP MW: 60, 67, 82 kDa; 25 nm, velikost 2.5x mAb
- Nálož ssDNA, 4.5 kb limit



- **Adeno Viry (AdV)**
- Středně velké viry, hmotnost 150 MDa (ekvivalent 100 mAb)
- AdV se skládá z 252 proteinů, 240 hexonů, 12 pentonů
- 129 kDa, 51.1 kDa; velikost 90-100 nm, 4x mAb
- Nálož dsDNA, 32-43 kb
- Sputnik V (AdV26, AdV5), Janssen (AdV26), AstraZeneca (AdV26)



Analýza virových částic



Zdroj: istockphoto.com

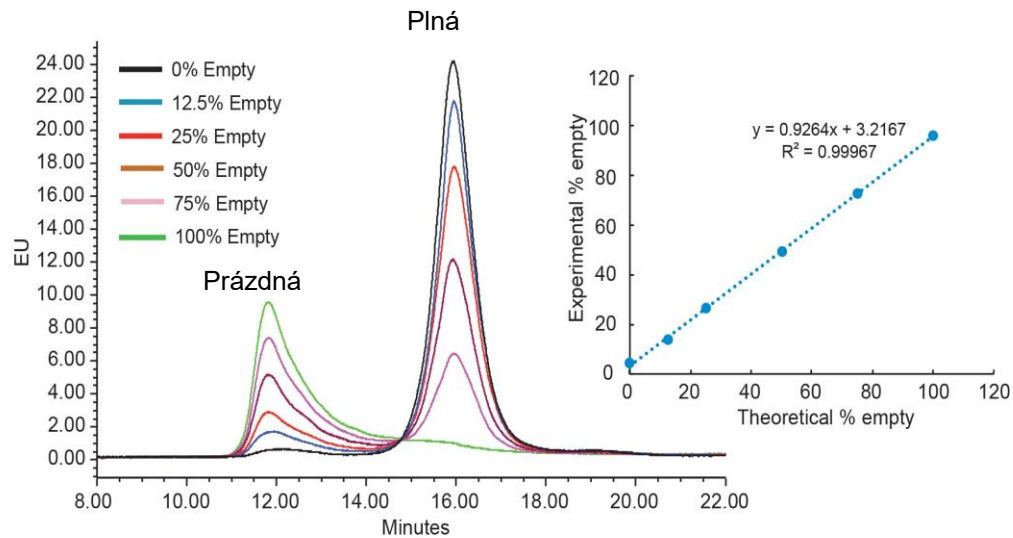
Prázdná
AAV obálka



Nekompletní
DNA obsah



AAV s
cílovou DNA

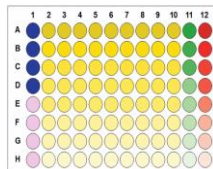


Hua Yang et al., Waters 720006825

LC and LC/MS technologie pro kontrolu AAV terapii

ELISA

Anti-Capsid Antibody Binding



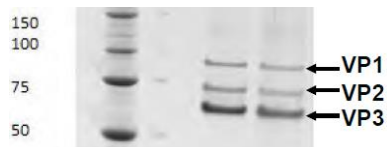
AUC

Measure difference in Sedimentation Coefficient



SDS-PAGE

Measure difference in separation profile



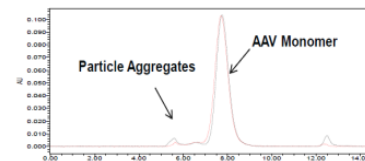
Western Blot

Resource intensive



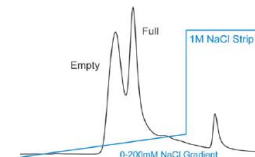
SEC-FLR-UV

Purify and measure intrinsic fluorescence



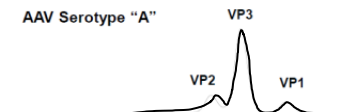
IEX-UV

Measure difference in surface charge profile



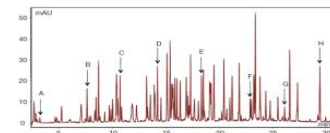
RPLC-UV-MS

Measure difference in hydrophobicity profile

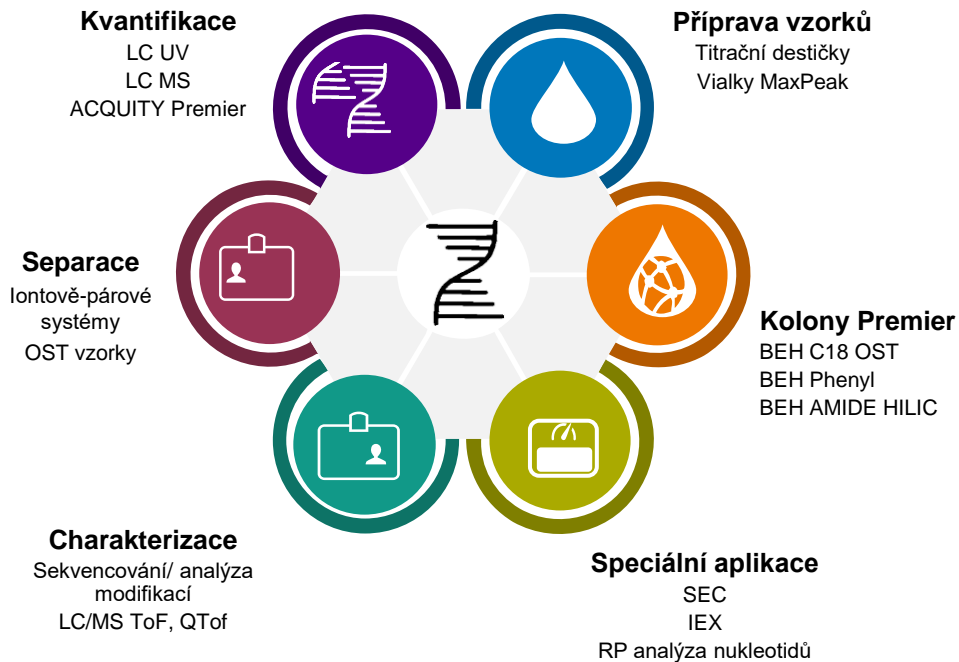


Peptide Mapping

AA sequence and PTMs



Analýza oligonukleotidů a nukleových kyselin



Acquity™ PREMIER



MAXPEAK™
HIGH PERFORMANCE SURFACES

BEH technology



MassPREP Standard:
Quality Control Reference
Material (QCRM)



Analyza nukleových kyselin s HPS technologií

High Performance Surfaces (HPS)

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analytical
chemistry

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Article

Using Hybrid Organic–Inorganic Surface Technology to Mitigate Analyte Interactions with Metal Surfaces in UHPLC

Mathew DeLano, Thomas H. Walter,* Matthew A. Lauber, Martin Gilar, Moon Chul Jung, Jennifer M. Nguyen, Cheryl Boissel, Amit V. Patel, Andrew Bates-Harrison, and Kevin D. Wyndham

Cite This: *Anal. Chem.* 2021, 93, 5773–5781

Read Online

CHROMATOGRAPHY
TODAY

February / March 2021

Faster Time to Results for Ultra-Performance Liquid Chromatographic Separations of Metal-Sensitive Analytes

Thomas H. Walter, Brian J. Murphy, Moon Chul Jung†, Martin Gilar, Robert E. Birdsall and Jacob Kellett, Waters Corporation
34 Maple Street, Milford, MA 01757

† Current address: Enanta Pharmaceuticals Inc, 500 Arsenal Street, Watertown, MA



ELSEVIER Journal of Chromatography A 1650 (2021) 462247

Mitigation of analyte loss on metal surfaces in liquid chromatography

Martin Gilar*, Mathew DeLano, Fabrice Gritti

Waters Corporation, 34 Maple Street, Milford, MA 01757, USA

Assessing the impact of nonspecific binding on oligonucleotide bioanalysis

Bioanalysis

Jennifer M Nguyen*,^{1,2} , Martin Gilar², Brooke Koshel², Michael Donegan², Jason MacLean², Zhimin Li² & Matthew A Lauber²

¹School of Science, University of Copenhagen, Rolighedsvej 30, 1958 Frederiksberg, Denmark

²Waters Corporation, 34 Maple Street, Milford, MA 01757, USA

*Author for correspondence: Jennifer.Nguyen@waters.com

Bioanalysis (2021) 13(16), 1233–1244

Journal of Pharmaceutical and Biomedical Analysis

208 (2021) 114439

Impact of Nonspecific Adsorption to Metal Surfaces in Ion Pair-RP LC-MS Impurity Analysis of Oligonucleotides

Guilherme J. Guimaraes^a, J. Michael Sutton^a, Martin Gilar^b, Michael Donegan^b, Michael G. Bartlett^{a,*}

^aDepartment of Pharmaceutical and Biomedical Sciences, The University of Georgia College of Pharmacy, 250W. Green Street, Athens, Georgia 30602, United States
^bWaters Corporation, Milford, Massachusetts 01757, United States



The background features a complex network diagram with various sized nodes (circles) connected by thin lines, set against a blue gradient background. A dark blue horizontal band is centered across the image, containing the text.

Waters

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