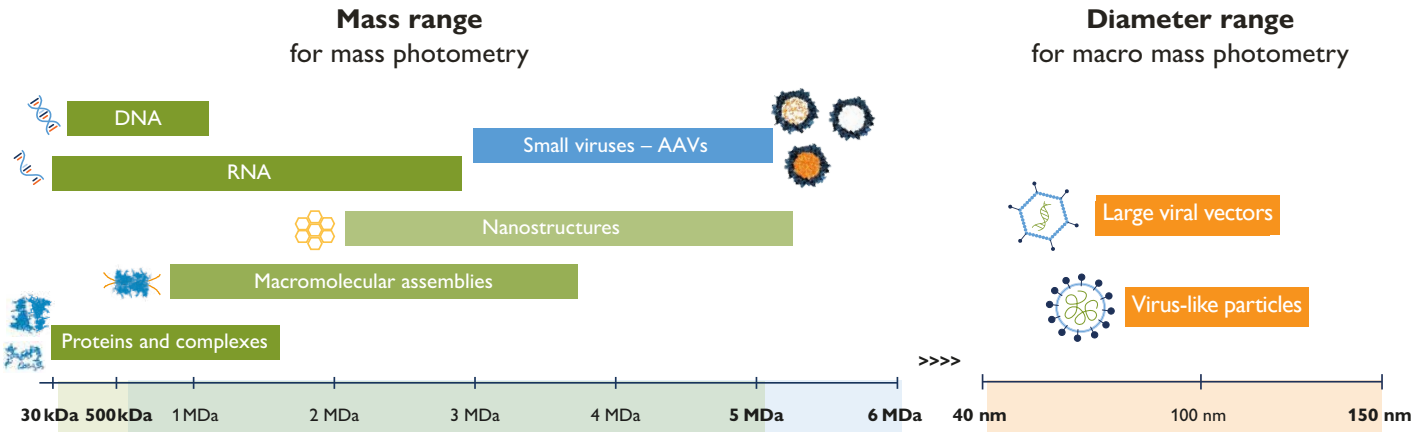
RE•FEYN®

Bioanalytics with Mass Photometry

Accelerate your discovery with fast, in-solution measurements

Refeyn's unique mass photometry technology is accelerating discovery, drug development and clinical manufacturing.
Measuring the mass of single proteins, nucleic acids and viral vectors in solution without labels, it delivers insights fast – on sample purity, biomolecular interactions, protein oligomerization, viral vector quality and more.

What will you measure?



The **TwoMP** product family (pp. 6-9) delivers accuracy and versatility, providing accurate mass measurement in the 30 kDa – 5 MDa mass range, including for:

- Antibodies
- Proteins
- Nucleic acids
- Protein-protein complexes
- Protein-nucleic acid complexes

The **SamuxMP** product family (pp. 10-13) is essential for laboratories working with adeno-associated viruses (AAV) analysis. Covering the 500 kDa – 6 MDa mass range, it offers:

- Empty/full and partials quantification
- Titer estimation
- Genome length measurement

The **KaritroMP** product family (pp. 14-15) makes it easy to quickly characterize samples of large viral vectors (e.g. adenovirus) and virus-like particles (VLPs) – covering the 40 – 150 nm range for particle size.
It leverages innovative macro mass photometry technology.

"Mass photometry fits perfectly into our analytical workflows when we know there are additional species in our samples [such as antibody aggregates] but we don't know their mass or their oligomeric state. Now we finally have a suitable technology to fill that gap."

Martin E., Scientist at a top 5 pharmaceutical company

Why choose mass photometry?

Label-free measurements, in solution

Fast: <5 min measurement to results

Little sample needed: 10–20 µL at 100 pM–100 nM or ~10^{11} particles/mL

Easy to use: Train new users in <1 day

Benchtop instruments

Cost efffective

Information on all subpopulations in samples

Founded 7 years ago

Mass photometry is in 90% of top biopharma companies

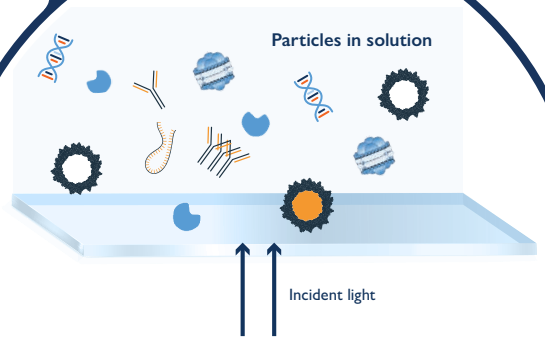
1500+ publications

Portfolio of 58 patents

~490 instruments in over 30 countries

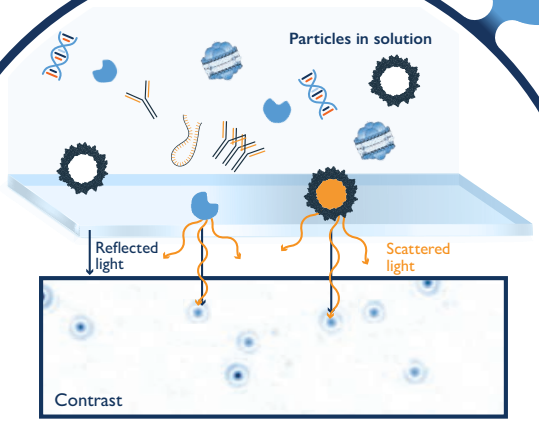
How does mass photometry work?

1



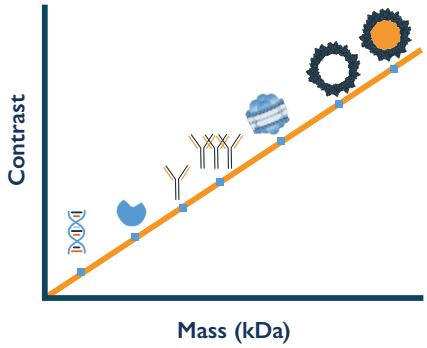
Particles in a sample on a glass surface are illuminated by a laser.

2



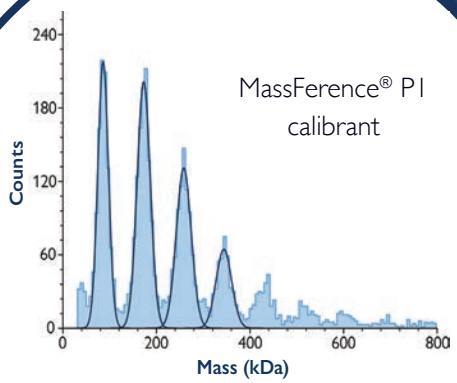
The particles scatter light, which interferes with the light reflected at the interface.

3



The resulting interference contrast scales linearly with the particles' mass.

4



A mass histogram is generated from the single-particle measurements.

“We are very limited in sample volume and concentration in some projects. We have been very surprised with how low you can go in terms of absolute sample concentration.”

Martin E., Scientist at a top 5 pharmaceutical company

“Mass photometry is very straightforward and convenient.”

Eduard Ebberink, Postdoc at Utrecht University

Analysis of proteins, including antibodies, and nucleic acids

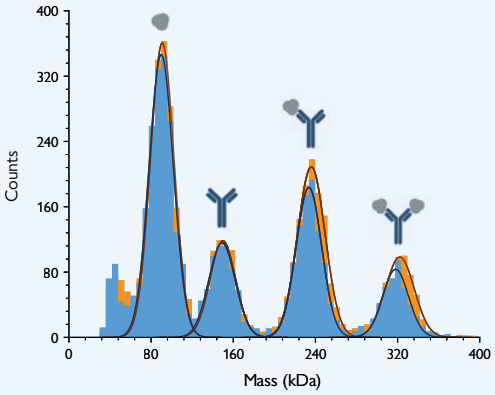
Explore the power of simple mass measurements:

- Oligomerization
- Protein-protein interactions
- Binding affinity
- Aggregation and fragmentation
- Sample stability
- Sample purity

Antibody-antigen affinity and stoichiometry

Antibody samples (X, Y, Z) were mixed 2:1 with the epidermal growth factor receptor (EGFR) and measured with mass photometry and biolayer interferometry (BLI). Mass photometry quantified the stoichiometries and their different affinities – which BLI could not.

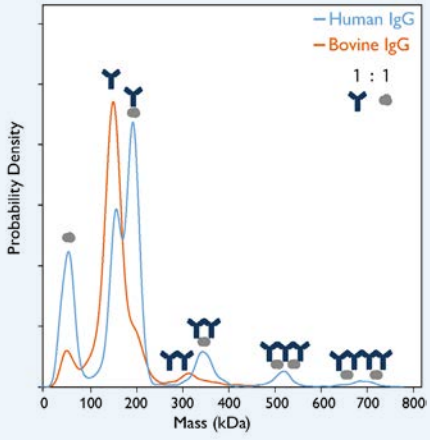
	Mass photometry		BLI
Antibody X	2.5 ± 0.7 nM	2.5 ± 0.7 nM	5.0 nM
Antibody Y	7.0 ± 2.0 nM	25.3 ± 6.8 nM	3.1 nM
Antibody Z	80.6 ± 17.7 nM	155.0 ± 86.0 nM	170.0 nM



This example duplicate measurement shows how mass photometry resolved and quantified species of EGFR, anti-EGFR antibody Y, and 1:1 and 2:1 complexes.

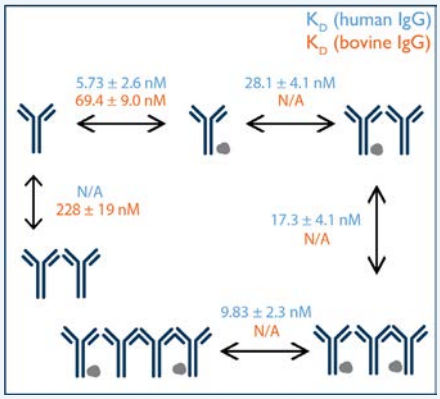
Complex binding

Protein A and IgG antibodies of human or bovine origin were mixed in a 1:1 molar ratio. Species of distinct, complex stoichiometries were resolved for each mixture.



Multiple binding affinities

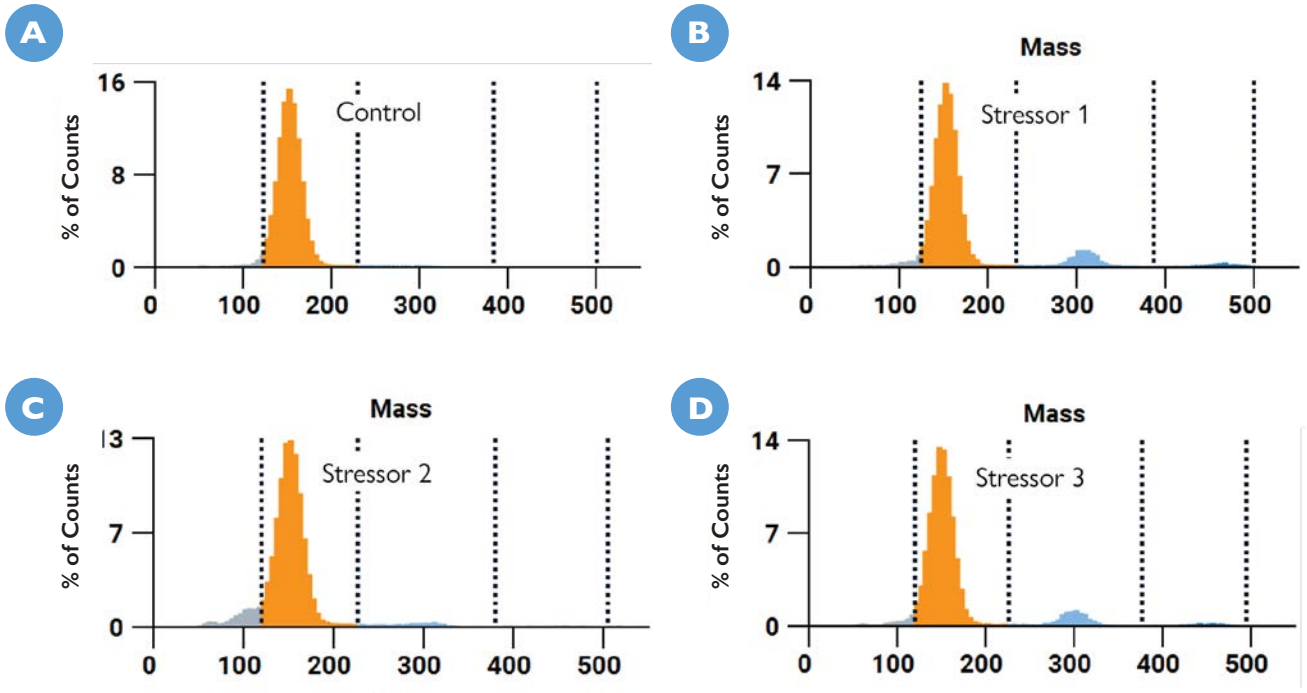
K_D values were calculated for the IgG-protein A interactions. The K_D values (mean ± SD) were calculated from triplicate measurements. (N/A = reaction not applicable).



Antibody aggregation and fragmentation

A therapeutic antibody was exposed to three different stress conditions, then analyzed with mass photometry and Refeyn's Antibody Stability software module. The data shows that Stressors 1 and 3 promoted aggregation (dimer and trimer formation).

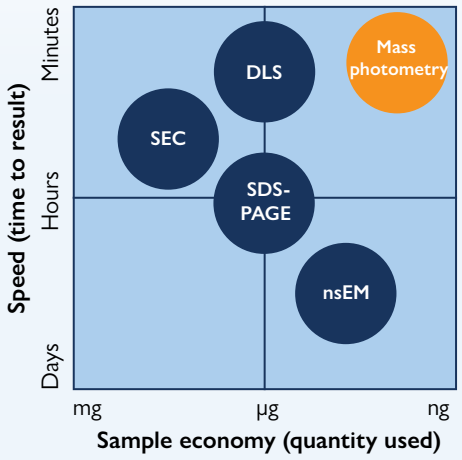
	Sample	Monomer (%)	Dimer (%)	Trimer (%)
Forced degradation	Control	98.9 ± 0.1%	1.1 ± 0.1%	0.0 ± 0.0%
	Stressor 1	87.8 ± 0.3%	9.6 ± 0.2%	1.8 ± 0.1%
	Stressor 2	96.3 ± 0.2%	3.4 ± 0.2%	0.2 ± 0.0%
	Stressor 3	89.6 ± 0.1%	8.9 ± 0.2%	1.3 ± 0.1%



Cryo-EM sample optimization and screening

Prior to cryo-EM analysis, it is critical to screen buffers and purification conditions, ideally with single-particle resolution. Sending substandard samples for cryo-EM often wastes time and may even result in structures remaining unsolved. Negative stain EM (nsEM) offers single-particle resolution (unlike DLS, SEC and SDS-PAGE), but it is costly, slow and requires non-native heavy metal staining.

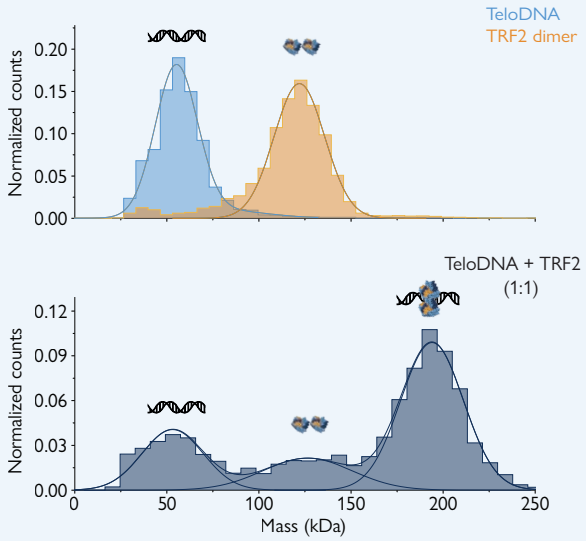
Mass photometry is fast and consumes little sample. It is also compatible with a wide range of buffers and membrane mimetic systems, so it is possible to analyze biomolecules, including membrane proteins and macromolecular complexes, in their native states.



Quantifying the mass and relative abundance of protein, DNA, and protein-DNA complexes

Telomeric DNA (teloDNA) and telomeric repeat–binding factor 2 (TRF2, dimer) were analyzed separately (top). They were then mixed in a 1:1 molar ratio (15 nM concentration) and analyzed (bottom). A TRF2-DNA complex with 2:1 stoichiometry was resolved in addition to the DNA and TRF2 dimers.

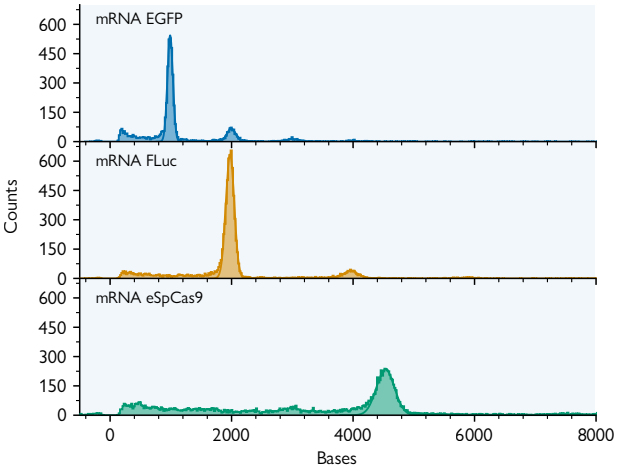
When the dissociation constant was measured with mass photometry and surface plasmon resonance (SPR), there was excellent agreement (K_D = 16.5 ± 5.1 nM with mass photometry vs. 14.8 nM with SPR).



Sizing mRNA

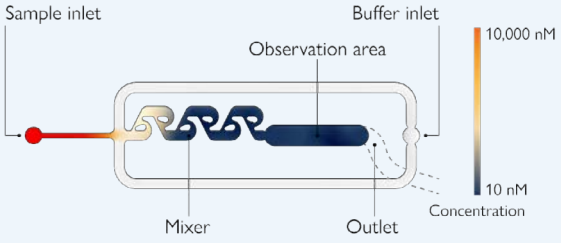
Three different messenger RNA (mRNA) transcripts of therapeutically relevant sizes were measured in triplicate with mass photometry. For all three constructs, average measured lengths were within 5% of the expected lengths. (EGFP = enhanced green fluorescent protein, FLuc = firefly luciferase, eSpCas9 = recombinant CRISPR–associated protein 9 from *Streptococcus pyogenes*).

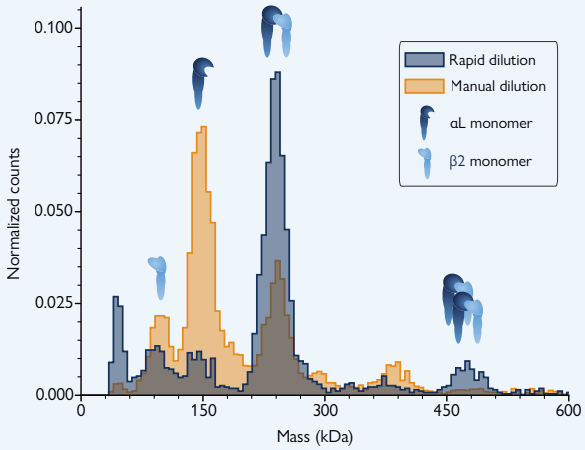
Unlike other techniques (e.g. CE, HPLC), mass photometry can be run in native buffer conditions, enabling detection of oligomeric RNA species that are not seen in denaturing conditions (not shown).



Low-affinity complexes

Samples containing integrin αL and β2 were measured following manual dilution (orange) or rapid dilution via the **MassFluidix HC system** (blue), from 2 µM to 5 nM. Rapid dilution enabled the detection of heterotetramers and significantly more heterodimers – complexes that are only stable at high concentration.

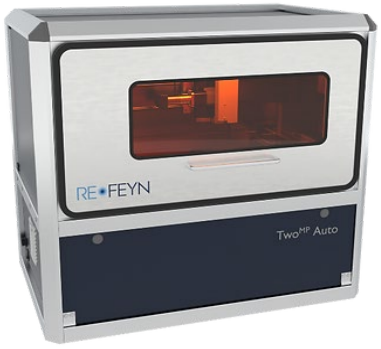




Introducing the TwoMP product family

An integrated solution for biomolecular analysis

The **TwoMP mass photometer** enables label-free mass measurement of single molecules, directly in solution. It fits on a lab bench and is easy to use.



The **TwoMP Auto mass photometer** automatically measures up to 24 samples in as little as 90 minutes, freeing up operator time.

The **MassFluidix HC microfluidics add-on** for the TwoMP enables the study of samples at higher (micromolar) concentration and low-affinity interactions.

Acquire and analyze your data using custom-designed software packages: **AcquireMP** and **DiscoverMP.**

Use the **StreamlineMP Antibody Stability** module to automatically characterize aggregation.

To facilitate the measurement process further, Refeyn offers dedicated mass photometry consumables, including:

- **The MassFerence P1 calibrant**, for use when measuring proteins in the 90 - 1000 kDa range

Learn more at refeyn.com/biomolecular-analysis

The TwoMP and TwoMP Auto are Class 1 laser products.

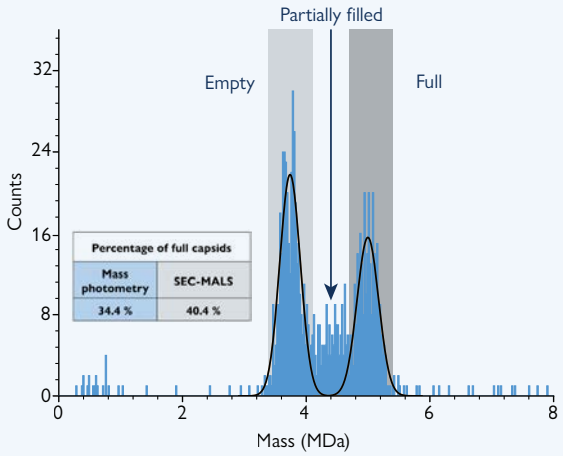
AAV analytics for cell & gene therapy

By enabling frequent checks of critical quality attributes (CQAs), mass photometry accelerates manufacturing and process development, helping better therapeutics reach patients faster. It quantifies:

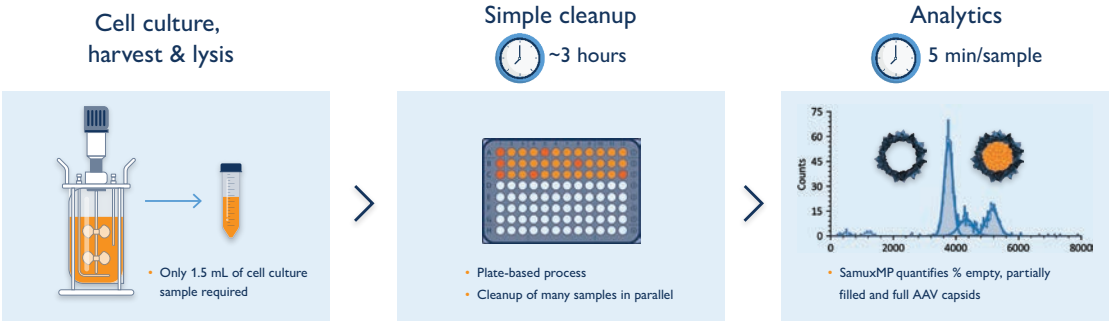
- Proportions of empty, partially filled, full and overfull capsids (supporting compliance in GMP-regulated environments)
- Capsid degradation
- Sample titer estimation
- Sample purity
- AAV genome length

Quantifying empty, full and partially filled AAVs

Subpopulations of empty and full AAV vectors form clearly visible peaks and represent the bulk of the sample, while partially filled capsids are distributed across an intermediate mass range. The mass photometry measurement was consistent with a SEC-MALS measurement of the same sample.



Upstream AAV characterization



Mass photometry can be applied downstream as well as upstream – to clarified lysates – following a simple, plate-based cleanup method created by Génethon. It takes 3 hours from bioreactor to results and uses 1.5 mL of cell culture sample.

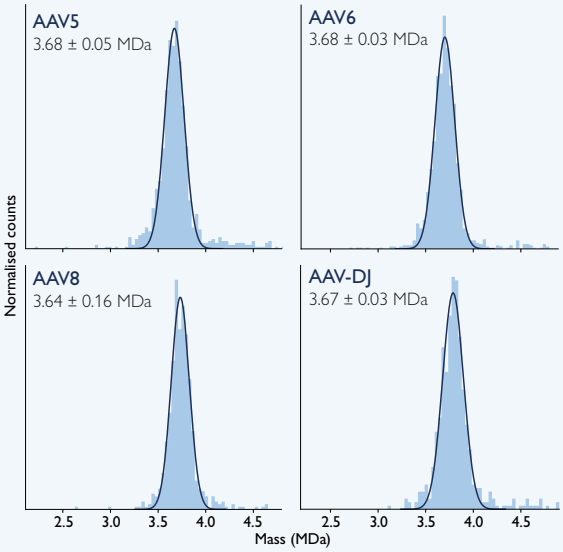
This approach eliminates the need for lengthy downstream purification and concentration procedures before AAV samples can be characterized – and before a judgement can be made on upstream performance.

Applying mass photometry upstream makes process optimization faster and more cost-effective than traditional post-purification checkpoint control.

Serotype-agnostic AAV analytics

Mass photometry can measure AAV capsids of any serotype without the need for protocol adjustments. This example shows SamuxMP measurements of empty AAV capsids of four different serotypes.

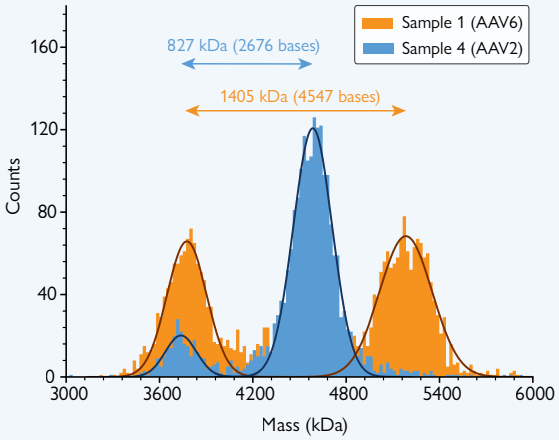
The measurements revealed a single, symmetric peak at the expected mass, confirming that the SamuxMP produces consistent results across serotypes.



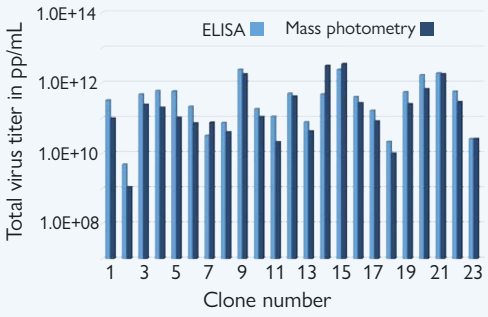
AAV genome length measurement

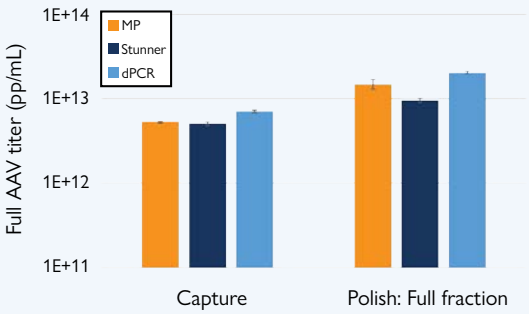
Mass histograms are shown of two AAV samples (of serotypes AAV2 and AAV6), each with empty and full populations and different genome lengths. The mass differences between the empty and full AAV populations results from the genetic material in the capsid and can be readily converted into genome length (number of bases).

When four different AAV samples were measured this way in triplicate, the results showed high levels of precision and accuracy.



	Sample number	1	2	3	4
	Serotype	AAV6	AAV6	AAV6	AAV2
Expected	Genome length (bases)	4543	4104	4292	2705
Expected	Genome mass (kDa)	1404	1268	1326	836
Measured	Empty AAV mass (kDa)	3751	3717	3737	3720
Measured	Full AAV mass (kDa)	5156	4995	5046	4547
Measured	Genome mass (kDa)	1405	1278	1308	827
	CV genome mass (%)	1.1	1.5	0.8	1.8
	Mass accuracy (%)	0.1	0.8	1.3	1.0





Estimating AAV titer

The SamuxMP titer estimation tool provides titer data on all populations in the sample – empty, full and partially filled AAV capsids – with minimal time, sample and expertise requirements.

The results agree with those from other methods, as shown in these examples of AAV9 clone screening (left) and analysis after different purification steps (right).

Introducing the SamuxMP product family

Integrated AAV analytics solutions

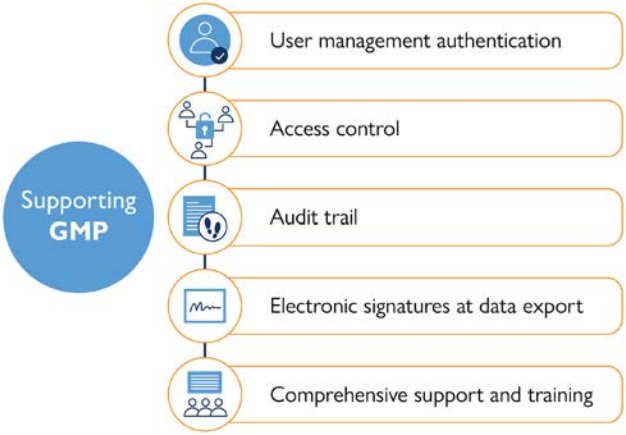
The **SamuxMP mass photometer** was designed specifically for AAV sample analysis. It takes under five minutes from sample loading to results and can be applied to AAVs of any serotype. Just one measurement enables:

- Resolution and quantification of subpopulations of differently filled capsids (empty, partially filled, full and overfilled)
- Determination of genome length in differently filled subpopulations
- Estimation of capsid titer
- Assessment of sample purity
- Detection of aggregation

The **SamuxMP Auto mass photometer** offers the capabilities of the SamuxMP, plus automation of up to 24 measurements at once.

Support for GMP-regulated environments

The **GMP software** package for the SamuxMP and SamuxMP Auto includes all the necessary features to comply with FDA 21 CFR 11 (US) and EU GMP Annex 11. Furthermore, Refeyn's service teams provide support and training to fulfill the necessary Installation Qualification (IQ) and Operational Qualification (OQ).



The **MassFerence P2 calibrant** facilitates measurements of samples containing AAVs with masses in the 670 kDa to 5 MDa range, while **MassGlass UC** sample carrier slides provide the ideal AAV measurement surface.

The SamuxMP and SamuxMP Auto are Class 1 laser products.

“We could not only differentiate full and empty capsids, but also estimate the size of the encapsidated genome from the MP data. This result really showcases the capability of the MP technique.”

Grzegorz Piszczek, Director of the Biophysics Core Facility
National Heart, Lung, and Blood Institute (NIH)

“We’re generating data to compare mass photometry with gold standards like AUC and cryoTEM. Early indications show that it’s much quicker and equally accurate. Partners who’ve compared mass photometry to other methods themselves vouch for its accuracy. It’s a game changer in AAV characterization, for us as well as our clients.”

Quentin Bazot, Process Development and Innovation Manager, ABL Europe

Learn more at refeyn.com/aav-vector-analytics

Next-generation analysis of large vectors for cell & gene therapy and vaccines

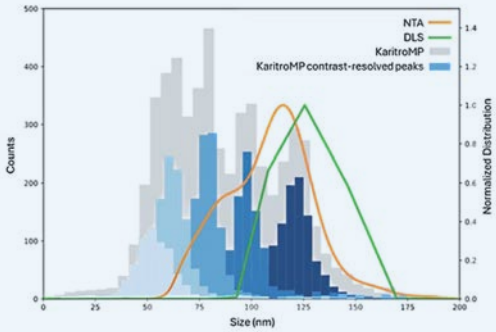
Characterization of large viral vectors and virus-like particles (VLPs), revealing more information than other methods while using less time and sample:

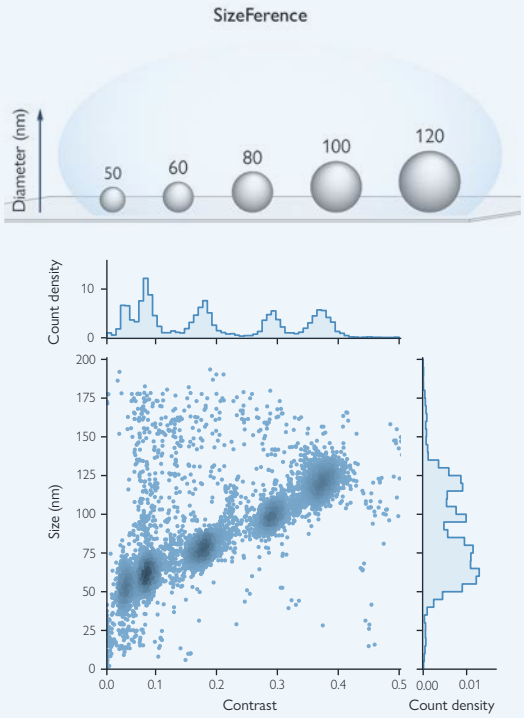
- Purity
- Stability
- Size distribution

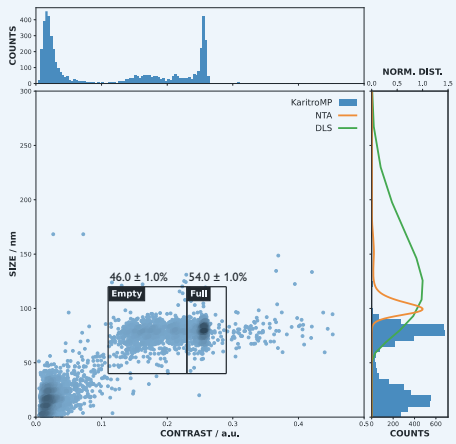
A new way to characterize large viral vectors

Macro mass photometry measures particle size as well as the scattering contrast, which is a proxy for mass and can be used to resolve particles of similar size but different mass. Refeyn's size calibrant, **SizeFerence**, is an equimolar mixture of silica beads of five diameters. The five populations of beads could only be resolved using both size and contrast information.

While macro mass photometry could resolve all five populations of beads, dynamic light scattering (DLS) and nanoparticle tracking analysis (NTA) could not.







Resolution of empty/full ratios

Unlike DLS and NTA, macro mass photometry can distinguish and quantify populations of particles with the same size but different mass, such as empty vs. full adenovirus capsids.

Learn more at refeyn.com/karitro-mp

The KaritroMP is a Class 1 laser product.

Introducing the KaritroMP product family

An innovative solution for large vector analytics

The **KaritroMP macro mass photometer** makes it easy to quickly characterize samples of large viral vectors and VLPs. Its single-particle analysis enables users to visualize the distributions of particles present in their samples in minutes.

The **SizeFerence calibrant** provides reliable calibrations for macro mass photometry measurements of particles in the 40 - 150 nm range, including adenoviruses, lentiviruses and VLPs. Ready-to-use MassGlass KV sample carrier slides are optimized for the KaritroMP, further simplifying workflows.

The software packages **AcquireMP** and **DiscoverMPK** provide intuitive environments for data acquisition and analysis.

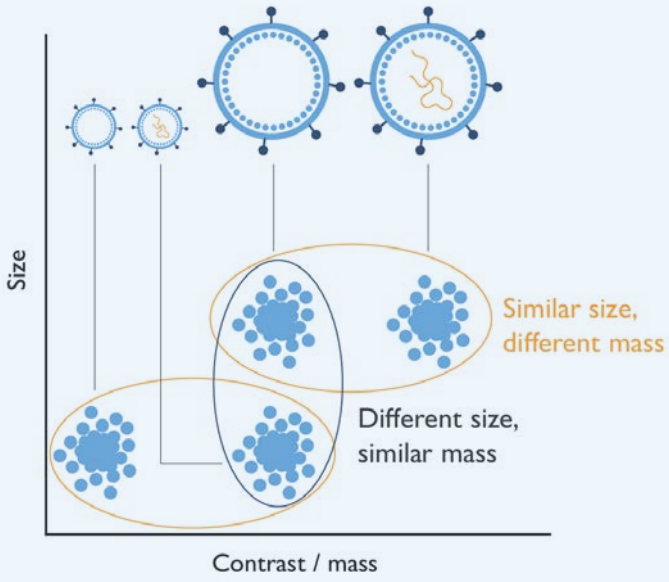
The KaritroMP is powered by macro mass photometry – a rapid, single-particle, multiparametric technique requiring no labels that builds on the principles of mass photometry.

How does macro mass photometry work?

In a macro mass photometry measurement, a sample droplet on a slide is illuminated from below and the scattering contrast is imaged as the stage sweeps vertically (along the z axis). Particles of different sizes reach their maximum contrast at different planes, so the vertical sweep enables the size measurement.

For each particle, the **KaritroMP** measures two distinct parameters:

- Contrast (a qualitative measure related to the particle's composition and mass)
- Size



Comparison guide

			TwoMP	SamuxMP	KaritroMP
Technology			Mass photometry		Macro mass photometry
Parameters measured			Mass		Diameter (size) Contrast (mass proxy)
Parameter range			30 kDa – 5 MDa	500 kDa – 6 MDa	40 – 150 nm diameter
Concentration range			100 pM – 100 nM*	10^{11} particles/mL	10^{8} – 10^{9} particles/mL
Particle type	Proteins		✓		
	Nucleic acids		✓		
	AAVs			✓	
	Large viruses (e.g. AdV)				✓
Add-ons			TwoMP Auto: Autonomous measurement of 24 samples in ~90 minutes MassFluidix HC: Microfluidics system to measure low-affinity interactions	SamuxMP Auto: Autonomous measurement of 24 samples in ~90 minutes	
Software	Data acquisition		AcquireMP		
	Analysis	Standard	DiscoverMP		DiscoverMPK
		Special workflows	StreamlineMP for specialized applications Available: Antibody stability module		
	GMP environments			GMP software package	
Consumables	Sample carrier slides		MassGlass UC Microfluidics chips for MassFluidix HC	MassGlass UC	MassGlass KV
	Calibrant		MassFerence P1	MassFerence P2	SizeFerence

*The MassFluidix HC add-on expands the TwoMP sample concentration range up to the tens of micromolar.

Learn more about consumables at refeyn.com/mass-photometry-consumables

Certified and accredited services & support for the life of your instruments

We take pride in our dedication to excellence, ensuring your mass photometer operates smoothly and delivers reliable, accurate and compliant data.

Our Field Service Engineers deliver personalized support and expertise, drawing on extensive experience and thorough knowledge of bioanalytical instruments.

Our services include:

- Repairs
- Preventive maintenance
- Packing and reinstallation for moves
- IQ & OQ

Service contract options

	Gold	Silver	Bronze
Labor	Yes	Yes	Yes
Parts	Yes Includes PC Includes Objective	Yes Includes PC Excludes Objective	Yes Excludes PC Excludes Objective
Travel and travel labor	Yes	Yes	Yes
Engineer onsite	Yes Highest Priority	Yes Second Priority	Yes Third Priority
Engineer remote diagnosis	Yes Within 1 business day M-F	Yes Within 2 business days M-F	Yes Within 3 business days M-F
Instrument/system replacement unit	Yes	No	No
Acurion replacement unit (where relevant)	Yes	No	No
Annual maintenance visit	Yes	Yes	Yes
1 instrument move per year	Yes	No	No

2018

First prototype debuts at Biophysical Society Meeting

Seminal paper in *Science* by Kukura lab, demonstrating mass photometry

Refeyn spun out of the University of Oxford

2019

OneMP launches

Opening of first US office in Portland, Oregon

20+ instruments installed

2020

Series A funding, led by Northpond Ventures ($24.4m)

Opening of US East Coast Office in Boston, Massachusetts

2021

Expansion of manufacturing facilities in Oxford, UK

TwoMP launches

100 instruments installed

Many publications now cite mass photometry

A clear indication of mass photometry's value is its rapid adoption by researchers, as evidenced by the scientific literature.

As of early 2025, over 1500 papers feature mass photometry – remarkable for a technology that was introduced in 2018.

Explore the 1500+ publications that use mass photometry at refeyn.com/featured-publications

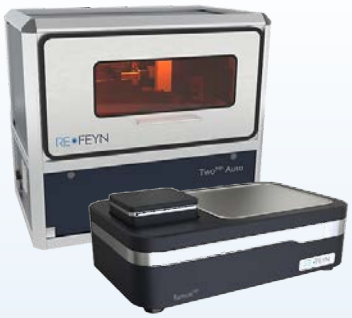
A story of innovation

Refeyn's story begins with a discovery that some had said was impossible – imaging a single protein without a label.

A research team led by Philipp Kukura at the University of Oxford achieved this and went a step further – measuring a single protein's mass.

Refeyn was established to make their technology – which we now know as mass photometry – available in an easy-to-use box.

Today, hundreds of labs around the world use mass photometry. It is accelerating scientific discovery, drug development and manufacturing.



2022

SamuxMP and **TwoMP Auto** launch

2023

SamuxMP Auto and **MassFluidix HC** launch

GMP compliance software launches for SamuxMP

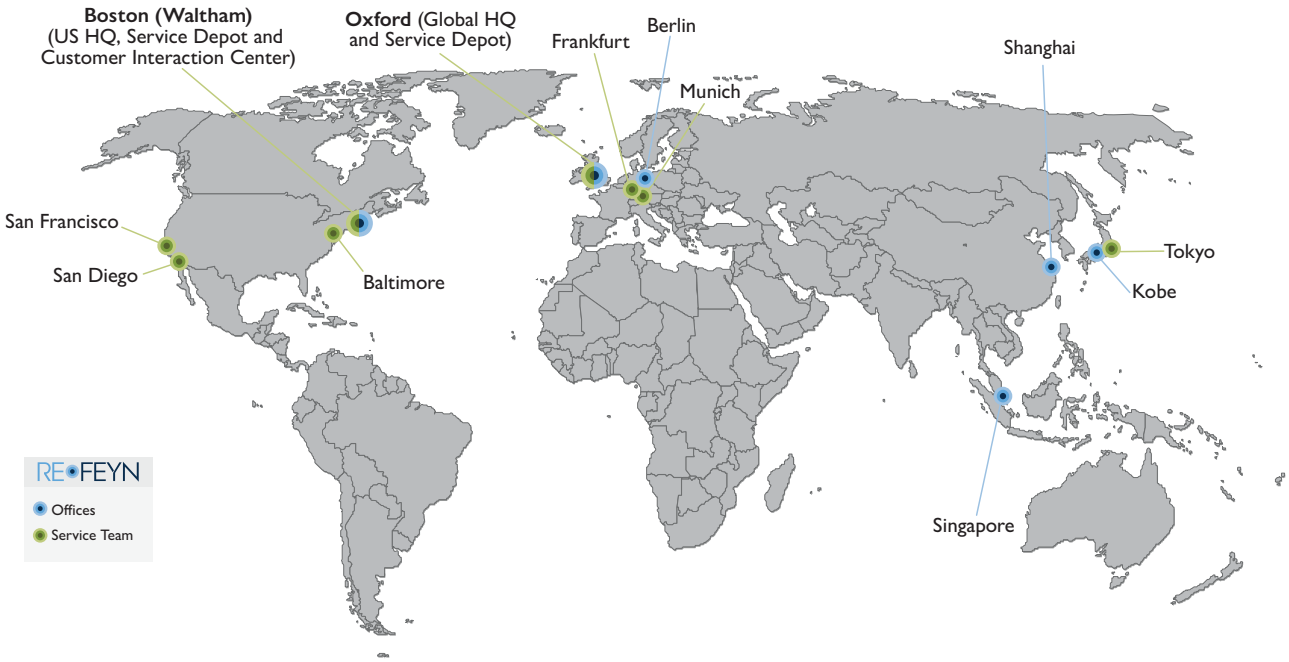
2024

KaritroMP launches

Customer Interaction Center opens in Waltham, Massachusetts with demo & service lab facilities

1500 papers feature mass photometry

Our vision is to accelerate discovery through innovation, empowering the latest scientific breakthroughs in basic research and transforming biotherapeutic development and manufacturing.



Refeyn Headquarters (UK)
Unit 9, Trade City
Sandy Lane West
Oxford OX4 6FF
United Kingdom
Phone: +44 1865 800175

Refeyn Headquarters (USA)
21 Hickory Drive
Suite 200A
Waltham MA 02451
USA
Phone: + 1 (971) 200 1370

Sales Directors:

EMEA – Rebecca Elston
Phone: +44 7804 629158
E-mail: rebecca.elston@refeyn.com

USA – Candi Mach
Phone: + 1 (971) 200 1370
E-mail: candice.mach@refeyn.com

APAC and Global – Guillaume Kohen
Phone: +44 7511 183320
E-mail: guillaume.kohen@refeyn.com

RE•FEYN®

Unit 9, Trade City, Sandy Lane West, Oxford OX4 6FF, United Kingdom

orders@refeyn.com
refeyn.com
Refeyn
@Refeyn