

Optical Sensing Strategies for Probing Single-Cell Secretion

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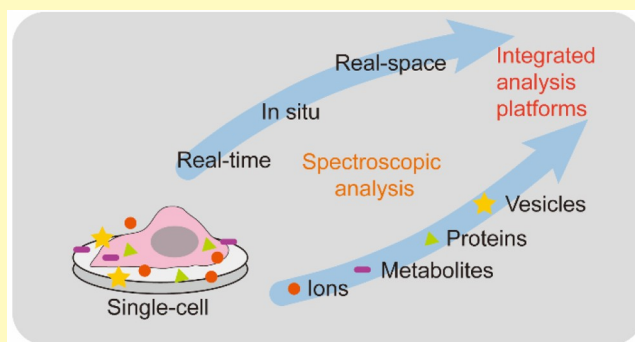
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ABSTRACT: Measuring cell secretion events is crucial to understand the fundamental cell biology that underlies cell–cell communication, migration, proliferation, and differentiation. Although strategies targeting cell populations have provided significant information about live cell secretion, they yield ensemble profiles that obscure intrinsic cell-to-cell variations. Innovation in single-cell analysis has made breakthroughs allowing accurate sensing of a wide variety of secretions and their release dynamics with high spatiotemporal resolution. This perspective focuses on the power of single-cell protocols to revolutionize cell-secretion analysis by allowing real-time and real-space measurements on single live cell resolution. We begin by discussing recent progress on single-cell bioanalytical techniques, specifically optical sensing strategies such as fluorescence-, surface plasmon resonance-, and surface-enhanced Raman scattering-based strategies, capable of in situ real-time monitoring of single-cell released ions, metabolites, proteins, and vesicles. Single-cell sensing platforms which allow for high-throughput high-resolution analysis with enough accuracy are highlighted. Furthermore, we discuss remaining challenges that should be addressed to get a more comprehensive understanding of secretion biology. Finally, future opportunities and potential breakthroughs in secretome analysis that will arise as a result of further development of single-cell sensing approaches are discussed.

KEYWORDS: *Single cell, secretion, bioanalysis, optical sensing, fluorescence, surface plasmon resonance, surface-enhanced Raman scattering*



Secretion is a fundamental and ubiquitous cellular process of delivering intracellular species, such as ions, metabolites, and proteins, to the cell exterior in a highly controlled way. These released substances execute a variety of key roles in maintaining normal cellular biology. Abnormal variations in secretion patterns and extracellular concentrations of the secretions can lead to cell dysfunction and diseases.^{1–3} For example, neurotransmitters, including some amino acids, biogenic amines, and neuropeptides, released from peripheral and autonomic nerves are well-known signaling molecules in mediating the stimulatory or inhibitory neuronal functions.^{4,5} An imbalance of neurotransmitter can provoke various disorders including Alzheimer's disease,⁶ Parkinson's disease,⁷ schizophrenia,⁸ inherited disorders of neurotransmitter metabolism,⁹ and malignant tumors.¹⁰ Precise measurement of cell secretion, therefore, is not only crucial to understanding the fundamental cell biology that underlies cell–cell communication, migration, proliferation, and differentiation, but also for discovering new biomarkers and therapy targets.^{11,12}

Conventionally, cell secretion is analyzed by ensemble biochemical assays of a large population of cells with relatively low sensitivity, temporal and spatial resolution, and throughput. They are unable to reveal the heterogeneous secretory

phenotype and function of individual cells, to quantify extremely trace amounts of released species including ions, molecules, and vesicles, to track the fast, dynamic, and site-specifically occurred secretion events.^{13,14} Especially, an increasing number of studies have revealed the pervasive existence of heterogeneity in cellular systems that is commonly manifested in phenotypic differences between cells.^{15,16} Cells possessing identical or near-identical genomic DNA sequences can have very different behaviors and biological functions, for example, the exocytotic rate.¹⁷ Ensemble-averaged measurements only reflect the dominant biological features in a cell population, whereas the cell-to-cell variations are usually masked. Furthermore, population-averaged analysis can obscure the presence of rare subpopulations of cells with distinct exocytotic activities, posing challenges for building accurate mechanistic models of secretion related diseases (e.g.,

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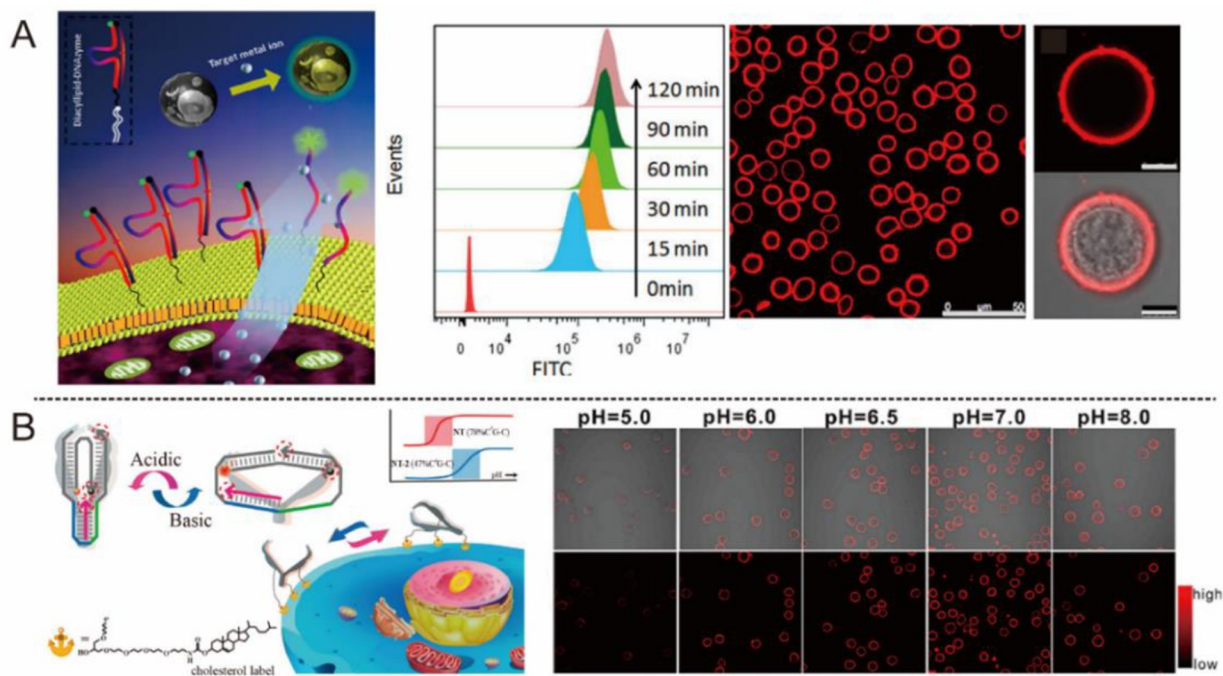


Figure 1. (A) Design of a cell membrane anchored DNAzyme for real-time monitoring of metal ions in the cellular microenvironment. Reprinted with permission from ref 42. Copyright 2014 American Chemical Society. (B) Schematic illustration of a cell surface-anchored DNA nanomachine as a reversible and tunable pH sensor. Reprinted with permission from ref 43. Copyright 2018 American Chemical Society.

neurological and metabolic diseases).¹⁸ Given these challenges, it is highly necessary to analyze cellular secretion at the single-cell level.

At present, electrochemical analysis represents one of the mainstream techniques for single-cell secretion analysis and relies on the electrical response of electrodes upon binding to the cell-released molecules.^{19–21} The design and preparation of micro/nano electrodes has allowed continuous detection and monitoring of molecular release with high resolution.²² However, the technical challenge of precisely positioning the probe electrode in the cellular microenvironment may compromise the spatial resolution. The selective detection of compounds with overlapping redox potentials (e.g., dopamine and ascorbic acid) by electrochemical assays is still difficult.²³ In addition, perturbation of cellular states by applying an extra voltage or current to living cells is unknown and needs to be further elucidated.

Optical spectroscopic analysis is attracting increasing attention in the research field of single-cell secretion. Chemical conversion or a physical interaction of the target analytes at a biosensing surface/interface produces the optical signal (e.g., photon emission or frequency shift).²⁴ Fluorescence imaging and surface plasmon resonance (SPR) imaging microscopies have permitted the in situ monitoring of secretion events with unprecedented sensitivity and resolution, down to the single-molecule level.²⁵ Although the number of molecules and ions secreted by a single cell to the extracellular space is usually small, the advances in the development of novel fluorescent probes and fluorescence signal-amplification techniques including the enzymatic and nonenzymatic approaches enable accurate detection and quantification of live cell secretions.^{26,27} Due to the large extinction coefficient, the plasmonic scattering of a single noble metal nanoparticle can be readily detected by a commercial microscope and imaged by a standard dark-field microscope. This enables analysis of trace molecules

by using a single nanoparticle as the optical biosensor. Similarly, with the rapid progress of bionanophotonics, surface-enhanced Raman scattering (SERS) has emerged as another powerful tool for highly sensitive analysis of cellular secretion with the single-cell resolution.^{28,29} The enhancement of Raman signal comes from the excitation of localized surface plasmons with metal nanostructures, especially nano assemblies with tiny interparticle gaps (the so-called SERS hot spots).³⁰ Compared with fluorescence and SPR-based strategies, SERS has an additional advantage of proving the “spectral fingerprint” of the analyte molecules which contains a wealth of information about the molecular composition, and thus enabling label-free detection and identification of the target molecules released from living cells.³¹ The aim of this Perspective is to detail important technological advances toward real-time, in situ, and high-resolution investigation of single-cell secretion. Specifically, we will focus on advances of fluorescence, SPR, and SERS assays for the qualitative and quantitative analysis of different species released by single living cells which include inorganic ions, small molecules, cytokines, and vesicles. We will discuss the pros and cons of each method and finally provide our version of the future of the single-cell secretion analysis.

■ APPROACHES TO SINGLE CELL

Ions. Ions play an important role in the regulation of cell function and enzyme catalysis.^{32–34} Although the concentration of these ions is usually low under normal conditions, it may increase by several orders of magnitude under some pathological conditions.³⁵ With the rapid progress of highly bright and specific fluorescent probes, fluorescence-based strategies have been extensively explored for analyzing and/or imaging ions secreted from single living cells.^{36–39} Because of the low abundance of specific ions released from a single cell, isolation and enrichment of the target ions in a confined

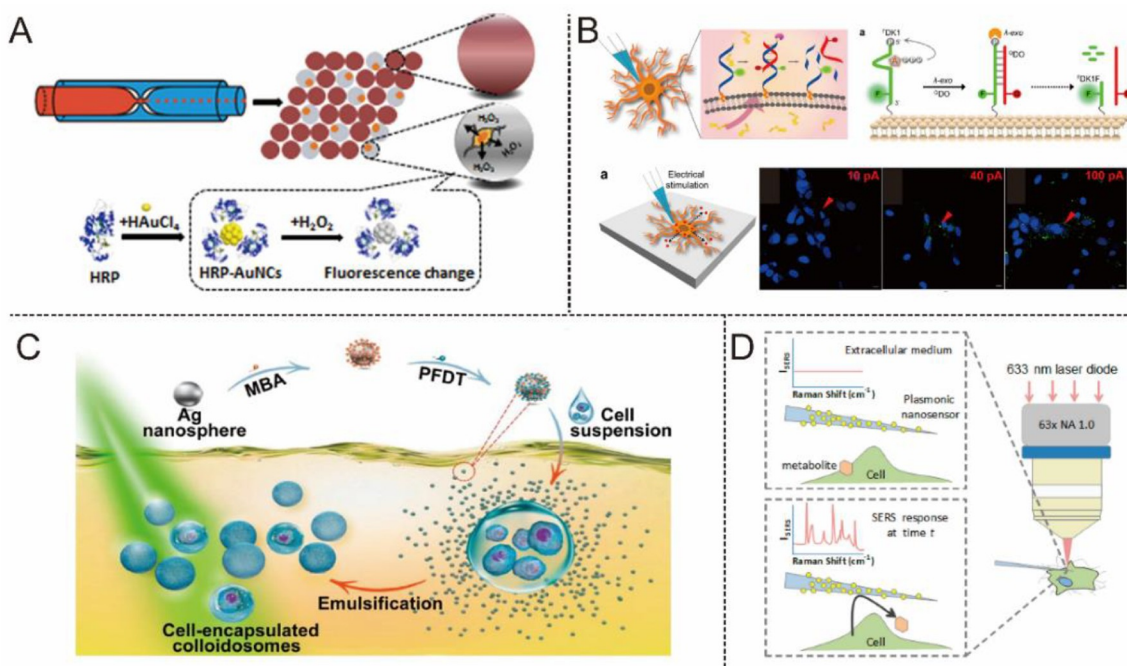


Figure 2. (A) Schematic illustration of detecting hydrogen peroxide in the single-cell encapsulated droplets in combination with HRP-AuNCs. Reprinted with permission from ref 63. Copyright 2018 American Chemical Society. (B) Schematic illustration of a cell-surface-anchored ^FDK1 sensor for fluorescence imaging of extracellular ATP. Reprinted with permission from ref 64. Copyright 2021 American Chemical Society. (C) Schematic illustrating the formation of a plasmonic colloidosome-based single cell detector. Reprinted with permission from ref 70. Copyright 2019 American Chemical Society. (D) Representation of the concept of a SERS nanosensor to monitor cellular secretion. Reprinted with permission from ref 73. Copyright 2016 American Chemical Society.

space is necessary to improve the fluorescence intensity and signal-to-noise ratio. The encapsulation of individual living cells in uniform, picoliter (pL) microfluidic droplets has already shown huge promise in elevating the local concentration of the analyte ions due to the largely decreased solution volume.⁴⁰ By combining single-cell droplet microfluidics with fluorescence cytometry, proton secretion from single circulation tumor cells was evaluated in a high-throughput (1 kHz) manner, which was a remarkable achievement.⁴¹ Considering the rapid diffusion and dilution of released ions in the bulk extracellular medium, fluorescent probes capable of anchoring at the cell membrane have been designed using dye-labeled DNA oligonucleotides and genetically encoded fluorescent proteins as recognition and signal reporters.^{42–44} A representative cell-surface anchored fluorescent biosensor used a diacyllipid-DNAzyme conjugate consisting of three parts: the DNAzyme sequence at the 3'-end region, a diacyllipid tail at the 5'-end region, and a PEG linker located between the two regions. The DNAzyme and the substrate strand were labeled with a fluorescent dye and a quencher, respectively. Target ions were detected based on the enzymatic reaction-induced structural changes of the membrane-anchored sensors in the presence of target ions (see Figure 1A).⁴² In the absence of target ions, fluorescence was quenched due to the close proximity between the fluorescent dye and the quencher. In the presence of target ions, the DNAzyme was activated to cleave the substrate strand into two fragments which dissociated from the DNAzyme strand due to a decrease of the hybridization stability. This resulted in separation of the quencher from the fluorophore and, in turn, the fluorescence restoration at the cell surface.³⁸ By adjusting the DNA sequence and the lipid unit, this fluorescence switching approach can be extended to other ions such as H⁺ and

K⁺.^{43,45,46} Recently, Jiang et al. reported a dynamic pH-responsive DNA nanodevice which is anchored on the cell surface via multiple cholesterol anchors. This nanodevice could experience a rapid reversible triplex–duplex conformation change accompanied by the off–on fluorescence switching, thus possessing an ability for dynamic detection and imaging of H⁺ excretion at the single-cell level (Figure 1B).⁴³ Despite this progress, the problem of photobleaching and phototoxicity needs to be considered in live fluorescence imaging.

SERS has a sensitivity comparable to that of fluorescence, but is less influenced by photobleaching. A simple yet efficient approach for SERS analysis of H⁺ excretion from living cells was developed by directly culturing cells on the SERS substrates premodified with pH-sensitive Raman probes such as 4-mercaptopyridine and 4-mercaptobenzoic acid.^{47–49} The detection was based on the deprotonation and protonation of the probe molecules at different pH conditions, which resulted in a detectable change of their SERS spectra.^{47–49} To avoid the effect of ion diffusion and dilution in the extracellular space, the strategy of tethering probes on the cell surface was also feasible for SERS analysis. For example, a cell membrane-anchored SERS biosensor was designed for measuring extracellular pH at micrometer-scale resolution.⁵⁰ To achieve that, the outer membrane surface of the living cell was first biotinylated via the NHS-ester amine reaction. Gold nanoparticles cofunctionalized with streptavidin and 4-mercaptobenzoic acid were then conjugated onto the cell surface by streptavidin–biotin interaction.⁵⁰ The SERS sensor was able to probe a highly localized variation of pH induced by H⁺ release which was particularly upregulated in tumor cells.⁵⁰ Despite this progress, robust and site-specific labeling of the cell membrane with metal nanoparticles is experimentally challenging that involves multistep biochemical operation and can

Table 1. Optical Strategies for Analysis of Metabolites Secreted from Single Cells

| analytical modality | probes/tools | targets | pros and cons | refs |
|---------------------|--|---|---|----------------|
| Fluorescence | Microdroplet and Au nanoclusters Photoactivatable DNAs NIR fluorescence carbon nanotube arrays Genetically encoded fluorescent proteins | H ₂ O ₂ , ATP, dopamine, serotonin, lactate | Pros • High throughput • High spatiotemporal resolution (100 ms; 60 μm) • High sensitivity (beyond 10 ⁻¹² M) Cons • Probes needed • Simultaneous multitarget analysis is difficult | 61,62 64–69 |
| SERS | Au/Ag-based plasmonic nanotips | H ⁺ , ROS, pyruvate, lactate, ATP, ADP, glucose, glutamine, urea | Pros • Direct label-free analysis is allowed • Good temporal resolution (500 ms–1 s) • High sensitivity (down to a single molecule) Cons • Low throughput (one tip one cell) | 70–74 |
| SPR | Au nanorods-based plasmonic hydrogel | H ₂ O ₂ | Pros • Label-free analysis is allowed • Easy-to-use Cons • Single-target analysis | 75 |

cause cellular damage. Another strategy for SERS sensing of cellular ions utilizes a SERS-active nanopipette.^{51–53} By using a three-dimensional micromanipulation system which has long been employed in patch-clamp electrophysiology, the plasmonic nanopipette could be positioned precisely in close proximity to the outer cell membrane and thus was able to measure metabolically induced changes in the extracellular pH of individual cancer cells by real-time recording of the SERS signature on the nanopipette.⁵¹ Although effective, the assay throughput of this approach is low; only one cell can be measured at a time. Furthermore, there is still a lack of enough Raman probes to target different ions. New probes could be synthesized, but screening effective dual-function molecules capable of specifically recognizing target ions and stably binding to the SERS substrate is time- and labor-intensive.^{54,55}

Metabolites. Metabolites secreted by single cells are important factors for cells to respond to microenvironmental stress.^{56–62} Single-cell-secreted H₂O₂ has been measured by coupling microfluidic droplet biosensors and fluorescent Au nanoclusters (Figure 2A).⁶³ In the presence of H₂O₂, redox reactions on the metal nanoclusters took place, which led to fluorescence quenching.⁶³ The method allowed sensitive quantification of H₂O₂ with a detection limit of 1.0 nM. However, change of cell status from the adherent state to the suspended state in microdroplet may affect the intrinsic secretion profile of cells. Similar to the analysis of secreted ions, the diffusion of metabolites in bulk extracellular space would cause a deviation between the measured value and the real value of the secretion activity. To address this problem, a cell-surface-anchored self-phosphorylating DNAzyme was designed for fluorescence imaging of ATP secreted from single cells. The presence of ATP resulted in a structural change of the DNA sequence accompanying a restoration of the prequenched fluorescence. The DNAzyme exhibited sub-second response kinetics, high specificity, and micromolar sensitivity (Figure 2B).⁶⁴ Such a strategy can be further extended to other metabolites such as dopamine and lactates.^{65,66} A drawback of these strategies is that they use

fluorophores with optical radiation in the visible spectral region which can be subject to influence of the intrinsic emission of cellular components. Recently, single-wall carbon nanotubes emitting near-infrared fluorescence have been used as optical probes for spatiotemporal imaging of neurotransmitter secretion from a single living cell.^{67–69} Although promising, this sensing strategy is limited by the availability of metabolites that are capable of binding carbon nanotubes and affecting their luminescence.

Recently, our group reported a SERS detection of lactic acid secreted from individual single cells by using 4-MBA functionalized plasmonic colloidosomes as biosensing units (Figure 2C).⁷⁰ This method demonstrates high sensitivity and reliability by ratiometric sensing, but colloidosomes prepared by manual emulsification show size variation and may cause signal fluctuation. Furthermore, the lack of automation and biodegradability may limit the practical sensing applications. To address these issues, a renewable nanotip manipulated by the optical fiber system was constructed to identify reactive oxygen species (ROS) from single living cells by SERS.⁷¹ The 4-mercaptophenol-modified Ag nanotip was used for SERS sensing of the intra- and extracellular ROS.⁷¹ To build upon this reversible SERS analysis, the nanopipette contributes to surmounting clearance-based problems.⁷¹ It should be noted that these Raman probe-based indirect measurements are still limited in multiplexing. Using a plasmonic nanosensor (so-called SERS optophysiology) prepared by coating borosilicate nanopipettes with gold nanoparticles, multiple metabolites, such as pyruvate, lactate, ATP, and urea were detected simultaneously in a label-free and real-time manner. However, a chemometric sorting algorithm or more advanced artificial neural network algorithm is required to identify the spectra (Figure 2D).^{72,73} Another multiplexing strategy is the development of a SERS-microfluidic droplet platform to realize the label-free simultaneous analysis of metabolites at the single-cell level. By analyzing the intrinsic SERS fingerprints of pyruvate, ATP, and lactate, the metabolic heterogeneity of single cancer cells has been evaluated, which represents a large advance

Table 2. Optical Strategies for Analysis of Proteins Secreted from Single Cells

| analytical modality | underlying principle | targets | pros and cons | ref |
|---------------------|---|--|---|-------|
| Fluorescence | <ul style="list-style-type: none"> • Sandwich immunoassay in microchambers • Fluorescence switch of cell surface-anchored aptamers/peptides • Signal-on imaging in microfluidic droplets | TNF- α , IL-6, IL-10, IFN- γ , protease | Pros <ul style="list-style-type: none"> • High throughput Cons <ul style="list-style-type: none"> • In situ real-time analysis is allowed | 80–83 |
| SERS | <ul style="list-style-type: none"> • Microdroplet-SERS immunoassay | VEGF, IL-8 | Pros <ul style="list-style-type: none"> • High sensitivity (1.0 fg/mL) • Multiplexed analysis (1.0 fg/mL) Cons <ul style="list-style-type: none"> • Weak stability of large SERS nanotags | 84 |
| SPR | <ul style="list-style-type: none"> • Immunobinding induced change of SPR frequency/intensity | TGF- β , IgG, Thrombopoietin, IL-2, IL-6, IL-8, VEGF | Pros <ul style="list-style-type: none"> • Label-free analysis is allowed • Single-molecule resolution • In situ real-time analysis is allowed Cons <ul style="list-style-type: none"> • Challenging in multiplexed analysis | 85–92 |

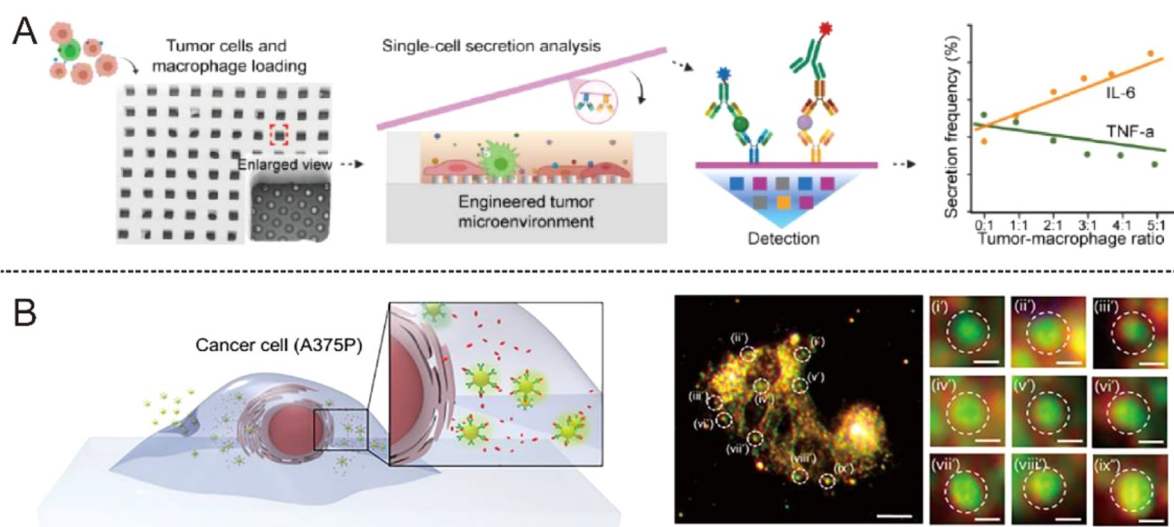


Figure 3. (A) Engineering and characterization of single-cell secretion analysis platform. Reprinted with permission from ref 82. Copyright 2021 American Chemical Society. (B) Immunoplasmonic approach for transforming growth factor- β . Reprinted with permission from ref 85. Copyright 2021 American Chemical Society.

toward real-time single-cell secretion analysis.⁷⁴ In addition, an SPR strategy has recently been developed for tracking the release of metabolites from single cells, although the analytes were limited to the highly reactive molecules such as hydrogen peroxide.⁷⁵ The pros and cons of each sensing modality are summarized in Table 1.

Proteins. The cell-released proteins, such as cytokines and proteases, play critical roles in regulating physiology and homeostasis in the change process of the extracellular environment.^{76–81} Optical spectroscopies based on fluorescence, SERS, and SPR have been exploited in the protein secretion analysis (Table 2). A fluorescent immunoassay-based single cell analysis platform has been developed for investigating the differential modulation effect in cytokine

secretions by the tumor microenvironment (Figure 3A).⁸² However, as other classical immunoassays, this method faces a problem for which multistep washing and incubation are needed; thus it is not compatible with real-time analysis. Recently, Figdor et al. developed a membrane anchored aptamer sensor combined with a droplet microfluidic platform to detect cytokine secretion.⁸³ Based on the hydrophobic interaction between the cholesterol tail and the cell phospholipid layer, the cholesterol-linked aptamer probe could be stably anchored on the cell surface. After binding to secreted target cytokines, fluorescence emission of the aptamer probe would be lightened up. By using a microfluidic chip system, aptamer-modified T cells can be individually encapsulated into droplets, which enabled high-throughput

Table 3. Optical Strategies for Analysis of Cell-Secreted Vesicles and Their Cargos

| strategy | target | LOD | real-time analysis | assay throughput | multiplexed analysis | ref |
|--|--------------------|-------------------------------------|--------------------|------------------|----------------------|-----|
| Antibody barcode-based fluorescent immunoassay | EV surface protein | / | No | >1000 samples | Yes | 99 |
| Fluorescence imaging of cellular membrane deformation during vesicle release | Vesicle | / | Yes | Single sample | No | 100 |
| Fluorescence imaging of vesicle fusion with cellular membrane | Exosome | / | Yes | Single sample | No | 101 |
| Ag staining-based immunoassay | EV surface protein | $\sim 10^5$ vesicles/ μL | No | >1000 samples | No | 102 |
| Metal-enhanced fluorescence detection after Immunomagnetic isolation | Exosomal miRNA124 | / | No | Single sample | No | 104 |
| Hybridization induced fluorescent lighting | Exosomal miRNA21 | 45.4 fM | No | >45 samples | No | 105 |
| Catalytic hairpin assembly driven fluorescence amplification with spatially confined DNA nanocubes | Exosomal miRNA21 | 9.8×10^7 particles/mL | No | Single sample | No | 106 |
| Hybridization induced decline of SERS emission | Exosomal let-7a | 5.3 aM | No | Single sample | No | 111 |

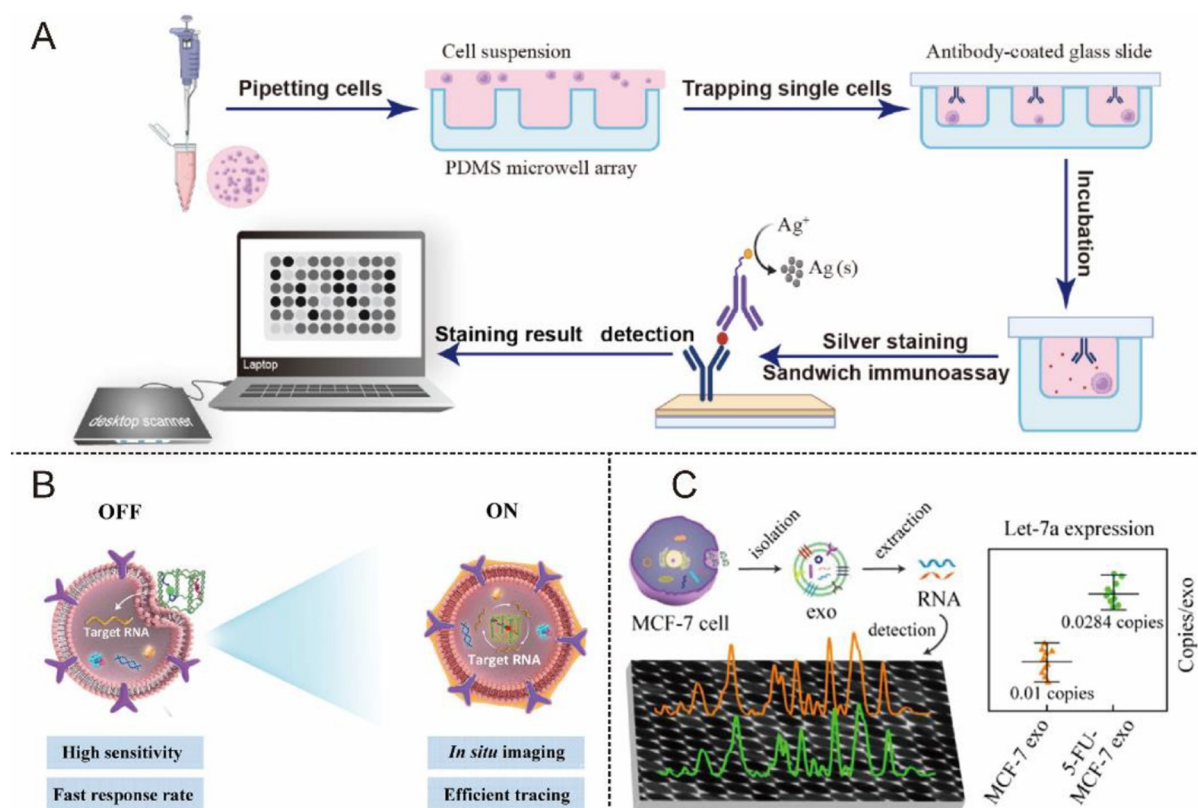


Figure 4. (A) Workflow illustration of trapping of single cells and using gold nanoparticle-enhanced silver staining to enable detection with the desktop scanner for the single-cell EV secretion assay. Reprinted with permission from ref 102. Copyright 2021 American Chemical Society. (B) In situ monitoring of exosomal miRNAs with double-accelerated DNA cascade amplifier nanocubes. Reprinted with permission from ref 106. Copyright 2022 American Chemical Society. (C) Schematic illustration of the SERS sensing exosomal microRNAs. Reprinted with permission from ref 111. Copyright 2021 American Chemical Society.

real-time detection of cytokine secretion at a single cell level, although simultaneous multiprotein quantification is still challenging.⁸³ To circumvent this issue, a SERS immunoassay combined with droplet microfluidics has been developed. The narrow vibrational spectra allowed simultaneous SERS detection of the vascular endothelial growth factor (VEGF) and interleukin-8 (IL-8) released from single living cells in monodispersed droplets.⁸⁴ A significant limitation of this method is that complex SERS nanotags are needed for signal transformation. The insufficient stability of metallic particles in

biological samples such as the extracellular medium may decrease the detection accuracy.

The protein secretion has also been studied by SPR-based strategies which allow label-free, real-time detection of molecular interactions occurring on or near a noble metal surface by monitoring changes in refractive index induced by molecular binding.^{85–92} For example, Choi et al. reported an immunoplasmonic approach for transforming growth factor- β (TGF- β) (Figure 3B).⁸⁵ The method used antibody-conjugated single gold nanoparticles as optical detection probes.

Adsorption of the secreted TGF- β on surface of the gold nanoparticle induced an apparent shift in the plasmonic scattering peak of the particle due to variation of the local refractive index.⁸⁵ The method was capable of detecting TGF- β with picomolar sensitivity and monitoring the extracellular TGF- β level secreted from cells under stress conditions.⁸⁵ In another work, two antibody-modified gold nanorods, which showed distinct SPR peaks, were used to create a plasmonic microdroplet platform for label-free, real-time, high-throughput, and multiplexed monitoring of the secretion of IL-8 and VEGF from single cancer cells.⁹³ Besides spectral analysis, SPR imaging has also been employed for real-time monitoring of protein secretion from single cells.^{94–96} These advanced methodologies not only expand the assay throughput but also bring an improvement for high spatiotemporal measurement. The major drawback of SPR strategies lies in the weak ability for multiplexing due to the limited resolution of spectrometers for the SPR peaks of metal nanostructures.

Vesicles. Extracellular vesicles (EVs) are important intercellular mediators regulating intercellular communications and transferring biological information molecules like cytosolic proteins, lipids, and nucleic acids.^{97,98} Various optical spectroscopic strategies have been proposed for EV quantification and functional analysis (Table 3). An antibody barcode-based fluorescence approach has been developed for high-throughput, multiplexed profiling of single-cell EV secretion. The approach used nanoliter microwell arrays for isolating and enriching EVs released from single cells and spatially resolved antibody barcode for fluorescence detection of EV surface proteins. Single-cell heterogeneity underlying EV secretion within a phenotypically similar cell population was revealed.⁹⁹ For a deep understanding of the biosynthesis and secretion of EVs, in situ real-time analysis is urgently needed.¹⁰⁰ Recently, Verweij et al. described a total internal reflection fluorescence microscopy that enabled imaging of vesicles based on tetraspanin reporters.¹⁰¹ The approach allowed real-time measurement of exosomes released from a single live event and the identification of subcellular sites of fusion events.¹⁰¹ However, these fluorescent methods mainly rely on expensive or unwieldy instruments, which hinder the practical application. On the bases of gold nanoparticle-enhanced silver staining and the Poisson distribution statistics, a home-use scanner platform was developed.¹⁰² After seeding single cells in microchamber arrays, gold nanoparticle-labeled antibodies were used to execute the sandwich immunoassay, which enabled further generation of a plasmonic silver coating with intense light scattering and reflection (Figure 4A).¹⁰² The method was used to analyze the different phenotypes and the number of extracellular vesicles secreted from the single cell, and has the characteristics of high-throughput and no cell counting.¹⁰²

Extracellular vesicles encapsulate a variety of substances such as microRNAs (miRNA) and proteins which play a pivotal role in the disease progression and have received wide attention as next-generation biomarkers.¹⁰³ However, the low abundance and protection of lipid bilayer make it challenging to sense these substances. Several signal amplification-based fluorescent strategies, such as metal-enhanced fluorescence, hybridization chain reaction, and confined space acceleration of hybridization, have been designed to quantify EV miRNAs.^{104–106} Li et al. developed a double-accelerated DNA nanocube, which combines the spatial confinement effect and the catalytic hairpin assembly reaction to achieve fast fluorescence signal

amplification, for in situ monitoring of miRNA21 in exosomes released from cancer cells (Figure 4B).¹⁰⁶ Furthermore, with the continuous progress in fabrication of novel SERS substrates via colloidal synthesis and interfacial self-assembly,^{107–109} SERS has emerged as a powerful analytical tool for analysis of EV miRNAs.^{110,111} By self-assembling nanoparticles at the oil–water interface, a close-packed and ordered Au octahedra array was developed. The Au nanoarray was used to construct a SERS sensor for exosomal miRNA let-7a, which exhibited broad linearity ranging from 10 aM to 10 nM and could discriminate the target from other miRNA sequences with single-base resolution (Figure 4C).¹¹¹ It should be noted that most existing methods, either fluorescence-based techniques or SERS-based ones, are not compatible with a single-cell EV miRNA analysis due to their inability to capture EVs and label the EV miRNAs in situ. However, recently it was reported that the rigid DNA nanostructures and liposome-based vesicle fusion techniques could be used to effectively deliver optical probes to into the EVs.^{112,113} The integration of these novel technologies with single-cell microfluids such as microchamber arrays may enable highly-throughput analysis of EV miRNAs released from single cells.

CONCLUSIONS AND OUTLOOK

New strategies for accurate detection and monitoring of single-cell secretion are critical to enable deeper understanding of the heterogeneous cell states between normal and pathological conditions. This knowledge will boost the development of precision medicine by the discovery of meaningful screening and diagnostic biomarkers and therapeutic targets, thereby allowing clinicians to tailor treatment according to the specific characteristics of each patient. They will be help to improve the outcome of patients with malignant diseases, both acutely and in the long term, by providing earlier medical intervention, precise management, and prognosis.

Compared to population-based methodologies, such as liquid chromatography–tandem mass spectrometry (LC-MS/MS) or immunoassays (e.g., ELISA in multiwell plates), single-cell techniques exhibit remarkable resolution. In general, LC-MS/MS methods require several hundred microliters of samples ($>10^5$ cells),¹¹⁴ whereas microscopic optical strategies have achieved nanoscale subcell resolution.^{50,115} Moreover, cells are lysed in LC-MS/MS assays, and are thus incapable of real-time and in situ recording of secretion events of live cells. Although advanced immunoassays such as digital ELISA has an improved sensitivity at the single-cell level, they use a sandwich-based approach, hence involve multistep operations, and are not applicable for measuring secretion events at a high spatial–temporal resolution.

Despite great progress in optical spectroscopic analysis of single-cell secretion over recent decades, formidable challenges remain to be addressed. First, new principles and methods for improving the signal-to-noise ratio (SNR), and hence the sensitivity and temporal resolution during the in situ observation of the secretion dynamics must be established.¹¹⁶ As detailed in this Perspective, current efforts to meet this challenge have largely focused on amplifying the signal generated by target analytes as well as on new insights into elimination of the nonspecific background noise. As SNR is related to both the signal and noise levels, preventing nonspecific binding would not only enable a sensitivity and resolution enhancement but also be helpful to avoid measurement bias. Second, as secretion events occur locally on the live

cell surface, methods with unprecedented spatial resolution must be developed. Recent advances in live-cell super-resolution imaging may facilitate observation of secretion with nanoscale resolution.¹¹⁷ Moreover, to continuously observe molecular efflux from the local cell surface for extended periods of time, facile methods for site-specific engineering of the outer cell membrane with rationally designed probes should be further developed. To this end, in addition to classical bioconjugation techniques (e.g., biotin–streptavidin coupling, *N*-hydroxysuccinimide (NHS) ester–primary amine reaction),¹¹⁸ biorthogonal click chemistry is playing an increasingly prominent role because of the high selectivity and biocompatibility.¹¹⁹ In addition, since oligonucleotide sequences can be facilely edited and labeled with other chemical/biological moieties (e.g., cholesterol), noncovalent anchoring of oligonucleotide-based optical probes such as aptamers at the cell surface would offer new access to single-cell secretion measurements. It should be noted that, in comparison to antibodies, currently available aptamers, especially the ones targeting specific proteins or small molecules, are still relatively insufficient. We expect that with the continuous development of aptamer discovery techniques (e.g., machine learning guided discovery),¹²⁰ this challenge can be effectively addressed. Furthermore, the fluorescence- and SPR-based techniques to date are only capable of detection and imaging of very few targets (≤ 3 kinds of targets) simultaneously due to spectral overlap. To truly enable high-throughput molecular profiling of single-cell secretion by these techniques, integrated platforms that combine optical spectroscopic analysis with other techniques such as spatial and spectral encoding, microfluidic chips, MS, or flow cytometry should be further studied.^{121–125} For SERS analysis, although the molecular narrow band spectra theoretically permit multiplexed monitoring of cellular species, accurately extracting and quantifying the intensities of the characteristic SERS peaks of the target molecules remain a challenge due to the heterogeneous distribution of SERS hot spots on the enhancing matrix. In this regard, the continuous progress in molecular manipulation by DNA origami and host-guest chemistry may facilitate the construction of highly reproducible SERS substrates and the precise placement of target analytes in the hot spots.^{126–129}

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The manuscript was written through contributions of all authors.

Notes

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