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One-step nanoscale expansion microscopy reveals individual protein shapes

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The attainable resolution of fluorescence microscopy has reached the subnanometer range, but this technique still fails to image the morphology of single proteins or small molecular complexes. Here, we expand the specimens at least tenfold, label them with conventional fluorophores and image them with conventional light microscopes, acquiring videos in which we analyze fluorescence fluctuations. One-step nanoscale expansion (ONE) microscopy enables the visualization of the shapes of individual membrane and soluble proteins, achieving around 1-nm resolution. We show that conformational changes are readily observable, such as those undergone by the ~17-kDa protein calmodulin upon Ca^{2+} binding. ONE is also applied to clinical samples, analyzing the morphology of protein aggregates in cerebrospinal fluid from persons with Parkinson disease, potentially aiding disease diagnosis. This technology bridges the gap between high-resolution structural biology techniques and light microscopy, providing new avenues for discoveries in biology and medicine.

Several recent studies have improved the localization precision of fluorescence microscopy to the 1-nm range or even below this value[1–4]. Nevertheless, the application of such techniques to biological samples has been limited by two fundamental problems. First, the achievable structural resolution depends on the labeling density because fluorescent proteins or chemical fluorophores cannot be packed closer than their molecular size (typically 1 nm or larger[5]) allows. This could be alleviated by having only one functional fluorophore physically present at one time point at the respective location[3,4]. Second, fluorophores can interact through energy transfer at distances below 10 nm, resulting in accelerated photoswitching (blinking) and photobleaching and, thus, in lower localization probabilities[6].

A simple solution would be to separate the labeling sites by the physical expansion of the specimen, in what is termed expansion microscopy (ExM)[7]. In addition, the samples can be labeled fluorescently after expansion, at a time point at which the fluorophore size becomes negligible and, therefore, no longer hinders the labeling density, while lowering the displacement error. To then reach molecular-scale imaging, one would combine ExM with optics-based super-resolution. This has been attempted numerous times[8–10] but

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the resulting performance typically reached only ~10 nm. ExM gels are dim because the fluorophores are diluted by the third power of the expansion factor, thus limiting optics techniques that prefer bright samples, such as stimulated emission depletion (STED), or saturated structured illumination. In addition, ExM gels need to be imaged in distilled water because the ions in buffered solutions shield the charged moieties of the gels and diminish the expansion factor. The use of distilled water reduces the performance of techniques that rely on special buffers, such as single-molecule localization microscopy[7]. A third class of optical super-resolution approaches is based on determining the higher-order statistical analysis of temporal fluctuations measured in a video, using algorithms applied to these images to generate super-resolution images, such as super-resolution optical fluctuation imaging (SOFI)[11] or super-resolution radial fluctuations (SRRF)[12,13]. The resolution of these approaches is inversely correlated to the distance between the fluorophores[12–14] and they do not require especially bright samples or special buffers, implying that they should benefit from ExM. To test this hypothesis, we combined X10 ExM[15,16] with SRRF[12–14] and established a technique we term one-step nanoscale expansion (ONE) microscopy (Fig. 1a,b). Using this technique, we aim to reveal the shape of single proteins of different sizes with near 1-nm resolution.

Results

Principles and validation of ONE microscopy

We first attached a gel-compatible anchor (Acryloyl-X) to protein molecules, either purified or in a cellular context, and then embedded these samples into a swellable X10 gel[15,16]. Proteins were hydrolyzed (homogenized) by proteinase K or by heating in alkaline buffers, leading to main-chain breaks. This enables a highly isotropic tenfold expansion of the sample, which is achieved by distilled water incubations[15,16]. We then imaged the samples using wide-field epifluorescence or confocal microscopy, acquiring series of hundreds to thousands of images as videos (ideally 1,500–2,000) in which the fluorescence intensity of the fluorophores fluctuates (Fig. 1b and Supplementary Fig. 1). Each pixel of a frame was then magnified into a large number of subpixels and the local radial symmetries of the frame (which are because of the radial symmetry of the microscope's point spread function (PSF)) were measured. This parameter, termed 'radiality' was analyzed throughout the image stack, by higher-order temporal statistics, to provide the final, fully resolved image[12–14]. To aid in the implementation of this procedure, we generated an ONE software platform as a plugin for the popular freeware ImageJ (Fiji) (Supplementary Fig. 2 and Supplementary Software).

In theory, the precision of the SRRF technique should reach values close to 10 nm (ref. 12). SRRF should, therefore, be able to separate fluorophores found at 20 nm from each other, provided the signal-to-noise ratio (SNR) is sufficiently high. We found this to be the case, using nanorulers (provided by GATTAquant[17]) of precisely defined size (Supplementary Figs. 4 and 5).

In practice, most previous implementations of SRRF have reached ~50–70 nm. This is partly because of the fact that the presence of overlapping fluorophores reduces radiality in conventional samples[12,13] and partly because of the aims of the respective SRRF implementations, which did not target ultimate performance in terms of resolution and, therefore, did not optimize a number of parameters. First, the highest resolutions are obtained by analyzing higher-order statistical correlations, whose precision is dependent on the number of frames acquired, as discussed not only for SRRF but also for SOFI[11]. While most publications used less than 300 frames, we found that results were optimal when using 1,500–2,000 frames (Supplementary Fig. 5). Working with low frame numbers reduces the achievable resolution, even when working with ExM gels[18,19]. Second, the SNR needs to be optimized carefully (Supplementary Fig. 6).

These limitations are alleviated by ExM (see Supplementary Discussion for more details). As the distance between the fluorophores increases, it enables the study of intensity fluctuations from individual dye molecules independently. The SNR also increases even for idealized samples consisting only of fluorescently conjugated nanobodies (Nbs) in solution (Supplementary Fig. 3a,b). This approach should, therefore, allow an optimal SRRF performance, which, divided by the expansion factor, should bring the resulting imaging precision to the molecular scale, as long as the gel expands isotropically in all dimensions. The X10 gel, based on *N,N*-dimethylacrylamide acid (DMAA), rather than the acrylamide used in typical ExM protocols, has a more homogeneous distribution of crosslinks[20], thus leading to fewer errors in expansion (a further discussion on gel homogeneity was provided in a previous study[21]). However, the use of gels with large expansion factors is prone to inducing imaging drift, which was only eliminated after we introduced specially designed imaging chambers (Supplementary Fig. 7). For correcting residual drifts, the ONE plugin automatically applies drift correction before computation (Supplementary Fig. 8). Drift compensation is explained in more detail in the Supplementary Information.

ONE microscopy reveals protein shapes

To reveal protein molecules, we labeled their peptide chains using *N*-hydroxysuccinimide ester (NHS-ester) fluorescein[22,23], which maintains a signal intensity of ~50% by the end of the video acquisition, under our imaging conditions, for this type of experiment (Supplementary Fig. 3c,d). This is possible because proteins are broken during homogenization at multiple main-chain positions and each resulting peptide has an exposed amino-terminal group that can be efficiently conjugated with NHS-ester-functionalized fluorophores. For an initial visualization, we applied this labeling method to a membrane protein, the full-length β3 human γ-aminobutyric acid receptor ($GABA_AR$) homopentamer, a ligand-gated chloride channel[24]. We analyzed purified receptors in solution and produced images that resembled 'front' and 'side' views of the receptor, similar to its structure, as derived from crystallography and single-particle cryogenic electron microscopy (cryo-EM) structures (Fig. 1b,c and Supplementary Fig. 9). It is worth noting that the particles observed by ONE microscopy are indeed single molecules and no averaging or classification was performed on these datasets.

We next applied this approach to antibody molecules and we could observe immediately recognizable outlines for immunoglobulins (IgGs, IgAs and IgMs) (Fig. 2a and Supplementary Fig. 10). Fluorescent labels attached to secondary IgG antibodies could also be observed in the same images (Fig. 2a) and in complexes between fluorescently conjugated primary and secondary antibodies or Nbs (Supplementary Fig. 10b).

We next investigated a protein of unknown structure, the ~225-kDa otoferlin, a Ca^{2+} sensor molecule that is essential for synaptic sound encoding[25]. The outlines provided by ONE microscopy imaging strongly resemble the AlphaFold[26] prediction for this protein (Fig. 2b and Supplementary Fig. 11). At the opposite end of the Ca^{2+} sensor size spectrum, we sought to visualize the small (~17 kDa) protein calmodulin, expressed as a green fluorescent protein (GFP) chimera. GFP itself was visualized as a small and compact structure, as expected (Fig. 2c and Supplementary Fig. 12). Calmodulin–GFP exhibited an elongated shape, as expected from its known structure (Fig. 2d). To our surprise, even for such small particles, it was possible to observe changes in their shape upon Ca^{2+} binding (Fig. 2d). We applied both heat denaturation and proteinase K treatments for the homogenization of calmodulin, to test whether these methods would lead to different results. The proteinase K presumably removes most of the amino acids that are not anchored into the gel and is, therefore, more aggressive than the heat denaturation[27]. However, both methods resulted in similar observations for calmodulin, implying that both can be used for observing the shape of purified proteins (Fig. 2d and Supplementary Fig. 13).

To validate our procedures, we proceeded to test the organization of a number of samples that were analyzed in the past using methods

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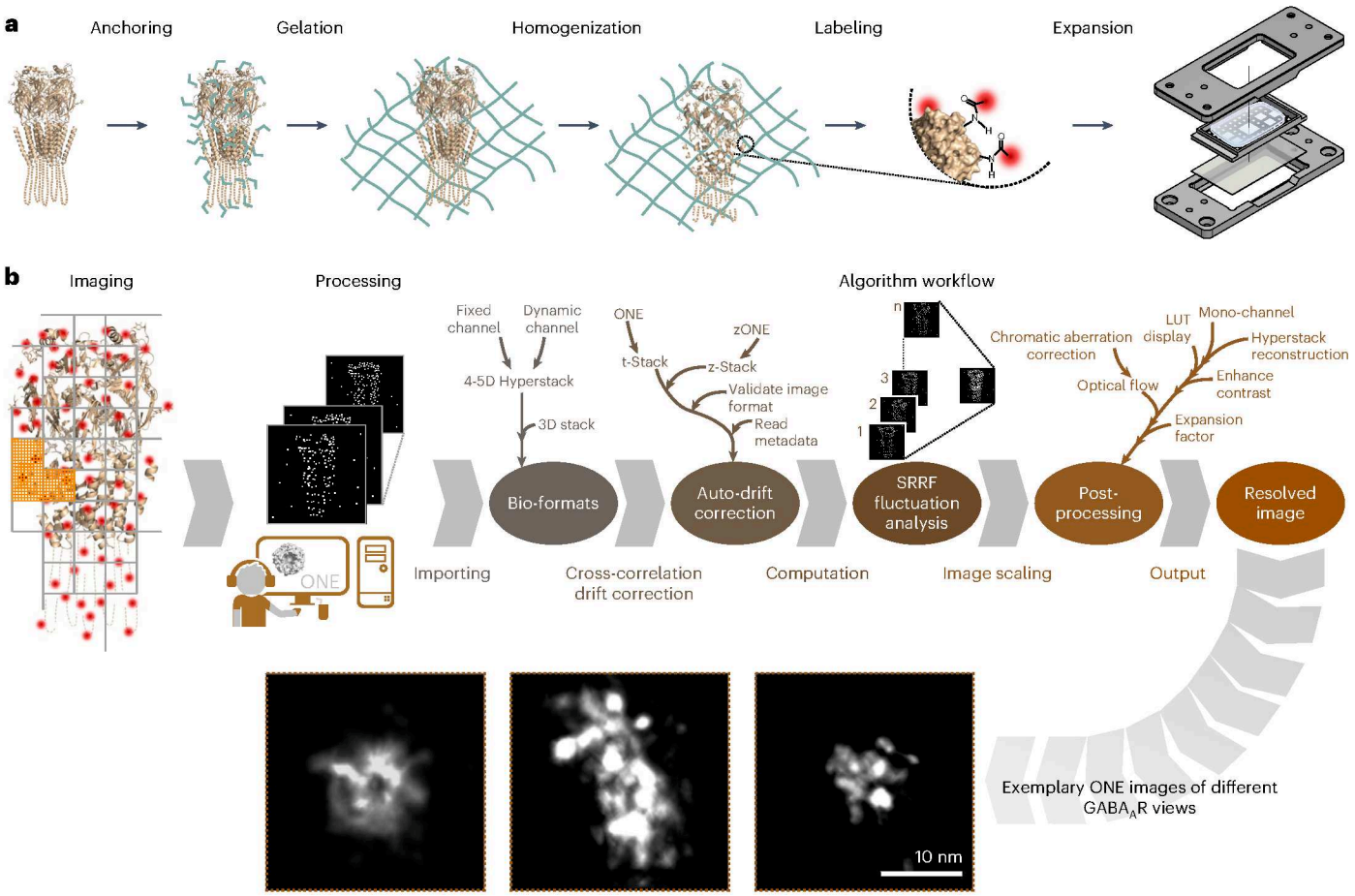

Fig. 1 | ONE microscopy concept. a, Biological samples are linked to gel anchors, relying on Acryloyl-X, followed by X10 gel formation and homogenization, which is achieved either by proteinase K digestion or by proteolysis induced by autoclaving in alkaline buffers. Full expansion is achieved by repeated washes with distilled H_2O and is followed by mounting gel portions in a specially designed chamber. **b**, Expansion separates the fluorophores spatially, allowing them to fluctuate independently[6]. Repeated imaging is performed (up to 3,000 images) in any desired imaging system (confocal, epifluorescence, etc.) to detect signal fluctuations, which are then computed through an open-source JAVA plugin (ONE platform) based on the SRRF algorithm, before assembling the final super-resolved exemplary images (here, GABA$_A$Rs). The analysis routine is explained in Supplementary Fig. 1 and a flowchart of the software implementation is shown in Supplementary Fig. 2. Further details on image acquisition and image processing can be found in the Methods. **c**, Superimposition of ONE microscopy images and cryo-EM data. A cartoon view of a complex consisting of a GABA$_A$R bound simultaneously by five Nbs (GABA$_A$R–Nb, PDB 5OJM). The red dots represent the two fluorophores on each Nb. The four cryo-EM images are representative 2D classes of the GABA$_A$R–Nb complexes, derived from the same samples as used for ExM. The overview panel shows an exemplary ONE image (from a total 648 ONE images, acquired from at least six gels) of GABA$_A$R–Nb that are postexpansion labeled with NHS-ester dyes described in Supplementary Fig. 3, followed by a magnified region of a single receptor. The last panel shows a cryo-EM–ONE overlay.

with very high resolution, such as MINFLUX. As shown in Supplementary Fig. 14, ONE microscopy could reproduce the expected signal patterns on isolated Nbs in vitro (Supplementary Fig. 14a–e). Moreover, the signals observed by immunostaining cultured neurons with a postsynaptic density protein 95 (PSD95) Nb (initially indicated in a previous study[28]) are very similar to results obtained more recently by MINFLUX microscopy[29] (Supplementary Fig. 14f). Lastly, microtubule images were also similar to their MINFLUX counterparts (Supplementary Fig. 14g).

For additional validation purposes, we evaluated a purified ALFA-tagged enhanced GFP (EGFP) construct bound simultaneously by two anti-GFP Nbs[30] and by an anti-ALFA Nb[31]. This results in a triangular semiflexible arrangement, which we termed a 'triangulate smart ruler' (TSR; Supplementary Fig. 15a–c). The TSR aspect observed in

ONE microscopy was consistent with crystal structures of Nb–EGFP and Nb–ALFA complexes (Supplementary Fig. 15d,e). The fluorophore positions on the individual Nbs were also consistent with their known size (Supplementary Fig. 16a,e). However, Nbs are 4–5 nm in length, implying that the fluorophores they carry are separated by relatively large distances. To test the performance of ONE microscopy on smaller structures, we turned to a polypeptide consisting of nine amino acids, termed membrane-binding fluorophore-cysteine-lysine-palmitoyl group (mCLING)[32]. mCLING contains seven lysines, thereby offering many anchor points for ExM, and can also carry on its C-terminal cysteine residue an additional Atto 647N moiety, resulting in a total molecular weight of 2,056 Da (Supplementary Fig. 17a). The whole length of mCLING is ~3 nm (according to our simulations; Supplementary Fig. 17d) and its expansion should place fluorophores at subnanometer distances. As expected, we indeed observed fluorophores separated by ~1 nm or below (Supplementary Fig. 17e–g).

We also sought to verify whether such analyses could be performed using a natural system rather than purified proteins. To test this, we turned to cell cultures subjected to detergent extraction during fixation. This procedure results in the preservation of actin filaments at the cell–glass interface, which could then be analyzed in ONE microscopy. We performed a simple manual averaging analysis on ~50 filaments and we obtained images that reproduce the known size of the actin filaments and the distance between the actin subunits, as well as providing views of the filament pitch (Supplementary Fig. 18).

Three-dimensional (3D) analysis of ONE images validates our imaging precision

The ability of ONE microscopy to reveal images of individual molecules opens a strong possibility of user bias. Users are naturally impressed by images showcasing the expected protein shapes, implying that such images would tend to be over-reported (akin to the 'Einstein from noise' problem known in single-particle cryo-EM[33]). Such bias is difficult to quantify and affects our understanding of the precision of the ONE technology. In principle, most ONE images may suffer from various degrees of distortion, from uneven expansion to inhomogeneous labeling, which a user-biased qualitative analysis would fail to report.

To address this, one could image the size and organization of known molecular structures, such as the nuclear pore complex (NPC; as performed in several recent studies, including our characterization of the X10 gels[27]), which would serve as molecular rulers to validate the ONE procedure. However, the NPC size (>100 nm) is far too large for ONE microscopy and we, therefore, applied this procedure on smaller molecules or assemblies, whose size is known or can be estimated from structural biology techniques, including Nbs, GFP, actin, $GABA_A$Rs, otoferlin, IgG, IgA and IgM (Supplementary Fig. 19). As presented in Supplementary Fig. 19, all measured parameters were very similar to the expected values and their variance was limited, suggesting that the expansion and labeling have isotropic, homogeneous performance.

While this approach has been sufficient for validating most super-resolution fluorescence microscopy tools in the past, we would like to point out that structure measurements do not constitute a complete solution to the issue of user bias because the particles measured are still selected by humans. In principle, one could turn to automated techniques of measuring image resolution, such as the Fourier ring correlation (FRC) determination[34]. We applied this approach to our images, relying on the NanoJ-SQUIRREL package[34] with a blockwise implementation, to provide FRC values for different regions within individual images (Supplementary Fig. 20). We obtained values within the low single-digit nanometer range and below 1 nm when suitably small pixels were used. This is in line with our ability to measure distances as low as 0.5 nm within single molecules (Supplementary Fig. 21). However, this remains only a partial solution to the bias issue because only the resolution and not the accuracy of fluorophore placement (that is, the degree of distortion) is measured.

We, therefore, turned to a completely automated analysis, in which the 3D shape of individual proteins is derived from the ONE images. To overcome human bias, ONE images were segmented using an automatic thresholding procedure (based solely on particle intensity) to identify hypothetical molecules. These were processed by deconvolution and normalization steps (Methods) and transferred to cryoFIRE, an unsupervised ab initio autoencoder for complex shape reconstruction with amortized inference[35], which was modified to accommodate fluorescence rather than cryo-EM signals. Importantly, the cryoFIRE algorithm does not place any bias on the expected molecular shape because there is no user input and no correlation to expected structures. The overall approach is illustrated in Supplementary Fig. 22a.

We first applied this procedure to the simple case of an Nb carrying two fluorophores (Fig. 3a). The deep learning analysis of 279 protein molecules resulted in the expected visualization of two fluorescent objects in 3D, spaced by a distance that is fully compatible with the known size of the respective Nbs (Fig. 3a). To proceed to a larger molecule, we targeted GFP (Supplementary Fig. 22a,b). The results, obtained from 885 protein molecules, are shown in Supplementary Fig. 22b. To obtain a numerical estimate for the precision of the 3D shape obtained by ONE, we turned to a Fourier shell correlation analysis[36], comparing the ONE results to the cryo-EM structure. A value of 18 Å was obtained, suggesting that the overall resolution of the ONE procedure, from imaging to 3D reconstruction, is between 1 and 2 nm.

We finally turned to a substantially more complex object, a human $GABA_A$R homopentamer[24].The analysis of 4,938 two-dimensional (2D) views of molecules resulted in the 3D shape depicted in Fig. 3b, in comparison to both AlphaFold[37] predictions and crystallography-derived structures (Fig. 3c). A Fourier shell correlation analysis provided a value of 16 Å, again suggesting that the precision of the technique, in 3D, lies between 1 and 2 nm.

Overall, these results demonstrate that the ONE microscopy images are representative of the respective molecular structures. While the 3D shapes obtained have a substantially lower resolution than structures derived from crystallography and cryo-EM, our results imply that the generation of protein structures from fluorescence images should be possible.

Clinical sample analysis: Parkinson disease (PD)

In principle, all of the observations made above could be reproduced, at higher resolution, in cryo-EM imaging. However, cryo-EM faces challenges in observing specific proteins or protein assemblies in complex mixtures, unless they have special density and/or shape features[38]. ONE microscopy can rely on specific epitope recognition, thereby avoiding this problem. To test this, we sought to address a pathology-relevant imaging challenge, focusing on PD, a neurodegenerative disease characterized by the accumulation of aggregates composed of several proteins, of which α-synuclein (ASYN) is the most prominent[39]. In the cell, ASYN can exist as a monomer or can assemble into species of different sizes, including soluble oligomers and fibrils. A substantial number of studies focused on ASYN as a PD biomarker. Genetic changes (mutations) in *SNCA* (the gene for ASYN) are poor biomarkers because familial PD accounts for a minority of all cases. Measuring the ASYN levels has also proven to lack diagnostic relevance. Measuring post-translational modifications (for example, phosphorylation) has similarly been difficult to use as a biomarker. The combination of ASYN phosphorylation analyses with other parameters, including nerve fiber morphology, amyloid deposition and skin histology, has been more successful[40], leading to a commercial PD biomarker test (Syn-One Test, CND Life Sciences). However, it is unclear whether phosphorylated ASYN is a toxic species because it seems to inhibit seeded fibril formation and toxicity[41] while also being a physiological form of ASYN involved in synaptic transmission.

The ideal diagnostic procedure would reveal the actual toxic species, which are thought to be ASYN oligomers (reviewed previously[42]). This has been exceedingly difficult because the performance

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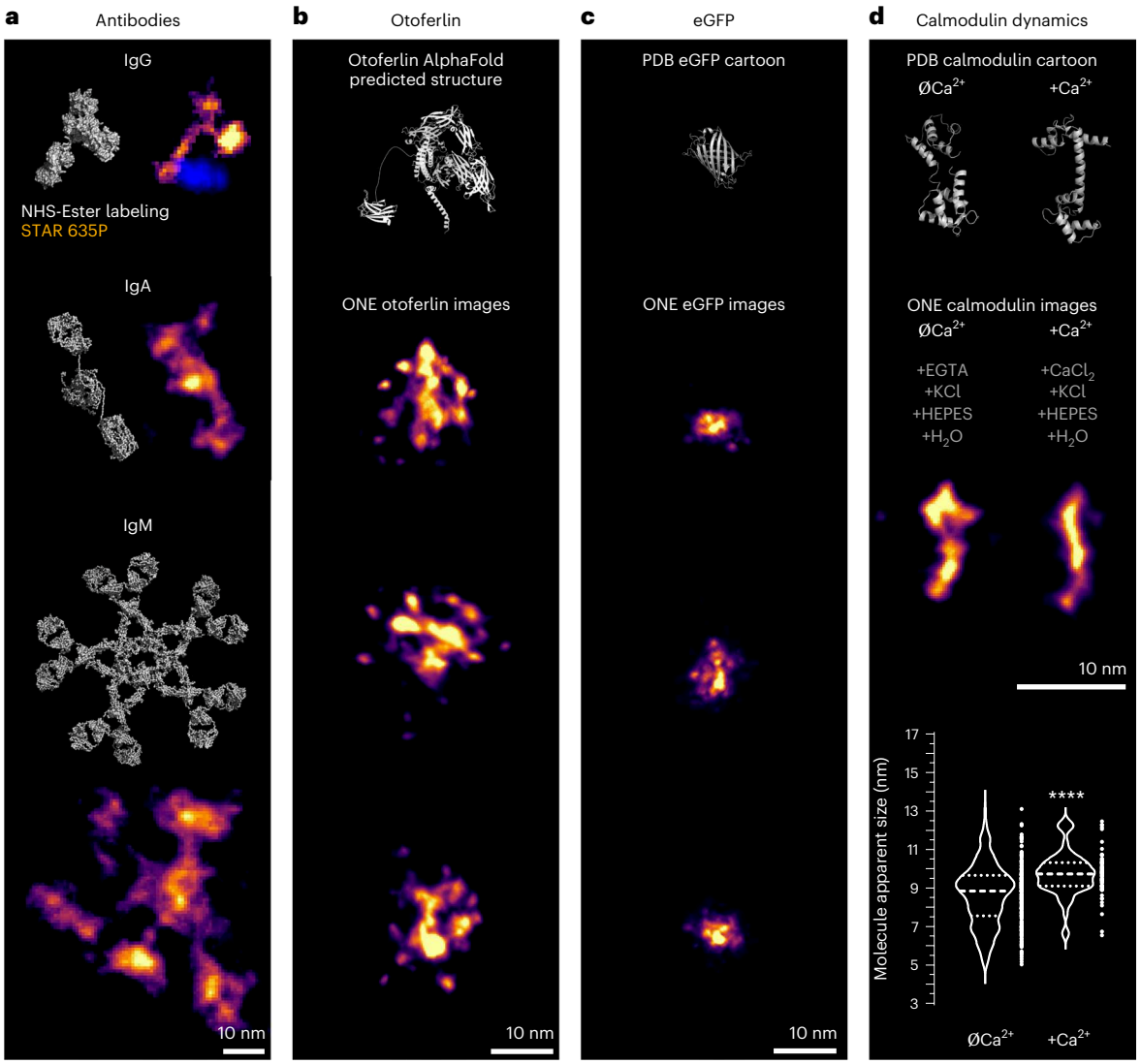

Fig. 2 | ONE analysis of single molecules. To delineate protein shapes, gels containing proteins were labeled with NHS-ester fluorescein after homogenization. **a**, ONE images of isolated immunoglobulins (secondary anti-mouse IgG conjugated to STAR 635P, human IgA and IgM and their respective PDB structures: 1HZH, 1IGA and 2RCJ) obtained from three independent experiments. Immunoglobulin ONE images were analyzed by a different fluctuation analysis, TRPPM, unlike the TRAC4 (ref. 12) approach used in most other figures. Unlike TRAC4, which aims to separate the individual fluorophores, TRPPM enhances the cohesiveness of the fluorophores decorating the single antibodies, resulting in cloud-like signals. Overviews and more analysis can be found in Supplementary Fig. 10. **b**, ONE examples of otoferlin images obtained from at least three independent experiments. The otoferlin model is an AlphaFold prediction. Overviews, control experiments and the otoferlin gallery can be found in Supplementary Fig. 11. **c**, GFP ONE images obtained from three independent experiments and the PDB 1EMA structure. Overviews, size measurements and the GFP gallery can be found in Supplementary Fig. 12. **d**, Structures (PDB 1CLL and 1CFD) of the Ca^{2+} sensor calmodulin, in the presence or absence of its ligand, respectively, along with ONE images after proteinase K-based homogenization and expansion. The expected elongation by ~1 nm was reproduced, as shown by the quantification, which indicates measurements of the longest axis of the calmodulin molecules, performed across all molecules, from all conditions, in a blind fashion ($P < 0.0001$, two-tailed nonparametric Mann–Whitney test; $n = 66–197$). Similar analysis, after homogenization using autoclaving ($P = 0.0006$, $n = 70–155$; Supplementary Fig. 13). The violin plot shows the median, the 25th percentile and the range of values.

of oligomer-specific ASYN antibodies is highly contested[43]. Importantly, ASYN-containing aggregates are present in the cerebrospinal fluid (CSF) and serum of both persons with PD and controls[44]. Thus, simply identifying aggregates (even oligomer-sized ones) is not useful for diagnostics; being able to reveal the toxic ones, those present specifically in persons with PD, would be much more valuable. Notably, a frequently used procedure for PD diagnostics, the seed amplification assay, does not even attempt to identify such species because of difficulties in their analysis.

We argued that insufficient resolution is the main problem in identifying such oligomers and ONE microscopy should be able to reveal them. We analyzed ASYN assemblies in the CSF of persons with PD versus controls (Supplementary Table 1) using an Nb[45]. Full-length immunoglobulins provide poor labeling because of their large size (Supplementary Fig. 24). Different types of ASYN assemblies could be detected (Fig. 4a,b) and persons with PD had higher levels of oligomer-like structures (Fig. 4c,d and Supplementary Fig. 25). All oligomer-like species were significantly more abundant in PD CSF than in control samples (Fig. 4f) and their cumulative analysis, which alleviated ambiguities because of imperfect classification of oligomer types, resulted in a good discrimination of persons with PD and age-matched controls (Fig. 4g,h). Analyses of the different ASYN species may prove to be relevant for diagnostics because some correlate to medication status while others may relate to clinical features (Supplementary Fig. 26). The analysis of ASYN aggregates by ONE microscopy is, therefore, a

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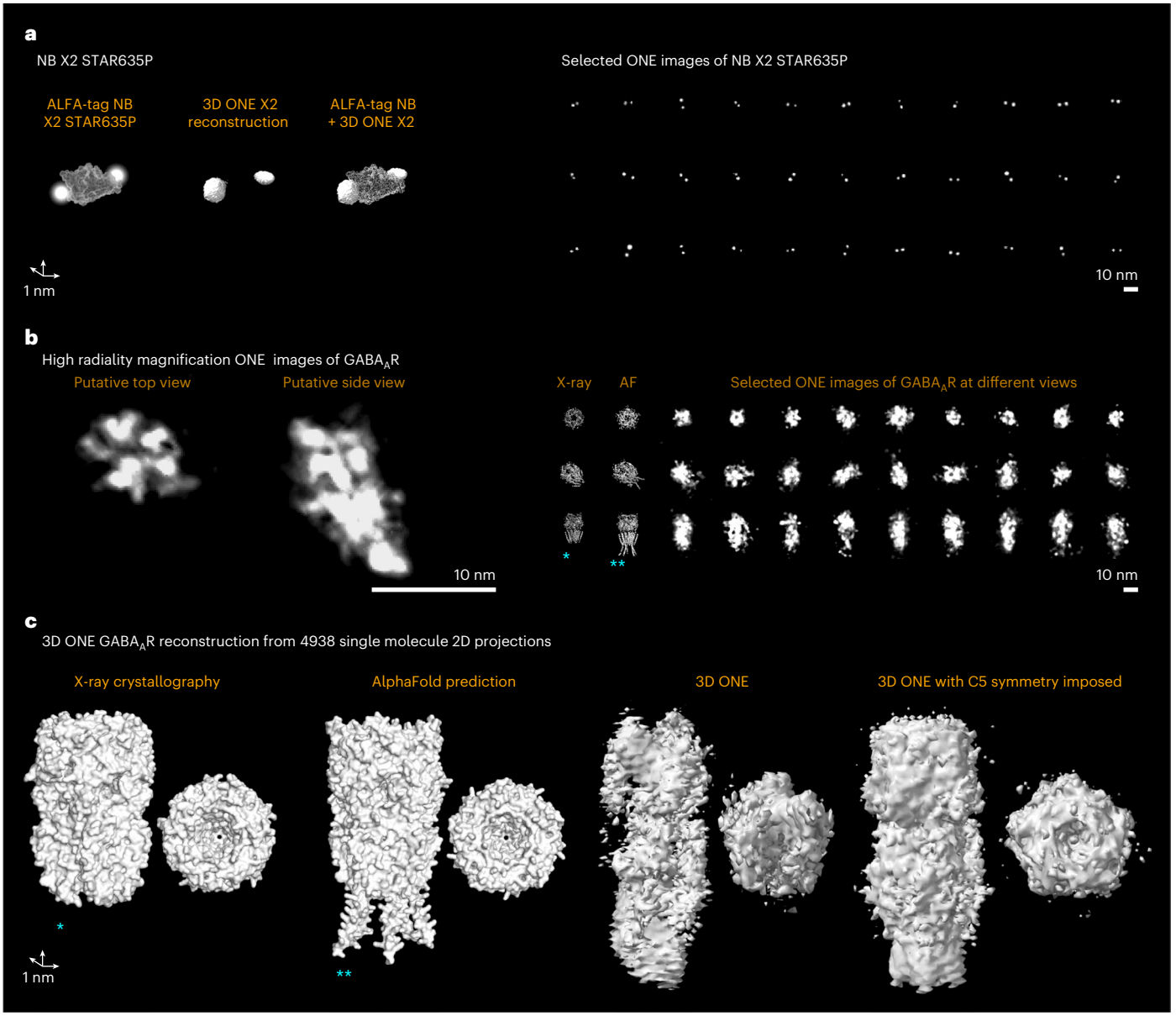

Fig. 3 | 3D ONE reconstruction using unsupervised ab initio artificial intelligence architecture. To reconstruct 3D models from 2D ONE images, segmented single molecules were transferred to a modified cryoFIRE neural network[35] (the neural network workflow can be found in Supplementary Fig. 22a). **a**, To run a sanity test on the reconstructed images, we used ONE images of 279 ALFA tag Nb STAR 635P with two fluorophores at known positions. This experiment used the inherent signal of the X2 STAR 635P fluorophores, foregoing additional labeling. The panel on the left shows the following: left, a model for the ALFA tag Nb structure (PDB 6I2G) in mesh representation, carrying two fluorophores; middle, 3D ONE X2 reconstruction; right, a view of both the 3D ONE X2 reconstruction and the Nb. The panel on the right shows selected ONE images of Nb X2 STAR 635P. The generated 3D positions of X2 fluorophores were at 4.6-nm distance, which correlates well with the measured line scans of 2D ONE images at 4.5 nm (Supplementary Fig. 14a–e). **b**, ONE images of NHS-ester fluorescein-labeled GABA$_A$R in top and side views, obtained with high-radiality magnification (Supplementary Discussion). A gallery of GABA$_A$R in different positions is shown. **c**, 3D representations of GABA$_A$R generated by crystal structure (PDB 4COF), by an AlphaFold-Multimer[37] prediction, by 3D ONE (raw) and by 3D ONE after imposing *C5* symmetry to the molecule. Side and top views are shown. The crystallography structure does not indicate segments that are shown in the AlphaFold model. These segments are visible in the 3D ONE reconstruction. The increased length of the 3D ONE reconstruction, when compared to the AlphaFold model, is probably accounted for by the fact that AlphaFold predicts a substantial unfolded coil in this region, which is not depicted (full AlphaFold-predicted models and error estimates can be found in Supplementary Fig. 23). 3D ONE reconstructions and AlphaFold-predicted models are provided in the Supplementary Information (PDB or MRC files; all reconstruction files have self-explanatory names). Fourier shell correlation analysis indicated that the 3D ONE reconstruction is generated at a resolution of 16 Å. The cyan asterisks indicate the following: *components known to be missing in the PDB 4COF structure; **AlphaFold prediction unclear in this area, as AlphaFold cannot reliably predict disordered domains.

promising procedure for PD diagnosis and possibly for monitoring the disease status.

Multilaboratory applications of ONE microscopy

An important issue for any new technology is its wide applicability in multiple laboratories. To test this issue, we collaborated with academic laboratories in Homburg and at Massachusetts Institute of Technology (MIT), as well as with the industrial laboratory of microscope developer Leica Microsystems. We focused on GABA$_A$Rs, samples that were well described in the rest of the work (Supplementary Figs. 27–29). We were able to show that ONE can be applied in different laboratories, with some of the experiments even surpassing our original applications by

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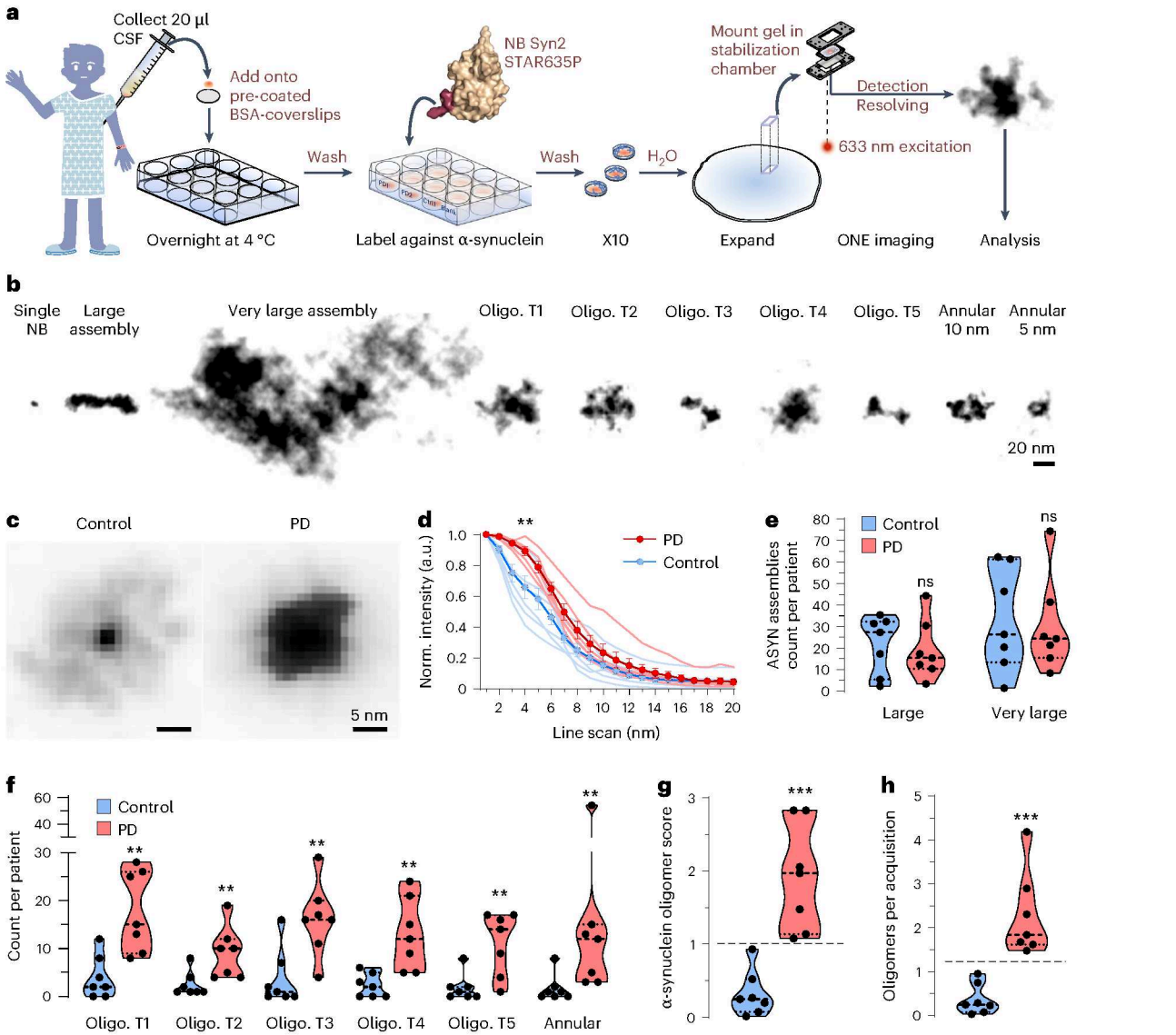

Fig. 4 | Detection of ASYN oligomers in human CSF. a, CSF probes were obtained from persons with PD and controls and 20-µl volumes were placed on BSA-coated coverslips, followed by ONE imaging after immunolabeling ASYN using a specific Nb[45]. **b**, A gallery of typical ASYN species observed in the CSF samples. Only the fluorophores contained by the Nbs are visualized here (no postexpansion labeling). **c**, Average ASYN assemblies from a person with PD and a control. **d**, An analysis of the spot profiles detects significant differences, with the average control object being smaller than the average PD object. All ASYN assemblies for the control and persons with PD were averaged from three independent experiments. Significant differences were determined by a Friedman test followed by Dunn–Šidák correction ($P = 0.0237$); errors show the s.e.m. AU, arbitrary units. **e**, An analysis of the number of larger assemblies in CSF samples. No significant differences were determined according to Mann–Whitney tests ($P = 1$ and 0.7104). NS, not significant. **f**, An analysis of the number of oligomers in CSF samples. All comparisons indicated significant differences according to Mann–Whitney tests followed by a Benjamini–Hochberg multiple-testing correction with a false discovery rate of 2.5% ($P = 0.0105$, 0.0023, 0.0111, 0.0012 and 0.0012, in the respective order of datasets). **g**,**h**, Analyses of the number of oligomers as a proportion of all ASYN assemblies analyzed (**g**) or as the number per acquisition (**h**). Both procedures discriminate fully between the persons with PD and the controls. For the second procedure, the lowest PD value is 50% larger than the highest control. Significant differences were determined by a two-tailed nonparametric Mann–Whitney test ($P < 0.0001$ for **h**,**g**); $n = 7$ persons with PD and $n = 7$ controls.

using either larger expansion factors (MIT laboratory, postexpansion stained bassoon in 20-fold expanded mouse brain tissue; Supplementary Fig. 29) or faster scanning to allow volumetric ONE imaging in two color channels (Leica Microsystems laboratory; Supplementary Fig. 27). We hope that future applications can be facilitated by the open-source software package we generated (Supplementary Fig. 30).

Discussion

ONE microscopy was applied here to analyze a variety of proteins, relying on conventional microscopes. No special handling, unusual fluorophores or reagents are necessary for this technique, which should enable the application of super-resolution analyses to laboratories without access to the best imaging instruments[46]. The initial immunostaining and expansion procedures take a total of 3–4 days, while imaging individual regions of interest only takes between 35 s and 2 min depending on the number of color channels; the SRRF-based procedure is then performed in minutes.

At the same time, several limitations should be considered carefully. Firstly, the ONE axial resolution surpasses that of confocal microscopy only by the expansion factor, implying that the axial and lateral resolutions differ by more than one order of magnitude. This can become a problem for dense samples; therefore, further improvements

in the axial resolution should be introduced in the future through methods such as total internal reflection fluorescence (TIRF), lattice light-sheet microscopy or multifocus microscopy. Secondly, applications to cell and tissue samples will require fixation, a procedure that can cause substantial artifacts. A combination of rapid freezing (or high-pressure freezing), fixation at subzero temperatures and rehydration would reduce such artifacts[32]. Thirdly, while ONE microscopy should be feasible for all ExM gel chemistries, it is likely that some gels will result in less homogeneous samples than others, thereby changing the signals in an unpredictable fashion. This implies that each gel type needs to be carefully calibrated before use.

Unlike fluorescence imaging techniques that are based on imaging native structures (that is, essentially all tools other than ExM), our approach is not limited by the size of the molecules to be analyzed. Normally, the shape of a small protein or peptide cannot be visualized in fluorescence because not enough fluorophores can be introduced into it. Our solution to this problem enables us to describe the shapes of molecules that could otherwise only be visualized by technologies such as cryo-EM. Lastly, a further advantage of ONE microscopy is that the fluorescence analysis is not dependent on molecular density, implying that extremely small objects, such as the peptide mCLING, can be analyzed, although they may be virtually invisible for density-based techniques such as EM.

Overall, ONE is a simple and easily applicable technology to study the morphology of proteins with high resolution and has the potential to bridge the gap between X-ray crystallography and EM-based techniques.

Online content

Any methods, additional references, Nature Portfolio reporting summaries, source data, extended data, supplementary information, acknowledgements, peer review information; details of author contributions and competing interests; and statements of data and code availability are available at https://doi.org/10.1038/s41587-024-02431-9.

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Methods

Nanorulers

Custom-designed linear nanorulers of varying length (80, 60, 50, 30, 20 and 10 nm), carrying one Atto 647N molecule on each end, were purchased from GATTAquant.

Cell cultures

Hippocampal cultured neurons. Animals (Wistar rats, P0–P1) were treated according to the regulations of the local authority, the Lower Saxony State Office for Consumer Protection and Food Safety (Niedersächsisches Landesamt für Verbraucherschutz und Lebensmittelsicherheit), under the license Tötungsversuch T09/08. In brief, the hippocampi were dissected from the brains and washed with Hank's balanced salt solution (14175-053, Invitrogen), before being incubated under slow rotation in a digestion solution containing 15 U per ml papain (LS003126, Worthington), 1 mM $CaCl_2$ (A862982745, Merck), 0.5 mM EDTA and 0.5 mg ml^{-1} L-cysteine (30090, Merck) in DMEM. This procedure was performed for 1 h at 37 °C, before enzyme inactivation with a buffer containing 10% fetal calf serum (FCS) and 5 mg ml^{-1} BSA (A1391, Applichem) in DMEM. The inactivation solution was replaced after 15 min with the growth medium, containing 10% horse serum (S900-500, VWR International), 1.8 mM glutamine and 0.6 mg ml^{-1} glucose in MEM (51200046, Thermo Fisher Scientific), which was used to wash the hippocampi repeatedly. The neurons were then isolated by trituration using a glass pipette and sedimented by centrifugation at 80*g* (8 min). The cells were then resuspended in the same medium and seeded on poly(L-lysine) (PLL)-coated coverslips for several hours, before replacing the buffer with Neurobasal A culture medium (10888-022, Thermo Fisher Scientific) containing 0.2% B27 supplement (17504-044, Thermo Fisher Scientific) and 2 mM GlutaMAX (35050-038, Thermo Fisher Scientific). The neurons were then maintained in a humidified incubator (5% CO_2, 37 °C) for at least 14 days before use.

Conventional cell cultures. Tubulin immunostaining was performed in the U2OS cell line, obtained from the Cell Lines Service (CLS). The cells were grown in a humidified incubator (5% CO_2, 37 °C) in DMEM (D5671, Merck) with the addition of 10% FCS (S0615, Merck), 4 mM glutamine (25030-024, Thermo Fisher Scientific) and an antibiotic mixture added at 1% (penicillin–streptomycin; Thermo Fisher Scientific). For imaging purposes, cells were grown overnight on PLL-coated coverslips (P2658, Merck).

Brain slices

We dissected rat brains from P0–P1 rat pups (Wistar). The brains were then fixed with 4% PFA (30525894, Merck) in PBS for 20 h. The fixed brains were then placed in agarose (4% solution; 9012366, VWR Life Science), before cutting to the desired thickness (100–200 µm) using a vibratome.

Participants

Participants were in treatment at the Paracelsus Elena Klinik. They were diagnosed with PD according to standard criteria[47–49]. Neurological control participants were diagnosed with a variety of non-neurodegenerative disorders. A detailed presentation of participants, their ages and their diagnoses can be found in Supplementary Table 1. The informed consent of all of the participants was obtained at the Paracelsus Elena Klinik, following the principles of the Declaration of Helsinki.

CSF samples

CSF samples were collected at the Paracelsus Elena Klinik following identical standard operating procedures. CSF was obtained by lumbar puncture in the morning with the participants fasting and in sitting position. The CSF was processed by centrifugation at 2,000*g* for 10 min at room temperature; aliquots of supernatant were frozen within 20–30 min and stored at −80 °C until analysis. Samples with a red blood cell count > 25 $µl^{-1}$ or indication for an inflammatory process were excluded.

Immunostaining procedures

Tubulin immunostaining. U2OS cells were first incubated with 0.2% saponin (47036, Sigma-Aldrich) to extract lipid membranes. This procedure was performed for 1 min in cytoskeleton buffer, consisting of 10 mM MES (M3671, Merck), 138 mM KCl (K42209636128, Merck), 3 mM $MgCl_2$ (M8266-100G, Sigma-Aldrich), 2 mM EGTA (324626-25GM, Merck) and 320 mM sucrose at pH 6.1. The cells were then fixed using 4% PFA and 0.1% glutaraldehyde (A3166, PanReac) in the same buffer. Unreacted aldehyde groups were quenched using 0.1% $NaBH_4$ (71320, Sigma-Aldrich now Merck) for 7 min in PBS, followed by a second quenching step with 0.1 M glycine (3187, Carl Roth) for 10 min in PBS. The samples were blocked and simultaneously permeabilized using 2% BSA and 0.1% Triton X-100 (9036-19-5, Sigma-Aldrich) in PBS (room temperature, 30 min). Primary anti-tubulin antibodies (T6199 Sigma-Aldrich; 302211, Synaptic Systems; 302203, Synaptic Systems; ab18251, Abcam) were applied for 60 min at room temperature and were then washed off with permeabilization buffer, followed by an incubation of the samples with secondary antibodies (ST635P-1001, Abberior). Five washes were performed with permeabilization buffer followed by three PBS washes (each for 10 min) before continuing with cellular expansion.

PSD95 immunostaining. Neurons were fixed with 4% PFA in PBS (D8537-500ML, Thermo Fisher Scientific) for at least 30 min before quenching with 50 mM glycine (in PBS) for 10 min and blocking and permeabilizing using 2.5% BSA (9048-46-8, Sigma-Aldrich), 2.5% normal goat serum (NGS) and 0.1% Triton X-100 (1003287133, Sigma-Aldrich) in PBS (30 min at room temperature, unless specified otherwise). The antibodies and/or primary Nbs were diluted in 2.5% BSA and 2.5% NGS in PBS and added to coverslips for 60 min at room temperature. This was followed by washing with the permeabilization buffer (30 min, three buffer exchanges) and by incubation with the primary Nb FluoTag-X2 anti-PSD95 (clone 1B2; N3702, NanoTag Biotechnologies) for 1 h at room temperature. Specimens were then washed five times with permeabilization buffer before a final wash with PBS (15–30 min, three buffer exchanges), followed by expansion procedures.

Immunostaining of CSF samples. CSF probes were obtained from persons with PD and controls at the Paracelsus Elena Klinik and stored at −80 °C before use. Then, 20 µl of CSF was placed on BSA-coated coverslips, enabling the sedimentation of multiprotein species overnight at 4 °C. Fixation with 4% PFA (10 min, room temperature) and quenching with 50 mM glycine (10 min, room temperature) were followed by the application of anti-ASYN antibodies (128211 and 128002, Synaptic Systems) or ASYN Nb2 (SynNb2 (ref. 45), custom-produced and fluorescently conjugated by NanoTag) for 1 h at room temperature in 2.5% BSA in PBS buffer. For the case of antibodies, secondary Abberior STAR 635P was applied for 1 h at room temperature. Five washes with 2.5% BSA in PBS were followed by mild postfixation with 4% PFA for 4 min and expansion procedures.

Brain slice immunostaining. The fixed brain slices were first quenched using 50 mM glycine (in PBS), followed by three washes with PBS (each for 5 min) and blocking and permeabilization in PBS containing 2.5% BSA and 0.3% Triton X-100 for 120 min at room temperature. The primary antibodies used (anti-bassoon, ADI-VAM-PS003-F, Enzo Life Sciences; anti-Homer 1, 160003, Synaptic Systems) were diluted in the same buffer (lacking Triton X-100) to 2 µg ml^{-1} and added to the slices overnight at 4 °C. Three washes with PBS (each for 5 min) removed the primary antibodies, enabling the addition of secondary antibodies conjugated with Abberior STAR 635P (ST635P-1001, Abberior)

for Basson identification. The secondary antibodies were diluted to 1 µg ml^{-1} in PBS containing 2.5% BSA and incubated for 3 h at room temperature. The brain slices were finally subjected to five washes with PBS containing 2.5% BSA (each wash for 5 min), followed by two final 5-min washes in PBS.

GFP–Nb complex (TSR) generation

The monomeric (A206K) and nonfluorescent (Y66L) EGFP (mEGFP*) was modified to have an ALFA tag on its N terminus and a HaloTag on its C terminus (ALFA-EGFP-HaloTag). This construct was expressed in a NebExpress bacterial strain and it had an N-terminal His-tag, followed by a bdSUMO domain, which enabled the specific cleavage of the His-tag[31] after the purification procedures. Bacteria were grown at 37 °C with shaking at 2*g* in Terrific Broth (TB) supplemented with kanamycin. Upon reaching an optical density (OD) of ~3, the temperature was reduced to 30 °C and bacteria were induced using 0.4 mM IPTG, with shaking for another ~16 h. Bacteria lysates were incubated with Ni^+ resin (Roche, cOmplete) for 2 h at 4 °C. After several washing steps, the ALFA-mEGFP(Y66L)-HaloTag protein was eluted by enzymatic cleavage on the column using 0.1 µM SENP1 protease for 15 min. Protein concentration was determined using Nanodrop (Thermo Fisher Scientific) and purity was assessed by Coomassie gels. Complex formation was performed by mixing the following for 1 h at room temperature in a final volume of 40 µl: 25 pmol of ALFA-EGFP-HaloTag and 30 pmol of three different single-domain antibodies: FluoTag-Q anti-ALFA (N1505), FluoTag-X2 anti-GFP (clone 1H1; N0301) and FluoTag-X2 anti-GFP (clone 1B2), all from NanoTag Biotechnologies. The control experiments were performed using a similar procedure without including the target protein ALFA-EGFP-HaloTag. The expression and purification of EGFP used in Supplementary Figs. 15 and 16 were performed as previously described[50]. Briefly, NebExpress *Escherichia coli* strain (New England Biolabs) was cultured in TB at 37 °C and induced using 0.4 mM IPTG for 16 h at 30 °C. Bacteria pellets were sonicated on ice in 50 mM HEPES pH 8.0, 500 mM NaCl, 5 mM $MgCl_2$ and 10% glycerol. After removing cell debris by centrifugation, the lysate was incubated for 1 h with cOmplete His-tag purification resin (Roche) at 4 °C. After washing the resin in batch mode with more than ten column volumes, eGFP was enzymatically eluted using 0.1 µM SUMO protease. Concentration was determined by absorbance at 280 nm using the molecular weight and extinction coefficient of eGFP. Purified protein was diluted in 50% glycerol and stored in small aliquots at −80 °C.

PAGE

A primary mouse monoclonal antibody to synaptobrevin 2 (104211, Synaptic Systems) and a secondary antibody conjugated to Abberior STAR 635P (ST635P-1002-500UG) were mixed with reducing 2× Laemmli buffer (63 mM Tris-HCl pH 6.8, 2% SDS, 100 mM DTT and 20% glycerol) and heated for 10 min at 96 °C. The denatured and reduced samples were then loaded in a self-cast Tris-glycine 12% polyacrylamide gel and 10 µg of total protein was loaded per lane. Electrophoresis was run at low voltage at room temperature. The gel was briefly rinsed using distilled water and fluorescence was read on a GE-Healthcare AI 600 imager using a far-red filter (Cy5 channel). Next, the gel was submerged for 4 h in Coomassie brilliant blue solution to stain all proteins, followed by incubation with destaining solutions, before finally being imaged using the same GE-Healthcare AI 600 gel documentation system.

Dot blot

In a stripe of nitrocellulose membrane (GE-Healthcare), 5 mg of BSA and 1 µg of ALFA-tagged EGFP-Y66L-HaloTag were spotted and left to dry at room temperature. Membranes were then blocked in PBS supplemented with 5% skim milk and 0.05% Tween-20 for 1 h with tilting and shaking. FluoTag-X2 anti-GFP Cy3 (clone 1B1), FluoTag-X2 anti-GFP Abberior STAR 635P (clone 1H1) and Fluotag-X2 anti-ALFA Abberior STAR 635P (all from NanoTag) were used at 2.5 nM final concentration in PBS with 5% milk and 0.05% Tween-20 for 1 h with gentle rocking. After 1-h incubation at room temperature while protected from light, five washing steps were performed each using 2 ml of PBS supplemented with 0.05% Tween-20 for a total of 30 min. Membranes were finally imaged using a GE-Healthcare AI 600 system.

1,6-Hexanediol treatments. 1,6-Hexanediol (240117-50G, Sigma-Aldrich) was diluted in neuronal Neurobasal A culture medium at 3% for 2 min and 10% for 12 min before fixation and further processing for immunostaining.

Purified proteins

IgA and IgM were purchased from Jackson ImmunoResearch and IgG was purchased from Abberior (AffinityPure IgA 109-005-011, ChromePure IgM 009-000-012 and ST635P-1001, respectively) and all immunoglobulins were diluted in PBS before expansion procedures. Otoferlin was produced according to standard procedures[51] and was diluted in 20 mM HEPES, 100 mM KCl and 0.05% DDM buffer, before being used at 0.4 mg ml^{-1} concentration. For $GABA_A$Rs, a construct encoding the full-length human $GABA_A$R β3 subunit (UniProt P28472) with an N-terminal TwinStrep tag was cloned into the pHR-CMV-TetO2 vector[52]. A lentiviral cell pool was generated in HEK293S GnTI-TetR cells as described previously[53]. Cells were grown in FreeStyle 293 expression medium (12338018, Gibco) supplemented with 1% FBS (11570506, Gibco), 1 mM L-glutamine (25030149, Gibco), 1% NEEA (11140050, Gibco) and 5 µg ml^{-1} blasticidin (ant-bl-5b, Invivogen) at 37 °C (130 r.p.m., 8% CO_2) and induced as described[54]. Following collection by centrifugation (2,000*g*, 15 min), the cell pellets were resuspended in PBS pH 8 supplemented with 1% (v/v) mammalian protease inhibitor cocktail (Sigma-Aldrich). Cell membranes were solubilized with 1% (w/v) DDM (D3105GM, Anatrace) for 1 h. The insoluble material was removed by centrifugation (12,500*g*, 15 min) and the supernatant was incubated with 300 µl of Strep-Tactin Superflow resin (IBA Lifesciences) while rotating slowly for 2 h at 4 °C. The beads were collected by centrifugation (300*g*, 5 min) and washed with 150 ml of 0.04% (w/v) DDM and PBS pH 8. The sample was eluted in 2.5 mM biotin, 0.02% (w/v) DDM and PBS pH 8 and used for imaging at 1 mg ml^{-1} concentration. For the purification of the $GABA_A$R in complex with the β3-specific Nb (Nb25)[55], Nb25 was fluorescently labeled with STAR 635P at the N and C termini, generating Nb25-STAR 635P. Then, 20 µl of 10 µM Nb25-STAR 635P was added to the sample before the elution step and incubated for 2 h at 4 °C while rotating. The excess Nb25-STAR 635P was removed by washing the beads with six bed volumes of 0.04% (w/v) DDM and PBS pH 8, eluted with 2.5 mM biotin, 0.02% (w/v) DDM and PBS pH 8 and used for imaging at 3 mg ml^{-1} concentration. The same procedure was applied for the negative control anti-eGFP Nbs. To test that Nb25-STAR 635P could still bind the receptor, 2 µM Nb25-STAR 635P was added to the β3 homomeric receptor reconstituted in nanodiscs as described previously[56]. Next, 3.5 µl of the sample was applied to a freshly glow-discharged (PELCO easiGlow, 30 mA for 120 s) 1.2/1.3 UltrAuFoil grid (Quantifoil), which was blotted for 2.5 s and plunge-frozen using a Leica EM GP2 plunger at 14 °C and 99% humidity. Imaging was performed at the Medical Research Council (MRC) Laboratory of Molecular Biology on a Titan Krios G2 microscope equipped with an F4 detector in electron counting mode at 300 kV at a nominal magnification of 96,000×, corresponding to a calibrated pixel size of 0.824 Å. A total of 300 movies were collected using EPU (Thermo Fisher Scientific, version 2.0–2.11) with a total dose of 38 e^- per Å^2 and 6.43 s of exposure time. The movies were motion-corrected using MotionCor2 (ref. 57). Contrast transfer function estimation was performed with CTFFIND-4.1.13 (ref. 58). Particle picking was performed using a retrained BoxNet2D neural network in Warp[59], followed by 2D classification in cryoSPARC[60]. Calmodulin was purified as previously described[61] and was used in calcium-free buffer (150 mM KCl, 10 mM HEPES and 5 mM EGTA) or calcium-containing buffer (150 mM KCL, 10 mM HEPES and 2 mM $CaCl_2$)

at pH 7.2 before expansion procedures. Briefly, calmodulin 1 (mRNA reference sequence number NM_031969.2) was tagged with mEGFP and an ALFA tag for affinity purification purposes. The construct was transfected in HEK293 cells using Lipofectamine 2000 (11668019, Invitrogen) following the manufacturer's protocol. After expression for ~24 h, the cells were lysed in PBS buffer containing 1% Triton X-100, 2 mM EDTA and a protease inhibitor cocktail. The debris was removed by centrifugation and the supernatant was added to an ALFA Selector PE resin (NanoTag Biotechnologies), where it was allowed to bind for 60 min (4 °C, under rotation). After two washes with lysis buffer and one wash with PBS (ice-cold), the bound proteins were eluted by adding the ALFA peptide. The purified protein was analyzed by Coomassie gel imaging as previously described[61].

X10 expansion procedures

X10 expansion of cultured cells was performed using proteinase K exactly as described in the protocol article[16]. X10 expansion relying on autoclaving (X10ht[62]) was performed as follows. The samples were incubated overnight with 0.3 mg ml^{-1} Acryloyl-X (A-20770, Thermo Fisher Scientific) in PBS pH 7.4 at room temperature. The samples were then subjected to three PBS washes (5 min each) while preparing the gel monomer solution as previously described[16]. The solution was pipetted on parafilm and was covered with upside-down coverslips containing cells or with brain slices that were then also covered with fresh coverslips. Polymerization was allowed to proceed overnight at room temperature in a humidified chamber. Homogenization of proteins and single molecules was performed using 8 U per ml proteinase K (P4850, Sigma-Aldrich now Merck) in digestion buffer (800 mM guanidine HCl, 2 mM $CaCl_2$ and 0.5% Triton X-100 in 50 mM Tris; 8382J008706, Merck) overnight at 50 °C. Homogenization of cell cultures and brain slices was performed by autoclaving for 60 min at 110 °C in disruption buffer (5% Triton X-100 and 1% SDS in 100 mM Tris pH 8.0) followed by a 90-min incubation to cool the temperature to safe levels. Before autoclaving, the gels were washed first in 1 M NaCl and then at least four times in disruption buffer for a total time of at least 120 min. Gel expansion was then performed by washing with double-distilled water (ddH_2O) for several hours, with at least five solution exchanges. Expansion was performed in 22 × 22-cm square culture dishes, carrying 400–500 ml of ddH_2O. When desired, the samples were labeled using a 20-fold molar excess of NHS-ester fluorescein (46409, Thermo Fisher Scientific) in $NaCHO_3$ buffer at pH 8.3 for 1 h before the washing procedure that induced the final expansion.

ZOOM expansion procedures

Following a previously described protocol[63], fixed U2OS cultured cells were incubated in anchoring solution (25 mM acrylic acid NHS-ester in 60% (v/v) DPBS and 40% (v/v) DMSO) for 60 min. Afterward, cells were moved to monomer solution (30% (w/v) acrylamide and 0.014% (w/v) *N*-*N*′-methylenbisacrylamide in PBS buffer). After 60 min, the gelation process was started by adding initiators (0.5% (w/v) TEMED and 0.5% (w/v) APS) to the monomer solution. The hydrogel–cell hybrid was homogenized in detergent solution (200 mM SDS and 50 mM boric acid in deionized water, with the pH titrated to 9.0) at 95 °C for 15 min, followed by 24 h at 80 °C. ZOOM-processed samples were then stained using the previously mentioned anti-α-tubulin antibodies (1:400 in PBST).

mCLING expansion

For mCLING gelation, we started with 2 µl of mCLING-Atto 647N (710 006AT1, Synaptic Systems), originally reconstituted to a concentration of 1.0 nmol ml^{-1} and mixed with 2 µl of 10 mg ml^{-1} Acryloyl-X, before bubbling with N_2 gas for a few minutes to purge oxygen. This mixture was incubated overnight at 4 °C and then mixed with 100 µl of freshly prepared X10 polymer solution. Next, 80-µl aliquots of this gel-sample mixture were placed on parafilm in a humidified chamber and were covered with a clean 18-mm coverslip. Homogenization was carried out by X10 proteinase K digestion protocol, as previously described. Gels were then postexpansion labeled with NHS-ester fluorescein (46409, Thermo Fisher Scientific) or NHS-ester STAR 635P (07679-1MG, Sigma-Aldrich). Images were acquired using HyD X detectors on a STELLARIS 8 microscope.

mCLING structure simulation

The equilibrium structure of mCLING peptide-bonded to Atto 647N was assessed using molecular dynamics simulations with the AMBER99 force field[64]. The molecule was simulated in water using the TIP4P/EW model[65] in a cubic system of length 6 nm with periodic boundaries. The topology for the fluorophore was generated using ACPYPE[66], which interfaces with Antechamber from the AMBER suite of tools to create compatible topology files. The molecular dynamics package GROMACS[64] was used with the leap-frog algorithm to integrate Newton's equations of motion with a time step of 1 fs. Conditionally convergent long-range electrostatic interactions were calculated by the smooth particle mesh Ewald method with a cutoff distance of 1.2 nm. Lennard–Jones interactions were assessed using a single cutoff distance of 1.2 nm, supplemented by long-range dispersion corrections for both energy and pressure. After energy minimization, the system was equilibrated for 300 ns, followed by a 300-ns production run. The pressure was fixed at 1 bar by the Parrinello–Rahman barostat.

Microscope systems

For image acquisition, small gel fragments were cut and placed in the imaging chamber presented in Supplementary Fig. 7. Paper tissues were used to remove any water droplets around the gels, before enabling the gels to equilibrate for at least 30 min on the microscope stage. Epifluorescence imaging was performed using an Olympus IX83 TIRF microscope equipped with an Andor iXon Ultra 888, ×100 (1.49 numerical aperture (NA)) TIRF objective and Olympus LAS-VC four-channel laser illumination system. Confocal imaging was performed for most experiments using a TCS SP5 STED microscope (Leica Microsystems) with a ×100 (1.4 NA) HCX Plan Apochromat STED oil-immersion objective. The LAS AF imaging software (Leica) was used to operate imaging experiments. Excitation lines were 633, 561 and 488 nm and emission was tuned using an acousto-optical tunable filter. Detection was ensured by PMT and HyD detectors. Images were taken using a resonant scanner at 8-kHz frequency. The five-dimensional (5D) stacks for zONE were performed using a 12-kHz resonant scanner mounted on a Leica TCSSP8 Lightning confocal microscope. Samples were excited with a 40% white-light laser at wavelengths of 633, 561 and 488 nm and acquisitions were carried out using HyD detectors in unidirectional *xyct* line scans or in unidirectional and bidirectional *xyczt* line scans.

Image acquisition

Objectives of 1.4, 1.45 and 1.51 NA were used to acquire images with a theoretical pixel size of 98 nm. For a higher resolution, the theoretical pixel size was set to 48 nm at the cost of a slightly lower detection rate. Images acquired on the camera-based system had a predetermined pixel size of 100 nm. The acquisition speeds were 20–40 ms and 25 ms on resonant scanners of 8 and 12 kHz and on a camera, respectively, for *xyct*. For hyperstacks of *xyczt* acquisitions, images were acquired using 8-kHz and 12-kHz scanners in bidirectional mode (after the necessary alignments), allowing an achieved speed of 16 kHz and 24 kHz, respectively. Images of 8-bit depth were acquired at a line format ranging from 128 × 128 to 256 × 256. The scanning modality on a confocal was set to 'minimize time interval' (Leica LAS software). To maintain natural fluctuations of fluorophores, we did not use line accumulation or line averaging during scanning. A frame count from 200 up to 4,000 was acquired. We recommend a frame count of at least 1,500–2,000 for optimal computed resolution in *xyct* scans and 200–1,000 for *xyczt* scans for volume reconstructions.

Image processing

ONE image processing is enabled through a Java-written ONE Platform under 'ONE microscopy' in Fiji. The ONE microscopy plugin uses open-source codes from Bioformats Java library, NanoJ-Core, NanoJ-SRRF, NanoJ-eSRRF and Image Stabilizer[12,13,67,68]. ONE plugin supports multiple video formats of single or batch analyses in *xyct*. Hyperstacks with 5D *xyczt* format were processed with the zONE module. This module allows the user to select the optical slices and channels to resolve at ultraresolution. Upon irregularities in resolving one or more channels within one or more planes, zONE leaves a blank image and computes the remaining planes within a stack. The image processing is fully automated and requires minimal initial user input. Aside from the expansion factor, preset values and analysis modalities are automatically provided (see Supplementary Fig. 1 for more details). The ONE plugin has a preinstalled safety protocol to skip failures in computations or uncompensated drifts, without affecting the progress of batch analysis. Data analyses, parameters and irregularities are reported in log files. The ONE plugin automatically linearizes the scale on the basis of radiality magnification and expansion factor corrections. In addition, ONE offers the possibility to correct for chromatic aberration by processing multichannel bead images as a template that is applied to super-resolved images of the biological samples. The correction is performed by applying a modified Lucas–Kanade algorithm[67]. For the ONE microscopy plugin to store complex multidimensional images from hyperstacks, we modified the Java code of the ImageJ library and adapted it locally. The ONE Platform source code and plugin are available from GitHub (https://github.com/Rizzoli-Lab/ONE-Microscopy-Java-Plugin). For best performance, we recommend to download a preinstalled version on Fiji, available from the same link. The ONE plugin comes with predefined parameters optimized for single molecules, particularly emphasizing the highest resolution. Next to each parameter, the user will find explanations and recommendations. When the cursor hovers over the parameters, pop-up text bubbles provide further details. Users can adjust all parameters as desired. Importantly, the expansion factor should be set in accordance with the results obtained in the respective laboratories because this parameter is particularly important for obtaining the correct image scale. In addition, the temporal analysis mode should be adjusted in accordance with the type of experiment performed. For example, the temporal radiality pairwise product mean (TRPPM) analysis suits continuous and diffuse signals, while temporal radiality autocorrelation (TRAC) analysis is recommended for sparse labels and for colocalization studies requiring higher resolution. A TRAC order of 4 is preset for the analysis of single molecules because it provides the highest achievable resolution. For colocalization analysis, we recommend using the chromatic aberration correction function. The resulting images have an additional suffix of '_CAC' (for chromatic aberration corrected). Additional parameters are available in the advanced options tab, which can be used to accommodate various experimental paradigms with different SNR and signal quality. When acquiring zONE images, where image quality becomes noisier and the acquisition rate slows down because of imaging in multiple axial planes, users may choose to analyze the images using a lower TRAC order of 3 or 2. However, users should note that, while zONE allows the collection of information across a volume, this comes at the cost of reducing the achieved resolution because of hardware limitations. Lastly, we recommend that the users thoroughly read Supplementary Fig. 30, in which we present the software in graphic format, and Supplementary Figs. 1 and 2, in which the imaging and analysis flowcharts are shown.

Image analysis and statistics

For single-object analyses, such as synaptic vesicle or antibody analyses, signal intensities and distances between objects were analyzed manually using ImageJ (W. Rasband and contributors, National Institutes of Health). Line scans were also performed and analyzed using ImageJ. For the analysis of PSDs (Fig. 2), spots were identified by thresholding bandpass-filtered images, relying on empiric thresholds and bandpass filters, organized in the form of semiautomated routines in Matlab (version 2017b). Spots were overlaid to determine their overall signal distributions or their center positions were determined to measure distances between spots (in the same or different channels). The same procedure was used for the averaging analysis of CSF samples (Fig. 4) and for the analysis of spot distances for the GFP–Nb assemblies (Supplementary Figs. 15 and 16). Full width at half maximum values were measured after performing line scans over small but distinguishable spots (Supplementary Fig. 16), followed by Gaussian fitting using Matlab. The averaging analysis of $GABA_AR$s is presented in detail in the main text and was performed using Matlab. In brief, receptors were detected automatically as particles with intensities above an empirically derived threshold. To remove particles with uncompensated drift, we eliminated all receptors coming from images in which a large proportion of the particles were oriented similarly. We then visually inspected all of the remaining particles to choose those that appeared to be in a 'front view', showing a reasonably round appearance, with Nbs placed at the edges of the receptor (visible in the second color channel). All particles were centered on the intensity maxima of the respective $GABA_AR$ channel images. The particles were subjected to an analysis of the peaks of fluorescence, using a bandpass procedure, followed by identification of maxima[69]; the positions of the peaks were calculated to below-pixel precision and were rounded off to a pixel size of 0.384 nm (the starting pixel size was 1 nm). These positions were then mapped into one single matrix, which represents the 'averaged receptor', as indicated in the main text. Averaging analyses of actin were performed similarly. In brief, actin strands were selected manually and were overlaid to generate average views. Model objects were generated as a comparison by convoluting the amino acid positions in the respective Protein Data Bank (PDB) structures with empirically derived ONE spots. All of these analyses were performed using Matlab. The SNR for single Nbs was determined by measuring the average pixel intensities within the Nb spots and away from them and then dividing the two measurements. Identically sized circular regions of interest, sufficient to capture the Nb spots completely, were used for both signal and background (noise) regions. Plots and statistics were generated using GraphPad Prism 9.3.1 (GraphPad Software), SigmaPlot 10 (Systat Software) or Matlab. Statistical details are presented in the respective figure captions. Figures were prepared with CorelDraw 23.5 (Corel Corporation).

Optimization

Overview of critical steps in ONE microscopy. The gel preparation for ONE microscopy in classical ExM cell imaging closely follows the recommendations in the X10 guide, which we published several years ago[16]. Here, we highlight briefly the crucial steps for ONE microscopy, which include anchoring, homogenization and oxygen purging. Proper anchoring is vital for maintaining labeled targets and fluorescence signals. Effective homogenization prevents the rupture of cell compartments and enables the proper expansion of proteins. To troubleshoot this step, one may consider tuning the strength of the homogenization process by testing both autoclave and proteinase K protocols. Milder digestion methods, including short autoclave times (<60 min) or trypsin-based digestion (instead of proteinase K), could also be considered. Improper oxygen purging results in inconsistent sticky gels, with varying expansion factors that are hard to handle. For optimal results, the user should always add the reaction initiator KPS and the catalyst TEMED to the polymer solution in a rapid fashion and then the gel amount used (typically 70–80 µl for an 18-mm coverslip) should be sealed off with a coverslip within, at most, 70 s. When preparing more than five gels simultaneously, we suggest having two people perform this step side by side to minimize oxygen exposure. In the special case of single-molecule analyses, it is crucial to work only with a thin film of

fluid containing the molecules to be analyzed, to which the gel solution is quickly added. Please be aware that thin films of protein-containing buffers tend to dry very rapidly. An indicator of failure in this step is the appearance of salt and protein precipitates, looking as white clumps, which will be visible on the coverslip.

Imaging chamber optimization. All of the chamber blueprints and data are available in the Supplementary Information. For chamber usage, a gel slightly larger than the chamber should be cut, before removing excess water and fitting the gel onto the stabilizing net. Any overhanging gel should be trimmed away. The tight gel–chamber fit minimizes drift but automated drift correction in the ONE plugin is also available to address any residual drift before processing. It is automatically implemented and operates independently for each color channel. If the correction fails for one channel, it attempts to implement the drift correction coordinates from another channel. The interchannel drift correction feature is exclusive to line-by-line scanning and should not be used in frame-by-frame or stack-by-stack scan modes. Users suspecting postcorrection artifacts should sum the intensity of the entire drift-corrected raw video. Comet effects in the summed images indicate a drift correction failure, suggesting the need to discard such acquisitions. Drift correction issues often stem from dim or poorly labeled specimens or strong vibrations from an unstable imaging system.

Optimizing objective type selection. For targets in cells, which are close to the glass–gel interface, or single molecules, oil objectives with NA ≥ 1.4 should be used. For optimal imaging of single molecules, which are typically less than 1 µm in size when expanded, high-NA oil objectives should be used. Additionally, maintaining an imaging distance of ≤5 µm, by removing excess water between the gel and glass surfaces, is essential. To image cellular targets at higher depths accurately, it is crucial to address the refractive index mismatch. Using water-immersion objectives for deeper specimens is recommended to reduce artifacts.

Microscope selection. The user should consider the resolution needed and the type of specimen analyzed before settling on a particular microscope. In general, confocal microscopes are preferred. However, for general cellular imaging, epifluorescence microscopes are sufficiently accurate. Confocal microscopes offer higher resolution for single molecules and should be preferred for such uses. When using a confocal microscope, optimal results are achieved with the following detectors: HyD detectors, especially HyD X for its high quantum yield and SNR, or HyD R for near-infrared applications in photon counting mode (avoid analog and digital modes). Gallium arsenide phosphide and Avalanche photodiodes are also recommended. Classical photomultiplier tubes can be used at moderate voltage with a corrected smart offset to minimize dark counts to 1–5 per field of view.

Imaging conditions to avoid. During sample preparation, imaging single molecules from sticky gels or gels with cracks should be avoided, while ensuring that the expansion factor is corrected using known structures as rulers. For sample imaging, using noisy detectors with high dark counts should be avoided. Bidirectional scanners without manual phase shift correction should also be avoided. When processing images, users should be wary of artifactual airy disks caused by brightly labeled molecules that are partially out of focus. We suggest to opt for NHS-ester fluorescein over bright and stable modern dyes for labeling multimeric protein complexes, as bright parts of large complexes may get out of focus and lead to artifacts. The lower photon output of fluorescein reduces this problem.

Software considerations. The generated images have a 32-bit depth with negative values. These negative values represent noise and should be ignored. The users should set the dynamic display range to a zero-value minimum to exclude the noise. If gridded patterns appear in processed images, this may indicate low SNR, out-of-focus signals or incorrect bidirectional line scanning. Such images should be discarded. One can troubleshoot this by optimizing the labeling and the fluorophore selection and/or by adjusting the pixel dwell time and detector sensitivity.

3D model reconstruction

To prepare the ONE images for suitable 3D model reconstruction, we applied automated thresholding algorithms to extract dense areas of intensity, in which the expected protein should be located. The extracted areas have a window size of 200 × 200 pixels. The next step involved deconvolving the images using the Lucy–Richardson[70] method with 80 iterations and a Gaussian PSF kernel of size 13 × 13 and $\sigma = 2$. Subsequently, the images were normalized to a range of 0–8 and then scaled down using bilinear interpolation to dimensions of 128 × 128 pixels. The processed images were transferred into cryoFIRE, an unsupervised ab initio autoencoder for complex shape reconstruction with amortized inference[35]. cryoFIRE consists of two components, the encoder f_{enc} and decoder f_{dec}. The encoder contains convolutional followed by fully connected layers. It takes a processed ONE image Y_i and estimates its pose R_i, translation t_i, expansion factor e_i and molecule confirmation z_i (that is, $f_{\text{enc}}(Y_i) = (R_i, t_i, e_i, z_i)$). Here, e_i was added to the original cryoFIRE approach to account for mild variations in the expansion factor between different gels. The decoder, a coordinate-based multilayer perceptron, represents the protein structure implicitly. For a given 3D coordinate, its output represents the density of the protein at this location. The decoder gets a 2D grid of coordinates, centered at the origin, which gets rotated and scaled by (R_i, e_i); therefore, the predicted image is $\hat{Y}_{k_x,k_y} = f_{\text{dec}}(z_i, e_i \cdot R_i \cdot (k_x, k_y, 0)^T)$ with $(k_x, k_y) \in R^2$. This prediction is then shifted by t_i to move it back to the original position. Because the predicted output represents a 2D central slice of the molecule in the Hartley domain, to compare the prediction $\hat{Y}$ to the input Y, it also needs to be transformed into the Hartley domain. Because of the deconvolution in the preprocessing step, we did not need to apply a contrastive transfer function to the prediction, as proposed in cryoFIRE. With the modified (symmetric) mean squared error loss, which takes account of the handedness of the protein, the parameters are optimized using stochastic gradient descent. The 3D reconstructed images can be inspected with UCSF ChimeraX. The computation and processing were hosted by the Norddeutscher Verbund für Hoch- und Höchstleistungsrechnen servers (https://hlrn.de/).

Reporting summary

Further information on research design is available in the Nature Portfolio Reporting Summary linked to this article.

Data availability

Image data are available from the corresponding authors on reasonable request. Source data are provided with this paper.

Code availability

The ONE platform plugin software (source code) is available from Zenodo (https://doi.org/10.5281/zenodo.13685267)[71].

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Author contributions

A.H.S. and S.O.R. conceptualized the project. A.A.C. and U.B. developed the ONE Platform plugin, which was supported for driver compatibility by M.M.A. A.H.S. and S.O.R. designed and performed the experiments. U.B. supervised the ONE experiments at the Center for Integrative Physiology and Molecular Medicine (CIPMM). J.A. and A.A.C. implemented the deep learning algorithms for 3D reconstructions under the supervision of A.H.S., C.P. and S.O.R. E.S.B. supervised the ONE experiments at MIT. S.K. supervised T. Mimoso's ONE experiments at the Institute for X-Ray Physics. M.S. supervised the ONE experiments at Würzburg University. A.H.S., V.I. and S.O.R. analyzed the data. R.C., N.M., P.F. and S.V.G. contributed to reproducing the ONE experiments. C.Z. performed the ONE experiments at MIT. J.K. contributed to the bassoon in tissues experiment. N.A. and U.B. performed the ONE experiments at the CIPMM. M.M., H.C. and J.P. purified otoferlin protein. H.C. and T.M. generated the otoferlin AlphaFold model. D.M. and A.R.A. generated the $GABA_A$Rs and the cryo-EM data. S.R. purified calmodulin protein. A.H.S. and D.K. performed the mCLING experiments and the mCLING simulation was performed by R.K.W.S., A.S. and M.M. J.E. performed the ONE experiments at Würzburg University. R.C. and L.A. contributed to the experiments at Leica. F.O. generated the TSRs. D.C. generated the tissue sections. K.A.S. assisted with the initial implementation of X10ht experiments. C.T. and B.M. provided the CSF specimens from participants. T.F.O. verified the analysis of PD data. M.S. contributed to the understanding of photophysics fluctuations and E.S.B. contributed to the understanding of ExM gel behavior. S.O.R. wrote the manuscript, which was revised by all other authors, with especially strong contributions from A.H.S., A.R.A., M.S. and E.S.B.

Competing interests

S.O.R. and F.O. are shareholders of NanoTag Biotechnologies GmbH. E.S.B. is an inventor on multiple patents related to ExM and co-founder of a company working on commercial applications of ExM. The other authors declare no competing interests.

Ethics statement

Animals (Wistar rats, P0–P1) were treated according to the regulations of the local authority, the Lower Saxony State Office for Consumer Protection and Food Safety (Niedersächsisches Landesamt für Verbraucherschutz und Lebensmittelsicherheit), under the license Tötungsversuch T09/08. The informed consent of all of participants was obtained at the Paracelsus Elena Klinik, following the principles of the Declaration of Helsinki.

Additional information

Supplementary information The online version contains supplementary material available at https://doi.org/10.1038/s41587-024-02431-9.

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Software and code

Policy information about availability of computer code

Data collection	Data was acquired using Leica Application Suite for SP5 version 1.6 and SP8 version 3.5.7.23225, STELLARIS 8 version 4.7.0.28176, Abberior Instruments Imspector v16.3 and Olympus CellSens Dimension 2.3.
Data analysis	Custom code written in Matlab2017b and 2019b, ImageJ versions 1.53j and 1.54f, GraphPad Prism 9, SigmaPlot 10 and Excel 2022.

For manuscripts utilizing custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors and reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Portfolio guidelines for submitting code & software for further information.

Data

Policy information about availability of data

All manuscripts must include a data availability statement. This statement should provide the following information, where applicable:

- Accession codes, unique identifiers, or web links for publicly available datasets
- A description of any restrictions on data availability
- For clinical datasets or third party data, please ensure that the statement adheres to our policy

Image data are available from the corresponding authors on reasonable request.

Research involving human participants, their data, or biological material

Policy information about studies with human participants or human data. See also policy information about sex, gender (identity/presentation), and sexual orientation and race, ethnicity and racism.

Reporting on sex and gender	Fourteen human participants (male, female) were involved in this study, seven of which were diagnosed with Parkinson's disease and the other seven patients served as neurological controls and have been diagnosed with a variety of non-neurodegenerative disorders.
Reporting on race, ethnicity, or other socially relevant groupings	No reporting on race, ethnicity, or other socially relevant groupings.
Population characteristics	The age of participants carried from 76.7 ± 2.3 years and 72.0 ± 2.9 years and more details about the population characteristics that include age, sex, and diagnosis is available in the manuscript, see Supplementary Table 1.
Recruitment	Patients were in treatment at the Paracelsus Elena Klinik, Kassel, Germany.
Ethics oversight	The informed consent of all of the participants was obtained at the Paracelsus Elena Klinik, following the principles of the Declaration of Helsinki.

Note that full information on the approval of the study protocol must also be provided in the manuscript.

Field-specific reporting

Please select the one below that is the best fit for your research. If you are not sure, read the appropriate sections before making your selection.

☒ Life sciences ☐ Behavioural & social sciences ☐ Ecological, evolutionary & environmental sciences

For a reference copy of the document with all sections, see nature.com/documents/nr-reporting-summary-flat.pdf

Life sciences study design

All studies must disclose on these points even when the disclosure is negative.

Sample size	The largest possible numbers of experiments were performed, taking into account the high number of different experimental settings, and is well within the range of typical imaging experiments. No formal sample size calculation was performed.
Data exclusions	No experiments or data points were excluded (unless stated in figure legends).
Replication	In general 2 to 5 independent experiments were performed (experimental N is indicated for every dataset in the figure legends, with tens or hundreds of items (molecules, purified proteins, protein assemblies, synapses, synaptic structures, etc.) analyzed. All replications were successful. For expanded samples, each experimental N encompassed from 2 and up to 4 gel replicates.
Randomization	Not relevant for this manuscript.
Blinding	Most analyses relied on automated procedures which are not influenced by the nature of the sample. Blind analysis was applied when meaningful for the manual analysis and for the calmodulin experiment of which image acquisition was carried out blindly as well. Parkinson's disease data were imaged blindly and the analysis was performed by two independent investigators using two different image processing paradigms which was in agreement with automated script results using Matlab.

Reporting for specific materials, systems and methods

We require information from authors about some types of materials, experimental systems and methods used in many studies. Here, indicate whether each material, system or method listed is relevant to your study. If you are not sure if a list item applies to your research, read the appropriate section before selecting a response.

Materials & experimental systems

n/a	Involved in the study
☐	☒ Antibodies
☐	☒ Eukaryotic cell lines
☒	☐ Palaeontology and archaeology
☐	☒ Animals and other organisms
☒	☐ Clinical data
☒	☐ Dual use research of concern
☒	☐ Plants

Methods

n/a	Involved in the study
☒	☐ ChIP-seq
☒	☐ Flow cytometry
☒	☐ MRI-based neuroimaging

Antibodies

Antibodies used

FluoTag-X2 anti-PSD95 anti-PSD95, clone 1B2, #N3702, NanoTag Biotechnologies, Göttingen, Germany, dilution 1:1000.
FluoTag-X2 anti-ALFA nanobody, Cat#N1502, NanotTag GmbH, Göttingen, Germany, dilution 1:500.
Alpha-Synuclein, Nb2, NanoTag Biotechnologies, Göttingen, Germany, dilution 1:200.
Alpha-Synuclein antibody, Synaptic Systems Cat#128 211, Göttingen, Germany, dilution 1:500.
Alpha/beta-Synuclein antibody, Synaptic Systems Cat#128 002, Göttingen, Germany, dilution 1:500.
GABAaR nanobody, Nb25, NanoTag Biotechnologies, Göttingen, Germany dilution : 20 µl of 10 µM Nb25-STAR635P was added to the sample prior to the elution step.
Rabbit alpha-Tubulin Abcam, Cat#ab18251, Cambridgshire, UK, dilution 1:1000.
Mouse alpha-Tubulin Sigma Cat#T6199; Sigma-Aldrich, Darmstadt, Germany, dilution 1:1000.
Rabbit alpha Tubulin Synaptic Systems Cat#302 203, Göttingen, Germany, dilution 1:1000.
Mouse alpha Tubulin Synaptic Systems Cat#302 211; Göttingen, Germany, dilution 1:1000.
Mouse Bassoon, #ADI-VAM-PS003-F, Enzo Life Sciences GmbH, Lörrach, Germany, dilution 1:500.
Abberior Star635P, Cat#ST635P-1001, Abberior, Göttingen, Germany, dilution 1:1000.
Abberior Star635P, Cat#ST635P-1002-500UG, Abberior, Göttingen, Germany, dilution 1:1000.

Validation

FluoTag-X2 anti-PSD95 anti-PSD95, clone 1B2, #N3702, NanoTag Biotechnologies GmbH, validated by NanoTag, see: https://nano-tag.com/product/fluotag-x2-anti-psd95/
FluoTag-X2 anti-ALFA nanobody, Cat#N1502, NanotTag GmbH, Göttingen, Germany; validated by NanoTag, see: https://nano-tag.com/product/fluotag-x2-anti-alfa/, and recently cited by Saal et la., 2022 - BioRxivs.
Alpha-Synuclein 2 nanobody, NanoTag GmbH, Göttingen, Germany; validated by: De Genst et al., 2010 - J Mol Biol.
Alpha-Synuclein antibody, Synaptic Systems Cat#128 211, Göttingen, Germany; recently validated by: Vinueza-Gavilanes et al., 2020 - Neurobiology of Disease.
Alpha/beta-Synuclein antibody, Synaptic Systems Cat#128 002, Göttingen, Germany; validated 13 times including Wilhelm et al., 2014 - Science, and Chandra,... Südhof, 2003 - J Biol Chem.
GABAaR nanobody, NanoTag GmbH, Göttingen, Germany; validated by NanoTag and A. Radu Aricescu lab, see: Miller et al., 2017 - Nat Struct Mol Biol.
Rabbit alpha-Tubulin Abcam, Cat#ab18251, Cambridgshire, UK; validation in 286 citations, Berbari et al., 2012 - Cytoskeleton.
Mouse alpha-Tubulin Sigma Cat#T6199; Sigma-Aldrich, Darmstadt, Germany; validated in 105 citations, recent validation: Latremoliere et al., 2018 - Cell Rep.
Rabbit alpha Tubulin Synaptic Systems Cat#302 203, Göttingen, Germany; 4 citations, Wilhelm et al., 2014 - Science.
Mouse alpha Tubulin Synaptic Systems Cat#302 211; Göttingen, Germany; 15 citations, Groffen et al., 2010 - Science.
Mouse Bassoon, #ADI-VAM-PS003-F, Enzo Life Sciences GmbH, Lörrach, Germany; validated 73 times, most recent: Yamamoto et al., 2022 - Cell Biol.

Eukaryotic cell lines

Policy information about cell lines and Sex and Gender in Research

Cell line source(s)	U2OS cell line from Cell Lines Service (CLS), Eppelheim, Germany. HEK 293T, Thermo Scientific, #HCL4517, Germany.
Authentication	STR analysis according to the global standard ANSI/ATCC ASN-0002.1-2021 (2021) resulted in an authentic STR profile of the reference STR database - confirmed by the company.
Mycoplasma contamination	Both lines are negative in PCR assay - confirmed by the companies.
Commonly misidentified lines (See ICLAC register)	Not listed in the ICLAC database.

Animals and other research organisms

Policy information about studies involving animals; ARRIVE guidelines recommended for reporting animal research, and Sex and Gender in Research

Laboratory animals	Rattus norvegicus, Wistar, P0 to P1 pups.
Wild animals	None
Reporting on sex	Both sexes
Field-collected samples	none
Ethics oversight	All animals were handled according to the specifications of the University of Gbttingen and of the local authority, the State of Lower Saxony (Landesamt fur Verbraucherschutz, LAVES, Braunschweig, Germany). All animal experiments were approved by the local authority, the Lower Saxony State Office for Consumer Protection and Food Safety (Niedersachsisches Landesamt fur Verbraucherschutz und Lebensmittelsicherheit).

Note that full information on the approval of the study protocol must also be provided in the manuscript.

Plants

Seed stocks	Not relevant for this study.
Novel plant genotypes	Not relevant for this study.
Authentication	Not relevant for this study.