A dynamic compositional equilibrium governs mRNA recognition by eIF3

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SUMMARY
Eukaryotic translation initiation factor (eIF) 3 is a multi-subunit protein complex that binds both ribosomes and messenger RNAs (mRNAs) in order to drive a diverse set of mechanistic steps during translation. Despite its importance, a unifying framework explaining how eIF3 performs these numerous activities is lacking. Using single-molecule light scattering microscopy, we demonstrate that *Saccharomyces cerevisiae* eIF3 is an equilibrium mixture of the full complex, subcomplexes, and subunits. By extending our microscopy approach to an *in vitro* reconstituted eIF3 and complementing it with biochemical assays, we define the subspecies comprising this equilibrium and show that, rather than being driven by the full complex, mRNA binding by eIF3 is instead driven by the eIF3a subunit within eIF3a-containing subcomplexes. Our findings provide a mechanistic model for the role of eIF3 in the mRNA recruitment step of translation initiation and establish a mechanistic framework for explaining and investigating the other activities of eIF3.

KEYWORDS
Translation, translation initiation, eIF3, mRNA, mRNA recruitment, ribosome, translational regulation, single-molecule, mass photometry, biophysics, biochemistry

INTRODUCTION

Initiation of translation at the start codon of a messenger RNA (mRNA) sets the reading frame for protein synthesis and is the most regulated stage of translation[1-5]. In eukaryotes, initiation is distinguished by an mRNA recruitment step during which a ribosomal pre-initiation complex (PIC) attaches to the 7-methylguanosine 'cap'-containing 5' end of the mRNA and then scans to locate the start codon. mRNA recruitment determines how a diverse set of mRNAs compete for the translational machinery.

Eukaryotic translation initiation factor (eIF) 3 is a multi-subunit protein complex that is required for mRNA recruitment to the 43S PIC during initiation[6-9]. eIF3 has more recently been implicated in mediating events during translation elongation[10] and termination[11], and has also emerged as a player in translational regulation at multiple stages and by various proposed mechanisms[12-18]. And yet, how the role of eIF3 in mRNA recruitment is related to these emerging regulatory roles and their underlying mechanism remains a mystery.

Each of these proposed roles suggest eIF3 interacts directly or indirectly with mRNA. During initiation, eIF3 binds the PIC[2,6] and its presence near the mRNA-entry channel of the small, or 40S, ribosomal subunit appears to facilitate loading of the mRNA onto the PIC and subsequent scanning of the PIC along the mRNA to locate the start codon[19-21]. At the mRNA-exit channel of the PIC, eIF3 makes critical contributions to stabilizing the binding of mRNA to the PIC[22]. However, the mechanistic origin of these effects remains unclear. Multiple lines of evidence also suggest eIF3 remains bound to post-initiation, ribosomal elongation complexes engaged in translating specific mRNAs to regulate their expression by an unknown mechanism[10,23] and that eIF3 can mediate sequence-specific re-initiation events[24]. Finally, multiple studies have reported that eIF3 binds specific mRNAs directly or indirectly and may thus dictate their translational fates[12,13,25]. Nonetheless, it remains unclear whether these interactions are mediated by the full eIF3 complex containing all of its component subunits (hereafter referred to as the full eIF3 complex) or by smaller multi-subunit eIF3 subcomplexes or even individual, complex-free, eIF3 subunits. In fact, some evidence suggests that distinct eIF3 subcomplexes associate with specific mRNA pools to differentially control their translation[26]. And yet, a mechanism for this compositional heterogeneity and how it might underlie these differential outcomes remains elusive.

The open questions of whether different molecular species underlie the multiple functions of eIF3 and, if so, which species might drive which functions are consonant with an emerging body of evidence that multi-subunit protein complexes—which are pervasive in biology and perform critical roles throughout gene expression and beyond[27-29]—are not indefinitely stable and compositionally uniform, but are instead metastable and compositionally heterogeneous[30,31]. In the yeast *Saccharomyces cerevisiae*, eIF3 is composed of five essential subunits that are conserved throughout eukaryotes and thought to represent a functional core complex[6] that in humans has expanded to 12 subunits[9]. The possibility that eIF3 behaves not as one molecular species but instead as a mixture of distinct species might explain the myriad roles attributed to eIF3 as well as its ability to mediate distinct but specific translational fates across various mRNAs. Nonetheless, such a model remains to be explored.

To directly test this hypothesis, we have combined a novel single-molecule light scattering microscopy technique and a battery of ensemble biophysical and biochemical assays to investigate the compositional integrity and biochemical functions of natively purified and *in vitro* reconstituted *S. cerevisiae* eIF3. Leveraging our ability to control the composition of our reconstituted eIF3, we conclusively demonstrate that, rather than functioning as a single, highly stable and uniformly composed entity, the full eIF3 complex is in a dynamic equilibrium with its constituent subcomplexes and subunits. Exploiting our capacity to characterize this dynamic equilibrium and detect the binding of individual eIF3 subspecies to mRNA at the single-molecule level, we interrogate the contributions that individual eIF3 subcomplexes and subunits make to mRNA binding by eIF3. Our findings provide a mechanistic framework for understanding how the

binding of mRNA by specific eIF3 subspecies contributes to the mechanism of mRNA recruitment by the PIC. More broadly, the framework we have uncovered can be extended to provide a rationale for how eIF3 can execute the many and diverse roles that have been attributed to it, particularly in higher eukaryotes, where the more complex subunit composition of eIF3 could enable a more multiplexed array of subspecies with distinct biochemical functions.

RESULTS

A dynamic equilibrium governs eIF3 composition

In vivo genetic and biochemical studies of eIF3 suggest that individual eIF3 subcomplexes and subunits might play functional roles in cells[26,32-35]. Contrasting with this possibility, analyses of data resulting from *in vitro* biochemical studies of eIF3 have universally made the simplifying assumption that eIF3 functions as a single, permanently stable complex uniformly containing the full set of eIF3 subunits (*i.e.*, the full eIF3 complex)[22,36]. Apparently consistent with this view, size-exclusion chromatography of eIF3 runs as a single peak, albeit typically exhibiting some broadness, shouldering, and/or splitting[37-40] (Figure S1A). Motivated by these contrasting perspectives, we first set out to characterize the compositional stability of eIF3 that we natively purified from *S. cerevisiae*. To this end, we employed a single-molecule interferometric scattering (iSCAT) microscopy (Refeyn, Inc.) technique that detects the adsorption of an individual particle onto the borosilicate glass surface of a microscopy sample well. iSCAT microscopy measures the interference between a reference laser light field that is reflected off of the surface of the well and the Rayleigh scattering of this light field that occurs when individual, subwavelength-sized particles adsorb to the surface. iSCAT is a wide-field microscopy technique in which the adsorption of hundreds to thousands of individual particles to the surface of the well can be spatially separated and imaged within a 10.9 μm × 4.3 μm field-of-view using a complementary metal-oxide semiconductor (CMOS) camera[41]. Because the amount of scattering increases as the size of the particle increases, the iSCAT microscope allows the particles present in a complex mixture to be distinguished as a function of their molecular masses. The conventional output of this 'mass photometry' technique is a one-dimensional histogram in which the number of peaks corresponds to the number of species that can be resolved. The mean and area of each peak correspond to the molecular mass and relative population of each species, respectively[42,43].

To reveal the solution composition of the full eIF3 complex, we began by characterizing a 30 nM sample of natively purified eIF3 that we have previously shown is biochemically functional[44]. Although this concentration is ten-fold lower than what is typically used in *in vitro* biochemical experiments[22,36] and 50-fold lower than estimates of eIF3 concentrations *in vivo*[45], it is near the maximum concentration at which mass photometry measurements retain single-molecule resolution (~80 nM)[41]. If a 30 nM sample of eIF3 contained a single, highly stable, and uniformly composed full eIF3 complex, we would expect to observe a single major species with a relative population of 100 % and a molecular mass of ~360 kDa. In contrast with this expectation, we observe at least four species present in the sample (Figure 1A). The largest of these species comprises just 47 % of the total population and has a molecular mass distribution centered at 368 kDa, consistent with the mass of the full eIF3 complex. The additional three species make up the remaining 14, 22, and 15 % of the total population and have molecular masses centered at 261, 158, and 70 kDa, respectively (Figure 1A), consistent with the expected molecular mass of various possible combinations of subcomplexes and subunits. We note that the lower mass resolution limit of the iSCAT microscope is ~60 kDa[41], such that peaks below ~60 kDa could represent multiple species with molecular masses at or lower than ~60 kDa. These results reveal that the composition of eIF3 is governed by an equilibrium involving the full complex and its constituent subcomplexes and subunits.

The equilibria that typically control multi-subunit biomolecular complexes are dynamic, such that individual subunits exchange between a full complex, subcomplexes, and/or complex-free subunits as a function of time. To assess whether the eIF3 compositional equilibrium is

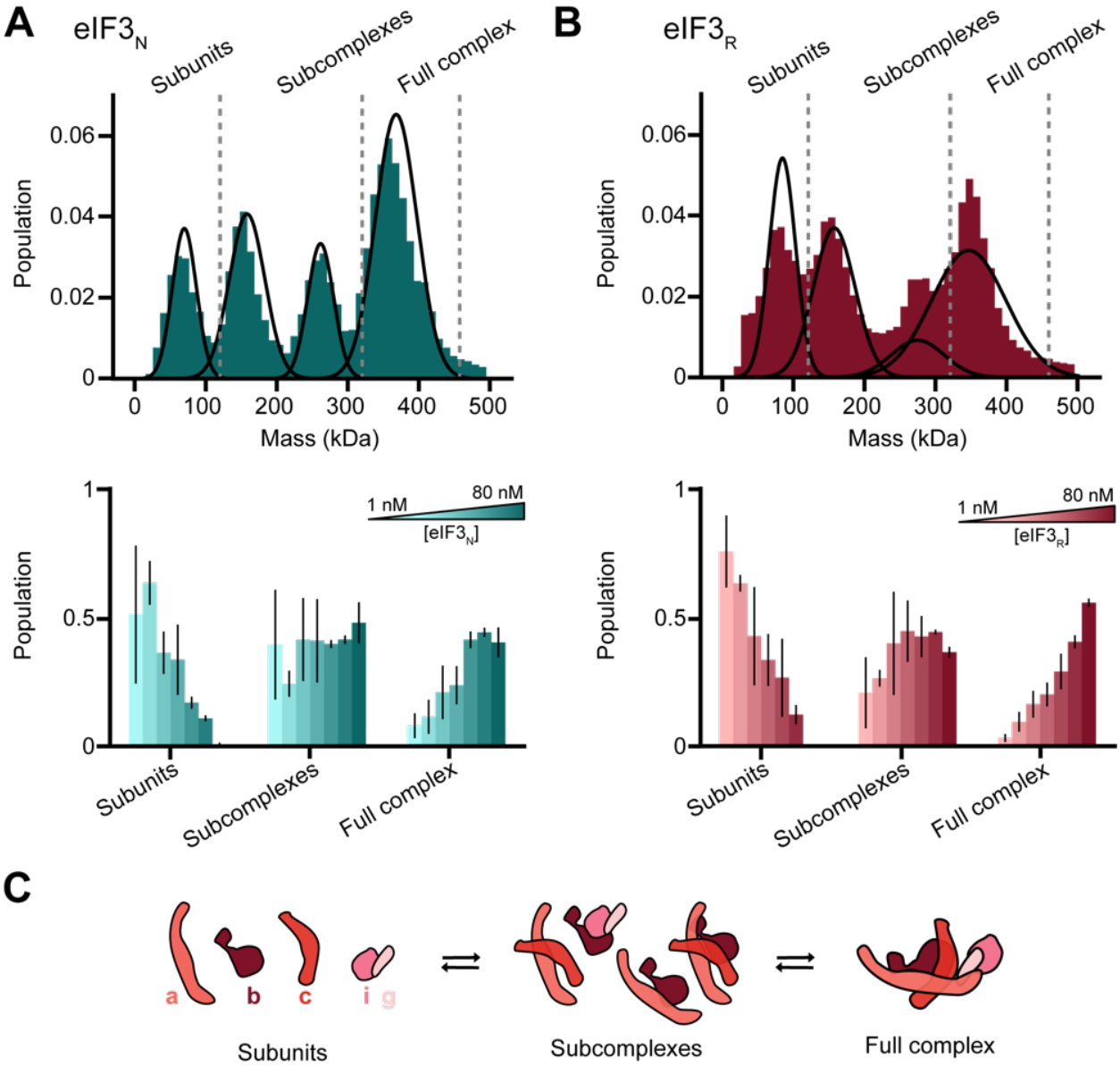

Figure 1. eIF3 exists as a dynamic equilibrium between subunits, subcomplexes, and the full complex. (A) *Histograms of the mass distribution of eIF3$_N$ at 30 nM from mass photometry (top) and a bar graph showing the change in fractional distribution as a function of concentration (bottom). Dashed grey lines indicate the threshold cutoffs defining 'subunits', 'subcomplexes', and the 'full complex' shown in the lower bar graph.* ***(B)*** *The equivalent plots as shown in (A) for eIF3$_R$* ***(C)*** *A simplified cartoon model of a dynamic equilibrium governing the composition of eIF3.*

dynamic on a relatively short timescale, we used mass photometry to characterize the compositional equilibrium of an 80 nM eIF3 sample which we then serially diluted down to 1 nM and characterized at each concentration (Figures 1A and S2C). As expected, at the highest eIF3 concentrations, eIF3 is primarily composed of the full complex, with a lower population of subcomplexes. We note here that, due to the high number of adsorption events at 80 nM, the spatial resolution between the full complex, subcomplexes, and subunits in the iSCAT microscope can become compromised[41], potentially resulting in under-sampling of low-molecular-mass species. Nonetheless, as the 80 nM sample is diluted to intermediate concentrations, the

equilibrium shifts, decreasing the population of the full complex and increasing the populations of the subcomplexes. Continued dilution to the lowest concentrations results in a further shift of the equilibrium away from the full complex and subcomplexes and toward individual subunits. Such concentration-dependent shifts in the compositional equilibrium demonstrate that this equilibrium is dynamic on the relatively short timescales over which dilution and imaging are executed (~20 min).

In vitro reconstitution of eIF3 allows the molecular species constituting the eIF3 compositional equilibrium to be identified and characterized

To assign the observed peaks to specific subcomplexes and subunits and explore the potential role of this equilibrium in regulating eIF3 function, we sought to control the presence and concentrations of the individual subunits. Because all five *S. cerevisiae* subunits are essential, it is difficult or impossible to natively purify eIF3 variants from *S. cerevisiae* that lack one or more subunits or contain other lethal mutations. To overcome this challenge, we optimized a system for *in vitro* reconstituting eIF3 from *S. cerevisiae* subunits that we recombinantly expressed in *Escherichia coli*[39,40] (Figure S1B, STAR*Methods). Briefly, we individually purified recombinant eIF3a, eIF3b, and eIF3c, as well as an eIF3i-eIF3g fusion that we subsequently separate *via* proteolytic cleavage during purification. Combining these purified subunits in near stoichiometric amounts yields a reconstituted eIF3 ($eIF3_R$) that, upon size-exclusion chromatography, runs as a single peak exhibiting broadness, shouldering, and/or splitting that is similar to that observed for eIF3 purified natively from *S. cerevisiae* ($eIF3_N$) (Figure S1A).

Using mass photometry, we assessed whether $eIF3_R$ exhibits a dynamic compositional equilibrium comparable to that which we observed for $eIF3_N$ (Figure 1B). A 30 nM sample of $eIF3_R$ exhibits at least four peaks with populations of 40, 8, 27, and 24 % and centered at molecular masses of 345, 274, 156, and 83 kDa, respectively, consistent with the populations and molecular mass centers of the peaks we observed for a 30 nM sample of $eIF3_N$. To assign these peaks to specific eIF3 species, we performed mass photometry measurements on 30 nM samples of the purified individual $eIF3_R$ subunits (Figure S3A) as well as selected combinations of $eIF3_R$ subunits (Figure S3B) that, assuming they could do so at a concentration of 30 nM, would form subcomplexes with molecular masses matching those observed in the 30 nM $eIF3_R$ and $eIF3_N$ samples. Based on these measurements, we were able to assign the species centered at 360 kDa to the full complex (364 kDa); the species centered at 274 kDa to the eIF3abig (268 kDa) and/or eIF3abc (292 kDa) subcomplexes; the species centered at 156 kDa to the eIF3big (157 kDa), eIF3ab (198 kDa), and/or eIF3ac (202 kDa) subcomplexes; and the species centered at 83 kDa to the eIF3ig (69 kDa) subcomplex and/or to the eIF3a (111 kDa), eIF3b (89 kDa), and/or eIF3c (93 kDa) subunits. Strikingly, the subcomplexes we assign our peaks to here are in excellent agreement with those predicted by genetic[46,47] and biochemical[32,48] studies as well as with the inter-subunit contacts observed in available structures of eIF3-bound 48S PICs[8,20,21,47,49-51].

Analogous to our studies of the $eIF3_N$ compositional equilibrium, we next performed mass photometry measurements of an 80 nM $eIF3_R$ sample and of serial dilutions of this sample down to 1 nM $eIF3_R$. In full agreement with the dynamic nature we observed for the $eIF3_N$ compositional equilibrium, the 80 nM $eIF3_R$ sample is primarily composed of the full complex, but dilution of this sample shifts the $eIF3_R$ compositional equilibrium away from the full complex, initially populating the subcomplexes at intermediate concentrations, and ultimately populating the individual subunits at the lower concentrations (Figure 1B). Collectively, our results using $eIF3_N$ and $eIF3_R$ demonstrate that the composition of eIF3 is governed by a dynamic equilibrium in which the full complex can dynamically dissociate into individual subcomplexes and subunits, components that can then reassociate into subcomplexes and the full complex.

$eIF3_R$ recapitulates the biochemical activities of $eIF3_N$

Before investigating the role that the dynamic eIF3 compositional equilibrium might play in regulating eIF3 function, we sought to characterize the biochemical activity of $eIF3_R$ and compare it to that of $eIF3_N$. To this end, we used two established, standard eIF3 activity assays. The first of these is an assay that monitors eIF3 binding to the PIC[22,52]. Using a previously described[22,52,53], uncapped and unstructured, 50-nucleotide model mRNA containing an AUG start codon at nucleotide positions 23-25 and a fluorescein label at the 3' end, we employed a previously reported *S. cerevisiae in vitro* reconstituted translation initiation system[37,38] to assemble PICs (STAR*Methods). Briefly, we combined mRNA and 40S subunits with saturating amounts of a ternary complex composed of eIF2, guanosine triphosphate (GTP), and initiator transfer RNA (eIF2(GTP)•$tRNA_i$), eIF1, and eIF1A to form PICs under conditions previously reported to yield start-codon-dependent formation of PICs in the absence of the eIF4 factors[22,36]. We then incubated these PICs with varying concentrations of either $eIF3_R$ or $eIF3_N$ and used native gel electrophoresis to separate free mRNA, eIF3-free PICs, and eIF3-bound PICs (Figure 2A). Consistent with a previous study that reported a mean apparent equilibrium dissociation constant (K_d^{app}) of 30 nM for $eIF3_N$ binding to the PIC[22], we observe a mean K_d^{app} of 23 nM for $eIF3_N$ binding to the PIC (Figure 2A, Cyan). More importantly, we observe a mean K_d^{app} of 14 nM for $eIF3_R$ binding to PICs (Figure 2A, Burgandy), demonstrating that our $eIF3_R$ binds the PIC nearly identically to $eIF3_N$.

The second activity assay we used leverages the fact that eIF3 is required for *in vitro* recruitment of capped mRNAs into PICs[22,36,44,53,54]. Using this mRNA recruitment assay, we compared the abilities of $eIF3_R$ and $eIF3_N$ to recruit a capped mRNA encoding the *S. cerevisiae rpl41a* gene into PICs as a function of time. The rpl41a mRNA has previously been used as a representative natural mRNA in numerous *in vitro* and *in vivo* biochemical studies[22,36,53,55]. Briefly, we prepared a mixture containing PICs (40S subunits in the presence of saturating concentrations of eIF1, eIF1A, ternary complex, and either $eIF3_R$ or $eIF3_N$), the eIF4 factors (eIF4G, eIF4E, eIF4A, and eIF4B, at concentrations that are saturating over the mRNA), and ATP (STAR*Methods). To begin each reaction, we added a sub-stoichiometric amount of the rpl41a mRNA prepared with a ^{32}P-labeled cap to the mixture, incubated for a variable amount of time, and used native gel electrophoresis to separate free mRNA from mRNA recruited to PICs. Under conditions in which they are saturating over the PIC, both $eIF3_R$ and $eIF3_N$ stimulate mRNA recruitment similarly across timepoints ranging from 30 seconds to 60 minutes (Figure 2B). Under conditions in which they are sub-saturating to saturating over the PIC, both $eIF3_R$ and $eIF3_N$ stimulate > 70 % mRNA recruitment. It should be noted that at the most sub-saturating concentrations (*i.e.*, < 100 nM), $eIF3_N$ exhibits a slightly higher recruitment efficiency than $eIF3_R$ (Figure S4). These modest differences likely derive from contamination of the $eIF3_N$ prep with additional proteins, which is routinely observed in preparations of $eIF3_N$[20,38]. Alternatively, or in addition, these slight activity differences might derive from previously observed variations in the mRNA recruitment activities of different preparations of eIF3[38], from the presence of post-translational modifications in $eIF3_N$ that are lacking in our $eIF3_R$, or from subtle variations in the subunit stoichiometry of $eIF3_N$ (as compared to $eIF3_R$). Regardless, the collective results of these assays demonstrate that $eIF3_R$ recapitulates the known *in vitro* biochemical functions of $eIF3_N$.

eIF3a is the only free eIF3 subunit that binds mRNA with high affinity

One of the most recently described functions of eIF3, an activity that is typically ascribed to the full complex, is its apparent ability to directly interact with specific mRNAs in cells[12,13,16,25]. This is an exciting development in that it suggests direct interactions between eIF3 and specific mRNAs could drive initiation of such mRNAs[13,14,56]. Consistent with this, previous *in vitro* mRNA binding assays have shown that eIF3 can bind mRNA with a K_d^{app} of 30 nM[36]. Complementing this, previous *in vivo* and *in vitro* biochemical studies have identified several eIF3 subunits from *S. cerevisiae* or higher eukaryotes that copurify or crosslink with either endogenous or model

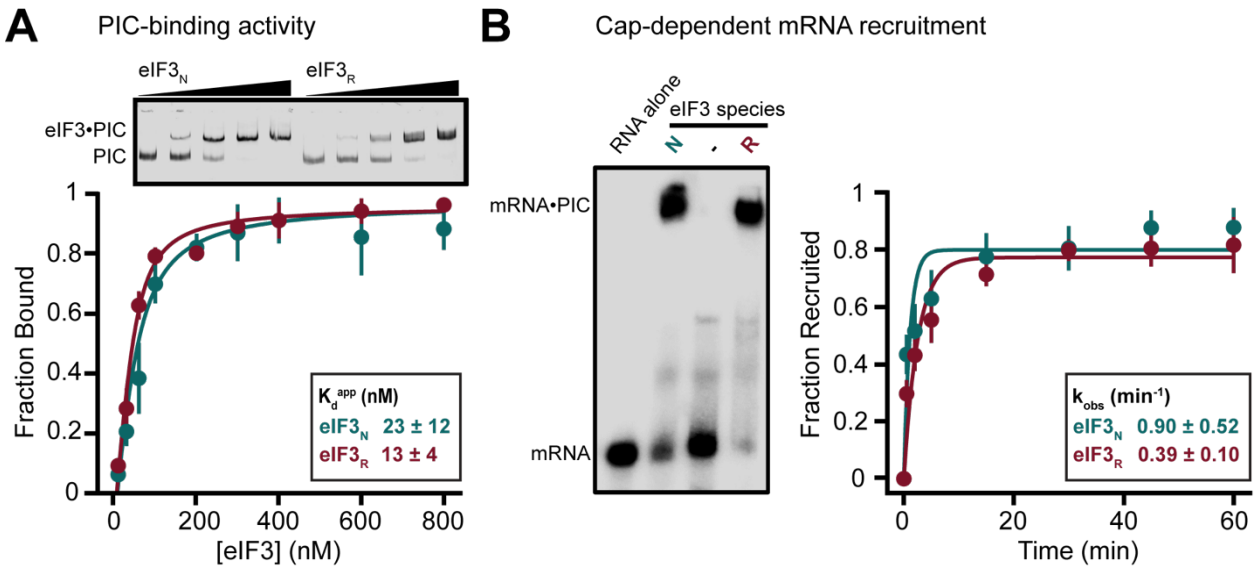

Figure 2. eIF3$_R$ is biochemically active. (A) *Electrophoretic mobility shift assay (EMSA) comparing eIF3$_N$ and eIF3$_R$ binding to the PIC. An example gel is shown (top) alongside the quantitation across three replicates (bottom), including the apparent binding affinities (K_d^{app}).* ***(B)*** *EMSA comparing the ability of eIF3$_N$ and eIF3$_R$ to stimulate recruitment of capped rpl41a mRNA. An example gel is shown (left) alongside the quantitation across three replicates (right), including the observed rate constants (k_{obs}).*

mRNAs[13-18,25,36,57-61]. These latter results motivated us to use our eIF3$_R$ system to ask whether individual eIF3$_R$ subcomplexes and/or subunits exhibit high-affinity mRNA binding and, if so, whether the dynamic eIF3 compositional equilibrium might regulate the ability of eIF3 to bind mRNA.

We began by testing whether eIF3$_R$ binds to RNA and compared it to what has been previously reported for eIF3$_N$ [36]. Using the same uncapped, 50-nucleotide, 3'-fluorescein-labeled model mRNA that we used in the PIC binding assays described above, we measured changes in the fluorescence anisotropy of mRNA upon titration with either eIF3$_R$ or eIF3$_N$ (Figures 3 and S6, STAR*Methods). Fitting plots of fluorescence anisotropy as a function of eIF3 concentration to a two-component, single-site binding model provides mean K_d^{app} values of 5 nM and 45 nM for eIF3$_N$ and eIF3$_R$, respectively (Figure 3A), in excellent agreement with the mean K_d^{app} of 30 nM that has been previously reported for eIF3[36]. We suspect that differences in the stoichiometries of the individual subunits within eIF3$_N$ versus those within the more compositionally controlled eIF3$_R$ underlie the ~10-fold lower mean K_d^{app} we observe for eIF3$_N$ relative to eIF3$_R$; this interpretation is supported by our experiments showing that distinct eIF3 species bind to mRNA with significantly different affinities, as described below. Nonetheless, these results demonstrate that eIF3$_R$ recapitulates the mRNA binding activity of eIF3$_N$.

We next leveraged our eIF3$_R$ system to test whether, and to what extent, individual eIF3 subunits can directly interact with mRNAs. To accomplish this, we adapted the fluorescence anisotropy-based mRNA binding assay described above to measure the change in fluorescence anisotropy of the mRNA upon titration with individual eIF3 subunits (Figures 3B, S6B, and S6D). Because we co-purify eIF3i and eIF3g and they form a high-affinity bimolecular complex that is not easily separated[39,40], we titrated these together. Surprisingly, despite the fact that both eIF3b and eIF3g contain RNA recognition motifs[58,59,61], plots of fluorescence anisotropy as a function of eIF3 subunit concentration reveal that neither eIF3b nor eIF3ig show an appreciable level of mRNA binding, even at the highest protein concentrations we tested (2 μM). Moreover, eIF3c exhibits only modest affinity for mRNA, with a K_d^{app} of > 600 nM (Figure S6B and Table S1). In stark contrast, eIF3a exhibits significant mRNA binding activity, yielding a mean K_d^{app} of 119 nM

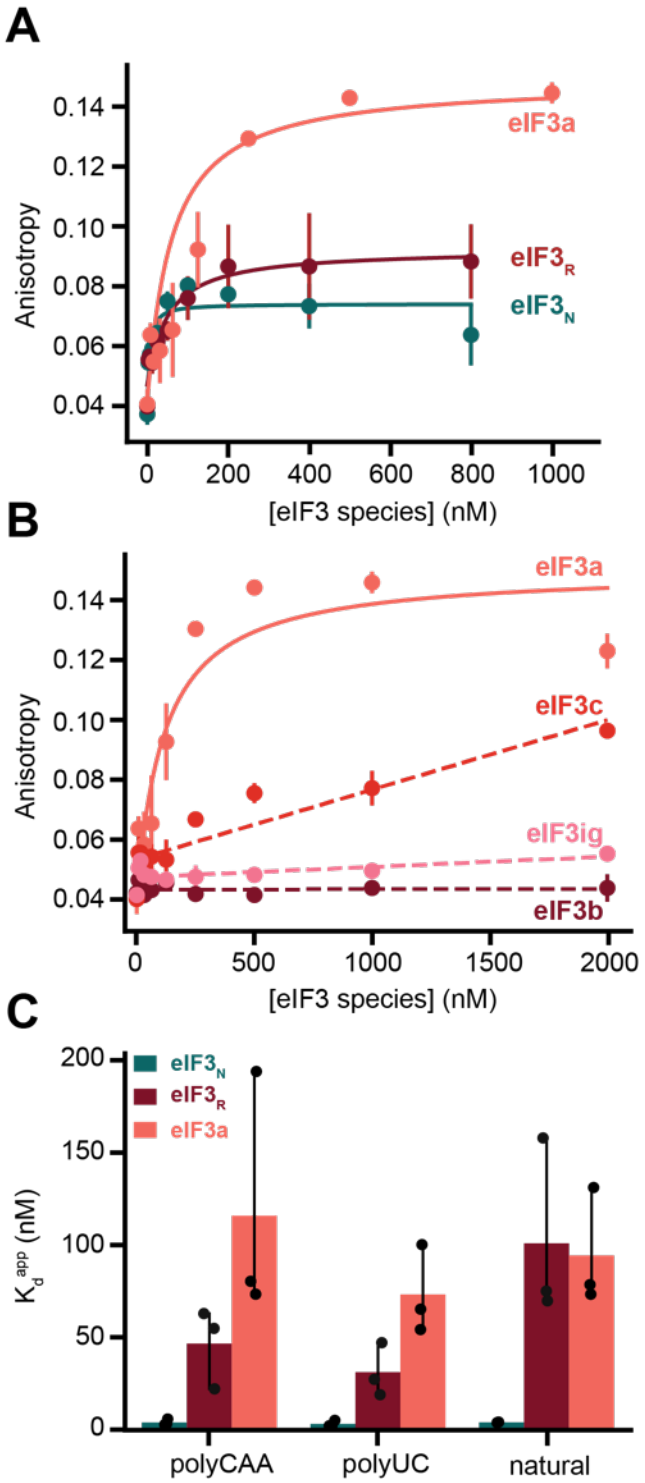

Figure 3. eIF3a is the only subunit that binds mRNA with high affinity. (A) *Fluorescence-anisotropy experiments comparing eIF3N, eIF3R, and eIF3a binding to an mRNA.* ***(B)*** *Fluorescence-anisotropy experiments comparing eIF3a, eIF3b, eIF3c, and a co-purified eIF3i-eIF3g binding to an mRNA.* ***(C)*** *Bar graph of the apparent binding affinities measured for three sequence-distinct mRNAs to eIF3N, eIF3R, and eIF3a.*

that could potentially account for a significant fraction the mRNA binding affinity we observed when titrating mRNA with $eIF3_N$ or $eIF3_R$ (mean K_d^{app} values of 5 and 45 nM, respectively). Notably, the relatively high mRNA binding affinities we observed here for $eIF3_N$, $eIF3_R$, and eIF3a all required an mRNA length of at least 45 nucleotides (Table S1 and Source Data). To test the effect of the model mRNA sequence on eIF3 binding, we tested a different previously employed model mRNA with a distinct repetitive sequence[37] (Figures S6B and S6D) as well as a model mRNA containing the first 51 nucleotides of the native rpl41a sequence (Figures S6A and S6C). Neither the repetitive nor the rpl41a model mRNAs showed significant differences in mRNA binding relative to the initial model mRNA (Figures 3, S6, and Table S1), demonstrating that mRNA binding is relatively sequence non-specific in the absence of additional interacting components.

Because the eIF3c C-terminal domain forms a stable heterodimer with the eIF3a N-terminal domain that has been shown to stabilize mRNA binding to the PIC[22,57], we wondered whether the inclusion of eIF3c would affect the high-affinity mRNA binding we observe for eIF3a. Consistent with these observations, eIF3a and eIF3c form the highest affinity subcomplex we identified in our mass photometry experiments and could be expected to predominantly form a 3ac subcomplex under our titration conditions (Figure S3B). In contrast, assessing whether and to what extent the other major subcomplexes we observed and identified in the $eIF3_N$ and $eIF3_R$ samples can directly interact with mRNA is complicated by the dynamic compositional equilibria of these subcomplexes and free subunits. Strikingly, we find that inclusion of eIF3c within an eIF3ac subcomplex results in a binding curve that matches nearly identically with that of $eIF3_R$, potentially indicating that the interaction between eIF3a and eIF3c enhances the ability of the eIF3ac subcomplex to bind mRNA relative to eIF3a alone (Figure S5A).

eIF3a-containing subcomplexes drive the reported mRNA binding activity of eIF3

The dynamic compositional equilibrium of eIF3 severely complicates the analysis and interpretation of mRNA-binding experiments because it invalidates assumptions inherent to two-component, single-site binding models. These models underlie the approaches that are most frequently used to analyze data from such experiments and have been employed as simplifying assumptions in previous studies of eIF3[22,36]. In contrast, mRNA binding by eIF3a is strictly bimolecular and therefore should more closely obey the assumptions of a two-component, single-site binding model than mRNA binding by $eIF3_N$ or $eIF3_R$. Furthermore, our fluorescence anisotropy data at concentrations below 50 nM (from experiments testing either $eIF3_N$ or $eIF3_R$) match nearly identically the anisotropy data we obtain within this concentration range from experiments testing eIF3a (Figures 3A, S6A, and S6B). Given that, at these concentrations, both $eIF3_N$ and $eIF3_R$ contain significant populations of free subunits (Figures 1A and 1B), we hypothesized that eIF3a might be primarily responsible for the observed mRNA-binding activity of eIF3 to mRNA in all cases and that the compositional heterogeneity of $eIF3_N$ and $eIF3_R$ could be modulating this activity. We therefore sought to directly test how the dynamic compositional equilibrium of eIF3 alters its observed mRNA-binding activity.

We first tested this using fluorescence anisotropy binding experiments where we increased the concentration of total mRNA in separate titrations. As the concentration of mRNA is increased, the amount of eIF3a or eIF3 required to saturate binding should increase if the assumptions of two-component, single-site binding hold. This should shift the binding curve to higher concentrations and, at concentrations near and above the K_d, result in a non-hyperbolic titration curve[62]. Because we have full control over the stoichiometry of eIF3 subunits as compared to $eIF3_N$, we performed these experiments comparing eIF3a and $eIF3_R$. As expected, when we increased the concentration of mRNA and performed binding experiments with eIF3a alone, the resultant plots of normalized anisotropy match closely with those modeled by a two-component, single-site binding model (Figure S7A). Strikingly, identical experiments with $eIF3_R$ as the titrant do not show this trend (Figure S7B). Rather, these binding curves saturate at concentrations >

500 nM $eIF3_R$ regardless of the mRNA concentration, followed by a decrease in anisotropy that continues as $eIF3_R$ concentrations increase. Notably, this decrease in anisotropy at higher eIF3 concentrations is also observed when $eIF3_N$ is the titrant (Figure 3A). These decreases in anisotropy led us to consider whether the dynamic compositional equilibrium of eIF3 at higher protein concentrations was leading to the accumulation of species that bind the mRNA with relatively low affinity. In other words, that the full eIF3 complex or other subcomplexes may exhibit a lower affinity for mRNA. This hypothesis, that the accumulation of specific eIF3 subspecies might enhance or diminish the affinity with which eIF3 binds mRNA is consistent with our observation that the inclusion of eIF3c enhances mRNA binding by the eIF3ac subcomplex (Figure S5A). Such a hypothesis is exceedingly difficult to experimentally verify with conventional approaches due to various technical challenges: (*i*) the probabilities with which specific subspecies in a dynamic compositional equilibrium of a multi-component complex become available for binding vary non-linearly as a function of concentration, (*ii*) the binding of specific subspecies to the target result in further changes to these probabilities, (*iii*) each subspecies may differentially contribute to the signal response in assays commonly used to measure binding (*e.g.*, components with different masses will contribute differently to the change in anisotropy signal upon binding), and (*iv*) ensemble averaging complicates deconvolution of *i-iii* using ensemble binding assays.

To overcome these difficulties and test this hypothesis directly, we adapted our mass photometry approach to use sample wells in which the borosilicate glass surface is derivatized with a mixture of polyethylene glycol (PEG) and biotinylated (biotin)-PEG (*i.e.*, PEG-derivatized) in a manner similar to the flow cells commonly employed in single-molecule florescence microscopy experiments[44,63-65] (Figure 4A). Derivatization of the surface in this way enables us to sparsely tether a 3'-biotinylated version of the model RNA we previously employed in our PIC-binding and mRNA-binding experiments within each sample well using a biotin-streptavidin-biotin bridge. While mass photometry experiments using conventional, underivatized sample wells report on the masses of biomolecules that irreversibly and non-specifically adsorb across the entire coverslip surface, mass photometry experiments using our PEG-derivatized and tethered-mRNA sample wells report instead on the masses of eIF3 species that reversibly and specifically bind to these sparsely tethered, single mRNA molecules (Figure S8A, STAR*methods).

We began these mRNA-binding mass photometry experiments by comparing the adsorption events we observed upon delivering 200 nM $eIF3_R$ to PEG-derivatized wells in either the absence or presence of tethered mRNA (Figure 4B). Under both conditions, the distribution of all detected adsorption events yielded a single large peak centered at a mass of 150 kDa, corresponding neither to eIF3a, any other subunit or subcomplex, or the full complex. However, in the presence of mRNA we additionally observe a second, broader peak centered at a molecular mass of 250 kDa that we hypothesized represents the binding of $eIF3_R$ components to mRNA. To confirm this hypothesis, we used two independent methods. First, we reasoned that events resulting from specific binding to the mRNA would be sensitive to ribonuclease (RNase) treatment. Thus, we repeated this experiment in the absence and presence of RNase and compared the distribution of all events observed in a well to the distribution of all events observed in the same well, but after adding RNase (Figure 4C). Subtraction of the events detected after RNase addition from those detected before RNase addition leaves only those events that depend on mRNA binding (Figure 4C). Second, we similarly reasoned that only at those PEG-derivatized well locations at which an mRNA was specifically tethered, would we expect the corresponding CMOS camera pixels to report multiple association/dissociation events, with dissociation events detected as events in which the amount of Rayleigh scattering decreases rather than increases. Consequently, we altered our analysis approach to consider only those events that were detected at pixels exhibiting multiple adsorption/desorption events (Figure 4D). Strikingly, both methods for identifying mRNA-dependent binding events yield similar mass distributions of the $eIF3_R$ species that specifically bind to mRNAs (*i.e.*, the mRNA-binding mass distribution). Unexpectedly, the

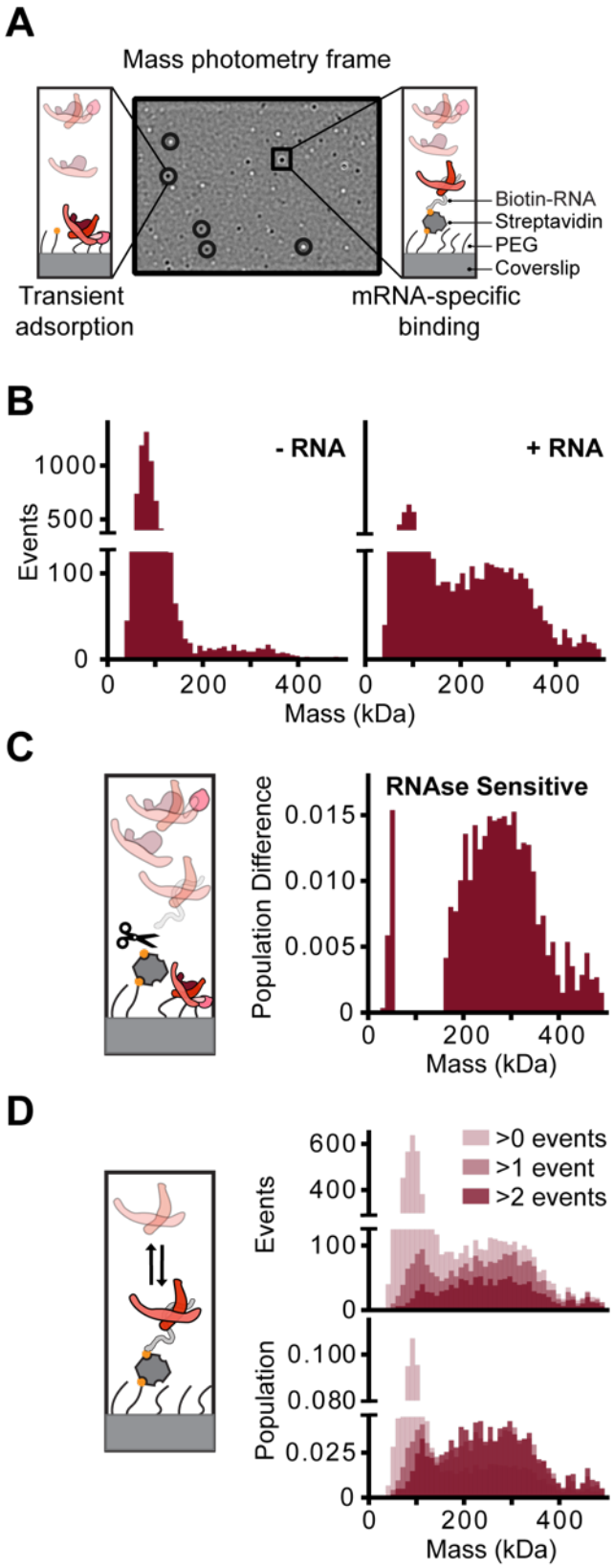

Figure 4. Distinguishing between transient adsorption and mRNA-specific binding events in mass photometry. (A) *An example frame from mass photometry depicting various events in the field of view. A*

cartoon illustrating events of transient adsorption to the surface (left) and mRNA-specific binding events (right). ***(B)*** *Histograms of the mass distribution from mass photometry experiments of 200 nM eIF3$_R$ using derivatized coverslips in the absence (left) and presence (right) of tethered mRNA.* ***(C)*** *The portion of the mass distribution of 200 nM eIF3$_R$ that is sensitive to addition of RNAse.* ***(D)*** *The mass distribution of 200 nM eIF3$_R$ exhibiting > 0, 1, or 2 events per pixel shown as either raw counts (top) or normalized population (bottom).*

mass eIF3 subcomplexes and the full complex (Figure 4D). Because we have previously determined the mass distribution of eIF3$_R$ in solution (*i.e.*, the solution mass distribution) at 30 nM, we repeated the mRNA-binding mass photometry experiment at 30 nM eIF3$_R$ and compared this distribution (built using events detected only at those pixels exhibiting > 2 adsorption/desorption events) to the solution mass distribution in the absence of mRNA (Figure 5A). To identify which eIF3 species bind mRNA and whether these are enriched or depleted in the mRNA-binding mass distribution as compared to the solution mass distribution in the absence of mRNA, we calculated the population difference between these two distributions (Figure 5B). Species that are equally represented in both distributions should yield peaks near zero, whereas enriched or depleted species appear as positive or negative peaks, respectively. This analysis reveals that high-molecular-mass subcomplexes and the full complex exhibit substantial affinity for the mRNA, while low-molecular-mass subcomplexes and subunits do not. The lack of low-molecular-mass subcomplexes and subunits in the mRNA-binding mass distribution, despite their prominence in the solution mass distribution, demonstrates that eIF3a, which we have shown tightly binds mRNA (Figure 3), is rapidly depleted from low-molecular-mass subcomplexes and subunits and incorporated into higher-molecular-mass subcomplexes bound to mRNA.

A deeper comparison of the mRNA-binding and solution mass distributions demonstrates that high-molecular-mass subcomplexes compete with, and may even outcompete, the full complex for mRNA binding. This can be readily concluded from the observation that the high-molecular-mass subcomplexes are enriched relative to the full complex in the population difference plot (Figure 5B). Consistent with this conclusion, while the concentration limits of mass photometry prevent us from determining the solution mass distribution at elevated concentrations in which the full complex is favored over subcomplexes, analysis of the mRNA-binding mass distribution at 200 nM eIF3$_R$ shows that certain higher-molecular-weight subcomplexes more effectively compete with the full complex for mRNA binding (Figure S8A). This result suggests that, by increasing the total concentration of eIF3 components, the compositional equilibrium of eIF3 is shifted so as to favor the formation of these mRNA-binding, higher-molecular-weight subcomplexes.

Our unique ability to compare the mRNA-binding and solution mass distributions provides an opportunity to identify the binding preferences of all possible subcomplexes. Given our observation that eIF3a appears to be the primary driver of mRNA binding, we sought to narrow the list of possible subcomplexes by testing the ensemble of subcomplexes that form in the absence of eIF3a (*i.e.*, eIF3b+c+i+g) (Figures S3B and S8B). The results of this experiment show that excluding eIF3a from the eIF3 compositional equilibrium abolishes mRNA binding, demonstrating that eIF3a is necessary for RNA binding. We therefore limited our studies of the remaining subcomplexes to only those containing eIF3a. In Figures 5C-F, a comparison of the mRNA-binding and solution mass distributions of all eIF3a-containing subcomplexes shows that each of these subcomplexes binds mRNA to varied extents. Therefore, eIF3a is necessary and sufficient for eIF3 to bind mRNA. While it is likely that different eIF3a-containing subcomplexes bind mRNA with different affinities, current limitations in the quantitative capabilities of mass photometry prevents us from quantifying such differences.

DISCUSSION

Prior studies of eIF3 function, including those in which mRNA binding by eIF3 has been

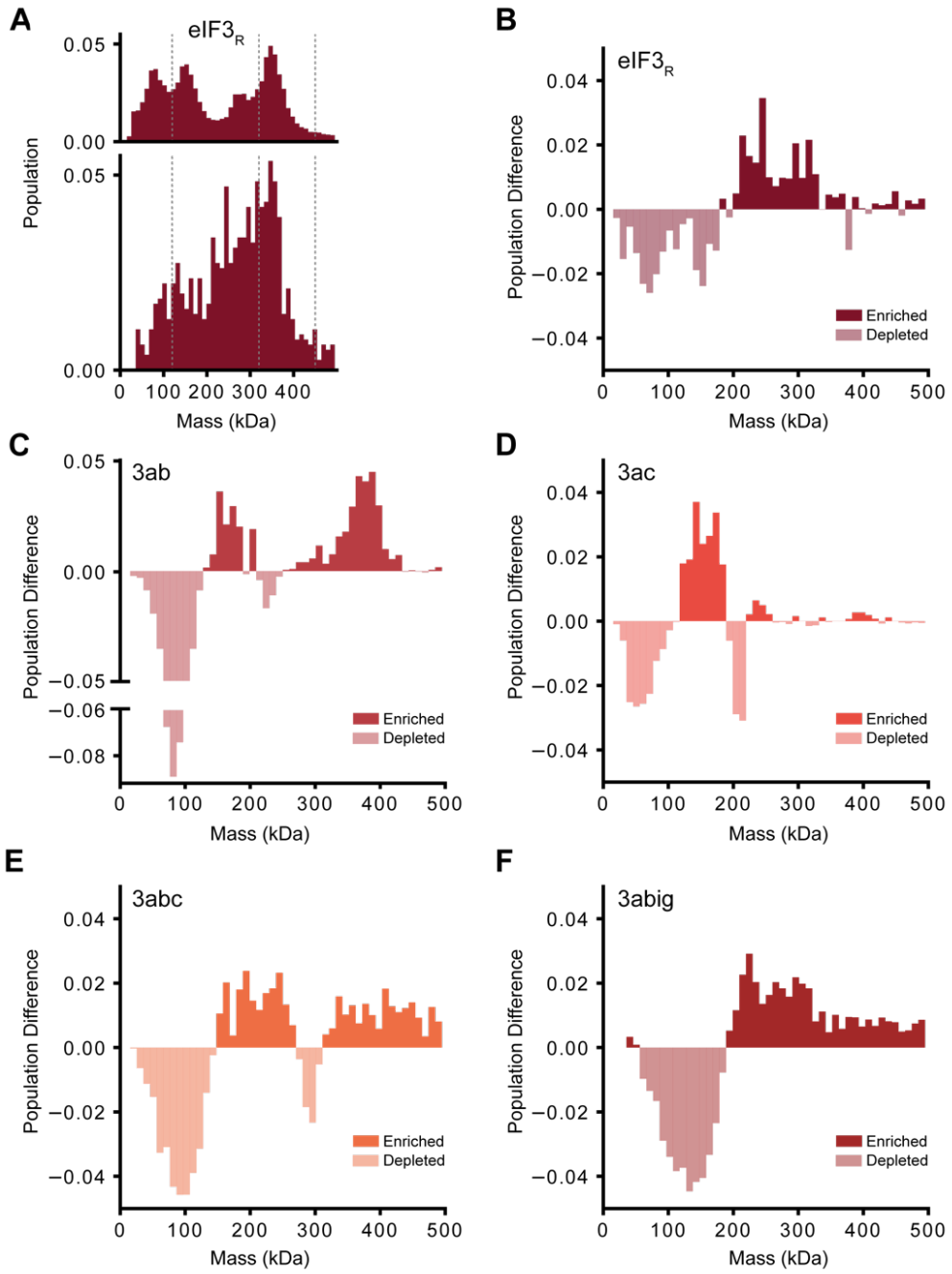

Figure 5. Comparison of the solution mass distribution to the mRNA-binding mass distribution reveals eIF3a-containing subcomplexes differentially bind mRNA. (A) *Solution mass distribution histogram (top) and the mRNA-binding mass distribution (bottom) of 30 nM eIF3R.* ***(B)*** *A population difference plot of the mRNA-binding mass distribution relative to the solution mass distribution for 30 nM eIF3R.* ***(C-F)*** *Population difference plots for eIF3a-containing subcomplexes at 30 nM: 3ab (C), 3ac (D), 3abc (E), and 3abig (F).*

homogenous entity[22,35,36]. In contrast, our work here establishes that the full eIF3 complex is in a dynamic compositional equilibrium with its constituent subcomplexes and subunits, and that this dynamic equilibrium governs mRNA binding by eIF3. Our experiments demonstrate that the eIF3a subunit is the primary driver of mRNA binding by the yeast core eIF3 complex and that the

interactions of eIF3a with eIF3c and other eIF3 subunits modulate its ability to associate with mRNA. Most importantly, even at eIF3 concentrations employed in previous biochemical studies[22,44,52-54] and that favor formation of the full eIF3 complex, we observe substantial mRNA binding by eIF3a-containing subcomplexes. Based on this observation, we expect the dynamic exchange of eIF3 subunits to have functional consequences for eIF3-mediated mRNA binding under physiological conditions.

The results we present here allow us to propose a model for eIF3 function that provides a molecular framework for investigating the numerous roles ascribed to eIF3 in translation (Figure 6). In our model, eIF3 is in a dynamic compositional equilibrium that is best described as a mixture of the full complex and the distinct subcomplexes and subunits with which the full complex can dynamically exchange. Because free subunits are rapidly sequestered into subcomplexes through the activity of eIF3a, this mixture is simplified to primarily consist of subcomplexes and the full complex. Here, we have used this framework to characterize how eIF3 interacts with mRNA. Specifically, we find that eIF3a is both necessary and sufficient for high-affinity association with mRNA, leading to a competition between eIF3a-containing subcomplexes and the full complex for binding sites on mRNA. Interestingly, the various eIF3a-containing subcomplexes possess varied affinities for mRNA that span those less than and greater than that of the full complex. This finding demonstrates that inter-subunit interactions within eIF3 subcomplexes and the full complex can modulate the activities of individual subunits and, in the case of the mRNA binding by eIF3, shows how subcomplexes can outcompete the full complex, even under conditions that otherwise strongly favor formation of the full complex.

Our model predicts two key regulatory routes through which the activities of eIF3 may be controlled. First, the degree to which individual subcomplexes or subunits partition between interacting with additional eIF3 subunits or translational components could be context-dependent, creating a regulatory paradigm in which the presence and concentration of additional translation components can modulate these compositional equilibria and, consequently, the functions of eIF3. As a physiologically important example of this, here we show how the interaction of mRNA with eIF3a-containing subcomplexes modulates these equilibria (Figure 6). In the presence of high concentrations of mRNA, we expect eIF3a-containing subcomplexes to effectively partition along the path of forming complexes with mRNA. This would have the effect of depopulating the path through which eIF3a-containing subcomplexes participate in the formation of higher-order subcomplexes and the full complex, consequently redistributing the species participating in these equilibria such that higher order eIF3 subcomplexes and the full complex would be relatively depleted, but complexes between eIF3a-containing subcomplexes and mRNA and a variety of eIF3 subcomplexes lacking both eIF3a and mRNA would be enriched.

In the second regulatory route predicted by our model, interactions between the translation machinery and individual subunits within the full complex may up- or downregulate the activities of individual subunits. Such interactions could modulate the dynamic eIF3 compositional equilibrium in a manner similar to that described above for mRNA binding in order to control additional eIF3-modulated steps in the initiation pathway, including PIC binding and mRNA recruitment, as well as more expanded activities, for example the recruitment of specific mRNAs, an activity that has been suggested from studies of eIF3 in higher eukaryotes[10,12,13,25]. Perhaps most excitingly, our model raises the possibility that, rather than stimulating translation initiation through the activity of the full complex, perhaps eIF3 accomplishes this through the action of different subcomplexes and subunits that act at different points along the initiation pathway.

Our observations that the mRNA binding activity of non-PIC-bound eIF3 is predominantly driven by eIF3a and that binding of other eIF3 subunits to eIF3a to form eIF3a-containing subcomplexes and the full complex can allosterically modulate this activity raises exciting possibilities for the mechanisms through which an mRNA is delivered to, loaded on, and then scanned by a PIC. One such possibility is that a complex between an mRNA-bound eIF3a-containing subcomplex and mRNA is delivered directly to an otherwise factor-bound PIC, serving

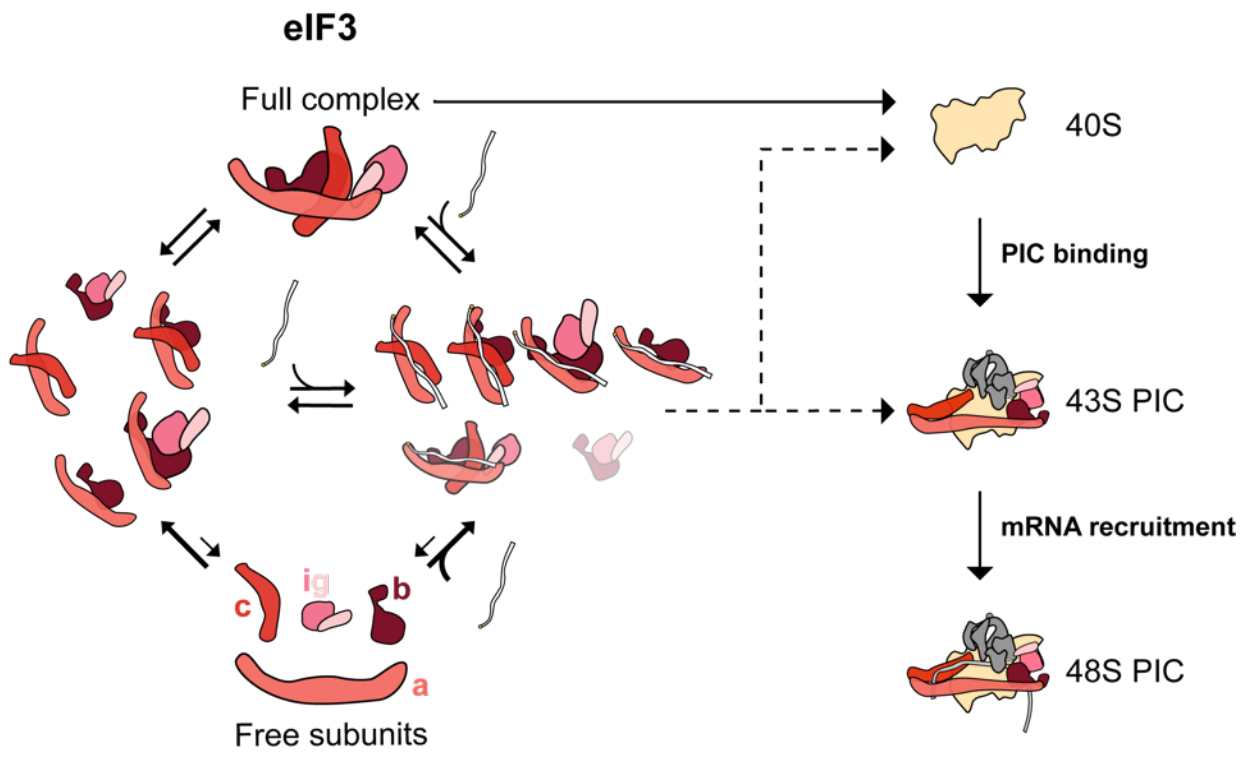

Figure 6. A molecular framework for modulation of eIF3 function by its underlying compositional equilibrium. *In contrast to existing as a stable, compositionally uniform protein complex, eIF3 exists in a dynamic equilibrium between the full complex, various subcomplexes, and free subunits. Additional eIF3-interacting factors likely alter this complex and dynamic compositional equilibrium. The presence eIF3a is required to enable mRNA binding by eIF3 subcomplexes, and eIF3a-containing subcomplexes may bind mRNA with a higher affinity than the full complex. The presence of mRNA thus biases the eIF3 compositional equilibrium to the formation of mRNA-bound eIF3a-containing subcomplexes, which may enable the delivery of mRNAs to free 40S subunits or PICs. Additional modulation of this compositional equilibrium may enable the formation of specific eIF3a-containing subcomplexes capable of dictating the translational fates of specific mRNAs.*

a major role in mRNA delivery to the PIC. Although we cannot discount this possibility, a more likely mechanism is one in which mRNA delivery is handled by the eIF4F mRNA-activation complex[4,5] and the mRNA-binding activity of eIF3a within the context of a PIC-bound, eIF3a-containing subcomplex or the full eIF3 complex is allosterically modulated in a manner that facilitates mRNA loading and/or scanning. Such a mechanism is supported by earlier studies attempting to reconstitute eIF3, which proposed allosteric modulation of the structure of eIF3 by the PIC[40]. Given that PIC-bound eIF3a spans both the mRNA-entry and -exit channels[20,22] and serves as the only physical connection between the domains of eIF3 at these two locations on the PIC[6], it is perhaps not surprising that eIF3a would play a central role in interacting with mRNA and in allosteric control of eIF3 activity. Beyond eIF3a, the numerous additional contacts that eIF3 makes with the PIC create expanded opportunities for allosteric control of other aspects of translation initiation by eIF3. Such opportunities are likely even further expanded in the case of higher eukaryotes, where an additional seven subunits of eIF3 are present[6,9,35]. Notably, these additional subunits are concentrated at the mRNA-exit channel[50,66,67]. This observation strongly suggests that whatever the expanded functions of these subunits may be, such roles are spatially localized to this region of eIF3 and/or the PIC and likely contribute to a narrowed set of mechanistic or regulatory steps in the initiation pathway of higher eukaryotes.

LIMITATIONS OF STUDY

A caveat to mass photometry is that the laser used for detection heats the sample, limiting the amount of time each field of view can be imaged, which has unknown effects on our derivatized coverslips, and required us to take a higher number of shorter movies as compared to underivatized coverslips (Figure S9C, and further discussed in STAR*Methods).

Several prior studies have suggested that eIF3 interacts with specific mRNAs dependent on sequence[12-18]**.** Seemingly in contrast, our anisotropy experiments testing the ability of eIF3 to bind a limited set of three mRNAs with distinct sequence content did not show a substantial difference in K_d^{app}. However, as we note above, it is possible that these observations could change in the context of PIC-bound eIF3. Moreover, these experiments did not test the binding of eIF3 to more complex mRNAs (*e.g.*, natural mRNAs with long or structured 5'-untranslated-region sequences or with post-transcriptional modifications, *etc.*). As a consequence, it is always possible that the binding affinity of eIF3a, eIF3a-containing subcomplexes, or other eIF3 subunits or subcomplexes, is altered in the presence of a unique set of mRNAs not tested in our study. Furthermore, additional mRNA-binding proteins present in the cell, but not in our *in vitro* experiments, may interact with eIF3 and modulate its apparent mRNA-binding activities.

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AUTHOR CONTRIBUTIONS

Conceptualization, N.A.I., R.C.G., C.D.K.-T., R.L.G., and C.E.A.; Methodology, N.A.I., R.C.G., C.D.K.-T., R.L.G., and C.E.A.; Investigation, N.A.I., R.C.G., and M.A.R.; Resources, N.A.I., R.C.G., V.M.C., K.Y., and E.W.H.; Validation, N.A.I., R.C.G., M.A.R., and P.K.V.; Writing – Original Draft, N.A.I., R.C.G., R.L.G., and C.E.A.; Writing – Review & Editing, N.A.I., R.C.G., R.L.G., and C.E.A.; Supervision, R.L.G. and C.E.A.; Funding acquisition, R.L.G. and C.E.A.

COMPETING INTERESTS

The authors declare no competing interests.

RESOURCE AVAILABILITY

Lead Contact

Further information and requests for resources and reagents should be directed to and will be fulfilled by either of the corresponding authors, Ruben L. Gonzalez, Jr. (rlg2118@columbia.edu), and/or Colin Echeverría Aitken (caitken@vassar.edu).

Materials Availability

All unique and stable reagents generated in this study are available from either of the corresponding authors with a completed Materials Transfer Agreement.

Data and Code Availability

All of the original source data is available in the supplemental information associated with this article. All code used to analyze the source data and generate plots is also available in the supplemental zipped folder associated with this article. The large, raw mass photometry movie files are available upon request to R.L.G.

EXPRIMENTAL AND SUBJECT DETAILS

Yeast Strains

40S subunits were purified from a wild-type, W303 *S. cerevisiae* strain, LSY679 (*MATα leu2-3,112 trp1-1 ura3-1 can1-100 ade2-1 his3-11,15 RAD5)*, a kind gift from L. Symington (Columbia University). eIF3 was natively purified from *S. cerevisiae* strain, LPY87 (pLPY-PRT1His-TIF34HA-TIF35Flag/pLPY-TIF32-NIP1 in *MATa/α ura3-52/ura3-52 trp1/ trp1 leu2-Δ1/leu2-Δ1 his3-Δ200/his3-Δ200 pep::HIS4/pep::HIS4 prb1-Δ1.6/prb1-Δ1.6 can1/can1 GAL*$^{+}$).[32] eIF2 was natively purified from *S. cerevisiae* strain GP3511 (pAV1089[*SUI2 SUI3* His-tagged *GCD11 URA3*] in *MATα leu2-3 leu2-112 ura3-52 ino1 gcn2Δ pep4::LEU2 sui2Δ HIS4-lac*).[68]

Bacterial Strains

All recombinant protein overexpression was performed in *Escherichia coli* BL21-CodonPlus (DE3)-RIPL cells (Agilent, Catalog Number 230280, F– ompT hsdS(rB – mB –) dcm+ Tetr gal l(DE3) endA Hte [argU proL Camr] [argU ileY leuW Step/Specr]). All cloning was performed using NEB DH5*α* (New England Biolabs, Catalog Number C2987H, *fhuA2Δ(argF-lacZ)U169 phoA glnV44 Φ80Δ(lacZ)M15 gyrA96 recA1 relA1 endA1 thi-1 hsdR17*).

METHOD DETAILS

Cloning, Expression, and Purification of Recombinant eIF3 Subunits

The expression plasmids used for eIF3a and eIF3b are identical to those previously reported[40]. The expression plasmid for eIF3c contains an N-terminal, six-histidine (6× His) tag, followed by a *Fasciola hepatica* 8 kDa (Fh8) solubility enhancer tag[69], a tobacco etch virus (TEV) protease recognition site. This results in a full-length, untagged eIF3c with no residual scar from the TEV cleavage site. The expression plasmid for eIF3i-eIF3g is identical to that previously reported[40], with the exception that the PreScission protease cleavage site between eIF3i and eIF3g was changed to a TEV protease cleavage site.

The expression protocol for each recombinant eIF3 subunit was as follows. Each subunit was overexpressed from a pET vector (Novagen) in *E. coli* BL21-CodonPlus (DE3)-RIPL cells (Agilent, Catalog Number 230280). Cells were grown at 37 °C to an optical density at 600 nm (OD_{600}) of 0.4-0.6. The temperature was then lowered to 17.5 °C. After 45-60 min, expression was induced by addition of 0.5 mM isopropyl ß-D-1-thiogalactopyranoside (IPTG) and the cells were grown overnight (16-20 hours). The next morning, these cell cultures were cooled by placing them in a plastic autoclave bin filled with ice and the cells were pelleted by repeated centrifugation at 8,000 relative centrifugal force (rcf) for 5 minutes. Pelleted cells were resuspended in 40-50 mL of eIF3 Lysis Buffer (20 mM 4-(2-hydroxyethyl)-1-piperazine ethanesulfonic acid (HEPES) at

a pH of 7.4, 400 mM potassium chloride (KCl), 10% glycerol, and 2 mM β-mercaptoethanol (βME)). The cell slurry was then flash frozen as droplets by slowly dropping the slurry into a bowl filled with liquid nitrogen. The resulting frozen droplets can be stored at –80 °C for at least 2 months. These droplets were then lysed using a freezer mill (SPEX, Catalog Number 6875D115) using 7 cycles of 2 minutes on-time at a rate of 10 cycles per second, followed by 1 minute of off-time. The resulting lysate powder was then stored at –80 °C.

To begin each purification, the lysate powder was resuspended in 100-200 mL of room temperature eIF3 Lysis Buffer supplemented with 2 ethylenediamine tetraacetic acid (EDTA)-free protease inhibitor tablets (Roche, Catalog Number 04693132001), 20 mM imidazole, 10 mM magnesium chloride ($MgCl_2$) and 50 µg of nuclease A from *Serratia marcescens* by slowly adding the powder to actively stirring eIF3 Lysis Buffer in a 0.5 L glass beaker. The lysate was then clarified at 31,500 rcf for 30 minutes and the supernatant was filtered through a 0.45-micron bottle-top filter before loading onto a HiTrap 5 mL chelating column (Cytiva, Catalog Number 17040901) that had been charged with nickel sulfate ($NiSO_4$) according to the manufacturer's instructions and pre-equilibrated with K-200 Buffer (20 mM HEPES at a pH of 7.4, 200 mM KCl, and 10 % glycerol). The subunit was then eluted using an 8× column-volume (c.v.) gradient of K-200 Buffer supplemented with 400 mM imidazole. Up to this point, the preparation for each subunit was identical. The next steps, which were unique to each subunit, are detailed in the following paragraphs.

For eIF3a and eIF3b, the entire volume eluted from the HiTrap 5 mL chelating column was pooled, diluted 2-fold in K-200 Buffer, and subsequently loaded onto a HiTrap Q 5 mL column (Cytiva, Catalog Number 17115401) that was in-line connected to a second HiTrap Q 5 mL column and that were pre-equilibrated with K-200 Buffer. The protein was eluted using a 15× c.v. gradient of K-1000 Buffer (20 mM HEPES at a pH of 7.4, 1,000 mM KCl, and 10% glycerol). For both eIF3a and eIF3b, there is largely a single, homogenous peak upon elution. The purities of the fractions were validated using sodium dodecyl sulfate-polyacrylamide electrophoresis (SDS-PAGE) followed by staining with Coomassie brilliant blue. The fractions with a single band corresponding to the molecular mass of the desired recombinant protein were pooled and the concentration of the protein was determined using a Bradford assay with bovine serum albumin as a standard. The protein was then aliquoted into 10 µL single-use aliquots and flash frozen in liquid nitrogen.

For eIF3c, the peak from the HiTrap 5 mL chelating column elution corresponding to eIF3a was pooled and treated with 1:100 (w/w) TEV protease and 2 mM βME. For efficient proteolysis of the Fh8 enhanced solubility tag, this mixture was incubated at room temperature for 2-3 hours followed by a further incubation at 4 °C overnight. The next day, this mixture was diluted 10-fold in K-200 Buffer in order to lower the concentration of imidazole. After dilution, to remove the TEV protease and any uncleaved Fh8-eIF3c, the mixture was passed through a HiTrap 5 mL chelating column freshly recharged with $NiSO_4$ and pre-equilibrated with K-200 Buffer. The flow-through was then pooled, loaded onto, and eluted from 2 HiTrap Q 5 mL columns in-line connected in a manner identical to that described for eIF3a and eIF3b above. As above, the purity of the fractions was validated using SDS-PAGE and the appropriate fractions were pooled prior to aliquoting and flash freezing.

For eIF3i-eIF3g, the peak from the HiTrap 5 mL chelating column elution was pooled and then diluted 2-fold using K-200 Buffer. The diluted protein fusion was then loaded onto, and subsequently eluted from, 2 HiTrap Q 5 mL columns in-line connected as described above. This peak was then pooled and, in order to cleave the eIF3i-eIF3g protein fusion, TEV protease and βME were added to final concentrations of 1:100 (w/w) TEV protease and 2 mM βME. For efficient proteolysis, this mixture was incubated at room temperature for 2-3 hours followed by further incubation at 4 °C overnight. The next day, TEV protease was removed by loading this mixture onto a Superdex 200 Increase 10/300 GL column (Cytiva, Catalog Number 28990944) that had been equilibrated in K-200 Buffer and was eluted using additional K-200 Buffer as a running

buffer. As described above for the other subunits, the purity of the fractions was checked using SDS-PAGE, the appropriate fractions were pooled, the concentration was determined, and single-use aliquots were flash frozen. Importantly, any fractions containing detectable uncleaved eIF3i-eIF3g protein fusion were removed prior to pooling.

Purification of eIF3$_N$

Native *S. cerevisiae* eIF3 was expressed using strain LPY87 as previously described[32,37,38]. Briefly, LPY87 was grown on selective media plates lacking uracil and leucine for 2-3 nights at 30 °C. A 50-100 mL starter culture was grown in liquid selective media overnight at 30 °C. After 16-20 hours, 5 mL of this starter culture was added to 1.5 L of yeast extract peptone dextrose (YPD) media and grown overnight again at 30 °C. The cells from these overnight cultures were then pelleted, resuspended, flash frozen, and lysed in eIF3 Lysis Buffer as described above.

To begin the eIF3$_N$ purification, the lysate was loaded onto and eluted from a HiTrap 5 mL chelating column charged with a $NiSO_4$ solution in a manner identical to that described for the recombinant subunits above.

The entire elution from the HiTrap 5 mL chelating column was pooled, diluted 2-fold in K-200 Buffer, and then loaded onto 2 HiTrapQ 5 mL columns in-line connected as described above. In an attempt to separate eIF3 complexes contaminated with eIF5 from those without eIF5[20], a shallow elution gradient was used; specifically, a 20× c.v. gradient between 0-50 % of K-200 Buffer and K-1000 Buffer. This elution resulted in two major peaks: one centered at a conductivity of 25 mS/cm and another, much broader peak, at a conductivity of > 27 mS/cm. The fractions corresponding to both peaks were analyzed using SDS-PAGE. Surprisingly, each fraction seemed to contain a population of full eIF3 complexes with varying levels of contamination. The fractions corresponding to the peak at 25 mS/cm were pooled and, separately, the fractions corresponding to the peak > 27 mS/cm were pooled. Each of these two mixtures were then separately loaded onto a Superose 6 Increase 10/300 column (Cytiva, Catalog Number 29091596) equilibrated in K-200 Buffer and eluted using additional K-200 Buffer as a running buffer. Each mixture resulted in two major peaks, one corresponding to a larger molecular mass complex and the other corresponding to a smaller molecular mass complex. However, the mixture containing the fractions corresponding to a conductivity of > 27 mS/cm produced a significantly larger population of the larger molecular mass complex. Therefore, only the fractions from the peak corresponding to the larger molecular mass complex obtained from the mixture containing the fractions corresponding to a conductivity of > 27 mS/cm were pooled and analyzed by SDS-PAGE to confirm the presence of the five core eIF3 subunits. As above, the concentration was determined using a standard Bradford assay and the sample was aliquoted into 10 µL single-use aliquots and flash frozen in liquid nitrogen.

Purification of eIFs 1, 1A, 2, 4GE, 4A, and 4B

eIF1, eIF1A, and eIF4A were expressed with N-terminal 6× His tags followed by a TEV protease cleavage site. eIF4B was expressed with a C-terminal TEV protease cleavage site followed by a 6× His tag. These factors were purified from *E. coli* BL21(DE3) RIPL cells (Agilent, Catalog Number 230280) following established procedures[36-38]. Native, 6× His-tagged eIF2 was expressed and purified from *S. cerevisiae* strain GP3511 as previously described[37]. eIF4G containing a C-terminal TEV protease cleavage site followed by an Fh8 tag and 6× His tag was co-expressed with full-length eIF4E. This results in an eIF4GE complex, which was purified from *E. coli* BL21(DE3) RIPL cells (Agilent, Catalog Number 230280) as previously described[44].

Purification of 40S Subunits

Native *S. cerevisiae* 40S subunits were purified from a wild-type, W303 *S. cerevisiae* strain, LSY679, largely following established protocols[37] with the deviations outlined here. First, cells

were grown at 30 °C to an OD_{600} of 0.8-1.2, then pelleted, resuspended in Ribosome Lysis Buffer (20 mM HEPES at a pH of 7.4, 100 mM potassium acetate (KOAc), 7.5 mM $Mg(OAc)_2$, and 5 mM βME), and flash frozen as droplets in liquid nitrogen. The frozen droplets were then lysed in a freezer mill as described above.

To begin the purification, the lysate powder was resuspended in 50-200 mL of room temperature Ribosome Lysis Buffer supplemented with 2 EDTA-free protease inhibitor tablets (Roche, Catalog Number 04693132001), Turbo DNAse (Invitrogen, Catalog Number AM2239), and 0.5-1 mg/mL heparin. The resuspended lysate was then clarified at 31,500 rcf for 30 minutes. A High-Salt Sucrose Cushion Buffer (20 mM HEPES at a pH of 7.4, 100 mM KOAc, 500 mM KCl, 2.5 mM $Mg(OAc)_2$, 34 % w/v sucrose, and 5 mM βME) was then layered underneath the supernatant of the clarified lysate. 80S ribosomes were then pelleted through the High-Salt Sucrose Cushion Buffer by ultracentrifugation at 60,000 rpm in a Ti 70 rotor (Beckman Coulter, Catalog Number 337922) for 2 hours at 4 °C. After the spin, the ribosome pellets were rinsed with 1 mL of Subunit Separation Buffer (50 mM HEPES at a pH of 7.4, 550 mM KCl, 2 mM $MgCl_2$, and 5 mM βME) and the centrifuge tubes were left inverted to dry for 10 minutes at room temperature. The pellets were then resuspended in ~400 uL of Subunit Separation Buffer.

The resuspended pellets across all tubes were pooled. To dissociate the the 40S subunits from the ribosomal large, or 60S, subunits, puromycin dihydrochloride (Goldbio, Catalog Number P-600-100) was added to a final concentration of 2 mM and the centrifuge tubes were inverted to mix, placed on ice for 10 minutes, and subsequently moved to a 37 °C water bath for 15 minutes. The mixture of dissociated subunits was then layered on top of a 10-35 % sucrose density gradient prepared using Subunit Separation Buffer supplemented with either 10 % or 35 % sucrose. The subunits were then separated by ultracentrifugation in an SW32 rotor (Beckman Coulter, Catalog Number 369694) at 22,000 rpm for 17 hours at 4 °C.

The next day, the sucrose density gradients were fractionated on a BioComp Instruments Piston Gradient Fractionator™. The fractions from the peaks corresponding to the 40S and 60S subunits were pooled separately and pelleted through a High-Salt Sucrose Cushion Buffer as above. The separated 40S and 60S subunit pellets were resuspended in Subunit Separation Buffer and each of the resulting 40S and 60S subunit samples were run through another 10-35% sucrose density gradient prepared as described above in order to separate any contaminating 40S or 60S subunits from the 60S and 40S subunit samples, respectively. The next day, the 40S and 60S subunit samples were fractionated and pooled as done on the previous day. Each of the subunit samples were then pelleted through a Ribosome Storage Cushion Buffer (20 mM HEPES at a pH of 7.4, 100 mM KOAc, 2.5 mM $Mg(OAc)_2$, 30 % w/v sucrose, and 2 mM dithiothreitol (DTT)). These pellets were resuspended in Ribosome Storage Buffer (20 mM HEPES at a pH of 7.4, 100 mM KOAc, 2.5 mM $Mg(OAc)_2$, 8.5 % w/v sucrose, and 2 mM DTT). The concentration of each subunit sample was determined using absorbance at 260 nm and extinction coefficients at 260 nm (ε_{260nm}s) of 2×10^7 $M^{-1}cm^{-1}$ and 4×10^7 $M^{-1}cm^{-1}$ for the 40S and 60S subunits, respectively[37] before aliquoting into 5 µL single-use aliquots that were flash frozen in liquid nitrogen and stored at –80 °C.

Transcription, Purification, and Aminoacylation of Initiator tRNA

S. cerevisiae initiator tRNA ($tRNA_i^{Met}$) was generated by *in vitro* transcription using T7 RNA polymerase (RNAP). To generate the DNA template, we used the polymerase chain reaction (PCR) to amplify the portion of a pUC19 vector that contained a T7 promoter followed by a hammerhead ribozyme construct and the $tRNA_i^{Met}$ sequence[70]. Because it starts with a 5' guanosine nucleotide, the hammerhead ribozyme construct enabled efficient transcription by T7 RNAP while subsequently allowing self-cleavage of the transcript by incubation at 65 °C for 1 hr after transcription so as to generate the native $tRNA_i^{Met}$ containing an adenosine nucleotide at the 5' end. After cleavage, the hammerhead ribozyme and $tRNA_i^{Met}$ fragments of the transcript were separated using denaturing (D)-PAGE on a 7 % polyacrylamide (19:1 acrylamide:bis-acrylamide)

gel prepared in TBE Buffer (90 mM tris-borate and 2 mM EDTA) supplemented with 7 M urea. The $tRNA_i^{Met}$ was then extracted from the gel *via* 'crush and soak'. Briefly, the $tRNA_i^{Met}$ within the gel was visualized by ultraviolet (UV) shadowing, the corresponding region of the gel containing the $tRNA_i^{Met}$ was excised, and then the excised gel piece was agitated at 4 ºC overnight in a solution of 300 mM sodium acetate at a pH of 5.2, supplemented with 1 mM EDTA. The extracted $tRNA_i^{Met}$ was then concentrated by ethanol precipitation.

The purified $tRNA_i^{Met}$ pellet was dissolved in 10 mM sodium acetate at a pH of 5.2. To fold the $tRNA_i^{Met}$, it was placed into boiling water that was allowed to slow cool to room temperature. Once the sample was near-room-temperature, 5 mM $Mg(OAc)_2$ was added to stabilize the folded $tRNA_i^{Met}$. The folded $tRNA_i^{Met}$ was then used to prepare an Aminoacylation Reaction Mixture (100 mM HEPES at a pH of 7.4, 10 mM $MgCl_2$, 10 mM KCl, 0.1 mM methionine, 10 mM ATP•Mg, 1 mM DTT, 1 μM *E. coli* methionyl-tRNA synthetase, and 12 μM folded $tRNA_i^{Met}$) based on previously established methods for *in vitro* aminoacylation of tRNAs[70]. This mixture was incubated at 37 °C for 30 minutes, followed by phenol-chloroform extraction and ethanol precipitation. The resulting pellet contains significant contaminating ATP, and was therefore resuspended in 10 mM sodium acetate at a pH of 5.2 and run through 3 sequential PD SpinTrap G-25 columns (Cytiva, Catalog Number 28918004) equilibrated in 10 mM sodium acetate at a pH of 5.2, following the manufacturer's protocol. The concentration of the Met-$tRNA_i^{Met}$ was then determined *via* its absorbance at 260 nm and an ε_{260nm} of 708,900 $M^{-1}cm^{-1}$, aliquoted into 5 μL single-use aliquots, flash frozen in liquid nitrogen, and stored at -80°C.

Standard Reaction Buffer

All measurements were performed in a Standard Reaction Buffer (20 mM HEPES at a pH of 7.4, 100 mM KOAc, and 3 mM $Mg(OAc)_2$) that has been previously shown to be optimal for studies of *S. cerevisiae in vitro* translation initiation[22,36-38].

PIC Binding Assays

The abilities of $eIF3_R$ and $eIF3_N$ to bind to PICs were assessed using a native gel electrophoresis-based assay to monitor the mobility of a fluorescein-labeled 'polyCAA' mRNA with the following sequence: GGCAACAACAACAACAACAACAAAUGGAACAACAACAACAAC AAAGUCGA-fluorescein. A 2× PIC Master Mix was prepared by combining 2 μM eIF1, 2 μM eIF1A, 600 nM eIF2, 750 nM Met-$tRNA_i^{Met}$, 100 nM 40S subunit, and 1 μM polyCAA-fluorescein mRNA. This 2× PIC Master Mix was then combined with stock solutions of $eIF3_R$ or $eIF3_N$ and Standard Reaction Buffer to make a series of solutions in which the final conditions were 1 μM eIF1, 1 μM eIF1A, 300 nM eIF2, 375 nM Met-$tRNA_i^{Met}$, 50 nM 40S subunit, 0.5 μM polyCAA-fluorescein RNA, and 10-800 nM $eIF3_R$ or $eIF3_N$, depending on the concentration of $eIF3_R$ or $eIF3_N$ to be tested. Reactions were incubated at 26 °C for 1 hr, after which time 8 μL of the reaction was combined with 1 μL of Native Loading Dye (0.05% bromophenol blue and 50% sucrose in Standard Reaction Buffer) and then loaded onto a 4%, polyacrylamide (37.5:1 acrylamide:bis-acrylamide) gel prepared in THEM Buffer (34 mM Tris Base, 57 mM HEPES, 0.1 mM EDTA, and 2.5 mM $MgCl_2$). This gel was then run for 1 hr at 200 Volts, and maintained at 16 °C with a circulating water cooler[22,37]. Subsequently, the gel was imaged for fluorescein fluorescence on an Amersham Typhoon 5 Biomolecular Imager (Cytiva, Catalog Number 29187191). Because a large excess of the polyCAA-fluorescein mRNA was used to saturate the PIC, the free mRNA signal saturated the corresponding pixels on the imager detector. This saturated signal was therefore ignored, and the fraction of eIF3-bound PICs was calculated using the total PIC concentration (see 'Quantification of eIF3 PIC Binding and mRNA Recruitment Assays' below).

mRNA Recruitment Assays

The kinetics with which a capped rpl41a mRNA was recruited to PICs was determined using a previously described native gel electrophoresis-based assay to monitor the mobility of a [^{32}P]-

cap-labeled rpl41a mRNA[22,36,53,54]. A 2× PIC Master Mix was formed by combining 2 μM eIF1, 2 μM eIF1A, 600 nM eIF2, 750 nM Met-tRNA$_i^{Met}$, 4 μM eIF4A, 800 nM eIF4B, 100 nM 40S subunit, and 4 mM ATP•Mg^{2+}. This 2× PIC Master Mix was then used to generate a 1× reaction by adding stock solutions of eIF3$_R$ or eIF3$_N$ to the final specified concentrations. mRNA recruitment reactions were initiated by adding [^{32}P]-cap-labeled rpl41a mRNA to a final concentration of 15 nM. mRNA recruitment reactions were incubated continuously at 26 °C. At each specified time point, 4 μL of the reaction was removed and combined with 1 μL of Native Loading Dye and loaded onto an actively running 4 % polyacrylamide (37.5:1 acrylamide:bis-acrylamide) gel prepared in THEM Buffer. This gel was then run for 70 min at 200 Volts, and maintained at 16 °C with a circulating water cooler[22,37]. Subsequently, the gel was exposed to a phosphor screen overnight and then imaged on an Amersham Typhoon 5 Biomolecular Imager (Cytiva, Catalog Number 29187191).

mRNA Binding Assays

mRNA binding was assessed using a fluorescence anisotropy-based assay. These assays were performed using chemically synthesized, 3'-fluorescein-labeled model mRNAs (Integrated DNA Technologies), with the following sequences:

- 'polyCAA'=GGCAACAACAACAACAACAACAAAUGGAACAACAACAACAACAAAGUCGA-Fluorescein
- 'polyUC'=GGAAUCUCUCUCUCUCUCUAUGCUCUCUCUCUCUCUCUCUCUC-Fluorescein
- 'Natural'=GGAGACCACAUCGAUUCAAUCGAAAUGAGAGCCAAGUGGAGAAAGAAGAGA- Fluorescein

For each set of affinity experiments, 1 mL of a 5 nM mRNA solution was prepared by supplementing Standard Reaction Buffer with mRNA. In parallel, the highest concentration protein sample (800 nM for eIF3$_R$ or eIF3$_N$ or 2 μM for eIF3 subunits) was also supplemented to 5 nM mRNA. This highest concentration protein sample was then 2-fold serially diluted using the 5 nM mRNA solution to generate all other, lower protein concentration points to the lowest concentration protein samples tested (3.1 nM for eIF3$_R$ or eIF3$_N$ or 7.8 nM for eIF3 subunits). The resulting concentration series was incubated in a black-bottomed, 96-well plate (Corning, Catalog Number 3916) that was placed in the dark and allowed to equilibrate at room temperature for 20 min. The fluorescence polarization of the concentration series in the plate was then measured on a BioTek Synergy Neo2 plate reader (Agilent) using a 485 nm excitation source and an Agilent Green FP filter cube (Agilent, Catalog Number 8040561).

For each set of stoichiometry experiments in the titration regime, the protocol is identical to that described above, with one exception. Briefly, the total concentration of polyCAA mRNA in the experiment was raised to 400 nM. This was achieved by mixing 50 nM of the fluorescein-labeled polyCAA mRNA with 350 nM of its unlabeled counterpart.

Mass Photometry Assays

Conventional mass photometry experiments were performed using a commercially purchased mass photometer (Refeyn, Inc., TwoMP). Borosilicate glass coverslips (Research Products International Corp, Catalog Number 246008) were cleaned by sonication in 100 % ethanol for 15 min, sonicated in 1 M KOH for 15 minutes, and then thoroughly washed with nanopure water and blow-dried with pre-purified argon gas. To generate sample wells, silicone gaskets (Grace Bio-Labs, Catalog Number GBL103250) were placed on the cleaned coverslips. Proteins were diluted to 30 nM in Standard Reaction Buffer prior to measurements, unless otherwise noted. Measurements were acquired as 60-sec movies in the 'regular' field-of-view recorded using the AcquireMP software (Refeyn, Inc.), and the resulting movies were analyzed using the DiscoverMP software (Refeyn, Inc.). Protein masses were determined using a calibration curve that was established using three protein standards taken from a High Molecular Weight Calibration Kit

(Cytiva, Catalog Number 28-4038-42): Conalbumin (75 kDa), aldolase (158 kDa), and thryoglobin (669 kDa).

Tethered mRNA mass photometry experiments were performed using derivatized coverslips. To derivatize a coverslip, the borosilicate glass surface was passivated with a monolayer mixture of methoxy-terminated PEG (mPEG, Laysan Bio, Catalog Number MPEGSIL50001G) and biotin-terminated PEG (biotin-PEG, Laysan Bio, Catalog Number Biotin-PEG-SIL-5K-1g) as previously described[44]. To make sample wells, small cups cut from p200 pipette tips were epoxied (Devcon Home, Catalog Number 20945) onto the surface of the coverslip. This was required because the surface of the derivatized coverslip is hydrophilic and therefore the sample leaks under the silicone gaskets used above. Prior to the addition of sample, wells were rinsed with 70 µL of Standard Reaction Buffer followed by 70 µL of Standard Reaction Buffer supplemented to 0.1 % Tween-20 detergent and then subsequently washed 3 times with 70 µL Standard Reaction Buffer. Streptavidin was bound to the biotin-terminated PEGs by addition of 20 µL of 10 nM streptavidin (Invitrogen, Catalog Number S888) and free streptavidin was removed by rinsing the well 4 times with 70 µL Standard Reaction Buffer. A 3'-biotinylated version of the polyCAA mRNA described above (Integrated DNA Technologies) was tethered to the biotin-PEG-bound streptavidin by incubating 10 nM mRNA in the well for 1 min at room temperature and subsequently removing free mRNA by rinsing 5 times with 70 µL Standard Reaction Buffer. To begin each measurement, 20 µL of 2× protein was then mixed with 20 µL of Standard Reaction Buffer in the well and imaged. Measurements were acquired as 10 15-sec movies in the 'regular' field-of-view and masses were determined as described above. After each measurement, 10 ng of nuclease A from *Serratia marcescens* was added to the well and allowed to incubate for 2 min. Following RNase treatment, 10 more 15-sec movies were acquired.

QUANTIFICATION AND STATISTICAL ANALYSIS

Mass Photometry Data Processing

For all mass photometry experiments, the events detected using the DiscoverMP software were exported as 'comma-separated-value' (csv) files. Because mass photometry detects both adsorption and desorption events, both adsorption events, denoted as positive masses, and desorption events, denoted as negative masses, are present in the exported events file. Normalized mass distribution histograms were calculated using only those adsorption events with masses between 0 and 500 kDa such that the sum of all the bars in each histogram sum to 1. To identify pixels where multiple events occur, the super-resolution *x*- and *y* coordinates for each event were rounded to the nearest integer and the number of events at each pixel were determined.

To calculate the RNase-sensitive mass distribution for each eIF3 species, the normalized mass distribution measured after addition of RNase was subtracted from the normalized mass distribution before addition of RNase. To calculate the population difference between mRNA-binding mass distribution and the solution mass distribution, the mRNA-binding distribution was filtered for events occurring in pixels which exhibited > 2 events and then normalized. The normalized solution mass distribution was then subtracted from this resulting normalized mRNA-binding mass distribution.

Gaussian Fitting of Solution Mass Distributions

Gaussian fitting of solution mass distributions was performed on samples that contained more than a single eIF3 subunit. These fits were calculated using the 'normalmixEM()' function in the 'mixtools' library in R, version 4.2.3.[71] For mixtures containing only 2 subunits, 2 initial guesses, at 80, and 160 kDa, were given as arguments. For mixtures containing 3 or more subunits, 4 initial guesses, at 80, 160, 290, and 365 kDa, were given as arguments.

Gaussian fitting of solution mass distributions was performed on samples composed of individual eIF3 subunits using the 'fitdisr()' function from the 'MASS' library in R, version 4.2.3.[72] No initial guesses were provided.

Quantification of PIC binding and mRNA Recruitment Assays

The TIFF images obtained from the Amersham Typhoon 5 Biomolecular Imager (Cytiva, Catalog Number 29187191) for both PIC binding and mRNA recruitment assays were analyzed using ImageQuant TL, version 8.2.0.0 (Cytiva). For PIC binding assays, there are three bands corresponding to free mRNA, mRNA•PIC complexes, and mRNA•PIC•eIF3 complexes. Only the relative amount of mRNA•PIC and mRNA•PIC•eIF3 complexes are compared. A minimum profile background was subtracted from each lane in the gel and the mRNA•PIC•eIF3 complex fraction was calculated by dividing the intensity of the band corresponding to the mRNA•PIC•eIF3 complex by the total intensity of the lane (excluding the band corresponding to the free mRNA). For mRNA recruitment assays, a 'rubber band' background correction was applied, and the fraction of recruited mRNA was calculated by dividing the intensity of the band corresponding to the PIC by the total intensity of the lane.

Determination of Equilibrium Dissociation Constants

All binding data were fit to the quadratic binding equation:

$$A\left(\frac{(R+x+K)-\sqrt{(R+s+K)^2-(4Rx)}}{2R}\right)+O,$$

where A is the amplitude, R is the known concentration of the labeled component, K is the K_d^{app}, and O is the response offset.

To model the expected stoichiometry experiments in the titration regime at increasing mRNA concentrations for $eIF3_R$ and eIF3a, the experimentally measured mean K_d^{app}s were used to fix the K in the quadratic binding equation shown above with no offsets.

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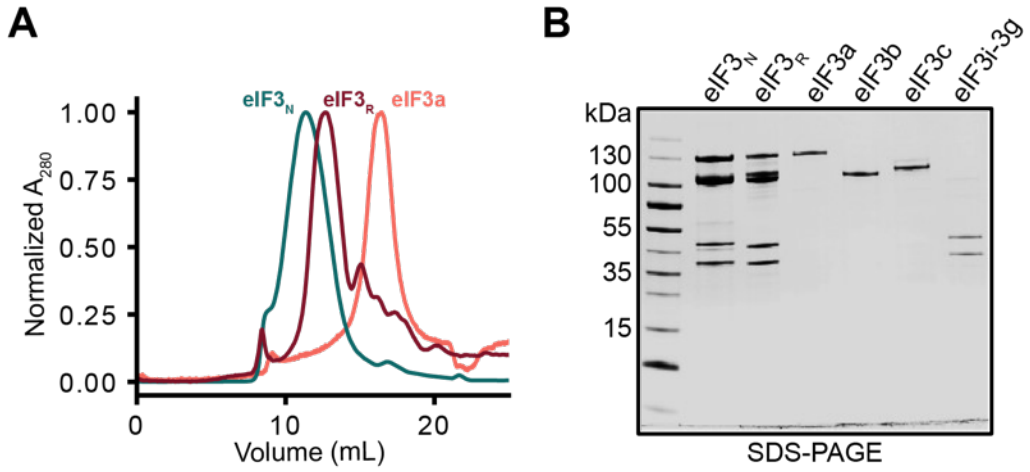
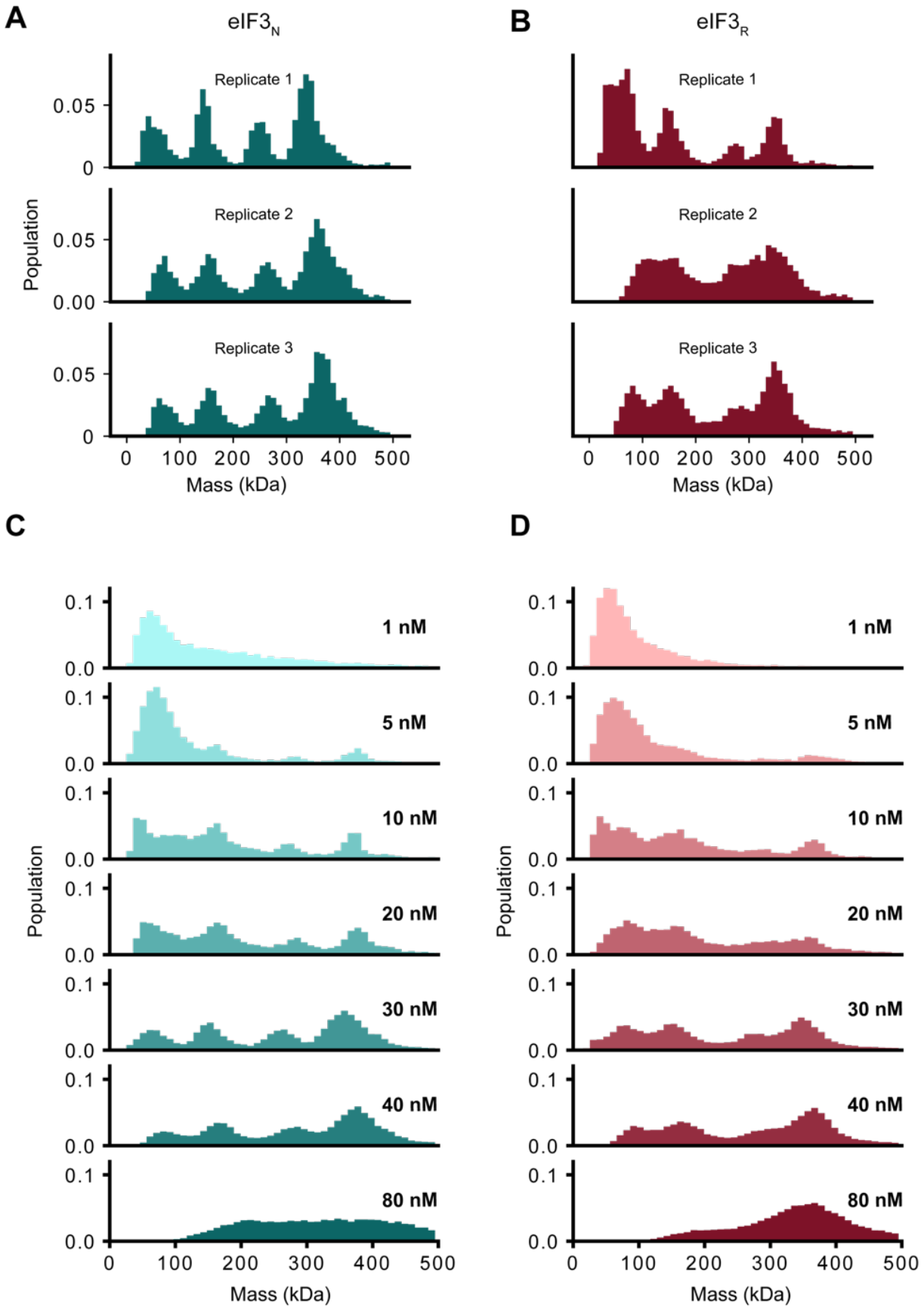
SUPPLEMENTAL FIGURES



Supplemental Figure 1. Preparation of eIF3$_N$ and eIF3$_R$ (A) Size-exclusion chromatograms for eIF3$_N$, eIF3$_R$, and eIF3a. **(B)** SDS-PAGE gel showing eIF3$_N$, eIF3$_R$, and each recombinant eIF3 subunit.


A
eIF3N
Replicate 1
Replicate 2
Replicate 3
Population
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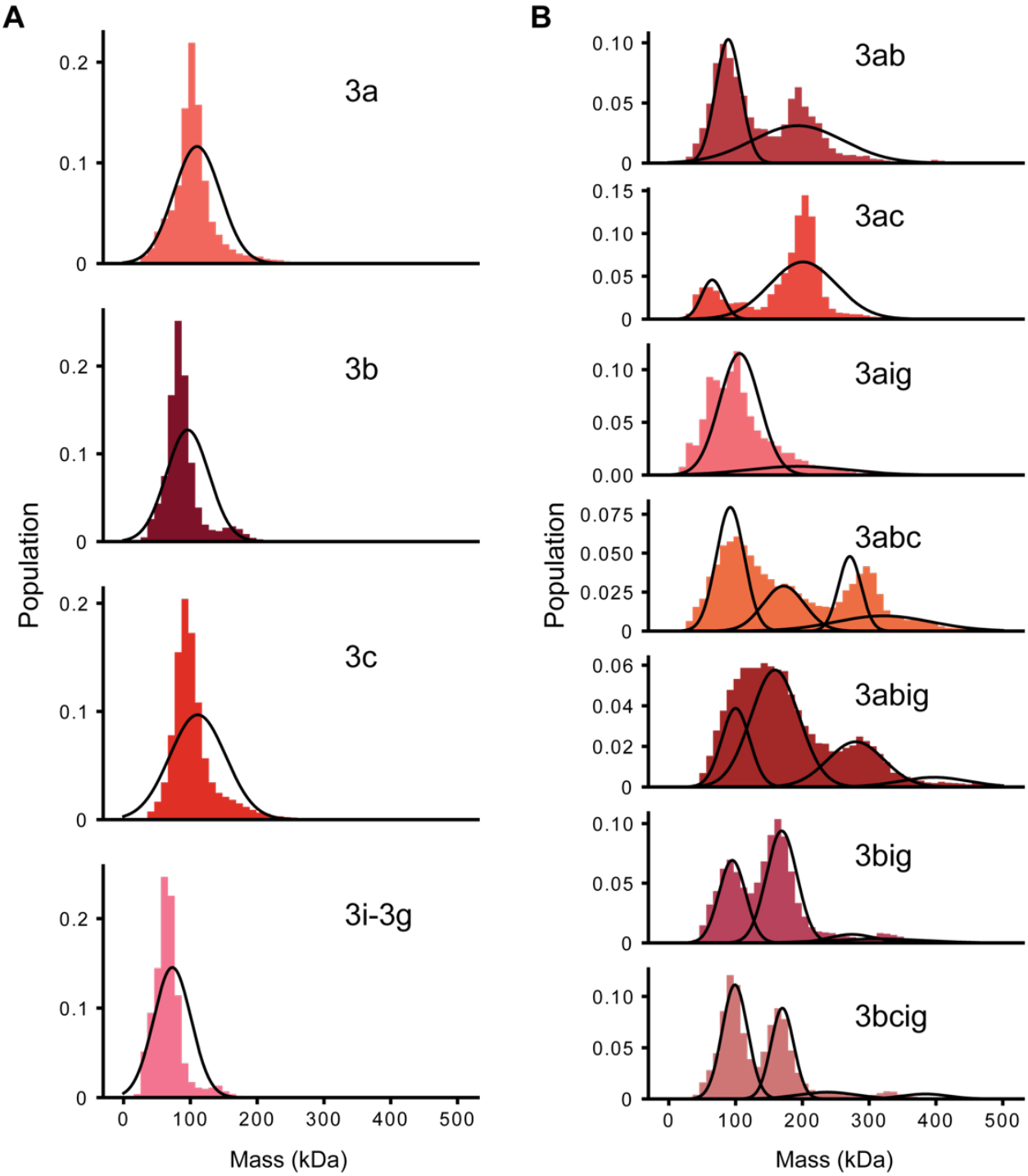
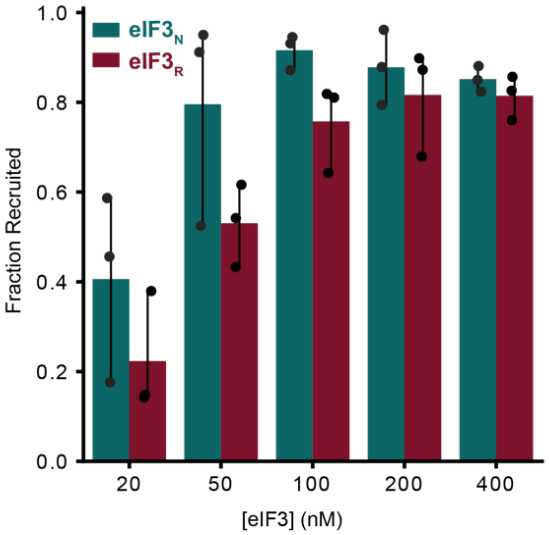
0
0.05
0.00
0.05
0
0 100 200 300 400 500
Mass (kDa)
B
eIF3R
Replicate 1
Replicate 2
Replicate 3
0 100 200 300 400 500
Mass (kDa)
C
D
1 nM
5 nM
10 nM
20 nM
30 nM
40 nM
80 nM
0.1
0.0
Population
0 100 200 300 400 500
Mass (kDa)

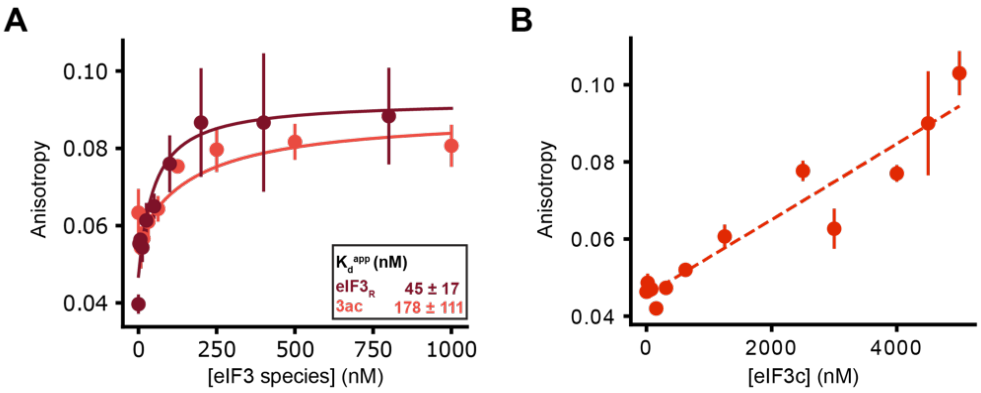
Supplemental Figure 2. Mass photometry of $eIF3_N$ and $eIF3_R$, related to Figure 1. (A) Individual replicates shown separately for experiments depicted in Figure 1A. **(B)** Individual replicates shown separately for experiments depicted in Figure 1B. **(C)** Histograms from mass photometry experiments at different $eIF3_N$ concentrations. **(D)** The same as depicted in (C) for $eIF3_R$.



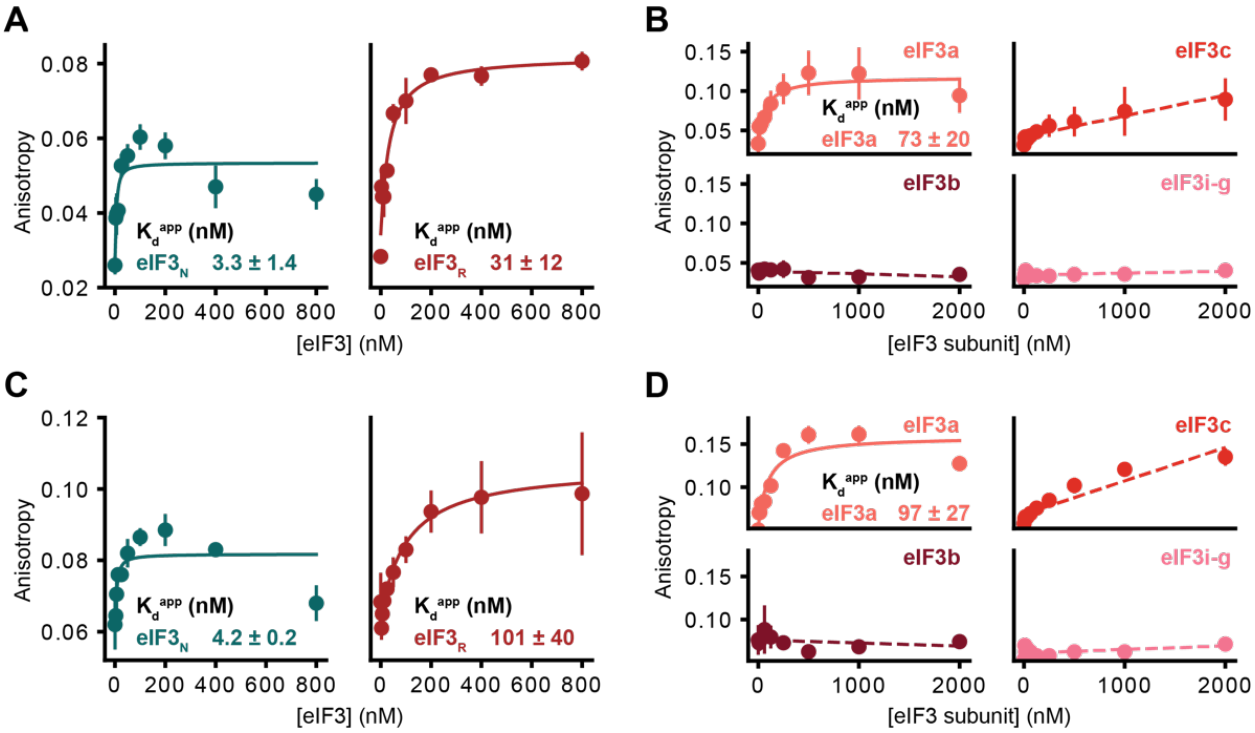
Supplemental Figure 3. Identification of eIF3-subcomplexes using mass photometry (A) Histograms of three combined replicates for each recombinant eIF3 subunit. **(B)** Histograms of three combined replicates for eIF3 subcomplexes. Gaussian distributions were fit to each individual replicate to understand the relative populations of each species. Overlayed Gaussians shown here are results of fitting either single Gaussians (subunits) or multiple (subcomplexes) to each individual replicate, then using the mean value of each fit parameter across replicates to define the final Gaussians shown.



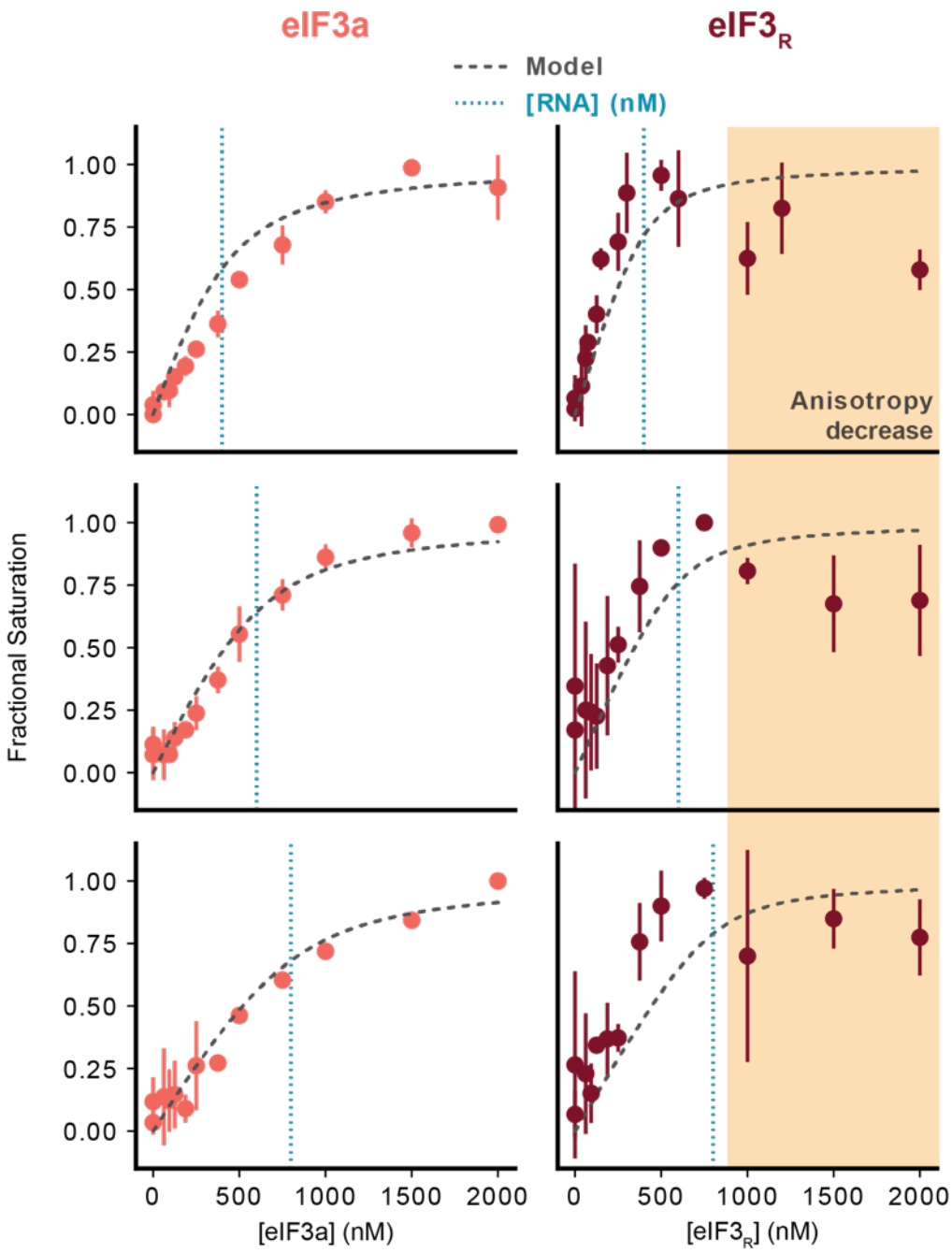
Supplemental Figure 4. Cap-dependent mRNA recruitment by eIF3$_N$ and eIF3$_R$. Extent of mRNA recruitment at various concentrations of eIF3$_N$ and eIF3$_R$.



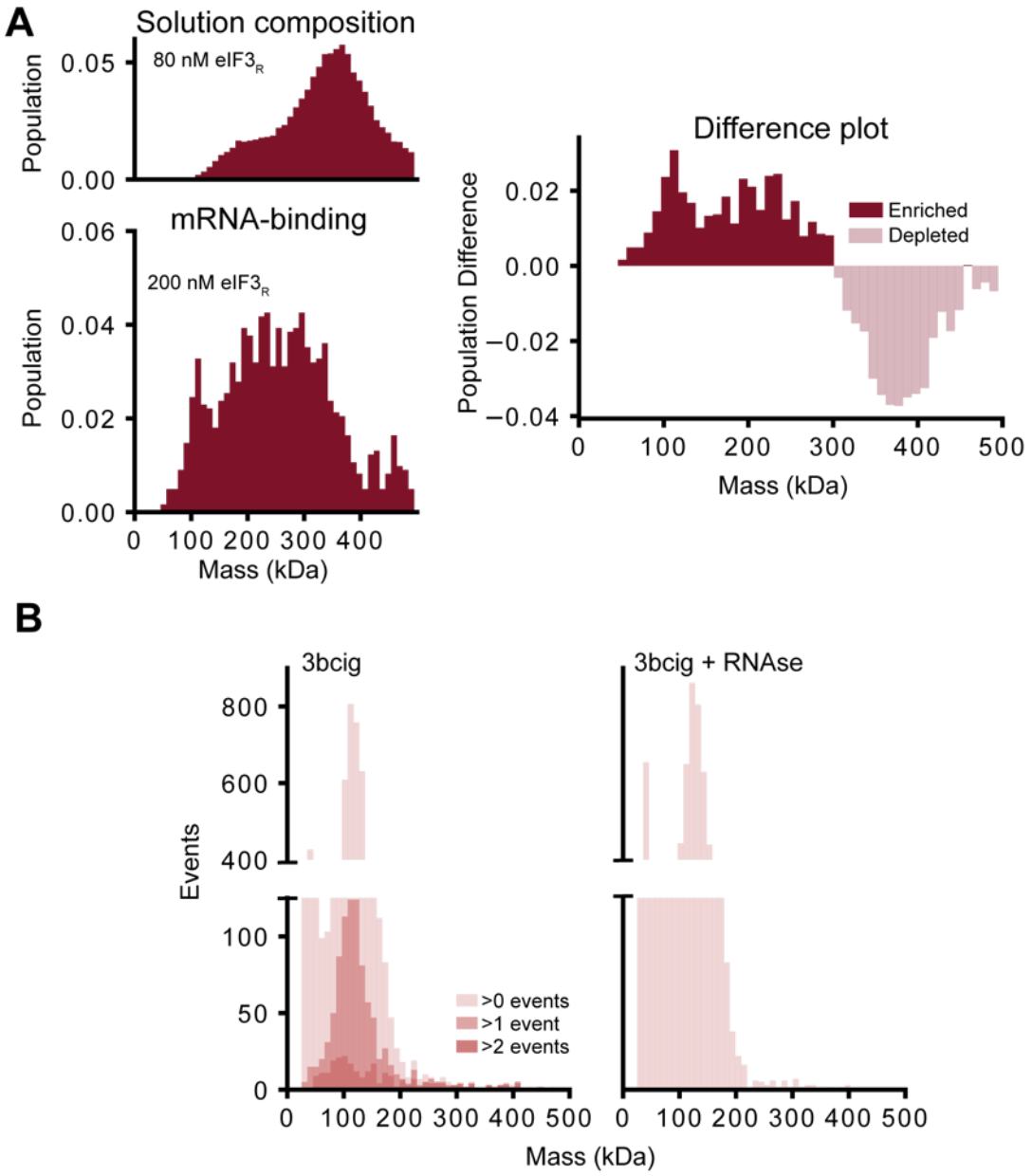
Supplemental Figure 5. eIF3ac binds mRNA nearly identically to eIF3$_R$ and an extended eIF3c titration does not saturate the mRNA (A) Fluorescence-anisotropy binding experiment comparing eIF3$_R$ and eIF3ac. **(B)** Fluorescence anisotropy binding experiment titrating up to 5000 nM eIF3c.



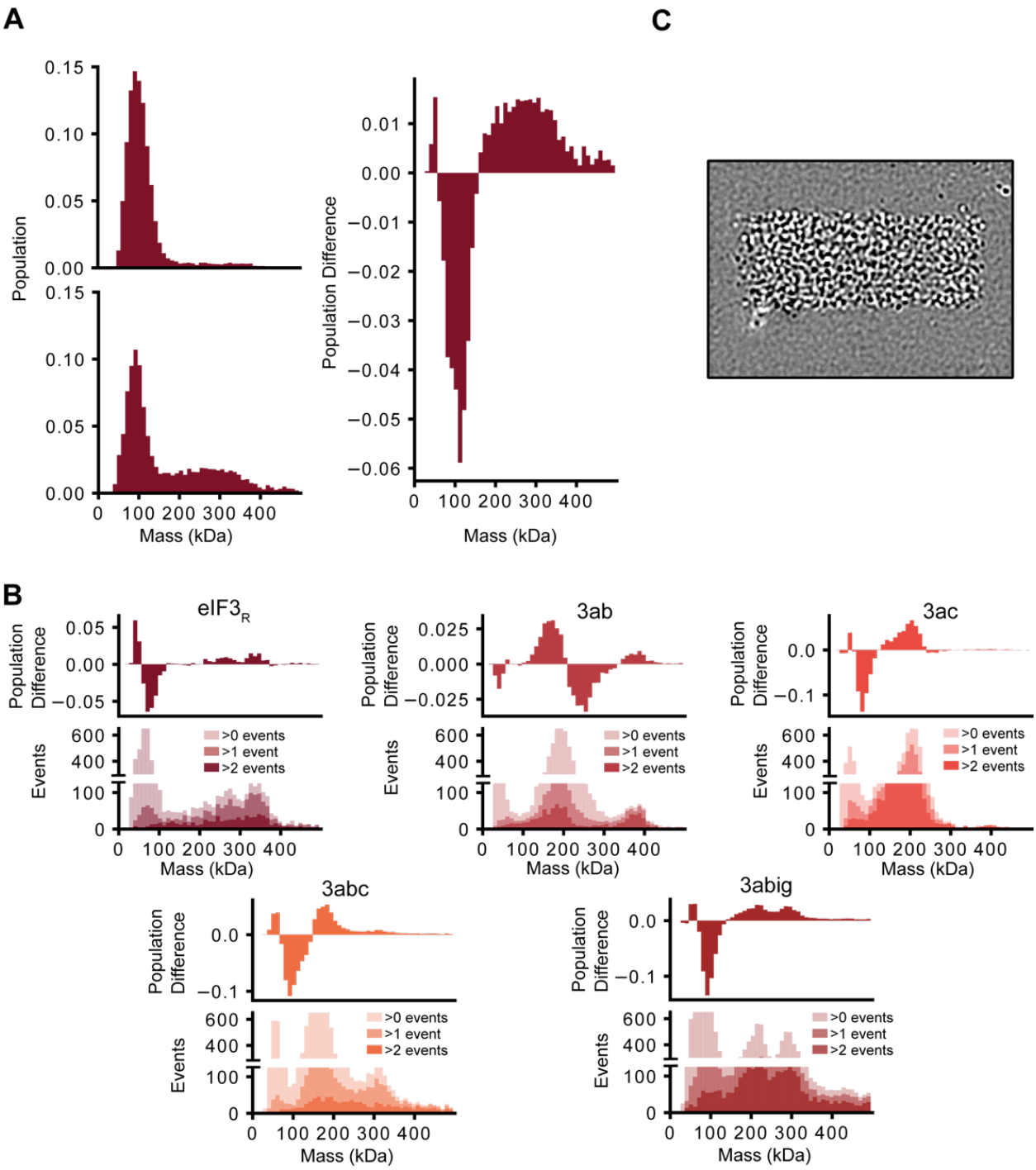
Supplemental Figure 6. $eIF3_N$, $eIF3_R$, and eIF3 subunits binding to two additional mRNAs. **(A)** Fluorescence-anisotropy RNA binding experiments comparing $eIF3_N$ and $eIF3_R$ binding to a model mRNA composed largely of a repetitive UC sequence ('polyUC') **(B)** The same experiments as (A) for individual eIF3 subunits **(C)** Fluorescence-anisotropy RNA binding experiments comparing $eIF3_N$ and $eIF3_R$ binding to the first 51 nucleotides of the rpl41a mRNA ('natural') **(D)** The same experiments as (C) for individual eIF3 subunits



Supplemental Figure 7. Fluorescence anisotropy binding experiments increasing the total concentration of mRNA (i.e. in the 'titration-regime'). (A) Fluorescence-anisotropy RNA binding experiments of eIF3a to the polyCAA mRNA sequence with increasing [mRNA]: 400 nM (top), 600 nM (middle), and 800 nM (bottom) compared to a model protein-RNA binding interaction with a K_d of 119 nM (Figure 3A). Normalized anisotropy is shown to compare experimental data to the modeled curves **(B)** The same experiments as in (A) for $eIF3_R$ (using a K_d of 45 nM for the model, Figure 3A).



Supplemental Figure 8. eIF3a-containing subcomplexes are over-represented in mRNA-binding relative to their solution distribution. (A) The solution composition of 80 nM $eIF3_R$ determined using standard mass photometry on underivatized coverslips is shown above the mRNA-binding mass distribution of 200 nM $eIF3_R$. To the right is the difference plot of the solution distribution of 80 nM $eIF3_R$ subtracted from the mRNA-binding distribution, highlighting that while the full complex is likely most abundant at 200 nM, subcomplexes are over-represented in mRNA-binding. . **(B)** mRNA-binding mass distributions of an eIF3a dropout mixture. Upon filtering for repetitive events at individual pixels (left) and upon addition of RNAse (right).



Supplemental Figure 9. The addition of RNAse highlights which part of the mass distribution makes specific mRNA interactions. (A) The mRNA-binding mass distributions of 200 nM eIF3$_R$ before (bottom) and after (top) addition of RNAse. Left is the population difference plot generated by subtracting the mass distribution after addition of RNAse from the mass distribution before addition of RNAse. . **(B)** The same difference plots as in (A) but for 30 nM of each indicated subcomplex. **(C)** An example frame after laser-induced heating of an mRNA-binding experiment with 30 nM eIF3$_R$. A 'small' field of view was imaged for ~ 2 minutes, then the field of view was changed to 'large' and this image was captured.

Supplemental Table 1. Summary of K_d^{app} values.

Summary of K_d^{app} values (nM)

	polyCAA (50nt)	polyCAA (45 nt)	polyCAA (40 nt)	polyUC	rpl41a
$eIF3_N$[a]	5.3 ± 1.1	7.5 ± 5.4	N.D.	3.3 ± 1.4	4.2 ± 0.2
$eIF3_R$[a]	45 ± 17	7.1 ± 0.6	N.D.	31 ± 12	101 ± 40
eIF3a	119 ± 56	88 ± 10	N.D.	73 ± 20	97 ± 27
eIF3b	N.D.	–	–	N.D.	N.D.
eIF3c	1229 ± 720	–	–	N.D.[b]	1219 ± 808
eIF3i-3g	N.D.	–	–	N.D.	N.D.

[a] K_d^{app} assuming two-component, single-site binding
[b] General anisotropy increase but unable to fit
N.D. Not Determined/unable to fit