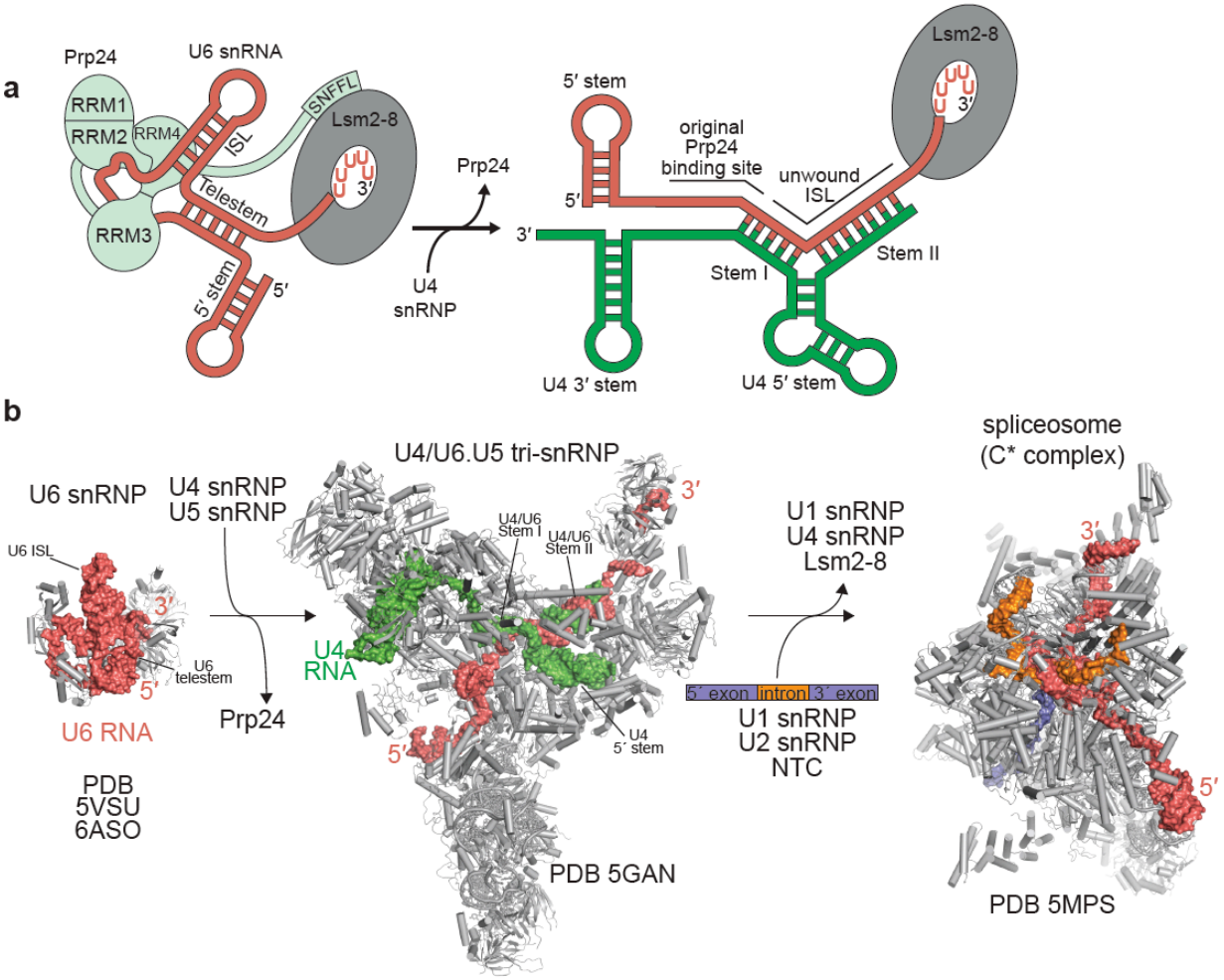
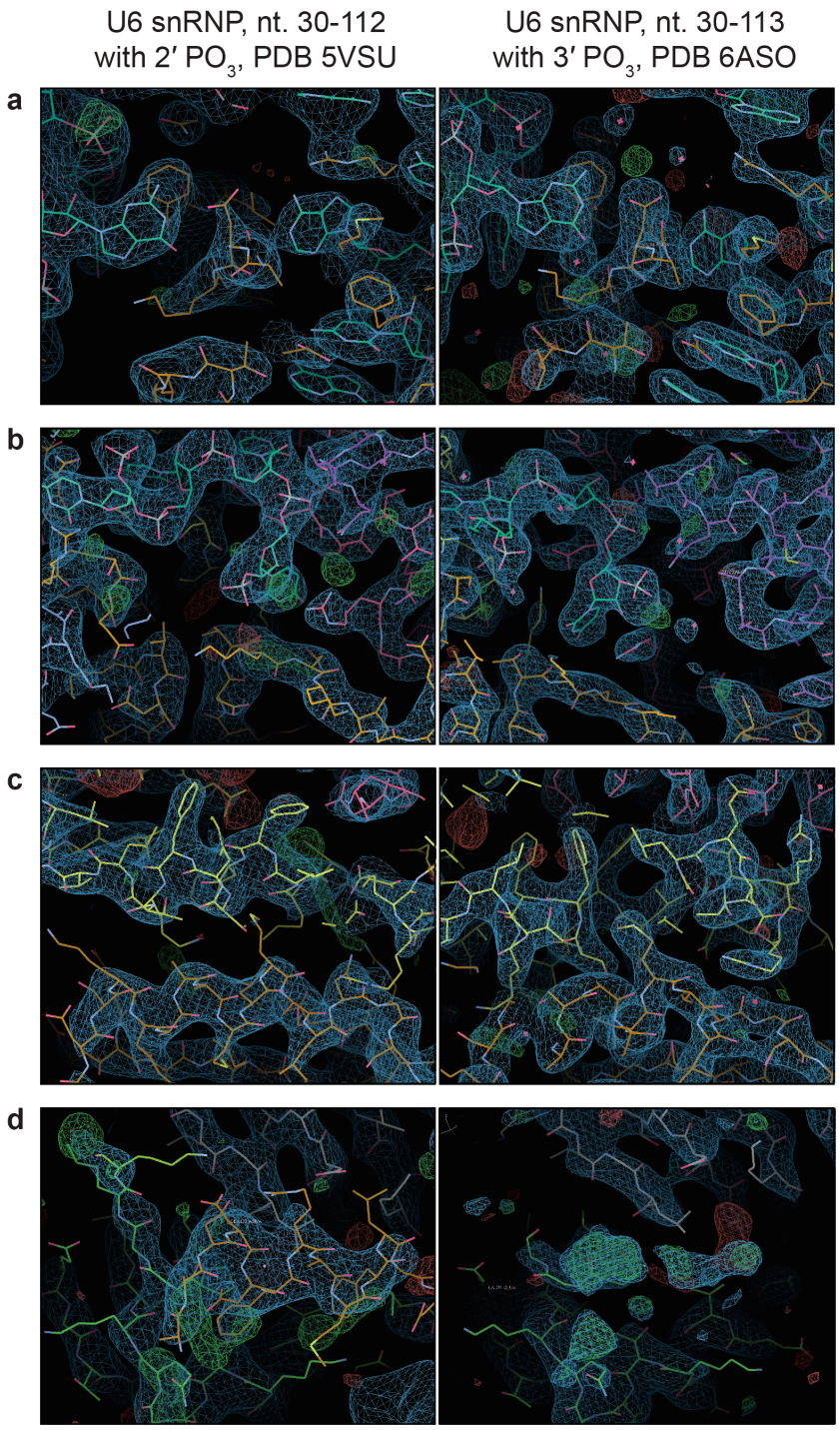
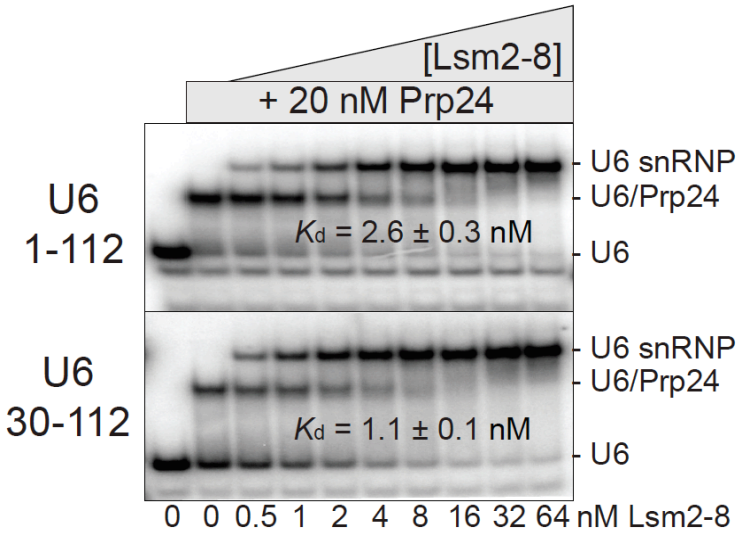


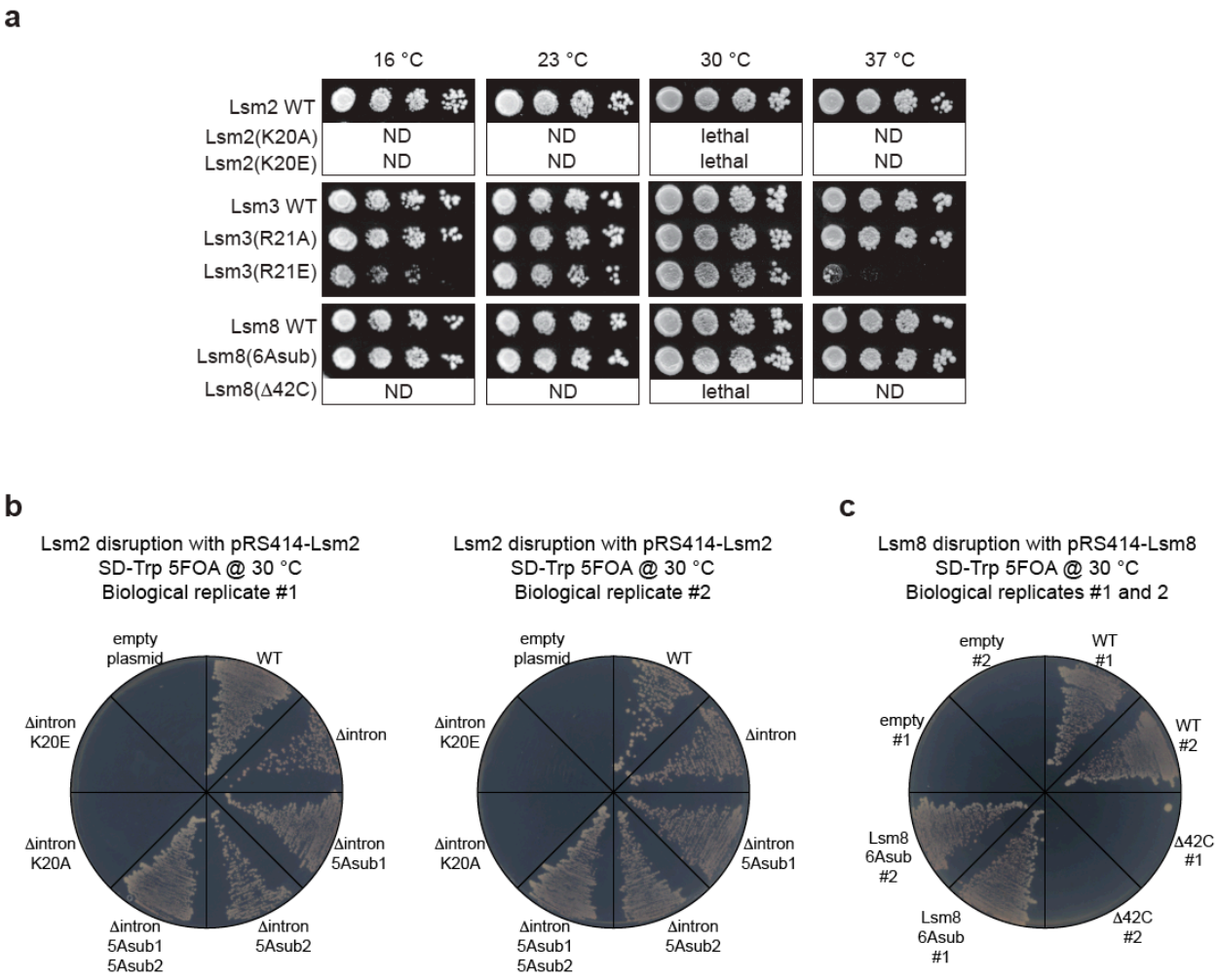

**Supplementary Fig 1** Overview of U6 snRNA structure and assembly into the spliceosome. **a** Simplified cartoon representation of the yeast U6 and U4/U6 snRNPs. For clarity, U4-associated proteins are not depicted. Prp24 binds U6 and catalyzes formation of the U4/U6 snRNP, which requires unwinding of the U6 internal stem loop (ISL). Lsm2-8 is known to bind the conserved C-terminal “SNFFL box” motif in Prp24 and the 3′ oligouridylate tract in U6, and accelerates Prp24-mediated annealing of U4/U6 through an unknown mechanism[1-3]. **b** U6 snRNA undergoes extensive structural remodeling during pre-mRNA splicing. U6 is highly compact in the U6 snRNP due to extensive intramolecular base-pairing. In contrast, U6 is highly extended in the U4/U6.U5 tri-snRNP, in which Prp24 is absent but the Lsm2-8 ring is still bound to U6. In activated spliceosomes the Lsm2-8 ring is gone, the ISL is mostly reformed, and U6 makes numerous protein-RNA contacts, in addition to pairing with U2 snRNA.



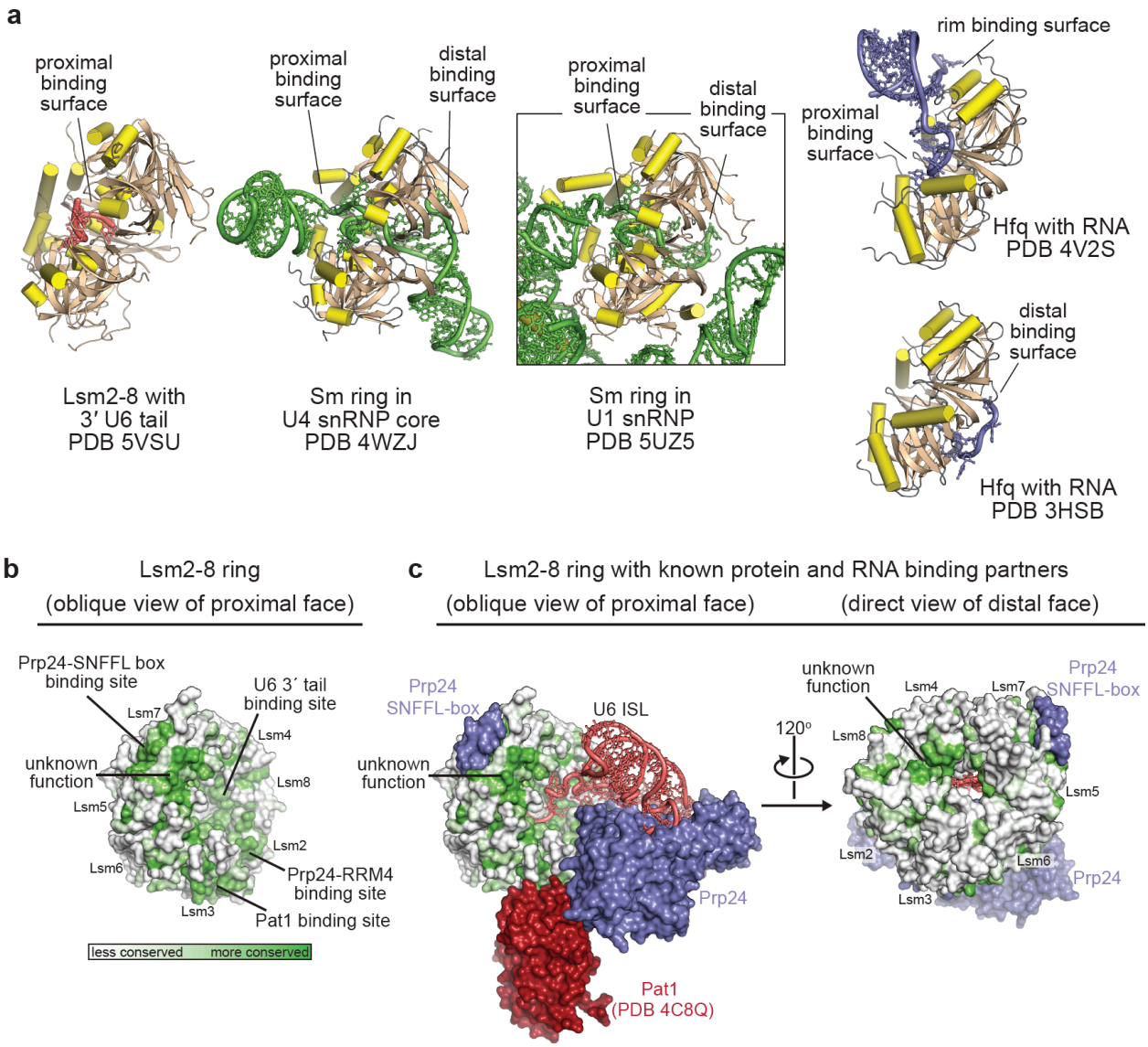

**Supplementary Fig 2** Representative electron density. Blue density is of form 2m$F_o$-D$F_c$ and is contoured at 1.5 rmsd. Positive and negative density (colored green and red, respectively) is of form m$F_o$-D$F_c$ and is contoured at 3.0 rmsd. **a** Density for the core of the U6-Prp24 interaction, centered at Asp288 (the aspartate bridge[4]) and U6 nucleotides A42 and G55. **b** Density for the 3′ tail of U6 RNA bound inside the Lsm2-8 ring. **c** Density for the Prp24-RRM4/Lsm2 interface. **d** Density for the Prp24-SNFFL box interaction with Lsm5 and Lsm7. Alpha helical density was modeled as the SNFFL box in PDB 5VSU in space group $P2_12_12_1$. Due to weak density, the SNFFL box was not modeled into PDB 6ASO in space group $P2_1$.



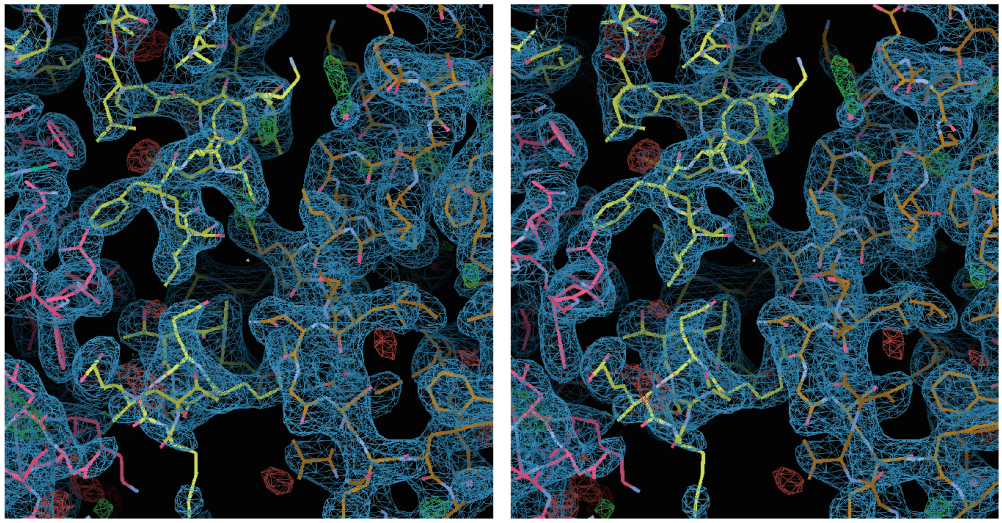

**Supplementary Fig 3** The 5′ stem of U6 does not contribute to U6 snRNP stability *in vitro*. Electrophoretic mobility shift was used to monitor formation of U6 snRNPs in the presence of 20 nM Prp24 and varying concentrations of Lsm2-8, using RNA that had been 5′ labeled with $^{32}$P. $K_d$ is the dissociation constant for Lsm2-8 from the ternary complex (Prp24•U6•Lsm2-8). Note that the binary complex of Prp24•U6 appears to be less stable in the absence of the U6 5′ stem.




**Supplementary Fig 4** Mutation of 3′ end binding residues in Lsm2-8. **a** Point mutant strains exhibit diverse growth phenotypes *in vivo*, which agree well with *in vitro* binding defects (Table 3). ND = not tested due to lethality during initial 5-FOA selection at 30 °C. **b** The intron in Lsm2 is not essential to viability, and mutation of Lsm2 residue K20 is lethal. The 5Asub1 and 5Asub2 alleles contain Lsm2 substitutions at the Prp24/Lsm2 interface (5Asub1 = S5A/K8A/T9A/V11A/D12A, 5Asub2 = L81A/D84A/R88A/E89A/T92A). **c** Removal of the C-terminal 42 residues of Lsm8 is also lethal. The Lsm8 6Asub allele contains K87A, D88A, T89A, K90A, N91A and K92A substitutions at the Lsm8 contact with the 3′ end of U6 snRNA. Lethality was determined via 5-FOA counter-selection of the wild-type Lsm alleles on solid media lacking tryptophan at 30 °C. Two independent transformants were tested for each allele.




**Supplementary Fig 5** Homology and surface conservation in protein-protein and protein-RNA binding surfaces of the Lsm2-8 ring. **a** Comparison of known binding mechanisms between RNA and Lsm2-8 or homologous protein ring structures. Unlike the Lsm2-8 ring[5], the U1 and U4 snRNAs are threaded through the homologous Sm ring[6,7] in the U1 and U4 snRNPs, respectively, and employ a mixture of proximal, rim, and distal RNA binding mechanisms like in the Hfq homologs of the Lsm2-8 ring[8-11]. **b** There are numerous patches of sequence conservation on the proximal and rim surfaces of the Lsm2-8 ring that can be attributed to binding of U6 snRNA and Prp24 in the U6 snRNP, or Pat1 in the Lsm1-7/Pat1 complex[12]. **c** Overlay of known binding partners in the U6 snRNP or Lsm1-7/Pat1 complex shows an additional patch of sequence conservation in the N-terminal region of Lsm5 (approximately residues 7-16 and 37) that is proximal to the bound C-terminal SNFFL-box motif of Prp24. There is an additional patch of sequence conservation along the distal face of the ring between Lsm4 (approximately residues 18-24) and Lsm8 (approximately residues 17-21) that does not interact with Prp24 or U6 in the U6 snRNP, or Pat1 in the Lsm1-7/Pat1 complex, that could provide a binding surface for protein and/or RNA during U4/U6 annealing, or partially comprise the nuclear localization sequence in the Lsm2-8 ring[13]. Conservation was determined with the program ConSurf[14] and the alignment in Supplementary Note 1.



**Supplementary Fig 6** Cross-eyed stereo view of electron density at the Lsm2/RRM4 interface. Blue density is of form 2m$F_o$-D$F_c$ and is contoured at 1 r.m.s.d. Positive and negative density (colored green and red, respectively) is of form m$F_o$-D$F_c$ and is contoured at 3.0 r.m.s.d. Prp24 RRM4 is colored orange, Lsm2 is colored yellow, and Lsm3 is colored pink.

Figure 3d

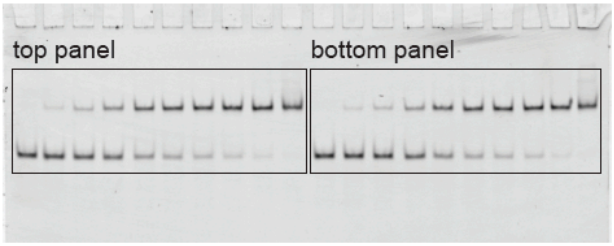



Figure 3e

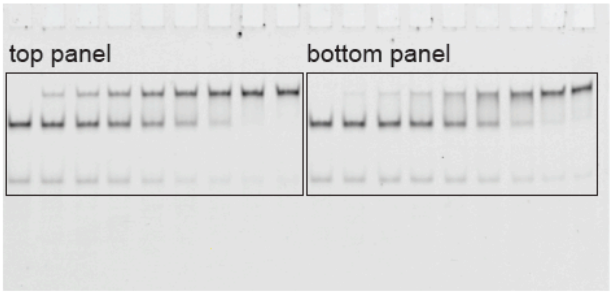
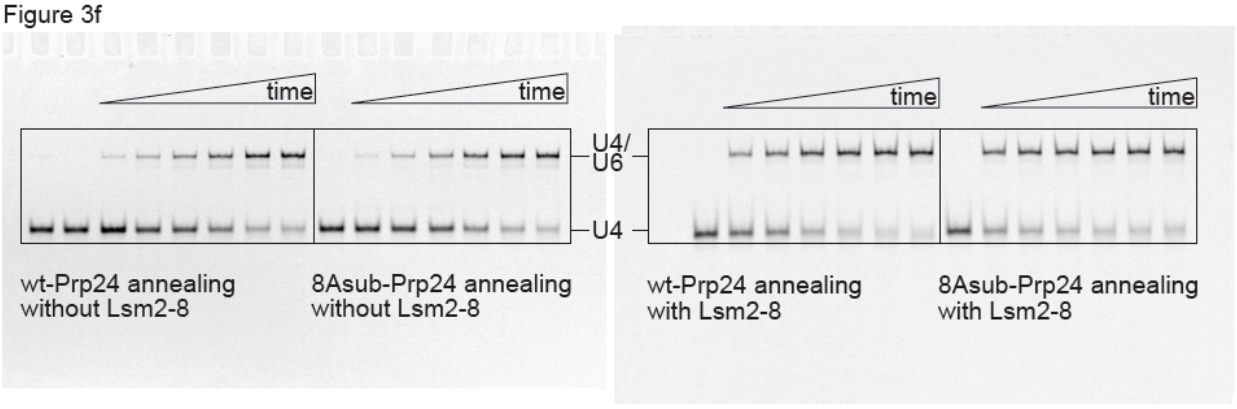
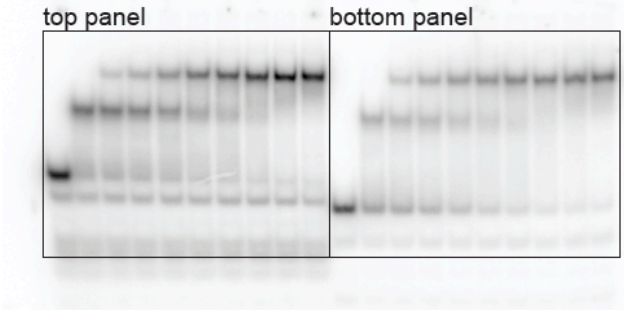



Figure 3f




Supplementary Figure 3




**Supplementary Fig 7** Representative, uncropped gel images.

**Supplementary Note 1: Sequence alignment of Lsm2-8 proteins**

**red** = truncations used for crystallization, or substitutions tested in this study
grey = disordered in yeast U6 snRNP crystal structure

```
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S.scrofa        MLFYSFFKSLVGKDVVVELKNDLSICGTLHSVDQYLNIKLTDISVTDPEKYPHMLSVKNCFIRGSVVRYVQLPADEVDTQLLQDAARKEALQQKQ-----
F.catus         MLFYSFFKSLVGKDVVVELKNDLSICGTLHSVDQYLNIKLTDISVTDPEKYPHMLSVKNCFIRGSVVRYVQLPADEVDTQLLQDAARKEALQQKQ-----
C.familiaris    MLFYSFFKSLVGKDVVVELKNDLSICGTLHSVDQYLNIKLTDISVTDPEKYPHMLSVKNCFIRGSVVHYVQLPADEVDTQLLQDAARKEALQQKQ-----
D.rerio         MLFYSFFKSLVGKDVVVELKNDLSICGTLHSVDQYLNIKLTDISVTDPEKYPHMLSVKNCFIRGSVVRYVQLPADEVDTQLLQDAARKEATQQKQ-----
X.laevis        MLFYSFFKSLVGKDVVVELKNDLSICGTLHSVDQYLNIKLTDISVTDPEKYPHMLSVKNCFIRGSVVRYVQLPADEVDTQLLQDAARKEAVQQKQ-----
A.thaliana      MLFFSYFKDLVGQEVTVELKNDLAIRGTLHSVDQYLNIKLENTRVVDQDKYPHMLSVRNCFIRGSVVRYVQLPKDGVDVDLLHDAARREARGG-------
O.sativa        MLFFSYFKELVGKEVTVELKNDLAIRGTLHSVDQYLNIKLENTRVVDQDKYPHMLSVRNCFIRGSVVRYVLLPQDGVDIDILHDATRREARGG-------
S.pombe         MLFYSFFKTLIDTEVTVELKNDMSIRGILKSVDQFLNVKLENISVVDASKYPHMAAVKDLFIRGSVVRYVHMSSAYVDTILLADACRRDLANNKRQ----
C.neoformans    MLIFSFFKTLTDQVITVELKNDLSITGTLKSVDQFLNIRLDNISVEDPERHPHMMAVKNCFIRGSVVRYVRMAARSVDTTLLEDATRREAKEGKK-----
N.crassa        MLFFSFFKTLIDHEVTVELKNDIQIRGVLKSVDQFLNIKLDNIQVVEELKYPHLSAVKNVFIRGSVVRYVHLPQESVDIQLLEDATRREAANQATKAKQG
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S.cerevisiae    MLFFSFFKTLVDQEVVVELKNDIEIKGTLQSVDQFLNLKLDNISCTDEKKYPHLGSVRNIFIRGSTVRYVYLNKNMVDTNLLQDATRREVMTERK-----
                **::*:** * .  :.*:****: * * *:****:**::* :    :  ::**: :*:: *****.*:** :    **  :* ** *::

Lsm3            1        10        20        30        40        50        60        70        80        90        100
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B.taurus        MADDVDQQQTTNTVEEPLDLIRLSLDERIYVKMRNDRELRGRLHAYDQHLNMILGDVEETVTTIEIDEETYEEIYKSTKRNIPMLFVRGDGVVLVAPPLRVG------
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F.catus         MADDVDQQQTTNTVEEPLDLIRLSLDERIYVKMRNDRELRGRLHAYDQHLNMILGDVEETVTTIEIDEETYEEIYKSTKRNIPMLFVRGDGVVLVAPPLRVG------
C.familiaris    MADDVDQQQTTNTVEEPLDLIRLSLDERIYVKMRNDRELRGRLHAYDQHLNMILGDVEETVTTIEIDEETYEEIYKSTKRNIPMLFVRGDGVVLVAPPLRVG------
G.gallus        MADEVDQQQTTNTVEEPLDLIRLSLDERIYVKMRNDRELRGRLHAYDQHLNMILGDVEETVTTIEIDEETYEEIYKSTKRNIPMLFVRGDGVVLVAPPLRVG------
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C.neoformans    -----MDAVVNSQIQEPLDLVKLALGERVLIKLRGDRIVTGVLHAYDAHMNVVISQAEESIHVVDVTEEGQPLPPRIERRTAEMLFVRGDGVILLSPAEQ--------
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C.glabrata      -----------MSLSTPLDLLKLNLDERVYVKLRGARAMEGVLQAFDSHCNIVLSDAVETIYELVDG------ELKSQERASEMIFVRGDSVTLITAVSEEE------
S.cerevisiae    -------------METPLDLLKLNLDERVYIKLRGARTLVGTLQAFDSHCNIVLSDAVETIYQLNNE------ELSESERRCEMVFIRGDTVTLISTPSEDDDGAVEI
                          :  *:**::* *.* : :*:*. * : * *:*:* * *:::.:. * :  .              :   ::*:*** * *::   .

Lsm4            1        10        20        30        40        50        60        70        80        90        100       110       120       130
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D.rerio         MLPLSLLKTAQNHPMLVELKNGETYNGHLVSCDNWMNINLREVICTSRDGDKFWRMPECYIRGSTIKYLRIPDEIIDMVKEEVVSKGRGRGGMQQNKPQ-(14aa)-GRGVFGGRGRGMQGSGRGQQQDKKPGKQQV--
X.laevis        MLPLSLLKTAQNHPMLVELKNGETYNGHLVSCDNWMNINLREVICTSRDGDKFWRMPECYIRGSTIKYLRIPDEIIDMVKEEVMSKGRGRGGMQQQKQMKGRGAGGGGRGVFGGRGR-GAPGGGRGQQDKKPGRQSGKQ
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O.sativa        MLPLSLLKTAQGHPMLVELKNGETYNGHLVNCDTWMNIHLREVICTSKDGDKFWRMPECYIRGNTIKYLRVPDEVIDKVQEET-(64aa)----------------------------------------------------
S.pombe         MLPLTLLNATQGRPILVELKNGETFNGHLENCDNYMNLTLREVIRTMPDGDKFFRLPECYIRGNNIKYLRIQDEVLSQVAKQQ-(38aa)----------------------------------------------------
C.neoformans    MLPLSLLTAAQGKPMLVELKNGVTFNGHLVECDTFMNVTLREVYQTSADGERFWKMKEMFIKGNIIKYFRIADNILEQAAEEQ-(64aa)----------------------------------------------------
N.crassa        MLPLGILTAAQGHPMLVELKNGETLNGHLIQCDTWMNLTLREVVQTSPEGDKFVRLPEVYVKGNNIKYLRVPDDVIDIAREQQ-(47aa)----------------------------------------------------
C.glabrata      MLPLYLLTNAKGQQMRIELKNGDIVEGELTNVDNWMNLTLANV-(15aa)-KVVKSKEIYVRGVYIKYITLQDDIIEKVKQQI-(80aa)----------------------------------------------------
S.cerevisiae    MLPLYLLTNAKGQQMQIELKNGEIIQGILTNVDNWMNLTLSNV-(18aa)-KAVKLNEIYIRGTFIKFIKLQDNIIDKVKQQI-(94aa)----------------------------------------------------
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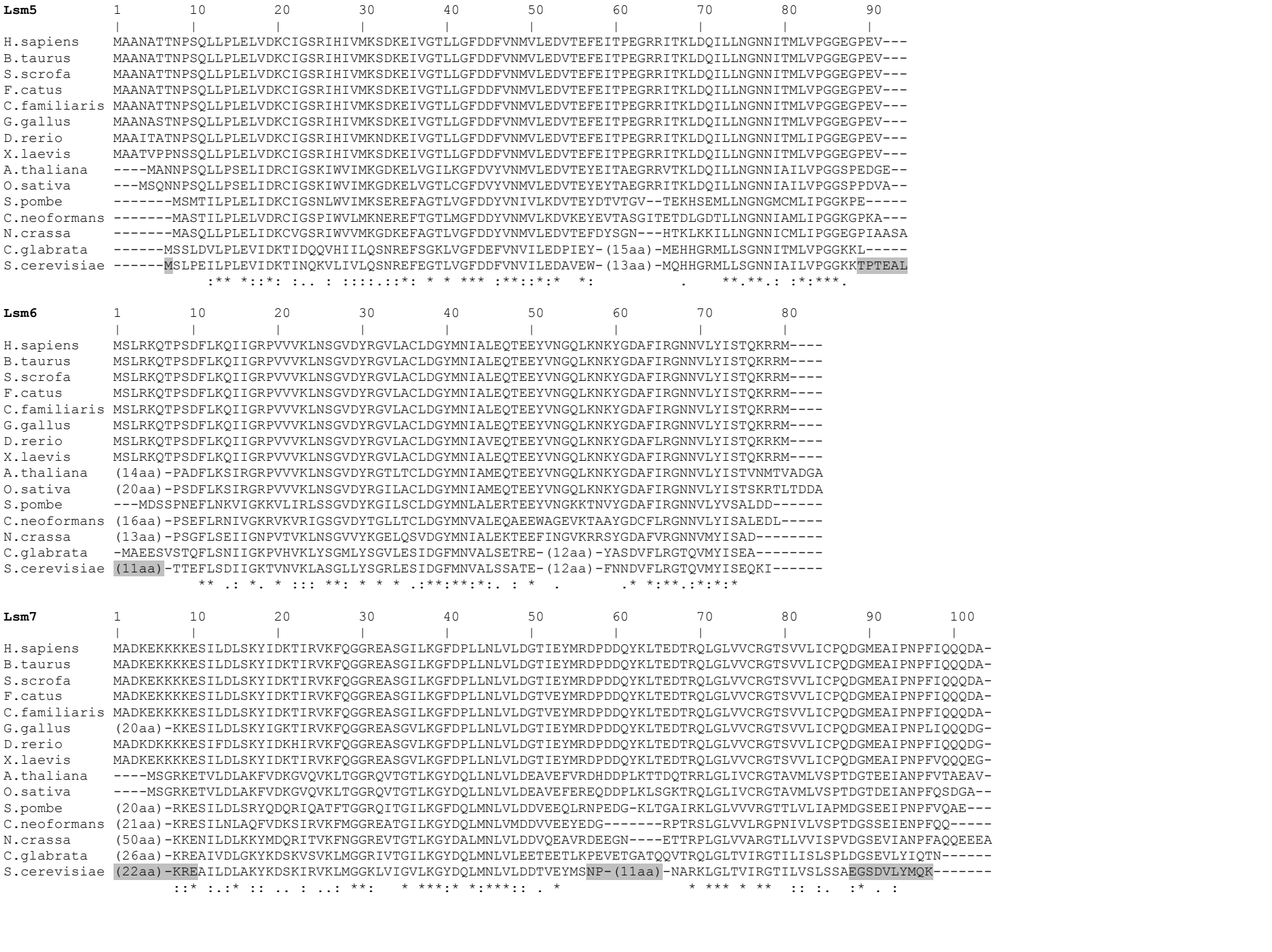
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C.familiaris MSLRKQTPSDFLKQIIGRPVVVKLNSGVDYRGVLACLDGYMNIALEQTEEYVNGQLKNKYGDAFIRGNNVLYISTQKRRM----
G.gallus MSLRKQTPSDFLKQIIGRPVVVKLNSGVDYRGVLACLDGYMNIALEQTEEYVNGQLKNKYGDAFIRGNNVLYISTQKRRM----
D.rerio MSLRKQTPSDFLKQIIGRPVVVKLNSGVDYRGVLACLDGYMNIAVEQTEEYVNGQLKNKYGDAFLRGNNVLYISTQKRKM----
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C.glabrata -MAEESVSTQFLSNIIGKPVHVKLYSGMLYSGVLESIDGFMNVALSETRE-(12aa)-YASDVFLRGTQVMYISEA--------
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B.taurus MADKEKKKKESILDLSKYIDKTIRVKFQGGREASGILKGFDPLLNLVLDGTIEYMRDPDDQYKLTEDTRQLGLVVCRGTSVVLICPQDGMEAIPNPFIQQQDA-
S.scrofa MADKEKKKKESILDLSKYIDKTIRVKFQGGREASGILKGFDPLLNLVLDGTIEYMRDPDDQYKLTEDTRQLGLVVCRGTSVVLICPQDGMEAIPNPFIQQQDA-
F.catus MADKEKKKKESILDLSKYIDKTIRVKFQGGREASGILKGFDPLLNLVLDGTVEYMRDPDDQYKLTEDTRQLGLVVCRGTSVVLICPQDGMEAIPNPFIQQQDA-
C.familiaris MADKEKKKKESILDLSKYIDKTIRVKFQGGREASGILKGFDPLLNLVLDGTVEYMRDPDDQYKLTEDTRQLGLVVCRGTSVVLICPQDGMEAIPNPFIQQQDA-
G.gallus (20aa)-KKESILDLSKYIGKTIRVKFQGGREASGVLKGFDPLLNLVLDGTIEYMRDPDDQYKLTEDTRQLGLVVCRGTSVVLICPQDGMEAIPNPLIQQQDG-
D.rerio MADKDKKKKESIFDLSKYIDKHIRVKFQGGREASGVLKGFDPLLNLVLDGTIEYMRDPDDQYKLTEDTRQLGLVVCRGTSVVLICPQDGMEAIPNPFIQQQDG-
X.laevis MADKEKKKKESILDLSKYIDKTIRVKFQGGREASGVLKGFDPLLNLVLDGTIEYMRDPDDQYKLTEDTRQLGLVVCRGTSVVLICPQDGMEAIPNPFVQQQEG-
A.thaliana ----MSGRKETVLDLAKFVDKGVQVKLTGGRQVTGTLKGYDQLLNLVLDEAVEFVRDHDDPLKTTDQTRRLGLIVCRGTAVMLVSPTDGTEEIANPFVTAEAV-
O.sativa ----MSGRKETVLDLAKFVDKGVQVKLTGGRQVTGTLKGYDQLLNLVLDEAVEFEREQDDPLKLSGKTRQLGLIVCRGTAVMLVSPTDGTDEIANPFQSDGA--
S.pombe (20aa)-RKESILDLSRYQDQRIQATFTGGRQITGILKGFDQLMNLVLDDVEEQLRNPEDG-KLTGAIRKLGLVVVRGTTLVLIAPMDGSEEIPNPFVQAE---
C.neoformans (21aa)-KRESILNLAQFVDKSIRVKFMGGREATGILKGYDQLMNLVMDDVVEEYEDG-------RPTRSLGLVVLRGPNIVLVSPTDGSSEIENPFQQ-----
N.crassa (50aa)-KKENILDLKKYMDQRITVKFNGGREVTGTLKGYDALMNLVLDDVQEAVRDEEGN----ETTRPLGLVVARGTLLVVISPVDGSEVIANPFAQQEEEA
C.glabrata (26aa)-KREAIVDLGKYKDSKVSVKLMGGRIVTGILKGYDQLMNLVLEETEETLKPEVETGATQQVTRQLGLTVIRGTILISLSPLDGSEVLYIQTN------
S.cerevisiae (22aa)-KREAILDLAKYKDSKIRVKLMGGKLVIGVLKGYDQLMNLVLDDTVEYMSNP-(11aa)-NARKLGLTVIRGTILVSLSSAEGSDVLYMQK-------


Lsm8
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H.sapiens MTSALENYINRTVAVITSDGRMIVGTLKGFDQTINLILDESHERVFSSSQGVEQVVLGLYIVRGDNVAVIGEIDEETDSALDLGNIRAEPLNSVAH----------
B.taurus MTSALENYINRTVAVITSDGRMIVGTLKGFDQTINLILDESHERVFSSSQGVEQVVLGLYIVRGDNVAVIGEIDEETDSALDLGNIRAEPLNSVAH----------
S.scrofa MTSALENYINRTVAVITSDGRMIVGTLKGFDQTINLILDESHERVFSSSQGVEQVVLGLYIVRGDNVAVIGEIDEETDSALDLGNIRAEPLNSVAH----------
F.catus MTSALENYINRTVAVITSDGRMIVGTLKGFDQTINLILDESHERVFSSSQGVEQVVLGLYIVRGDNVAVIGEIDEETDSALDLGNIRAEPLNSVAH----------
C.familiaris MTSALENYINRTVAVITSDGRMIVGTLKGFDQTINLILDESHERVFSSSQGVEQVVLGLYIVRGDNVAVIGEIDEETDSALDLGNIRAEPLNSVAH----------
G.gallus MTSALENYINRTVAVITSDGRMIVGTLKGFDQTINLILDESHERVFSSSQGVEQVVLGLYIVRGDNVAVIGEIDEETDSALDLGNIRAEPLNSVVH----------
D.rerio MSTALESYIHRTVAIVTSDGRMIVGTLKGFDQAINLILDESHERVFSSSQGVEQVVLGLYIVRGDNVAVIGEIDEETDSALDLGNIRAEPLNSVVH----------
X.laevis MASALENYINRTVAVITADGRMIVGTLKGFDQTINLILDESHERVFSSSQGVEQVVLGLYIVRGDNVAVIGEIDEETDSSLDLGNIRAEPLNSVVN----------
A.thaliana (13aa)-LVDQIISVITNDGRNIVGVLKGFDQATNIILDESHERVFSTKEGVQQHVLGLYIIRGDNIGVIGELDEELDASLDFSKLRAHPLKPVVH----------
O.sativa (9aa)-SLVDQIISVITNDGRNIVGTLRGFDQATNIILDESHERVYSTREGVQQLVLGLYIIRGDNISVVGEVDEELDARLDLSNLRAHPLKPVIH----------
S.pombe --MSLADFMEQRVQVITNDGRVVLGSLKGFDHTTNLILSDSFERIISMDQDMETIPLGVYLLRGENVAMVGLVNEELDSEIEWTKIRGEAIPDVVH----------
C.neoformans -MASIESYVDHTVQVILQDGRVIVGKLKGYDPRTNLILSDSVEREFSMDQGVEMIPLGLYVIKGDNVAVVAELDEEKDSTINYNDIRAEPLAELRY----------
N.crassa (7aa)-SYLNKKVCIITVDGRTLVGTLISVDMSTNVFLQRAVERVI-(11aa)-IELGTHMIRGDTVCLVGLVDEPLDESIDWTKVKGATIGTTKH----------
C.glabrata MSPLLKQYLNKDIVVVTTAGEVMHVILDGYDKYTNLVVKEG----------DKIRLLRGSEIVVCGLLEDAKALEGLPMDS---HVYKDTKNVIKDEYLIWEAVNKKHQSTHKKRKLK
S.cerevisiae MSATLKDYLNKRVVIIKVDGECLIASLNGFDKNTNLFITNVFNRISKE------FICKAQLLRGSEIALVGLIDAENDDSLAPIDEKKVPMLKDTKNKIENEHVIWEKVYESKTK--------

**Supplementary Table 1** Diffraction data collection and structure refinement statistics

| | U6 snRNP nt. 30-112 with 2′ $PO_3$ | U6 snRNP nt. 30-113 with 3′ $PO_3$ |
|---|---|---|
| PDB ID | 5VSU | 6ASO |
| **Data Collection** | | |
| Wavelength (Å) | 0.9792 | 0.9786 |
| Resolution range (Å)* | 179.8-3.10 (3.29-3.10) | 90.59-2.80 (2.91-2.80) |
| Space group | $P2_12_12_1$ | $P2_1$ |
| Unit cell dimensions (Å) | 70.2, 114.7, 179.8 | 94.2, 77.4, 118.6 |
| | | $\beta$ = 105.9° |
| Total reflections* | 1,389,951 (206,204) | 2,475,089 (267,471) |
| Unique reflections* | 27,164 (4,321) | 40,745 (4,574) |
| Multiplicity* | 51.2 (47.7) | 60.7 (58.5) |
| Completeness (%)* | 100 (100) | 100 (100) |
| Mean I/σ(I)* | 13.0 (1.2) | 8.7 (0.5) |
| Wilson B-factor ($Å^2$) | 129.7 | 79.1 |
| anisotropic $\Delta B$ ($Å^2$) | 17.4 | 87.2 |
| $R_{merge}$* | 0.25 (4.03) | 0.45 (16.6) |
| $R_{pim}$* | 0.035 (0.59) | 0.058 (2.18) |
| $CC_{1/2}$* | 1.00 (0.445) | 0.997 (0.418) |
| **Refinement** | | |
| Resolution | 96.7-3.10 | 55.6-2.71 |
| $R_{work}/R_{free}$* | 0.234/0.298 | 0.195/0.247 |
| Total number of atoms | 9,240 | 8,863 |
| macromolecules | 9,240 | 8,724 |
| ligands | 0 | 5 |
| water | 0 | 134 |
| RMS(bonds) | 0.011 | 0.011 |
| RMS(angles) | 1.667 | 1.656 |
| Ramachandran favored | 93.1 | 94.8 |
| Ramachandran outliers | 1.81 | 1.02 |
| Average B factor ($Å^2$) | 133.4 | 79.5 |
| macromolecules | 133.4 | 79.5 |
| ligands/ions | NA | 74.5 |
| solvent | NA | 45.6 |

*Values shown in parentheses are for the highest resolution shell. Isotropic data statistics are only shown to 2.8 Å for the anisotropic 3′ $PO_3$ dataset, where ellipsoidal truncation was used to generate the final dataset for structure refinement with resolution limits of 2.71 x 3.50 x 3.59 Å. Ellipsoidal truncation was performed on the StarAniso web server with the default I/σ(I) cutoff of 1.2.

**Supplementary Table 2** Growth rate of wild-type and *prp24* strains of *S. cerevisiae* in liquid media

| | doubling time in YEPD (minutes) | |
|---|---|---|
| strain | 30 °C | 37 °C |
| *PRP24* | 94 ± 3 | 88 ± 4 |
| *prp24-8Asub* | 112 ± 5 | 150 ± 9 |
| *prp24-ΔSNFFL* | 106 ± 1 | 114 ± 1 |
| *prp24-8Asub-ΔSNFFL* | 132 ± 0 | 188 ± 6 |

**Supplementary Table 3** Binding affinity of wild-type and mutant Lsm2-8 for the 3′ region of *S. cerevisiae* U6 RNA (nucleotides 104-113) with either a 2′,3′-*cis* diol or a 3′ phosphate.

| | diol | $PO_3$ | $K_d$ ratio diol/$PO_3$ | $K_d$ ratio $PO_3$/diol |
|---|---|---|---|---|
| WT | 37.4 ± 4.5 | 6.13 ± 0.87 | 6.11 | 0.16 |
| Lsm2-K20A | 522 ± 48 | 841 ± 89 | 0.62 | 1.61 |
| Lsm2-K20E | 1,870 ± 370 | 2,320 ± 450 | 0.81 | 1.24 |
| Lsm3-R21A | 40.8 ± 3.3 | 123 ± 12 | 0.33 | 3.01 |
| Lsm3-R21E | 195 ± 27 | 1,150 ± 190 | 0.17 | 5.89 |
| Lsm8-6Asub | 132 ± 16 | 301 ± 33 | 0.44 | 2.29 |
| Lsm8-delC | 277 ± 32 | 502 ± 47 | 0.55 | 1.81 |

Affinities are reported as $K_d$ values with units of nM. Binding data were obtained via fluorescence polarization with 5′ FAM labeled oligonucleotides (Fig. 5) and are from two technical replicates.

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