*Supplementary Data*

# Structural basis for snRNA recognition by the double WD40-repeat domain of Gemin5

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Figure S1. Two G5N-RNA complexes in one crystallographic asymmetric unit.

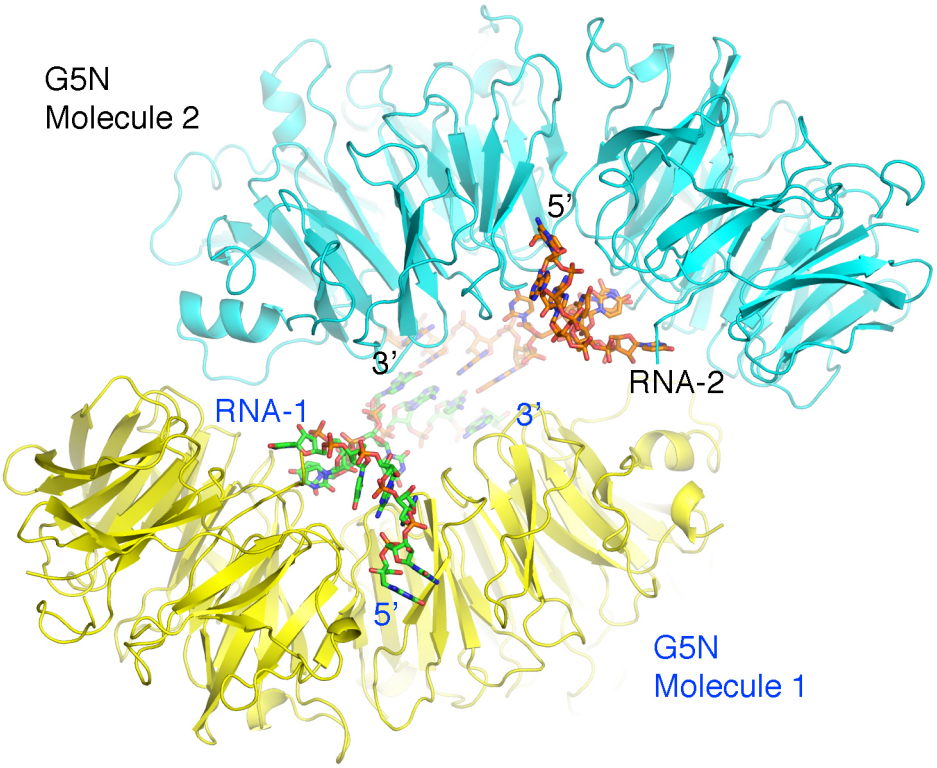
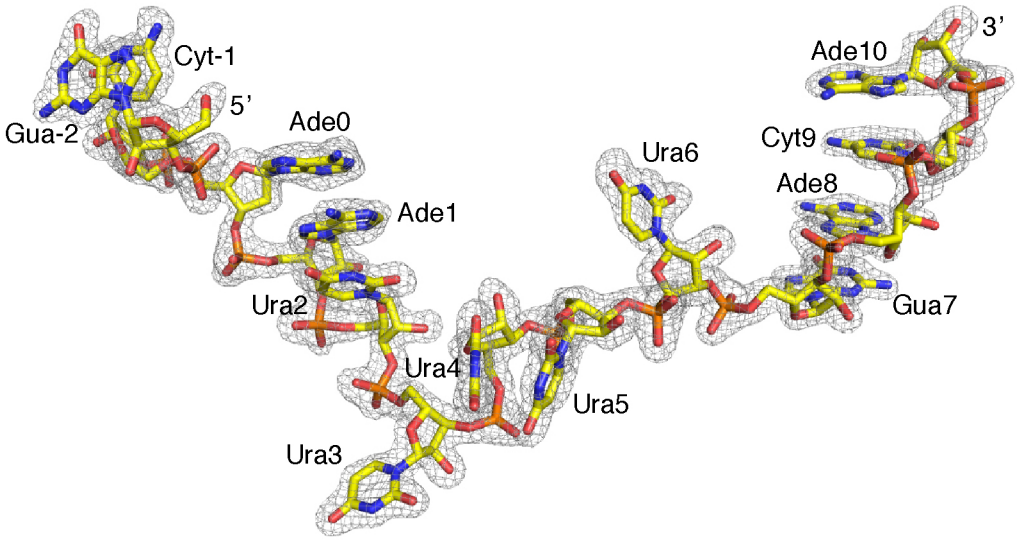



Figure S2. Simulated annealing omit difference electron density map of the bound RNA molecule. The Fo-Fc map is contoured at 3σ level. A stick model of the RNA molecule is superimposed.



Table_S1. Statistics of crystallographic analyses

| | $K_2Pt(NO_2)_4$ derivative | Native | G5N-13nt RNA (cocrystallization) | G5N-7nt RNA (soak) | G5N-m7GTP (soak) |
|---|---|---|---|---|---|
| **Data collection** | | | | | |
| Space group | $P2_1$ | $P2_1$ | $P2_12_12_1$ | $P2_1$ | $P2_1$ |
| Cell dimensions | | | | | |
| a, b, c (Å) | 59.61, 124.70, 61.64 | 60.26, 123.59, 61.73 | 98.65, 107.19, 151.48 | 59.54, 124.79, 61.02 | 60.53, 120.91, 61.26 |
| α, β, γ (°) | 90, 118.70, 90 | 90, 119.27, 90 | 90, 90, 90 | 90, 117.97, 90 | 90, 117.42, 90 |
| Wavelength (Å) | 0.9786 | 0.9786 | 0.9792 | 0.9785 | 0.9788 |
| Resolution (Å) | 50.00-3.00 (3.11-3.00) | 50.00-2.00 (2.07-2.00) | 50.00-1.90 (1.97-1.90) | 50.00-2.10 (2.18-2.10) | 50.00-2.50 (2.59-2.50) |
| Rmerge | 0.143 (0.699) | 0.116 (0.504) | 0.116 (0.683) | 0.090 (0.533) | 0.070 (0.609) |
| I / σI | 12 (3.0) | 11.5 (2.6) | 17.4 (2.8) | 13.0 (2.8) | 15.9 (2.1) |
| Completeness (%) | 100.0 (100.0) | 99.9 (99.9) | 99.7 (99.0) | 99.7 (99.7) | 99.1(99.6) |
| Redundancy | 6.9 (6.8) | 4.8 (4.8) | 7.9 (7.9) | 3.4 (3.4) | 3.3(3.3) |
| Total/Unique reflections | 215832/31097 | 255144/53257 | 1002669/126392 | 152592/45763 | 88710/26965 |
| **Refinement** | | | | | |
| Resolution (Å) | | 50.00-2.00 (2.03-2.00) | 50.00-1.90 (1.95-1.90) | 50.00-2.10 (2.15-2.10) | 50.00-2.50 (2.58-2.50) |
| No. reflections | | 52884 (2466) | 125759 (8413) | 45665 (2849) | 26936 (2527) |
| Rwork / Rfree | | 0.157(0.200)/0.199(0.242) | 0.170(0.242)/0.206(0.298) | 0.195(0.333)/0.241(0.354) | 0.183(0.241)/0.234(0.296) |
| No. atoms, B-factors ($Å^2$) | | | | | |
| Protein | | 5509, 28.1 $Å^2$ | 10899, 24.0 $Å^2$ | 5378, 34.5 $Å^2$ | 5319, 70.9 $Å^2$ |
| RNA | | | 522, 22.7 $Å^2$ | 142, 54.5 $Å^2$ | |
| Ligand | | | | 6, 29.4 $Å^2$ | 29, 86.8 $Å^2$ |
| Water | | 623, 35.3 $Å^2$ | 1330, 33.3 $Å^2$ | 417, 38.7 $Å^2$ | 33, 58.4 $Å^2$ |
| R.m.s deviations | | | | | |
| Bond length (Å) | | 0.005 | 0.009 | 0.005 | 0.003 |
| Bond angles (°) | | 0.911 | 1.256 | 0.936 | 0.661 |
| Ramachandran plot | | | | | |
| Favored | | 96.5% | 96.3% | 95.5% | 97.3% |
| Allowed | | 3.5% | 3.7% | 4.5% | 2.6% |
| Outliers | | 0 | 0 | 0 | 0.1% |