

Table S1 EM data and refinement, related to Figures 1, 4, S1-S6, and STAR Methods.

	NEXT-substrate 1 complex			NEXT-substrate 2 complex			Apo-NEXT
Data collection	Dataset 1 (MSKCC)	Dataset 2 (MSKCC)	Data collection	Dataset 1 (NYSBC)	Dataset 2 (MSKCC)	Dataset 3 (MSKCC)	Dataset 1 (MSKCC)
Magnification	22,500x	22,500x	Magnification	22,500x	22,500x	22,500x	22,500x
Voltage (kV)	300	300	Voltage (kV)	300	300	300	300
Electron exposure (e-/Å ²)	67.6	67.6	Electron exposure (e-/Å ²)	77.5	66	66	67.6
Defocus range (µm)	-1.0 to -3.0	-1.0 to -3.0	Defocus range (µm)	-1.0 to -3.0	-1.0 to -3.0	-1.0 to -3.0	-1.0 to -3.0
Super-resolution pixel size (Å)	0.544	0.544	Super-resolution pixel size (Å)	0.55	0.534	0.532	0.544
Fourier cropped pixel size (Å)	1.088	1.088	Fourier cropped pixel size (Å)	1.1	1.1	1.1	1.088
Initial particle projections (#)	960,423		Initial particle projections (#)	822,892			465,038
Final particle projections (#)			Final particle projections (#)				
Overall map	614,412		Overall map	252,638			52,777
Focused Refinement (Foc. Ref.) MTR4 (A)	225,213		Foc. Ref. MTR4 ^{core}	252,638			
Foc. Ref. MTR4 (B)	37,088		Foc. Ref. MTR4 ^{core} -ZCCHC8 ^{PSP} -RBM7-RNA	252,638			
Foc. Ref. MTR4 ^{KOW} -ZCCHC8 ^{HD} KID (CC-1)	117,561		Foc. Ref. RBM7-ZCCHC8 ^{PSP} -RNA	252,638			
Foc. Ref. MTR4 ^{core} -ZCCHC8 ^{PSP} -RBM7 (A)	44,800		Foc. Ref. MTR4-ZCCHC8 ^{HD} KID	252,638			
Foc. Ref. MTR4 ^{core} -ZCCHC8 ^{PSP} -RBM7 (B)	37,088		Foc. Ref. MTR4 ^{KOW} -ZCCHC8 ^{HD} KID	252,638			
Symmetry imposed	C1		Symmetry imposed	C1			C1
Map resolution (Å)			Map resolution (Å)				
FSC threshold = 0.143			FSC threshold = 0.143				
Overall map	4.06		Overall map	3.62			8.36
Focused Refinement (Foc. Ref.) MTR4 (A)	3.42		Foc. Ref. MTR4 ^{core}	3.50			
Foc. Ref. MTR4 (B)	3.54		Foc. Ref. MTR4 ^{core} -ZCCHC8 ^{MR} -RBM7-RNA	3.42			
Foc. Ref. MTR4 ^{KOW} -ZCCHC8 ^{HD} KID	3.26		Foc. Ref. RBM7-ZCCHC8 ^{MR} -RNA	3.94			
Foc. Ref. MTR4 ^{core} -ZCCHC8 ^{MR} -RBM7 (A)	4.26		Foc. Ref. MTR4-ZCCHC8 ^{HD} KID	3.62			
Foc. Ref. MTR4 ^{core} -ZCCHC8 ^{MR} -RBM7 (B)	4.40		Foc. Ref. MTR4 ^{KOW} -ZCCHC8 ^{HD} KID	3.34			
Map resolution range (Å)			Map resolution range (Å)				
Overall map	3.24 – 5.23		Overall map	3.00 – 6.56			6.52-13.1
Focused Refinement (Foc. Ref.) MTR4 (A)	3.06 – 6.05		Foc. Ref. MTR4 ^{core}	2.80 – 5.25			
Foc. Ref. MTR4 (B)	3.02 – 5.26		Foc. Ref. MTR4 ^{core} -ZCCHC8 ^{MR} -RBM7-RNA	2.73 – 5.03			
Foc. Ref. MTR4 ^{KOW} -ZCCHC8 ^{HD} KID	2.96 – 7.56		Foc. Ref. RBM7-ZCCHC8 ^{MR} -RNA	3.05 – 7.00			
Foc. Ref. MTR4 ^{core} -ZCCHC8 ^{MR} -RBM7 (A)	3.40 – 6.28		Foc. Ref. MTR4-ZCCHC8 ^{HD} KID	2.84 – 4.75			
Foc. Ref. MTR4 ^{core} -ZCCHC8 ^{MR} -RBM7 (B)	3.71 – 8.58		Foc. Ref. MTR4 ^{KOW} -ZCCHC8 ^{HD} KID	2.82 – 4.82			
Refinement			Refinement				
Initial model used (PDB code)	6C90, 5LXR		Initial model used (PDB code)	6C90, 5LXR			
Model resolution (Å)	3.57		Model resolution (Å)	3.74			
FSC threshold = 0.5			FSC threshold = 0.5				
Map sharpening B factor (Å ²)			Map sharpening B factor (Å ²)				
Overall map	-104		Overall map	-126			-429
Focused Refinement (Foc. Ref.) MTR4 (A)	-66		Foc. Ref. MTR4 ^{core}	-110			
Foc. Ref. MTR4 (B)	-82		Foc. Ref. MTR4 ^{core} -ZCCHC8 ^{PSP} -RBM7-RNA	-98			
Foc. Ref. MTR4 ^{KOW} -ZCCHC8 ^{HD} KID	-54		Foc. Ref. RBM7-ZCCHC8 ^{PSP} -RNA	-153			
Foc. Ref. MTR4 ^{core} -ZCCHC8 ^{PSP} -RBM7 (A)	-80		Foc. Ref. MTR4-ZCCHC8 ^{HD} KID	-113			
Foc. Ref. MTR4 ^{core} -ZCCHC8 ^{PSP} -RBM7 (B)	-91		Foc. Ref. MTR4 ^{KOW} -ZCCHC8 ^{HD} KID	-128			
Model composition			Model composition				
Non-hydrogen atoms	22,217		Non-hydrogen atoms	13,851			
Protein residues	2,709		Protein residues	1,629			
Nucleic acid residues	22		Nucleic acid residues	37			
Ligand (Zn ²⁺)	2		Ligand (Zn ²⁺)	1			
Mean B factors			Mean B factors				
Protein	109.45		Protein	79.1			
Nucleic acid	136.73		Nucleic acid	165.58			
Ligand (Zn ²⁺)	255.2		Ligand (Zn ²⁺)	182.12			
RMS deviations			RMS deviations				
Bond lengths (Å)	0.005		Bond lengths (Å)	0.003			
Bond angles (°)	0.917		Bond angles (°)	0.485			
Validation			Validation				
Molprobity score	2.08		Molprobity score	2.00			
Clashscore	8.35		Clashscore	8.82			
Rotamer Outliers (%)	1.54		Rotamer Outliers (%)	1.10			
C-beta deviations	0		C-beta deviations	0			
Ramachandran plot			Ramachandran plot				
% favored	92.11		% favored	91.68			
% allowed	7.89		% allowed	8.32			
% outliers	0		% outliers	0			

Table S2. Sequences of primers used for qPCR analysis, Related to Figure 5 and Star Methods

Name	Sequence (5' to 3')	Manufacturer
GAPDH qPCR forward	GTCAGCCGCATCTTCTTTTG	IDT
GAPDH qPCR reverse	GCGCCCAATACGACCAAATC	IDT
proPOGZ qPCR forward	AGTTCCAAGAAACCACACAC	IDT
proPOGZ qPCR reverse	GGTCGTTTGAGTGGACTAAC	IDT
proEXT1 qPCR forward	TCTAATGGCTGCAGGGAAAC	IDT
proEXT1 qPCR reverse	TAGCTGGGACAGTTGGCAAT	IDT
proKLF6 qPCR forward	AAGTTTTAGAGGGTCCGGCA	IDT
proKLF6 qPCR reverse	CTCTGCATAACCTTCACCGC	IDT
proSERINC3 qPCR forward	GCAGAGTGAGAACGTCCCAT	IDT
proSERINC3 qPCR reverse	GCATGGTTGCCTGTTTGAGA	IDT
proTTC32 qPCR forward	GTCTGTTCCACGGTCCAAAC	IDT
proTTC32 qPCR reverse	ACAGCAGGCATGTAGGGTAG	IDT
proRBM39 qPCR forward	AATAGATTTCCCTGTCATTTGGAGC	IDT
proRBM39 qPCR reverse	TTTCCAAGGTTGTTTCAAAGCTCG	IDT