Table S1 | X-ray data collection and refinement statistics for TEFM. *Related to Figure 1*

	TEFM CTD PDB ID: 5OL8	TEFM CTD SeMet-SAD [a]	TEFM NTD PDB ID: 5OL9	TEFM NTD S-SAD
Data collection				
Space group	C2	C2	$P4_32_12$	$P4_32_12$
Cell dimensions				
a, b, c (Å)	98.48, 112.54, 88.84	97.57, 112.79, 88.84	47.67, 47.67, 93.40	47.72, 47.72, 93.32
α, β, γ (°)	90.00, 110.13, 90.00	90, 109.76, 90.00	90.00, 90.00, 90.00	90.00, 90.00, 90.00
Wavelength	1.0000	0.9765	1.0000	2.0664
Resolution (Å)[a]	46.23 – 1.90 (1.94 – 1.90) [b]	48.32 – 2.68 (2.74 – 2.68) [b]	42.46 – 1.30 (1.33 – 1.30) [b]	42.49 – 2.10 (2.14 - 2.10) [b]
R_{meas}	0.056 (2.78)	0.24 (3.50)	0.107 (4.67)	0.096 (2.51)
$I/\sigma(I)$	17.92 (0.79)	9.45 (0.62)	20.26 (0.60)	41.67 (7.74)
$CC_{1/2}$	100.0 (35.3)	99.7 (32.6)	100.0 (41.3)	100.0 (95.1)
Completeness (%)	98.1 (89.5)	99.7 (98.8)	99.7 (98.1)	99.4 (96.1)
Redundancy	6.60 (5.04)	11.86 (6.25)	25.05 (24.01)	37.62 (25.64)
Refinement				
Resolution (Å)	46.23 – 1.90		42.46 – 1.30	
No. reflections	70117		27057	
R_{work} / R_{free}	0.195 / 0.228		0.190 / 0.197	
No. atoms				
Protein	6724		692	
Ligands	24		4	
Water	129		80	
B factors				
Protein	67.33		27.16	
Ligands	79.72		56.01	
Water	57.78		38.21	
r.m.s deviations				
Bond lengths (Å)	0.003		0.009	
Bond angles (°)	0.51		0.95	
Ramachandran Preferred / allowed / disallowed (%)	97.5 / 2.5 / 0.0		98.7 / 1.3 / 0.0	

[a] The data reflect the merged results from several crystals
[b] Values in parentheses are for highest-resolution shell.

Table S2 | X-ray data collection and refinement statistics for the EC-TEFM complex.

Related to Figure 4.

	EC-TEFM Complex [a] PDB ID: 5OLA
Data collection	
Space group	*C2*
Cell dimensions	
a, *b*, *c* (Å)	224.53, 155.55, 164.19
α, β, γ (°)	90.00, 113.59, 90.00
Wavelength	1.0000
Resolution (Å)[a]	49.16 – 3.90 (4.00 – 3.90)[b]
R_{meas}	0.258 (2.187)
$I/\sigma(I)$	9.72 (1.44)
$CC_{1/2}$	99.7 (54.5)
Completeness (%)	99.6 (97.7)
Redundancy	13.12 (12.50)
Refinement	
Resolution (Å)	48.87 – 3.90
No. reflections	46930
R_{work} / R_{free}	0.243 / 0.276
No. atoms	
Macromolecules	25122
Ligands	0
Water	0
B factors	
Macromolecules	160.94
Ligands	0
Water	0
r.m.s deviations	
Bond lengths (Å)	0.004
Bond angles (°)	0.63
Ramachandran Preferred / allowed / disallowed (%)	94.2 / 5.1 / 0.6

[a] The data reflect the merged results from two datasets.
[b] Values in parentheses are for highest-resolution shell.

Table S3 | List of oligonucleotides used. *Related to STAR Methods.*

REAGENT OR RESOURCE[a]	SOURCE	IDENTIFIER
RNA14mt agucugcggcgcgc	(Schwinghammer et al, 2013)	N/A
NT25HH GAACATGGTGTAATTATTTCGACGCCAG ACGAAC	This paper	N/A
TS22HH GTTCGTCTGGCGTGCGCGCCGCTACAC CATGTTC	This paper	N/A
TS26 GGGCTTAGTTCGTCTGGCGTGCGCGCC GCTACACCATGTTTGCTGACC	This paper	N/A
NT26A GGTCAGCAAACATGGTGTAAGTATTACG ACGCCAGACGAACTAAGCCC	This paper	N/A
RNA14HH ugaugguaaugcuccugucgugauc	This paper	N/A
NT19HH CATGGGGTAACTAGTTCGA CGCCAGACG	This paper	N/A
TS16HH CGTCTGGCGTGATCACGACTACCCCAT G	This paper	N/A
NT_LSP TGTTAGTTGGGGGGTGACTGTTAAAAGT GCATACCTATCCCCGATAGGCC	This paper	N/A
TS_LSP GGCCTATCTTTTGGCGGTATGCACTTTT AACAGTCACCCCCCAACTAACA	This paper	N/A
RNA10 cugcgcgcau	This paper	N/A
TS1 GGGTCCTGTCTGAAATCGACATCGCCG C	This paper	N/A
NT1 CGATTTCAGACAGGACCC	This paper	N/A

[a] DNA = UPPERCASE; RNA = lowercase