

Table S2. Summary of crystallographic information (Related to Figures 6 and 7)

Structure	DXO 3'-NADP⁺-Ca²⁺ complex	SsRai1 3'-NADP⁺-Ca²⁺ complex
Data Collection		
Space group	<i>P2</i> ₁	<i>P2</i> ₁
Cell dimensions		
a,b,c (Å)	49.9, 87.7, 53.2	89.4, 102.5, 101.2
α,β,γ (°)	90, 113.0, 90	90, 112.8, 90
Resolution (Å) ¹	48.9-2.1 (2.2-2.1)	49.7-1.9 (1.96-1.9)
<i>R</i> _{merge} (%)	7.2 (39.6)	8.3 (48.3)
<i>I</i> /σ	12.1 (2.8)	14.2 (2.0)
Completeness (%)	99.5 (98.2)	99.6 (97.9)
No. of reflections	26169	69282
Redundancy	2.9 (2.8)	3.6 (3.0)
Refinement		
Resolution (Å)	48.9-2.1	49.7-1.9
<i>R</i> _{work} / <i>R</i> _{free} (%)	16.1 (23.1) / 20.8 (26.5)	20.8 (26.9) / 25.4 (31.4)
Number of atoms	3142	13483
Protein	2941	12529
Ligand/Ion	49	96
Water	151	858
B-factors (Å ²)	30.6	29.7
Protein	30.0	29.4
Ligand	52.3	36.8
Water	34.9	33.6
r.m.s.d.		
Bond lengths (Å)	0.013	0.003
Bond angles (°)	1.4	0.69

1. The numbers in parentheses are for the highest resolution shell.

Table S3. DNA Primer Sequences (Related to the STAR Methods section):

ϕ2.5A-CA2: 5'-
CAGTAATACGACTCACTATTAGGCCTCTCGCTCTGCTGGGTGTGCGCTTGCTTGGCTTGCTT
GTGGTCTGCGGTTTCGTTCCCGCTTTGGT -3'

NAD-Transcription Forward Primer: 5'-CAGTAATACGACTCACTATTAGGCC-3'
NAD-Transcription Reverse Primer: 5'-CCCCCCCCCCCCCCCCACCAAAGCGGGAACGAACC-3'

ϕ2.5-Luc Forward Primer: 5'-ggtaccCAGTAATACGACTCACTATTAGGCC-3'
ϕ2.5-Luc Reverse Primer: 5'-ctcgagACCAAAGCGGGAACGAACC-3'

F-Luc Forward Primer: 5'-CAGTAATACGACTCACTATTAGGCC-3'
F-Luc-A₆₀ Reverse Primer: 5'-T₆₀ACCTACTCAGACAATGCGATGC-3'

R-Luc Forward Primer: 5'-TAATACGACTCACTATAGGG-3'
R-Luc-A₆₀ Reverse Primer: 5'-T₆₀GTACGACACTCATACTAACGCC-3'

F-Luc RT Primer: 5'-CGAAGATGTTGGGGTGTGG-3'

F-Luc P1: 5'-CGAAATGTCCGTTTCGGTTGG-3'
F-Luc P2: 5'-CGAAATGCCCATACTGTTGAGC-3'

GAPDH P1: 5'-AGGTGAAGGTCCGAGTCAAC-3'
GAPDH P2: 5'-TTCTCAGCCTTGACGGTGC-3'

DXO-gRNA1: 5' CACCGACAGCCCCCAACCTGCTATG3'
DXO-gRNA2: 5' AAACCATAGCAGGTTGGGGGCTGTC3'

TMSB10 P1: 5' ACCAGACATGGGGGAAATCG-3'
TMSB10 P2: 5' CACATCACGACTGGGGTCTC-3'

CKS2 P1: 5'-TCTCGTTTCATTTTCTGCAGCG-3'
CKS2 P2: 5'-GTTGGACACCAAGTCTCCTCC-3'

COX7B P1: 5'-TGCCGCAGTTCTAGCTTCAC-3'
COX7B P2: 5'-AGGTGTACGTTTCTGGTGGC-3'

LSM3 P1: 5'-TCCGGAGATTGACGTTGCTC-3'
LSM3 P2: 5'-GTCCGCCATGTTTCAAACCC-3'
LSM3 P3: 5'- ATGACCGAGAGCTTCGAGG -3'
LSM3 P4: 5'- CCCGGACAAAGAGCATTGG -3'

NDUFS5 P1: 5'-AAGATGGCTGGTCGATGCC-3'
NDUFS5 P2: 5'-TGATGGTACCTGCACGTCTC-3'

TIMP1 P1: 5'-CTTCTGGCATCCTGTTGTTGC-3'
TIMP1 P2: 5'-GGTTGACTTCTGGTGTCCCC-3'

EXOSC2 P1: 5'-TGCCGGGGGATAACAATCAC-3'
EXOSC2 P2: 5'-TCTGTGATTTCGTCCCCTACG-3'

ID2 P1: 5'-CTATTGTCAGCCTGCATCACC-3'
ID2 P2: 5'-TATCCGTGTTGAGGGTGGTC-3'

RHOA P1: 5'-CATTTCTGTCCCAACGTGCC-3'
RHOA P2: 5'-GCCTTCTTCAGGTTTCACCG-3'

VIM P1: 5'-TGGACCAGCTAACCAACGAC-3'
VIM P2: 5'-AAGGTCAAGACGTGCCAGAG-3'

MRPL33 P1: 5'-ACCAAGAGAAACCGACTGCG-3'
MRPL33 P2: 5'-TCAGTATCCCCGCCCTCAG-3'

MRPL13 P1: 5'-ACCTGTGTACCATGCACTGAG-3'
MRPL13 P2: 5'-CAATTGCCACTGGATCCCTC-3'

SNORA49 P1: 5'-CTTCCTCAGCCTTACTCCAGG-3'
SNORA49 P2: 5'-TGTCAGCTCAACTTGTAGGCC-3'

SNORA76 P1: 5'-GCGCTGTCTTTGAGCCC-3'
SNORA76 P2: 5'-GGCGGCCCCAGTTATGC-3')

SNORA20 P1: 5'-GCTGCTTGTAGTCTCACAGTG-3'
SNORA20 P2: 5'-ATGTCTAGTCCCTGCAGAAGAG-3'
SNORA20 P3: 5'-CCTTAAGTCCTGCCTACACAGG-3'

SNORA7B P1: 5'-GACCTCCTGGGATCGCATC-3'
SNORA7B P2: 5'-ACTGTCGCAGAGTGTCTTCC-3'

SCARNA7 P1: 5'-GTGTGCTTGTGGTGGCTATG-3'
SCARNA7 P2: 5'-CCAGGCTAGTTAGGTGAGCTG-3'

SNORD17 P1: 5'-TGACCTTCTTCCAAGCCTCAG-3'
SNORD17 P2: 5'-ATTCTTACCGGTAGCCTGCC-3'

SCARNA5 P1: 5'-TTGCACTGAATGTCACGGTC-3'
SCARNA5 P2: 5'-ATACTCGTCAGCTGTGAGCC-3'

SNORA6 P1: 5'-TCTGAGTGTCGGAAGTGTGC-3'
SNORA6 P2: 5'-ACTCCAGTCATAGAGGCAAGC-3'

SCARNA10 P1: 5'-AGGGGTGATTCTTCCAGTTGC-3'
SCARNA10 P2: 5'-AAGTCCTTTAGGACCCTTGGC-3'

SNORA46 P1: 5'-ATTCCCCATTCTTGGTTACGC-3'
SNORA46 P2: 5'-ATACAGCAACAGCAGAATGGC-3'

SNORA11B P1: 5'-CTCCTCTGTTTACAACACACCC-3'
SNORA11B P2: 5'-TTGTAGGGAGGTCACAAGCTC-3'

18S rRNA P1 : 5' -TTCGATGGTAGTCGCCGTG- 3'
18S rRNA P2 : 5' -GCTGCCTTCCTTGGATGTG- 3'

Anchor-d(T)₁₈: 5'-CTGCAGGTCGACCATATGGGTTTTTTTTTTTTTTTTTTT-3'
Anchor Primer: 5'-CTGCAGGTCGACCATATGGG-3'