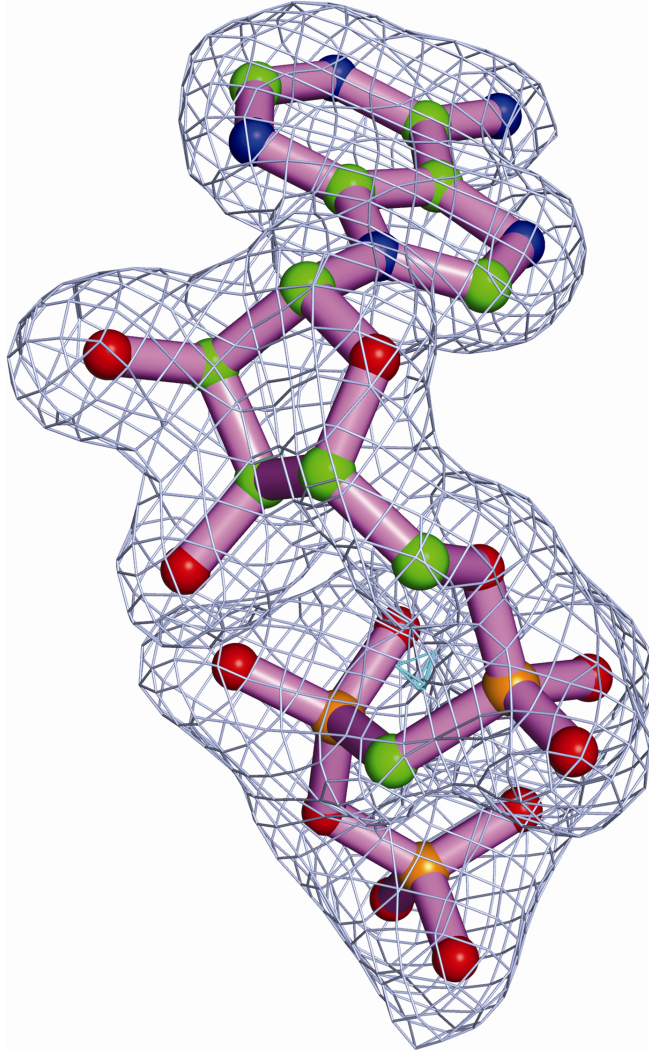


Supplementary material

AMP-CPP



(a)

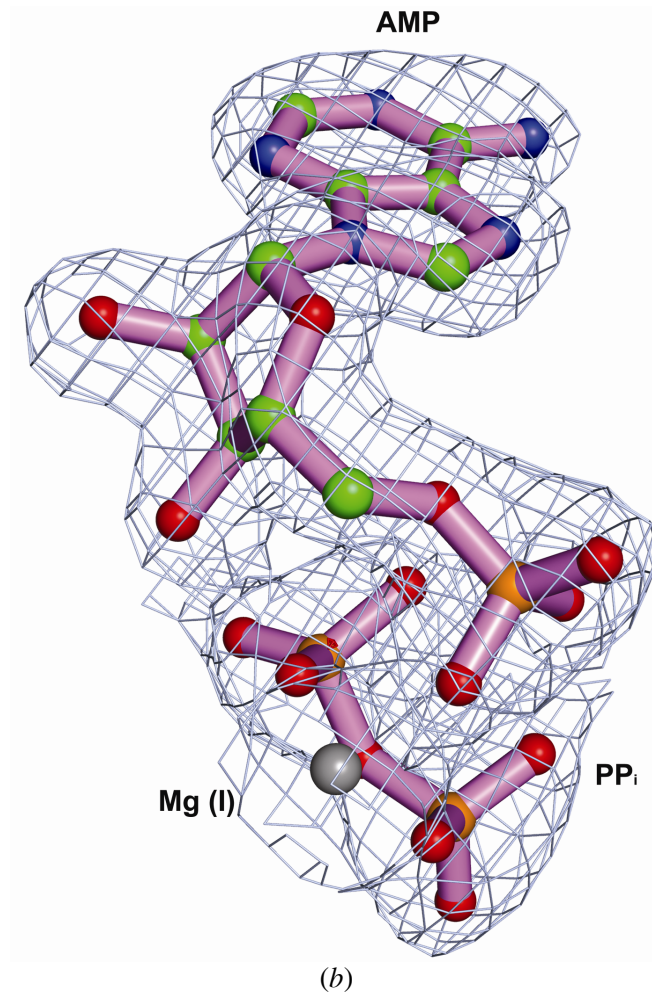


Figure 11. (a)  $2F_o-F_c$  electron density at  $1\sigma$  (gray),  $F_o-F_c$  at  $3\sigma$  (red) and  $F_o-F_c$  at  $3\sigma$  (cyan) of AMP-CPP ligand *banNADS* complex form III. (b)  $2F_o-F_c$  electron density at  $1\sigma$  (blue-gray),  $F_o-F_c$  at  $3\sigma$  (red) and  $F_o-F_c$  at  $3\sigma$  (cyan) of AMP and  $PP_i$  ligands and  $Mg^{2+}$ -I ion *banNADS* complex form II.  $Mg^{2+}$ -II not shown.

Table 2. NAD<sup>+</sup> Synthetase ATP Binding Site Comparison<sup>1</sup>

PDB Code	Species	Ligands	Mg <sup>2+</sup> (I, II, or III)	G45	S47	S52	Q50	R79	L80	Q85	T158	K187	T209
Form II	<i>ban</i>	AMP + PP <sub>i</sub>	I, II						All interactions present				
Form III	<i>ban</i>	AMP-CPP	II						All interactions present				
1NSY	<i>bsu</i>	ATP, AMP + PP <sub>i</sub>	I						All interactions present				
2NSY	<i>bsu</i>	NAD-adenylate	I, II					Not applicable					
1FYD	<i>bsu</i>	AMP + PP <sub>i</sub>	II					All interactions present					
1EE1	<i>bsu</i>	NaAD, ATP	II					All interactions present					
1IH8	<i>bsu</i>	AMP-CPP	II, III					All interactions present					
1WXE	<i>eco</i>	AMP	I	Y G46	N/A	N/A	N/A	N	Y L83	N	Y T160	N/A	No P2 Loop
1WXI	<i>eco</i>	AMP + PP <sub>i</sub>	I, II	Y G46	Y S48	Y S53	N	Y R82	Y L83	Y Q88	Y T160	Y K189	No P2 Loop
1WXG	<i>eco</i>	NaAD	I	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	No P2 Loop
1XNG	<i>hpy</i>	NaAD, ATP	II	Y G31	Y S33	Y S38	Y L36	N (L57)	Y M58	N (M64)	Y T132	Y K161	Y S183

<sup>1</sup>Y: Interaction is present between residue and ligand, N: No interaction is seen with homologous residue, N/A: Interaction is not applicable; the relevant ligand atoms (e.g., pyrophosphate groups in 1WXE and entire ATP ligand in 1WXG) are not present in the structure, therefore the respective interaction with the protein cannot exist.

Table 3. Root Mean Squared Deviation Between C $\alpha$  Atoms<sup>1</sup> (Å)

	Complex <i>ban</i> NADS(III)	<i>bsu</i> NADS 1IH8.pdb	<i>eco</i> NADS 1WXE.pdb	<i>hpy</i> NADS 1XNG.pdb	Apo <i>ban</i> NADS (I)
Complex <i>ban</i> NADS(III)	0	0.42	0.97	1.72	1.18
<i>bsu</i> NADS 1IH8.pdb	0.42	0	0.88	1.69	1.22
<i>eco</i> NADS 1WXE.pdb	0.97	0.88	0	1.5	1.38
<i>hpy</i> NADS 1XNG.pdb	1.72	1.69	1.5	0	2.35
Apo <i>ban</i> NADS (I)	1.18	1.22	1.38	2.35	0

<sup>1</sup>RMS deviations were calculated using a C $\alpha$  atom least squares fit in the software O.