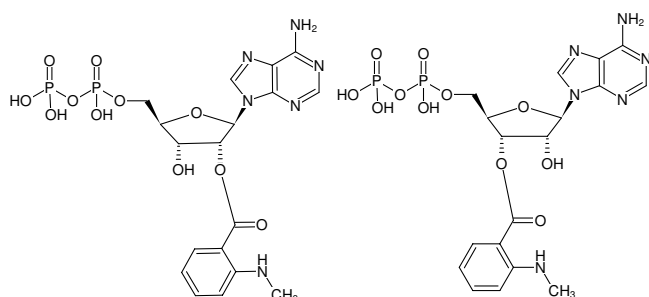


**Mant-ADP**

2'/3'-O-(N-Methyl-anthraniloyl)-adenosine-5'-diphosphate, Triethylammonium salt

Cat. No.	Amount
NU-201S	150 µl (10 mM)
NU-201L	5 x 150 µl (10 mM)



Structural formula of Mant-ADP

For research use only!**Shipping:** shipped on gel packs**Storage Conditions:** store at -20 °C

Short term exposure (up to 1 week cumulative) to ambient temperature possible.

Shelf Life: 12 months after date of delivery**Molecular Formula:** C₁₈H₂₂N₆O₁₁P₂ (free acid)**Molecular Weight:** 560.35 g/mol (free acid)**Exact Mass:** 560.08 g/mol (free acid)**CAS#:** 151481-85-5**Purity:** ≥ 95 % (HPLC)**Form:** solution in water**Color:** colorless to slightly yellow**Concentration:** 10 mM - 11 mM**pH:** 7.5 ± 0.5**Spectroscopic Properties:** λ_{max} 255/355 nm, ε 23.3/5.8 L mmol⁻¹ cm⁻¹ (Tris-HCl pH 7.5), λ_{exc} 355 nm, λ_{em} 448 nm**Applications:**MYOSIN-ATPase cycle^[1]SecA cycle^[2]Dissociation kinetic protein kinase A^[3]FRET: kinesin^[4], myosin^[5, 1]Conformational dynamic: DnaC-protein^[6]**Specific Ligands:**Kinesin head domains^[4]Myosin^[5]**Selected References:**[1] Robertson *et al.* (2005) Structural rearrangements in the active site of smooth muscle myosin. *Biophysical J.* **89**:1882.[2] Fak *et al.* (2004) Nucleotide exchange from the high-affinity ATP-binding site in SecA is the rate-limiting step in the ATPase cycle of the soluble enzyme and occurs through a specialized conformational state. *Biochemistry* **43**:7307.[3] Ni *et al.* (2000) Insights into nucleotide binding in protein kinase A using fluorescent adenosine derivatives. *Protein Science* **9**:1818.[4] Hackney *et al.* (2009) Half-site inhibition of dimeric kinesin head domains by monomeric tail domains. *Biochemistry* **48**:3448.[5] Sun *et al.* (2006) Dynamics of the upper 50-kDa domain of myosin V examined with fluorescence resonance energy transfer. *J. Biol. Chem.* **281**:5711.[6] Galletto *et al.* (2005) The nucleotide-binding site of the Escherichia coli DnaC protein: Molecular topography of DnaC protein-nucleotide cofactor complex. *Cell Biochem. and Biophys.* **43**:331.Pinto *et al.* (2011) Structure-activity relationships for the interactions of 2'- and 3'- (O)- (N-methyl)anthraniloyl-substituted purine and pyrimidine nucleotides with mammalian adenylyl cyclases. *Molecular Pharmacology* **82** (4):358.Chen *et al.* (2009) ADP but Not Pi Dissociation Contributes to Rate Limitation for Escherichia coli Rho*. *J. Biol. Chem.* **284** (49):33773.Taha *et al.* (2009) Molecular Analysis of the Interaction of Anthrax Adenylyl Cyclase Toxin, Edema Factor, with 2' (3')-O- (N-(methyl)anthraniloyl)-Substituted Purine and Pyrimidine Nucleotides. *Molecular Pharmacology* **75** (3):693.Del Toro Duany *et al.* (2008) The reverse gyrase helicase-like domain is a nucleotide-dependent switch that is attenuated by the topoisomerase domain. *Nucleic Acids Research* **36** (18):5882.Kainov *et al.* (2008) Structural Basis of Mechanochemical Coupling in a

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