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ProductInformation

PIPES SigmaUltra

Product Number **P8203**
Store at Room Temperature

Product Description

Molecular formula: $C_8H_{18}N_2O_6S_2$

Molecular weight: 302.4

CAS Number: 5625-37-6

pK_a : 6.2 (25 °C)

Synonyms: piperazine-N,N'-bis(2-ethanesulfonic acid), piperazine-1,4-bis(2-ethanesulfonic acid), 1,4-piperazinediethanesulfonic acid

Trace elemental analyses have been performed on the SigmaUltra PIPES free acid. The Certificate of Analysis provides lot-specific results. SigmaUltra PIPES free acid is for applications which require tight control of elemental content.

PIPES is a zwitterionic buffer used in biochemistry and molecular biology research. It is one of the Good buffers developed in the 1960's to provide buffers in the pH range of 6.15 - 8.35 for wide applicability to biochemical studies. The pioneering publication by Good and co-workers describes the synthesis of PIPES and its physical properties.¹

Protocols have been reported on the use of PIPES for separation of glyoxylated RNA in agarose gels, nuclease S1 mapping of RNA, and in ribonuclease protection assay protocols.² PIPES has been used as a buffer in glutaraldehyde fixation of tissue samples.^{3,4}

PIPES has been utilized in protein crystallization.^{5,6} The use of PIPES in the reconstitution of dissociated tubulin β - and γ -subunits after their resolution on immunoabsorbent gels has been described.⁷ PIPES has been recommended for use in buffers for the *in vitro* study of caspases 3, 6, 7, and 8.⁸

A study that demonstrates the usefulness of PIPES as a non-metal ion complexing buffer in such applications as protein assays has been published.⁹ PIPES has been used in cell culture for such applications as the engineering of a thermostable mutant membrane protein in *Escherichia coli*.¹⁰

Precautions and Disclaimer

For Laboratory Use Only. Not for drug, household or other uses.

Preparation Instructions

This product is soluble in 1 M NaOH (151 mg/ml, 0.5 M).

References

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6. Moore, S. A., et al., The structure of truncated recombinant human bile salt-stimulated lipase reveals bile salt-independent conformational flexibility at the active-site loop and provides insights into heparin binding. *J. Mol. Biol.*, **312(3)**, 511-523 (2001).
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9. Yu, Q., et al., Avoiding interferences from Good's buffers: A contiguous series of noncomplexing tertiary amine buffers covering the entire range of pH 3-11. *Anal. Biochem.*, **253(1)**, 50-56 (1997).
10. Zhou, Y., and Bowie, J. U., Building a thermostable membrane protein. *J. Biol. Chem.*, **275(10)**, 6975-6979 (2000).

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