

## Data Sheet

### MMP2

Human, recombinant, C-terminal His-tag

Catalog #: 80213

Lot #: 130730      Conc.: 1.27 mg/ml

**Formulated in:** 40 mM Tris-HCl, pH 8.0, 110 mM NaCl, 2.2 mM KCl, 200 mM imidazole, and 20% glycerol.

**Stability:** >6 months at -80°C. Avoid freeze/thaw cycles.

**References:**

1. Van Dijk, M., *et al.*, *Front Genet.* 2012; **3**:22.
2. Klotzsche-von Ameln, A., *et al.*, *Cancer Biol Ther.* 2012 Feb 15; **13(4)**: 216 – 223.

**Description:** Human matrix metallopeptidase-2 (MMP2), also known as gelatinase A (GenBank Accession No. NM\_004530), a.a. 30 – 660 (end), with C-terminal His-tag, MW=72 kDa, expressed in an HEK293 cell expression system.

**Specific Activity:** 511 pmole/min/μg

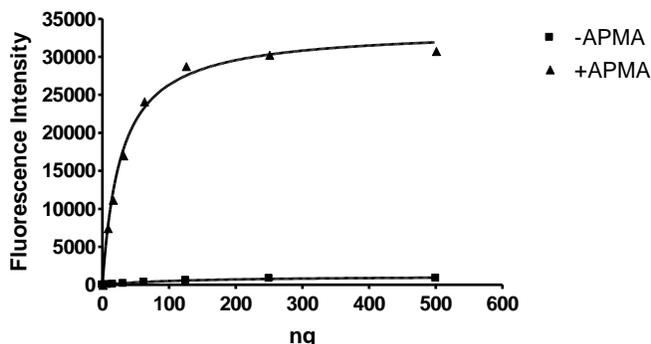
**Activation:** This is a proform enzyme and requires activation prior to testing activity. Dilute the enzyme to 100 ng/μl in a solution containing 50 mM HEPES, pH 7.4, 10 mM CaCl<sub>2</sub>, 0.05% Brij-35, and 1 mM APMA (amino-phenyl mercuric acetate). Incubate at 37°C for 2 hours.

**Assay conditions:** Reaction mixture with 10 μM 390 MMP substrate 1 (Anaspec). Incubate for 30 minutes at room temperature. Fluorescence intensity is measured at exc328/em393.

**Application:** Useful for the study of enzyme kinetics, screening inhibitors, and selectivity profiling.

### Quality Assurance

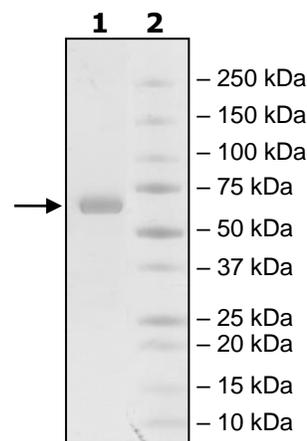
#### Specific Activity



#### 4-20% SDS-PAGE Coomassie staining

**Lane 1:**  
2.5 μg MMP2  
**Lane 2:**  
Protein Marker

**MW:** 72 kDa  
**Purity:** ≥90%



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6045 Mira Mesa Blvd, Suite 100  
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Tel: 1.858.202.1401  
Fax: 1.858.481.8694  
Email: [support@bpsbioscience.com](mailto:support@bpsbioscience.com)

**Sequence:**

APSPIIKFPGDVAPKTDKELAVQYLNTFYGCPKESC�LFVLKDTLKKMQKFFGLPQTG  
DLNQNTIETMRKPRCGNPDVANYNFFPRKPKWDKNQITYRIIGYTPDLDPETVDDAFA  
RAFQVWSDVTPLRFSRIHDGEADIMINFRWEHGDGYPFDGKDGLLAHAFAPGTGVG  
GDSHFDDDELWTLGEGQVVRVKYGNADGEYCKFPFLFNGKEYNSCTDTGRSDGFL  
WCSTTYNFEKDGKYGFCPHEALFTMGGNAEGQPCKFPFRFQGTSYDSCTTEGRTDG  
YRWCGTTEDYDRDKKYGFCPETAMSTVGGNSEGAPCVFPFTFLGNKYESCTSAGRS  
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FFFKDRFIWRTVTPRDKPMGPLLVATFWPELPEKIDAVYEAPQEEKAVFFAGNEYWIY  
SASTLERGYPKPLTSLGLPPDVQRVDAAFNWSKNKKTIFAGDKFWRYNEVKKKMD  
PGFPKLIADAWNAIPDNLDVVDLQGGGHSYFFKGAYYKLENQSLKSVKFGSIKSD  
WLGCHHHHHHHHHH

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