

Data Sheet

MMP9 (Q279R)

Human, recombinant, C-terminal His-tag
 Catalog #: 80215
 Lot #: 130730 Conc.: 1.26 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. Wenham, R.M., *et al.*, *J. Soc. Gynecol. Investig.* 2003 Sep;**10(6)**:381-7.
2. Li, X., *et al.*, *J. Cancer Res. Clin. Oncol.* 2013 Sep;**139(9)**:1433-47.

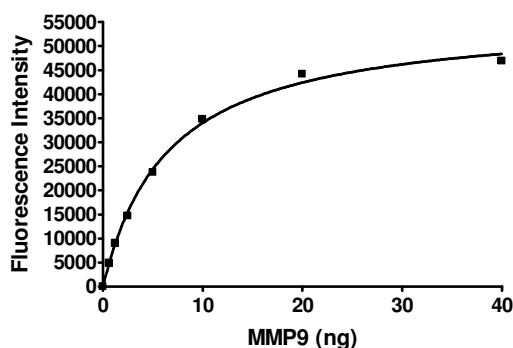
Description: Human matrix metalloproteinase-9 (MMP9), also known as gelatinase B, MANDP2, CLG4B, Macrophage gelatinase, GELB and EC 3.4.24, with Gln to Arg mutation on a.a. 279, GenBank Accession No. NM_004994), a.a. 20-707 (end) with C-terminal His-tag, MW=77.8 kDa, expressed in an HEK293 cell expression system.

Specific Activity: 2500 pmole/min/μg
Activation: This is a proform enzyme and requires activation prior to testing activity. Dilute the enzyme to 100 ng/ml in a solution containing 50 mM HEPES, pH 7.4, 10 mM CaCl₂, 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

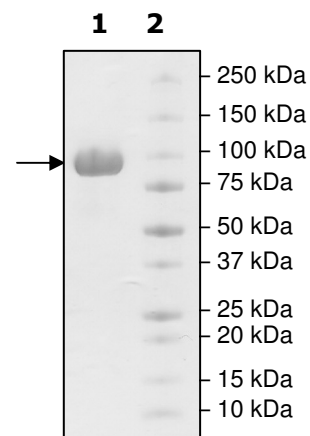


4-20% SDS-PAGE Coomassie staining

Lane 1:
6.3 μg MMP9

Lane 2:
Protein Marker

MW: 77.8 kDa
Purity: ≥90%



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Sequence:

APRQRQSTLVLFPGDLRTNLTDRQLAEEYLYRYGYTRVAEMRGESKSLGPALLLLQK
QLSLPETGELDSATLKAMRTPRCGVPLGRFQTFEGDLKWHHHNITYWIQNYSEDLP
RAVIDDAFARAFALWSAVTPLTFTRVYSRDADIVIQFGVAEHGDGYPFDGKDGLLAHA
FPPGPGIQGDAHFDDELWSLGKGVVVPTRFGNADGAACHFPFIFEGRSYSACTTDG
RSDGLPWCSTTANYDTDDRFGFCPSERLYT**R**DGNADGKPCQFPFIFQGQSYSACTTD
GRSDGYRWCATTANYDRDKLFGFCPTRADSTVMGGNSAGELCVFPFTFLGKEYSTC
TSEGRGDGRLWCATTSNFDSDKKWGFCPDQGYSLFLVAAHEFGHALGLDHSSVPEA
LMYPMYRFTEGPPLHKDDVNGIRHLYGPRPEPEPRPPTTTTPQPTAPPTVCPTGPPTV
HPSERPTAGPTGPPSAGPTGPPTAGPSTATTVPLSPVDDACNVNIFDAIAEIGNQLYLF
KDGKYWRFSEGRGSRPQGPFLIADKWPALPRKLDVFEERLSKLLFFFSGRQVWVY
TGASVLGPRRLDKLGLGADVAQVTGALRSGRGKMLLFSGRRLWRFDVKAQMVDPR
SASEVDRMFPGVPLDTHDVFQYREKAYFCQDRFYWRVSSRSELNQVDQVGYVTYDIL
QCPED**HHHHHHHHHH**

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