



arigoQIK™ Human MMP9 ELISA Development Kit

ARG83526 arigoQIK™ Human MMP9 ELISA Development Kit is designed for the development of sandwich ELISA to measure Matrix Metalloproteinase 9 in serum, plasma, cell culture supernatants.

Catalog number: ARG83526

Package: 1 kit (5 plates)
(15 plates)

For research use only. Not for use in diagnostic procedures.

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INTRODUCTION

Proteins of the matrix metalloproteinase (MMP) family are involved in the breakdown of extracellular matrix in normal physiological processes, such as embryonic development, reproduction, and tissue remodeling, as well as in disease processes, such as arthritis and metastasis. Most MMP's are secreted as inactive proproteins which are activated when cleaved by extracellular proteinases. The enzyme encoded by this gene degrades type IV and V collagens. Studies in rhesus monkeys suggest that the enzyme is involved in IL-8-induced mobilization of hematopoietic progenitor cells from bone marrow, and murine studies suggest a role in tumor-associated tissue remodeling. [provided by RefSeq, Jul 2008]

PRINCIPLE OF THE ASSAY

This pair employs the quantitative sandwich enzyme immunoassay technique. Coating specific MMP9 antibody on a microtiter plate. Standards or samples are pipetted into the wells and any MMP9 present is bound by the immobilized antibody. After washing away any unbound substances, a MMP9 Detection is added to each well and incubate. Following a washing to remove unbound substances, HRP-Streptavidin Solution is added to each microplate well and incubated. After washing away any unbound antibody, a substrate solution (TMB) is added to the wells and color develops in proportion to the amount of GM-CSF bound in the initial step. The color development is stopped by the addition of acid and the intensity of the color is measured at a wavelength of 450nm. The concentration of MMP9 in the sample is then determined by comparing the O.D of samples to the standard curve.

MATERIALS PROVIDED & STORAGE INFORMATION

Upon received, store 100X Human GM-CSF Detection at $\leq -20^{\circ}\text{C}$.

Store other components at 2-8°C at all times. Use the kit before expiration date.

Component	Package (5 plates)	Package (15 plates)	Storage information
100X Matrix Metalloproteinase 9 Capture Antibody	1 vial	3 vial	4°C
Matrix Metalloproteinase 9 Standard	1 vial	3 vial	4°C
100X Matrix Metalloproteinase 9 Detection Antibody	1 vial	3 vial	$\leq -20^{\circ}\text{C}$
100X HRP-Streptavidin Solution	1 vial	3 vial	4°C

MATERIALS REQUIRED BUT NOT PROVIDED

- Phosphate buffered saline (PBS)
- Wash buffer
- Antibody Diluent Buffer, Standard / Sample Diluent Buffer
- Blocking Buffer
- Substrate Solution, Stop Solution
- Deionized or distilled water
- 96-well plate
- Pipettes and pipette tips
- Multichannel micropipette reservoir
- Microplate reader capable of reading at 450 nm
- Microtiter plate washer (optional)
- For commercial reagents required for [arigoQIK™ ELISA Development Kit](#), please refer [ARG83524 Integral Reagent Kit \(ELISA Development Kit\)](#)

SAMPLE COLLECTION & STORAGE INFORMATION

The following recommendations are only guidelines and may be altered to optimize or complement the user's experimental design.

Cell Culture Supernatants - Remove particulates by centrifugation for 10 min at 1500 x g at 4°C and aliquot & store samples at -20°C up to 1 month or -80°C up to 6 months. Avoid repeated freeze-thaw cycles.

Serum- Use a serum separator tube (SST) and allow samples to clot for 30 minutes before centrifugation for 15 minutes at 1000 x g. Collect serum and assay immediately or aliquot & store samples at -20°C up to 1 month or -80°C up to 6 months. Avoid repeated freeze-thaw cycles.

Plasma - Collect plasma using EDTA or heparin as an anticoagulant. Centrifuge for 15 minutes at 1000 x g. within 30 minutes of collection. Collect the supernatants and assay immediately or aliquot and store samples at -20°C up to 1 month or -80°C up to 6 months. Avoid repeated freeze-thaw cycles.

Note:

- a) Do not use haemolytic, icteric or lipaemic specimens.
- b) Samples containing sodium azide should not be used in the assay.
- c) Avoid disturbing the white buffy layer when collection serum / plasma sample.

REAGENT PREPARATION

- **Phosphate buffered saline (PBS):** Prepared with 137 mM NaCl, 2.7 mM KCl, 8.1 mM Na₂HPO₄, and 1.5 mM KH₂PO₄. The solution is adjusted to a pH range of 7.2 to 7.4 and is filtered using a 0.2 µm filter.
- **10X Wash Buffer:** Add Tween-20 to the previously prepared PBS to achieve a final concentration of 0.5%. The solution is adjusted to a pH range of 7.2 to 7.4 and is filtered using a 0.2 µm filter.
Dilute 10X Wash Buffer with distilled water to yield 1X Wash Buffer. The diluted 1X Wash Buffer is stable for 4 weeks at 2°C to 8°C.
- **Standard / Sample Diluent Buffer:** Add BSA and Tween-20 to the previously prepared PBS to achieve a final concentration of 1% BSA and 0.05% Tween-20. The solution is adjusted to a pH range of 7.2 to 7.4 and is filtered using a 0.2 µm filter.
- **Antibody Diluent Buffer:** Add BSA and Tween-20 to the previously prepared PBS to achieve a final concentration of 1% BSA and 0.1% Tween-20. The solution is adjusted to a pH range of 7.2 to 7.4 and is filtered using a 0.2 µm filter.
- **Blocking Buffer:** Add BSA and Tween-20 to the previously prepared PBS to achieve a final concentration of 1% BSA and 0.05% Tween-20. The solution is adjusted to a pH range of 7.2 to 7.4 and is filtered using a 0.2 µm filter.

- **1X Matrix Metallopeptidase 9 Capture:** It is recommended to prepare this reagent immediately prior to use and use it within 15 min after preparation. Dilute 100X Matrix Metallopeptidase 9 Capture with prepared **PBS** previously, to yield 1X Matrix Metallopeptidase 9 Capture. The diluted 1X Matrix Metallopeptidase 9 Capture is stable for 8 weeks at 2-8°C. For long-term storage, aliquot and store at -20°C to -70 °C.
- **1X Matrix Metallopeptidase 9 Detection:** It is recommended to prepare this reagent immediately prior to use and use it within 15 min after preparation. Dilute 100X Matrix Metallopeptidase 9 Detection with prepare **Antibody Diluent Buffer** previously, to yield 1X Matrix Metallopeptidase 9 Detection. The diluted 1X Matrix Metallopeptidase 9 Detection is stable for 8 weeks at 2-8°C. For long-term storage, aliquot and store at -20°C to -70 °C.
- **1X HRP-Streptavidin Solution:** It is recommended to prepare this reagent immediately prior to use and use it within 15 min after preparation. Dilute 100X HRP-Streptavidin Solution with prepare **Antibody Diluent Buffer** previously, to yield 1X HRP-Streptavidin Solution. The diluted 1X HRP-Streptavidin Solution is stable for 4 weeks at 2-8°C. Do NOT freeze 1X HRP-Streptavidin Solution.
- **Sample:** If the initial assay found samples contain proteins higher than the highest standard, the samples can be diluted with Standard / Sample Diluent Buffer and then re-assay the samples.

Standard: Centrifuge the un-reconstituted standard at 6000 x g for 1 minute to bring down the material prior to open the vial. Reconstituted Standard as label on the Standard vial. The reconstituted Standard stock concentration would be 20000 pg/ml. Vortex for few seconds (Do not induce foaming) and allow it to sit for 15 minutes as stock. The Standard stock is stable for 4 weeks at 2-8°C. For long-term storage, aliquot and store at -20°C to -70 °C.

- Make sure the standard is dissolved completely before making serial dilutions. The **Standard / Sample Diluent Buffer** serves as zero standard (0 pg/ml), and the rest of the standard serial dilution can be diluted with **Standard / Sample Diluent Buffer**. Diluted the standard as below:

Standard tube	MMP9 (pg/mL)	Standard / Sample Diluent Buffer (µL)	Standard stock (µL)
Pre1	2000	900	100 (<u>20000 pg/ml Standard Stock</u>)
S1	1000	500	500 (<u>2000 pg/ml, Pre1</u>)
S2	500	500	500 of S1
S3	250	500	500 of S2
S4	125	500	500 of S3
S5	63	500	500 of S4
S6	31.25	500	500 of S5
S7	15.63	500	500 of S6
S0	0	500	0

ASSAY PROCEDURE

All materials should be equilibrated to room temperature before use.

1. Add **100 µL** of **1X Matrix Metallopeptidase 9 Capture** into respective well.
2. Cover the plate and incubate for **16-20 hours** at 4°C.
3. Remove the cover and discard the liquid in the wells.
4. Add **250 µL** of **Blocking Buffer** to each well.
5. Cover the plate and incubate for **2 hours** at room temperature.
6. Remove the cover and discard the liquid in the wells.
7. Add **100 µL** of **samples** and **each diluted Standard** into respective well.
8. Add **50 µL** of **1X Matrix Metallopeptidase 9 Detection** into each well.
9. Cover the plate and incubate for **1 hour** at room temperature on a microplate shaker set at 500 rpm.
10. Aspirate each well and wash, repeating the process 4 time for a **total 5 washes**. Wash by filling each well with **1X Wash Buffer (300 µL)** using a squirt bottle, manifold dispenser, or auto-washer. Complete removal of liquid at each is essential to good performance. After the last wash, remove any remaining Wash Buffer by aspirating, decanting or blotting against clean paper towels.
11. Add **100 µL** of **1X HRP-Streptavidin Solution** into each well.
12. Cover the plate and incubate for **30 min** at room temperature in the dark on a microplate shaker set at 500 rpm.
13. Aspirate each well and **wash plate as step 10**.
14. Add **100 µL** of **TMB Substrate** in each well.
15. Incubate for **5-30 mins** at room temperature in the dark.
16. Add **100 µL** of **Stop Solution** to each well to stop the reaction.

17. Read the absorbance with a plate reader at **O.D. 450 nm** within 10 minutes after adding the stop solution.

CALCULATION OF RESULTS

1. Calculate the average absorbance values for each set of standards, control and samples.
2. Using log-log, semi-log or linear graph paper, construct a standard curve by plotting the mean absorbance obtained from each standard against its concentration with absorbance value on the vertical (Y) axis and concentration on the horizontal (X) axis.
3. Using the mean absorbance value for each sample determine the corresponding concentration from the standard curve.
4. Automated method: The results in the IFU have been calculated automatically using a 4 PL (4 Parameter Logistics) curve fit. 4 Parameter Logistics is the preferred method. Other data reduction functions may give slightly different results.
5. arigo provides GainData®, an in-house development ELISA data calculator, for ELISA data result analysis. Please refer our GainData® website for details. (<https://www.arigobio.com/elisa-analysis>)
6. If the samples have been diluted, the concentration read from the standard curve must be further converted by the appropriate dilution factor according to the sample preparation procedure as described above.