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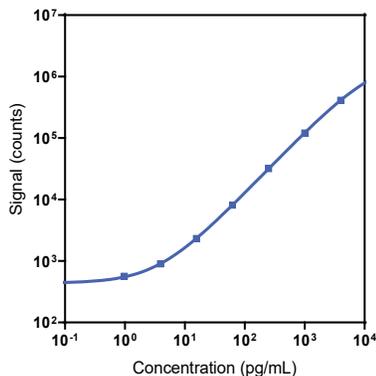
Company Address

Meso Scale Discovery, a
 division of Meso Scale
 Diagnostics
 , LLC.
 1601 Research Boulevard
 Rockville, MD 20850-3173 USA

| Product Options | Catalog Number | Description |
|---------------------|--|---|
| Multiplex | K151AEM, K251AEM | U-PLEX Immuno-Oncology Group 1 (human) |
| Singleplex | K151AGYK-1/-2/-4 | U-PLEX Human MIG Assay with SECTOR™ plates |
| | K151AGYK-21/-22/-24 | U-PLEX Human MIG Assay with QuickPlex Ultra™ plates |
| | K251AGYK-2/-4 | U-PLEX Human MIG Assay with 384-well plates |
| Antibody Set | B21AGY-2/-3 | U-PLEX Human MIG Antibody Set |
| Protocol | U-PLEX Product Inserts are available at www.mesoscale.com . | |

The U-PLEX® platform was designed to provide ultimate flexibility for the detection of biomarkers in a wide variety of sample types. This datasheet provides the representative performance of the U-PLEX Human MIG Assay tested on U-PLEX plates run as a multiplex. The data do not represent the product specifications. Under your experimental conditions, the assay may perform differently from the representative data. U-PLEX assays are offered in either singleplex or multiplex; both are available on 96- or 384-well plates. See a U-PLEX product insert for instrument compatibility.

Representative Calibration Curve and Sensitivity



| Assay | Median LLOD (pg/mL) | LLOD Range (pg/mL) |
|-------|---------------------|--------------------|
| MIG | 0.73 | 0.41–1.06 |

The Calibrator curve was fitted with a 4-parameter logistic model with a $1/Y^2$ weighting. The lower limit of detection (LLOD) is a calculated concentration corresponding to 2.5 standard deviations above the background (zero Calibrator).

Precision

| Control | Average Conc. (pg/mL) | Average Intra-run Conc. (%CV) | Inter-run Conc. (%CV) |
|---------|-----------------------|-------------------------------|-----------------------|
| High | 977 | 3.7 | 7.7 |
| Mid | 200 | 2.9 | 11.4 |
| Low | 48 | 2.2 | 15.0 |

Controls were made by spiking Calibrator into assay diluent at 3 levels within the quantitative range of the assay. Average intra-run concentration %CV is the average %CV of the control replicates within an individual run. Inter-run concentration %CV is the variability of controls across multiple runs.

For Research Use Only.
 Not for use in diagnostic
 procedures.

MSD® U-PLEX Human MIG

Tested Samples

| Sample Type | Serum (N = 9) | EDTA Plasma (N = 9) | Citrate Plasma (N = 9) | Normal Lysate (N = 5) | Tumor Lysate (N = 5) |
|----------------|------------------|------------------------|---------------------------|--------------------------|-------------------------|
| Median (pg/mL) | 112 | 109 | 89 | 22 | 240 |
| Range (pg/mL) | 52–178 | 51–177 | 43–147 | 6.7–100 | 18–1,700 |
| % Detected | 100 | 100 | 100 | 40 | 80 |

Normal serum and plasma samples were diluted 4-fold prior to the assay. Lysates were tested at a protein concentration of 0.5 mg/mL.

Dilution Linearity

| Serum | | | EDTA Plasma | | |
|---------------|--------------------|------------------|---------------|--------------------|------------------|
| Fold Dilution | Average % Recovery | % Recovery Range | Fold Dilution | Average % Recovery | % Recovery Range |
| 2 | 81 | 63–94 | 2 | 98 | 86–106 |
| 8 | 141 | 129–153 | 8 | 153 | 136–172 |
| 16 | 171 | 156–183 | 16 | 211 | 178–244 |

Samples were spiked with calibrator and serially diluted. Percent recovery at each dilution was normalized to the dilution-adjusted 4 (or 100)-fold concentration. Samples may benefit from additional dilution with assay diluent to reduce matrix effects.

$$\% \text{ Recovery} = (\text{measured concentration} / \text{expected concentration}) \times 100$$

Spike Recovery

| Spike Level | Serum | | EDTA Plasma | |
|-------------|--------------------|------------------|--------------------|------------------|
| | Average % Recovery | % Recovery Range | Average % Recovery | % Recovery Range |
| High | 44 | 35–52 | 31 | 24–40 |
| Mid | 48 | 39–55 | 34 | 25–40 |
| Low | 52 | 41–64 | 40 | 32–48 |

Samples were spiked with calibrator at three levels within the range of the assay.

$$\% \text{ Recovery} = (\text{measured concentration} / \text{expected concentration}) \times 100$$

Specificity

To assess specificity, the MIG Antibody Set was tested individually against a larger panel of analytes for nonspecific binding: APRIL/TNFSF13, BAFF-R/TNFRSF13C, BCMA/TNFRSF17, CD20, CD27, CD276/B7-H3, CD28, CD40L (soluble), CTACK, CTLA-4, ENA-78, Eotaxin, Eotaxin-2, Eotaxin-3, EPO, E-Selectin, FGF (basic), FLT3L, Fractalkine, G-CSF, Galectin-9, GITR/TNFRSF18, GITRL/TNFSF18, GM-CSF, gp130 (soluble), Granzyme A, Granzyme B, GRO- α , HAVCR2/TIM-3, HVEM/TNFRSF14, I-309, ICOS, ICOSL/B7-H2, IFN- α 2a, IFN- β , IFN- γ , IL-1 α , IL-1 β , IL-1RA, IL-10, IL-12/IL-23p40, IL-12p70, IL-13, IL-15, IL-16, IL-17A, IL-17A/F, IL-17C, IL-17D, IL-17E/IL 25, IL-17F, IL-18, IL-2, IL-21, IL-22, IL-23, IL-27, IL-29/IFN- λ 1, IL-2R α , IL-3, IL-31, IL-33, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IP-10, I-TAC, LAG-3, LIGHT/TNFSF14, MCP-1, MCP-2, MCP-4, M-CSF, MDC, MIF, MIG, MIP-1 α , MIP-5, MMP-1, MMP-2, MMP-7, MMP-9, Nectin-4, OX40/TNFRSF4, PD1, PD-L1, PD-L2, Pentraxin 3, Perforin, PIGF, P-Selectin, RAGE (soluble), RANKL/TNFSF11, RANTES, S100A12, TARC, Tie-2, TIGIT, TLR-1, TNF-RI, TNF-RII, TNF- α , TNF- β , TPO, TRAIL, TSLP, VEGF-A, VEGF-D, VEGFR-1/Fit-1 and YKL-40. Nonspecific binding was less than 2.0%.

$$\% \text{ Nonspecificity} = (\text{nonspecific signal} / \text{specific signal}) \times 100$$

Diluent Compatibility

Diluents 58 and 3 are provided with this assay. MSD offers a range of assay and antibody diluents for separate purchase. Depending on your assay needs, other diluents may be tested.

Assay Components

Calibrator: MIG is included in Calibrator 27. The human MIG Calibrator is a full-length recombinant protein.

Antibodies: The U-PLEX Human MIG Assay uses a mouse monoclonal antibody for capture and a mouse monoclonal antibody for detection.

Assay generation: A

Note: This datasheet contains representative assay performance data. In custom multiplex formats, the assay may perform differently from the representative data shown.

