Human GIP (total)

	Product Options	Catalog Number	Description				
9M®	Multiplex	K151ACM, K251ACM	U-PLEX Metabolic Group 1 (human)				
		K1515SK-1/-2/-4	U-PLEX Human GIP (total) Assay with SECTOR™ plates				
	Singleplex	K1515SK-21/-22/-24	U-PLEX Human GIP (total) Assay with QuickPlex Ultra [™] plates				
5		K2515SK-2/-4	U-PLEX Human GIP (total) Assay with 384-well plates				
D	Antibody Set	B215S-2/-3	U-PLEX Human GIP (total) Antibody Set				
y	Protocol	U-PLEX Product Inserts are available at <u>www.mesoscale.com</u>					

The MESO SCALE DISCOVERY® U-PLEX platform was designed to provide ultimate flexibility for detection of biomarkers in a wide variety of sample

types. This datasheet provides the representative performance of the U-PLEX® Human GIP (inactive) Assay tested on U-PLEX 96-well SECTOR

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.

Scientific Support Phone: 1-240-314-2798

www.mesoscale.cor

Ordering Information MSD Customer Service Phone: 1-240-314-2795 Fax: 1-301-990-2776 Email: CustomerService@ mesoscale.com

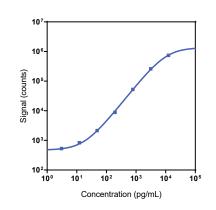
Email: ScientificSupport@ mesoscale.com

Company Address

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

Representative Calibration Curve and Sensitivity

See a U-PLEX product insert for instrument compatibility.



Assay	Median LLOD (pg/mL)	LLOD Range (pg/mL)		
GIP (total)	3.7	3.2-3.8		

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 2.5X the standard deviations above the background (zero Calibrator).

Precision

Control	Average Conc. (pg/mL)	Average Intra-run Conc. (%CV)	Inter-run Conc. (%CV)		
High	3,370	8.3	107		
Mid	622	4.0	13.7		
Low	158	11.1	16.9		

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 GIP (total)

Tested Samples

Sample Type	Serum (N=12)	EDTA Plasma (N=12)	P800 Plasma (N=8)		
Median (pg/mL)	16	14	93		
Range (pg/mL)	ND-27	8.9-218	42-260		
% Detected	83	100	100		

Normal serum, EDTA plasma, and P800 plasma samples were diluted 4-fold prior to the assay. ND = non-detectable (<LLOD)

Dilution Linearity

Serum			EDTA Plasma			P800 Plasma			Cell Culture Media		
Fold Dilution			Fold Dilution	Average % Recovery	% Recovery Range	Fold Dilution	Average % Recovery	% Recovery Range	Fold Dilution	Average % Recovery	% Recovery Range
2	82	56-107	2	90	72-136	2	83	64-106	2	97	74-123
8	111	106-120	8	115	102-128	8	112	96-126	8	115	96-169
16	134	107-183	16	130	107-149	16	125	103-149	16	120	105-167

Normal human serum, EDTA plasma, P800 plasma, and cell culture media were spiked with Calibrator and tested at different dilutions. Percent recovery at each dilution level was normalized to the dilution-adjusted, 4-fold concentration. Samples may benefit from additional dilution with assay diluent to reduce matrix effects.

% Recovery = (measured concentration / expected concentration) x 100

Spike Recovery

	Sei	Serum		EDTA Plasma		P800 Plasma		Cell Culture Media	
Spike Leve	Average % Recovery	% Recovery Range							
High	79	68-88	95	91-101	71	62-85	93	74-113	
Mid	78	62-82	92	84-103	72	61-83	95	84-102	
Low	76	62-83	91	81-102	74	58-87	91	82-101	

Normal serum, EDTA plasma, P800 plasma, and cell culture media were spiked with Calibrator at 3 levels. Spiked samples were diluted 4-fold to determine the expected concentration of the analyte. Samples may benefit from additional dilution with assay diluent to reduce matrix effects.

% Recovery = (measured concentration / expected concentration) x 100

Specificity

To assess specificity, the GIP (total) Antibody Set was tested individually against a larger panel of analytes for nonspecific binding (BAFF, BDNF, C-Peptide, CTACK, Desghrelin, ENA-78, Eotaxin, Eotaxin-2, Eotaxin-3, EPO, FGF-21, FGF-23, FLT3L, Fractalkine, FSH, G-CSF, Ghrelin (Ser3-octanoylated), GIP (1–42), GIP (3-42), GLP-1 (7–36), GLP-1 (9–36), GM-CSF, GRO- α , I-309, IFN- α 2a, IFN- β , IFN- γ , IL-1 α , IL-1 β , IL-1RA, IL-2, IL-2R α , IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, 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-21, IL-22, IL-23, IL-27, IL-29/IFN- λ 1, IL-31, IL-33, Insulin, IP-10, I-TAC, Leptin, LH, MCP-1, MCP-2, MCP-4, M-CSF, MDC, MIF, MIP-1 α , MIP-1 β , MIP-5, PIGF, PP, Proinsulin, PYY (3-36), SDF-1 α , TNF- α , TNF- β , TPO, TRAIL, TSLP, VEGF-A, YKL-40, and β -NGF). Nonspecific binding was less than 2.0%.

% Nonspecificity = (nonspecific signal / specific signal) x 100

GIP (1-42; active) cross-reacts with the GIP (total) assay as expected. We do not recommend multiplexing the GIP (total) assay with the GIP (active) or GIP (inactive) assays on the same plate.

Diluent Compatibility

The data included in this document were collected with Assay Diluent 13 (supplemented with 1,000 KIU/mL Aprotinin [provided] and 100 μ M diprotin A [not provided]) and Antibody Diluent 11. MSD offers a range of assay and antibody diluents for separate purchase. Depending on your assay needs, other diluents may be tested. Diprotin A should be purchased separately.

Assay Components

Calibrator: GIP (3-42) is included in Calibrator 13. The human GIP (total) Calibrator is a synthetic peptide.

Antibodies: the U-PLEX® Human GIP (total) Assay uses a mouse monoclonal antibody for capture and a rabbit polyclonal 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.

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