

Introduction

Inflammation and disruptions in immune response are central mechanisms in the development and treatment of many diseases. Detecting and measuring key immune-related proteins offer crucial insights for identifying and screening biomarkers associated with disease progression or therapeutic responses. The NULISAseq Inflammation

Panel 250 measures the presence and relative quantitation of 250 cytokines, chemokines and immune related proteins simultaneously from less than 25µl sample input. The analytical performance of the product has been carefully validated and the results are presented below.

NULISA™ Technology

NULISAseq is a sandwich immunoassay in which 2 target specific antibodies, conjugated with unique oligonucleotide tags, bind and form a complex with the specific protein in solution. The resulting immunocomplex is purified in sequential capture and release steps to remove background and unbound antibodies. Successful formation of the immunocomplex brings the two oligonucleotide tags into proximity for a ligation reaction and amplification. The resulting unique oligonucleotide reporters containing both target and sample information are then pooled to a library for analysis on an NGS sequencer. The assay protocol

is fully automated on the ARGO HT System and data is analyzed using the NULISA Analysis Software. More details on the assay protocol can be found [here](#).



Data Normalization & Calculation of NULISA Protein Quantification (NPQ) Values

NULISA Protein Quantification (NPQ) units are log₂-scale values used to quantify relative protein abundances. NPQ is derived from the raw sequencing reads using the following normalization and transformation steps. First, to control for intra-plate well-to-well variation, the raw sequencing read count for each analyte for a given sample well is divided by that well's internal control (IC)

raw count. Second, to control for plate-to-plate variation, the IC-normalized values for each analyte are divided by the analyte-specific median IC-normalized counts from the 3 inter-plate controls (IPCs) on the plate. Data is then rescaled and log₂-transformed to obtain the data in NPQ, which are approximately normally distributed values amenable to downstream statistical analysis.

Sensitivity & Detectability

The limit of detection (LOD), or the lowest concentration of the analyte that can be distinguished from the background signal of the assay, is calculated for each target as the mean plus three standard deviations of the 4 negative control (NC) wells' normalized reads. These values are rescaled and log₂-transformed to obtain LOD in NPQ. A maximum of one outlier NC value may be omitted.

Validation data LOD median and interquartile ranges (IQR) summarize LODs generated across 15 runs (Table 3). Target detectability is the percentage of samples above LOD. Detectability was assessed in 50 healthy and 62 disease EDTA plasma samples. More than 99% of targets were detectable in at least 50% of samples (Table 3, Figure 1).

Inflammation Panel 250 Detectability: Healthy + Disease Plasma Samples

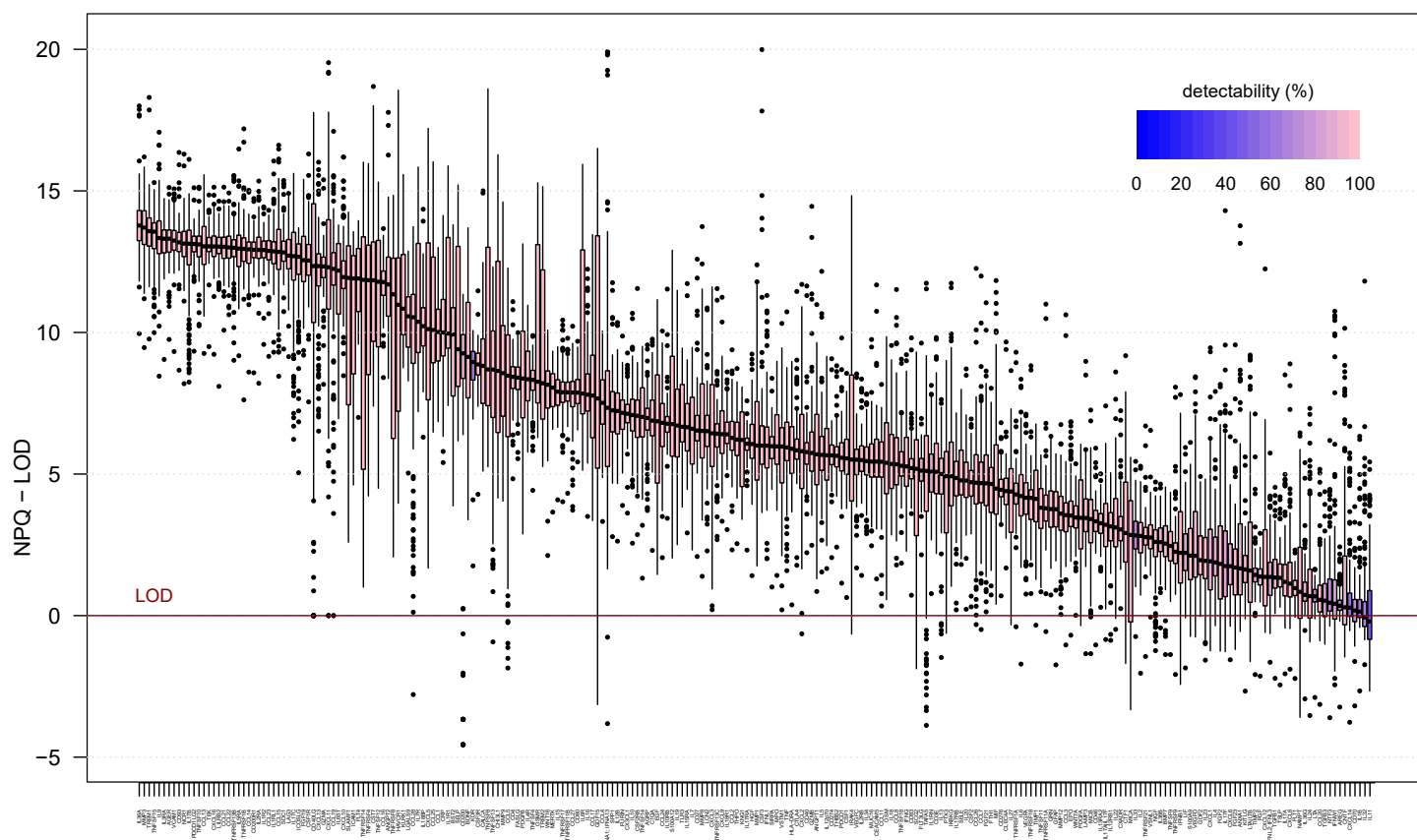


Figure 1. Detectability was assessed in 50 healthy and 62 disease EDTA plasma samples. More than 99% of targets were detectable in at least 50% of samples.

Dynamic Range

Dynamic range was determined using a set of 6 NULISaseq runs that included calibration standards comprising a mixture of recombinant antigens corresponding to each target in a dilution series extending to concentrations above and below each target's expected quantifiable range. For each target, a 4-parameter logistic regression (4PL) curve was fit to the calibration standards to form a standard curve which models the relationship between normalized counts and concentration. These curves were used to assess recovery of standards at various concentration levels. Precision was assessed using a precision profile model where intra-plate CV was modeled as a function of concentration.

The dynamic range for each target was defined as the largest concentration range for which the intra-plate CV is below 30% and the mean recovery error is within 30% of expected.

The log₁₀ range for each target is calculated as $\log_{10}(\text{range}) = \log_{10}(\text{ULoQ}) - \log_{10}(\text{LLoQ})$, where ULoQ and LLoQ represent the upper and lower limits of quantification, respectively.

Dynamic range was assessed for targets with commercially available recombinant antigens (Table 3).

Precision

Intra-assay precision, or repeatability, was measured to assess the variation in technical replicates within the same assay run; this is reported in Tables 1-3 as intra-plate coefficient of variation (CV). Inter-assay precision, or reproducibility, was measured to assess the variation in technical replicates across different assay runs or on different days; this is reported in Tables 1-3 as inter-plate CV. For each target, CV was determined using a variance component analysis model to assess the contribution of various factors to the total CV of the normalized reads. Six plasma samples with 3 technical replicates each were measured across a set of 10 runs which included 2 reagent lots and 2 instruments across 5 days. Variance component analysis models were fit for each sample and target and included the factors reagent lot, instrument, instrument bay, inter-plate, and intra-plate (Tables 1-3). To assess inter-site variability, the analysis was repeated with site included as an additional factor to account for runs performed at 2 external sites (Tables 1-2). For each target, the estimated CV for each component was averaged across the 6 samples. Values below LOD were excluded from CV calculations.

Table 1: Across-target Median Coefficients of Variation

CV component	Median CV (%), one site	Median CV (%), all sites
Intra-plate	7.15	7.17
Inter-plate	4.06	4.04
Bay	0.47	0.53
Instrument	0.62	0.47
Reagent Lot	1.88	1.72
Site	N/A	6.48
Total	9.98	12.62

Table 2: Percentage of Targets with CV Below 30%

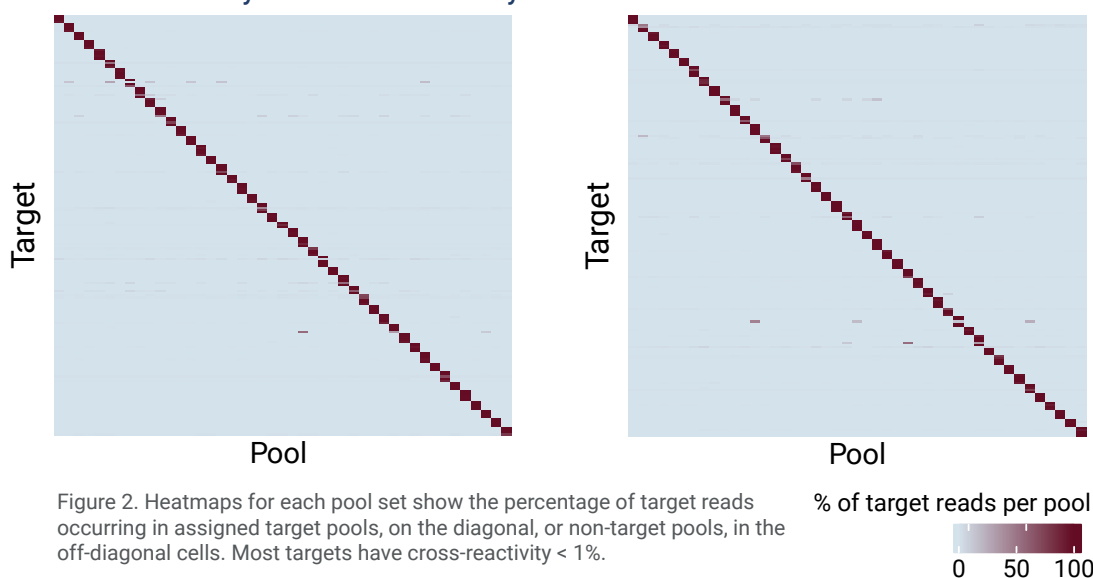
CV component	% targets < 30%, one site	% targets < 30%, all sites
Intra-plate	99.6	100.0
Inter-plate	99.2	99.2
Total	96.0	95.6

Cross-Reactivity

To assess cross-reactivity, targets were randomly assigned to two sets of 45 pools containing either four or five targets each, such that no two targets shared a pool for both sets. Counts were normalized using an internal control. Cross-reactivity for each target was quantified as (maximum non-target pool count – background)/(average target

pool counts – background) * 100, where the background was calculated as the median count across nontarget pools. Cross-reactivity was only assessed for targets with commercially available recombinant antigen (Table 3, Figure 2).

Analysis of Cross Reactivity Potential in Inflammation Panel 250



NULISAs^{seq}™ Inflammation Panel 250

Table 3: Performance Validation Data by Target

Target	UniProt ID	Protein Name	Detectability (%)		CV (%), one site			LOD (NPQ) Median (IQR)	LOD (pg/mL)	LLOQ (pg/mL)	ULOQ (pg/mL)	log10 Dynamic Range	Cross Reactivity
			Plasma		Plasma								
			Healthy n=50	Disease n=62	Intra	Inter	Total						
AGER	Q15109	Advanced glycosylation end product-specific receptor	100	100	5.2	4.2	7.3	2.9 (0.0, 3.8)	0.56	8.69	87525	4.0	< 1%
AGRP	O00253	Agouti-related protein	100	100	4.9	4.3	8.6	5.3 (5.0, 5.8)	0.17	0.50	260845	5.7	< 1%
ANGPT1	Q15389	Angiopoietin-1	100	100	6.3	2.5	7.8	7.4 (7.2, 7.7)	30.64	47.92	1136822	4.4	< 1%
ANGPT2	O15123	Angiopoietin-2	100	100	6.2	4.6	8.5	4.0 (3.5, 4.3)	5.43	36.95	26035	2.8	< 1%
ANXA1	P04083	Annexin A1	100	97	9.9	5.9	15.9	8.7 (8.6, 9.0)	2.97	4.49	1984450	5.6	< 1%
AREG	P15514	Amphiregulin	96	97	4.6	2.8	13.0	9.9 (9.8, 10.0)	4.43	92.47	23548	2.4	< 1%
BDNF	P23560	Brain-derived neurotrophic factor	100	100	6.8	6.7	10.1	3.4 (0.0, 5.4)	8.68	174.68	131086	2.9	< 1%
BMP7	P18075	Bone morphogenetic protein 7	100	100	4.6	3.2	7.0	10.3 (10.2, 10.4)	0.28	0.28	54945	5.3	< 1%
BST2	Q10589	Bone marrow stromal antigen 2	100	100	8.3	1.7	9.3	3.0 (0.0, 3.8)	2.05	8.52	711743	4.9	< 1%
C1QA	P02745	Complement C1q A chain	100	100	6.5	7.4	10.0	6.3 (5.7, 6.6)	n/a	n/a	n/a	n/a	3.4%
CALCA	P01258	Calcitonin [Cleaved into: Calcitonin; Katalcalcin	100	100	6.9	4.2	8.4	5.7 (5.1, 5.9)	0.57	1.69	290335	5.2	< 1%
CCL1	P22362	C-C motif chemokine 1	100	100	5.6	5.8	8.1	3.0 (0.0, 4.0)	< 0.01	0.61	41	1.8	< 1%
CCL11	P51671	Eotaxin	100	100	5.4	3.7	7.8	7.8 (7.5, 8.3)	0.32	0.59	304940	5.7	< 1%
CCL13	Q99616	C-C motif chemokine 13	100	100	7.6	5.2	10.6	0.0 (0.0, 2.4)	0.21	1.96	51891	4.4	< 1%
CCL14	Q16627	C-C motif chemokine 14	100	100	10.2	2.5	13.2	0.0 (0.0, 0.0)	n/a	n/a	n/a	n/a	< 1%
CCL15	Q16663	C-C motif chemokine 15	100	100	9.1	3.0	11.4	0.0 (0.0, 3.1)	45.65	317.91	597170	3.3	< 1%
CCL16	O15467	C-C motif chemokine 16	100	100	8.2	1.1	10.2	0.0 (0.0, 0.0)	< 0.01	296.43	432019	3.2	< 1%
CCL17	Q92583	C-C motif chemokine 17	100	100	8.9	4.8	10.3	5.1 (4.7, 6.2)	7.81	67.81	43129	2.8	< 1%
CCL19	Q99731	C-C motif chemokine 19	100	100	9.1	1.4	10.6	0.0 (0.0, 0.0)	< 0.01	3.81	54437	4.2	< 1%
CCL2	P13500	C-C motif chemokine 2	100	100	10.7	5.3	13.1	6.7 (6.4, 7.2)	2.97	36.32	34661	3.0	< 1%
CCL20	P78556	C-C motif chemokine 20	68	86	11.9	4.9	20.1	11.5 (11.1, 11.7)	3.09	4.72	31918	3.8	< 1%
CCL21	O00585	C-C motif chemokine 21	100	100	6.1	3.8	7.3	0.0 (0.0, 1.0)	0.83	13.46	15740	3.1	< 1%
CCL22	O00626	C-C motif chemokine 22	100	100	8.0	1.4	10.5	0.0 (0.0, 0.0)	< 0.01	126.85	104646	2.9	< 1%
CCL23	P55773	C-C motif chemokine 23	100	100	9.2	2.3	11.7	0.0 (0.0, 0.0)	2.87	29.65	282683	4.0	< 1%
CCL24	O00175	C-C motif chemokine 24	100	100	7.9	7.0	11.3	6.8 (6.4, 7.2)	197.44	272.84	270533	3.0	< 1%
CCL25	O15444	C-C motif chemokine 25	100	100	9.5	5.8	11.9	0.0 (0.0, 0.0)	0.05	0.27	610	3.4	< 1%
CCL26	Q9Y258	C-C motif chemokine 26	100	100	8.5	4.4	11.2	6.7 (6.3, 6.8)	0.12	10.65	25617	3.4	< 1%
CCL27	Q9Y4X3	C-C motif chemokine 27	100	100	5.2	1.4	6.1	4.3 (3.8, 4.7)	0.96	3.74	121037	4.5	< 1%
CCL28	Q9NRJ3	C-C motif chemokine 28	100	100	6.5	2.0	8.6	3.2 (2.3, 3.9)	0.04	3.78	272	1.9	< 1%
CCL3	P10147	C-C motif chemokine 3	100	100	10.4	2.5	12.0	8.1 (8.0, 8.6)	0.26	0.61	5529	4.0	< 1%
CCL4	P13236	C-C motif chemokine ligand 4	100	100	7.5	1.6	9.8	5.7 (5.0, 6.1)	0.79	6.45	119055	4.3	< 1%
CCL5	P13501	C-C motif chemokine 5	100	100	11.6	4.9	14.7	4.5 (4.3, 5.0)	588.52	693.31	520050	2.9	< 1%
CCL7	P80098	C-C motif chemokine 7	100	100	7.2	3.6	9.7	7.7 (7.0, 7.9)	0.02	0.02	89	3.6	< 1%
CCL8	P80075	C-C motif chemokine 8	100	100	10.4	4.1	11.8	7.4 (7.0, 7.7)	0.85	6.96	440	1.8	< 1%
CD200	P41217	OX-2 membrane glycoprotein	94	86	6.6	3.0	7.8	0.0 (0.0, 4.0)	0.11	1.75	51315	4.5	< 1%
CD200R1	Q8TD46	Cell surface glycoprotein CD200 receptor 1	100	100	10.4	4.4	13.2	0.0 (0.0, 0.0)	9.18	105.92	1149278	4.0	< 1%
CD27	P26842	CD27 antigen	100	100	8.4	5.0	10.7	7.2 (6.4, 7.4)	65.26	124.02	2796868	4.4	< 1%
CD274	Q9NZQ7	Programmed cell death 1 ligand 1, PD-L1	100	100	7.6	3.1	9.4	7.9 (7.5, 8.2)	0.53	1.69	156370	5.0	< 1%
CD276	Q5ZPR3	CD276 molecule	100	100	6.9	4.2	8.2	8.8 (8.6, 9.1)	n/a	n/a	n/a	n/a	< 1%
CD3E	P07766	T-cell surface glycoprotein CD3 epsilon chain	100	100	13.6	7.0	16.8	6.7 (6.4, 7.0)	n/a	n/a	n/a	n/a	n/a
CD4	P01730	T-cell surface glycoprotein CD4	100	100	4.2	2.5	5.8	5.3 (4.6, 5.4)	3.18	8.33	2557538	5.5	< 1%
CD40	P25942	CD40 molecule	100	100	10.6	5.1	13.9	7.8 (7.6, 8.1)	3.43	10.03	70528	3.8	< 1%

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			Plasma		Plasma								
			Healthy n=50	Disease n=62	Intra	Inter	Total						
CD40LG	P29965	CD40 ligand	100	100	9.5	0.7	10.9	0.0 (0.0, 0.0)	0.01	0.66	463354	5.8	< 1%
CD46	P15529	Membrane cofactor protein	100	100	5.8	3.1	8.0	9.8 (9.7, 9.9)	992.40	3400.01	2360181	2.8	< 1%
CD70	P32970	CD70 antigen	64	87	10.5	7.2	14.9	8.9 (8.8, 9.1)	11.90	69.20	532797	3.9	< 1%
CD80	P33681	T-lymphocyte activation antigen CD80	100	100	5.8	1.8	8.0	4.3 (3.5, 4.8)	0.63	1.76	100647	4.8	< 1%
CD83	Q01151	CD83 antigen	100	100	5.8	2.7	7.5	8.1 (7.8, 8.3)	0.07	0.11	109641	6.0	< 1%
CD93	Q9NPY3	Complement component C1q receptor	100	100	7.0	4.6	9.0	0.0 (0.0, 0.0)	19.51	3177.65	2611930	2.9	< 1%
CEACAM5	P06731	Carcinoembryonic antigen related cell adhesion molecule 5	100	100	7.2	6.0	9.9	8.4 (8.2, 8.6)	29.13	47.43	1442122	4.5	< 1%
CHI3L1	P36222	Chitinase-3-like protein 1	100	100	10.0	2.1	10.6	6.0 (5.6, 6.6)	139.32	1273.68	2116366	3.2	< 1%
CLEC4A	Q9UMR7	C-type lectin domain family 4 member A	100	100	5.2	4.5	7.0	9.4 (9.2, 9.6)	1.57	1.57	136135	4.9	< 1%
CNTF	P26441	Ciliary neurotrophic factor	48	60	10.0	2.1	18.1	7.8 (7.6, 7.9)	n/a	n/a	n/a	n/a	2.3%
CRP	P02741	C-reactive protein	100	100	11.1	22.8	32.8	21.9 (21.3, 22.4)	n/a	34193.60	403082691	4.1	< 1%
CSF1	P09603	Macrophage colony-stimulating factor 1	100	100	8.1	2.4	8.8	7.5 (7.3, 7.8)	14.75	37.36	192657	3.7	< 1%
CSF1R	P07333	Macrophage colony-stimulating factor 1 receptor	100	100	9.9	5.5	12.9	0.0 (0.0, 0.0)	n/a	n/a	n/a	n/a	< 1%
CSF2	P04141	Granulocyte-macrophage colony-stimulating factor	100	100	4.7	3.0	6.3	7.9 (7.7, 8.1)	< 0.01	< 0.01	850	5.5	< 1%
CSF2RB	P32927	Cytokine receptor common subunit beta	100	100	4.3	2.4	5.1	6.3 (5.9, 6.4)	0.54	0.64	493569	5.9	< 1%
CSF3	P09919	Granulocyte colony-stimulating factor, G-CSF	100	100	4.6	2.7	6.9	7.8 (7.2, 8.0)	0.55	0.99	19459	4.3	< 1%
CSF3R	Q99062	Granulocyte colony-stimulating factor receptor	100	100	5.7	2.1	8.5	5.4 (4.9, 6.1)	1.47	4.16	832878	5.3	< 1%
CST7	O76096	Cystatin-F	100	100	7.8	2.6	9.9	0.0 (0.0, 0.0)	0.19	7.95	6896	2.9	< 1%
CTF1	Q16619	Cardiotrophin-1	100	100	7.4	3.5	37.2	8.5 (8.3, 8.7)	0.20	0.29	66838	5.4	< 1%
CTLA4	P16410	Cytotoxic T-lymphocyte protein 4	100	100	4.7	5.2	7.4	7.0 (6.9, 7.4)	< 0.01	0.01	2568	5.6	< 1%
CTSS	P25774	Cathepsin S	52	68	6.0	2.3	7.1	4.6 (4.2, 5.1)	0.58	7.44	1407326	5.3	< 1%
CX3CL1	P78423	Fractalkine	100	100	5.8	5.8	12.6	6.8 (6.5, 7.3)	3.46	10.95	829581	4.9	< 1%
CXADR	P78310	Coxsackievirus and adenovirus receptor	100	100	7.5	6.8	11.1	9.5 (9.3, 9.7)	1.46	1.72	75556	4.6	< 1%
CXCL1	P09341	Growth-regulated alpha protein	90	98	10.2	3.5	12.6	10.6 (10.2, 10.8)	9.71	12.37	346108	4.4	< 1%
CXCL10	P02778	C-X-C motif chemokine 10	100	100	8.9	4.5	11.1	3.2 (0.0, 5.2)	0.35	4.20	66158	4.2	< 1%
CXCL11	O14625	C-X-C motif chemokine 11	100	100	12.7	4.8	15.3	0.0 (0.0, 0.0)	0.13	2.50	5448	3.3	< 1%
CXCL12	P48061	Stromal cell-derived factor 1	94	76	6.3	3.2	12.6	9.1 (9.0, 9.3)	n/a	n/a	n/a	n/a	n/a
CXCL13	O43927	C-X-C motif chemokine 13	100	100	10.7	2.5	12.0	0.0 (0.0, 0.0)	< 0.01	7.96	120919	4.2	< 1%
CXCL14	O95715	C-X-C motif chemokine 14	64	71	5.8	6.8	12.9	11.6 (11.4, 11.6)	n/a	n/a	n/a	n/a	n/a
CXCL16	Q9H2A7	C-X-C motif chemokine 16	100	100	6.5	4.3	8.5	0.0 (0.0, 2.0)	0.16	54.59	372422	3.8	< 1%
CXCL2	P19875	C-X-C motif chemokine ligand 2	100	100	13.4	5.1	17.9	7.9 (7.6, 8.2)	2.94	50.51	1359	1.4	< 1%
CXCL3	P19876	C-X-C motif chemokine ligand 3	100	100	10.7	4.3	12.4	7.6 (7.1, 7.8)	5.21	10.71	55794	3.7	< 1%
CXCL5	P42830	C-X-C motif chemokine 5	100	100	9.4	2.0	10.2	4.2 (1.3, 5.3)	0.33	2.12	323571	5.2	< 1%
CXCL6	P80162	C-X-C motif chemokine 6	100	98	11.4	7.5	21.9	10.1 (9.9, 10.3)	0.36	0.38	12623	4.5	< 1%
CXCL8	P10145	Interleukin-8, IL8	92	100	5.5	5.0	19.8	5.9 (5.8, 6.0)	1.41	2.45	10024	3.6	< 1%
CXCL9	Q07325	C-X-C motif chemokine 9	100	100	8.7	0.8	9.1	0.0 (0.0, 0.7)	0.01	0.17	1590	4.0	< 1%
EGF	P01133	Pro-epidermal growth factor	100	100	7.9	3.5	9.9	5.6 (5.3, 6.2)	6.52	16.96	625510	4.6	< 1%
EPO	P01588	Erythropoietin	100	100	6.7	4.9	9.7	9.6 (9.4, 9.8)	2.18	2.85	43643	4.2	< 1%

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			Plasma		Plasma								
			Healthy n=50	Disease n=62	Intra	Inter	Total						
FASLG	P48023	Tumor necrosis factor ligand superfamily member 6	100	100	4.7	3.9	7.5	5.0 (4.2, 5.8)	0.05	0.31	53823	5.2	< 1%
FGF19	O95750	Fibroblast growth factor 19	100	100	9.1	3.9	12.9	0.0 (0.0, 0.0)	0.09	6.45	120337	4.3	< 1%
FGF2	P09038	Fibroblast growth factor 2	88	90	10.7	3.3	12.1	10.2 (10.1, 10.5)	0.42	0.65	146244	5.4	< 1%
FGF21	Q9NSA1	Fibroblast growth factor 21	100	100	8.1	2.3	8.9	7.3 (6.8, 7.6)	65.22	93.57	2324015	4.4	< 1%
FGF23	Q9GZV9	Fibroblast growth factor 23	98	100	11.4	13.8	20.4	10.0 (9.4, 10.5)	10.51	400.95	10256	1.4	< 1%
FLT1	P17948	Vascular endothelial growth factor receptor 1	100	100	8.0	3.9	10.7	11.9 (11.7, 12.1)	1275.35	2453.82	27524	1.0	< 1%
FLT3LG	P49771	Fms-related tyrosine kinase 3 ligand	100	100	8.9	5.2	20.5	3.8 (3.4, 4.1)	0.58	1.81	48139	4.4	< 1%
FLT4	P35916	Vascular endothelial growth factor receptor 3	100	100	7.9	1.8	9.6	2.7 (0.0, 3.2)	n/a	n/a	n/a	n/a	< 1%
FBXO1	P02794	Ferritin heavy chain 1	100	100	6.8	5.3	9.8	9.0 (8.9, 9.3)	160.94	242.45	337576	3.1	< 1%
FURIN	P09958	Furin	100	100	5.0	5.2	8.1	5.6 (5.3, 6.2)	0.29	0.64	480305	5.9	< 1%
GDF15	Q99988	Growth/differentiation factor 15	100	98	8.5	2.6	10.3	0.0 (0.0, 5.8)	8.18	169.19	1065905	3.8	< 1%
GDF2	Q9UK05	Growth/differentiation factor 2	100	100	9.3	4.2	17.8	9.5 (9.1, 9.6)	29.39	43.55	434348	4.0	< 1%
GFAP	P14136	Glial fibrillary acidic protein	100	100	8.9	6.0	10.8	9.9 (9.7, 10.2)	0.17	0.33	336664	6.0	< 1%
GRN	P28799	Progranulin	100	100	8.9	3.2	10.6	9.2 (8.8, 9.3)	1023.94	3063.49	2974903	3.0	< 1%
GZMA	P12544	Granzyme A	100	100	6.7	3.3	8.7	0.0 (0.0, 3.0)	0.12	1.52	67012	4.6	< 1%
GZMB	P10144	Granzyme B	100	100	8.6	3.4	10.4	5.7 (5.5, 5.9)	0.50	1.11	1301682	6.1	< 1%
HAVCR1	Q96D42	Hepatitis A virus cellular receptor 1	100	100	8.2	2.3	9.9	0.0 (0.0, 0.0)	0.03	1.16	246852	5.3	< 1%
HGF	P14210	Hepatocyte growth factor	100	100	7.5	1.9	8.7	7.1 (6.8, 7.4)	0.73	1.16	31729	4.4	< 1%
HLA-DRA	P01903	Major histocompatibility complex, class II, DR alpha	100	100	5.8	3.8	18.1	7.3 (7.0, 7.7)	0.05	0.12	182484	6.2	< 1%
ICAM1	P05362	Intercellular adhesion molecule 1	100	100	6.8	0.4	7.7	4.4 (1.6, 4.8)	506.27	6079.56	1366993	2.4	< 1%
ICOSLG	O75144	ICOS ligand	100	100	8.1	4.0	10.5	0.0 (0.0, 0.0)	107.78	2047.42	5838791	3.5	< 1%
IFNA1; IFNA13	P01562; P01562	Interferon alpha-1; Interferon alpha-13	100	97	15.2	7.5	18.0	2.5 (0.0, 5.1)	< 0.01	0.01	20912	6.4	< 1%
IFNB1	P01574	Interferon beta	98	100	14.0	3.8	21.5	11.2 (11.0, 11.3)	< 0.01	< 0.01	1191	5.6	< 1%
IFNG	P01579	Interferon gamma	100	100	6.2	2.8	8.7	5.7 (5.3, 6.0)	0.01	0.03	29847	6.0	< 1%
IFNL1	Q8IU54	Interferon lambda-1	100	100	4.9	3.1	7.7	8.4 (8.3, 8.8)	< 0.01	< 0.01	449	5.3	< 1%
IFNL2; IFNL3	Q8IZJ0; Q8IZI9	Interferon lambda-2; Interferon lambda-3	100	97	12.6	28.6	42.0	3.7 (3.3, 4.2)	0.02	0.04	7206	5.3	< 1%
IFNW1	P05000	Interferon omega-1	74	89	18.4	37.4	48.3	9.6 (9.4, 10.2)	< 0.01	< 0.01	963	5.7	< 1%
IKBKG	Q9Y6K9	Inhibitor of nuclear factor kappa B kinase subunit gamma	100	100	9.0	4.4	10.7	6.8 (6.7, 7.0)	3.39	7.42	1418988	5.3	< 1%
IL10	P22301	Interleukin-10	100	100	6.3	4.5	13.8	5.3 (4.9, 5.7)	< 0.01	0.02	30893	6.3	< 1%
IL10RB	Q08334	Interleukin-10 receptor subunit beta	100	100	6.0	6.2	9.3	6.2 (5.9, 6.6)	10.01	24.08	2098001	4.9	< 1%
IL11	P20809	Interleukin-11	38	47	14.1	5.0	18.2	8.6 (8.5, 8.6)	n/a	n/a	n/a	n/a	n/a
IL12B	P29460	Interleukin-12 subunit beta	100	100	5.3	1.6	7.2	5.5 (5.3, 5.7)	0.34	0.69	169166	5.4	n/a
IL12p70	P29459; P29460	Interleukin-12 subunit beta Interleukin-12 subunit alpha	100	100	6.2	3.1	7.3	7.6 (7.3, 8.1)	< 0.01	< 0.01	2960	5.9	< 1%
IL12RB1	P42701	Interleukin-12 receptor subunit beta-1	98	100	5.4	5.5	8.0	9.5 (9.2, 9.8)	8.41	8.41	353628	4.6	< 1%
IL13	P35225	Interleukin-13	96	97	5.2	4.7	7.4	8.5 (8.2, 9.0)	0.07	0.18	10175	4.8	< 1%
IL13RA2	Q14627	Interleukin 13 receptor subunit alpha 2	100	100	9.0	6.4	14.7	8.4 (8.2, 8.8)	1.89	4.78	464967	5.0	< 1%
IL15	P40933	Interleukin-15	100	100	3.9	4.2	6.2	5.8 (5.6, 6.2)	< 0.01	< 0.01	1790	6.1	< 1%

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Table 3: Performance Validation Data by Target

Target	UniProt ID	Protein Name	Detectability (%)		CV (%), one site			LOD (NPQ) Median (IQR)	LOD (pg/mL)	LLOQ (pg/mL)	ULOQ (pg/mL)	log10 Dynamic Range	Cross Reactivity
			Plasma		Plasma								
			Healthy n=50	Disease n=62	Intra	Inter	Total						
IL15RA	Q13261	Interleukin-15 receptor subunit alpha	100	100	7.9	2.2	9.6	7.1 (6.7, 7.3)	0.50	1.23	137287	5.0	< 1%
IL16	Q14005	Pro-interleukin-16	100	100	4.3	2.8	6.2	4.9 (4.7, 5.2)	4.08	7.62	889925	5.1	< 1%
IL17A	Q16552	Interleukin-17A	98	100	6.3	2.2	11.4	6.4 (6.3, 6.5)	0.01	0.01	5185	5.6	< 1%
IL17A IL17F	Q16552 Q96PD4	Interleukin-17A Interleukin-17F	100	100	11.5	7.8	16.5	4.3 (3.4, 4.5)	0.01	0.02	13997	6.0	< 1%
IL17B	Q9UHF5	Interleukin-17B	100	100	5.8	2.2	6.9	3.2 (0.0, 4.8)	< 0.01	0.02	20351	6.0	< 1%
IL17C	Q9P0M4	Interleukin-17C	100	100	7.9	2.3	9.3	0.0 (0.0, 0.0)	< 0.01	0.11	22080	5.3	< 1%
IL17F	Q96PD4	Interleukin-17F	94	94	6.9	1.8	10.5	9.6 (9.4, 9.6)	22.68	23.15	95047	3.6	n/a
IL17RA	Q96F46	Interleukin-17 receptor A	100	100	7.0	2.7	8.5	6.6 (6.4, 6.7)	0.05	0.12	59210	5.7	3.2%
IL17RB	Q9NRM6	Interleukin-17 receptor B	100	100	5.8	4.0	7.7	8.0 (7.9, 8.2)	0.12	0.14	112164	5.9	< 1%
IL18	Q14116	Interleukin-18	100	100	8.9	4.5	14.8	7.9 (7.3, 8.1)	3.80	22.89	439049	4.3	< 1%
IL18BP	O95998	Interleukin-18-binding protein	100	100	5.4	5.9	8.1	3.8 (3.6, 4.2)	8.29	28.40	3231589	5.1	< 1%
IL18R1	Q13478	Interleukin-18 receptor 1	100	100	6.6	4.6	8.3	6.3 (6.0, 6.9)	0.39	0.70	124893	5.2	< 1%
IL19	Q9UHD0	Interleukin-19	100	100	5.0	3.8	7.5	6.8 (6.3, 7.1)	0.02	0.07	61685	5.9	< 1%
IL1B	P01584	Interleukin-1 beta	58	66	4.8	3.1	13.9	8.4 (8.4, 8.5)	0.01	0.02	2852	5.2	< 1%
IL1R1	P14778	Interleukin-1 receptor type 1	100	100	4.8	3.2	6.2	0.0 (0.0, 3.2)	1.98	39.85	5829100	5.2	< 1%
IL1R2	P27930	Interleukin-1 receptor type 2	100	100	6.8	1.7	8.2	0.0 (0.0, 0.0)	1.68	1211.31	3152783	3.4	< 1%
IL1RL1	Q01638	Interleukin-1 receptor-like 1	100	100	11.3	3.2	14.0	0.0 (0.0, 0.0)	32.46	1747.84	1908982	3.0	< 1%
IL1RN	P18510	Interleukin-1 receptor antagonist protein	100	100	5.7	2.9	8.2	7.1 (7.0, 7.4)	5.38	6.95	133301	4.3	51.5%
IL2	P60568	Interleukin-2	100	100	8.7	4.1	12.1	6.8 (6.7, 7.0)	0.11	0.14	17887	5.1	< 1%
IL20	Q9NYY1	Interleukin-20	100	100	7.4	6.1	10.4	8.1 (7.9, 8.5)	0.01	0.03	19353	5.9	< 1%
IL22	Q9GZX6	Interleukin-22	100	100	10.2	2.3	14.1	8.9 (8.6, 9.5)	< 0.01	0.01	1468	5.4	< 1%
IL23	P29460 Q9NPF7	Interleukin-12 subunit beta Interleukin-23 subunit alpha	100	100	9.4	7.6	36.7	12.1 (11.8, 12.6)	0.01	0.02	52627	6.3	< 1%
IL24	Q13007	Interleukin-24	74	68	6.9	23.3	31.3	10.2 (9.4, 10.9)	n/a	n/a	n/a	n/a	n/a
IL27	Q8NEV9 Q14213	Interleukin 27 Interleukin-27 subunit beta	100	100	8.6	4.1	11.0	8.5 (8.0, 9.2)	< 0.01	0.01	5792	6.0	< 1%
IL2RA	P01589	Interleukin-2 receptor subunit alpha	100	100	6.8	5.8	9.3	0.0 (0.0, 0.0)	0.07	49.64	244875	3.7	< 1%
IL2RB	P14784	Interleukin-2 receptor subunit beta	100	100	8.0	5.9	10.4	7.3 (7.1, 7.8)	2.17	6.09	118886	4.3	< 1%
IL32	P24001	Interleukin-32	58	55	5.8	4.5	17.1	8.9 (8.8, 9.0)	5.00	5.36	1322652	5.4	1.7%
IL33	O95760	Interleukin 33	100	100	9.5	2.5	13.8	6.9 (6.6, 7.1)	0.01	0.02	3183	5.2	< 1%
IL34	Q6ZMJ4	Interleukin-34	100	100	4.8	4.6	6.9	7.5 (7.3, 7.8)	0.02	0.03	1848	4.8	< 1%
IL36A	Q9UHA7	Interleukin-36 alpha	100	100	6.6	6.8	10.9	0.0 (0.0, 0.0)	0.01	0.38	72067	5.3	1.0%
IL36B	Q9NZH7	Interleukin-36 beta	100	100	8.2	4.1	17.8	5.9 (5.7, 6.1)	< 0.01	< 0.01	6985	6.4	< 1%
IL36G	Q9NZH8	Interleukin-36 gamma	100	98	10.5	8.0	21.3	8.1 (7.7, 8.3)	0.99	3.83	93261	4.4	< 1%
IL3RA	P26951	Interleukin-3 receptor subunit alpha	100	100	6.5	3.4	8.7	0.0 (0.0, 4.8)	0.62	22.45	435659	4.3	< 1%
IL4	P05112	Interleukin-4	100	100	11.9	13.6	23.2	7.6 (7.0, 8.0)	< 0.01	< 0.01	940	5.7	< 1%
IL4R	P24394	Interleukin-4 receptor subunit alpha	100	100	8.2	3.1	9.8	0.0 (0.0, 4.5)	6.25	515.03	1059120	3.3	< 1%
IL5	P05113	Interleukin-5	100	100	6.0	3.5	8.1	6.6 (6.1, 7.0)	< 0.01	< 0.01	1570	5.9	< 1%
IL5RA	Q01344	Interleukin-5 receptor subunit alpha	100	100	8.0	5.4	10.2	0.0 (0.0, 0.0)	0.19	124.38	1535097	4.1	< 1%
IL6	P05231	Interleukin-6	100	100	7.3	4.3	9.7	8.2 (7.7, 8.4)	0.04	0.06	16542	5.4	< 1%
IL6R	P08887	Interleukin-6 receptor subunit alpha	100	100	9.4	4.8	12.2	0.0 (0.0, 4.1)	297.36	6693.02	5117188	2.9	< 1%

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Table 3: Performance Validation Data by Target

Target	UniProt ID	Protein Name	Detectability (%)		CV (%), one site			LOD (NPQ) Median (IQR)	LOD (pg/mL)	LLOQ (pg/mL)	ULOQ (pg/mL)	log10 Dynamic Range	Cross Reactivity
			Plasma		Plasma								
			Healthy n=50	Disease n=62	Intra	Inter	Total						
IL6ST	P40189	Interleukin-6 receptor subunit beta	100	100	6.0	1.5	6.7	1.7 (0.0, 3.8)	n/a	n/a	n/a	n/a	< 1%
IL7	P13232	Interleukin-7	100	100	5.5	2.9	7.1	6.7 (6.2, 6.9)	0.01	0.01	2219	5.2	< 1%
IL7R	P16871	Interleukin-7 receptor subunit alpha	100	100	4.8	4.6	7.0	0.0 (0.0, 0.0)	0.97	110.75	2220151	4.3	< 1%
IL9	P15248	Interleukin-9	100	100	8.8	8.1	13.9	0.0 (0.0, 5.8)	< 0.01	0.08	28778	5.6	< 1%
IRAK4	Q9NWX3	Interleukin-1 receptor-associated kinase 4	100	100	12.2	4.9	15.0	6.8 (6.3, 7.0)	0.37	0.61	99093	5.2	< 1%
KDR	P35968	Vascular endothelial growth factor receptor 2	100	100	7.2	4.8	9.3	3.1 (2.9, 4.0)	27.89	160.14	3846324	4.4	< 1%
KITLG	P21583	Kit ligand	100	100	5.1	4.8	10.1	8.9 (8.7, 9.0)	1.22	1.22	2610	3.3	< 1%
KLRK1	P26718	NKG2-D type II integral membrane protein	100	100	5.1	3.2	6.9	0.0 (0.0, 3.4)	3.66	51.96	2559555	4.7	< 1%
KNG1	P01042	Kininogen-1	100	100	6.8	9.3	18.3	20.0 (19.6, 20.2)	n/a	419208.33	24605458	1.8	< 1%
LAG3	P18627	Lymphocyte activation gene 3 protein	100	100	8.9	7.5	12.5	0.0 (0.0, 0.0)	< 0.01	69.14	556542	3.9	< 1%
LAMP3	Q9UQV4	Lysosomal associated membrane protein 3	100	100	6.0	3.3	7.8	8.5 (8.2, 8.7)	4.29	19.41	12318	2.8	< 1%
LCN2	P80188	Neutrophil gelatinase-associated lipocalin	100	100	7.6	2.3	9.1	7.0 (6.6, 7.3)	n/a	n/a	n/a	n/a	1.0%
LGALS9	O00182	Galectin-9	100	100	5.4	1.7	6.1	3.6 (1.6, 3.8)	0.61	22.34	1682474	4.9	< 1%
LIF	P15018	Leukemia inhibitory factor	98	100	7.4	4.1	9.1	7.3 (6.9, 7.5)	0.01	0.02	2480	5.1	< 1%
LILRB2	Q8N423	Leukocyte immunoglobulin-like receptor subfamily B member 2	100	100	7.0	3.2	8.7	0.0 (0.0, 3.0)	70.70	1648.73	7319637	3.6	< 1%
LTA	P01374	Lymphotoxin-alpha	98	95	9.1	6.1	40.9	7.8 (7.6, 8.1)	0.14	0.30	11793	4.6	< 1%
LTA LTB	P01374 Q06643	Lymphotoxin-alpha Lymphotoxin-beta	90	89	7.9	3.4	18.1	8.5 (8.3, 8.8)	n/a	n/a	n/a	n/a	n/a
MERTK	Q12866	MER proto-oncogene, tyrosine kinase	100	100	5.9	5.1	8.1	6.2 (5.8, 6.5)	382.65	3542.54	5490472	3.2	< 1%
MICA	Q29983	MHC class I polypeptide-related sequence A	56	89	5.4	5.5	8.2	9.7 (9.4, 9.8)	n/a	n/a	n/a	n/a	< 1%
MICB	Q29980	MHC class I polypeptide-related sequence B	100	100	4.8	5.0	9.3	9.4 (9.2, 9.4)	8.02	10.97	4387913	5.6	< 1%
MIF	P14174	Macrophage migration inhibitory factor	100	100	8.1	5.9	18.0	7.7 (7.5, 7.8)	648.13	772.89	3739366	3.7	< 1%
MMP1	P03956	Interstitial collagenase	100	100	11.1	1.9	18.4	7.1 (6.6, 7.5)	3.62	5.00	530956	5.0	< 1%
MMP12	P39900	Macrophage metalloelastase	100	100	7.1	4.0	9.3	9.9 (9.7, 10.1)	6.40	8.11	432460	4.7	< 1%
MMP3	P08254	Stromelysin-1	100	100	7.0	2.2	9.3	0.0 (0.0, 0.0)	1.07	230.20	2193844	4.0	< 1%
MMP8	P22894	Neutrophil collagenase	100	100	5.1	3.8	7.6	6.5 (6.2, 6.8)	4.96	13.98	2586587	5.3	< 1%
MMP9	P14780	Matrix metalloproteinase-9	100	100	7.2	5.5	10.4	4.7 (4.2, 5.1)	24.05	237.89	1574852	3.8	< 1%
MPO	P05164	Myeloperoxidase	100	100	6.8	5.3	9.7	6.5 (6.3, 6.9)	n/a	n/a	n/a	n/a	< 1%
MUC16	Q8WXI7	Mucin-16	100	100	12.1	14.2	21.3	7.9 (7.5, 8.2)	169.74	485.91	1041973	3.3	< 1%
NAMPT	P43490	Nicotinamide phosphoribosyl-transferase	62	71	17.8	21.7	30.1	11.0 (10.3, 11.7)	n/a	n/a	n/a	n/a	n/a
NCR1	O76036	Natural cytotoxicity triggering receptor 1	100	100	7.1	4.8	10.1	0.0 (0.0, 0.0)	0.03	3.10	161778	4.7	< 1%
NGF	P01138	Beta-nerve growth factor	100	100	8.3	1.6	9.9	9.0 (8.8, 9.1)	0.89	0.89	38071	4.6	< 1%
NTF3	P20783	Neurotrophin-3	82	84	5.2	3.3	21.2	11.6 (11.5, 11.7)	n/a	n/a	n/a	n/a	n/a
OSM	P13725	Oncostatin-M	100	100	5.2	6.7	10.1	8.9 (8.4, 9.2)	0.02	0.02	5249	5.5	< 1%
OSMR	Q99650	Oncostatin-M-specific receptor subunit beta	100	100	6.3	5.2	8.4	6.2 (5.6, 7.0)	44.47	223.66	980170	3.6	< 1%
PDCD1	Q15116	Programmed cell death protein 1	100	100	8.2	3.7	10.0	6.5 (2.7, 6.9)	2.59	12.91	154325	4.1	< 1%

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Table 3: Performance Validation Data by Target

Target	UniProt ID	Protein Name	Detectability (%)		CV (%), one site			LOD (NPQ) Median (IQR)	LOD (pg/mL)	LLOQ (pg/mL)	ULOQ (pg/mL)	log10 Dynamic Range	Cross Reactivity
			Plasma		Plasma								
			Healthy n=50	Disease n=62	Intra	Inter	Total						
PDC-D1LG2	Q9BQ51	Programmed cell death 1 ligand 2	100	100	6.5	4.2	9.8	0.0 (0.0, 0.0)	0.11	63.94	679015	4.0	< 1%
PDGFA	P04085	Platelet-derived growth factor subunit A	100	100	4.4	3.6	6.1	10.2 (10.1, 10.3)	10.30	15.72	26493	3.2	< 1%
PDGFB	P01127	Platelet-derived growth factor subunit B	100	100	7.4	2.6	8.4	4.8 (2.5, 5.4)	1.18	5.92	57555	4.0	< 1%
PGF	P49763	Placenta growth factor	100	100	4.8	3.9	6.4	12.1 (12.0, 12.2)	1.38	1.38	48244	4.5	< 1%
PTX3	P26022	Pentraxin-related protein PTX3	100	100	5.8	5.1	11.3	8.4 (8.1, 8.6)	8.62	8.62	281721	4.5	< 1%
S100A12	P80511	Protein S100-A12	100	100	7.0	7.9	18.4	6.1 (5.5, 7.0)	54.57	106.64	154460	3.2	1.4%
S100A9	P06702	Protein S100-A9	90	92	7.8	6.1	10.2	10.8 (10.6, 11.1)	n/a	n/a	n/a	n/a	n/a
SCG2	P13521	Secretogranin II	98	100	10.1	6.0	19.3	8.2 (7.7, 8.4)	15.82	132.76	31200	2.4	1.7%
SDC1	P18827	Syndecan 1	100	100	6.1	4.0	7.7	1.8 (0.0, 4.1)	0.35	5.03	102768	4.3	< 1%
SELE	P16581	E-selectin	100	100	8.0	6.2	11.0	7.6 (7.2, 8.3)	623.41	1190.05	2735589	3.4	< 1%
SELP	P16109	P-selectin	100	100	7.7	4.0	9.6	0.0 (0.0, 0.0)	54.11	1457.54	2704555	3.3	< 1%
SIRPA	P78324	Tyrosine-protein phosphatase non-receptor type substrate 1	100	100	6.3	2.7	8.0	7.1 (6.8, 7.7)	599.86	818.32	3299634	3.6	< 1%
SLAMF1	Q13291	Signaling lymphocytic activation molecule	100	100	7.7	3.9	9.6	0.0 (0.0, 0.0)	0.09	17.62	248076	4.1	< 1%
SPP1	P10451	Osteopontin	100	100	9.7	3.8	16.2	6.2 (5.7, 6.7)	186.38	613.40	890274	3.2	< 1%
TAFA5	Q7Z5A7	Chemokine-like protein TAFA-5	98	100	16.0	6.4	23.8	8.0 (7.3, 8.6)	33.15	83.02	100656	3.1	< 1%
TEK	Q02763	Angiopoietin-1 receptor	100	100	7.7	4.0	9.1	4.0 (0.8, 5.0)	22.61	n/a	635763	n/a	< 1%
TGFB1	P01137	Transforming growth factor beta-1 proprotein	100	100	4.4	1.9	6.5	11.9 (11.8, 12.0)	n/a	n/a	n/a	n/a	< 1%
TGFB3	P10600	Transforming growth factor beta-3 proprotein	76	86	32.0	31.8	61.7	11.5 (11.1, 12.0)	0.29	4.76	96370	4.3	< 1%
THBS2	P35442	Thrombospondin-2	100	100	6.3	2.2	8.2	6.8 (6.4, 7.2)	675.46	1318.99	5016819	3.6	< 1%
THPO	P40225	Thrombopoietin	100	100	6.9	2.5	9.6	6.1 (5.7, 6.6)	3.08	21.57	765785	4.6	< 1%
TIMP1	P01033	Metalloproteinase inhibitor 1	100	100	10.4	6.4	13.9	8.9 (8.7, 9.1)	n/a	n/a	n/a	n/a	< 1%
TIMP2	P16035	Metalloproteinase inhibitor 2	100	100	6.6	2.0	13.4	8.9 (8.7, 9.0)	59.92	754.65	21238	1.4	2.2%
TLR3	O15455	Toll-like receptor 3	100	100	7.1	3.2	9.1	5.5 (5.2, 6.5)	18.30	152.43	1654834	4.0	< 1%
TNF	P01375	Tumor necrosis factor	100	100	8.7	3.9	11.4	7.7 (7.3, 8.4)	0.46	13.72	1017	1.9	< 1%
TNFRS-F11A	Q9Y6Q6	TNF receptor superfamily member 11a	100	100	5.7	4.5	8.9	9.2 (9.0, 9.4)	0.26	0.59	295511	5.7	< 1%
TNFRS-F11B	O00300	Tumor necrosis factor receptor superfamily member 11B	100	100	5.8	1.9	8.3	5.3 (4.9, 5.5)	8.23	20.39	98164	3.7	< 1%
TNFRS-F13B	O14836	Tumor necrosis factor receptor superfamily member 13B	100	100	6.4	2.1	8.6	0.0 (0.0, 0.8)	0.10	0.73	94561	5.1	< 1%
TNFRS-F13C	Q96RJ3	Tumor necrosis factor receptor superfamily member 13C	100	100	4.5	5.4	8.3	6.8 (6.5, 7.4)	1.40	1.63	528634	5.5	< 1%
TN-FRSF14	Q92956	Tumor necrosis factor receptor superfamily member 14	100	100	8.6	6.0	10.7	5.1 (0.0, 6.2)	17.22	130.88	310970	3.4	< 1%
TN-FRSF17	Q02223	Tumor necrosis factor receptor superfamily member 17	100	100	8.8	4.1	12.2	5.3 (4.5, 5.9)	25.87	96.40	600189	3.8	< 1%
TN-FRSF18	Q9Y5U5	Tumor necrosis factor receptor superfamily member 18	100	100	5.3	4.6	7.3	9.8 (9.6, 10.0)	0.09	0.13	9526	4.9	< 1%
TNFRS-F1A	P19438	Tumor necrosis factor receptor superfamily member 1A	100	100	6.5	2.2	7.5	9.1 (8.8, 9.3)	133.74	243.97	1480215	3.8	< 1%
TNFRS-F1B	P20333	Tumor necrosis factor receptor superfamily member 1B	100	100	8.5	3.0	10.0	0.0 (0.0, 0.0)	8.52	582.93	2459820	3.6	< 1%
TN-FRSF21	O75509	Tumor necrosis factor receptor superfamily member 21	100	100	6.5	5.2	39.8	9.2 (8.8, 9.3)	0.18	0.47	1147247	6.4	n/a

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Table 3: Performance Validation Data by Target

Target	UniProt ID	Protein Name	Detectability (%)		CV (%), one site			LOD (NPQ) Median (IQR)	LOD (pg/mL)	LLOQ (pg/mL)	ULOQ (pg/mL)	log10 Dynamic Range	Cross Reactivity
			Plasma		Plasma								
			Healthy n=50	Disease n=62	Intra	Inter	Total						
TNFRSF4	P43489	Tumor necrosis factor receptor superfamily member 4	100	100	6.8	7.3	12.3	4.1 (0.0, 6.1)	0.02	0.80	131185	5.2	< 1%
TNFRSF8	P28908	Tumor necrosis factor receptor superfamily member 8	100	100	8.1	6.0	11.2	0.0 (0.0, 5.3)	1.52	33.77	309797	4.0	< 1%
TNFRSF9	Q07011	Tumor necrosis factor receptor superfamily member 9	100	100	4.7	4.6	7.1	8.8 (8.6, 8.8)	4.33	83.50	2256	1.4	n/a
TNFSF10	P50591	Tumor necrosis factor ligand superfamily member 10	100	100	9.5	2.2	10.2	0.0 (0.0, 0.0)	0.27	11.31	176218	4.2	< 1%
TNFSF11	O14788	Tumor necrosis factor ligand superfamily member 11	100	100	6.8	5.3	9.5	9.3 (9.0, 9.6)	6.05	10.86	53905	3.7	< 1%
TNFSF12	O43508	Tumor necrosis factor ligand superfamily member 12	100	100	6.8	4.6	8.5	5.3 (0.0, 5.9)	0.17	0.80	14969	4.3	< 1%
TNFSF13	O75888	TNF superfamily member 13	100	100	12.4	2.5	15.2	4.9 (4.6, 5.2)	n/a	n/a	n/a	n/a	< 1%
TNFSF14	O43557	Tumor necrosis factor ligand superfamily member 14	100	100	4.7	4.7	7.3	4.6 (4.1, 4.9)	1.39	8.53	2732	2.5	< 1%
TNFSF15	O95150	Tumor necrosis factor ligand superfamily member 15	100	100	7.2	5.4	9.3	0.0 (0.0, 0.0)	< 0.01	0.24	29126	5.1	< 1%
TNFSF18	Q9UNG2	Tumor necrosis factor ligand superfamily member 18	100	100	4.6	4.1	7.0	8.0 (7.8, 8.2)	< 0.01	< 0.01	2102	5.9	< 1%
TNFSF4	P23510	Tumor necrosis factor ligand superfamily member 4	100	100	5.0	2.6	7.6	5.8 (5.1, 6.1)	0.02	0.10	18763	5.3	< 1%
TNFSF8	P32971	Tumor necrosis factor ligand superfamily member 8	100	100	7.0	4.1	12.8	5.3 (2.2, 6.1)	1.06	20.70	571859	4.4	< 1%
TNFSF9	P41273	Tumor necrosis factor ligand superfamily member 9	100	100	6.9	1.6	7.7	7.3 (7.1, 7.5)	0.32	0.39	132209	5.5	n/a
TREM1	Q9NP99	Triggering receptor expressed on myeloid cells 1	100	100	8.8	7.5	12.1	0.0 (0.0, 2.0)	< 0.01	5.54	482107	4.9	< 1%
TREM2	Q9NZC2	Triggering receptor expressed on myeloid cells 2	100	100	5.0	1.9	7.3	3.2 (0.0, 4.0)	2.97	47.90	492122	4.0	< 1%
TSLP	Q969D9	Thymic stromal lymphopoietin	100	100	3.9	2.1	9.7	11.1 (11.1, 11.2)	0.55	0.55	4482	3.9	n/a
VCAM1	P19320	Vascular cell adhesion protein 1	100	100	7.2	5.2	9.5	0.0 (0.0, 0.0)	280.41	6802.91	9248786	3.1	< 1%
VEGFA	P15692	Vascular endothelial growth factor A	100	100	4.4	3.9	6.8	9.7 (9.6, 9.9)	90.54	132.16	311777	3.4	< 1%
VEGFC	P49767	Vascular endothelial growth factor C	100	100	4.3	4.7	6.8	7.7 (7.3, 8.0)	0.46	0.62	86542	5.1	< 1%
VEGFD	O43915	Vascular endothelial growth factor D	100	100	6.5	2.3	16.6	6.4 (6.3, 6.5)	10.32	165.11	37512	2.4	< 1%
VSNL1	P62760	Visinin-like protein 1	100	100	5.5	3.0	6.6	9.0 (8.9, 9.2)	0.12	0.17	44393	5.4	< 1%
VSTM1	Q6UX27	V-set and transmembrane domain containing 1	100	100	9.2	5.0	12.4	7.2 (6.8, 7.6)	0.29	2.28	1079	2.7	< 1%
WNT16	Q9UBV4	Wnt family member 16	100	100	3.8	3.3	5.8	5.4 (5.2, 6.0)	0.01	0.03	42643	6.1	< 1%
WNT7A	O00755	Protein Wnt-7a	100	100	11.2	1.4	16.1	6.7 (6.5, 7.4)	0.05	0.07	39089	5.7	< 1%

NULISaseq™ Inflammation Panel 250

Ordering Information

NULISaseq Panels

Product Name	Plate Format	Sample Type	Catalog Number
NULISaseq Inflammation Panel	96	plasma/serum	800103

Consumables & Buffers

Product Name	Qty	Catalog Number
NULISA Wash Buffer (3L)	3L	801035

Instrument

Product Name	Qty	Catalog Number
Alamar ARGO HT System	1	800101

Alamar Biosciences, Inc.
47071 Bayside Parkway
Fremont, CA 94538

T +1 (510) 626-9888
E info@alamarbio.com

Visit [AlamarBio.com](https://www.alamarbio.com) to learn more.

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