EVE DIAGNOSTICS
3415A 3 Ave NW, Calgary, Alberta, T2N 0M4, Canada

Patient Name: PATIENT, NAME
Specimen ID (SID): 26-0000-05
DOB: 01-Jan-2000
PHN: AB 00000000
Reason for Testing: FIRES
Relevant Medications: -

External SID: 123456789
Doctor: Dr. Doctor
Report Date: 31-Mar-2026

Specimen Type: Serum
Date/Time Collected: 01-Jan-2026 / 00:00

Cytokine, Chemokine & Growth Factor Panel

Laboratory Developed Test (LDT)

Report Summary:

Sample Comments:

-

Results Summary:

High Analytes: IFNω, IL-20, IL-29, IL-31, IL-34, IL-35, LIF
High Normal Analytes: CCL28, Eotaxin-3, HMGB1, IFNβ, IL-33, MCP-3
Low Analytes: PDGF-AB/BB

Results Interpretation:

Grouping Summary:
The grouping profile shows moderate elevations in group D2, which may suggest a moderate mucosal immune response.

Profile Overview:
- The results suggest a pronounced type I/III interferon signature, supported by high IFNω, IL-29, and high normal IFNβ, which could indicate active antiviral or innate immune signaling.
- Regulatory and anti-inflammatory signals are evident, including high IL-35 and LIF, which may reflect a counter-regulatory response to ongoing immune activation.
- Type 2 immune activation is also suggested, with high IL-31 and high normal CCL28, Eotaxin-3, and IL-33, which may be consistent with allergic or mucosal immune processes. Together, these patterns could indicate a mixed immune milieu with concurrent antiviral, regulatory, and type 2-associated signaling.

Disclaimer:

The interpretation of these test results should be correlated with clinical findings and other diagnostic tests. Biomarker levels can vary due to many biological, physiological, and diurnal factors; their clinical significance must be assessed by a qualified healthcare professional. This information is not intended to be used as the sole basis for diagnosis or treatment decisions.

Reviewed by: DP
Eve Technologies Corporation is a CLIA certified High Complexity International Laboratory

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Cytokine, Chemokine & Growth Factor Panel

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Analyte	Results (pg/ml)		Reference Interval†
6CKine	857		325 - 1345
APRIL	1374		180 - 5514
BAFF	1414		329 - 2260
BCA-1	68.7		28 - 249
CCL28	720		0 - 800
CTACK	1020		235 - 1379
EGF	22.1		0 - 191
ENA-78			207 - 1563
Eotaxin	33.8		7.5 - 90.9
Eotaxin-2	284		73 - 1309
Eotaxin-3	89.7		7.7 - 93.2
FGF-2	51.6		0 - 215
FLT-3L	23.2		0 - 51.1
Fractalkine	212		0 - 441
GCP-2	101		30 - 258
G-CSF	< 6.0		0 - 88.5
GM-CSF	20.1		0 - 99.4
Granzyme A	79.5		9 - 120
Granzyme B	5.7		0.9 - 26.3
GROα	20.3		0 - 62.3
HMGB1	4009		0 - 4078
I-309	26.8		0.8 - 66.4
IFN-α2	32.6		0 - 139
IFNβ	161		0 - 161
IFNγ	3.5		0 - 18.3
IFNω	153	**HIGH**	0 - 67.3
IL-1α	< 3.0		0 - 82.5
IL-1β	9.9		0 - 89.4
IL-1RA	3.0		0 - 40.9
IL-2	< 0.4		0 - 9.9
IL-3	< 0.4		0 - 1.1
IL-4	3.0		0 - 8.1
IL-5	6.8		0.4 - 18.4
IL-6	2.6		0 - 10.6
IL-7	2.4		0 - 17.4
IL-8	5.3		0 - 26.0
IL-9	7.2		0 - 27.2
IL-10	2.4		0 - 21.6
IL-11	24.6		0 - 41.2
IL-12p40	23.4		14 - 186
IL-12p70	19.1		0 - 25.2
IL-13	147		0 - 229
IL-15	15.6		0 - 65.1
IL-16	363		19 - 788
IL-17A	1.5		0 - 23.3
IL-17E/IL-25	165		0 - 1785
IL-17F	17.0		0 - 69.8
IL-18	40.3		6 - 283

Analyte	Results (pg/ml)		Reference Interval†
IL-20	198	**HIGH**	12 - 126
IL-21	13.7		0 - 32.5
IL-22	65.6		0 - 164
IL-23	2794		0 - 6719
IL-24	1307		0 - 2732
IL-27	2659		167 - 4330
IL-28A	51.9		0 - 76.3
IL-29	121	**HIGH**	0 - 31.8
IL-31	74.5	**HIGH**	0 - 55.3
IL-33	32.1		0 - 36.5
IL-34	198	**HIGH**	6 - 149
IL-35	852	**HIGH**	0 - 371
IP-10	38.2		19 - 334
I-TAC	31.4		18 - 220
LIF	84.2	**HIGH**	0 - 24.3
Lymphotactin	79.0		0 - 100
MCP-1	302		72 - 723
MCP-2	33.1		5.7 - 88.5
MCP-3	33.8		0 - 41.2
MCP-4	89.7		22 - 156
M-CSF	62.3		0 - 321
MDC	774		167 - 1214
MIG	783		380 - 6176
MIP-1α	15.8		0 - 88.1
MIP-1β	46.4		8 - 115
MIP-1δ	1639		1166 - 7149
MIP-3α	10.0		2.7 - 44.3
MIP-3β	66.8		26 - 237
MPIF-1	271		69 - 715
PDGF-AA	638		202 - 4693
PDGF-AB/BB	9618	**LOW**	11200 - 34600
Perforin	6054		1119 - 10192
RANTES	500		389 - 2464
sCD137	27.5		3.7 - 40.4
sCD40L	1065		361 - 11200
SCF	804		382 - 1908
SDF-1	3547		868 - 4506
sFas (ng/ml)	12.6		2.9 - 44.8
sFasL	37.4		24 - 428
TARC	21.6		7 - 245
TGFα	3.7		0 - 30.5
TNFα	51.8		15 - 167
TNFβ	12.5		0 - 54.7
TPO	171		36 - 1231
TRAIL	34.5		4.4 - 87.6
TSLP	1.1		0 - 2.6
VEGF-A	337		13 - 495

† Reference intervals estimated by data-mining ≥1000 SERUM samples drawn from both healthy and pathological subjects.

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Cytokine Groupings - Immune Signatures

Groupings represent co-expressing cytokines identified by non-biased clustering of >130 clinical plasma-EDTA samples

Analyte	Results (pg/ml)		Reference Interval†
GROUP A1 - INNATE/AUTOIMMUNE INFLAMMATION			
FGF-2	51.6		0 - 215
IFN-α2	32.6		0 - 139
IL-1α	< 3.0		0 - 82.5
IL-1β	9.9		0 - 89.4
IL-1RA	3.0		0 - 40.9
IL-2	< 0.4		0 - 9.9
IL-17A	1.5		0 - 23.3
GROUP A2 - PRO-INFLAMMATORY/T CELL BIOMARKERS			
Fractalkine	212		0 - 441
IFNγ	3.5		0 - 18.3
IL-4	3.0		0 - 8.1
IL-5	6.8		0.4 - 18.4
IL-9	7.2		0 - 27.2
IL-12p40	23.4		14 - 186
IL-12p70	19.1		0 - 25.2
IL-13	147		0 - 229
IL-17F	17.0		0 - 69.8
IL-22	65.6		0 - 164
MCP-3	33.8		0 - 41.2
MIP-1α	15.8		0 - 88.1
TGFα	3.7		0 - 30.5
TNFα	51.8		15 - 167
TNFβ	12.5		0 - 54.7
GROUP A3 - HEMATOPOIETIC GROWTH FACTORS			
GM-CSF	20.1		0 - 99.4
G-CSF	< 6.0		0 - 88.5
IL-3	< 0.4		0 - 1.1
IL-7	2.4		0 - 17.4
GROUP B - INNATE INFLAMMATION/CYTOKINE STORM			
BAFF	1414		329 - 2260
FLT-3L	23.2		0 - 51.1
IL-27	2659		167 - 4330
IL-6	2.6		0 - 10.6
IL-8	5.3		0 - 26.0
IP-10	38.2		19 - 334
I-TAC	31.4		18 - 220
IL-10	2.4		0 - 21.6
IL-15	15.6		0 - 65.1
IL-18	40.3		6 - 283
MCP-1	302		72 - 723
MCP-2	33.1		5.7 - 88.5
M-CSF	62.3		0 - 321
MIG	783		380 - 6176
MIP-1β	46.4		8 - 115
MIP-3α	10.0		2.7 - 44.3
MIP-3β	66.8		26 - 237
GROUP C - CELL DEATH BIOMARKERS			
Perforin	6054		1119 - 10192
sFas (ng/ml)	12.6		2.9 - 44.8
TRAIL	34.5		4.4 - 87.6

Analyte	Results (pg/ml)		Reference Interval†
GROUP D1 - LYMPHOCYTE RECRUITMENT/ACTIVATION			
BCA-1	68.7		28 - 249
CCL28	720		0 - 800
Granzyme A	79.5		9 - 120
Granzyme B	5.7		0.9 - 26.3
I-309	26.8		0.8 - 66.4
IL-16	363		19 - 788
IL-23	2794		0 - 6719
IL-35	852	**HIGH**	0 - 371
Lymphotactin	79.0		0 - 100
sCD137	27.5		3.7 - 40.4
sFasL	37.4		24 - 428
TPO	171		36 - 1231
GROUP D2 - MUCOSAL INFLAMMATION/DAMAGE			
Eotaxin-3	89.7		7.7 - 93.2
HMGB1	4009		0 - 4078
IFNβ	161		0 - 161
IFNω	153	**HIGH**	0 - 67.3
IL-11	24.6		0 - 41.2
IL-17E/IL-25	165		0 - 1785
IL-20	198	**HIGH**	12 - 126
IL-21	13.7		0 - 32.5
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IL-31	74.5	**HIGH**	0 - 55.3
IL-33	32.1		0 - 36.5
IL-34	198	**HIGH**	6 - 149
LIF	84.2	**HIGH**	0 - 24.3
TSLP	1.1		0 - 2.6
GROUP E - IMMUNE CELL TRAFFICKING/ACTIVATION			
6CKine	857		325 - 1345
CTACK	1020		235 - 1379
Eotaxin	33.8		7.5 - 90.9
Eotaxin-2	284		73 - 1309
MDC	774		167 - 1214
MIP-1δ	1639		1166 - 7149
MPIF-1	271		69 - 715
RANTES	500		389 - 2464
SCF	804		382 - 1908
SDF-1	3547		868 - 4506
GROUP F - PLATELET ACTIVATION/WOUND HEALING			
APRIL	1374		180 - 5514
EGF	22.1		0 - 191
ENA-78			207 - 1563
GCP-2	101		30 - 258
GROα	20.3		0 - 62.3
MCP-4	89.7		22 - 156
PDGF-AA	638		202 - 4693
PDGF-AB/BB	9618	**LOW**	11200 - 34600
sCD40L	1065		361 - 11200
TARC	21.6		7 - 245
VEGF-A	337		13 - 495

† Reference intervals estimated by data-mining ≥1000 SERUM samples drawn from both healthy and pathological subjects.

Cytokine Groupings Descriptions

GROUP A1 - INNATE / AUTOIMMUNE INFLAMMATION
The analytes in this group are associated with innate immunity (IL-1α/β, IL-17E/IL-25, IFNα2), type 1 (IFNα2, IL-2, MIP-1α), and type 3 (IL-17A, IL-1) immune responses. IL-1, type I interferons, IL-17, MIP-1α, and FGF-2 contribute to autoimmune diseases, while IL-2 and IL-17E/IL-25 can either promote or suppress autoimmunity. IL-17A and FGF-2 synergistically drive inflammation in autoimmune arthritis. IL-1, IL-17, and FGF-2 potentiate Th17-mediated immunity, a key driver of autoimmunity, whereas IL-2 and IL-17E/IL-25 negatively regulate Th17 activity. IFNα2 exacerbates Th17-mediated inflammation, as seen in systemic lupus erythematosus (SLE), where IFNα2 and IL-17A form a pathogenic signaling axis. IL-1α/β also drive innate inflammatory responses and autoinflammatory conditions, and IL-1RA is expressed as a negative regulator of IL-1 signaling.
GROUP A2 - PRO-INFLAMMATORY/T CELL BIOMARKERS
This group of analytes includes pro-inflammatory cytokines involved in initiating innate inflammation and adaptive immune responses. The cytokine profile reflects Th1 (IFNγ, IL-12p70, TNFβ; intracellular pathogens/autoimmunity), Th2 (IL-4, IL-5, IL-13, IL-9; helminths/allergy/tissue repair), Th17 (IL-17F, IL-22; extracellular pathogens/autoimmunity), Th9 (IL-9), and Th22 (IL-22, IL-13) responses, which influence allergy and autoimmunity. Mixed T cell cytokine patterns may indicate diverse inflammatory responses, T cell heterogeneity and plasticity, or hybrid cells expressing multiple cytokines (e.g., IL-4 with IFNγ, IFNγ with IL-17A). These patterns may also reflect regulatory mechanisms, such as type 2 cytokine release following tissue damage from type 1 or type 3 responses.
GROUP A3 - HEMATOPOIETIC GROWTH FACTORS
The analytes in this group are hematopoietic growth factors and could indicate the expansion and activation of lymphocytes (IL-7) and/or leukocytes (GM-CSF, G-CSF, IL-3).
GROUP B - INNATE INFLAMMATION/CYTOKINE STORM
High levels of these analytes may indicate innate immune responses. IL-6 drives acute phase protein release, IL-18 acts as a pro-inflammatory alarmin via inflammasome activation, and Flt-3L supports innate lymphoid cell development. Elevated levels can signify severe systemic inflammation, such as cytokine storm (CRS). Key cytokines involved in CRS include IL-6, IL-10, IL-18, IL-8, MIG, IP-10, MIP-1ß, and MCP-1. IL-10, despite its anti-inflammatory role, is upregulated in CRS, reflecting an insufficient regulatory response. High analyte levels are common in CRS-related conditions like macrophage activation syndrome (MAS), adult-onset Still's disease (AOSD), systemic arthritis, hemophagocytic lymphohistiocytosis (HLH), and lymphocytic leukemia.
GROUP C - CELL DEATH BIOMARKERS
The analytes in this group promote cell death through facilitating (perforin) or directly inducing apoptosis (sFas, TRAIL).
GROUP D1 - LYMPHOCYTE RECRUITMENT/ACTIVATION
Elevated levels of these analytes may reflect the recruitment and activation of NK, T, and B cells. Granzyme A and B are cytotoxic mediators from NK and CD8+ T cells. sCD137 indicates NK and T cell activity, while sFasL regulates apoptosis and is shed by NK and CD8+ T cells. Lymphotactin (CD8+ T cells), CCL28 (NK and T cells), I-309 and IL-16 (CD4+ T cells) recruit lymphocytes to inflammation sites. IL-23 has context-specific pro-inflammatory effects on NK cells, CD4+ and CD8+ T cells, while IL-35 suppresses inflammation and cytotoxic cell function.
GROUP D2 - MUCOSAL INFLAMMATION/DAMAGE
Elevated levels of these analytes may indicate tissue injury and mucosal inflammation. IL-17E/IL-25, TSLP, and IL-33 are epithelial alarmins that activate type 2 immune responses. IFNβ and IFNω (type 1 interferons) and IL-28A and IL-29 (type 3 interferons) are linked to innate antiviral responses and mucosal immunity. HMGB1, released by damaged cells, promotes interferon expression. IL-34 supports mucosal-resident macrophages, while IL-11, IL-20, and IL-21 contribute to epithelial defense and tissue repair.
GROUP E - IMMUNE CELL TRAFFICKING/ACTIVATION
The analytes in this group drive the recruitment, homing and activation of leukocytes and lymphocytes.
GROUP F - PLATELET ACTIVATION/WOUND HEALING
High levels of these analytes suggest platelet activation and wound healing, as they are released by platelets and involved in angiogenesis, tissue remodeling, and inflammation. Elevated levels are seen in conditions linked to vascular injury, angiogenesis, and thrombocytosis, such as AOSD, Kawasaki disease, juvenile arthritis, FMF, COVID-19, and Crohn's disease. Lower levels are associated with thrombocytopenia-related conditions like HLH, lymphocytic leukemia, and hematopoietic stem cell transplantation. Notably, serum samples show significantly higher analyte levels than plasma samples from the same individuals.

Descriptions of the analytes and groupings with citations are available from Eve Diagnostics.
Clusters of co-expressing cytokines were determined with unsupervised clustering analysis of >130 plasma-EDTA specimens, using a similar approach as described in our publication: Polley DJ, et al. (2023) Identification of novel clusters of co-expressing cytokines in a diagnostic cytokine multiplex test. Front. Immunol. 14:1223817. doi: 10.3389/fimmu.2023.1223817. The designations of physiological/pathological significance assigned to each grouping are speculative, based on an analysis of the immune signatures in our database of clinical specimens and on the functional/pathological roles of the analytes in each grouping established in the scientific literature.