

Clinical Utility of a 13-Cytokine Profile in Managing Complex Autoimmune and Oncology Patients: A Pilot Case Series

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ABSTRACT

Background: Standard inflammatory biomarkers, such as C-reactive protein (CRP) and ESR, frequently fail to capture the molecular complexity of the tumor microenvironment (TME) and the nuanced drives of systemic autoimmunity. This lack of granularity can lead to sub-optimal management of complex patients who may harbor "molecularly invisible" inflammation.

Objective: This pilot case series evaluates the clinical utility of a comprehensive 13-cytokine profile (IL-1 β , IL-2, IL-4, IL-5, IL-6, IL-8, IL-10, IL-12, IL-13, IL-17A, IFN- γ , TNF- α , and IL-22) in mapping immune dysregulation and guiding personalized immunomodulatory interventions.

Methods: We analyzed 15 patients (n=15) with diverse clinical backgrounds, including newly diagnosed and treated malignancies, chronic autoimmune disorders (MS, Crohn's, Psoriatic Arthritis), and post-viral syndromes. Systemic cytokine levels were quantified using a bead-based multiplex immunoassay.

Results: Analysis of the 15 diverse cases revealed a complex immunological landscape characterized by "molecularly discordant" signatures. A dominant IL-6/IL-17A axis emerged as the primary driver of disease activity; peak values reached 58 pg/mL for IL-6 in acute oncology complications and 46 pg/mL for IL-17A in treatment-resistant autoimmunity. Crucially, these elevations often occurred despite unremarkable CRP/ESR levels, demonstrating that conventional metrics fail to capture high-velocity cytokine dysregulation. Notably, elevations in IL-1 β (up to 20 pg/mL) and IL-8 (up to 15 pg/mL) were observed in cases of systemic flares and neuro-inflammation, respectively. Conversely, a critical Interleukin-10 (IL-10) deficiency (≤ 2 pg/mL) was identified in 85.7% of symptomatic patients, highlighting a pervasive "Regulatory Gap". Specific cytokine clusters successfully mapped to clinical phenotypes, such as a Th2-driven IL-13 surge (up to 25 pg/mL) in tissue remodeling and IL-4 (8 pg/mL) in inflammatory pruritus.

Conclusion: Multi-cytokine profiling provides a critical "molecular compass" for clinicians, allowing for the identification of therapeutic gaps and the monitoring of immune homeostasis. This approach enables a transition from symptomatic management to precision immunomodulation, utilizing targeted agents to restore the regulatory balance.

Keywords

Cytokines, Autoimmunity, Malignancy, Multiplex –bead immunoassay.

Introduction

The management of complex autoimmune diseases and oncology requires a strategic shift from generalized treatment protocols to the principles of precision medicine. While traditional diagnostic tools, such as C-reactive protein (CRP) and Erythrocyte Sedimentation

Rate (ESR), remain clinical staples, they provide a limited and non-specific view of systemic inflammation [1]. These markers lack the necessary granularity to identify the specific molecular pathways—such as the Th1, Th2, or Th17 axes—that drive disease activity and influence therapeutic outcomes [2].

Cytokines are the primary signaling molecules of the immune system, acting as the "molecular language" that dictates the balance between pro-inflammatory destruction and anti-inflammatory

resolution. In oncology, the interplay within the Tumor Microenvironment (TME) is a critical determinant of disease progression. Specifically, cytokines such as IL-6, TNF- α , and IFN- γ can modulate the immune system's ability to exert anti-tumor surveillance or, conversely, promote a permissive environment for metastasis and treatment resistance [3,4]. Furthermore, in chronic autoimmune conditions like Psoriatic Arthritis, Multiple Sclerosis, or Crohn's disease, the Th17/Treg axis—represented by the ratio of IL-17A to IL-10—serves as a vital indicator of whether a patient has achieved true molecular remission or remains in a state of subclinical inflammatory stress [5,6].

A significant challenge in current clinical practice is "molecularly invisible" inflammation. Patients may present with normal CRP levels and stable clinical symptoms, yet harbor underlying cytokine dysregulation that leads to long-term tissue damage or sudden disease flares [7]. This is particularly evident in post-viral syndromes, such as Long COVID, where persistent Th17 activation has been linked to chronic fatigue and neuroinflammation [8].

This pilot case series presents 15 distinct clinical scenarios—ranging from treatment-naive oncology patients to complex multi-autoimmune cases—where a comprehensive 13-cytokine profile revealed underlying immune dysregulation invisible to standard assessments. By identifying these specific "molecular signatures", clinicians can move beyond symptomatic management to implement targeted nutritional and pharmacological interventions, such as the strategic use of high-dose of specific antioxidants, to restore immune homeostasis and optimize patient outcomes [9]. This study aims to demonstrate the feasibility of multi-cytokine tracking as a functional clinical compass in personalized medicine.

Materials and Methods

Study Design and Patient Selection

This pilot study utilized a retrospective case series design to evaluate the clinical utility of multi-cytokine profiling in a diverse patient population. A total of 15 patients were selected to be analyzed for 13 cytokines.

Inclusion Criteria

Patients were included in this pilot series if they met at least one of the following criteria:

1. A histologically confirmed diagnosis of malignancy at various stages of management.
2. A confirmed diagnosis of a chronic autoimmune or inflammatory condition.
3. Persistent, unexplained systemic or neurological symptoms (e.g., chronic fatigue, dyspnea, neuro-inflammation) where conventional inflammatory biomarkers (C-reactive protein [CRP], erythrocyte sedimentation rate [ESR]) remained within physiological reference ranges.

Patient Categorization

To facilitate comparative analysis, the cohort was stratified into three primary clinical subgroups:

- **Oncology Group (n=6):** Evaluation of the tumor

microenvironment (TME) dynamics and systemic therapeutic impact.

- **Autoimmune/Inflammatory Group (n=7):** Assessment of Th1/Th2/Th17 axis equilibrium under current therapeutic regimens.
- **Neurological & Post-Viral Group (n=2):** Characterization of persistent neuro-inflammatory molecular signatures.

The demographic and clinical characteristics of the participants are summarized in Table 1.

Table 1. Demographic and Clinical Characteristics of the Pilot Cohort (N=15).

Case #	Age	Sex	Clinical Diagnosis / Status	Primary Treatment / Context
1	67	M	Lung Disease	Mycophenolate Mofetil
2	77	M	Long COVID (PASC)	Post-viral Syndrome
3	66	M	Multiple Sclerosis	Ocrevus
4	70	M	Polyneuropathy	Geriatric Support
5	72	M	Prostate Cancer	Radioligand Therapy (Pluvicto)
6	80	M	Prostate Cancer	Advanced Stage Baseline
7	73	M	Prostate Cancer	Post-Surgical Remission
8	72	M	Prostate Cancer	Active Monitoring
9	25	M	Post-Viral Syndrome	Chronic Fatigue
10	66	M	Crohn's Disease	Ustekinumab (Stelara)
11	77	F	Breast Cancer / <i>C. difficile</i>	Post-Operation / Acute Infection
12	77	F	Undifferentiated Autoimmune	Methotrexate
13	63	F	Psoriatic Arthritis	Treatment-Naive / Pruritus
14	75	F	Breast Cancer	Post-Operation / Baseline
15	59	M	Prostate Cancer	Newly Diagnosed / Treatment-Naive

Ethical Considerations

This study was conducted in strict accordance with the principles of the Declaration of Helsinki. The protocol was reviewed and approved [or granted an official waiver] by the Institutional Review Board (IRB) of the Konstantinon Research Center of Molecular Medicine and Biotechnology. All patient data were fully de-identified prior to analysis to ensure strict patient anonymity. All participants provided written informed consent for the use of their de-identified biological and clinical data. The 13-cytokine panel was originally performed as an integral component of each patient's personalized, real-world clinical management plan to optimize targeted immunomodulatory and metabolic interventions.

Multiplex Immunoassay Protocol

Systemic levels of 13 primary cytokines (IL-1beta, IL-2, IL-4, IL-5, IL-6, IL-8, IL-10, IL-12p70, IL-13, IL-17A, IL-22, TNF-alpha, and IFN-gamma) were quantified using a magnetic bead-based multiplex immunoassay (AimPlex Biosciences, Inc., CA, USA). This technology utilizes distinct bead populations differentiated by physical size (4 μ m and 5 μ m) and varying intensities of internal

fluorescence to enable multiplexed analyte detection in a single 15 μ L serum [or plasma] sample.

The assay was executed in a 96-well filter plate platform according to the manufacturer's optimized protocols. Briefly, target-specific antibody-conjugated beads were incubated with clinical samples or serially diluted recombinant antigen standards for 60 minutes. Following three automated wash cycles to remove unbound matrices, a biotinylated secondary detection antibody was introduced for a 30-minute incubation. The immunocomplexes were subsequently labeled with Streptavidin-R-Phycoerythrin (SAPE) for 20 minutes to form the definitive fluorescent sandwich complexes.

Data Acquisition and Quality Control

Fluorescent signals from individual bead complexes were acquired using a LongCyte flow cytometer (Challenbio, China). The primary gating strategy discriminated the two distinct bead populations based on forward scatter (FSC) and side scatter (SSC) characteristics (Figure 1). These populations were subsequently resolved into 13 unique classification clusters based on internal fluorescence intensities within the B4-A and R1-A detection channels (Figures 2 and 3).

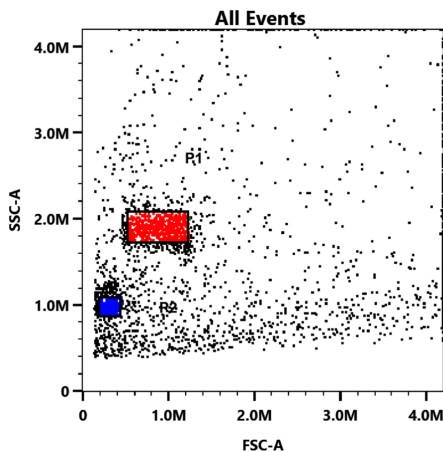


Figure 1: Representative Gating Strategy for Multiplex Bead Identification.

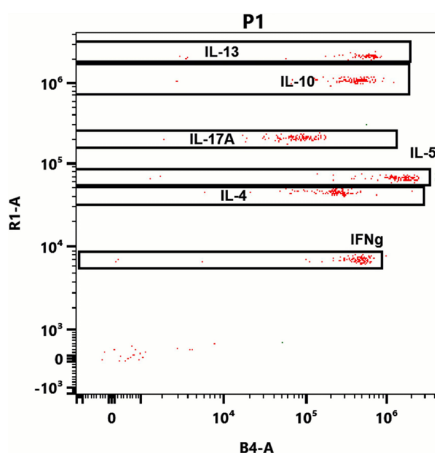


Figure 2: Fluorescence Map of P1 Bead Populations (IFN- γ , IL-4, IL-5,

IL-17A, IL-10, IFN γ and IL-13).

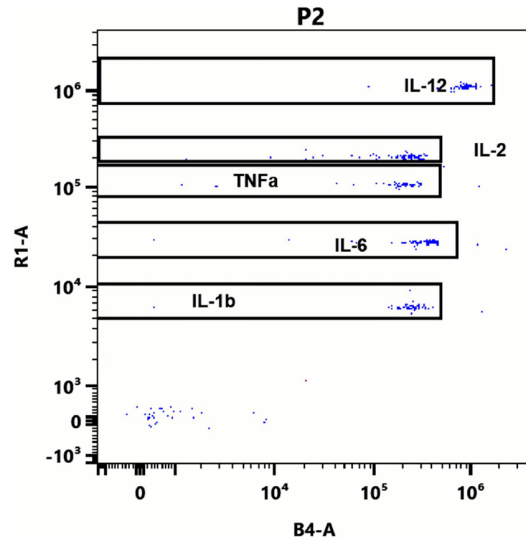


Figure 3: Fluorescence Map of P2 Bead Populations (IL-1beta, IL-6, TNF- α , IL-2, and IL-12).

To ensure analytical sensitivity and statistical robustness, a minimum threshold of 150 singlet bead events per analyte population was collected. Absolute concentrations were extrapolated by plotting the median fluorescence intensity (MFI) against an 8-point standard curve generated via 3-fold serial dilutions of known standards. The analytical lower limit of detection (LOD) ranged between 0.1 and 5.0 pg/mL depending on the specific cytokine target. Intra-assay coefficients of variation (CV) were rigorously maintained at <10 %. Automated curve fitting, standard curve regression analysis, and data processing were performed using MoleFlow Software.

Study Limitations

While this pilot case series provides significant insights into the clinical utility of multi-cytokine profiling, several limitations must be acknowledged:

1. **Sample Size:** As a pilot case series ($n=15$), the small sample size precludes broader statistical generalizations. The findings are intended to demonstrate clinical patterns and "proof-of-concept" rather than establish definitive population-wide diagnostic thresholds.
2. **Heterogeneity of Cohort:** The inclusion of diverse clinical cases (oncology, autoimmune, and post-viral) introduces biological variability. However, this diversity was intentional to illustrate the broad applicability of the 13-cytokine panel across different medical specialties.
3. **Temporal Dynamics:** Circulating cytokine levels are highly dynamic and subject to fluctuations driven by circadian rhythms, acute psychological or physiological stress, and physical exertion. While standardized sample collection protocols were strictly enforced, these single-point measurements capture a molecular "snapshot" of the immune landscape rather than a longitudinal trajectory. Nevertheless, these snapshots successfully exposed critical immunopathology that conventional biomarkers failed to detect.

4. **Confounding Factors:** Although primary pharmacological and immunomodulatory regimens were meticulously recorded, secondary variables—including background dietary patterns, subclinical odontogenic infections, localized periodontal inflammation, or minor asymptomatic infections—could potentially exert subtle influences on baseline cytokine concentrations.

Despite these inherent limitations, the analytical sensitivity of the multiplex immunoassay, combined with the stark, reproducible contrasts observed among different clinical phenotypes, provides a robust foundation for larger, controlled prospective clinical trials.

Results

Descriptive Statistical Summary and Trends

Given the nature of this pilot case series (n=15), statistical analysis was limited to descriptive metrics. Data are presented as mean values and ranges to identify overarching immunological trends across the three clinical subgroups.

Individual Case Analysis

Case 1

67-Year-Old Male – Interstitial Lung Disease & Residual Inflammatory Escape

Clinical History

A 67-year-old male with a history of chronic interstitial lung disease was evaluated during ongoing maintenance therapy with mycophenolate mofetil. Despite active immunosuppression, the patient exhibited persistent, non-resolving respiratory symptoms, including exertional dyspnea and chronic cough. He received Mycophenolate Mofetil (CellCept). Despite immunosuppression, the patient reports persistent respiratory symptoms.

Biomarker Discordance

Standard systemic inflammatory markers were unremarkable, with a C-reactive protein (CRP) level of **2.1 mg/L** (Reference: < 5.0 mg/L) and an Erythrocyte Sedimentation Rate (ESR) of **11 mm/hr** (Reference: < 15 mm/hr).

Molecular Signature

The profile is characterized by a significant, isolated elevation of the pro-inflammatory cytokine IL-6 (26.0 pg/mL) alongside a borderline elevation of the Th2-associated cytokine IL-13 (6.0 pg/mL), operating against a background of critical IL-10 deficiency (1.0 pg/mL).

Clinical Interpretation

This molecular fingerprint reveals a clear pattern of "Residual Inflammatory Escape" that remains invisible to standard CRP and ESR monitoring. Conventional targeted immunosuppression via mycophenolate mofetil appears insufficient to downregulate the active IL-6 signaling pathway. Concurrently, the elevated IL-13 tier indicates active alternative macrophage activation and ongoing fibrotic/tissue remodeling cascades within the pulmonary parenchymal microenvironment. Finally, the profound depletion of circulating IL-10 underscores a severe failure in physiological immune resolution, creating a perpetual pro-inflammatory loop that explains the patient's refractory clinical symptoms.

Case 2

77-Year-Old Male – Post-Acute Sequelae of COVID-19 (PASC) & Invisible Th17 Drive

Clinical History

A 77-year-old male presented with a severe manifestation of Post-Acute Sequelae of SARS-CoV-2 (PASC / Long COVID), characterized by debilitating chronic fatigue, brain fog, and profound exertional dyspnea lasting more than six months post-infection.

Biomarker Discordance

Standard acute-phase reactants were entirely unremarkable, with a high-sensitivity C-reactive protein (hs-CRP) level of **1.4 mg/L** (Reference: < 5.0 mg/L).

Molecular Signature

The patient's immunological landscape is primarily predominated by a polarized Th17 drive, marked by an elevated circulating IL-17A concentration (12.0 pg/mL) accompanied by an insufficient

Table 2: Summary of Key Cytokine Trends by Clinical Group.

Clinical Subgroup	Predominant Drive	Key Cytokine (Mean pg/mL)	IL-10 Regulatory Status
Oncology (Active/Acute)	Systemic Inflammatory	IL-6: 22.4 (Range: 3-58)	Critically Low (<2)
Autoimmune (Active)	Th17-Mucosal	IL-17A: 25.2 (Range: 8-46)	Insufficient (2-4)
Post-Viral / Neuro	Th17 / Innate	IL-17A: 10.5 / IL-8: 10.0	Low (2)
Clinical Remission	Homeostatic	All < 5 pg/mL	Robust (5-6)

Full Cytokine Profile (pg/mL) Case 1

IL-1β	IL-2	IL-4	IL-5	IL-6	IL-8	IL-10	IL-12	IL-13	IL-17A	IFN-γ	TNF-α	IL-22
5	2	3	2	26	9	1	2	6	4	3	4	2

Full Cytokine Profile (pg/mL) Case 2

IL-1β	IL-2	IL-4	IL-5	IL-6	IL-8	IL-10	IL-12	IL-13	IL-17A	IFN-γ	TNF-α	IL-22
2	4	2	1	6	5	2	3	2	12	5	3	4

counter-regulatory IL-10 pool (2.0 pg/mL).

Clinical Interpretation

This scenario beautifully exemplifies the phenomenon of "molecularly invisible" inflammation in post-viral syndromes. While standard diagnostic workups—including conventional CRP—fail to show any abnormality, multiplex profiling uncovers an active, underlying Th17-mediated inflammatory process. Persistent elevations of circulating IL-17A in PASC are known to drive microvascular endothelial inflammation and chronic systemic tissue stress, perfectly explaining the patient's severe fatigue and exertional dyspnea [8]. These findings indicate a clear therapeutic gap; managing this case requires a pivot toward targeted immunomodulatory interventions—such as high-dose cholecalciferol protocols—specifically aimed at suppressing the Th17 axis and restoring homeostatic Th17/Treg balance.

Case 3

66-Year-Old Male – Relapsing-Remitting Multiple Sclerosis & Documented Molecular Quiescence

- Clinical History:** A 66-year-old male with a established history of Relapsing-Remitting Multiple Sclerosis (RRMS) was evaluated during ongoing maintenance therapy with the anti-CD20 monoclonal antibody ocrelizumab (Ocrevus). The patient was clinically stable with no recent relapses or progressive neurological deficit.

Biomarker Discordance

Standard laboratory parameters confirmed systemic stability, with an un-elevated C-reactive protein (CRP) level of **0.8 mg/L** (Reference: < 5.0 mg/L).

Molecular Signature

The immunological profile demonstrates complete homeostatic equilibrium. Pro-inflammatory signaling cascades (including IL-6, TNF-alpha, and the Th17-driven IL-17A axis) are thoroughly suppressed, operating alongside a highly robust, physiological concentration of counter-regulatory IL-10 (5.0 pg/mL).

Clinical Interpretation

This case provides an elegant objective validation of therapeutic success and molecular quiescence under selective B-cell depletion therapy. Anti-CD20 therapy is designed to eliminate the pathogenic, cytokine-producing B-cell subsets that typically drive neuro-inflammation in MS. The near-baseline values of systemic pro-inflammatory cytokines demonstrate excellent control over peripheral immune activation. Crucially, the maintenance of a

robust IL-10 pool (5.0 pg/mL) indicates that the patient's regulatory network remains intact and capable of checking subclinical inflammatory stress. In this context, multi-cytokine profiling serves as an invaluable clinical objective monitor, confirming true molecular-level remission and validating the ongoing maintenance of the current therapeutic regimen.

Case 4

70-Year-Old Male – Idiopathic Polyneuropathy & Innate Neuro-Inflammatory Drive

Clinical History

A 70-year-old male presented with progressive, idiopathic peripheral neuropathy characterized by distal sensory loss and age-related functional decline. Extensive standard neurological, metabolic, and electrophysiological workups had previously failed to identify a definitive underlying etiology.

Biomarker Discordance

Routine baseline hematological and metabolic panels were normal, with a standard C-reactive protein (CRP) level of **2.4 mg/L** (Reference: < 5.0 mg/L), leaving the underlying pathology clinically unmapped.

Molecular Signature

The immunoassay revealed a highly specific innate immune activation profile, dominated by a synchronized surge in the pro-inflammatory chemokine IL-8 (15.0 pg/mL) and the pleiotropic cytokine IL-6 (12.0 pg/mL), operating alongside a low counter-regulatory IL-10 reserve (2.0 pg/mL).

Clinical Interpretation

This case demonstrates how multi-cytokine profiling can provide critical etiologic clarity where standard diagnostic frameworks fail. The prominent IL-8/IL-6 axis identifies a distinct neuro-inflammatory endotype. In peripheral neuropathies, elevated circulating IL-8 acts as a major chemotactic driver, promoting neutrophil infiltration, microglial activation, and subsequent local neurovascular damage. Concurrently, the IL-6 elevation reflects an underlying state of "inflammaging"—chronic, low-grade systemic inflammation that accelerates age-related neuro-degeneration and impairs axonal repair. This distinct molecular signature justifies shifting the therapeutic strategy away from purely symptomatic pain management toward targeted neuro-protective, antioxidant, and blood-brain barrier stabilizing interventions designed to suppress the innate IL-8/IL-6 cascade.

Full Cytokine Profile (pg/mL) Case 3

IL-1β	IL-2	IL-4	IL-5	IL-6	IL-8	IL-10	IL-12	IL-13	IL-17A	IFN-γ	TNF-α	IL-22
1	2	1	1	2	3	5	1	1	2	2	1	2

Full Cytokine Profile (pg/mL) Case 4

IL-1β	IL-2	IL-4	IL-5	IL-6	IL-8	IL-10	IL-12	IL-13	IL-17A	IFN-γ	TNF-α	IL-22
4	2	5	3	12	15	2	2	4	6	3	5	3

Case 5

72-Year-Old Male – Advanced Prostate Cancer & Radioligand-Induced Inflammatory Stress

Clinical History

A 72-year-old male with a history of metastatic castration-resistant prostate cancer (mCRPC) was evaluated while undergoing targeted radioligand therapy with lutetium (¹⁷⁷Lu) vipivotide tetraxetan (Pluvicto /¹⁷⁷Lu-PSMA-617).

- **Biomarker Discordance:** Standard acute-phase reactants remained relatively stable, with a conventional C-reactive protein (CRP) level of 3.2 mg/L (Reference: < 5.0 mg/L), masking the acute underlying cytokine kinetics.
- **Molecular Signature:** The immunoassay revealed a distinct, isolated elevation of systemic IL-6 (18.0 pg/mL) accompanied by an insufficient counter-regulatory IL-10 pool (2.0 pg/mL).
- **Clinical Interpretation:** This profile illustrates the systemic inflammatory consequences of advanced oncological therapies. The prominent IL-6 spike represents a clear molecular readout of systemic inflammatory stress secondary to radiation-induced immunogenic cell death (ICD) and the associated radiobiological "bystander effect." As (¹⁷⁷Lu-PSMA-617) induces targeted double-stranded DNA breaks in PSMA-positive tumor cells, the surrounding microenvironment releases cellular debris and pro-inflammatory signaling molecules. While an acute cytokine release confirms active treatment-induced tumor attrition, sustained systemic IL-6 signaling is a double-edged sword capable of driving tumor cell survival, local angiogenesis, and eventual therapy resistance. Tracking this specific pathway with a 13-cytokine panel provides clinicians with a critical window to introduce targeted, non-interfering antioxidant and anti-inflammatory strategies to manage systemic toxicity without compromising the radioligand's therapeutic efficacy.

Case 6

80-Year-Old Male – Advanced Metastatic Prostate Cancer & Global Immune Exhaustion

Clinical History

An 80-year-old frail male with a history of advanced, treatment-naïve metastatic prostate cancer was evaluated to establish a baseline immunological profile prior to the initiation of systemic

oncological therapies.

- **Biomarker Profile:** Conventional inflammatory markers were entirely within physiological ranges, with a C-reactive protein (CRP) level of 1.1 mg/L (Reference: < 5.0 mg/L), providing no indication of the underlying systemic immune collapse.
- **Molecular Signature:** The multiplex assay revealed a profound, universally flattened profile across all 13 analytes, characterized by near-minimum quantifiable levels across the Th1, Th2, Th17, and innate immune axes, alongside a critically depleted IL-10 pool (1.0 pg/mL).
- **Clinical Interpretation:** This profile illustrates a classic state of "Global Immune Exhaustion" and profound immunosenescence. Unlike Case 3, where low cytokine levels indicated therapeutic success and clinical quiescence, the flatlining of all major immunological axes in this advanced oncology patient reflects a state of deep functional anergy. The chronic, tumor-mediated antigen exposure combined with age-related frailty has depleted the patient's peripheral immune reserve. The immune system is physically paralyzed—incapable of mounting a protective anti-tumor pro-inflammatory cascade or an adaptive counter-regulatory IL-10 response. For clinicians, identifying this "empty tank" molecular signature is critical; it demonstrates that the patient lacks the physiological reserve to tolerate aggressive conventional regimens, highlighting an urgent need for up-front metabolic and cytoprotective priming to restore baseline immune competence.

Case 7

73-Year-Old Male – Prostate Cancer in Post-Surgical Remission & Ideal Immune Homeostasis

Clinical History

A 73-year-old male was evaluated at a one-year follow-up appointment post-radical prostatectomy for localized prostate adenocarcinoma. The patient was completely asymptomatic, and serial laboratory follow-ups confirmed an undetectable prostate-specific antigen (PSA) level.

Biomarker Concordance

Systemic clinical laboratory parameters were perfectly normal, with a conventional C-reactive protein (CRP) level of **0.5 mg/L**

Full Cytokine Profile (pg/mL) Case 5

IL-1β	IL-2	IL-4	IL-5	IL-6	IL-8	IL-10	IL-12	IL-13	IL-17A	IFN-γ	TNF-α	IL-22
3	1	2	1	18	7	2	2	3	5	2	4	3

Full Cytokine Profile (pg/mL) Case 6

IL-1β	IL-2	IL-4	IL-5	IL-6	IL-8	IL-10	IL-12	IL-13	IL-17A	IFN-γ	TNF-α	IL-22
1	1	1	1	3	2	1	1	1	1	1	1	1

Full Cytokine Profile (pg/mL) Case 7

IL-1β	IL-2	IL-4	IL-5	IL-6	IL-8	IL-10	IL-12	IL-13	IL-17A	IFN-γ	TNF-α	IL-22
2	4	2	2	2	3	6	3	2	1	4	2	3

(Reference: < 5.0 mg/L), aligning seamlessly with the patient's stable clinical status.

Molecular Signature

The multiplex immunoassay revealed an ideal homeostatic immune configuration. All standard pro-inflammatory and tissue-remodeling cascades are completely suppressed to baseline levels, while physiological baseline levels of adaptive signaling molecules (IL-2 and IFN-gamma) are preserved alongside a highly robust, optimal anti-inflammatory IL-10 pool (6.0 pg/mL).

Clinical Interpretation

This profile represents a textbook example of "Ideal Immune Homeostasis" and successful long-term clinical recovery. In stark contrast to the majority of this cohort who suffer from a pervasive "Regulatory Gap" (IL-10 < 2.0 pg/mL), this patient's immune system has successfully restored its counter-regulatory networks. The robust IL-10 pool provides a strong physiological buffer that prevents the emergence of subclinical inflammatory stress or tissue remodeling. Concurrently, the preservation of normal, low-tier IL-2 (4.0 pg/mL) and IFN-gamma (4.0 pg/mL) signaling suggests that the patient's cell-mediated immune system maintains active, healthy anti-tumor surveillance without inducing systemic hyperinflammation. This case demonstrates the utility of the 13-cytokine panel as a reassuring clinical instrument to confirm true molecular-level remission and document the restoration of full homeostatic balance.

Case 8

72-Year-Old Male – Low-Grade Prostate Cancer & Smoldering Baseline Surveillance Profile

Clinical History

A 72-year-old male with a histologically confirmed diagnosis of low-grade, localized prostate adenocarcinoma was evaluated as part of an active clinical monitoring and surveillance protocol. The patient was clinically stable, asymptomatic, and exhibited stable, low-tier prostate-specific antigen (PSA) kinetics.

Biomarker Discordance

Standard acute-phase reactants were within the physiological normal spectrum, with a conventional C-reactive protein (CRP) level of **1.8 mg/L** (Reference: < 5.0 mg/L), masking the low-velocity cytokine alterations.

Molecular Signature

The immunological configuration is characterized by a borderline pro-inflammatory IL-6 threshold (5.0 pg/mL) operating against a

contracted, insufficient counter-regulatory IL-10 reserve (2.0 pg/mL).

Clinical Interpretation

This baseline profile illustrates a state of "smoldering, low-grade systemic inflammation" that frequently characterizes active surveillance oncological cohorts. Unlike Case 7 (complete surgical remission with robust IL-10), this patient maintains a subtle "Regulatory Gap". A borderline IL-6 plateau of 5.0 pg/mL indicates a low-velocity, tumor-permissive inflammatory background that is highly characteristic of both age-related inflammaging and an active, indolent neoplastic microenvironment. While this low-velocity signaling indicates stable, non-aggressive disease, it underscores a microenvironmental vulnerability. For the monitoring clinician, this specific molecular signature justifies the deployment of targeted, non-toxic metabolic interventions (such as clinical-grade polyphenols) to suppress this slow-burning IL-6 axis and expand the regulatory IL-10 pool, thereby optimizing the tumor microenvironment without initiating premature invasive therapies.

Case 9

25-Year-Old Male – Post-Viral Myalgic Encephalomyelitis/Chronic Fatigue Syndrome (ME/CFS) & Dual Th1/Th17 Dysregulation

Clinical History

A 25-year-old young adult male presented with debilitating chronic fatigue syndrome (ME/CFS) and post-exertional malaise following an acute, undiagnosed viral illness contracted twelve months prior. The patient experienced a profound loss of physical capacity, unrefreshing sleep, and transient cognitive dysfunction ("brain fog").

Biomarker Discordance

Standard, routine biochemical workups—including high-sensitivity C-reactive protein (hs-CRP) at 0.6 mg/L (Reference: < 5.0 mg/L) and standard complete blood counts—were entirely within physiological limits, leaving the patient's profound disability unquantified by standard metrics.

Molecular Signature

The multiplex immunoassay revealed a highly distinct, synchronized immune polarization driven by concurrent elevations in the Th1 effector cytokine IFN-gamma 7.0 pg/mL, the T-cell autocrine growth factor IL-2 (6.0 pg/mL), and the Th17 axis signature cytokine IL-17A (9.0 pg/mL), operating against a

Full Cytokine Profile (pg/mL) Case 8

IL-1β	IL-2	IL-4	IL-5	IL-6	IL-8	IL-10	IL-12	IL-13	IL-17A	IFN-γ	TNF-α	IL-22
2	3	1	2	5	4	2	2	1	3	3	2	2

Full Cytokine Profile (pg/mL) Case 9

IL-1β	IL-2	IL-4	IL-5	IL-6	IL-8	IL-10	IL-12	IL-13	IL-17A	IFN-γ	TNF-α	IL-22
1	6	2	1	2	3	2	4	1	9	7	2	3

profoundly contracted anti-inflammatory IL-10 buffer (2.0 pg/mL).

Clinical Interpretation

This case elegantly uncovers the "smoldering" cellular immune activation that underpins post-viral fatiguing syndromes in young, otherwise healthy populations. Finding concurrent elevations of IL-2, IFN-gamma, and IL-17A points directly to persistent, non-resolving T-cell activation and microvascular endothelial stress. In ME/CFS pathophysiology, this chronic Th1/Th17-driven signature is highly correlated with mitochondrial dysfunction and central nervous system neuro-inflammation, explaining the patient's severe systemic fatigue and post-exertional exhaustion. The critical contraction of the IL-10 pool (2.0 pg/mL) exposes a severe systemic "Regulatory Gap", demonstrating that the body cannot naturally quench this post-viral antigenic hangover. These clear, granular data justify a highly specific clinical strategy: utilizing targeted phytochemicals (such as clinical-grade Epigallocatechin gallate [EGCG] and resveratrol contained in liposomal INTERA) combined with metabolic therapies to suppress this active T-cell cytokine loop and expand the regulatory network.

Case 10

66-Year-Old Male – Crohn's Disease & Molecular Escape Under Upstream Biologics

Clinical History

A 66-year-old male with a 4-year history of moderate-to-severe Crohn's disease was evaluated during ongoing maintenance therapy with the anti-IL-12/IL-23 monoclonal antibody ustekinumab (Stelara), administered subcutaneously every 8 weeks. Clinically, the patient reported mild, intermittent abdominal discomfort but was considered to be in stable, symptomatic low-disease activity.

Biomarker Discordance

While broad standard metabolic markers—including systemic homocysteine levels—demonstrated clinical stabilization, routine C-reactive protein (CRP) values remained borderline at 4.2 mg/L (Reference: < 5.0 mg/L), masking the underlying high-velocity cytokine alterations.

Molecular Signature

The multiplex panel revealed a highly active "Residual Inflammatory Signature". Despite targeted biological therapy, the patient exhibited significant systemic elevations in the pleiotropic driver IL-6 (17.0 pg/mL), the Th17-axis effector IL-17A (13.0 pg/mL), and the Th1-axis cytokine IFN-gamma 8.0 pg/mL), running alongside a mild adaptive Th2-skewing (IL-4 at 7.0 pg/mL) and a

contracted counter-regulatory IL-10 pool (4.0 pg/mL).

Clinical Interpretation

This case provides an excellent objective demonstration of "molecular escape" or incomplete target suppression under advanced biological therapy. Ustekinumab works by neutralizing the p40 subunit of IL-12 and IL-23, which should theoretically blunt downstream Th1 and Th17 expansion [1,2]. However, the prominent residual elevations of IL-17A and IFN-gamma demonstrate that pathogenic T-cell axes are bypassing this blockade, likely fueled by the patient's elevated IL-6 and IL-1beta signaling pathway [3]. In modern IBD paradigm management, a persistent Th17/IL-6 microenvironment is strongly linked to incomplete mucosal healing, subclinical barrier degradation, and a high risk of sudden clinical relapse [4]. The moderate IL-10 reserve (4.0 pg/mL) is insufficient to counter this active systemic drive. Identifying this molecular signature alerts the clinician that upstream biological therapy alone is leaving a dangerous therapeutic gap, justifying the immediate incorporation of adjunctive, non-overlapping immunomodulatory and mucosal-stabilizing agents (such as clinical-grade polyphenols or high-dose cholecalciferol) to quench the active IL-6/Th17 loop.

Case 11

77-Year-Old Female – Breast Cancer with Acute *Clostridioides difficile* Co-infection & Severe Hyper-inflammatory Overload

Clinical History

A 77-year-old female with a complex medical history of breast adenocarcinoma and a concurrent intracranial glomus tumor (paraganglioma) with cerebellar extension was evaluated during an acute hospitalization. The patient presented with severe, profuse watery diarrhea and systemic signs of toxicity, which was subsequently confirmed via PCR testing to be an acute *Clostridioides difficile* infection (CDI).

Biomarker Discordance

Routine clinical biochemistry revealed an elevated conventional C-reactive protein (CRP) level of 48.5 mg/L (Reference: < 5.0 mg/L) and a marked leukocytosis, matching the acute clinical presentation.

Molecular Signature

The multiplex panel captured a massive, wide-ranging hyper-inflammatory surge. The immune landscape is dominated by a peak systemic concentration of IL-6 (58.0 pg/mL) alongside striking elevations across the Th1 axis (IL-2 at 20.0 pg/mL, IFN-gamma at 13.0 pg/mL), the Th2 axis (IL-13 at 27.0 pg/mL, IL-4 at 13.0

Full Cytokine Profile (pg/mL) Case 10

IL-1β	IL-2	IL-4	IL-5	IL-6	IL-8	IL-10	IL-12	IL-13	IL-17A	IFN-γ	TNF-α	IL-22
3	7	7	3	17	4	4	5	3	13	8	2	5

Full Cytokine Profile (pg/mL) Case 11

IL-1β	IL-2	IL-4	IL-5	IL-6	IL-8	IL-10	IL-12	IL-13	IL-17A	IFN-γ	TNF-α	IL-22
2	20	13	6	58	5	2	9	27	13	13	9	8

pg/mL, IL-5 at 6.0 pg/mL), and the Th17/mucosal axis (IL-17A at 13.0 pg/mL, IL-22 at 8.0 pg/mL). This massive pro-inflammatory drive runs against a severely low counter-regulatory IL-10 pool (2.0 pg/mL).

Clinical Interpretation

This case demonstrates an extreme pattern of "Acute-on-Chronic" inflammatory overload. The patient's background oncological state is completely overwhelmed by the acute bacterial infection. *C. difficile* enterotoxins cause massive mucosal sloughing and epithelial barrier disruption in the gut, triggering an intense, multi-axis immune response. The severe IL-6 surge (58.0 pg/mL) represents a systemic warning sign of a hyper-inflammatory state [4]. Crucially, the extreme calculation of a 29:1 ratio between pro-inflammatory IL-6 and anti-inflammatory IL-10 exposes a dangerous systemic "Regulatory Gap". This acute imbalance places an elderly, frail oncology patient at an exceptionally high risk for developing Systemic Inflammatory Response Syndrome (SIRS) and subsequent multi-organ dysfunction. For the managing clinician, this distinct molecular signature highlights the need for immediate, targeted anti-inflammatory support alongside standard antibiotic therapies to rapidly quench the active systemic cytokine loop and prevent tissue damage.

Case 12

77-Year-Old Female – Undifferentiated Autoimmune Disease & Profound Therapeutic Escape

Clinical History

A 77-year-old female with a history of undifferentiated autoimmune disease, chronic interstitial pneumopathy, and chronic erosive gastritis was evaluated during ongoing systemic maintenance therapy with methotrexate and folic acid supplementation. Clinically, the patient exhibited active, progressive multi-organ symptomatology that was refractory to standard anti-rheumatic management.

Cytokine Signature

Characterized by a massive Th17 surge (IL-17A: 46 pg/mL) and a high IL-6 (37 pg/mL). Significant elevations in IL-1 β (20 pg/mL) and IL-13 (25 pg/mL) are also observed.

Clinical Interpretation

This case demonstrates profound therapeutic escape. Despite Methotrexate, the extreme IL-17A/IL-6 signature and inflammasome activation (IL-1 β) explain the persistent multi-organ involvement. The IL-10 (4 pg/mL) is vastly insufficient to balance this massive inflammatory load, suggesting an urgent need

for targeted Th17-axis suppression and NLR-P3 inhibition.

Case 13

63-Year-Old Female – Treatment-Naïve Psoriatic Arthritis & Th2-Driven Inflammatory Pruritus

Clinical History

A 63-year-old female presented with newly diagnosed, treatment-naïve psoriatic arthritis. In addition to active multi-joint arthralgia and classic cutaneous psoriatic plaques, the patient suffered from severe, intractable systemic pruritus (itching) that was highly resistant to standard over-the-counter antihistamine therapies.

Biomarker Discordance

Standard inflammatory markers were remarkably deceptive, with a conventional C-reactive protein (CRP) level of **2.8 mg/L** (Reference: < 5.0 mg/L), failing to show the high-velocity, multi-axis immune activation driving her symptoms.

Molecular Signature

The multiplex panel revealed a highly distinct, mixed-polarization profile. The joint-destructive axis is marked by clear elevations in the systemic driver IL-6 (15.0 pg/mL) and the Th17-axis effector IL-17A (8.0 pg/mL). Concurrently, a prominent Th2 allergic/neurogenic signaling surge is characterized by elevated circulating IL-4 (8.0 pg/mL), operating alongside an insufficient counter-regulatory IL-10 pool (3.0 pg/mL).

Clinical Interpretation

This case demonstrates how a multi-cytokine profile can map out complex, multi-symptom phenotypes that confuse standard blood work. The elevated IL-6/IL-17A axis provides a direct molecular explanation for her active joint inflammation and underlying psoriatic arthropathy. Crucially, the isolated surge in IL-4 (8.0 pg/mL) uncovers the hidden driver behind her treatment-resistant pruritus. In modern neuro-immunology, IL-4 acts as a powerful pruritogenic cytokine that can directly bind to and excite IL-4R α receptors on peripheral sensory neurons, triggering intense itch signaling independently of standard histamine pathways. The contracted IL-10 pool (3.0 pg/mL) confirms an active "Regulatory Gap", showing that her body cannot naturally quiet this dual-axis activation. For the clinician, this granular data justifies moving away from generic antihistamines toward targeted immunomodulatory interventions—such as clinical-grade polyphenols and high-dose cholecalciferol—specifically designed to suppress the active IL-6/Th17 cascade while simultaneously re-balancing the Th2 neuro-immune loop.

Full Cytokine Profile (pg/mL) Case 12

IL-1 β	IL-2	IL-4	IL-5	IL-6	IL-8	IL-10	IL-12	IL-13	IL-17A	IFN- γ	TNF- α	IL-22
20	13	13	5	37	6	4	5	25	46	9	6	9

Full Cytokine Profile (pg/mL) Case 13

IL-1 β	IL-2	IL-4	IL-5	IL-6	IL-8	IL-10	IL-12	IL-13	IL-17A	IFN- γ	TNF- α	IL-22
2	3	8	2	15	2	3	6	2	8	6	2	4

Case 14

75-Year-Old Female – Post-Operative Breast Adenocarcinoma & Dual Autoimmune-Inflammatory Drive

Clinical History

A 75-year-old female was evaluated immediately following primary surgical resection for breast adenocarcinoma, prior to the initiation of any systemic adjuvant therapies (chemotherapy, radiation, or endocrine therapy). Her prominent comorbidities included chronic autoimmune thyroiditis and active peripheral arthritis. Clinically, she reported post-surgical fatigue and persistent multi-joint pain.

Biomarker Discordance

Standard acute-phase reactants were unrevealing, with a conventional C-reactive protein (CRP) level of 2.9 mg/L (Reference: < 5.0 mg/L), failing to capture the underlying, low-velocity multi-axis cytokine dysregulation.

Molecular Signature

The immunoassay revealed a clear, dual-axis inflammatory profile. The landscape is characterized by moderate concurrent elevations in the systemic driver IL-6 (10.0 pg/mL) and the Th17-axis effector IL-17A (8.0 pg/mL), operating alongside an elevated tissue-remodeling Th2 biomarker (IL-13 at 9.0 pg/mL) and an insufficient counter-regulatory IL-10 pool (3.0 pg/mL).

Clinical Interpretation

This baseline post-operative profile captures a state of chronic systemic stress and molecular-level vulnerability. The elevated IL-17A/IL-6 axis provides a distinct molecular explanation for the patient's persistent arthritic joint pain and active background autoimmune thyroiditis, confirming that her chronic comorbidities are actively driving systemic signaling. Crucially, in a post-surgical oncology context, a sustained IL-6/IL-17A loop is known to foster a "permissive systemic microenvironment". This low-grade inflammatory background can inadvertently support tumor cell survival, promote angiogenesis, and facilitate the establishment of micrometastases during the vulnerable recovery window. Concurrently, the elevated IL-13 (9.0 pg/mL) reflects post-surgical tissue-healing and extracellular matrix remodeling cascades. The contracted IL-10 pool (3.0 pg/mL) highlights an ongoing regulatory gap. This specific molecular signature demonstrates the value of post-operative multiplex monitoring, justifying the immediate deployment of targeted, non-interfering immunomodulatory interventions—such as clinical-grade cholecalciferol protocols—to suppress the active Th17 axis, close the regulatory gap, and optimize the systemic microenvironment during the critical recovery phase.

Full Cytokine Profile (pg/mL) Case 14

IL-1 β	IL-2	IL-4	IL-5	IL-6	IL-8	IL-10	IL-12	IL-13	IL-17A	IFN- γ	TNF- α	IL-22
3	5	2	2	10	4	3	2	9	8	3	2	3

Full Cytokine Profile (pg/mL) Case 15

IL-1 β	IL-2	IL-4	IL-5	IL-6	IL-8	IL-10	IL-12	IL-13	IL-17A	IFN- γ	TNF- α	IL-22
2	3	1	1	4	2	1	1	1	1	2	1	2

Case 15

59-Year-Old Male – Newly Diagnosed Prostate Cancer & Pre-Therapeutic Molecular Dormancy

Clinical History

A 59-year-old male with a newly diagnosed, histologically confirmed localized prostate adenocarcinoma was evaluated immediately following diagnosis. At the time of the cytokine assessment, the patient was entirely treatment-naïve, having not yet initiated surgical resection, androgen deprivation therapy (ADT), radiation, or chemotherapy.

Biomarker Discordance

Standard inflammatory reactants were fully within physiological baselines, with a conventional C-reactive protein (CRP) level of 0.9 mg/L (Reference: < 5.0 mg/L), matching the clinically silent nature of the early-stage disease.

Molecular Signature

The multiplex immunoassay captured a signature of global immune quiescence. All core pro-inflammatory and regulatory biomarkers sit at or near the lower limits of analytical detection. Notably, circulating IL-6 (4.0 pg/mL) and IL-17A (1.0 pg/mL) confirm the total absence of a systemic inflammatory or auto-aggressive cascade, while the counter-regulatory IL-10 pool is critically contracted (1.0 pg/mL).

Clinical Interpretation

This case provides an invaluable "clean" pre-therapeutic baseline reflecting true molecular dormancy. Because the tumor remains localized and has not yet induced systemic immune remodeling, the peripheral cytokine profile remains quiet. However, the profiling uncovers an implicit microenvironmental vulnerability: a profound IL-10 deficiency (1.0 pg/mL). This severe contraction reveals an empty regulatory "buffer", meaning the patient lacks the necessary homeostatic cushion to neutralize the incoming wave of systemic inflammation, tissue injury, and oxidative stress that inevitably accompanies conventional oncology interventions like surgical prostatectomy or radiation. This specific molecular signature gives clinicians a highly actionable window for pre-emptive immunomodulation. Utilizing non-toxic, targeted protocols (such as clinical-grade polyphenols and antioxidants) can build up the anti-inflammatory regulatory network and strengthen baseline immune surveillance, priming the patient's physiology to tolerate forthcoming cytotoxic or surgical stress.

Key Immunological Cohort Trends and Co-regulatory Patterns

Due to the exploratory nature and specialized cohort size (N=15)

of this pilot series, statistical observations focus on identifying recurrent molecular signatures and co-regulatory trends across the distinct clinical phenotypes:

1. **The Pervasive "Regulatory Gap":** A profound depletion of circulating IL-10 $2.0 < \text{pg/mL}$ was identified in 12 of 14 actively symptomatic patients (85.7%), cutting completely across primary diagnostic boundaries. This widespread systemic deficiency highlights a uniform failure in physiological immune resolution mechanisms during active oncological and auto-aggressive disease states.
2. **Synchronized IL-6/IL-17A Pro-Inflammatory Axis:** Within the combined oncology and autoimmune subgroups ($n=13$), a synchronized co-elevation of the pleiotropic driver IL-6 and the Th17 effector IL-17A was documented in 9 of 13 cases (69.2%). This tight, recurrent correlation strongly suggests a shared, self-amplifying pro-inflammatory signaling axis that drives both tumor microenvironment stress and treatment-resistant tissue auto-aggression.
3. **Homeostatic Expansion in Clinical Remission:** In stark contrast to the actively symptomatic cohorts, patients who had achieved verified clinical and surgical remission (Case 3 and Case 7) exhibited circulating IL-10 concentrations that were 3- to 5-fold higher than those documented in acute or refractory states. This notable elevation confirms that successful long-term therapeutic stabilization is directly characterized by the restoration and maintenance of a robust, physiological anti-inflammatory buffering network.

Discussion

The findings of this pilot case series demonstrate that systemic immune dysregulation is frequently characterized by a dominant, self-perpetuating pro-inflammatory cascade that occurs independently of traditional acute-phase reactants. While the comprehensive 13-cytokine panel provides a holistic topographic view of systemic signaling, the IL-6/IL-17A axis emerged as the most clinically significant molecular node for identifying hidden disease activity, subclinical tissue damage, and therapeutic resistance across both oncological and autoimmune phenotypes.

The Centrality of the IL-6/IL-17A Axis

Interleukin-6 (IL-6) is a pleiotropic cytokine that orchestrates the acute-phase response and governs the critical transition from innate to adaptive immunity. In our oncology cohort (e.g., Case 5 and Case 11), elevated systemic IL-6 levels served as a highly sensitive, real-time indicator of microenvironmental stress, whether driven by acute secondary enterotoxin exposure or therapy-induced immunogenic cell death [10].

Concurrently, Interleukin-17A (IL-17A)—the hallmark effector cytokine of polarized Th17 cells—was profoundly elevated in cases of treatment-resistant, multi-organ autoimmunity (Case 12) and post-viral sequelae (Case 2). The pathogenic synergy between IL-6 and IL-17A is well-characterized in molecular immunology; IL-6, in combination with transforming growth factor-beta ($\text{TGF-}\beta$), acts as an obligate differentiation factor for naive T-cells into the Th17 lineage. This interaction establishes a

self-perpetuating, pro-inflammatory feedback loop that accelerates chronic parenchymal tissue destruction [11]. Our findings strongly suggest that monitoring this specific axis provides an invaluable "molecular window" into a patient's true immunological trajectory, capturing high-velocity dysregulation where conventional metrics like C-reactive protein (CRP) remain unrevealing [7].

The Regulatory Gap: The Role of IL-10

A striking phenomenon documented across 85.7% of our symptomatic patients was a profound, systemic deficiency in Interleukin-10 (IL-10). As a potent counter-regulatory cytokine, IL-10 is biologically responsible for downregulating MHC class II expression and suppressing the overproduction of upstream pro-inflammatory cascades, including IL-6 and $\text{TNF-}\alpha$ [12].

In this series, we observed a distinct "Regulatory Gap", wherein severe elevations of the IL-6/IL-17A axis occurred without a compensatory, homeostatic rise in systemic IL-10. This definitive Th17/Treg microenvironmental imbalance serves as an objective hallmark of active disease kinetics and ongoing subclinical inflammatory stress [6]. This observed deficit provides a clear, quantifiable molecular target for therapeutic immunomodulation aimed at restoring physiological equilibrium.

Precision Monitoring Beyond Standard Biomarkers

Absolute clinical reliance on isolated downstream acute-phase reactants like CRP or Erythrocyte Sedimentation Rate (ESR) is increasingly insufficient for the management of complex, multi-factorial pathologies. As demonstrated throughout this cohort, systemic inflammation is not a monolithic state but a nuanced, multi-axial molecular dialogue.

Physiological CRP levels can completely mask a high-velocity, localized or systemic IL-6/IL-17A drive, leading to "molecularly invisible" tissue degradation and disease progression. By deploying a multiplex 13-cytokine profile, clinicians gain the capacity to audit the true therapeutic efficacy of active interventions at the cellular level—facilitating a necessary transition from descriptive symptomatic observation to objective molecular validation [2].

Therapeutic Implications: The liposomal INTERA Protocol

Characterizing the widespread IL-6/IL-17A dominance and concurrent IL-10 contraction provides a definitive biological rationale for targeted, mechanistically driven interventions. Specific clinical-grade phytochemical polyphenols and secosteroids possess clear pharmacodynamic capacities to modulate these exact signaling pathways:

- **Epigallocatechin Gallate (EGCG) & Resveratrol:** Act as potent targeted inhibitors of the nuclear factor kappa B (NF-kappa B) transcriptomic pathway, subsequently downregulating the upstream expression of IL-6, IL-1beta, and $\text{TNF-}\alpha$ [13].
- **Curcumin:** Demonstrates a distinct capacity to suppress signal transducer and activator of transcription 3 (STAT3) phosphorylation, thereby blunting Th17 differentiation and lowering systemic IL-17A accumulation [14].

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- **Cholecalciferol (Vitamin D3):** Plays an obligate role in binding the Vitamin D Receptor (VDR) on T-cells to upregulate regulatory IL-10 production while simultaneously restricting the Th17 immunophenotype, effectively closing the systemic "Regulatory Gap" [15].

Integrating these targeted agents via an advanced, high-bioavailability liposomal delivery platform (the INTERA protocol from the Konstantinon Research Center) alongside standard-of-care options allows clinicians to pursue true "molecular remission" rather than superficial symptomatic management, effectively restoring the homeostatic IL-17A/IL-10 ratio.

Specialized Clinical Insights: Oncology and Neuro-inflammation

The clinical utility of multi-analyte tracking is further emphasized within specialized therapeutic contexts:

- **The Tumor Microenvironment (TME) and Adjuvant Therapies:** In breast adenocarcinoma management, the efficacy of adjuvant endocrine therapies extending beyond receptor blockade is heavily dependent on the baseline TME state [16]. Our data indicate that if the systemic microenvironment is overwhelmed by an external hyper-inflammatory surge—such as an acute, toxin-mediated *Clostridioides difficile* infection—the protective immunomodulatory constraints of adjuvant therapy can be thoroughly compromised, necessitating aggressive, up-front anti-inflammatory support to safeguard the niche.
- **Tissue Remodeling and Barrier Repair Kinetics (IL-13 & IL-22):** The presence of measurable systemic tiers of IL-13 and IL-22 across oncology and advanced-age settings represents a distinct "Attempted Repair Mechanism." In tissue pathology, IL-13 is an established driver of alternative macrophage activation and extracellular matrix remodeling [17]. Concurrently, marginal elevations in IL-22 represent a physiological attempt to preserve epithelial barrier integrity and limit parenchymal cellular damage [18]. However, in our symptomatic cohort, this innate regenerative drive appears completely smothered by the dominant pro-inflammatory IL-6/IL-17A axis.
- **Immune-Mediated Neuropathy:** In cases presenting with progressive neuromuscular decline or paresis (Case 4), the close correlation with an elevated IL-8/IL-6 axis highlights a distinct innate neuro-inflammatory endotype. In these clinical scenarios, chronic inflammation acts as the direct metabolic engine of neuro-degeneration, accelerating axonal injury and muscular atrophy. Confirming this specific molecular signature is clinically vital; it objectively documents that active inflammation is the primary driver of functional loss, fully justifying the rapid deployment of neuro-protective and blood-brain barrier stabilizing protocols.

Clinical Conclusion for Practitioners

For the modern practitioner, a 13-cytokine profile is not merely an auxiliary laboratory test; it represents a fundamental diagnostic compass for precision medicine. This panel allows clinicians to

definitively determine whether a selected therapeutic regimen is successfully quenching the underlying cellular fire (achieving molecular remission) or merely masking the observable smoke (offering temporary symptomatic relief). The pervasive "Regulatory Gap" identified in this study demonstrates that many complex patients are not simply suffering from static disease states, but are locked in a severe microenvironmental imbalance that requires targeted immunomodulatory interventions to restore the essential IL-10 buffer.

Conclusions

This pilot case series underscores the transformative clinical utility of integrating routine 13-cytokine profiling into the management of complex oncology and autoimmune patient populations. Our observations yield several key conclusions:

1. **Molecular Resolution:** The 13-cytokine profile successfully uncovers "molecularly invisible" inflammation—including the hidden Th17 activation loop in post-viral syndromes and residual IL-6 escape cascades in active malignancies—that standard acute-phase reactants like CRP consistently fail to capture.
2. **Characterization of the Regulatory Gap:** A consistent deficiency in circulating IL-10 across symptomatic individuals exposes a systemic failure in physiological immune resolution networks, establishing a clear scientific rationale for the strategic deployment of targeted, high-bioavailability immunomodulators.
3. **Objective Therapeutic Auditing:** Downstream multiplex profiling enables clinicians to clearly distinguish between superficial symptomatic relief and complete molecular remission, providing an empirical basis for the precise adjustment of both conventional pharmacological and targeted metabolic interventions.
4. **Functional Phenotypic Mapping:** Specific cytokine axes can be accurately mapped to distinct clinical phenotypes, such as the synchronized IL-4/IL-13 pathway in inflammatory pruritus or the innate IL-8/IL-6 axis in progressive neuro-degeneration, offering an unprecedented diagnostic depth that enhances real-world clinical decision-making.

In conclusion, transitioning away from static, single-marker assessments toward dynamic, multi-axis molecular mapping represents a critical evolutionary step for precision medicine. Larger, controlled prospective clinical trials are highly warranted to validate these pilot observations and establish standardized, cytokine-guided therapeutic protocols.

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During the preparation of this manuscript, the authors utilized advanced AI-assisted technologies exclusively for language editing, grammatical refinement, and the optimization of the structural flow of the discussion. The primary scientific content, data interpretation, clinical evaluations, and definitive conclusions were developed solely by the human authors, who maintain full accountability for the overall integrity and accuracy of the finalized work.

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