

Association between specific timothy grass antigens and changes in T_H1- and T_H2-cell responses following specific immunotherapy

Véronique Schulten, PhD,^a Victoria Tripple, BSc,^a John Sidney, MSc,^a Jason Greenbaum, PhD,^a April Frazier, PhD,^a Rafeul Alam, MD,^b David Broide, MD,^c Bjoern Peters, PhD,^a and Alessandro Sette, PhD^a La Jolla, Calif, and Denver, Colo

Background: Different populations of T cells are involved in the pathogenesis of allergic diseases.

Objective: We investigated changes in T_H-cell populations in patients with allergies after specific immunotherapy (SIT).

Methods: PBMCs were isolated from patients with allergies who received SIT and those who did not (controls). We tested the ability of peptides from 93 timothy grass (TG) proteins to induce T-cell responses (cytokine production). We used ELISPOT and staining assays for intracellular cytokines to measure the production of IL-4, IL-5, IL-13, IFN- γ , and IL-10.

Results: Compared with PBMCs from controls, PBMCs from patients who received SIT produced lower levels of T_H2 cytokines on incubation with several different TG peptides. These data were used to select 20 peptides to be tested in an independent cohort of 20 patients with allergies who received SIT and 20 controls. We again observed a significant decrease in the production of T_H2 cytokines, and an increase in the production of the T_H1 cytokine IFN- γ , in PBMCs from the validation groups. These changes correlated with improved symptoms after SIT. Immunization with this selected pool of peptides (or their associated antigens) could protect a substantial proportion of the population from TG allergy.

Conclusions: We observed a significant decrease in the production of T_H2 cytokines by PBMCs from patients who received SIT for TG allergy compared to those who did not. These changes might be used to monitor response to therapy.

The decrease occurred in response to antigens that elicit little (if any) IgE responses; these antigens might be developed for use in immunotherapy. (J Allergy Clin Immunol 2014;■■■:■■■-■■■.)

Key words: T cells, specific immunotherapy, timothy grass, cytokine

Abbreviations used

ATGA: Additional timothy grass antigen
KTGA: Known timothy grass antigen
MNA: Modulated novel antigen
SFC: Spot-forming cell
SIT: Specific immunotherapy
TG: Timothy grass

Sensitization to common environmental allergens such as grass pollen is a feature of type I allergy, which affects as much as 20% of the general population.^{1,2} Despite increasing awareness and research efforts, several studies have reported a worldwide increase in allergy prevalence over the last decades.³⁻⁵ There is an urgent need for strategies to reduce or stop pathogenesis of severe allergies, rather than just reduce symptoms. The only treatment with long-term clinical efficacy is specific immunotherapy (SIT). Little is known about the mechanisms by which SIT produces its beneficial effects.

Type I allergy is mediated by activated allergen-specific T_H2 cells, which produce cytokines such as IL-4, IL-5, and IL-13.^{6,7} In healthy individuals, the allergen-specific T-cell response is mediated predominantly by T_H1 cells.⁸ SIT reduces the ratio of T_H2:T_H1 cells and alters the cytokine profile, reducing the production of IL-4, IL-5, and IL-13 and increasing the production of IFN- γ .⁹⁻¹¹ In addition, SIT has been associated with the induction of IL-10-secreting regulatory T cells, which are detected in greatest abundance in the first 3 to 6 months of treatment and their numbers decrease after 12 months of treatment.^{12,13} In addition, SIT induces the production of IgG₄, which could compete with IgE for binding to allergen.^{14,15} However, there is no dependable immune correlate of clinical response to SIT that can be measured by standardized reagents in the clinic; evaluation of clinical response depends on clinical tests and evaluation of patient-reported symptoms.

Despite its efficacy, SIT has several limitations, including safety concerns about giving patients allergenic substances. Because most SIT regimens involve the administration of whole, unfractionated, allergen extracts, adverse IgE-mediated events are a considerable risk. SIT is therefore not recommended for patients who are at high risk for serious adverse reactions (such as patients with asthma with forced expiratory volumes <70%). Significant efforts have been devoted to developing approaches to modulate allergen-specific T-cell responses without inducing IgE-mediated, immediate-type reactions. These approaches include developing hypoallergens that do not contain IgE-binding epitopes,^{16,17} allergens that are coupled to adjuvants and carriers of bacterial or viral origin,¹⁸ or peptides that contain dominant T-cell epitopes¹⁹ and do not react with IgE in allergic individuals.

From ^athe Division of Vaccine Discovery, La Jolla Institute for Allergy & Immunology, La Jolla; ^bthe Department of Medicine, National Jewish Health, Denver; and ^cthe Department of Medicine, University of California, San Diego, La Jolla.

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Corresponding author: Alessandro Sette, PhD, La Jolla Institute for Allergy and Immunology, 9420 Athena Circle, La Jolla, CA 92037. E-mail: alex@liai.org. 0091-6749/\$36.00

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We previously identified a set of 93 additional timothy grass (TG) antigens and assessed their ability to induce IL-5 production by PBMCs from TG-allergic patients.²⁰ Here, we investigate the TG-specific T-cell responses induced by these antigens in patients who have undergone SIT, compared with TG-allergic patients who did not receive SIT (controls).

METHODS

Study participants

Participants were recruited after Institutional Review Board approval (Federal Wide Assurance no. 00000032). As control group, 40 patients with TG allergy who developed a skin reaction, based on a wheal of 5 mm or more in diameter after a skin prick test with the TG extract, and had histories of seasonal grass pollen allergies were included in the study. For the treated group, 40 patients who received subcutaneous SIT within the last 12 months and were receiving maintenance therapy were recruited. General information was collected by interviews and questionnaires at the time of enrollment, including participants' assessments of whether the SIT regimens had been effective in ameliorating their symptoms. Patients' demographic and clinical information is presented in [Table E1, A](#), in this article's Online Repository at www.jacionline.org. HLA type information is presented in [Table E1, B](#).

Assembly of a peptide panel from additional TG antigens

The discovery of additional TG antigens and the assembly of a set of peptides that bind HLA class II molecules has been previously described.²⁰

Isolation of PBMCs and *in vitro* expansion of TG extract-specific T cells

PBMCs were isolated from study participants and stored in liquid nitrogen until further use. For experimental testing, PBMCs were thawed and expanded *in vitro* with TG pollen extract (50 µg/mL) (Greer, Lenoir, NC) or the peptide pool (5 µg/mL), as described previously.^{20,21} The TG extract and peptide pools had each been previously titrated to determine optimal stimulation concentrations.

ELISPOT assays

Cytokine production by cultured PBMCs in response to antigen stimulation was measured by ELISPOT, as described previously.^{20,21} Cells (1×10^5 cells/well) were plated and incubated with peptide (10 µg/mL), the peptide pool (5 µg/mL), or the TG extract (50 µg/mL). Phytohemagglutinin (10 µg/mL) and medium alone were used as positive and negative controls, respectively. Samples were considered to produce a cytokine if 100 spot-forming cells (SFCs)/ 10^6 PBMCs were detected, with $P \leq .05$ and a stimulation index of 2 or more. Criteria for individual peptides were the same except that a minimum of 20 SFCs were required for a sample to be counted as positive.

Binding assays

We determined the MHC binding capacity of 50 peptides, in different pools of interest (a P20, P19, and the modulated novel antigen [MNA] pool), for a panel of common HLA class II alleles. Purified MHC molecules were used in competition assays, as described previously.^{22,23} Binding data are presented in [Table E2](#) in this article's Online Repository at www.jacionline.org.

Intracellular cytokine staining

Cultured PBMCs were restimulated with 5 µg/mL of modulated peptide pool in complete RPMI medium at 37°C in 5% CO₂. Unstimulated PBMCs were used to assess nonspecific/background cytokine production. Phorbol 12-myristate 13-acetate and ionomycin were used as the positive

control. After the initial 2 hours of stimulation, 4 µL/mL of Golgiplug (BD Biosciences, San Diego, Calif) was added. After 7 hours of total incubation time, cells were collected and stained for cell surface antigens (CD4, CD3, CD8, CD14, and CD19) and Fixable Viability Dye (all from eBioscience, San Diego, Calif). After washing, cells were fixed with 4% paraformaldehyde, placed in permeabilization buffer (0.5% saponin, 0.1% sodium azide, 1% BSA in PBS), and stained for IFN-γ, IL-4, and IL-13. Samples were analyzed using a BD LSR II flow cytometer. We created dotblots of CD4⁺ T cells that responded to the modulated peptide pool by gating for CD4⁺CD3⁺CD8⁺CD14⁺CD19⁺ and cytokine-positive cells using FlowJo software (TreeStar, Ashland, Ore).

Two-dimensional gel electrophoresis and immunoblotting

Detailed methods have been previously described.²⁰ Proteins on nitrocellulose membranes were probed with serum samples from 8 controls, as described,²⁰ or serum samples from 6 participants who received SIT, to detect antigen-specific IgG and IgE.

Population coverage analysis

The potential population coverage afforded by the panel of TG epitopes we identified was determined on the basis of their predicted ability to bind 47 different human leukocyte antigen DR, DQ and DP molecules (see [Table E4](#) in this article's Online Repository at www.jacionline.org). The panel of class II specificities to be used in the analysis was selected on the basis of availability of reagents that would allow for further characterization of response, such as in MHC-peptide binding assays,²² with tetramer reagents, or with cell lines transfected with single alleles.²³ Binding was predicted using tools available from the Immune Epitope Database (www.iedb.org).^{24,25} We used the prediction method recommended by the Immune Epitope Database for each HLA; binding was defined conservatively, as a consensus percentile score of less than 10. Population coverage was estimated using the Immune Epitope Database's population coverage tool,²⁶ based on HLA frequency data available from the MHC database (<http://www.ncbi.nlm.nih.gov/gv/mhc/main.fcgi?cmd=init>) and the Allele Frequencies database (<http://www.allele-frequencies.net/>).²⁷

RESULTS

Decrease in IL-5 production in response to TG antigens after SIT

Previous studies^{21,28-30} described a set of 10 TG pollen-derived antigens (referred to in this report as known timothy grass antigens [KTGAs]). We recently identified and characterized the immune responses of TG-allergic patients to a panel of 93 additional timothy grass antigens (referred to in this report as ATGAs).²⁰ Here, we investigated immune responses from patients who received grass pollen SIT, to peptides derived from the ATGAs and KTGAs. The 822 peptides from the ATGAs were assembled into 42 pools and tested for PBMC responses from study participants along with 5 pools of 105 peptides from the 10 KTGAs (~20 peptides per pool).

Production of IL-5 was detected in PBMCs from 20% or more of control patients in response to 4 of the 5 KTGA pools and 13 of the 42 ATGA pools; the average response was 262 SFCs among the 5 KTGA pools (range, 44-498 SFCs) and 107 SFCs among the 42 ATGA pools (range, 48-197 SFCs)²⁰ ([Fig 1, A and B](#)). PBMCs from all control subjects reacted to the TG extract (average response of 1012 SFCs). In contrast to control subjects, only 1 of the KTGA pools (109 SFCs) and none of the ATGA pools tested induced IL-5 production by PMBCs from 20% or more of patients who received SIT ([Fig 1, A and B](#)). IL-5 was produced in response to the TG extract in PBMCs from 75% of subjects who received SIT, eliciting an average of 460 SFCs.

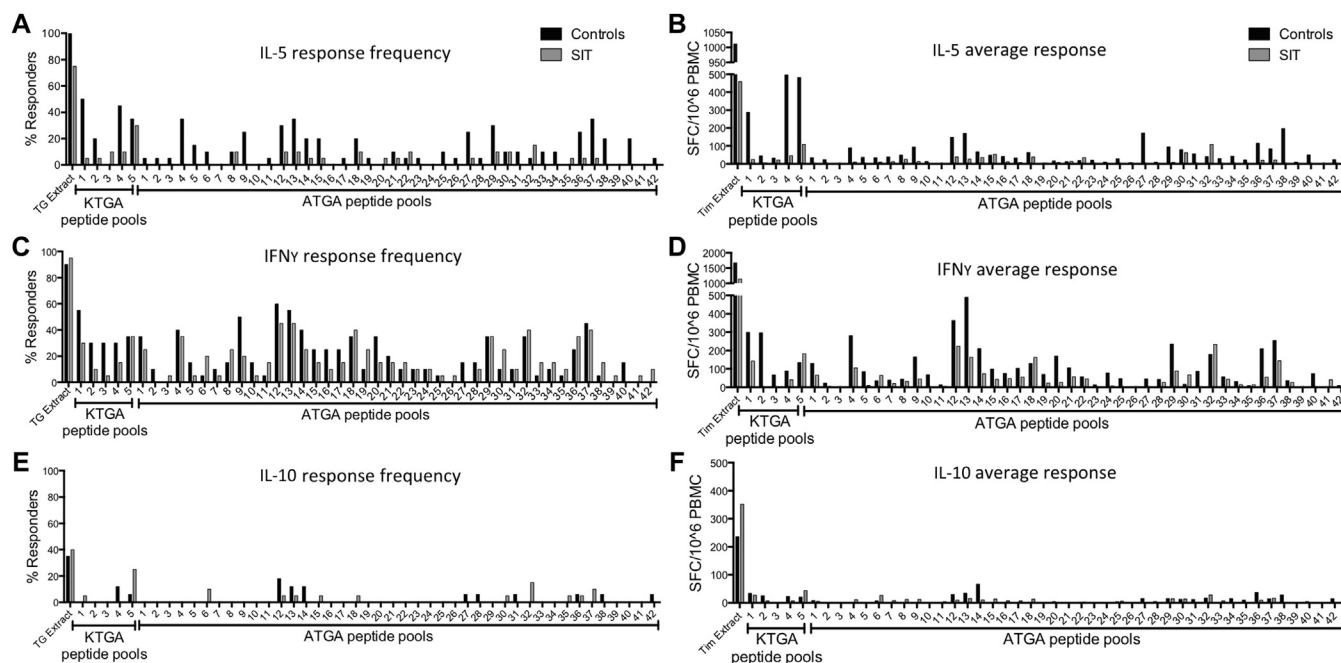


FIG 1. Cytokine production by PBMCs in response to the TG extract and peptide pools. Peptides that induce the production of IL-5 (**A** and **B**), IFN- γ (**C** and **D**), and IL-10 (**E** and **F**) by PBMCs from 20 patients receiving SIT and 20 controls. Panels **A**, **C**, and **E** show the percentage of PBMC samples from patients who responded to each antigen. Panels **B**, **D**, and **F** show average responses of PBMCs from 20 patients to each antigen.

Production of IFN- γ and IL-10 in response to TG antigens

The efficacy of SIT has been proposed to partly depend on a switch from a T_H2 - to a T_H1 -cell response, and/or the upregulation of IL-10 production by regulatory T cells. We therefore measured the production of IFN- γ and IL-10 by PBMCs in response to the TG extract, KTGA, and ATGA.

IFN- γ production in both control subjects and patients who received SIT was of similar frequency and magnitude (**Fig 1, C** and **D**). All 5 KTGA-derived pools elicited IFN- γ in PBMCs from 20% or more control subjects (average of 177 SFCs), as did 16 of the 42 ATGA pools (average, 200 SFCs). Production of IFN- γ in response to the TG extract was observed in PBMCs from 90% of control subjects (average, 1668 SFCs). In patients who received SIT, 2 of the 5 KTGA pools (average, 163 SFCs) and 15 of the 42 ATGA pools (average, 103 SFCs) induced IFN- γ production by PBMCs from 20% or more of the subjects (**Fig 1, C** and **D**). The TG extract induced IFN- γ production by PBMCs from 95% of the subjects who received SIT (average, 1139 SFCs).

In contrast to IFN- γ , IL-10 was produced at a relatively low frequency, by PMBCs from patients of both cohorts, in response to KTGA and ATGA peptide pools (**Fig 1, E** and **F**). IL-10 production was detected in 10% or more of control subjects and patients who received SIT in response to only 1 of the 5 KTGA pools (average, 23 and 44 SFCs for control subjects and patients who received SIT, respectively). Three of the 42 ATGA peptide pools induced IL-10 production by PBMCs from 10% or more of both control subjects and subjects who received SIT (average, 44 and 24 SFCs for control subjects and patients who received SIT, respectively) (**Fig 1, E** and **F**). IL-10 was produced in response to the TG extract by PBMCs from 35% of the control

subjects (average, 352 SFCs) and 40% of the patients who received SIT (average, 236 SFCs). IL-10 production measured against the TG extract indicates that the median response magnitude in SIT donors is slightly increased than in controls. To further assess this difference, we plotted individual responses and found that differences in IL-10 production by PBMCs did not differ significantly between groups (see **Fig E1** in this article's Online Repository at www.jacionline.org).

Summary of T-cell reactivity among patients who received SIT

Next, we analyzed the data on a per-patient rather than a per-pool basis. Averages of the sum responses to KTGA and ATGA pools of all subjects are shown in **Fig 2**. The KTGA pools elicited reduced IL-5 production by PBMCs from patients who received SIT (average, 145 SFCs) compared with controls (average, 1249 SFCs) ($P = .006$) (**Fig 2, A**). IL-5 responses to ATGA from patients who received SIT were also reduced (average, 373 SFCs) compared with controls (average, 1463 SFCs) ($P = .003$) (**Fig 2, A**).

In contrast, the production of IFN- γ by PBMCs from patients who received SIT versus controls did not differ significantly in response to ATGA or KTGA pools (**Fig 2, B**). In IFN- γ assays, KTGA pools induced an average of 569 SFCs in controls and 405 SFCs in patients who received SIT; ATGA pools induced an average of 2876 SFCs in controls and 2220 SFCs in patients who received SIT (**Fig 2, B**). Similarly, IL-10 production did not differ between groups (**Fig 2, C**). KTGA pools induced 51 SFCs in controls and 46 SFC in patients who received SIT; ATGA pools induced 49 SFCs in controls and 19 SFCs in patients who received SIT (**Fig 2, C**).

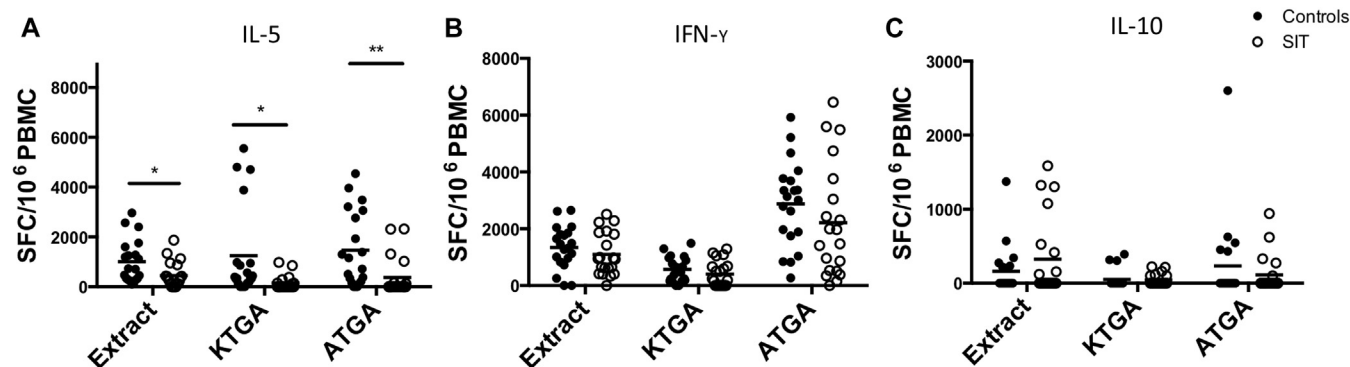


FIG 2. Cytokine production by PBMCs from control subjects and patients who received SIT in response to TG antigens. Circles indicate the number of SFCs in PBMCs from individual donors (black circles, from 20 controls; white circles, from 20 patients who received SIT), indicating the production of IL-5 (A), IFN- γ (B), and IL-10 (C) in response to the TG extract, known allergens, and additional TG antigens. * $P < .05$, ** $P < .005$, based on the Student t test.

TABLE I. Immunologic characteristics of 13 additional TG antigens inducing IL-5 production in 20% or more of control donors*

Antigen	Control cohort						SIT cohort					
	IL-5		IFN- γ		Antibody reactivity		IL-5		IFN- γ		Antibody reactivity	
	No. of responders	Total SFCs	No. of responders	Total SFCs	IgE	IgG	No. of responders	Total SFCs	No. of responders	Total SFCs	IgE	IgG
2	7	3447	10	8200	+	+	3	130	4	2790	+	+
62	5	1927	6	2827	+	+	2	80	3	1417	+	+
49	5	7417	1	990	–	–	0	0	0	0	–	+
53	6	1750	6	3693	–	+	1	30	3	903	–	+
54	4	2647	7	1133	–	–	2	387	3	1510	–	+
91	4	1904	2	1430	–	–	1	23	1	270	–	–
6	11	7003	11	7490	+	+	5	1087	10	6163	+	+
89	9	2360	11	5560	–	–	6	883	6	5470	–	–
24	6	1327	5	2443	+	–	2	603	3	3307	+	+
52	6	930	5	1293	–	+	0	0	1	27	–	+
7	5	1657	5	5603	+	+	1	567	3	1270	+	+
46	5	533	2	227	+	+	0	0	3	100	+	+
22	4	367	1	667	–	–	0	0	1	103	–	–

*The 6 highly modulated antigens (MNA) are shown at the top, and the remaining 7 ATGAs are shown on the bottom for reference.

Effects of SIT on antigen and epitope specificity

To identify the individual peptides within the ATGA pools that produced the observed responses, pools that elicited cytokine production were deconvoluted and PBMC reactivity to individual peptides was determined (Table E3, A). We were specifically interested in mapping T-cell epitopes of each antigen and assessing the modulation of T_H2-cell responses on a per-antigen level. T-cell reactivity to each antigen is presented in Table E3, B.

Immunologic characteristics of the 13 antigens that were recognized by PBMCs from 20% or more of control subjects are presented in Table I. The deconvolution experiments identified 6 specific ATGAs (Table I, top) that induced strong IL-5 production in control subjects, which was reduced in PBMCs from patients who received SIT (antigens 2, 49, 53, 54, 69, and 91; Fig 3, A and B). PBMCs from 15 of 20 controls recognized 1 or more of these antigens (on average, each antigen elicited IL-5 production in 5.2 control patients; range, 4–7), whereas PBMCs from only 7 of 20 patients who received SIT responded to 1 or more of these antigens (on average, each antigen elicited responses in 1.5 patients who received SIT; range, 0–3) (Fig 3, A). The average response to these antigens was reduced from 3182

SFCs detected in controls (range, 1750–7417 SFCs) to 108 SFCs in patients who received SIT (range, 0–387 SFCs) (Fig 3, B).

Two-dimensional gel electrophoresis and immunoblot analyses were used to assess antibody reactivity to all 13 antigens in both control subjects (pool of 8 patients) and patients with SIT (pool of 6 patients) (Fig 4, B and C). Five of the antigens were recognized by both IgE and IgG (antigens 2, 6, 7, 46, and 62) in controls, and this reactivity was not appreciably modulated by SIT treatment. One antigen (antigen 24) was IgE reactive in both controls and patients who received SIT but was recognized only by IgG from donors who had received SIT. The remaining 7 antigens were IgE unreactive in controls as well as in SIT-treated patients. Interestingly, for 2 of them (antigens 49 and 54), IgG reactivity was detected only in SIT-treated patient's sera (Table I).

SIT alters T-cell responses to specific epitopes

We investigated whether T_H2 responses to a specific mixture of peptides are downregulated after SIT. If so, these might be used to track response to therapy or develop new treatment regimens. We assessed whether the significant IL-5 reduction we observed after

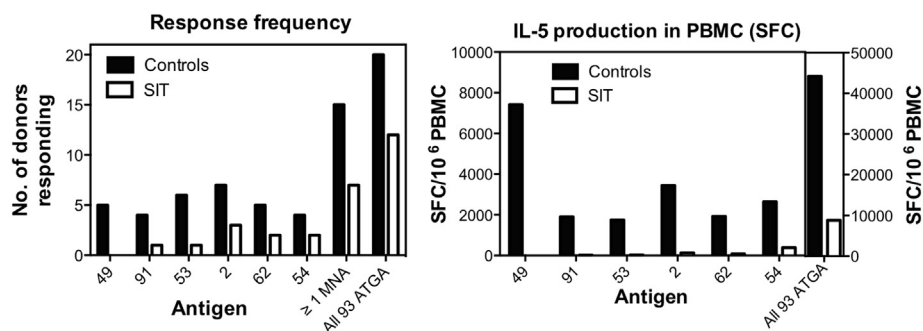


FIG 3. IL-5 production by PBMCs in response to modulated ATGAs. The left panel shows the number of responding patients who received SIT (white bar) and controls (black bar) whose PBMCs produced IL-5 in response to a subset of ATGAs that show modulated IL-5 production after SIT treatment. The right panel shows the magnitude of the IL-5 response to the subset of antigens in PBMCs from patients who received SIT (white bar) or control (black bar) subjects.

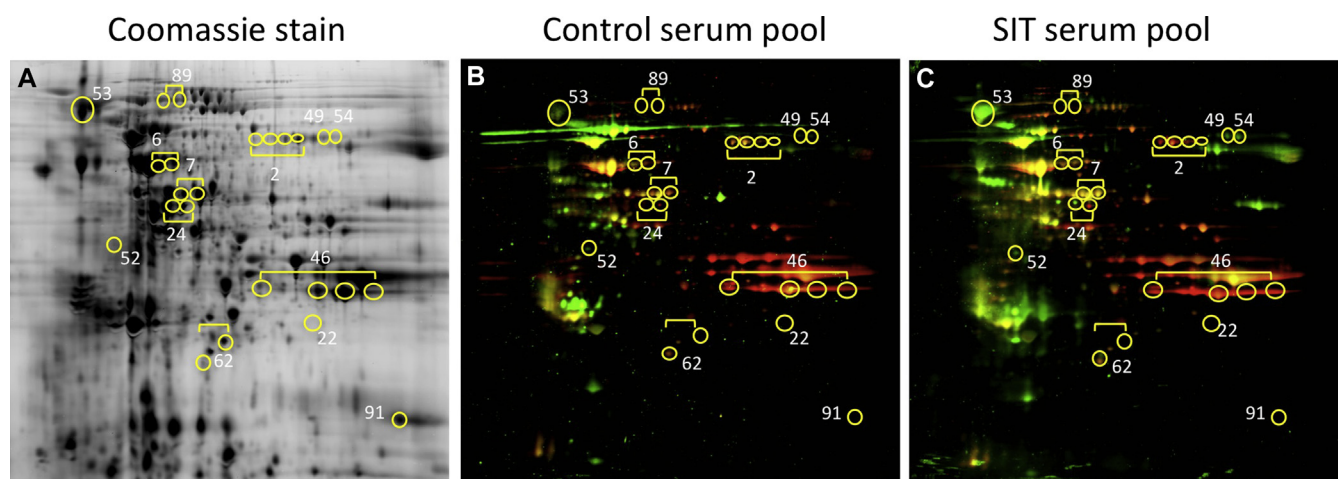


FIG 4. Two-dimensional (2D) gel electrophoresis and immunoblot analysis of the TG extract, using pooled serum samples from controls and patients who received SIT. Coomassie-stained 2D gel of the TG extract (**A**). Immunoblot analysis shows proteins that react with IgG (green spots), IgE (red spots), or both (yellow spots) in sera from controls (**B**) and patients who received SIT (**C**). Yellow circles indicate locations of the 13 ATGAs that induce IL-5 production in PBMCs from controls.

SIT could be validated in an independent group of patients (20 new patients who received SIT and 20 new controls). In these experiments, we tested a pool of 20 peptides from the 6 ATGAs (2, 49, 53, 54, 62, and 91), which had showed strongest modulation of IL-5 responses after SIT (referred to hereafter as the MNA pool).

In ELISPOT assays, PBMCs from controls produced significantly lower levels of IFN- γ (average, 1588 SFCs) than did PBMCs from patients who received SIT (average, 2560 SFCs) ($P = .00006$) (Fig 5, A). IL-5 production was higher in PBMCs from controls (average, 957 SFCs) than in PBMCs from patients who received SIT (average, 425 SFCs) ($P = .015$). No significant difference in IL-10 production was observed between controls (average, 467 SFCs) and patients who received SIT (average, 388 SFCs) ($P = .65$).

We performed intracellular cytokine staining experiments to investigate whether SIT leads to changes in other T_H2-cell responses, beyond reducing the production of IL-5. We measured levels of the T_H2 cytokines IL-4 and IL-13, as well as the T_H1 cytokine IFN- γ , in PBMCs stimulated with the MNA pool. In support of findings from ELISPOT assays, we observed reduced

production of IL-4 and IL-13 by CD4 T cells from patients who received SIT than from CD4 T cells from controls (see Fig E2 in this article's Online Repository at www.jacionline.org).

Production of IL-5 in response to the MNA pool

Using the data from the original ELISPOT assays assessing cytokine production in PBMCs in response to all 822 ATGA peptides, in the case of IFN- γ , a reactivity of 2200 SFCs or higher was associated with 75% of the patients who received SIT, whereas a response of 2200 SFCs or lower identified 75% of controls. Similarly, for IL-5 production, correct classification of approximately 67% of SIT-treated individuals was associated with reactivity below the 1000 SFC level.

We investigated whether a reduction in the T_H2-cell response specific to the MNA pool correlated with a reduction in symptoms, as subjectively judged by patients who received SIT. Subjects undergoing maintenance SIT were divided into groups that did and did not report improved symptoms from the treatment. PBMCs from patients who reported improved symptoms

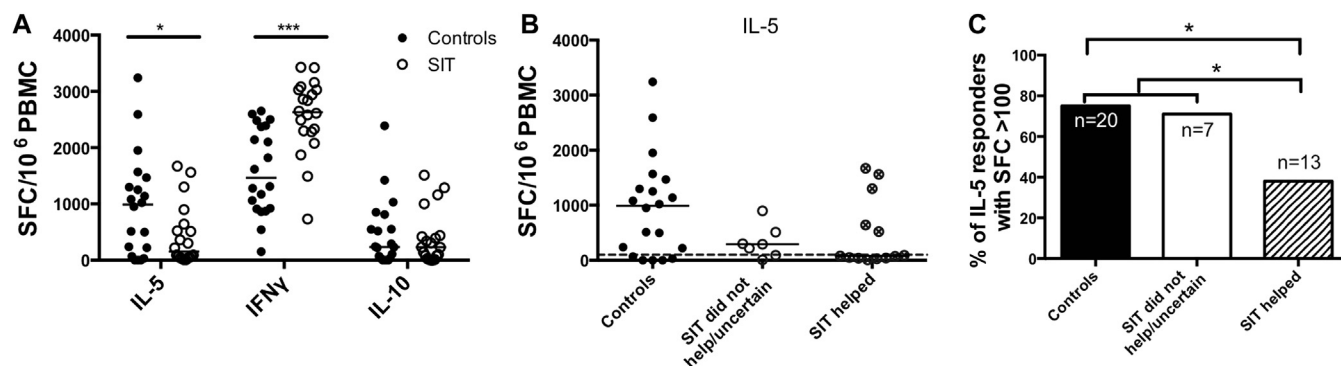


FIG 5. Modulation of cytokine production by PBMCs from patients who received SIT in response to the MNA pool. **A**, Cytokine production (measured as SFCs) from patients receiving SIT (white dots) or controls (black dots). Line indicates median values. * $P < .05$, *** $P < .001$, determined by Student t test. **B**, IL-5 production by PBMCs from controls (black dots, left), patients who did not respond to SIT or were uncertain of their response (white dots, middle), or patients who reported improved symptoms after receiving SIT (dots with X, right) in response to the MNA pool. The dashed line (at 100 SFCs) indicates a strong response. **C**, A bar chart showing the percentage of patients in each group who had PBMC responses of more than 100 SFCs for IL-5. * $P < .05$, determined by Fisher exact test.

after SIT produced lower levels of IL-5 than did PBMCs from patients who were uncertain or did not feel that their symptoms had improved (Fig 5, B).

The percentage of patients with PBMCs that formed 100 or more SFCs (which we considered a strong response) was plotted for each group (Fig 5, C). PBMCs from 75% (15 of 20) of the controls produced IL-5 in response to the MNA pool, with 100 or more SFCs. Similarly, PBMCs from 71.4% (5 of 7) of the patients who were unsure of their improvement or did not report reduced symptoms after SIT produced IL-5 at the 100 or more SFC threshold. However, among patients who felt that SIT reduced their symptoms, only 38.5% (5 of 13) produced IL-5 at levels of 100 or more SFCs (Fig 5, C; $P < .05$, by the Fisher exact test). Among all 20 patients who received SIT, 10 had PBMCs that produced IL-5 at levels of less than 100 SFCs; 8 patients stated that SIT improved their symptoms. This assay therefore identifies 80% of the patients who report that SIT reduces their symptoms.

Percentage of population with MNA peptide-binding HLA

The ability to use the MNA pool as a diagnostic or in SIT would depend on the ability of the epitopes to bind the HLA of a broad fraction of the target population. We investigated the percentage of the population with HLA types that would bind MNA peptides using 2 approaches. First, we simply reviewed data collected from PBMCs of controls, restimulated with the MNA pool, and made a minimal estimate of reactivity because immunization occurred only once *in vitro*. We found that PMBCs from 90% of the controls responded to at least 1 epitope and, on average, each individual responded to 3.75 epitopes (range, 0-14) (Table II). The HLA types of individual subjects are presented in Table E1, B. An analysis of the HLA type data from the control and SIT groups revealed a statistically significant difference for 2 alleles between groups (DPB1*04:02 and DRB1*04:01; Fisher exact test, with Bonferroni correction), although neither allele was present in more than 20% of either group.

In the second approach, we estimated the maximum potential population coverage using the Population Coverage Calculation Tool, available from the Immune Epitope Database and Analysis

TABLE II. Patient coverage of the control patient cohort experimentally determined by PBMC cytokine production elicited by the set of peptides from the modulated pool

Patient	No. of positive peptides
U00098	5
D00016	6
D00073	2
D00084	12
D00089	2
D00090	1
D00092	2
D00102	0
D00104	1
D00117	14
U00058	5
U00095	2
U00106	5
U00125	4
U00129	0
U00140	3
U00147	2
U00150	3
U00151	3
U00153	3
Average	3.75

Resource (www.iedb.org).²⁶ Here, coverage is based on predicted binding to a panel of the most common HLA DR, DQ, and DP allelic variants. It is estimated that more than 95% of the general population expresses HLA molecules predicted to bind at least 1 epitope(s), and on average each individual would be expected to present 12.6 epitope-HLA combinations (range, 6.8-17.6) (Table III). These data indicate that most of the population's HLAs should bind the MNA peptides.

DISCUSSION

We recently reported that the number of TG antigens recognized by T_H2 cells in TG-allergic patients is much broader than previously recognized and that many of these antigens are not

TABLE III. Predicted HLA binding of MNA pool peptides in different populations

Population/area	Coverage (%) [*]	Average hit [†]	PC90 [‡]
Australia	98.0	11.4	2.64
Europe	95.2	12.5	1.96
North Africa	96.5	13.7	4.36
North America	99.3	13.3	6.26
North-East Asia	87.2	9.5	0.78
Oceania	89.4	8.1	0.94
Other	99.7	17.6	8.42
South America	99.8	11.5	6.27
South-East Asia	91.1	6.8	1.12
South-West Asia	99.7	17.1	8.06
Sub-Saharan Africa	99.1	17.3	6.44
Average	95.90	12.6	4.3

^{*}Projected population coverage.

[†]Average number of epitope hits/ HLA combinations recognized by the population.

[‡]Minimum number of epitope hits/HLA combinations recognized by 90% of the population.

recognized by IgE.²⁰ Herein, we examined whether reactivity to these additional antigens is modulated by SIT. To address this question, we compared the responses of PBMCs from 20 TG-allergic subjects (controls) with those of patients who had received SIT.

Findings from our cross-sectional study indicated that PBMCs from patients who received SIT produced lower levels of IL-5, in response to previously known and recently discovered TG antigens, than did PBMCs from controls. Conversely, the overall production of IFN- γ did not differ significantly between patients who received SIT and controls. However, PBMCs produced higher levels of IFN- γ in response to peptides derived from ATGAs than from known allergens (KTGAs). This may indicate that ATGAs more frequently activate T_H1 cells than T_H2 cells. Alternatively, the observed difference in IFN- γ production may simply be because the ATGAs comprised 822 predicted peptides, whereas the KTGAs comprised only 105 peptides. We observed no difference in the production of IL-10 by PBMCs from patients who received SIT versus controls.

The significant increase in the production of IFN- γ by PBMCs from patients who received SIT was not observed in our first study. This difference could result from different stimulation conditions (pools vs TG extracts); it is possible that peptides and extract affect patients in different ways (depending on exact sensitization), interacting with different types of T cells or receptors. Additional experiments are required to evaluate the different effects of TG extracts versus peptides on T-cell activation and cytokine production.

Our results are consistent with those from other studies reporting a shift in the immune response from T_H2 to T_H1 after SIT for grass pollen allergy.^{31,32} Interestingly, we did not observe any obvious differences in protein size or abundance in TG extracts among MNAs (data not shown). The observation that there was no difference in IL-10 production from patients who received SIT versus controls, in response to either KTGAs or ATGAs, is consistent with reports that IL-10 production after SIT is an initial and transient event.¹⁵ IL-10 produced in response to whole TG extract by patients who received SIT was slightly higher than in controls. However, in an analysis of individual responses, this difference was not statistically significant. IL-10 production might differ on the basis of whether it is induced in response to extract or peptide, and which T-cell population produces it.

Our findings indicate that reduced production of T_H2 cytokines by PBMCs could be a biomarker of SIT. Importantly, because the modulation of T_H-cell function occurs in response to known allergens and recently identified TG antigens, the effects of SIT, in terms of T-cell activity, could be much broader than currently recognized. Although beyond the scope of this article, it would be interesting to investigate whether the TG MNA peptides stimulate different T-cell repertoires and to determine whether the downmodulation affects different T-cell receptor subsets.

Our observed association between reduced IL-5 production and SIT efficacy, based on patient-reported improvements in symptoms, might lead to the development of an assay to measure or predict responses to therapy. However, it is important to recognize the caveat that these PBMC samples are collected from separate allergic (control) and SIT cohorts rather than from the same patients before and throughout SIT. Also, patient-reported improvement in symptoms is a subjective end point. More detailed analyses of T-cell reactivity to TG antigens in longitudinal studies are required to evaluate the clinical potential of these peptides and assays. The observed modulation in T_H2 response must be correlated with objective clinical end points such as levels of IgG₄, increased lung function, and reduced responses to skin prick tests. Such studies will also help determine how soon the downregulation of T_H2 responses can be detected after the initiation of the SIT regimen.

Our findings have led us to speculate whether ATGAs might be used in SIT. T cells are involved in the pathogenesis of asthma and allergic disease.^{33,34} The T-cell modulation we observed occurs not only in response to ATGA peptides but also KTGAs and whole TG extract. However, the pollen extracts administered for SIT contain allergens that interact strongly with IgE. Many patients, most in need of SIT, such as those with severe asthma, do not receive this therapy because of concerns about anaphylactic reactions. However, many ATGAs do not appear to bind IgE, indicating that this property is not required to alter IL-5 production. The ATGAs might be used to modulate the T_H2 response with fewer safety concerns. Further study of antibody reactivity is required to determine actual antigen-specific levels of IgE and IgG, based on RAST analysis of serum from each subject.

If ATGAs are to be considered for inclusion in immunotherapy, several important questions must be answered. What are the mechanisms by which ATGAs alter the responses of T_H2 cells? Are ATGAs more effective than allergen extracts, which contain allergens and nonallergenic proteins? Does the observed downregulation of the T_H2 response result from direct activation and modulation of KTGA- or ATGA-specific T cells, or both?

SIT is believed to reduce the allergic response by induction of IL-10-producing regulatory T cells and modulating T_H2 cell activity. It could have broad effects, in that regulatory T cells specific for a given molecule in pollen might be able to downregulate the T-cell response against a different pollen antigen. Alternatively, SIT may be highly allergen-specific at the T-cell level, yet have strong bystander effects on other non-T cells. The generalized downregulation of T_H2-cell responses we observed is compatible with both these models.

Several reports from clinical trials³⁵⁻³⁸ support the potential use of peptides as immunomodulators. Our study identifies a set of TG antigen epitopes that downregulate the production of T_H2 cytokines and upregulate the T_H1-cell response. It is important to note, however, that the set of epitopes we identified did not alter T_H2 responses in PBMCs from 100% of study participants. Further

studies are required to determine the optimal number and composition of epitopes required to produce these effects. Here, we have identified a pool of peptides that could alter immune responses in a large proportion of the population, worldwide.

Our findings provide evidence that SIT downregulates the T_H2 response to both known allergens and recently identified additional TG antigens. These antigens or their associated epitopes could be used to measure or predict patients' response to SIT or as immunotherapeutic agents. Studies to evaluate the clinical potential of our findings are underway, and include whole-pollen sensitization of animal models immunized with peptides, as well as longitudinal studies of patients who have received SIT regimens.

Clinical implications: PBMCs from patients with allergies who received SIT produce lower levels of T_H2 cytokines and higher levels of IFN- γ in response to specific peptides from TG antigens.

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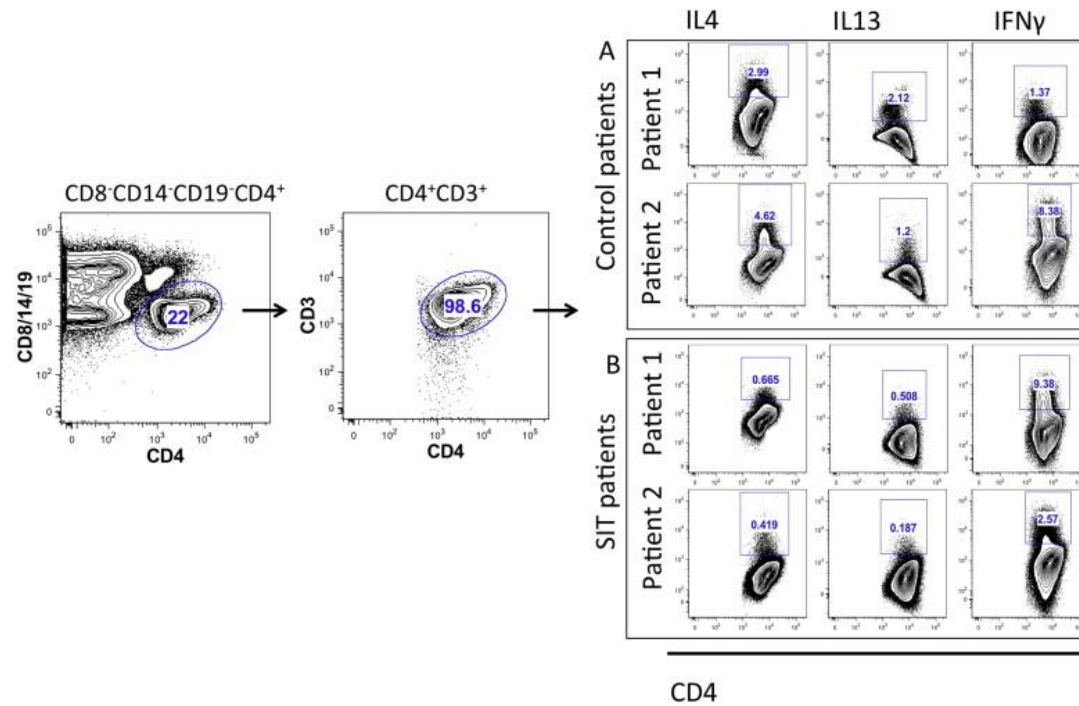


Fig E2

Véronique Schulten , Victoria Tripple , John Sidney , Jason Greenbaum , April Frazier , Rafeul Alam , David Broid...

Association between specific timothy grass antigens and changes in TH1- and TH2-cell responses following specific immunotherapy

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Patient ID	Status	Sex	Age	Wheal	Ethnicity	Allergen	Date	Dose dil.	Duration (years)	Type	Positive response
D00008	Allergic	Male	34	11	White	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
D00016	Allergic	Male	59	16	White	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
D00045	Allergic	Female	26	9	Hispanic	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
D00052	Allergic	Female	45	10	White	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
D00067	Allergic	Female	54	19	White	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
D00073	Allergic	Female	48	12	Black	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
D00084	Allergic	Male	34	17	White	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
D00090	Allergic	Male	46	10	Native American, Hispanic	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
D00096	Allergic	Female	60	34	White	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
D00102	Allergic	Male	31	29	White	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
D00104	Allergic	Male	64	12	White	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
D00117	Allergic	Female	55	36	White	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
U00032	Allergic	Female	26	30	Asian/Pacific Islander	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
U00034	Allergic	Male	32	10	White	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
U00036	Allergic	Male	26	10	White	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
U00058	Allergic	Female	26	15	White	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
U00095	Allergic	Male	57	5	White	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
U00098	Allergic	Male	25	10	Asian/Pacific Islander	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
U00106	Allergic	Male	22	16	1/2 White 1/2 Hispanic	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
U00125	Allergic	Male	26	20	Asian/Pacific Islander	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.

U00129	Allergic	Male	25	10	Black	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
U00140	Allergic	Male	31	10	1/2 Asian 1/2 White	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
U00147	Allergic	Male	25	10	Asian/Pacific Islander	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
U00150	Allergic	Female	21	20	Asian/Pacific Islander	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
U00151	Allergic	Male	25	30	Asian/Pacific Islander	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
U00153	Allergic	Female	23	10	Asian/Pacific Islander	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
D00089	Allergic	Female	67	12	White	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
D00092	Allergic	Female	44	6	Hispanic	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
D00015	Allergic	Female	45	7	Hispanic	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
U00001	Allergic	Female	25	12	White	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
D00168	Allergic	Male	44	21	White	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
D00083	Allergic	Female	45	10	White	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
U00114	Allergic	Male	34	10	Asian/Pacific Islander	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
D00169	Allergic	Female	46	9	White	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
D00172	Allergic	Female	60	12	White	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
D00158	Allergic	Male	31	31	White	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
D00170	Allergic	Male	47	37	White	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
D00122	Allergic	Female	41	20	White	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
D00160	Allergic	Female	49	31	Black	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
D00171	Allergic	Male	64	14	White	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
D00017	SIT	Female	67	14	White	T/G/W*	12-Aug	1:10**	4	C***	Yes
D00031	SIT	Female	44	7	Hispanic	T/G/W/D	11-Aug	1:10	3	C	Yes

D00044	SIT	Female	54	8	White	T/GW	8-Mar	1:10	5	C	No
D00063	SIT	Male	43	15	Asian/Pacific Islander	T/GW/C/D	9-Jun	1:100	3	R	No
D00072	SIT	Female	59	8		T/GW/C/D	12-Jul	1:10	5	C	Yes
D00080	SIT	Male	40	25	White	T/GW/C/D/DM	13-Aug	1:10	5	C	Yes
D00087	SIT	Male	40	18	White	T/GW/C/D	12-Sep	1:10	3	R	Yes
D00093	SIT	Female	43	10	White	T/GW	11-Sep	1:10	2	C	No
D00101	SIT	Male	49	17	White	T/GW/C	11-Sep	1:10	2	C	Yes
D00106	SIT	Female	42	9	White	T/G/D	11-Sep	1:10	2	R	Yes
D00109	SIT	Female	33	10	Black	T/GW/C/D/M	13-Sep	1:10	4	R	Yes
D00111	SIT	Male	50	11	White	T/GW/DM	12-Sep	1:10	3	C	Yes
D00114	SIT	Female	52	11	White	GW/DM/C/D/M	12-Sep	1:10	3	R	No
D00116	SIT	Male	54	14	White	T/GW/C/D	11-Apr	1:10	7	C	Yes
D00119	SIT	Female	59	12	White	GW/C/DM	12-Jul	1:10	5	C	Yes
D00120	SIT	Female	67	16	Declined to answer	T/GW	10-current	1:10	3	R	Yes
D00126	SIT	Male	44	17	White	T/GW/C/D/DM/M	10-current	1:10	3	R	Yes
D00129	SIT	Female	23	17	White	T/GW/C	11-current	1:10	2	C	Yes
D00130	SIT	Male	40	15	White	T/GW/C/D/DM	12-Aug	1:10	4	C	Yes
D00132	SIT	Male	44	11	White	n.a.	12-current	n.a.	1	n.a.	Yes
D00133	SIT	Male	40	11	White	T/GW/C/D	12-Sep	1:10	3	R	Yes
D00134	SIT	Female	59	15	White	T/GW	11-Sep	1:10	2	R	Yes
D00135	SIT	Male	51	13	White	T/G/C/D/M	12-current	n.a.	1	n.a.	Yes
D00136	SIT	Female	67	10	White	T/G/C/D	12-current	n.a.	1	n.a.	Yes
D00142	SIT	Female	29	5	White	T/GW/M	12-current	1:10	1	R	Yes

D00143	SIT	Female	53	7	White	T/G/W/C/D/DM	13-Aug	1:10	5	R	Yes
D00144	SIT	Male	35	9	White	T/G/W	12-current	1:10	1	R	Yes
D00146	SIT	Male	31	7	Black	T/G/W/C/D	12-current	1:10	1	C	Yes
D00147	SIT	Male	32	6	White	T/G/C/D	12-current	1:10	2	R	Yes
D00148	SIT	Female	46	10	Black	G/C/D	12-current	n.a.	1	n.a.	No
D00150	SIT	Female	47	6	White	T/G/W	12-Oct	1:100	2	C	Yes
D00151	SIT	Female	52	9	White	T/G/C/D	12-current	n.a.	1	n.a.	No
D00152	SIT	Female	39	10	White	T/G/W/C/D/M	12-current	1:10	2	C	Yes
D00153	SIT	Male	46	5	White	T/G/C	10-current	1:10	3	C	Yes
D00155	SIT	Male	28	9	Black	T/G/DM	12-current	n.a.	1	n.a.	Yes
D00157	SIT	Female	26	10	White	T/G/W/C/D/DM	12-current	1:10	1	R	Yes
D00162	SIT	Female	57	7	White	G/C	12-current	n.a.	1	n.a.	Yes
U00065	SIT	Female	22	8	White	C/G/T/W	9-Aug	1:10	1	C	Yes
U00141	SIT	Female	33	3	Hispanic	C/D/DM/G/T/W	11-Sep	1:10	2	C	Yes
U00158	SIT	Female	32	4	White	C/D/DM/G/T/W/M	12-Oct	1:10	2	C	Yes

*T: trees; G: grasses; W: weeds; C: cats; D: dogs; DM: dust mites; M: molds

** 1:10 dilution of the full allergen concentration supplied by the vendor for IT

***R: Rush immunotherapy; C: conventional immunotherapy

Controls												
ID	DRB1	DRB1	DRB3/4/5	DRB3/4/5	DQA1	DQA1	DQB1	DQB1	DPA1	DPA1	DPB1	DPB1
D00008	DRB1*13:01	DRB1*15:01	DRB3*02:02	DRB5*01:01	DQA1*01:02	DQA1*01:03	DQB1*06:02	DQB1*06:03	DPA1*01:03	DPA1*01:03	DPB1*02:01	DPB1*20:01
D00015	DRB1*15:01	DRB1*16:02	DRB5*01:01	DRB5*02:02			DQB1*03:01	DQB1*06:02			DPB1*02:01	DPB1*04:01
D00016	DRB1*01:02	DRB1*04:02		DRB4*01:03	DQA1*01:01	DQA1*03:01	DQB1*03:02	DQB1*05:01	DPA1*01:03	DPA1*01:03	DPB1*04:01	DPB1*04:01
D00045	DRB1*08:04	DRB1*15:01		DRB5*01:01	DQA1*01:02	DQA1*04:01	DQB1*04:02	DQB1*06:02	DPA1*01:03	DPA1*01:03	DPB1*04:01	DPB1*04:02
D00052	DRB1*07:01	DRB1*15:01	DRB4*01:03	DRB5*01:01	DQA1*01:02	DQA1*02:01	DQB1*06:02	DQB1*06:02	DPA1*01:03	DPA1*01:03	DPB1*04:01	DPB1*51:01
D00067	DRB1*13:02	DRB1*15:01	DRB3*01:01	DRB5*01:01	DQA1*01:02	DQA1*01:02	DQB1*06:02	DQB1*06:04	DPA1*01:03	DPA1*01:03	DPB1*04:01	DPB1*04:01
D00073	DRB1*03:01	DRB1*08:04	DRB3*02:02		DQA1*04:01	DQA1*05:01	DQB1*02:01	DQB1*03:19	DPA1*02:01	DPA1*02:02	DPB1*01:01	DPB1*01:01
D00083	DRB1*11:04	DRB1*13:02	DRB3*02:02	DRB3*03:01			DQB1*03:01	DQB1*06:04			DPB1*04:01	DPB1*14:01
D00084	DRB1*07:01	DRB1*07:01	DRB4*01:01	DRB4*01:03	DQA1*02:01	DQA1*02:01	DQB1*02:02	DQB1*03:03	DPA1*01:03	DPA1*01:03	DPB1*04:01	DPB1*04:01
D00089	DRB1*03:01	DRB1*11:04	DRB3*01:01	DRB3*02:02			DQB1*02:01	DQB1*03:01			DPB1*03:01	DPB1*04:01
D00090	DRB1*11:01	DRB1*11:04	DRB3*02:02	DRB3*02:02	DQA1*05:01	DQA1*05:05	DQB1*03:01	DQB1*03:01	DPA1*02:01	DPA1*02:01	DPB1*10:01	DPB1*10:01
D00092	DRB1*01:01	DRB1*08:02					DQB1*04:02	DQB1*05:01			DPB1*04:01	
D00096	DRB1*04:07	DRB1*03:02	DRB3*03:01	DRB4*01:03	DQA1*01:02	DQA1*03:03	DQB1*03:01	DQB1*06:09	DPA1*01:03	DPA1*01:03	DPB1*02:01	DPB1*03:01
D00102	DRB1*03:01	DRB1*04:01	DRB3*02:02	DRB4*01:03	DQA1*03:01	DQA1*05:01	DQB1*02:01	DQB1*03:02	DPA1*01:03	DPA1*02:02	DPB1*01:01	DPB1*02:02
D00104	DRB1*04:01	DRB1*13:01	DRB3*01:01	DRB4*01:03	DQA1*01:03	DQA1*03:03	DQB1*03:01	DQB1*06:03	DPA1*01:03	DPA1*01:03	DPB1*02:01	DPB1*04:01
D00117	DRB1*08:01	DRB1*15:01		DRB5*01:01	DQA1*01:02	DQA1*04:01	DQB1*04:02	DQB1*06:02	DPA1*01:03	DPA1*01:03	DPB1*04:01	DPB1*04:01
D00168	DRB1*07:01	DRB1*10:03	DRB4*01:01	DRB4*01:01	DQA1*01:01	DQA1*01:06	DQB1*02:02	DQB1*05:01	DPA1*01:03	DPA1*01:03	DPB1*02:01	DPB1*04:01
D00169	DRB1*13:02	DRB1*15:01	DRB3*03:01	DRB5*01:01	DQA1*01:02	DQA1*01:02	DQB1*06:02	DQB1*06:04	DPA1*01:03	DPA1*02:01	DPB1*01:01	DPB1*03:01
U00001	DRB1*03:01	DRB1*07:01	DRB3*01:01	DRB4*01:03			DQB1*02:01	DQB1*02:02			DPB1*04:01	DPB1*04:01
U00032	DRB1*09:01	DRB1*11:01	DRB3*02:02	DRB4*01:03	DQA1*03:02	DQA1*05:05	DQB1*03:01	DQB1*03:03	DPA1*02:01	DPA1*02:02	DPB1*05:01	DPB1*14:01
U00034	DRB1*04:03	DRB1*15:01	DRB4*01:03	DRB5*01:01	DQA1*01:02	DQA1*03	DQB1*03:02	DQB1*06:02	DPA1*01:03	DPA1*01:03	DPB1*04:01	DPB1*04:01
U00036	DRB1*03:01	DRB1*07:01	DRB3*01:01	DRB4*01:03	DQA1*02:01	DQA1*05:01	DQB1*02:01	DQB1*02:02	DPA1*01:03	DPA1*01:03	DPB1*04:01	DPB1*04:01
U00058	DRB1*03:01	DRB1*13:01	DRB3*01:01	DRB3*02:02	DQA1*01:03	DQA1*05:01	DQB1*02:01	DQB1*06:03	DPA1*01:03	DPA1*01:03	DPB1*04:01	DPB1*04:01
U00095	DRB1*04:02	DRB1*04:04	DRB4*01:03	DRB4*01:03	DQA1*03:01	DQA1*03	DQB1*03:02	DQB1*04:02	DPA1*01:03	DPA1*01:03	DPB1*04:01	DPB1*04:02
U00098	DRB1*03:01	DRB1*07:01	DRB3*02:02	DRB4*01:03	DQA1*02:01	DQA1*05:01	DQB1*02:01	DQB1*02:02	DPA1*01:03	DPA1*02:01	DPB1*04:01	DPB1*26:01
U00106	DRB1*04:04	DRB1*07:01	DRB4*01:03	DRB4*01:03	DQA1*02:01	DQA1*03:01	DQB1*02:02	DQB1*03:02	DPA1*01:03	DPA1*02:01	DPB1*04:01	DPB1*14:01

U00114	DRB1*12:01	DRB1*15:06	DRB3*02:02	DRB5*01:01	DQA1*01:02	DQA1*05:05	DQB1*03:01	DQB1*05:02	DPA1*01:03	DPA1*02:02	DPB1*02:01	DPB1*13:01
U00125	DRB1*03:01	DRB1*08:02	DRB3*02:02		DQA1*03:01	DQA1*05:01	DQB1*02:01	DQB1*03:02	DPA1*01:03	DPA1*02:02	DPB1*04:01	DPB1*05:01
U00129	DRB1*04:07	DRB1*11:01	DRB3*02:02	DRB4*01:03	DQA1*03:03	DQA1*05:05	DQB1*03:01	DQB1*03:19	DPA1*01:03	DPA1*02:01	DPB1*01:01	DPB1*03:01
U00140	DRB1*11:01	DRB1*13:02	DRB3*02:02	DRB3*03:01	DQA1*01:02	DQA1*05:05	DQB1*03:01	DQB1*06:09	DPA1*01:03	DPA1*02:01	DPB1*04:02	DPB1*09:01
U00147	DRB1*08:02	DRB1*15:01		DRB5*01:01	DQA1*01:02	DQA1*04:01	DQB1*06:02	DQB1*06:02	DPA1*01:03	DPA1*01:03	DPB1*02:01	DPB1*02:01
U00150	DRB1*11:01	DRB1*15:01	DRB3*02:02	DRB5*01:01	DQA1*01:02	DQA1*05:05	DQB1*03:01	DQB1*06:01	DPA1*01:03	DPA1*02:02	DPB1*03:01	DPB1*05:01
U00151	DRB1*12:02	DRB1*15:01	DRB3*03:01	DRB5*01:01	DQA1*01:02	DQA1*06:01	DQB1*03:01	DQB1*06:01	DPA1*01:03	DPA1*02:02	DPB1*05:01	DPB1*21:01
U00153	DRB1*15:02	DRB1*15:02	DRB5*01:01	DRB5*01:08	DQA1*01:02	DQA1*01:02	DQB1*05:02	DQB1*05:02	DPA1*02:02	DPA1*02:02	DPB1*01:01	DPB1*05:01
D00158	DRB1* 03:01	DRB1* 15:01	DRB3*01:01	DRB5*01:01	DQA1* 01:02	DQA1* 05:01	DQB1* 02:01	DQB1* 06:02	DPA1* 01:03	DPA1* 02:01	DPB1* 04:01	DPB1* 11:01
D00160	DRB1* 07:01	DRB1* 11:01	DRB3*02:02	DRB4*01:03	DQA1* 02:01	DQA1* 05:05	DQB1* 02:01	DQB1* 02:02	DPA1* 02:01	DPA1* 02:01	DPB1* 11:01	DPB1* 17:01
D00122	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
D00170	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
D00171	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
D00172	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.

SIT

ID	DRB1	DRB1	DRB3/4/5	DRB3/4/5	DQA1	DQA1	DQB1	DQB1	DPA1	DPA1	DPB1	DPB1
D00017	DRB1*03:01	DRB1*11:04	DRB3*01:01	DRB3*02:02			DQB1*02:01	DQB1*03:01			DPB1*03:01	DPB1*04:01
D00031	DRB1*01:01	DRB1*08:02					DQB1*04:02	DQB1*05:01			DPB1*04:01	
D00044	DRB1*04:01	DRB1*15:01	DRB4*01:03	DRB5*01:01			DQB1*03:01	DQB1*06:02			DPB1*02:01	DPB1*04:01
D00072	DRB1*04:01	DRB1*11:01	DRB3*02:02	DRB4*01:03	DQA1*03	DQA1*05	DQB1*03:01	DQB1*03:01	DPA1*01:03	DPA1*01:03	DPB1*04:01	DPB1*04:02
D00087	DRB1*04:01	DRB1*11:01	DRB3*02:02	DRB4*01:03	DQA1*03:03	DQA1*05:09	DQB1*03:01	DQB1*03:02	DPA1*01:03	DPA1*02:01	DPB1*03:01	DPB1*14:01
D00093	DRB1*01:01	DRB1*15:01	DRB5*01:01				DQB1*05:01	DQB1*06:02			DPB1*04:02	DPB1*09:01
D00101	DRB1*03:01	DRB1*13:02	DRB3*01:01	DRB3*03:01	DQA1*05:01	DQA1*01:02	DQB1*02:01	DQB1*06:04	DPA1*01:03	DPA1*02:01	DPB1*05:01	DPB1*01:01
D00106	DRB1*03:01	DRB1*08:01	DRB3*01:01	DRB3*01:01	DQA1*04:03	DQA1*05:01	DQB1*02:01	DQB1*04:02	DPA1*01:03	DPA1*02:01	DPB1*01:01	DPB1*04:02
D00109	DRB1*08:04	DRB1*15:03		DRB5*01:01	DQA1*01:02	DQA1*05:05	DQB1*03:01	DQB1*06:02	DPA1*01:03	DPA1*02:01	DPB1*02:01	DPB1*11:01
D00111	DRB1*03:01	DRB1*15:01	DRB3*01:01	DRB5*01:01	DQA1*01:02	DQA1*05:01	DQB1*02:01	DQB1*06:02	DPA1*01:03	DPA1*01:03	DPB1*02:01	DPB1*03:01
D00116	DRB1*04:01	DRB1*15:01	DRB4*01:03	DRB5*01:01	DQA1*01:02	DQA1*03:01	DQB1*03:02	DQB1*06:02	DPA1*01:03	DPA1*01:03	DPB1*02:01	DPB1*04:01
D00119	DRB1*04:01	DRB1*11:01	DRB3*02:02	DRB4*01:03	DQA1*03	DQA1*05	DQB1*03:01	DQB1*03:01	DPA1*01:03	DPA1*01:03	DPB1*04:01	DPB1*04:02

[illegible]

Peptide sequence	LQGFNFRFLTEKGMKNVFDDVWPEKY TIG	AVQVFTTVQKGSDPKKLVLNIIKYTRPGD SL	EEWEPLTKKGNVWEV	NVWEVKSSKPLVGPF	LVGPFNFRFMSKGGMRNVFDEVIPT	INAGFKAALAAAAGVPPADKY	AFKVAATAANAAPAN	PANDKFTVFEEAFNDAIKE	ATVATAPEVKYTVFETALKKAITAMS	STWYGKPTGAGPKDN
Pool	P20	P20	P20	P20	P20	P20	P20	P20	P20	P20
Protein	Phl p 2	Phl p 3	Phl p 3	Phl p 3	Phl p 3	Phl p 5a/5b	Phl p 5a	Phl p 5a/5b	Phl p 5a/5b	Phl p 1
DPA1*01:03/DPB1*03:01	226.2	41.7	26158.5	5889.2	290.7	48.5	26.9	660.8	2348.6	3887.4
DPB1*02:01	103.8	103.5	18002.6	9616.8	25.7	4486.4	27973.6	100.0	2.2	7459.3
DPB1*20:01	74.2	18.2	12918.0	2912.7	48.7	33.9	7.7	491.2	1011.0	3193.6
DRB1*04:05	199.1	487.2	32308.4	10366.8	814.7	208.3	183.2	51.1	110.2	4568.5
DRB1*15:01	811.9	216.9	30341.6	4634.2	150.0	62.2	10928.6	604.6	128.4	13661.1
DRB1*04:01	121.3	1822.9	14260.2	2961.7	1615.5	5.4	5.8	72.7	22.3	2448.7
DRB1*04:04	958.7	121.5	<46728.9	862.6	1388.8	150.7	47.3	287.6	44.2	5390.3
DRB1*01:01	13.8	31.5	990.5	261.5	32.1	1.0	6.3	12.9	53.4	366.4
DRB1*03:01	57.9	235.1	2964.9	5462.6	5174.7	<33358.0	<46728.9	2889.9	938.6	<46728.9
DRB1*07:01	2460.6	92.8	<46728.9	373.5	216.1	83.0	77.1	222.8	185.4	4024.3
DRB3*02:02	<23364.5	117.6	26615.3	20986.9	457.0	28.2	680.4	242.2	376.6	5908.73
DRB1*10:01	8.1	43.5	637.9	542.4	46.5	1.9	1.9	4.8	83.9	125.23
DRB1*08:02	90.9	9.8	113.6	63.2	5.2	10.7	44.1	858.8	13.2	34.49

DRB4*01:01	541.5	306.2	20595.6	220.2	474.1	1816.4	2529.6	693.1	7.3	17935.62
DQA1*01:02/DQB1*06:02	5454.7	542.0	<46728.9	828.5	1308.6	11.7	95.7	173.6	82.0	8311.61
DQA1*04:01/DQB1*04:02	1652.2	<23364.5	<46728.9	4564.4	10055.5	1155.5	1565.2	656.5	2730.8	38760.85
DQA1*05:01/DQB1*02:01	107.0	6275.5	7915.9	422.9	43.9	988.3	1259.0	80.6	2735.7	5042.37
DQA1*01:01/DQB1*05:01	410.5	<23364.5	27058.8	<46728.9	28.3	869.5	<46728.9	39.3	12965.9	1810.78
DPA1*03:01/DPB1*04:02	5432.2	2308.7	43033.1	28416.4	5313.4	1860.9	10123.0	7681.6	48.3	11104.43
DPA1*02:01/DPB1*01:01	251.4	622.7	21126.8	2921.1	256.3	830.2	<46728.9	3371.5	15.1	<46728.9
DPB1*14:01	1865.2	557.9	22730.6	8378.4	5423.6	142.1	14.6	957.5	129.5	2786.13
DPA1*01:03/DPB1*04:01	5204.9	5279.1	<46728.9	12514.0	1003.5	17039.7	<46728.9	4054.6	11.0	5369.03
DRB1*16:02	60.5	42.8	8154.7	107.0	55.1	23.9	193.6	15.1	322.6	864.50
DRB1*11:01	111.2	24.2	645.5	853.7	27.0	138.7	197.5	5845.4	194.1	4710.24
DRB5*01:01	43.1	28.2	5169.2	2421.3	33.9	41.7	741.3	499.3	19.8	7574.92
DPA1*02:01/DPB1*05:01	64.1	41.7	5076.0	4643.0	276.2	4576.1	548.7	272.4	10.7	5120.64
DQA1*05:01/DQB1*03:01	7369.9	211.5	8015.9	34.7	523.6	8.8	16.5	322.3	89.0	102.43
DQA1*03:01/DQB1*03:02	1191.3	3088.7	39460.0	1601.7	4465.7	481.3	3347.3	181.0	1647.9	10548.54
DRB1*12:01	236.9	503.3	<46728.9	9435.9	1978.6	5931.2	<46728.9	<36855.0	668.5	28922.24
DRB1*13:02	400.6	119.0	5660.5	58.0	294.6	251.2	49.6	239.2	387.1	16279.77
DRB1*09:01	393.6	472.7	21501.5	2037.7	115.4	14.6	108.7	77.8	128.9	3559.64
DRB3*01:01	2568.1	<23348.1	<46728.9	<46728.9	<28019.1	<33355.6	<46728.9	407.0	7050.8	19106.03

Peptide sequence										
	KPPFSGMTGCGNTPi	FEIKCTKPEACSGEPVVVHI	SGIAFGSMAKKGDEQ	GELELQFRRVKCKYP	TFHVEKGSNPNYLALLVKYVNGDGD	EHGSDEWVAMTKGEGGVWTF	NRNNTFKPFAEYKSDYVYQPFPK	VIPAGELQVIEKVDAAFKVA	AYESYKFIPALEAAVKQAYAAATVAAA	LAKYKANWIEIMRIK
Pool	P20	P20	P20	P20	P20	P20	P20	P20	P20	P20
Protein	Phl p 1	Phl p 1	Phl p 1	Phl p 1	Phl p 1	Phl p 2	Phl p 4	Phl p 5a	Phl p 5a/5b	Phl p 13
DPA1*01:03/DPB1*03:01	<46728.9	457.9	12834.8	11849.0	17589.7	<46728.9	2020.0	9752.8	4.2	246.9
DPB1*02:01	35448.5	12169.8	<46728.9	181.4	85.9	7066.0	45.6	1103.6	404.2	95.3
DPB1*20:01	16060.3	1313.9	33279.9	8655.0	18194.5	27906.0	861.7	13547.5	44.1	4592.3
DRB1*04:05	2905.2	771.8	32247.9	34441.7	55.7	4265.0	926.2	1487.6	9.3	485.5
DRB1*15:01	3947.5	1781.1	3794.8	4532.2	84.1	3750.6	12.6	135.5	146.8	503.5
DRB1*04:01	1099.5	478.7	15304.5	15880.6	683.8	954.7	92.5	111.5	11.5	279.3
DRB1*04:04	2107.4	1733.2	4174.8	18554.3	59.1	1191.7	17297.8	187.2	54.6	106.5
DRB1*01:01	81.8	460.4	250.9	7305.9	7.0	51.3	96.5	51.8	1.2	20.8
DRB1*03:01	44207.1	26820.5	<46728.9	5889.1	35480.6	<46728.9	6427.2	141.1	33.7	1401.6
DRB1*07:01	8963.4	1546.7	20748.8	4874.0	253.6	446.0	1485.6	150.6	33.2	385.2
DRB3*02:02	<46728.9	1348.16	11589.77	<46728.9	5012.35	5602.78	616.04	5659.06	108.67	16.01
DRB1*10:01	4.64	321.74	808.88	3037.77	13.27	110.54	26.55	316.89	8.05	12.50
DRB1*08:02	6989.14	1210.04	986.92	101.27	52.50	184.33	744.86	371.15	26.11	53.93

DRB4*01:01	9179.50	751.30	13321.23	1513.25	4669.89	350.12	4134.66	10.77	730.64	9.48
DQA1*01:02/DQB1*06:02	22185.87	8188.95	176.19	10680.69	1320.85	1195.97	24533.69	9154.38	14.82	478.77
DQA1*04:01/DQB1*04:02	<46728.9	12075.71	<46728.9	<46728.9	19522.36	1204.09	14128.01	2584.20	423.31	8704.67
DQA1*05:01/DQB1*02:01	23608.96	8037.30	<46728.9	<46728.9	1487.26	835.96	650.41	1554.48	303.18	681.85
DQA1*01:01/DQB1*05:01	18971.27	32787.06	<46728.9	<46728.9	23313.13	<46728.9	2120.04	4866.30	304.45	853.25
DPA1*03:01/DPB1*04:02	35353.57	3713.37	<46728.9	10311.47	1171.01	13404.87	7207.50	837.29	1368.76	185.17
DPA1*02:01/DPB1*01:01	<46728.9	6454.39	<46728.9	3909.30	763.44	1514.54	692.04	1091.15	321.36	97.75
DPB1*14:01	6594.13	7911.75	28361.55	28342.38	432.40	3815.03	2803.04	318.88	27.78	709.07
DPA1*01:03/DPB1*04:01	29971.72	10930.53	<46728.9	7006.82	1441.71	25972.67	580.58	2734.11	1314.71	532.64
DRB1*16:02	3605.51	6066.43	9940.53	4642.56	84.13	376.73	5.58	106.08	2.72	429.69
DRB1*11:01	6562.64	3004.27	893.76	278.74	77.48	533.90	362.75	555.97	38.85	331.33
DRB5*01:01	2727.33	7910.00	2724.12	171.57	1826.33	3492.89	171.43	22.19	22.52	317.68
DPA1*02:01/DPB1*05:01	12142.59	4314.20	746.80	3690.05	33.18	1096.27	248.78	48.79	7.28	336.22
DQA1*05:01/DQB1*03:01	5090.22	256.66	84.46	2736.57	92.98	354.92	8053.52	247.48	6.99	618.92
DQA1*03:01/DQB1*03:02	29901.31	7373.62	17981.88	<46728.9	3184.40	851.69	9207.30	811.77	184.71	2586.60
DRB1*12:01	14829.87	6155.06	<46728.9	11029.57	89.44	6166.46	7701.28	194.02	2071.82	1356.89
DRB1*13:02	7933.13	1939.94	31963.80	28776.87	70.50	618.66	4685.61	69.00	7.81	59.85
DRB1*09:01	2792.29	5288.01	5318.47	11613.23	99.52	656.60	126.61	187.58	4.21	159.82
DRB3*01:01	<46728.9	18044.05	<46728.9	<46728.9	3378.84	9604.44	32.12	540.58	2010.78	440.00

Peptide sequence

AAYLATRGLDWDAV

APSGRIVMELYADV

AVMLTFDNAGMWNVR

CDASILIDPLSNQSA

ELRKTYNLLDAVSRH

GDLYIFESRAICKYA

GEVLNALAYDVPIPG

HYKGSSFHHRVIPGFM

IGSFFYFPSIGMQRT

IIELFTAKGFTVQEM

Pool	P19	P19/MNA	P19/MNA	P19	P19/MNA	P19	P19	P19/MNA	P19/MNA	P19/MNA
Protein	M82	MN26	M76	M81	M76	MN10	MN23	MN26	M83	M34
DPA1*01:03/DPB1*03:01	130.5	817.3	1740.2	313.8	4147.7	33.0	3697.8	8137.4	2993.6	1609.6
DPB1*02:01	78.2	734.5	957.1	2595.9	1626.3	599.5	5388.2	931.8	89.0	64.3
DPB1*20:01	864.9	848.7	31085.3	904.3	8061.6	1473.8	<46728.9	<46728.9	35007.0	4241.4
DRB1*04:05	9.4	291.2	60.2	208.5	6.1	70.8	1046.8	55.7	0.7	312.6
DRB1*15:01	38.3	289.5	58.5	363.4	973.5	0.8	30.0	1385.4	0.2	9.7
DRB1*04:01	11.9	774.2	35.6	41.6	59.4	2523.2	728.2	739.6	0.4	744.7
DRB1*04:04	390.2	2602.8	1.3	2.8	58.6	3.8	152.6	390.4	1.0	6.1
DRB1*01:01	3.6	561.2	501.8	1267.9	13.6	80.3	104.4	86.5	2.8	17.4
DRB1*03:01	23436.5	5558.7	1335.3	15.5	<46728.9	82.5	243.9	<46728.9	7492.3	4214.0
DRB1*07:01	2.5	330.1	358.5	1151.8	130.7	8.0	60.5	1.3	2.9	17.5
DRB3*02:02	3.2	4560.2	12.6	10088.7	464.1	636.8	9611.7	3906.6	2.7	4405.5
DRB1*10:01	0.6	780.2	75.5	49.6	3.6	1279.6	346.4	9.1	2.9	18.3
DRB1*08:02	111.1	439.8	2.8	17.7	54.0	11.0	56.2	199.9	0.6	4.6
DRB4*01:01	79.2	949.8	2004.4	1501.4	37885.6	5523.8	5919.5	17288.9	78.4	2880.7

DQA1*01:02/DQB1*06:02	6.4	65.3	1103.9	225.4	6684.5	779.0	413.0	5.8	1609.4	1376.0
DQA1*04:01/DQB1*04:02	5057.09	5438.71	5907.67	798.40	<46728.9	2007.20	3499.44	8868.76	7348.78	422.82
DQA1*05:01/DQB1*02:01	11.03	10.85	2280.93	2641.30	6523.87	17960.26	53.64	296.06	621.43	216.22
DQA1*01:01/DQB1*05:01	855.08	915.51	73.89	17881.81	2434.67	865.65	15.74	2141.62	883.24	68.58
DPA1*03:01/DPB1*04:02	259.57	71.61	1228.95	2714.00	2304.51	1385.56	1798.34	45.53	151.67	108.20
DPA1*02:01/DPB1*01:01	6458.68	50.14	8267.17	<46728.9	19820.45	5263.84	25749.24	522.54	1109.95	1870.51
DPB1*14:01	153.32	32799.10	23700.39	<46728.9	1960.54	5174.59	26116.87	13721.21	9754.48	1168.26
DPA1*01:03/DPB1*04:01	177.6	2.0	254.9	5337.3	3746.3	319.7	8995.9	19.5	64.2	436.1
DRB1*16:02	0.26	2297.04	665.07	324.01	244.45	9.90	315.98	262.22	1.38	65.29
DRB1*11:01	53.0	10998.0	2881.4	3995.1	1342.8	182.3	5653.9	349.2	11.9	495.1
DRB5*01:01	24.5	14033.3	325.0	2871.3	6.5	14.4	6089.8	145.9	4.8	140.1
DPA1*02:01/DPB1*05:01	14273.02	7362.39	3679.67	30548.06	209.48	674.58	21098.74	23063.28	8964.95	2483.95
DQA1*05:01/DQB1*03:01	124.6	3623.8	3128.6	5596.2	<46728.9	904.9	324.0	7964.9	4870.6	743.4
DQA1*03:01/DQB1*03:02	3522.0	3771.2	9589.5	382.8	<46728.9	714.0	930.2	5987.0	10483.2	313.5
DRB1*12:01	1069.9	100.0	2687.1	1332.3	33923.3	455.3	21.5	789.2	749.6	15.0
DRB1*13:02	16.9	550.6	17.1	221.5	77.5	5.2	45.4	4.2	159.5	107.2
DRB1*09:01	1.3	324.7	200.9	2224.5	643.6	10.9	52.7	62.1	0.8	18.3
DRB3*01:01	83.9	550.8	80.3	136.8	1989.3	419.5	531.5	876.3	5.5	3060.1

Peptide sequence	LVSKLYEVVPGILTE	NFTVGRIIELFTAKG	NGSQFFLCTAKTAWL	NPMTVFWSKMAQSMIT	PRRWLRFNPELSEI	QVYPRSWSAVMLTFD	QYAKEIWGITANPVP	VKLRRSSAAQVDGFY	VVSRLLIPVPFDPPA
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Pool	P19	P19/MNA	P19	P19	P19	P19/MNA	P19	P19/MNA	P19
Protein	MN11	M34	MN26	MN01	MN23	M76	MN23	M82	M83
DPA1*01:03/DPB1*03:01	1060.2	799.2	1238.9	24.4	95.0	0.6	36.3	43.0	4.4
DPB1*02:01	6.3	715.7	0.3	11.9	1044.3	1219.9	6.5	7657.9	308.5
DPB1*20:01	2737.5	4839.8	7124.3	41.2	865.1	46.2	252.3	109.2	112.6
DRB1*04:05	6.4	7.0	45.7	3410.4	7.6	60.6	3.0	430.1	3380.6
DRB1*15:01	488.6	89.3	618.8	6.7	24.8	1.9	8.6	2088.4	10099.8
DRB1*04:01	55.2	304.9	44.8	316.4	25.5	2.8	2.1	133.6	42898.2
DRB1*04:04	46.3	5.5	4053.3	70.0	63.1	18.7	0.3	211.9	2114.7
DRB1*01:01	6.7	112.7	19.3	76.2	39.5	34.0	2.3	115.1	5375.4
DRB1*03:01	3065.0	<46728.9	4318.5	15451.9	1452.2	17261.8	8578.9	4551.2	27550.6
DRB1*07:01	3.0	2.5	14.4	23.3	7.1	5.1	2.4	6.4	229.9
DRB3*02:02	4122.0	965.8	2035.7	453.8	226.0	60.7	28.0	116.7	5626.2
DRB1*10:01	23.8	86.7	66.8	325.3	11.7	22.2	25.0	114.6	279.6
DRB1*08:02	14.0	7.8	3258.6	37.0	40.6	177.1	0.4	62.4	256.2
DRB4*01:01	10257.6	5006.6	35054.4	2711.3	313.4	1590.0	986.0	573.5	173.4

DQA1*01:02/DQB1*06:02	1742.9	59.4	1758.0	0.3	756.5	64.5	7.5	518.1	8650.7
DQA1*04:01/DQB1*04:02	8619.72	4091.38	15618.21	33127.11	35778.23	724.25	1036.84	1024.81	12173.56
DQA1*05:01/DQB1*02:01	694.88	476.71	546.93	5985.30	1204.37	64.11	42.85	395.32	744.39
DQA1*01:01/DQB1*05:01	8067.92	712.42	1613.80	7766.08	94.71	8.10	78.30	6664.63	59.06
DPA1*03:01/DPB1*04:02	181.32	153.41	917.37	40.22	2933.37	5663.50	589.74	23294.62	182.00
DPA1*02:01/DPB1*01:01	102.90	7676.56	5742.34	4597.98	10110.17	7784.50	69.41	<46728.9	3134.74
DPB1*14:01	23.10	3481.31	31212.58	3310.23	33759.07	60.82	11.43	569.99	749.56
DPA1*01:03/DPB1*04:01	3.6	2146.7	680.6	29.0	615.4	393.0	41.7	21418.5	798.7
DRB1*16:02	1.01	62.22	124.24	13.92	3.11	36.59	13.48	652.26	13568.53
DRB1*11:01	123.5	2920.1	139.0	110.1	1201.2	265.1	1799.8	965.2	5246.9
DRB5*01:01	591.7	2399.5	384.6	191.9	248.4	118.8	117.8	8406.6	<46728.9
DPA1*02:01/DPB1*05:01	146.68	9531.86	1635.65	567.24	7576.80	1164.68	19700.38	24320.89	1172.16
DQA1*05:01/DQB1*03:01	489.2	738.7	1646.0	128.1	9182.3	94.3	4.2	175.7	1518.3
DQA1*03:01/DQB1*03:02	3544.7	2387.9	3202.2	26483.8	26160.2	197.5	183.6	792.9	10369.1
DRB1*12:01	1903.3	13009.6	3048.7	2006.5	4198.8	4411.2	12.9	1873.2	204.8
DRB1*13:02	6.2	932.1	73.7	92.6	100.6	198.4	0.6	1.2	203.4
DRB1*09:01	2.4	234.5	19.6	12.6	7.0	7.5	5.7	34.3	839.7
DRB3*01:01	550.5	4755.1	312.8	3343.1	2048.9	122.5	9036.9	5282.5	17022.4

Antigen	Peptide	Sequence	Control patients						SIT patients					
			IFN γ		IL5		IL10		IFN γ		IL5		IL10	
			Donors	Sum SFC	Donors	Sum SFC	Donors	Sum SFC	Donors	Sum SFC	Donors	Sum SFC	Donors	Sum SFC
1	1 ₁₂	SDGTFARAAVPSGAS	0	0	0	0	0	0	1	540	0	0	0	0
	1 ₁₈	RAAVPSGASTGVYEA	0	0	0	0	0	0	1	67	0	0	0	0
	1 ₂₄	GASTGVYEALELRDG	0	0	0	0	0	0	0	0	0	0	0	0
	1 ₄₃	LGKGVLKGNRANVEL	0	0	0	0	0	0	0	0	0	0	0	0
	1 ₅₁	NRANVELFHIAVLLA	0	0	0	0	0	0	1	30	0	0	0	0
	1 ₇₀	QTELDNFMVHQLDGT	0	0	0	0	0	0	0	0	0	0	0	0
	1 ₉₁	CKQKVFFNISADADA	0	0	0	0	0	0	0	0	0	0	0	0
	1 ₁₅	PAMAATIQSVKARQI	0	0	0	0	0	0	2	197	0	0	0	0
	1 ₈₄	VDNVNSIIGPALIGK	0	0	0	0	0	0	0	0	0	0	0	0
	1 ₁₂₇	KLGANAILAVSLAVC	0	0	0	0	0	0	1	67	0	0	0	0
	1 ₁₄₈	KKIPLYQHIANLAGN	0	0	0	0	0	0	1	27	0	0	0	0
	1 ₁₆₁	GNKQLVLPVPFNV	1	190	0	0	0	0	1	47	0	0	0	0
	1 ₁₈₄	KLAMQEFMILPTGAS	0	0	0	0	0	0	1	63	0	0	0	0
	1 ₂₀₅	KMGVEVYHNLKSVIK	0	0	0	0	0	0	0	0	0	0	0	0
	1 ₂₆₀	GKVVIGMDVAASEFY	0	0	0	0	0	0	0	0	0	0	1	23
	1 ₃₀₄	VYKSFVSEYPIVSIE	0	0	1	20	0	0	2	107	0	0	0	0
	1 ₃₄₂	IVGDDLLVTNPTRVA	1	193	0	0	0	0	2	267	0	0	0	0
	1 ₃₆₅	NALLKVNQIGSVTE	1	170	0	0	0	0	0	0	0	0	0	0
	1 ₄₀₂	ETEDTFIADLAVGLS	0	0	0	0	0	0	1	40	0	0	0	0
	1 ₄₂₉	ERLAKYNQLLRIEE	0	0	0	0	0	0	0	0	0	0	0	0
	1 ₄₄₄	LGAAAVYAGLKFRAP	1	153	0	0	0	0	1	43	0	0	0	0
2	2 ₁	AEFEGVFLDFARQQA	0	0	2	137	0	0	0	0	0	0	0	0
	2 ₂₀	VDKLFKLAEEAKLKE	2	610	2	200	0	0	2	133	1	67	0	0

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[illegible]

6	5 ₁₅₉	DHLRQVFTAQMGLSD	0	0	0	0	0	0	0	0	0	0	0	
	5 ₂₀₂	NPLIFDNSYFTELLT	0	0	0	0	0	0	0	0	0	0	0	
	5 ₂₄₈	EDAFFADYAE AHLKL	0	0	0	0	0	0	0	0	0	0	0	
	6 ₁	TLLFPHTQISLPSVR	1	140	2	63	0	0	2	383	1	70	0	0
	6 ₁₄	VRTRKHLAATMADEK	0	0	0	0	0	0	1	20	0	0	0	0
	6 ₄₄	DNEKSGFISLSRYL	0	0	2	77	0	0	2	93	0	0	0	0
	6 ₅₀	FISLSRYLSGEEEH	0	0	0	0	0	0	0	0	0	0	0	0
	6 ₉₂	EATKALLNKLAVLKL	0	0	1	33	0	0	0	0	0	0	0	0
	6 ₁₂₃	IEVRNGFTFLDLIVL	0	0	2	110	0	0	0	0	0	0	0	0
	6 ₁₃₁	FLDLIVLQIESLNKK	0	0	1	33	0	0	2	200	0	0	0	0
	6 ₁₄₂	LNKKYGSNVP LLLMN	0	0	1	353	0	0	1	63	0	0	0	0
	6 ₁₄₉	NVPLL MN SFNTHED	0	0	1	153	0	0	0	0	0	0	0	0
	6 ₁₆₅	LKIVEKYANSSIDIH	2	1967	3	587	1	57	3	583	3	237	0	0
	6 ₁₇₅	SIDIHTFNQSQYPRV	0	0	2	227	0	0	0	0	1	30	0	0
	6 ₂₂₄	GKLDLLLSQGKEYVF	2	130	2	173	0	0	0	0	0	0	0	0
	6 ₂₃₃	GKEYVFIANS DN LGA	0	0	3	330	0	0	2	787	2	57	0	0
	6 ₂₄₂	SDNLGAIVDMKILNH	1	30	3	137	0	0	0	0	0	0	0	0
	6 ₂₄₈	IVDMKILNHLIHKQN	2	320	4	393	0	0	1	507	1	137	0	0
	6 ₂₈₂	ISYEGRVQLLEIAQV	0	0	0	0	0	0	0	0	0	0	0	0
	6 ₂₈₈	VQLLEIAQVPDAHVD	0	0	1	107	2	43	1	43	0	0	0	0
	6 ₃₀₄	FKSIEKFKIFNTNNL	1	393	1	67	0	0	2	177	1	77	0	0
	6 ₃₁₀	FKIFNTNNLWVNLKA	0	0	3	203	0	0	1	90	1	20	0	0
	6 ₃₁₆	NNLWVNLKAIKRLVE	2	1757	3	1550	2	527	3	273	2	140	0	0
	6 ₃₂₅	IKRLVEADALKMEII	1	417	2	227	0	0	1	83	0	0	0	0
	6 ₃₄₈	VKVLQLETAAGAAIR	1	53	3	180	0	0	2	183	0	0	0	0
	6 ₃₅₉	AAIRFFDHAIGINVP	4	1377	5	470	1	43	6	1267	3	320	1	57

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9	8 ₃₁₃	KQMDWVSKLSAPQLK	0	0	0	0	0	0	0	0	0	0	0
	8 ₃₈₂	KPILFMNEYNTIEEP	0	0	0	0	0	0	0	0	0	0	0
	8 ₄₀₄	TKYLAKLKQIQSYPG	0	0	0	0	0	0	0	0	0	0	0
	8 ₄₃₈	PYVRGSLDTLAQAKV	0	0	0	0	0	0	0	0	0	0	0
	8 ₄₆₅	PKQVEYLEEVMREGF	0	0	0	0	0	0	0	0	0	0	0
	8 ₁₇₂	NVTAEVDSMSLQPF	1	293	0	0	0	0	0	0	0	0	0
	9 ₅₆	TDTIVYCAGRTFFFR	1	180	0	0	0	0	0	0	0	0	0
	9 ₆₄	GRTFFFRRLDAPLDA	1	383	0	0	0	0	1	163	0	0	0
	9 ₁₅₂	KSLVRAFMWDGSGTV	0	0	0	0	0	0	0	0	0	0	0
	9 ₁₇₅	RVLSCDFKPTRPFRI	2	270	0	0	0	0	1	60	0	0	0
	9 ₂₆₀	HTGSIYAVSWSADSK	0	0	0	0	0	0	0	0	0	0	0
	9 ₃₄₉	AGHLKTVSSLTYFPQ	0	0	0	0	0	0	0	0	0	0	0
	9 ₃₅₅	VSSLTYFPQSNPRTM	0	0	1	23	0	0	0	0	0	0	0
	9 ₃₇₃	SYDGVIIRWIQGVGY	0	0	0	0	0	0	0	0	0	0	0
	9 ₃₉₇	TQIKCFVAAEEELIT	0	0	1	20	0	0	0	0	0	0	0
	9 ₄₄₁	NALNIAVQQPEFALI	0	0	1	60	0	0	1	20	0	0	0
	9 ₄₅₀	PEFALITTDSAIVLL	0	0	1	33	0	0	1	223	1	667	0
	9 ₄₅₇	TDSAIVLLHKSTVTS	0	0	0	0	0	0	1	47	0	0	0
	9 ₄₇₃	TKVSYTITSSAVSPD	0	0	0	0	0	0	0	0	0	0	0
	9 ₄₉₉	KLRIYSISGDTLTEE	1	53	0	0	0	0	0	0	0	0	0
9 ₅₂₆	IHYSPDVSMFASADA	1	77	2	47	0	0	1	50	1	23	0	
9 ₅₅₄	IKLKNMLFHTARINC	1	20	1	33	0	0	1	47	0	0	0	
10	10 ₁₀	GRYFSKDAVQIITKM	1	170	1	43	0	0	1	40	0	0	0
	10 ₁₆	DAVQIITKMAAANGV	1	83	1	160	0	0	0	0	0	0	0
	10 ₂₉	GVRRVWVGQDSLLST	2	60	0	0	0	0	1	237	0	0	0
	10 ₃₉	SLLSTPAVSAIRER	2	60	1	37	0	0	1	173	1	33	0

11	10 ₄₅	AVSAIRERIAADGS	1	47	1	60	0	0	1	27	0	0	0	0
	11 ₅₈	SVGFVETLENDLAQL	1	47	1	30	0	0	1	27	0	0	0	0
	11 ₁₁₁	LGEAPYKFKSALEAV	2	977	1	110	0	0	0	0	0	0	0	0
	11 ₁₁₇	KFKSALEAVKTLRAE	0	0	1	43	0	0	0	0	0	0	0	0
	11 ₁₃₇	QYLPAFVIVDESGKS	0	0	1	23	0	0	0	0	0	0	0	0
	11 ₁₆₁	VVTFNFRADRMVMLA	0	0	2	100	0	0	0	0	0	0	0	0
	11 ₁₆₈	ADRMVMLAKALEFAD	0	0	1	40	0	0	0	0	0	0	0	0
	11 ₁₈₃	FDKFDRVRVPKIKYA	0	0	0	0	0	0	0	0	0	0	0	0
	11 ₁₉₂	PKIKYAGMLQYDGEL	0	0	0	0	0	0	1	47	0	0	0	0
12	11 ₂₀₆	LKLPNKFLVSPPLIE	0	0	1	30	0	0	1	43	0	0	0	0
	12 ₅	YKLLCSSFPVITYHQ	0	0	2	120	0	0	1	203	1	37	0	0
	12 ₁₂	FPVITYHQGRNGNLS	0	0	1	103	0	0	0	0	0	0	0	0
13	12 ₂₁	RNGNLSALACPLNQK	0	0	1	20	0	0	1	20	0	0	0	0
	13 ₂₁	ECILSGLSVDGLKV	0	0	0	0	0	0	0	0	0	0	0	0
	13 ₂₇	LLSVDGLKVLHMDRN	0	0	0	0	0	0	0	0	0	0	0	0
	13 ₈₁	VPKFMMANGALVRVL	0	0	0	0	0	0	0	0	1	37	0	0
	13 ₉₂	VRVLIRTSVTKYLN	0	0	0	0	0	0	0	0	0	0	0	0
	13 ₁₀₁	TKYLNFKAVDGSFVY	0	0	0	0	0	0	0	0	1	50	0	0
	13 ₁₂₆	TDVEALKSNLMGLFE	0	0	0	0	0	0	0	0	0	0	0	0
	13 ₁₄₀	EKRRARKFFIYVQDY	0	0	0	0	0	0	0	0	0	0	0	0
	13 ₁₄₆	KFFIYVQDYEEEDPK	0	0	0	0	0	0	1	33	0	0	0	0
	13 ₁₈₅	TVDFIGHALALHRDD	0	0	0	0	0	0	0	0	0	0	0	0
	13 ₂₁₀	VKRMKLYAESLARFQ	0	0	0	0	0	0	1	57	0	0	0	0
	13 ₂₃₇	GELPQAFARLSAVYG	0	0	0	0	0	0	0	0	0	0	0	0
	13 ₂₄₃	FARLSAVYGGTYMLN	0	0	0	0	0	0	0	0	0	0	0	0
	13 ₃₅₂	KGKFIAFVSTEAETD	0	0	0	0	0	0	1	153	0	0	0	0

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21	20 ₅₅	RGYAAAAAPSPAVF	0	0	0	0	0	0	0	0	0	0	0
	20 ₁₁₄	LGLPVFNSVAEAKAE	0	0	0	0	0	0	0	0	0	0	0
	20 ₁₂₉	TKANASVIYVPPFA	0	0	0	0	0	0	0	0	0	0	0
	20 ₁₃₅	VIYVPPFAAAAIME	0	0	0	0	0	0	0	0	0	0	0
	20 ₁₄₁	PFAAAAIMEALEAEL	0	0	0	0	0	0	0	0	0	0	0
	20 ₁₆₇	QHDMVKVKAALNRQS	0	0	0	0	0	1	1003	0	0	0	0
	20 ₂₂₂	TLTYEAVFQTTAVGL	0	0	0	0	0	0	0	0	0	0	0
	20 ₂₉₄	DKPVVAFIAGLTAPP	0	0	1	23	0	0	0	0	0	0	0
	20 ₃₂₉	KIKALREAGVTVVES	0	0	1	23	0	0	0	0	0	0	0
	20 ₃₄₈	GSTMFEIFKQRMVE	0	0	0	0	0	0	0	0	0	0	0
	21 ₂	GSGDFKTIKEALAKV	0	0	0	0	0	0	0	0	0	0	0
	21 ₂₃	MYVMYIKEGTYKEYV	0	0	0	0	0	0	0	0	0	0	0
	21 ₃₃	YKEYVTVPRVTNLV	0	0	0	0	0	1	1020	0	0	0	0
	21 ₄₃	VTNLVMIGDGAAKTI	0	0	0	0	0	0	0	0	0	0	0
	21 ₆₃	NFKMNLTSMVAVSLV	0	0	0	0	0	0	0	0	0	0	0
	21 ₁₀₉	YQDTLYTHAQRQFFR	0	0	0	0	0	0	0	0	0	0	0
	21 ₁₂₉	GTIDFIGNSQVVIQ	0	0	0	0	0	0	0	0	0	0	0
	21 ₅₃	AKTIILKFLLPVMIV	0	0	0	0	0	0	0	0	0	0	0
22	22 ₁₅	NTRVLLLRRTSPFSA	0	0	1	63	0	0	0	0	0	0	0
	22 ₁₂₄	DGYIYHGQCAIIMFD	0	0	1	80	0	0	0	0	0	0	0
	22 ₁₃₁	QCAIIMFDVTSRLTY	0	0	1	27	0	0	0	0	0	0	0
	22 ₁₈₇	RKKNLQYYEISAKSN	0	0	0	0	0	0	0	0	0	0	0
	22 ₁₉₇	SAKSNYNFEKPFLYL	0	0	0	0	0	1	47	0	0	0	0
	22 ₂₀₆	KPFLYLARKLAGDAN	1	603	2	177	0	0	0	0	0	0	0
	22 ₂₁₉	ANIHFVEAVALKPPE	1	63	0	0	0	0	0	0	0	0	0
	22 ₂₄₅	EAELAAAAQPLPDD	0	0	1	20	0	0	1	57	0	0	0

23	23 ₁	RTSSWGSGLKIDR	0	0	2	67	0	0	0	0	0	0	0	0
	23 ₁₀	SLKIDRRELVTTIRY	0	0	0	0	0	0	0	0	0	0	0	0
24	24 ₂₁	RFLHAAVAMATKRSV	1	150	0	0	0	0	0	0	0	0	0	0
	24 ₄₄	KGKKVFLRADLNVPL	3	703	2	60	0	0	4	180	0	0	0	0
	24 ₆₈	TRIRASIPTIKFLE	1	140	0	0	0	0	1	210	0	0	0	0
	24 ₇₆	TIKFLLEKGAKVILA	0	0	2	93	0	0	1	83	1	33	0	0
	24 ₈₂	EKGAKVILASHLGRP	0	0	1	63	0	0	0	0	0	0	0	0
	24 ₁₀₉	VPRLSELLGVEVMA	2	237	2	140	0	0	3	333	0	0	0	0
	24 ₁₄₁	GGVLLLENVRFYKEE	1	33	2	97	0	0	2	87	0	0	0	0
	24 ₁₆₀	PEFAKKLASVADLYV	0	0	2	90	0	0	0	0	0	0	0	0
	24 ₁₉₃	KFLRPSVAGFLMQKE	1	177	3	113	0	0	1	37	0	0	0	0
	24 ₁₉₉	VAGFLMQKELDYLVG	0	0	1	90	0	0	0	0	0	0	0	0
	24 ₂₀₆	KELDYLVGAVANPKK	1	160	1	47	0	0	2	843	1	107	0	0
	24 ₂₃₄	KIGVIESLLAKVDIL	0	0	1	57	0	0	0	0	0	0	0	0
	24 ₂₅₃	GMIFTFYKAQKGAVG	2	793	2	277	0	0	6	1493	2	463	0	0
	24 ₂₇₂	EEDKLELATSLIETA	1	50	2	110	0	0	1	20	0	0	0	0
	24 ₂₉₀	GVSLLLPTDVVVADK	0	0	1	90	0	0	1	20	0	0	0	0
25	25 ₂	SAPALRILRSFPSHS	1	143	1	100	0	0	1	27	0	0	0	0
26	26 ₂	VELVAVNDPFITTDY	0	0	0	0	0	0	0	0	0	0	0	0
	26 ₁₅	DYMTYMFKYDTVHGQ	0	0	0	0	0	0	0	0	0	0	0	0
	26 ₉₀	GGAKKVIISAPSKDA	0	0	0	0	0	0	0	0	0	0	0	0
	26 ₁₁₆	YTSDITIVSNASCTT	0	0	0	0	0	0	0	0	0	0	0	0
	26 ₁₃₈	KVINDRFGIVEGLMT	1	37	0	0	0	0	1	87	0	0	0	0
	26 ₁₄₄	FGIVEGLMTTVHAMT	0	0	0	0	0	0	1	33	0	0	0	0
	26 ₁₇₄	GGRAASFNIIPSSTG	0	0	0	0	0	0	0	0	0	0	0	0
	26 ₂₂₁	LTVRLEKAATYEQIK	0	0	0	0	0	0	1	47	0	0	0	0

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31	30 ₅₂₇	IRKISANIAAKVAAK	0	0	0	0	0	0	1	37	0	0	0	0
	31 ₆	QIIRKGFYLTKNVEH	0	0	0	0	0	0	0	0	0	0	0	0
	31 ₁₂	FYLTKNVEHKGQVDL	0	0	0	0	0	0	0	0	0	0	0	0
	31 ₁₈	VEHKGQVDLVTETDK	0	0	0	0	0	0	0	0	0	0	0	0
	31 ₃₀	TDKACEDLIFNHLRK	0	0	0	0	0	0	0	0	0	0	0	0
32	31 ₃₆	DLIFNHLRKLYPDHK	0	0	0	0	0	0	1	20	0	0	0	0
	32 ₄₁	IEIDSLFEGIDFYST	1	27	0	0	0	0	0	0	0	0	0	0
	32 ₅₀	IDFYSTITRARFEEL	0	0	1	20	0	0	0	0	0	0	0	0
	32 ₁₀₂	IPKVQQLLQDFFNGK	0	0	0	0	0	0	0	0	0	0	0	0
	32 ₁₂₆	EAVAYGAAVQAAILS	1	30	0	0	0	0	0	0	0	0	0	0
33	32 ₁₄₇	VQDLLLDVTPSLG	1	47	0	0	0	0	0	0	0	0	0	0
	33 ₁	QEMAYWSLKAIEIG	0	0	0	0	0	0	0	0	0	0	0	0
	33 ₂₀	DAASSLYLFGENLPR	0	0	0	0	0	0	0	0	0	0	0	0
	33 ₆₀	GYNISLASMIPDYDT	0	0	0	0	0	0	0	0	0	0	0	0
	33 ₇₂	YDTVITNVRRSLAVA	0	0	0	0	0	0	0	0	0	0	0	0
34	33 ₁₁₆	LEKIVAILSAFVDAA	0	0	0	0	0	0	0	0	0	0	0	0
	33 ₇	NVRRSLAVAKKNHLA	0	0	0	0	0	0	0	0	0	0	0	0
	33 ₁₄	VAKKNHLAWNCERCR	0	0	0	0	0	0	0	0	0	0	0	0
	33 ₂₀	LAWNCERCRKGESKK	0	0	0	0	0	0	0	0	0	0	0	0
	33 ₃₃	KKTVDAILSAFVDAA	0	0	0	0	0	0	0	0	0	0	0	0
34	34 ₁	LMSFSWICACVRAAA	0	0	0	0	0	0	0	0	0	0	0	0
	34 ₇	ICACVRAAAVAWEAG	0	0	0	0	0	0	0	0	0	0	0	0
	34 ₃₉	VRVKILFTALCHTDV	0	0	0	0	0	0	2	303	1	90	0	0
	34 ₁₁₄	MCDLLRINTDRGVMI	0	0	0	0	0	0	1	37	1	77	0	0
	34 ₁₄₀	KPIHFVGTSTFSEY	0	0	1	40	0	0	0	0	0	0	0	0
	34 ₁₄₆	VGTSTFSEYTMHVG	0	0	0	0	0	0	2	57	0	0	0	0

35	34 ₂₀₀	VAIFGLGAVGLAAAE	0	0	0	0	0	0	2	297	0	0	0	0
	34 ₂₀₆	GAVGLAAEGARIAG	0	0	0	0	0	0	1	33	0	0	0	0
	34 ₂₇₅	GNINAMIQAFECVHD	0	0	0	0	0	0	1	40	0	0	0	0
	34 ₃₁₉	LKGTFFGNFKPRTDL	0	0	0	0	0	0	0	0	0	0	0	0
	34 ₃₄₉	KFITHSVTFSEINKA	1	110	1	87	0	0	0	0	0	0	0	0
	34 ₃₅₅	VTFSEINKAFDLMAK	1	103	0	0	0	0	0	0	0	0	0	0
	35 ₁	ALRWNLQMGHSLPK	0	0	1	47	0	0	0	0	0	0	0	0
	35 ₂₅	NLDVYDWSIPDDLLA	1	67	1	90	0	0	0	0	0	0	0	0
	35 ₃₅	DDLLAKFSEIKQTRL	0	0	1	30	0	0	0	0	0	0	0	0
	35 ₄₁	FSEIKQTRLIMGNFI	0	0	0	0	0	0	2	207	0	0	0	0
36	35 ₄₇	TRLLMGNFIVNKDSV	0	0	0	0	0	0	0	0	1	7	0	0
	36 ₁	QDFKKVNEIYAKYFP	0	0	0	0	0	0	0	0	1	107	0	0
	36 ₇	NEIYAKYFPPAPAR	0	0	0	0	0	0	0	0	0	0	0	0
	36 ₁₃	YFPSPAPARSTYQVA	0	0	0	0	0	0	0	0	0	0	0	0
	36 ₂₀	ARSTYQVAALPLDAR	0	0	0	0	0	0	0	0	0	0	0	0
37	36 ₂₉	LPLDARIEICIAAL	0	0	0	0	0	0	0	0	0	0	0	0
	37 ₅	EEAASTLPGLSSSTL	0	0	0	0	0	0	0	0	0	0	0	0
38	38 ₃	STKIFLESSTMESRA	0	0	0	0	0	0	1	160	0	0	0	0
	38 ₅₃	CAAVLAASAVVVLVV	0	0	0	0	0	0	1	47	0	0	0	0
	38 ₆₂	VVVLVVASGLAGSRV	0	0	0	0	0	0	0	0	0	0	0	0
	38 ₇₁	LAGSRVVRVAVDVAT	0	0	0	0	0	0	0	0	0	0	0	0
	38 ₁₅₉	GWYHLFYQYNPEGAV	0	0	0	0	0	0	0	0	0	0	0	0
	38 ₁₈₄	SRDLIHWRHLPLAMV	0	0	0	0	0	0	0	0	0	0	0	0
	38 ₂₂₁	LNMLYTGSTNASVQV	0	0	0	0	0	0	0	0	0	0	0	0
	38 ₃₀₂	IAMVYKTKDFVSYEL	0	0	0	0	0	0	1	143	0	0	0	0
	38 ₃₀₈	TKDFVSYELIPGLLH	0	0	0	0	0	0	2	630	1	63	0	0

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43	42 ₂₇	SSMVLIKMREIAEAF	0	0	0	0	0	0	1	73	1	47	0	0
	42 ₄₅	SIKNAVVTVPAYFND	0	0	0	0	0	0	0	0	0	0	0	0
	42 ₆₉	GVIAGLNVLRINEP	1	33	0	0	0	0	0	0	0	0	0	0
	42 ₇₆	VLRIINEPTAAAIAY	0	0	0	0	0	0	1	47	0	0	0	0
	43 ₁	GILLDFVWYEPLTYN	0	0	0	0	0	0	0	0	0	0	0	0
	43 ₄₄	ETMQRLVADRLPNFT	0	0	0	0	0	0	1	77	0	0	0	0
	43 ₁₁₄	GYSKWLYVVPWGFYK	0	0	0	0	0	0	0	0	0	0	0	0
	43 ₁₂₀	YVVPWGFYKAVMHVK	0	0	1	20	0	0	0	0	0	0	0	0
	43 ₁₆₄	KFRIDYFDQYLHELK	0	0	0	0	0	0	2	1223	1	80	0	0
44	43 ₁₈₅	ARVTGYFAWSLLDNF	0	0	0	0	0	0	0	0	0	0	0	0
	43 ₁₉₁	FAWSLLDNFEWRMGF	0	0	1	27	0	0	1	37	0	0	0	0
	44 ₇₁	FKDDPYIYAFDSLKY	0	0	0	0	0	0	0	0	0	0	0	0
	44 ₇₉	AFDSLKYIGIELWQV	0	0	0	0	0	0	0	0	0	0	0	0
	44 ₈₈	IELWQVKSGTLFDNI	0	0	0	0	0	0	0	0	0	0	0	0
	44 ₉₆	GTLFDNILITDDAAL	0	0	0	0	0	0	0	0	0	0	0	0
45	44 ₁₀₂	ILITDDAALAKTFAE	0	0	0	0	0	0	0	0	0	0	0	0
	45 ₅	KRPPRCCQDLVVLPL	0	0	0	0	0	0	0	0	0	0	0	0
46	46 ₃	RGLLRARGGPHHRR	0	0	1	40	0	0	1	27	0	0	0	0
	46 ₁₉	RGARRVPLRPLRHR	1	60	0	0	0	0	0	0	0	0	0	0
	46 ₄₀	EGRRAKLRSAGEVEI	0	0	1	177	0	0	0	0	0	0	0	0
	46 ₅₀ *	GEVEIQFRRVKCKYP*	0	0	4	240	0	0	1	53	0	0	0	0
47	46 ₆₇	TKVTFHVVGVPPLLH	1	167	1	77	0	0	1	20	0	0	0	0
	47 ₂₆	EDVAVSLAKYTAELS	0	0	0	0	0	0	0	0	0	0	0	0
	47 ₄₁	GKFAAERGAFVVLS	0	0	1	30	0	0	0	0	0	0	0	0
	47 ₄₉	AFTVVLSSGGTLIDTL	0	0	1	43	0	0	0	0	0	0	0	0
	47 ₉₆	DSNYKLAVDGLLSKV	0	0	1	53	0	0	0	0	0	0	0	0

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77	76 ₃₃	KDKLVVSTSCSLMHT	0	0	0	0	0	0	0	0	0	0	0
	76 ₄₀	TSCSLMHTAVDLVNE	0	0	1	160	0	0	0	0	0	0	0
	76 ₅₅	TKLDSEIKSWLAFAA	1	323	1	200	0	0	1	43	0	0	0
	76 ₆₁	IKSWLAFAAQKVVEV	0	0	0	0	0	0	0	0	1	50	0
	76 ₇₁	KVVEVNALGKALVGL	0	0	0	0	0	0	0	0	0	0	0
	76 ₈₅	LKDEAYFAANAAAQA	1	153	1	203	0	0	0	0	0	0	0
	76 ₁₇₅	EAYVSAIKEEISKVV	0	0	0	0	0	1	207	1	197	0	0
	76 ₁₈₅	ISKVVKIQEELDIDV	0	0	0	0	0	0	0	0	0	0	0
	76 ₂₁₀	MVEYFGEQLSGFAFT	0	0	0	0	0	0	0	0	0	0	0
	76 ₂₁₈	LSGFAFTANGWVQSY	0	0	1	63	0	0	1	20	0	0	0
	76 ₂₅₀	NPMTVFWSKMAQSMT	0	0	2	250	0	0	1	37	0	0	0
	77 ₃	EGPLMLYVSKMIPAS	0	0	0	0	0	0	0	0	1	23	0
	77 ₁₉	KGRFFAFGRVFAGRV	0	0	0	0	0	0	1	237	1	77	0
	77 ₇₉	GNTVALVGLDQFITK	0	0	0	0	0	0	0	0	1	97	0
	77 ₈₅	VGLDQFITKNATLTG	0	0	0	0	0	0	0	0	0	0	0
	77 ₁₀₇	PIRAMKFSPVVRV	0	0	0	0	0	0	0	0	0	0	0
	77 ₁₇₉	FMGGAEIIVSPPVVS	0	0	0	0	0	0	0	0	0	0	0
	77 ₁₈₈	SPPVVSFRETVLDKS	0	0	1	107	0	0	0	0	0	0	0
	77 ₂₁₂	NKHNRLYMEARPLEE	0	0	1	107	0	0	0	0	0	0	0
	77 ₃₃₈	PTARRVIFASQLTAK	0	0	0	0	0	0	1	117	1	37	0
	77 ₃₅₁	AKPRLLEPVYLVEIQ	0	0	0	0	0	0	0	0	0	0	0
	77 ₃₅₇	EPVYLVEIQAPEGAL	0	0	0	0	0	0	0	0	0	0	0
	77 ₃₉₅	PLYNIKAYLPVIESF	0	0	0	0	0	0	0	0	0	0	0
78	77 ₄₀₃	LPVIESFGFSATLRA	1	333	0	0	0	0	0	0	0	0	0
	77 ₄₀₉	FGFSATLRAATSGQA	1	30	0	0	0	0	0	0	0	0	0
	78 ₅	SLKLHKACEAFNPYD	0	0	0	0	0	0	1	87	0	0	0

79	78 ₁₃	EAFDPYYGKISLSKV	0	0	0	0	0	0	3	863	0	0	1	23
	78 ₂₅	SKVRSFLTEAKAKHI	0	0	0	0	0	0	2	87	0	0	0	0
	78 ₃₁	LTEAKAKHIEWNCDV	0	0	0	0	0	0	2	187	0	0	0	0
	78 ₁₁₆	KEKRWNAALTSISAS	0	0	0	0	0	0	0	0	0	0	1	27
	78 ₁₃₃	GSAYVDLGSLLAERT	0	0	0	0	0	0	2	80	0	0	0	0
	78 ₁	RHLARQFIPHLHQRF	0	0	0	0	0	0	2	93	0	0	0	0
	78 ₇	FIPHLHQRFIHPPIH	0	0	0	0	0	0	1	33	0	0	0	0
	78 ₂₄	NTMENLSSTIFSFI	0	0	0	0	0	0	2	60	0	0	0	0
	78 ₃₂	TIFSFIILLSASASL	0	0	0	0	0	0	2	70	0	0	1	23
	78 ₃₈	ILLSASASLVVAGDP	0	0	0	0	0	0	1	20	0	0	0	0
	78 ₈₅	ELAEMEVSAAFHLFS	2	433	0	0	0	0	1	183	0	0	1	27
	78 ₉₂	SAAFHLFSMAVTAAR	0	0	0	0	0	0	0	0	0	0	0	0
	78 ₉₈	FSMAVTAARSQQWND	0	0	0	0	0	0	0	0	0	0	0	0
	78 ₁₄₃	KISLSKVRSFLTEAK	1	783	0	0	0	0	2	1143	1	1677	0	0
	79 ₁₃₂	QQYTAALSPILFECL	0	0	1	183	0	0	1	160	0	0	0	0
	79 ₁₃₈	LSPILFECLIHPMLG	0	0	1	83	0	0	0	0	0	0	0	0
	79 ₁₆₀	VEDNLVKLKNVLNVY	0	0	1	100	0	0	0	0	0	0	0	0
	79 ₁₆₆	KLKNVLNVYEARLTK	0	0	0	0	0	0	0	0	0	0	0	0
	79 ₁₁	EVYEARLTKFKYLAG	1	47	1	143	0	0	0	0	0	0	0	0
	79 ₁₈	TKFKYLAGDYLSLAD	0	0	1	37	0	0	1	170	0	0	0	0
	79 ₂₄	AGDYLSLADLNHVST	0	0	0	0	0	0	0	0	0	0	0	0
80	79 ₅₇	VKAWWTDLLAKPSVQ	1	33	1	100	0	0	0	0	0	0	0	0
	80 ₁	KLRFTCLSSTGSSCL	0	0	1	133	0	0	0	0	0	0	0	0
	80 ₇	LSSTGSSCLFVLILF	1	63	1	147	0	0	0	0	0	0	0	0
81	81 ₁	EKLKKVLEVYEARLS	0	0	2	200	0	0	2	50	0	0	0	0
	81 ₁₈	SYLAGDFVSFADLNH	0	0	1	40	0	0	0	0	0	0	0	0

82	81 ₂₄	FVSFADLNHFPKTFY	0	0	0	0	0	0	0	0	0	0	0	
	81 ₃₃	FPKTFYFMATPHASL	0	0	0	0	0	0	1	63	0	0	0	
	81 ₅₃	HVKAWWERIMARPAV	0	0	0	0	0	0	1	53	0	0	0	
	81 ₆₁	IMARPAVKKIAAMV	0	0	0	0	0	0	0	0	0	0	0	
	82 ₃₃	KRKVRGFWRVHQISA	0	0	0	0	0	0	1	23	0	0	0	
	82 ₃₉	FWRVHQISARMAPVK	0	0	0	0	0	0	5	187	0	0	0	
	82 ₄₉	MAPVKLYGATLSWNV	0	0	0	0	0	0	1	130	1	33	0	
83	82 ₁₀₉	GDLYIFESRAICKYA	0	0	1	290	0	0	5	593	3	300	1	23
	82 ₁₅₀	EANQYTAALGPILFE	0	0	0	0	0	0	2	523	0	0	0	0
	83 ₅	ACSLFLNYAVSFNYF	0	0	1	57	0	0	0	0	0	0	0	0
	83 ₁₂	YAVSFNYFVCNLLQE	1	37	0	0	0	0	0	0	1	23	0	0
	83 ₂₂	NLLQERLKKLKSEHG	1	47	1	83	0	0	0	0	0	0	0	0
	83 ₅₄	GMTGMLWETSLDPE	0	0	1	107	0	0	0	0	0	0	0	0
	83 ₉₆	PEGLLWLLTGKVPT	1	33	1	93	0	0	0	0	0	0	0	0
	83 ₁₃₀	YVYKAIDALPVT AHP	0	0	0	0	0	0	0	0	0	0	0	0
	83 ₁₄₇	QFTTGVMALQVESEF	0	0	0	0	0	0	0	0	1	67	0	0
	83 ₁₈₀	EDCLNLIARLPQVAS	0	0	1	137	0	0	1	540	1	117	0	0
	83 ₁₈₆	IARLPQVASYVYRRI	1	33	1	187	0	0	0	0	0	0	0	0
	83 ₂₀₉	ADNSLDYAANFSHML	1	53	1	130	0	0	0	0	0	0	0	0
	83 ₂₂₇	DPKMLELMRLYITI H	1	40	0	0	0	0	0	0	0	0	0	0
	83 ₂₆₀	ALSDPYLSFAAALNG	1	70	1	130	0	0	0	0	0	0	0	0
	83 ₂₆₆	LSFAAALNGLAGPLH	0	0	1	103	0	0	0	0	0	0	0	0
	83 ₂₇₈	PLHGLANQEVLLWIK	0	0	0	0	0	0	0	0	0	0	0	0
	83 ₂₈₅	QEVLLWIKSVMEETG	0	0	0	0	0	0	0	0	0	0	0	0
	83 ₃₀₆	QLKEYVWKT LKSGKV	1	40	1	90	0	0	0	0	0	0	0	0
	83 ₃₄₉	EDPLFQLVSKLYEVV	0	0	1	160	0	0	0	0	0	0	0	0

[illegible]

[illegible]

89	261	EGKLLRLKQQFFLCS	0	0	0	0	0	0	2	140	0	0	0	0
	267	LKQQFFLCSASLQDI	0	0	0	0	0	0	1	40	0	0	0	0
	313	PTLAIPELMRLLMDE	0	0	0	0	0	0	1	110	0	0	0	0
	360	QSVMRKLLPRQMEII	0	0	0	0	0	0	2	170	0	0	0	0
	375	EEIDKRFRMVISTR	0	0	0	0	0	0	1	90	1	27	0	0
	406	PQKPVVRMANLCVVS	0	0	0	0	0	0	3	270	0	0	0	0
	434	ILKEELFADYVSIWP	0	0	0	0	0	0	1	40	1	33	0	0
	460	PRRWLRFCNPELSEI	1	153	1	240	0	0	1	137	1	23	0	0
	501	EKLHAEWAAAKLASK	0	0	0	0	0	0	0	0	0	0	0	0
	540	IKRIHEYKRQLMNIL	2	90	0	0	0	0	1	110	0	0	0	0
	546	YKRQLMNILGAVYRY	1	77	2	187	0	0	2	137	0	0	0	0
	554	LGAVYRYKKLEMSA	1	63	3	163	0	0	0	0	0	0	0	0
	583	GKAFATYTNKRIVK	0	0	2	137	0	0	0	0	0	0	0	0
	593	KRIVKLVNDVGAVVN	2	413	1	107	0	0	2	357	1	47	0	0
	612	VNKYLKVVFI PNYNV	1	220	1	120	0	0	3	290	1	67	0	0
	619	VFI PNYNVSVAEVL I	5	1413	2	110	0	0	4	537	2	167	0	0
	681	EDNFFLFGAKADQVA	1	503	2	97	0	0	1	107	0	0	0	0
	723	TFGTDYDTPLLDSLE	0	0	0	0	0	0	1	150	0	0	0	0
	748	FLVG YDFPSYIDAQA	0	0	0	0	0	0	1	123	0	0	0	0
	772	KRWIKMSILNTAGSG	3	407	1	120	0	0	2	537	1	97	0	0
	796	QYAKEIWGITANPVP	3	303	2	253	0	0	0	0	0	0	0	0
90	90 ₃₃	KT LAVALGGARPLAT	1	30	0	0	0	0	0	0	0	0	0	0
	90 ₄₅	LATRGVATFTLPDLP	2	60	0	0	0	0	0	0	0	0	0	0
	90 ₅₆	PDLPYDYGALEPAIS	1	73	2	73	0	0	0	0	0	0	0	0
	90 ₈₂	HATYVANYNKALEQL	1	57	0	0	0	0	1	63	0	0	0	0
	90 ₁₀₃	GDASAVVQLQGAIKF	0	0	0	0	0	0	0	0	1	43	0	0

91	90 ₁₉₈	DPLVTKGANLIPLL	1	87	0	0	0	0	1	53	0	0	0	0
	90 ₂₀₅	ANLIPLLIDVWEHA	1	113	0	0	0	0	1	20	0	0	0	0
	90 ₂₁₈	HAYYLQYKNVRPDYL	2	110	1	83	0	0	0	0	0	0	0	0
	90 ₂₂₉	PDYLTNIWKVVNWKY	1	70	2	110	0	0	0	0	0	0	0	0
	91 ₃₅	APSGRIVMELYADV	2	247	3	737	0	0	0	0	0	0	0	0
	91 ₄₁	VMELYADVVPKTAEN	2	140	0	0	0	0	0	0	0	0	0	0
	91 ₇₄	HYKGSSFHVRIPGFM	1	537	3	623	0	0	0	0	0	0	0	0
	91 ₁₀₄	SIYGAKFADENFIKK	1	60	0	0	0	0	0	0	1	23	0	0
	91 ₁₃₅	NGSQFFLCTAKTAWL	2	447	1	543	0	0	1	270	0	0	0	0
	92	92 ₁	SQVHIRRPGGAGR	1	113	0	0	0	0	0	0	0	0	0
92	92 ₇	RPGGAGR	1	130	0	0	0	0	0	0	0	0	0	0
	92 ₁₃	RDGGQLRIP	1	97	0	0	0	0	0	0	0	0	0	0
	92 ₂₇	GHGCAQPAMERRKHI	2	590	0	0	0	0	0	0	0	0	0	0
	92 ₃₈	RKHIEWNCDCR	1	83	0	0	0	0	0	0	0	0	0	0
	93	93 ₁	WTTVMRASC	1	87	0	0	0	0	0	1	43	0	0
93	93 ₁₃	RFRDCVISSL	2	93	0	0	0	0	0	0	0	0	0	0
	93 ₁₉	ISSLADFKL	1	67	0	0	0	0	0	0	0	0	0	0
	93 ₂₉	PVLQHIISIAV	1	140	0	0	0	0	0	0	1	47	0	0
	93 ₃₅	ISIAVLAIF	2	247	0	0	0	0	0	0	1	37	0	0

*peptide is 100% identical to a peptide sequence in Phl p 1 and was therefore not included in any pools of interest for subsequent screens, namely the MAA pool and P19.

Control patients							SIT patients					
Antigen	IL5		IFN γ		Ab reactivity		IL5		IFN γ		Ab reactivity	
	Patients	Sum SFC	Patients	Sum SFC	IgE	IgG	Patients	Sum SFC	Patients	Sum SFC	IgE	IgG
1	1	20	1	707	+	+	0	0	3	1493	+	+
2	7	3447	10	8200	+	+	3	130	4	2790	+	+
3	1	20	0	0	+	+	0	0	0	0	-	-
4	3	597	4	923	-	-	1	93	2	537	+	+
5	0	0	1	73	-	+	0	0	0	0	+	+
6	11	7003	11	7490	+	+	5	1087	10	6163	+	+
7	5	1657	5	5603	+	+	1	567	3	1270	+	+
8	0	0	0	293	+	-	0	0	0	0	+	-
9	3	217	2	983	-	-	2	690	4	610	+	+
10	1	300	2	420	+	+	1	33	3	477	+	+
11	3	377	2	1023	+	+	0	0	1	117	+	+
12	2	243	0	0	-	+	1	37	2	223	+	+
13	0	0	0	0	+	+	2	87	3	373	+	+
14	1	110	0	0	+	-	0	0	0	0	+	-
15	0	0	0	0	+	-	0	0	0	0	+	+
16	0	0	2	823	-	-	0	0	0	0	-	-
17	3	167	0	0	+	-	1	20	0	0	+	+
18	0	0	0	0	-	-	0	0	1	353	+	-
19	0	0	0	0	-	+	0	0	0	0	+	+
20	1	47	0	0	+	+	0	0	1	1003	+	-
21	0	0	0	0	+	+	0	0	1	1020	-	+
22	4	367	1	667	-	-	0	0	1	103	-	-
23	2	67	0	0	-	-	0	0	0	0	+	+
24	6	1327	5	2443	+	-	2	603	3	3307	+	+
25	1	100	1	143	+	-	0	0	2	27	+	-

26	0	0	1	37	-	+	0	0	2	167	+	+
27	2	230	2	267	-	-	0	0	0	0	+	-
28	1	540	2	953	-	-	1	143	1	453	+	+
29	2	380	1	247	+	-	1	20	1	260	+	+
30	1	67	0	0	+	+	0	0	1	37	+	+
31	0	0	0	0	+	+	0	0	1	20	+	+
32	1	20	1	103	+	+	0	0	0	0	+	+
33	0	0	0	0	-	+	0	0	0	0	-	+
34	1	127	1	213	-	-	2	167	3	767	+	+
35	1	167	1	67	-	-	0	0	3	210	+	-
36	0	0	0	0	-	-	1	107	0	0	-	+
37	0	0	0	0	-	+	0	0	0	0	-	+
38	0	0	0	0	-	+	1	63	2	1430	-	+
39	1	67	2	103	-	+	0	0	2	530	-	+
40	1	67	0	0	-	+	0	0	0	0	-	+
41	0	0	0	0	-	+	0	0	0	0	-	+
42	0	0	1	33	+	+	1	47	2	120	+	+
43	1	47	0	0	-	+	1	80	3	1337	-	+
44	0	0	0	0	-	+	0	0	0	0	-	+
45	0	0	0	0	-	+	0	0	0	0	-	+
46	5	533	2	227	+	+	0	0	3	100	+	+
47	2	210	0	0	+	+	0	0	1	57	+	+
48	0	0	1	297	-	+	0	0	1	400	-	+
49	5	7417	1	990	-	-	0	0	0	0	-	+
50	1	120	3	957	-	+	0	0	1	57	-	+
51	1	27	1	90	+	+	0	0	0	0	+	+
52	6	930	5	1293	-	+	0	0	1	27	-	+
53	6	1750	6	3693	-	+	1	30	3	903	-	+
54	4	2647	7	1133	-	-	2	387	3	1510	-	+
55	0	0	2	1070	-	+	0	0	0	0	-	+

56	0	0	1	343	-	-	0	0	0	0	-	+
57	0	0	0	0	+	-	0	0	1	480	+	-
58	0	0	0	0	-	+	0	0	0	0	-	+
59	2	67	3	620	+	-	0	0	0	0	-	+
60	0	0	0	0	-	-	0	0	0	0	-	+
61	0	0	0	0	-	+	1	137	1	27	-	+
62	5	1927	6	2827	+	+	2	80	3	1417	+	+
63	0	0	1	70	-	+	0	0	1	190	-	+
64	2	283	1	47	+	-	0	0	0	0	+	-
65	1	240	1	527	+	+	0	0	1	267	-	+
66	0	0	0	0	n.d.	n.d.	0	0	0	0	n.d.	n.d.
67	0	0	0	0	n.d.	n.d.	0	0	0	0	n.d.	n.d.
68	0	0	0	0	n.d.	n.d.	0	0	0	0	n.d.	n.d.
69	0	0	0	0	n.d.	n.d.	0	0	0	0	n.d.	n.d.
70	0	0	0	0	n.d.	n.d.	0	0	0	0	n.d.	n.d.
71	0	0	0	0	n.d.	n.d.	0	0	0	0	n.d.	n.d.
72	2	230	2	110	n.d.	n.d.	1	313	1	780	n.d.	n.d.
73	1	967	0	0	n.d.	n.d.	0	0	0	0	n.d.	n.d.
74	0	0	0	0	n.d.	n.d.	0	0	0	0	n.d.	n.d.
75	0	0	0	0	n.d.	n.d.	0	0	0	0	n.d.	n.d.
76	3	923	3	867	-	-	2	330	3	357	-	-
77	1	213	1	363	-	-	1	233	1	353	-	-
78	0	0	3	1217	-	-	1	1677	4	2907	-	-
79	1	647	2	80	-	-	0	0	1	330	-	-
80	1	280	1	63	-	-	0	0	0	0	-	-
81	2	240	0	0	-	-	0	0	2	167	-	-
82	1	290	0	0	-	-	2	333	3	1457	-	-
83	1	1747	1	410	-	-	1	207	1	540	-	-
84	1	220	1	310	-	-	0	0	1	473	-	-
85	0	0	0	0	-	-	0	0	1	20	-	-

86	0	0	1	73	-	-	0	0	1	193	-	-
87	0	0	0	0	-	-	0	0	1	100	-	-
88	0	0	0	0	-	-	0	0	0	0	-	-
89	9	2360	11	5560	-	-	6	883	6	5470	-	-
90	3	267	4	600	-	-	1	43	2	137	-	-
91	4	1904	2	1430	-	-	1	23	1	270	-	-
92	0	0	2	1013	-	-	0	0	0	0	-	-
93	0	0	2	633	-	-	2	127	0	0	-	-

Allele	Alpha chain	Percent of haplotypes	Phenotype frequency
DPB1*0101	DPA1*0201	8.4	16.0
DPB1*0201	DPA1*0103	9.2	17.5
DPB1*0401	DPA1*0103	20.1	36.2
DPB1*0402	DPA1*0103	23.6	41.6
DPB1*0501	DPA1*0202	11.5	21.7
DQB1*0201	DQA1*0501	5.8	11.3
DQB1*0301	DQA1*0501	19.5	35.1
DQB1*0302	DQA1*0301	10.0	19.0
DQB1*0402	DQA1*0401	6.6	12.8
DQB1*0501	DQA1*0101	7.6	14.6
DQB1*0602	DQA1*0102	7.6	14.6
DRB1*0101	DRA1*0101	2.8	5.4
DRB1*0102	DRA1*0101	1.7	3.3
DRB1*0301	DRA1*0101	7.1	13.7
DRB1*0302	DRA1*0101	1.1	2.12
DRB1*0401	DRA1*0101	2.3	4.6
DRB1*0402	DRA1*0101	1.1	2.18
DRB1*0403	DRA1*0101	2.3	4.5
DRB1*0404	DRA1*0101	1.9	3.8
DRB1*0405	DRA1*0101	3.1	6.2
DRB1*0407	DRA1*0101	2.4	4.8
DRB1*0411	DRA1*0101	1.6	3.3
DRB1*0701	DRA1*0101	7.0	13.5
DRB1*0802	DRA1*0101	2.5	4.9
DRB1*0803	DRA1*0101	3.8	7.4
DRB1*0901	DRA1*0101	3.1	6.2
DRB1*1001	DRA1*0101	1.9	3.8
DRB1*1101	DRA1*0101	6.1	11.8
DRB1*1102	DRA1*0101	1.1	2.21
DRB1*1103	DRA1*0101	0.2	0.50
DRB1*1104	DRA1*0101	1.4	2.77
DRB1*1201	DRA1*0101	2.0	3.9
DRB1*1301	DRA1*0101	3.2	6.3
DRB1*1302	DRA1*0101	3.9	7.7
DRB1*1303	DRA1*0101	1.2	2.40
DRB1*1304	DRA1*0101	0.1	0.17
DRB1*1401	DRA1*0101	3.4	6.7
DRB1*1402	DRA1*0101	2.8	5.6
DRB1*1501	DRA1*0101	6.3	12.2
DRB1*1601	DRA1*0101	1.0	1.9
DRB1*1602	DRA1*0101	3.9	7.7

DRB3*0101	DRA1*0101	14.0	26.1
DRB3*0202	DRA1*0101	18.9	34.3
DRB3*0301	DRA1*0101	7.6	14.5
DRB4*0101	DRA1*0101	23.7	41.8
DRB5*0101	DRA1*0101	8.3	16.0
DRB5*0102	DRA1*0101	5.1	9.8
