

Supplementary data for the article:

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1 **Supporting information**

2 **The cat lipocalin Fel d 7 and its cross-reactivity with the dog lipocalin Can f 1**

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## 33 **Methods**

### 34 **Allergen preparations**

35 BL21 Star (DE3) *Escherichia coli* (Invitrogen, Carlsbad, CA) were transformed with the  
36 p80QE plasmid containing the gene for Fel d 7 (1). Cells were grown for four hours at 37°C  
37 and protein expression was induced by addition of isopropyl-b-thiogalactopyranoside (IPTG)  
38 to a final concentration of 0.5 M for three hours and the cells were subsequently pelleted  
39 (16 800 g, 10min). After sonication (Soniprep 150 ultrasonic disintegrator, Sanyo  
40 Gallenkamp, Uxbridge, UK) by 10 sec (10ma) bursts and centrifugation (16 800 g, 10 min),  
41 the soluble supernatant fraction was sterile filtered and purified twice on 6-His-tag affinity  
42 IMAC Ni<sup>2+</sup> column (GE healthcare, Uppsala, Sweden) using an ÄKTA purifier (GE  
43 Healthcare) followed by Amicon Ultra 15 (Merck Millipore, Darmstadt, Germany) filtration  
44 in the range from 3 to 30 kDa range.

45 Recombinant (r) Can f 1 protein was prepared as previously described (2). Briefly, 6-His-  
46 tagged Can f 1 was produced by BL21 (DE3) pLysS (Novagen, EMD Chemicals, Darmstadt,  
47 Germany) *E.coli* transformed with pET20b (Novagen) containing the gene for Can f 1.  
48 Protein concentrations were determined by BCA™ protein assay (Pierce, Rockford, IL).

### 49 **Circular dichroism spectroscopy**

50 Circular dichroism (CD)-spectra were recorded on a JASCO J-815 spectropolarimeter  
51 (JASCO, Tokyo, Japan). Samples (0.5 mg/ml of rFel d 7 and rCan f 1 in PBS, pH 7.4) were  
52 analyzed at 25°C in a 0.1 mm path length quartz cell for far-UV and a 10 mm path length  
53 quartz cell for near-UV spectra. The spectra were collected in 0.1 nm steps at a rate of 50  
54 nm/min over the wavelength range 195-260 nm for far-UV and 260–320 nm for near-UV.  
55 Each spectrum was acquired five times and the results were averaged. Results were recorded

56 in mdeg and converted to molar  $\Delta\epsilon$  in  $M^{-1} \text{ cm}^{-1}$  and mean residue  $\Delta\epsilon_{MRV}$  for near UV and  
57 far UV, respectively. The percentage of secondary structure motifs were determined in the  
58 CONTIN software with the SP37 protein set in CDPro.

### 59 **IgE ELISA for Fel d 7 and Can f 1**

60 IgE levels to rFel d 7 and rCan f 1 were determined by enzyme-linked immunosorbent assay  
61 (ELISA) (2, 3). Half-area microtiter plates (96 wells, Greiner bio-one, Frickenhausen,  
62 Germany) were coated overnight at 4°C with 0.5  $\mu\text{g}$  of rFel d 7 or rCan f 1, followed by  
63 blocking (PBS containing 1% BSA and 0.5% Tween 20, pH 7.4) for 2 h at room temperature.  
64 Standard curves created with active human IgE (Abcam, Cambridge, UK) and undiluted  
65 serum samples were incubated for 2 h. Detection was performed with rabbit anti-human IgE  
66 antibody (1h, 1:2000; MIAB, Uppsala, Sweden) followed by alkaline phosphatase (AP)  
67 conjugated goat anti-rabbit antibody (1h, 1:1000; Jackson ImmunoResearch Laboratories,  
68 West Grove, PA). Finally, p-nitrophenyl phosphate substrate (Sigma, St. Louis, MO) was  
69 added and incubated for 15 min. The absorbance was measured at 405 nm. Sera with an IgE  
70 antibody level  $>100 \text{ kU}_A/\text{l}$  were re-run at 1:10 dilution. The IgE ELISAs were repeated with  
71 an inter-assay variation of 12%. IgE values to rFel d 7 were considered positive when the IgE  
72 level exceeded the mean of the 45 negative controls + 3 SD ( $\text{kU}_A/\text{l} \geq 0.12$  to Fel d 7). IgE  
73 values to rCan f 1 were regarded as positive when the IgE level exceeded the previously  
74 established cut-off for rCan f 1 ( $\geq 0.1 \text{ kU}_A/\text{l}$ ) (3). Spearman's correlation test was used for  
75 comparing rFel d 7- and rCan f 1-specific IgE levels, where  $p < 0.05$  was considered  
76 significant. Analyses were performed using Graphpad Prism 5 software (Graphpad Software  
77 Inc., San Diego, CA).

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## 80 **Basophil activation test**

81 Allergen-specific basophil degranulation was analyzed by monitoring the basophil activation  
82 markers CD203c and CD63, as previously described (4). Briefly, 10-fold serial dilutions of  
83 rFel d 7, rCan f 1 (10 µg/ml to 10<sup>-7</sup> µg/ml) or two irrelevant control allergens (BSA from New  
84 England BioLabs, MA and rLep d 2.01, in house production), medium (negative control) and  
85 1 µg/ml rabbit anti-human IgE (Phadia AB, Uppsala, Sweden) were added to heparinized  
86 venous blood samples from four patients with doctor's diagnosed allergy to cat and IgE  
87 positive to Fel d 7, whereof two were also co-sensitized to Can f 1. Serum from a non-atopic  
88 subject IgE negative to rFel d 7 (and Can f 1) was included as control. The samples were  
89 further incubated with FITC conjugated anti-CD63 and PE conjugated anti-CD203c  
90 monoclonal antibodies (clones CLBGran/12 and 97A6, respectively, Immunotech, Marseille,  
91 France) and analyzed by flow cytometry using a BD FACSCanto II (BD Biosciences, San  
92 Jose, CA). Data were analyzed using FlowJo (Treestar, Ashland, OR). Basophils were  
93 identified by gating for CD203c positive cells and the magnitude of allergen-activation was  
94 calculated and expressed as the percentage of CD63 positive cells among the gated basophils.

## 95 **Measurement of IgE cross-reactivity between Fel d 7 and Can f 1**

96 The potential cross-reactivity between IgE to Fel d 7 and Can f 1 was investigated by  
97 inhibition ELISA. The sera were diluted to 1 kU<sub>A</sub>/l and incubated at 1:1 v/v with 10-fold  
98 dilutions (range 10<sup>1</sup>–10<sup>-7</sup> µg/ml) of rFel d 7, rCan f 1 or PBS for 2 h at room temperature (5).  
99 Inhibition of IgE binding was analyzed by ELISA and calculated as  $[(OD_{no\ inhibitor} -$   
100  $OD_{inhibitor})/OD_{no\ inhibitor}] \times 100$ . Additionally, inhibition ELISA was performed using sera from  
101 two patients with IgE reactivity to rCan f 1 but not to rFel d 7.

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## 104 **Synthesis and characterization of Can f 1 derived peptides and immunization of rabbits**

105 Six overlapping peptides spanning the Can f 1 sequence with a length between 30 and 36  
106 amino acids were designed based on the prediction of surface exposure of amino acids as  
107 determined by the ProtScale bioinformatics tool from the ExPASy server (6) and were  
108 synthesized using an Applied Biosystems peptide synthesizer Model 433A (Foster City, CA).  
109 The peptides contained cysteins for coupling to keyhole limpet hemocyanin (KLH) either at N  
110 termini (Peptide 3, Peptide 4, Peptide 5 and Peptide 6) or at C termini (Peptide 1 and Peptide  
111 2) (Table S1). One Peptide, P4, contains a highly hydrophobic region of Can f 1 and was  
112 not used in further studies due to non-solubility in water or biological buffers. All the other  
113 peptides were purified by preparative HPLC (Dionex, Thermofischer Scientific, Waltham,  
114 MA) and their identities were confirmed by mass spectrometry (Bruker, Bremen, Germany).  
115 Can f 1 peptides were coupled to KLH (Pierce, ThermoFisher Scientific, Waltham, MA) and  
116 purified using a conjugation kit according to manufacturer`s instructions. The concentration  
117 of KLH-conjugated Can f 1 peptides was measured using the Micro BCA Assay Kit (Pierce,  
118 Rockford, IL).

119 Peptide-specific IgG antibodies were obtained by immunizing rabbits three times (first  
120 booster injection after 4 weeks and a second booster injection after 7 weeks) with each of the  
121 KLH-conjugated peptides (200 µg/injection) and, for control purposes, with recombinant Can  
122 f 1 (200 µg/injection) using once Freund`s complete and twice Freund`s incomplete adjuvant  
123 (Charles River, Chatillon sur Chalaronne, France). The “Directive 2010/63/EU of the  
124 European parliament and of the council (22 September 2010) on the protection of animals  
125 used for scientific purposes” were followed for the care and use of the animals. Five rabbit  
126 anti-Can f 1 peptide sera (diluted from 1:2000 to 1:50000) were used to evaluate cross-  
127 reactive binding sites between Can f 1 and Fel d 7. IgG binding was analyzed by ELISA using  
128 rFel d 7, rCan f 1 and rFel d 1 coated plates incubated with rabbit anti-Can f 1 peptide

129 antisera. Detection was performed with alkaline phosphatase conjugated goat-anti-rabbit IgG  
130 antibodies (1:1000, Jackson ImmunoResearch Laboratories, West Grove, PA). Detection was  
131 carried on like in IgE ELISA.

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154 **Table S1.** Characteristic of synthetic Can f 1-derived peptides.

No.	Position (AA)*	Sequence**	# AA	Molecular mass (Da)	pI
Peptide 1	1-35	CQDTPALG <b><u>DTVA</u></b> <b><u>VSGKWYLKAM</u></b> TADQEVPE <b><u>KPDSV</u></b>	36	3879.37	4.53
Peptide 2	31-60	<b><u>CKPDSVTPMILKAQKGGNLEAKITMLTNGQ</u></b>	30	3187.78	9.11
Peptide 3	56-85	<b><u>TNGQCQNITVVLHKTSEPGKYTAYEGQRVVC</u></b>	31	3424.85	7.74
Peptide 4	78-107	CAY <b><u>EGQRVVFIQPSVPRDHYILYCEGELHGR</u></b>	31	3636.12	6.03
Peptide 5	101-132	<b><u>CEGELHGRQIRMAKLLGRDPEQSQEALDFWF</u></b>	33	3919.36	4.59
Peptide 6	127-156	<b><u>EDFWEFSRAKGLNQEILELAQSETCSPGGQC</u></b>	31	3473.79	4.14

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156 \*, Position of amino acid without signal peptide;

157 \*\*, Bold and underlined sequences represent identical portions with Fel d 7;

158 C, Addition of cysteine.

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161 **Table S2.** Serological characteristics of the 65 rFel d 7-positive patients.

Patient ID	Cat (kU <sub>A</sub> /l)*	Dog (kU <sub>A</sub> /l)*	rFel d 7 (kU <sub>A</sub> /l)**	rCan f 1 (kU <sub>A</sub> /l)**
1	2.2	19	2.3	7.9
2	3.4	14	7.2	13
3	44	2.9	4.6	2.5
4	14	16	37	33
5	4.5	21	18	20
6	24	12	11	8.3
7	19	27	7.4	15
8	110	29	11	18
9	2.6	0.26	2.5	0.64
10	190	58	14	29
11	5.2	0.62	2.2	0.76
12	60	7.2	28	9.9
13	50	7	3.5	1.5
14	17	12	9.1	11
15	24	10	2.8	4.0
16	6.6	2	2.6	2.4
17	9.7	3.4	2.6	1.9
18	2.5	7.4	2.0	1.9
19	160	59	1.9	26
20	44	36	1.6	31
21	14	26	1.4	17
22	16	11	1.3	2.2
23	11	1.5	1.3	0.87
24	6.1	0.87	1.2	0.38
25	5.1	0.19	1.1	0.27
26	14	1.1	1.1	1.4
27	16	0.86	1.0	<0.10
28	30	18	0.97	5.9
29	34	3.7	0.70	<0.10
30	19	8.9	0.62	1.2
31	3.2	0.12	0.53	0.43
32	9.4	16	0.44	29
33	7.2	0.97	0.43	0.17
34	14	36	0.35	0.89
35	3.8	0.69	0.16	<0.10
36	3	7.3	0.24	<0.10
37	2.7	25	0.16	19
38	9.6	10	0.93	4.2
39	29	11	28	26
40	165	11	27	4.8

41	82	13	28	26
42	6.0	41	2.8	1.4
43	189	17	0.26	<0.10
44	12	12	7.5	9.5
45	111	24	28	29
46	120	25	28	28
47	67	54	25	25
48	3.5	48	2.8	29
49	12	56	1.4	29
50	6.9	63	3.3	9.6
51	13	66	27	26
52	13	95	5.6	12
53	68	80	26	28
54	11	78	25	27
55	105	60	29	28
56	42	14	15	5.8
57	11	51	0.9	0.67
58	22	1.7	1.7	0.70
59	6.2	7.9	17	16
60	36	9.0	1.5	3.5
61	69	18	32	32
62	91	22	0.45	0.50
63	88	28	30.5	7.4
64	13	38	13	14
65	4.0	22	9.5	25

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\*, Specific IgE levels in kU<sub>A</sub>/l to cat and dog dander (ImmunoCAP; e1 and e5, respectively);

\*\*, Allergen-specific IgE levels in kU<sub>A</sub>/l (ELISA).

168 **Table S3.** Serological characteristics of patients in basophil activation test.

Patient	Cat (kU <sub>A</sub> /l)*	Dog (kU <sub>A</sub> /l)*	rFel d 7 (kU <sub>A</sub> /l)**	rCan f 1 (kU <sub>A</sub> /l)**
I	1.6	0.31	0.46	0.1
II	8.9	4.0	3.4	3.9
III	10	1.8	5.1	<0.10
IV	12	0.91	1.5	<0.10

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170 \*, Specific IgE levels in kU<sub>A</sub>/l to cat and dog dander (ImmunoCAP; e1 and e5, respectively);

171 \*\*, Allergen-specific IgE levels in kU<sub>A</sub>/l (ELISA).

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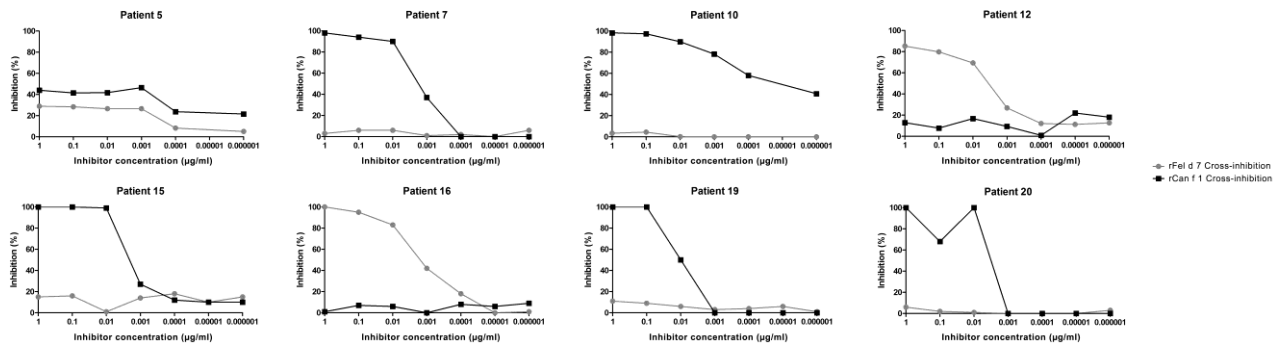
175 **Table S4.** Percentages of secondary structure calculated in CDPro with CONTINILL  
 176 algorithm using SP37 base.

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Secondary structure	rFel d 7 (%)	rCan f 1 (%)	Δ sum of α and β (%)
α- helix	5.0	10.7	14.2
β- sheets	36.0	40.9	
β-turn	24.2	27.8	
unfolded	34.8	20.6	

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181 **Figure S1** - IgE cross-reactivity between rFel d 7 and rCan f 1 in eight additional patients.  
 182 Percentages of inhibition (y-axes) are plotted against different concentrations of inhibitor  
 183 allergens (x-axes) in eight additional patients (5, 7, 10, 12, 15, 16, 19 and 20 in Table S2).  
 184 IgE-binding to rCan f 1 in sera pre-incubated with rFel d 7–cross-inhibition (grey dots); IgE-  
 185 binding to rFel d 7 in sera pre-incubated with rCan f 1–cross-inhibition (black squares).

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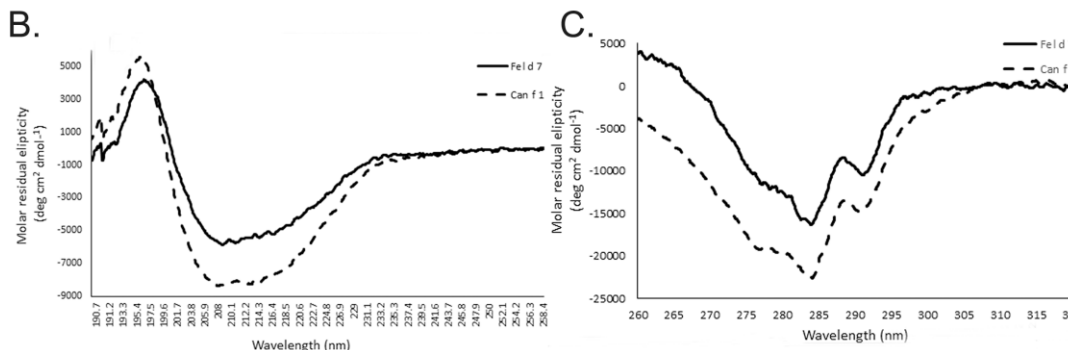
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**A.**

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Fel d 7 1 MKALLLAVGLSLITVLQAQDPASPAGEDTMAMSGKWLKAMITDRETSWKKPELVTPMTLT 60
Can f 1 1 MKTLLLTIGFSLIAILQAQDTPALGKDTVAVSGKWLKAMTADQVEP-EKPDSVTPMILK 59
P31025 1 MKPLLLAVSLGLIAALQAHLLASDEEIQDVSQTWYWKAMTVDFPEMNNLESVTPMTLT 60
      * * * * * . . . . . * : : : * : : * * * * * . * : * : * * * * .
Fel d 7 61 VLEGGNLKAETLLTNGQCKEVELILEKTSEPKKYTTYGGKRVVYIEPTEVKDHYIFYCE 120
Can f 1 60 AQKGGNLEAKITMLTNGQCQNITVVLHKTSEPGKYTAYEGQRVVF IQPSPVRDHYIILYCE 119
P31025 61 TLEGGNLEAKVTMLISGRCEQVKAVLEKTDEPGKYTAGGKHVAYIIRSHVKDHYIFYCE 120
      . . * * * * . * : * * * * * : : * : * * * * * * * : * : * * * * * : * : * * * * *
Fel d 7 121 GEMQGEQARMALVGRDPESNEEALFNREFFLRAKGFNQ-EIFSPKQSDTCPPTDQPEV 180
Can f 1 120 GELHGRQIRMAKLLGRDPEQSQALEDFFREFSRAKGLNQ-EILELAQSETCSPGGQ----- 174
P31025 121 GELHGKPVRGVKLVGRDPKNNLEALEDFEKAAGARGLSTESILIPRQSETCSPGSD----- 176
      * * : : * * . * . * . * * * * . . * * * * . * : * : * * * * * : * : * * * * *

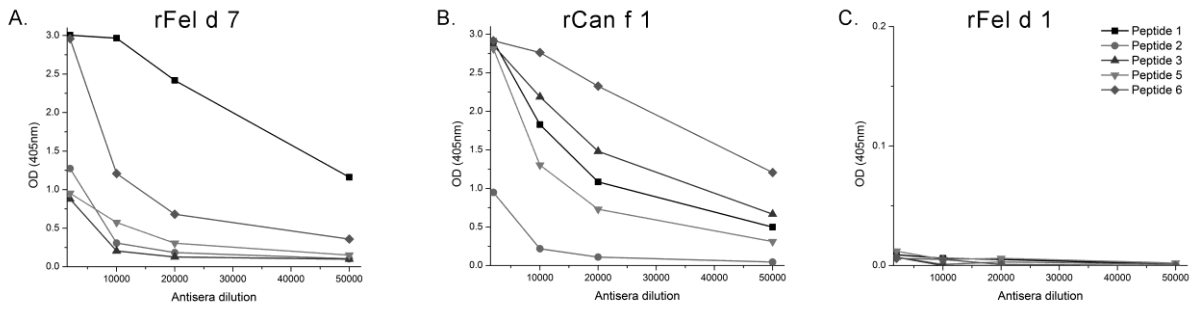
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189 **Figure S2** - Structural similarities between Fel d 7 and Can f 1. (A) Sequence alignment of  
 190 Fel d 7, Can f 1 and human tear lipocalin (hTL). Underlined sequences show the signal  
 191 peptide and symbols underneath the alignment indicate: positions which have a single, fully  
 192 conserved residue (\*), conservation between groups of strongly similar properties (:)  
 193 and weakly similar properties (.). Percentages of sequence identity between: Fel d 7 vs Can f 1  
 194 63%, Fel d 7 and hTL 55%, Can f 1 and hTL 60%.; (B) Far UV CD spectra of rFel d 7 (solid  
 195 line) and rCan f 1 (dashed line); (C) Near UV CD spectra of rFel d 7 (solid line) and rCan f 1  
 196 (dashed line).

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199 **Figure S3** - Can f 1 peptide-specific IgG binding. (A) to rFel d 7; (B) to rCan f 1; (C) to the  
 200 unrelated allergen rFel d 1. Optical density values corresponding to allergen-specific IgG  
 201 levels (y-axis) of different dilutions of peptide-specific antisera (x-axis).