

**Supplementary Table 1. Allele carrier frequencies of anti-AK5 LE patients compared to controls.**

Allele	Controls, n=442 (%)	Patients, n=11 (%)	Uncorrected p value	Corrected p value
A*01:01	92 (20.8)	7 (63.6)	0.002995	0.12579
A*01:23	1 (0.2)	0 (0.0)		
A*02:01	161 (36.4)	4 (36.4)		
A*02:02	11 (2.5)	0 (0.0)		
A*02:03	2 (0.5)	0 (0.0)		
A*02:05	12 (2.7)	0 (0.0)		
A*02:06	3 (0.7)	0 (0.0)		
A*02:17	2 (0.5)	0 (0.0)		
A*02:38	1 (0.2)	0 (0.0)		
A*03:01	88 (19.9)	0 (0.0)	0.133190	
A*03:02	3 (0.7)	0 (0.0)		
A*11:01	41 (9.3)	1 (9.1)		
A*11:02	1 (0.2)	0 (0.0)		
A*23:01	33 (7.5)	1 (9.1)	0.580313	
A*23:17	2 (0.5)	0 (0.0)		
A*24:02	78 (17.6)	1 (9.1)	0.698098	
A*24:03	6 (1.4)	0 (0.0)		
A*24:10	1 (0.2)	0 (0.0)		
A*25:01	12 (2.7)	0 (0.0)		
A*26:01	37 (8.4)	1 (9.1)		
A*26:08	1 (0.2)	0 (0.0)		
A*29:01	6 (1.4)	0 (0.0)		
A*29:02	41 (9.3)	0 (0.0)	0.609694	
A*30:01	16 (3.6)	0 (0.0)		
A*30:02	11 (2.5)	0 (0.0)		
A*30:04	7 (1.6)	0 (0.0)		
A*31:01	24 (5.4)	1 (9.1)	0.468294	
A*31:04	1 (0.2)	0 (0.0)		
A*32:01	57 (12.9)	1 (9.1)		
A*32:26	1 (0.2)	0 (0.0)		
A*33:01	13 (2.9)	1 (9.1)	0.294786	
A*33:03	10 (2.3)	1 (9.1)	0.239268	
A*33:05	1 (0.2)	0 (0.0)		
A*34:02	5 (1.1)	0 (0.0)		
A*36:01	4 (0.9)	0 (0.0)		
A*66:01	4 (0.9)	0 (0.0)		
A*66:02	1 (0.2)	0 (0.0)		
A*66:03	1 (0.2)	0 (0.0)		
A*68:01	25 (5.7)	0 (0.0)		
A*68:02	18 (4.1)	1 (9.1)	0.379186	
A*74:01	3 (0.7)	0 (0.0)		
A*80:01	1 (0.2)	0 (0.0)		
B*07:02	74 (16.7)	0 (0.0)	0.224724	
B*07:05	3 (0.7)	0 (0.0)		
B*07:06	3 (0.7)	0 (0.0)		
B*08:01	51 (11.5)	7 (63.6)	0.000088	0.005808
B*13:02	13 (2.9)	2 (18.2)	0.047399	
B*14:01	21 (4.8)	0 (0.0)		
B*14:02	36 (8.1)	2 (18.2)	0.233546	
B*15:01	29 (6.6)	0 (0.0)		
B*15:03	13 (2.9)	0 (0.0)		
B*15:09	1 (0.2)	0 (0.0)		
B*15:10	2 (0.5)	0 (0.0)		
B*15:16	1 (0.2)	0 (0.0)		
B*15:17	6 (1.4)	1 (9.1)	0.159065	
B*15:18	5 (1.1)	0 (0.0)		
B*15:24	1 (0.2)	0 (0.0)		
B*15:25	1 (0.2)	0 (0.0)		
B*18:01	52 (11.8)	0 (0.0)	0.623491	
B*18:02	1 (0.2)	0 (0.0)		
B*18:26	1 (0.2)	0 (0.0)		
B*27:02	5 (1.1)	0 (0.0)		
B*27:03	1 (0.2)	0 (0.0)		
B*27:05	27 (6.1)	0 (0.0)		
B*27:06	1 (0.2)	0 (0.0)		
B*27:07	1 (0.2)	0 (0.0)		
B*35:01	48 (10.9)	0 (0.0)	0.615755	
B*35:02	6 (1.4)	1 (9.1)	0.159065	
B*35:03	14 (3.2)	0 (0.0)		
B*35:08	3 (0.7)	0 (0.0)		
B*37:01	15 (3.4)	0 (0.0)		
B*38:01	22 (5.0)	0 (0.0)		

B*38:02	2 (0.5)	0 (0.0)		
B*39:01	5 (1.1)	0 (0.0)		
B*39:06	1 (0.2)	0 (0.0)		
B*39:10	3 (0.7)	0 (0.0)		
B*39:31	1 (0.2)	0 (0.0)		
B*40:01	27 (6.1)	0 (0.0)		
B*40:02	13 (2.9)	0 (0.0)		
B*41:01	6 (1.4)	0 (0.0)		
B*41:02	9 (2.0)	0 (0.0)		
B*42:01	6 (1.4)	0 (0.0)		
B*44:02	40 (9.0)	2 (18.2)	0.271266	
B*44:03	62 (14.0)	1 (9.1)		
B*44:04	2 (0.5)	0 (0.0)		
B*44:05	2 (0.5)	0 (0.0)		
B*44:115	1 (0.2)	0 (0.0)		
B*45:01	13 (2.9)	0 (0.0)		
B*47:01	1 (0.2)	0 (0.0)		
B*48:01	2 (0.5)	0 (0.0)		
B*49:01	24 (5.4)	0 (0.0)		
B*50:01	24 (5.4)	1 (9.1)	0.468294	
B*50:02	3 (0.7)	0 (0.0)		
B*51:01	55 (12.4)	1 (9.1)		
B*51:02	1 (0.2)	0 (0.0)		
B*51:07	1 (0.2)	0 (0.0)		
B*51:08	1 (0.2)	0 (0.0)		
B*51:165	1 (0.2)	0 (0.0)		
B*52:01	10 (2.3)	0 (0.0)		
B*53:01	24 (5.4)	0 (0.0)		
B*55:01	7 (1.6)	1 (9.1)	0.179805	
B*56:01	9 (2.0)	0 (0.0)		
B*57:01	21 (4.8)	2 (18.2)	0.102628	
B*58:01	16 (3.6)	0 (0.0)		
B*58:02	2 (0.5)	0 (0.0)		
B*73:01	3 (0.7)	0 (0.0)		
B*81:01	2 (0.5)	0 (0.0)		
B*82:01	1 (0.2)	0 (0.0)		
C*01:02	25 (5.7)	0 (0.0)		
C*02:02	51 (11.5)	0 (0.0)	0.621312	
C*02:10	13 (2.9)	0 (0.0)		
C*03:02	5 (1.1)	0 (0.0)		
C*03:03	26 (5.9)	1 (9.1)	0.495305	
C*03:04	33 (7.5)	0 (0.0)		
C*04:01	108 (24.4)	2 (18.2)		
C*04:09	6 (1.4)	0 (0.0)		
C*05:01	48 (10.9)	1 (9.1)		
C*06:02	83 (18.8)	5 (45.5)	0.042990	
C*07:01	86 (19.5)	8 (72.7)	0.000253	0.008349
C*07:02	83 (18.8)	0 (0.0)	0.228408	
C*07:04	16 (3.6)	0 (0.0)		
C*07:06	2 (0.5)	0 (0.0)		
C*07:18	13 (2.9)	0 (0.0)		
C*08:02	56 (12.7)	2 (18.2)	0.639443	
C*08:03	2 (0.5)	0 (0.0)		
C*12:02	10 (2.3)	0 (0.0)		
C*12:03	52 (11.8)	1 (9.1)		
C*14:02	7 (1.6)	0 (0.0)		
C*14:03	3 (0.7)	0 (0.0)		
C*15:02	24 (5.4)	1 (9.1)	0.468294	
C*15:04	3 (0.7)	0 (0.0)		
C*15:05	8 (1.8)	0 (0.0)		
C*15:06	2 (0.5)	0 (0.0)		
C*15:13	2 (0.5)	0 (0.0)		
C*16:01	45 (10.2)	0 (0.0)	0.611857	
C*16:02	4 (0.9)	0 (0.0)		
C*16:04	1 (0.2)	0 (0.0)		
C*16:35	2 (0.5)	0 (0.0)		
C*17:01	10 (2.3)	0 (0.0)		
C*17:03	9 (2.0)	0 (0.0)		
C*18:01	2 (0.5)	0 (0.0)		
DRB1*01:01	53 (12.0)	1 (9.1)		
DRB1*01:02	40 (9.0)	1 (9.1)		
DRB1*01:03	1 (0.2)	0 (0.0)		
DRB1*03:01	69 (15.6)	8 (72.7)	0.000054	0.002214
DRB1*03:02	4 (0.9)	0 (0.0)		
DRB1*04:01	35 (7.9)	0 (0.0)		

DRB1*04:02	13 (2.9)	0 (0.0)		
DRB1*04:03	17 (3.8)	0 (0.0)		
DRB1*04:04	14 (3.2)	0 (0.0)		
DRB1*04:05	13 (2.9)	0 (0.0)		
DRB1*04:06	11 (2.5)	0 (0.0)		
DRB1*04:07	1 (0.2)	0 (0.0)		
DRB1*04:08	1 (0.2)	0 (0.0)		
DRB1*04:38	1 (0.2)	0 (0.0)		
DRB1*07:01	101 (22.9)	5 (45.5)	0.139286	
DRB1*08:01	22 (5.0)	0 (0.0)		
DRB1*08:03	4 (0.9)	0 (0.0)		
DRB1*08:04	7 (1.6)	0 (0.0)		
DRB1*09:01	9 (2.0)	0 (0.0)		
DRB1*10:01	9 (2.0)	0 (0.0)		
DRB1*11:01	66 (14.9)	0 (0.0)	0.379627	
DRB1*11:02	14 (3.2)	1 (9.1)	0.312456	
DRB1*11:03	4 (0.9)	0 (0.0)		
DRB1*11:04	41 (9.3)	0 (0.0)	0.609694	
DRB1*12:01	14 (3.2)	0 (0.0)		
DRB1*12:02	5 (1.1)	0 (0.0)		
DRB1*13:01	62 (14.0)	1 (9.1)		
DRB1*13:02	40 (9.0)	3 (27.3)	0.076680	
DRB1*13:03	13 (2.9)	0 (0.0)		
DRB1*13:04	2 (0.5)	0 (0.0)		
DRB1*13:05	5 (1.1)	0 (0.0)		
DRB1*14:01	6 (1.4)	0 (0.0)		
DRB1*14:04	1 (0.2)	0 (0.0)		
DRB1*14:17	2 (0.5)	0 (0.0)		
DRB1*14:54	28 (6.3)	0 (0.0)		
DRB1*15:01	76 (17.2)	1 (9.1)	0.699032	
DRB1*15:02	11 (2.5)	0 (0.0)		
DRB1*15:03	11 (2.5)	0 (0.0)		
DRB1*15:04	1 (0.2)	0 (0.0)		
DRB1*16:01	14 (3.2)	0 (0.0)		
DRB1*16:02	4 (0.9)	0 (0.0)		
DQB1*02:01	73 (16.5)	8 (72.7)	0.000080	0.00128
DQB1*02:02	88 (19.9)	3 (27.3)	0.467823	
DQB1*03:01	162 (36.7)	0 (0.0)	0.009340	0.14944
DQB1*03:02	70 (15.8)	0 (0.0)	0.227910	
DQB1*03:03	22 (5.0)	2 (18.2)	0.110473	
DQB1*03:05	3 (0.7)	0 (0.0)		
DQB1*03:19	12 (2.7)	1 (9.1)	0.276703	
DQB1*04:02	39 (8.8)	0 (0.0)	0.610103	
DQB1*05:01	108 (24.4)	2 (18.2)		
DQB1*05:02	27 (6.1)	0 (0.0)		
DQB1*05:03	33 (7.5)	0 (0.0)		
DQB1*06:01	10 (2.3)	0 (0.0)		
DQB1*06:02	81 (18.3)	1 (9.1)	0.697573	
DQB1*06:03	59 (13.3)	1 (9.1)		
DQB1*06:04	30 (6.8)	3 (27.3)	0.038913	0.622608
DQB1*06:09	9 (2.0)	0 (0.0)		
DQA1*01:01	91 (20.6)	2 (18.2)		
DQA1*01:02	140 (31.7)	4 (36.4)	0.749087	
DQA1*01:03	69 (15.6)	1 (9.1)		
DQA1*01:04	35 (7.9)	0 (0.0)		
DQA1*01:05	11 (2.5)	0 (0.0)		
DQA1*02:01	100 (22.6)	5 (45.5)	0.137924	
DQA1*03:01	59 (13.3)	0 (0.0)	0.373234	
DQA1*03:02	8 (1.8)	0 (0.0)		
DQA1*03:03	51 (11.5)	0 (0.0)	0.621312	
DQA1*04:01	26 (5.9)	0 (0.0)		
DQA1*04:02	3 (0.7)	0 (0.0)		
DQA1*04:04	1 (0.2)	0 (0.0)		
DQA1*05:01	69 (15.6)	8 (72.7)	0.000054	0.000918
DQA1*05:05	143 (32.4)	1 (9.1)	0.185944	
DQA1*05:09	5 (1.1)	0 (0.0)		
DQA1*05:11	1 (0.2)	0 (0.0)		
DQA1*06:01	5 (1.1)	0 (0.0)		
DPB1*01:01	62 (14.0)	5 (45.5)	0.013812	0.441984
DPB1*02:01	133 (30.1)	4 (36.4)	0.741271	
DPB1*02:02	3 (0.7)	0 (0.0)		
DPB1*03:01	62 (14.0)	1 (9.1)		
DPB1*04:01	239 (54.1)	7 (63.6)	0.761026	
DPB1*04:02	92 (20.8)	1 (9.1)	0.474008	
DPB1*05:01	27 (6.1)	2 (18.2)	0.152026	

DPBI*06:01	8 (1.8)	0 (0.0)		
DPBI*09:01	5 (1.1)	0 (0.0)		
DPBI*10:01	14 (3.2)	0 (0.0)		
DPBI*11:01	20 (4.5)	0 (0.0)		
DPBI*13:01	34 (7.7)	2 (18.2)	0.214926	
DPBI*14:01	11 (2.5)	0 (0.0)		
DPBI*15:01	4 (0.9)	0 (0.0)		
DPBI*16:01	3 (0.7)	0 (0.0)		
DPBI*17:01	22 (5.0)	0 (0.0)		
DPBI*18:01	5 (1.1)	0 (0.0)		
DPBI*19:01	4 (0.9)	0 (0.0)		
DPBI*20:01	5 (1.1)	0 (0.0)		
DPBI*21:01	1 (0.2)	0 (0.0)		
DPBI*23:01	9 (2.0)	0 (0.0)		
DPBI*29:01	1 (0.2)	0 (0.0)		
DPBI*34:01	4 (0.9)	0 (0.0)		
DPBI*39:01	1 (0.2)	0 (0.0)		
DPBI*40:01	1 (0.2)	0 (0.0)		
DPBI*50:01	1 (0.2)	0 (0.0)		
DPBI*63:01	3 (0.7)	0 (0.0)		
DPBI*104:01	23 (5.2)	0 (0.0)		
DPBI*105:01	5 (1.1)	0 (0.0)		
DPBI*131:01	5 (1.1)	0 (0.0)		
DPBI*351:01	1 (0.2)	0 (0.0)		
DPBI*370:01	1 (0.2)	0 (0.0)		

**Supplementary Table 2. AK5-derived peptides predicted as strong binders for HLA class I molecules.**

Peptide	Position (AK5-1)	Position (AK5-2)	Position (AK5-3)	A*01:01	Rank % <sup>a</sup> B*08:01	C*07:01
LARREIPQL	10				0.4167	
ARREIPQLF	11					0.01
SKPEDPVEY	29		3			0.2572
SCLQKVKEL	40		14		0.2183	
SRRSFLRNV	75		49			0.2908
RRSFLRNVN	76		50			0.1216
NSNFPYRRY	87		61	0.3328		
FPYRRYDRL	90		64		0.0247	
RRYDRLPPI	93		67			0.0843
DRLPPIHQF	96		70			0.0306
LPPIHQFSI	98		72		0.4884	
ETAELIEEY	114		88	0.0649		
TRPRPKIIL	128		102			0.1409
RPRPKIILV	129		103		0.0738	
QSLKIAERY	148		122	0.2671		
IAERYGFQY	152		126	0.0703		
LLRKKIHST	166		140		0.0956	
TSSNRKWSL	174		148		0.1764	
EIKQKLMQI	201		175		0.0157	
FPRDVAQAL	220		194		0.048	
NQRLKERLL	247		221		0.1629	
NAAPLVKYF	281		255			0.2465
YFQEKGLIM	288		262		0.2436	0.3075
QCEKLVEKY	392	27	366	0.3852		
RRIGDPQLV	475	110	449			0.0799
LLQRSRSSL	497	132	471		0.2989	
YYRASIPVI	521	156	495			0.4896
YRASIPVIA	522	157	496			0.2965
RASIPVIAY	523	158	497			0.331
ASIPVIAYY	524	159	498	0.1899		0.1448
AYYETKTQL	530	165	504			0.0961

<sup>a</sup>Rank value is only provided for the strong binders for each HLA.

**Supplementary Table 3. AK5-derived peptides predicted as strong binders for HLA class II molecules.**

Peptide	Core	Position (AK5-1)	Position (AK5-3)	HLA class II	Rank %
EDEVFYDISMAVDNK	VFYDISMAV	304	278	DRB1*03:01	0.98
FYDISMAVDNKLFPN	MAVDNKLFP	308	282	DRB1*03:01	0.99
YDISMAVDNKLFPNK	MAVDNKLFP	309	283	DRB1*03:01	0.32
DISMAVDNKLFPNKE	MAVDNKLFP	310	284	DRB1*03:01	0.21
ISMAVDNKLFPNKEA	MAVDNKLFP	311	285	DRB1*03:01	0.88
HQFSIESDTDLSETA	IESDTDLSE	102	76	DQA1*05:01-DQB1*02:01	0.66
QFSIESDTDLSETAE	IESDTDLSE	103	77	DQA1*05:01-DQB1*02:01	0.34
YGFQYISVGELLRKK	YISVGELLR	156	130	DQA1*05:01-DQB1*02:01	0.78
IAKIITTGELAPQET	IITTGELAPQ	183	157	DQA1*05:01-DQB1*02:01	0.92
AKIITTGELAPQETT	IITTGELAPQ	184	158	DQA1*05:01-DQB1*02:01	0.94
IPDEEGIVIDGFPRD	EEGIVIDGF	209	183	DQA1*05:01-DQB1*02:01	0.70
QEKGLIMTFDADRDE	IMTFDADR	290	264	DQA1*05:01-DQB1*02:01	0.99
EKGLIMTFDADRDED	IMTFDADR	291	265	DQA1*05:01-DQB1*02:01	0.38
KGLIMTFDADRDEDE	IMTFDADR	292	266	DQA1*05:01-DQB1*02:01	0.22
GLIMTFDADRDEDEV	IMTFDADR	293	267	DQA1*05:01-DQB1*02:01	0.66
DTGSDYEDQGDDQLN	YEDQGDDQL	345	319	DQA1*05:01-DQB1*02:01	0.64
TGSDYEDQGDDQLNV	YEDQGDDQL	346	320	DQA1*05:01-DQB1*02:01	0.52
GSDYEDQGDDQLNVF	YEDQGDDQL	347	321	DQA1*05:01-DQB1*02:01	0.57

**Supplementary Table 4. Statistically significant up-regulated CSF proteins in anti-AK5 LE compared to anti-LGII/CASPR2 and anti-Yo/Ma2 patients.**

Abbreviation	Protein	vs. Controls		vs. LGII/CASPR2		vs. Yo/Ma2 <sup>a</sup>	
		logFold Change	Corrected P value	logFold Change	Corrected P value	logFold Change	Corrected P value
CA3*	Carbonic anhydrase 3	0.31	0.02	5.85	0.005	3.84	0.0007
CAPG	Macrophage-capping protein	0.25	0.005	2.11	0.03		
CD209*	CD 209 antigen	0.13	0.004	1.00	0.03	0.76	0.02
CD300C	CMRF35-like molecule 6	0.11	0.002	1.42	0.03		
CSF3	Granulocyte colony-stimulating factor	0.25	0.007	1.13	0.04		
C1R	Complement 1r	0.25	0.0002	3.27	0.01		
C4A/C4B*	Complement c4-a/c4-b	0.06	0.0001	1.28	0.001	0.71	0.005
FAM3B	Protein FAM3B	0.14	0.003	1.04	0.01		
GFAP	Glial fibrillary acidic protein	0.16	0.0003	1.42	0.03		
GRN	Progranulin	0.10	0.0008	1.32	0.003		
HAVCR2*	Hepatitis A virus cellular receptor 2	0.13	0.0007	1.20	0.04	1.07	0.03
ISG15	Ubiquitin-like protein 15	0.23	0.0004	1.74	0.001		
LYZ	Lysozyme C	0.09	0.0009	1.10	0.03		
MB*	Myoglobin	0.22	0.002	3.44	0.003	3.04	0.0007
MRC1	Macrophage mannose receptor 1	0.08	0.01	1.14	0.03		
PEBP1	Phosphatidylethanolamine-binding protein 1	0.03	0.04	0.84	0.04		
PGAM1	Phosphoglycerate mutase 1	0.26	0.0009	1.73	0.008		
PPIA	Peptidyl-prolyl cis-trans isomerase A	0.05	0.0001	0.50	0.03		
PSME1*	Proteasome activator complex subunit 1	0.15	0.0002	0.68	0.03	0.85	0.04
SLAMF7	SLAM family member 7	0.39	0.004	1.88	0.04		
SI00A4	Protein SI00-A4	0.09	0.04	0.81	0.04		
UBE2I	SUMO-conjugating enzyme UBC9	0.12	0.0005	0.68	0.04		
UFC1	Ubiquitin-fold modifier-conjugating enzyme 1	0.09	0.01	0.91	0.04		
YWHAB/E/G/H/Q/Z & SFN	Protein 14-3-3 (beta/alpha, epsilon, eta, gamma, theta, zeta/delta, sigma)	0.19	0.0004	2.48	0.003		
YWHAB	Protein 14-3-3 beta/alpha	0.08	0.003	1.11	0.01		
YWHAZ	Protein 14-3-3 zeta/delta	0.07	0.002	1.18	0.01		

<sup>a</sup>Blank spaces correspond to non-significant differences in CSF protein expression between anti-AK5 and anti-Yo/Ma2 patients.

**Supplementary Table 5. Biological processes in which up-expressed CSF proteins in anti-AK5 LE, compared to anti-LGII/CASPR2 patients, were involved.**

GO term	Description	FDR
GO:1900740	Positive regulation of protein insertion into mitochondrial membrane involved in apoptotic signalling pathway	4.81x10 <sup>-11</sup>
GO:1904951	Positive regulation of establishment of protein localization	7.61x10 <sup>-7</sup>
GO:0051050	Positive regulation of transport	4.90x10 <sup>-6</sup>
GO:0002376	Immune system process	7.50x10 <sup>-6</sup>
GO:0048584	Positive regulation of response to stimulus	8.04x10 <sup>-6</sup>
GO:0006955	Immune response	1.75x10 <sup>-5</sup>
GO:0048583	Regulation of response to stimulus	3.01x10 <sup>-5</sup>
GO:0002252	Immune effector process	5.28x10 <sup>-5</sup>
GO:0051707	Response to other organism	5.28x10 <sup>-5</sup>
GO:0006950	Response to stress	6.67x10 <sup>-5</sup>
GO:0051704	Multi-organism process	7.30x10 <sup>-5</sup>
GO:0010638	Positive regulation of organelle organization	7.65x10 <sup>-5</sup>
GO:0010647	Positive regulation of cell communication	0.00014
GO:0023056	Positive regulation of signalling	0.00014
GO:0050896	Response to stimulus	0.00016
GO:0002250	Adaptive immune response	0.00017
GO:0002443	Leukocyte mediated immunity	0.00017
GO:0098542	Defence response to other organism	0.00017
GO:0051130	Positive regulation of cellular component organization	0.00019
GO:0051049	Regulation of transport	0.00021
GO:0045087	Innate immune response	0.00023
GO:0009967	Positive regulation of signal transduction	0.00029
GO:0044419	Interspecies interaction between organisms	0.00036
GO:0006952	Defence response	0.00036
GO:0061024	Membrane organization	0.00037
GO:0051246	Regulation of protein metabolic process	0.00054
GO:0009617	Response to bacterium	0.00056
GO:0006958	Complement activation, classical pathway	0.00065
GO:0016032	Viral process	0.00065
GO:0052548	Regulation of endopeptidase activity	0.00078
GO:0010951	Negative regulation of endopeptidase activity	0.00090
GO:0006810	Transport	0.00090
GO:0002449	Lymphocyte mediated immunity	0.0011
GO:0033043	Regulation of organelle organization	0.0011
GO:2000427	Positive regulation of apoptotic cell clearance	0.0016
GO:0030449	Regulation of complement activation	0.0016
GO:0048522	Positive regulation of cellular process	0.0017
GO:2000257	Regulation of protein activation cascade	0.0018
GO:0048518	Positive regulation of biological process	0.0019
GO:0051128	Regulation of cellular component organization	0.0020
GO:0030162	Regulation of proteolysis	0.0023
GO:0032269	Negative regulation of cellular protein metabolic process	0.0024
GO:0065007	Biological regulation	0.0033
GO:0002682	Regulation of immune system process	0.0034
GO:0072376	Protein activation cascade	0.0036
GO:0032268	Regulation of cellular protein metabolic process	0.0036
GO:0010646	Regulation of cell communication	0.0036
GO:0065009	Regulation of molecular function	0.0036
GO:0023051	Regulation of signalling	0.0039
GO:0050789	Regulation of biological process	0.0043
GO:0002253	Regulation of immune response	0.0050
GO:0050776	Regulation of immune response	0.0050
GO:0002684	Positive regulation of immune system process	0.0052
GO:0009966	Regulation of signal transduction	0.0052
GO:0048523	Negative regulation of cellular process	0.0057
GO:0002673	Regulation of acute inflammatory response	0.0058
GO:0046718	Viral entry into host cell	0.0058
GO:0046827	Positive regulation of protein export from nucleus	0.0075
GO:0006959	Humoral immune response	0.0083
GO:0070613	Regulation of protein processing	0.0104
GO:0035329	Hippo signalling	0.0111
GO:0001775	Cell activation	0.0111
GO:0051171	Regulation of nitrogen compound metabolic process	0.0114
GO:0002275	Myeloid cell activation involved in immune response	0.0145
GO:0010605	Negative regulation of macromolecule metabolic process	0.0146
GO:0080090	Regulation of primary metabolic process	0.0154
GO:0043086	Negative regulation of catalytic activity	0.0167
GO:0002237	Response to molecule of bacterial origin	0.0169
GO:0044092	Negative regulation of molecular function	0.0169
GO:0071222	Cellular response to lipopolysaccharide	0.0175



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GO:0060255	Regulation of macromolecule metabolic process	0.0175
GO:0050794	Regulation of cellular process	0.0175
GO:0065008	Regulation of biological quality	0.0191
GO:0051172	Negative regulation of nitrogen compound metabolic process	0.0220
GO:0032480	Negative regulation of type I interferon production	0.0221
GO:0048167	Regulation of synaptic plasticity	0.0221
GO:1901990	Regulation of mitotic cell cycle phase transition	0.0221
GO:0031400	Negative regulation of protein modification process	0.0221
GO:0002697	Regulation of immune effector process	0.0235
GO:0045321	Leukocyte activation	0.0235
GO:0051222	Positive regulation of protein transport	0.0239
GO:0010033	Response to organic substance	0.0253
GO:0010941	Regulation of cell death	0.0290
GO:0031324	Negative regulation of cellular metabolic process	0.0312
GO:0035308	Negative regulation of protein dephosphorylation	0.0326
GO:0031347	Regulation of defence response	0.0342
GO:0031399	Regulation of protein modification process	0.0415
GO:0031323	Regulation of cellular metabolic process	0.0428
GO:0031329	Regulation of cellular catabolic process	0.0488

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**Supplementary Table 6. Biological processes in which up-expressed CSF proteins in anti-AK5 LE, compared to anti-Yo/Ma2 patients, were involved.**

GO term	Description	FDR
GO:0002250	Adaptive immune response	0.00070
GO:2000427	Positive regulation of apoptotic cell clearance	0.00094
GO:0002253	Activation of immune response	0.00094
GO:0051707	Response to other organism	0.0014
GO:0002376	Immune system process	0.0014
GO:0031347	Regulation of defence response	0.0022
GO:0045087	Innate immune response	0.0022
GO:0006958	Complement activation, classical pathway	0.0027
GO:0030449	Regulation of complement activation	0.0040
GO:2000257	Regulation of protein activation cascade	0.0040
GO:0032101	Regulation of response to external stimulus	0.0040
GO:0006950	Response to stress	0.0040
GO:0002697	Regulation of immune effector process	0.0044
GO:0072376	Protein activation cascade	0.0053
GO:0052548	Regulation of endopeptidase activity	0.0053
GO:0002673	Regulation of acute inflammatory response	0.0070
GO:0042102	Positive regulation of T cell proliferation	0.0070
GO:0006954	Inflammatory response	0.0070
GO:0051704	Multi-organism process	0.0077
GO:0070613	Regulation of protein processing	0.0093
GO:0009617	Response to bacterium	0.0093
GO:0045807	Positive regulation of endocytosis	0.0101
GO:0019882	Antigen processing and presentation	0.0129
GO:0002758	Innate immune response-activating signal transduction	0.0143
GO:0051050	Positive regulation of transport	0.0230
GO:0010951	Negative regulation of endopeptidase activity	0.0239
GO:0002252	Immune effector process	0.0244
GO:0046677	Response to antibiotic	0.0318
GO:0002237	Response to molecule of bacterial origin	0.0334
GO:0044092	Negative regulation of molecular function	0.0345
GO:0032268	Regulation of cellular protein metabolic process	0.0394
GO:0043687	Post-translational protein modification	0.0397
GO:0006979	Response to oxidative stress	0.0397
GO:0006508	Proteolysis	0.0397
GO:0043902	Positive regulation of multi-organism process	0.0423