SUPPLEMENTAL INFORMATION

Supplemental Methods

Mass spectrometry

Sample preparation - Established methods of in-gel digestion were used for processing of IEF gel¹. In brief, slices were washed with 25 mM ammonium bicarbonate (ABC)/50 % acetonitrile for removal of the stain agent. Supernatant was removed and gel pieces covered in100% acetonitrile until gel pieces were dehydrated. Acetonitrile was removed and gel pieces were vacuum dried. Next, the gel pieces were rehydrated and reduced in 10 mM dithiothreitol (DTT) (Sigma), for 45 min at 56°C. Supernatant was removed and gel pieces alkylated with 55mM iodoacetamide (IAA) (Sigma) in the dark for 30 minutes. At the end of the alkylation step, the gel pieces were washed 25 mM ABC, then dehydrated with neat acetonitrile and vacuum dried. Gel pieces were rehydrated in sequencing grade trypsin (12.5 ng/µl prepared in 25 mM ammonium bicarbonate) (Promega) at 4°C for 45 minutes, after which excess trypsin solution was removed and 25 mM ABC was placed on the top of the rehydrated gel pieces to ensure submersion in solution. After an overnight incubation at 37°C, digestion was stopped by the addition of .1% formic acid (FA). Samples were spun down and the water extract containing the peptides collected. Remaining peptides were extracted by shaking the gel pieces with .1% FA for 15 minutes at room temperature. This step was repeated one more time and extracts were combined. Peptide solutions were concentrated down to 10 µl by vacuum centrifugation. LCMS analysis was performed using an Eksigent NanoLC Ultra 2D Plus

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HPLC system coupled to a Thermo Scientific LTQ Orbitrap Velos (Waltham, MA) via an Advance CaptiveSpray Ionization source (Michrom BioResources, Auburn, CA).

Database Searches - The raw files generated on Orbitrap LTQ Velos mass spectrometer were converted to [mgf] format using Mascot Daemon software version 2.2.2 (Matrix Science) with prior to their submission to the search engine ProteinPilot [™] (release 4.5, revision 1656, AB Sciex) that uses the Paragon algorithm². The initial search of peptides mapping to CSF-associated IgG-VH clusters were performed against the VHref-CSF database appended with the UniProtKB database of human isoform sequences of common contaminants of human origin (release 31-Oct-2012), and of peptides exclusively mapping to PBMC-derived sequences the initial search was performed against the VHref-PB database appended with UniProtKB. The search databases contained 41,473 (VHref-CSF plus UniProtKB) and 489,419 (VHref-PB plus UniProtKB) total entries. Thus, our approach permitted only detection of OCB peptides that were represented either in our VHref databases containing over 450,000 IgG-VH transcripts and/or could be matched to UniProtKB. Next generation immune repertoire sequencing used to generate our IgG-VH reference databases is far-more comprehensive than Sanger-sequencing based approaches, and has a greater chance of capturing the true diversity of IgG-VH transcripts present in CSF samples, and a significant portion of IgG-VH diversity in PB. Nonetheless, it is likely that an undeterminable number of tryptic OCB peptides present after the in-gel digestion, were eliminated from further analysis if their respective IgG-VH transcript was not found in VHref-CSF or VHref-PB. All peptides were blasted against the IMGT IGHV germline database³ using IgBLAST (http://www.ncbi.nlm.nih.gov/igblast/).

Confirmatory searches were then performed against a combination of all three datasets (VHref-CSF plus VHref-PB plus UniProtKB). OCB peptides from a certain patient's CSF mapping to only the same patient's IgG-VH were identified as "patient-specific" (Tables S2 and S3). Patient non-specific OCB peptides mapped to IgG-VH transcripts of >1 patient or could not be assigned to the same patient's IgG-VH (Table S4) and were not analyzed further. Mass spectra of all "patient-specific" peptides were manually inspected to assess the quality of the match and importantly, to establish the extent of peptide sequence coverage by the detected product ions. Only OCB peptide sequences for which full tandem mass-spectrometry evidence was seen were utilized in further analysis.

Supplemental References

- 1. Jimenez CR, Huang L, Qiu Y, Burlingame AL. In-gel digestion of proteins for MALDI-MS fingerprint mapping. Curr Protoc Protein Sci. 2001;Chapter 16:Unit 16 14
- 2. Shilov IV, Seymour SL, Patel AA et al. The Paragon Algorithm, a next generation search engine that uses sequence temperature values and feature probabilities to identify peptides from tandem mass spectra. Mol Cell Proteomics. 2007;6:1638-1655
- 3. Lefranc MP, Giudicelli V, Ginestoux C et al. IMGT, the international ImMunoGeneTics information system. Nucleic Acids Res. 2009;37:D1006-1012

Supplemental Tables

ID	Age	Sex	Duration (months)	# Attacks	EDSS	Most recent MRI (months)	Gd
MS-1	29	F	11	3	1.	7	+
MS-2	37	F	24	1	2.	1	-
MS-3	39	F	>3	>1	2.	7	-
MS-4	39	F	24	2	1.5	2	-
MS-5	22	Μ	9	2	1.5	.25	+

Table S1. Additional clinical information of patients studied. *Duration* is disease duration in months, "# *Attacks*" refers to number of clinical MS attacks since diagnosis, *EDSS* is the Expanded Disability Scoring Scale at the time of lumbar puncture, "*Most recent MRI*" is time in months since last brain or spinal cord MRI, "*Gd*" indicates whether the most recent MRI displayed pathological contrast enhancement.

CSF	Total peptides	Not patient-specific	Patient-specific	Tandem Mass-Spec confirmed
MS-1	29	13	16	7
MS-2	106	42	64	20
MS-3	129	40	89	38
MS-4	10	5	5	3
MS-5	111	35	76	12
Sum	385	135	250	80

Table S2. OCB peptides identified by Mass-Spectrometry. *CSF*, ID of patient from which CSF OCB peptides were obtained; *Total peptides*, all peptides identified by mass-spectrometry; *Not patient-specific*, OCB peptides mapping to >1 patient in VHref-CSF; *Patient-specific*, OCB peptides uniquely mapping to the same patient's IgG-VH sequences in VHref-CSF or VHref-PB (see Methods); *Tandem Mass-Spec confirmed*, fully sequence confirmed OCB peptides per patient used for mapping to IgG-VH clusters. Refer to Tables S3 and S4 for further details on confirmed OCB peptides.

Pat ID	OCB Peptide	Mutated?	Cluster Compartment	IPG BAND	Multi band?	IGHV	H-CDR 3	IGHJ
MS-1	LACTASGFR	У	С	F	n	3-48	CVRDQGGYYGNFFLDYW	4
MS-1	G T GG GW YY R	У	С	F	n	3-23	CARGTGGGWYYRIHFDYW	4
MS-1	V EDSGVYYCA GR	У	С	D	n	3-48	CAGRRYLESSGPPEFPW	5
MS-1	VMGFYEDSGYR	CDR3	В	F	n	4-4	CARVMGFYEDSGYRYFTGLNDYW	4
MS-1	SIF DGGTTD F AAPV R	у	С	D	n	3-15	CTTDEGGNSGYYFEYW	4
MS-1	VAMSIDTSR	у	С	F	n	4-59/61	CARSGPGGEPVYYFDPW	5
MS-1	L T SVTAADTAK	У	С	F	n	4-59/61	CARSGPGGEPVYYFDPW	5
MS-2	AFFNPFDY WGQGALVTVSSASTK	CDR3	С	J	n	4-39	CARHPDSSDNTGRAFFNPFDYW	4
MS-2	YFAWSAGK	CDR3	B,C	D	n	4-39	CVAVRYFAWSAGKLFDYW	4
MS-2	ASDTAMYYCAR*	n	С	н	n	5-51	CARRIAPLRGTYSMFAFDIW	3
MS-2	VTISV VP SK	У	С	С	n	4-59/61	CAKRAAYCDGKRCSRAFDYW	4
MS-2	FDQ WGQGTLVTVSSASTK	CDR3	С	J	n	4-39	CAGDGSGSYYTRFDQW	4
MS-2	GLLWLDGDYR	CDR3	С	D	У	3-30/33rn	CTRGLLWLDGDYRDYW	4
MS-2	AEDTA I YYC T R	У	С	D	У	3-30/33rn	CTRGLLWLDGDYRDYW	4
MS-2	Y TL N LQM D SLR	У	С	J	У	3-30/33rn	CTRGLLWLDGDYRDYW	4
MS-2	FTFT SYGMHWVR	У	С	J	У	3-30/33rn	CTRGLLWLDGDYRDYW	4
MS-2	LTISMDTSR	у	С	D	n	4-30-4/31	CARRASPHHYDGSGEDYW	4
MS-2	VTISVETSK	у	С	J	n	4-30-4/31	CGRDGRGRELLPFPGFDSW	4
MS-2	ELLPFPGFDS WGQGTLVTVSSASTK	CDR3	С	J	n	4-30-4/31	CGRDGRGRELLPFPGFDSW	4
MS-2	GRELLPFPGFDS WGQGTLVTVSSASTK	CDR3	С	J	n	4-30-4/31	CGRDGRGRELLPFPGFDSW	4
MS-2	GLEWVS T IYR	у	С	J	У	3-53/66	CAGGQTGYCTGGNSQRCYGMDVW	6
MS-2	D G A T S YAD T VK	у	С	А	У	3-53/66	CAGGQTGYCTGGNSQRCYGMDVW	6
MS-2	VTISVDTS N NHFSLK	у	С	J	n	4-59/61	CARGSDILTGYSLGGWFDPW	5
MS-2	AEDTGVYYCAK	у	С	С	n	3-53/66	CAKVKGRQLVHYYYGMDVW	6
MS-2	VAISADAPK	у	С	J	n	4-39	CARGLPRLLSPHSDW	4
MS-2	S T STA N L H WSSLK	у	С	J	n	5-a	CARPQRSSSSTFDHW	4
MS-2	LSSVTAADTAVYHCAR	У	С	J	n	4-30-4/31	CARVDRTAGYYFDNW	4
MS-3	VILSVDTSK	у	С	К	У	4-39	CARHELVQTPATSKFGPW	5
MS-3	GLEWIGSV y K	У	С	J	У	4-39	CAGHELLHTPTTSKFGPW	5
MS-3	HEFLQTPTTSK	CDR3	С	J	У	4-39	CARHEFLQTPTTSKFGPW	5
MS-3	HELLQTPTTSK	CDR3	С	J	У	4-39	CVRHELLQTPTTSKFGPW	5
MS-3	HELVQTPATSK	CDR3	С	D	У	4-39	CARHELVQTPATSKFGPW	5
MS-3	HELVQTPTTSK	CDR3	С	А	У	4-39	RARHELVQTPTTSKFGPW	5

MS-3	NGIAYYNPSLTSR	У	С	J	У	4-39	CARHELVQTPATSKFGPW	5
MS-3	SG IAF YNPSL T SR	У	С	J	У	4-39	CARHELVQRPAISKFGPW	5
MS-3	SG IA YHNPSL T SR	У	С	J	У	4-39	CARHEAVQTPTTSKFGPW	5
MS-3	SG IA YYNPSL TT R	У	С	В	У	4-39	GARHELLQTPSTSKFGPW	5
MS-3	SG IV YYNPSL T SR	У	С	J	У	4-39	CARHELVQTPATSKFGPW	5
MS-3	SG VA YYNPSL TT R	У	С	J	У	4-39	CVRHELLQTPTTSKFGPW	5
MS-3	S VIA YYNPSL TG R	У	С	J	У	4-39	CARHELVQTPTTSKFGPW	5
MS-3	LNSVAAADTAFYYCAR	У	С	J	У	4-39	CARHELVQAPTTSKFGPW	5
MS-3	L N SV A AADTA I YYCAR	У	С	J	У	4-39	CARHELLQTPTTSKFGPW	5
MS-3	YGP WGQGTLVTVSSASTK	У	С	J	У	4-39	CARHELVQTPATSKYGPW	5
MS-3	L T SVTAADTAVYYC V R	У	С	J	n	4-30-4/31	CVRSKYDILTGYYDKGHAFHIW	3
MS-3	AEDTAVYYC V K	У	С	J	n	3-23	CVKDQGDYIWGTYPSTFDYW	4
MS-3	GLEWIGSI HSG GSTYYNP VV K	У	С	J	n	4-39	CASPRAIGATGPFDYW	4
MS-3	SVTAADTA M Y F CAR	У	С	J	n	4-59/61	CARTYGSGTYSRGYYYGMDVW	6
MS-3	EDGSESYYVDSVK	У	С	J	n	3-7	CARRGTTTPRGRTPDSW	4
MS-3	TLDS WGQGTLVTVSSASTK	CDR3	С	J	n	3-7	CTRRGATTPRGRTLDSW	4
MS-3	GLEWIG NMQ Y R	У	С	J	n	4-39	CASSRSWKGHFQHW	1
MS-3	NTLYLQM T SLR	У	С	К	n	3-30/33rn	CARKPDRGYNLDDYGEYKPTSPFDYW	4
MS-3	SAMDV WGQGTTVTVSSASTK	CDR3	С	J	n	4-59	CARVRSAMDVW	6
MS-3	SVTAADTAVYYCR	У	С	В	n	4-34	CRWGGDMDVW	6
MS-3	SHFAD WGQGTLVSVSSPSTK	CDR3	С	J	n	4-39	CASSTGTTLRRSHFADW	4
MS-3	LSSVTAADT GI YY CASSTGTTLR	CDR3	С	J	n	4-39	CASSTGTTLRRSHFADW	4
MS-3	DHQWLVLGR	CDR3	С	1	n	3-7	CVRDHQWLVLGRRCDSW	5
MS-3	GL Q WVANIK	У	С	1	n	3-7	CARVLTVRGVSSQGFDSW	4
MS-3	GVSSQGFDSWGQGTLVSVSSASTK	CDR3	С	J	n	3-7	CARVLTVRGVSSQGFDSW	4
MS-3	LSCAASGF I F R	У	С	К	n	3-15	CTTVKLGWRSSYYDTAFDYW	4
MS-3	GLEWVANI NPE G N EK	У	С	К	n	3-7	CAKDWTDAGAVTNVFDYW	4
MS-3	AEDTAVYYCANR	У	С	В	n	3-23	CANRYLVDSSGSYRDDPFDIW	3
MS-3	DAPDCGGDCYSLPTVR	CDR3	С	К	n	3-7	CARDAPDCGGDCYSLPTVRFDYW	4
MS-3	DYNPSVDS SGSTYYNPSLK	У	С	К	n	4-30-4/31	CARDYDYGDKWFDPW	5
MS-3	AEDT G VYYCAR	У	С	J	n	3-7	CARDYGSATYYASYYHGMGVW	6
MS-3	VTISVDTAK	У	С	К	n	4-39	CARHIALPARAMYYHDTIGTPGPLDFW	5
MS-4	AEDTAVYFCAR	У	С	D	n	3-53/66	CARDVFDAWCDHRFDFW	4
MS-4	NTL F LQMNSLR	У	С	D	n	3-53/66	CARDVFDAWCDHRFDFW	4
MS-4	LSCAASNFR	у	С	D	n	3-23	CAKSDDYDFHNIDSW	4

MS-5	NSLYLQMN T LR	У	B,C	I	У	3-9	CAKEPDSSGWSTGGFDPW	5
MS-5	VEDTALYYCAK	У	B,C	G	У	3-9	CAKEPDSSGWSTGGFDPW	5
MS-5	AEDTALYYCAK*	n	B,C	G	У	3-9	CAKEILRSKYDLWSGYYKPFDIW	3
MS-5	NSLYLQM S SLR	У	B,C	L	У	3-9	CAKEILRSKYDLWSGYYKPFDIW	3
MS-5	VTITADESTR*	n	B,C	I	n	1-69	CAPGIYIAGAGGKTYFDYW	4
MS-5	NTLYLQMNSLK*	n	B,C	I	n	3-15	CTTDRTVGATRDFGYW	4
MS-5	AEDTAVYYC S R	У	B,C	I	n	3-74	CSRDQHNFWTGSPYYMDAW	6
MS-5	QDG TD KYYVDSVK	У	С	I	n	3-7	CVGFNPPIDYR	4
MS-5	LNMSVDASK	У	С	L	n	4-30-4/31	CARRTSRREGMNWFDPW	5
MS-5	IYTSGSTNYNPSLK*	n	B,C	К	n	4-59/61	CAGRGFWSPYYYYMDAW	6
MS-5	VG DTA I YYCAR	У	С	А	n	3-7	CARGSAVAGNYW	4
MS-5	NS V YLQM H SLR	У	С	I	n	3-7	CARNADYDILTGYYRPGNFDFW	4

Table S3: <u>OCB Peptides</u>. Summary of patient-specific and fully sequence-confirmed OCB peptides. Peptides are ordered by patient (*Pat ID*); shown are the peptide AA sequences (*OCB Peptide*), IGHV/IGHJ usage, and *H-CDR3* regions representative of the associated IgG-VH cluster. Peptides marked with a "*" are identical to the respective IGHV germline sequence; AA mutations in comparison to the closest IGHV are in bold letters and shaded in gray. The column "Mutated?" lists whether a peptide is identical to germline ("n", not mutated); different from germline ("y"; yes); or contains >2 aminoacids mapping to the H-CDR region (*CDR3*). Compartmental distribution of IgG-VH clusters is "*Cluster Compartment*"; "C" are CSF-restricted clusters identified in VHref-CSF; "B,C" are clusters identified in VHref-CSF with contributions from blood and CSF; "B" is a cluster in patient MS-1 identified in VHref-PB. IEF gel band from which a peptide was obtained by mass-spectrometry is shown in column "*IEF*". Peptides belonging to IgG-VH clusters detected in >1 band on IEF of the same patient's OCB are labeled "y" (yes) in column "*Multi band*", "n" (no) if only detected in a single band. Boxed are peptides belonging to the same IgG-VH cluster. *Shaded in gray* is an OCB peptide that could not be matched to the same patient's VHref-CSF but instead mapped exclusively to this patient's IgG-VH in VHref-PB; this peptide is highly private to patient MS-1 as it is entirely H-CDR derived.

	OCP Pontido	Dto in Munof CCC	VHref-CSF					
CSF	OCB Peptide	Pts in VHrei-CSF	MS-1	MS-2	MS-3	MS-4	MS-5	
MS-1	GTGGGWYYR	1	12					
MS-1	VAMSIDTSR	1	8					
MS-1	SIFDGGTTDFAAPVR	1	3					
MS-1	VEDSGVYYCAGR	1	29					
MS-1	LACTASGFR	1	24					
MS-1	LTSVTAADTAK	1	8					
MS-2	GLEWVSTIYR	1		1				
MS-2	AEDTAIYYCTR	1		1				
MS-2	VTISVVPSK	1		18				
MS-2	GLLWLDGDYR	1		1				
MS-2	FDQWGQGTLVTVSSASTK	1		2				
MS-2	YTLNLQMDSLR	1		1				
MS-2	AFFNPFDYWGQGALVTVSSASTK	1		2				
MS-2	VTISVDTSNNHFSLK	1		6				
MS-2	VAISADAPK	1		4				
MS-2	GRELLPFPGFDSWGQGTLVTVSSASTK	1		1				
MS-2	AEDTGVYYCAK	1		5				
MS-2	DGATSYADTVK	1		2				
MS-2	YFAWSAGK	1		3				
MS-2	LSSVTAADTAVYHCAR	1		3				
MS-2	ASDTAMYYCAR*	1		6				
MS-2	VTISVETSK	1		1				
MS-2	LTISMDTSR	1		5				
MS-2	ELLPFPGFDSWGQGTLVTVSSASTK	1		1				
MS-2	FTFTSYGMHWVR	1		1				
MS-2	STSTANLHWSSLK	1		1				
MS-3	YGPWGQGTLVTVSSASTK	1			1			
MS-3	SHFADWGQGTLVSVSSPSTK	1			1			
MS-3	SVTAADTAVYYCR	1			1			
MS-3	SGIVYYNPSLTSR	1			1			
MS-3	SGIAYYNPSLTTR	1			176			
MS-3	DYNPSVDSSGSTYYNPSLK	1			1			
MS-3	TLDSWGQGTLVTVSSASTK	1			15			
MS-3	LSCAASGFIFR	1			1			

MS-3	LSSVTAADTGIYYCASSTGTTLR	1		1		
MS-3	SGIAYHNPSLTSR	1		2		
MS-3	GVSSQGFDSWGQGTLVSVSSASTK	1		1		
MS-3	AEDTGVYYCAR	1		1		
MS-3	GLEWVANINPEGNEK	1		1		
MS-3	GLEWIGSIHSGGSTYYNPVVK	1		22		
MS-3	HELVQTPTTSK	1		98		
MS-3	HELLQTPTTSK	1		117		
MS-3	SAMDVWGQGTTVTVSSASTK	1		1		
MS-3	GLEWIGNMQYR	1		21		
MS-3	SGVAYYNPSLTTR	1		27		
MS-3	LNSVAAADTAFYYCAR	1		20		
MS-3	LNSVAAADTAIYYCAR	1		6		
MS-3	GLQWVANIK	1		1		
MS-3	DAPDCGGDCYSLPTVR	1		2		
MS-3	SVIAYYNPSLTGR	1		1		
MS-3	GLEWIGSVYK	1		6		
MS-3	SGIAFYNPSLTSR	1		2		
MS-3	NGIAYYNPSLTSR	1		24		
MS-3	EDGSESYYVDSVK	1		16		
MS-3	VTISVDTAK	1		2		
MS-3	HEFLQTPTTSK	1		1		
MS-3	HELVQTPATSK	1		76		
MS-3	NTLYLQMTSLR	1		10		
MS-3	VILSVDTSK	1		38		
MS-3	DHQWLVLGR	1		2		
MS-3	AEDTAVYYCANR	1		1		
MS-3	AEDTAVYYCVK	1		13		
MS-3	SVTAADTAMYFCAR	1		21		
MS-3	LTSVTAADTAVYYCVR	1		2		
MS-4	AEDTAVYFCAR	1			6	
MS-4	LSCAASNFR	1			11	
MS-4	NTLFLQMNSLR	1			6	
MS-5	NSLYLQMNTLR	1				3
MS-5	AEDTAVYYCSR	1				21
MS-5	NSLYLQMSSLR	1				3
MS-5	VTITADESTR*	1				16

MS-5	VGDTAIYYCAR	1		7
MS-5	AEDTALYYCAK*	1		14
MS-5	LNMSVDASK	1		47
MS-5	IYTSGSTNYNPSLK*	1		15
MS-5	NTLYLQMNSLK*	1		6
MS-5	VEDTALYYCAK	1		2
MS-5	QDGTDKYYVDSVK	1		34
MS-5	NSVYLQMHSLR	1		1

Table S4: "Patient-specific" and fully sequence-confirmed OCB peptides. OCB peptides were termed "patient-specific" if they were found in the same patient's CSF IgG proteome and transcriptome (column "Pts in VHref-CSF"). In this table, the first column (*CSF*) denotes the CSF in which the indicated peptide (*OCB Peptide*) was identified using mass-spectrometry. In column "*VHref-CSF*" numbers of individual IgG-VH sequences containing exact sequence matches of the indicated OCB peptides as found in each patient are shown. The same OBC peptides as in Table S3 are represented here, except for peptide VMGFYEDSGYR from patient MS-1 which was private to this patient in VHref-PB.

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Supplemental Figure S1

Supplemental F	igure S1							
	•	CDR1		CDR2			CDR3	
		CBITE		CBILE	_		00103	
GYUR81E01AETCT_MS1_CSF/1-125 G60B31IT02IK3SY_MS3_CSE/16-131	EVQLVESGGTLVKPGGSR	R L S C V G S G F S F Y S A WM Y W V R Q A P	GKGLEWVGLSK	G G G T D F A A P V	GRETISRDDSKKTLY	LHMNSLQTEDTGVYYCT	T D E G G N S G Y -	VFEYWGQGTLVSSAPTK
G50A0Cl02F9BG0_MS5_PBMC/14-127	P G G P V	R L S C A A S G F T F S N T WMGWV R Q A P	GKGLEWVGRIKSKTD	G G T T NY A A P V	KGRFTISRDDSKNTLYI	LQMNSLKTEDTAVYYCT	TD R	TVGATRDFGYWGQGTLVTVSSASTK
G7D8SE001DXTQT_MS4_CSF/1-124	- EVQLVESGEAWSTGGSL	R L S C A A S G F I V S D N Y M S W V R Q A P	G K G L E W V S L I Y S	G G S T Y Y A N S V	/ K G R F T I S R D N S K <mark>N T L F I</mark>	LQMN S L R <mark>AEDTAVY F C A</mark> •••	<mark>R</mark> D V F	DAWYDHR FDFWGLGTLVTVSSASTK
G57NQVN02IF79M_MS2_CSF/1-125		R L S C A V S G F I V S G G Y MT W V R Q A P	GKGLEWVSTIYRD	G AT S - Y A D T V	K G R F T V S R H S S N S T L S I	LQMNSLRTEDTAVYYCA	GGQTGYCTGG	IN SQR CYGMDVWGQGSTVIVSSASTK
G57NQVN02J4GFD_M52_C3F/1-151 G57NQVN02JZSBT_MS5_CSF/1-120	EVQLVESGGGLVQPGESL	R L S C A S G F T L N T HWT SWV RQAP	GKGLEWVANIKO D	G T D K Y Y V D S V	K GR F T I SR D N A K N S L Y I	LQMNSERTODIA VIICA	- G	FNPPIDYRGQG51VTV55A5TK
G57NQVN02FIMLX_MS2_CSF/1-127	EVQLVESGGGLVQPGGSL	R V S C V V S G F T V S S N Y I T W V R Q A P	GKGLEWVSVI-YS	G G D T Y Y A R S V	/ K G R F A V S R D N S K N T V Y	LQMN S L R A E D T G V Y Y C A K V K	G R Q L	- VHYYYGMDVWGQGTTVTVP SASTK
G6QB3UT02JITYB_MS3_CSF/1-135	QVQLVESGGGLVQPGGSL	RLSCVASDFTFSNYDMHWVRQAP	GKGLEWVALIWF D	G T H E Y Y R D S V	/ K G R F T I S R D N S K N T L Y I	LQMT S L R A E D T A M Y Y C A R K P	DRGYNLDDYGEY-	- K - PT SP F DYWGQ GT L V T V S S A ST K
GYUR81E01APMCR_MS1_CSE/1-126	EVOLVESGEAWSQ <u>PGGSL</u>	RIACTASGEREH NYEMNWVROAP	GKGLEWVAVISTD	SATIYYADSU	K G R F T T S R D N S R Y T L N K G R F T T S R D N A R N S V Y T	I OMH S I SA EDTA I YYCI	- ROLLWLD- GDT-	- I DYWGQGTLVTVSSASTK
G57NQVN02GRIQT_MS5_CSF/1-121	EVQVVESGGGLVQPGGSL	RLSCAASGFTFR SYWMSWVRQTP	GTGLEWVALINQ D	G S E N H Y V D S V	KGRFTISRDNAK <u>NALY</u>	LQMN SPRVGDTALYYCA	- RGSAVAG	NYWGQGTLVSVSSAPTK
G50A0Cl02GBX2E_MS5_PBMC/1-132	EVQLVESGEGLEQPGRSL	T L S C A A S G F T F D D Y S M H W V R Q A P	GRGLEWVSGINW N	S D A L G Y A D S V	/ R G R F T I S R D N A K <mark>N S L Y I</mark>	LQMSSLR <mark>AEDTALYYCA</mark>	- KEILRSKYDLW-	- SGYYKPFDIWGPGTMVTVSSASTK
G50A0CI02E9JWC_MS5_PBMC/1-131 G50A0CI02EU1N4_MS5_PBMC/1-127	EVOLVESGGGLVOPGRSL	KLSCAASGETED - EYSMHWVRQAP RISCAASGETED - DYAMHWVRQAP	GRGLEWVSGINW N	S DNLGYADSV	/ R G R F T T S R D N A K N S L Y I	LOMN SER AEDTALYYCA	- KEVLRSKYDLW-	- SGYYKPFDIWGPGIMVIVSSASIK
G7D8SE001AQ1AP_MS4_CSF/1-124	EVQLLESGGGLVQPGGSL	R L S C A A S N F R F R NY AM SWV R Q A P	GKGLEWVSDISG S	GGLTHHADFV	K G R F T I S R D N S K N T L Y I	LQMNSLRAEDTALYFCA	KSDDY-	DFHNIDSWGQGTLVIVSSASTK
GYUR81E01DMLKI_MS1_CSF/1-124	L L E S G G G L V Q P G G S L	R L S C A A S G F A F G S H A M T W V R Q A P	G R G L E W V S A I N G R	G G S T Y C A D S V	K G R F T I S R D N S N S T L Y	LQINNLRPEDTAVYFCA	- RGT GGGWY -	YR I H F D YWGR GA L V T V S S A S T K
G6QB3UT02JWZG1_MS3_CSF/16-138	LGRLGTAWGSL	R L S C A A S G F T F S S Y A M S W V R Q A P	GKGLEWVSGISG S	G G ST YYAV SV	K G R F T I S R D N S K N T L Y I	LQMNSLRAEDTAVYYCA	- NRYLVDSSGSY-	R D D P F D I W G Q G T M V T V S S A S T K
G50A0Cl02IEWIE_MS5_PBMC/1-129	GIVOPGGSI	R L S C A A S G F A F S S H A M S W V R Q A P R L S C A A S G F A F S G Y WMHW V R O V P	GKGLEWVSGISGS	G	/ K G R F T V S R D N S K K T L Y I / K G R F T I S R D N A K N T I Y I	LUMNSER AEDTAVYYC		- AGSPYYMDVWGKGTTVTVSSASTK
G6QB3UT02IX7GT_MS3_CSF/1-112		RLSCTTSGFISS SFWMSWVRQAP	GKGLEWVANIKE D	G S E K Y Y V D S V	KGRFTISRDNAKNSLF	LQMNSLRVEDTAVYYCV	- R DH QW-	- LVLGRRCDSWGQGALVTVSSASTK
G6QB3UT02H7XHJ_MS3_CSF/1-117	G L V Q P G G S L	R L S C A A S G F T F S N Y WMT W V R Q P P	GKGLEWVANIKE D	G <u>S G S Y Y V D S V</u>	/	LQMNSLRAEDTAVYYCA	- R R G T T -	- TPRGRTLDSWGQGTLVTVSSASTK
G6QB3UT02ITNCQ_MS3_CSF/1-126 G6QB3UT02IKD2S_MS3_CSF/1-121	EVQLVEVWGGLVQPGGSL	R L S C A A S R F T F S H F WMT W V R Q P P P L S C A A S G F S L P N Y WMS W V P O G P	GKGLEWVANIKE D	G SESYYVDSV	K G R F T M S R D N A K N S L Y I	LQMNSLRAEDTAVYYCA	- R R G A T -	- TPRGRTLDSWGQGTLVTVSSASTK
G6QB3UT025KBP MS3_C5F/10-132	GGGLIQPGGSL	R L S C A A P G F S F S T Y WMT W V R Q A P	RKGLEWVANIKQ D	G TEKYYVDSV	KGRFJISRDNAKNSLY	LQMNSLRAEDTGVYYCA	- RDYGSAT YY-	- ASYYHGMGVWGQGTTVTVSSASTK
G6QB3UT02JXJV4_MS3_CSF/14-136	R L G P A W G S L	R L S C A A S G F T F S S F WM S W V R Q A P	GKGLEWVANIKE D	G <u>SEK</u> YYVDSV	K G R F T T S R D N A K N L L Y	LQMNSLRAEDTAVYYCA	- R D A P D C G G D C Y -	- SLPTVRFDYWGQGTLVTVSPASTK
G6QB3UT02GPL8K_MS3_CSF/17-133	L GP A G G S L	R L S C A A S G F I F P N S WM S W V R Q A P	GKGLEWVANINP E	G NEK YYEGSV	K GR ST I SR DNAKNSLF	LQVNTLRADDTAVYYCA	- K DWT D A G	AVTNVFDYWGQGILVTVSSASTK
G5/NQVN02JVN5L_M55_C5F/12-136 GVLIB81E01AIV71_M51_C5E/7-125		R L S C A A S G F S F S I Y R M S W V R Q A P R I S C A A S G F S F S N F F M N W V R O A P	GKGLEGVANTNQQ	G SETSYVDSV	K GREALSR DNAKNSLY	OMNSLKVEDSGVYYCA	BRYFESSGPPFF-	TRPGNEDEWGQGTLVTVSSASTK
GYUR81E01CYU1J_MS1_PBMConly/1-116	TL	SLTCAVSGGSISPGSW-WSWVRQPP	GKGLEWIGEINH G	GSTNYNPSL	LKSRVFISVDKSKNQFS	LKLTSVTAADTAIYYCARVM	GEYEDSGYRYFT-	- GL NDYR GQ GT L V I V S ST ST K
G57NQVN01CN4DI_MS4_PBMConly/1-117	TL	S L T C S V S G L S I L S S N Y Y W A W I R Q S P	G K G L E W I G S I Y T T	G D S Y Y N P S L	K SRVA I SHDT SNNR <mark>V S</mark>	LSLSSLTAADTAVYYCASPP	SGRRGYTFDQFV-	- DV FEIWGHGTMVTVSAASTK
G6QB3UT02G5R2I_M53_C5F7/1-123 G6QB3UT02IVOR7_M52_C5F7/1-121		SLICTVSGGSISSGSHYWNWIHQRP	GKGLEWIGHIYYS	G S R DY NP SV D S S G S T Y Y NP S L	K SRVT I SVDA SKNQFSI	LEVSSVTVADTAVYFCARDY	DYGDKW	FDPWGQGTLVTVSSASTK
G60B3UT02105BN_MS3_CSF/T-124	OVRIGOWGAGLIKPSETL	SITCAVYGGSES FYYWTWIROTP	GKGLECIGEVNH S	G STNYKPSI	RSRVTISVDTSKNQFS	LK LR SVT AADT AV YYCRWGG	D	MDVWG0GITVTVSSASTK
G6QB3UT02GUOXE_MS3_CSF/10-133	SGPGLVKPSQTL	SLTCNVFGDSISNVGYYWSWVRQLP	GRGLEWIGHISH S	G T T Y Y N S T L	LK SR <mark>LT I SVDT SN</mark> NQF SI	L K L G S V T A A D T A V Y Y C A R G P	AVLRYFDRLLR	F D Y W G Q G A L V T V S S A S T K
G57NQVN02FGWNS_MS2_CSF/1-128	Q V Q L K E S G P G L V R P S Q T L	S L T C T V S G G S I S S G G Y F W S W F R Q H P	ETGLEWIGYVYY G	G I T SYTP SL	LESR LT I SMDT SR NQ F SI	L K L S S V T A A D T A M Y Y C A R R A	S P H H Y D G S G E	DYWGQGTLVIVSSASTK
G57NQVN02INEYU_MS5_CSF/1-127 G57NQVN02GMNER_MS2_CSE/1-124	Q V Q L Q E S G P G L V K P S Q T L	SETCAVSGGSESSGGYYWSWIRQHP SETCAVSGGSETRGGYCWSWVROLP	EKGLEWIGDIYHI GKGLEWIGYIYDS	G	LK SRLNM SV DA SK REFSI	L K L R S V I A A D A A V Y Y C A R R I L N L T S V T V A D T A V Y Y C G R D G	SKREGVNW RGRELIPEPG	FDPRGQGTLVSVSSASTK
G57NQVN02JN2K7_MS2_CSF/1-128	- VQLQESGPGLVKPSQTL	SLTCAVSGGSITSGGYCWSWVRQLP	GKGLEWIGYIYD S	G S T Y Y N P S L	L K S R V T V S V E T S K N Q F S I	LNLTSVTVADTAVYYCGRDG	R GRELLPFPG	F D S W G Q G T L V T V S S A S T K
G57NQVN02GQN5J_MS2_CSF/1-121	G S G P G L V K P S E T L	S L T C T V S G G S I S S S T Y Y W G W I R Q P P	GKGLEWIGSIYY S	G S T Y Y N P S L	LK SRVIISVAT SKNQFS	LKLTSVTAADTAVYYCAGD-	<u>G S G S Y Y T R</u>	<mark>F DQWGQ GT L V T V S S A S T K</mark>
G6QB3UT02GJFMW_MS3_CSF/1-127 G6QB3UT02IB65C_MS3_CSF/1-128	Q L Q L Q E S G P G L V K P S E I L	SLICIVPGGSIISSNYYWGWIRQPP TITCSVSGGSITSSRYYWSWIROPPGK	GKGLEWIGSVFW S	G SI YYSASL	LKGRVIISVDISKNQFS TSRVIVSVDTSKSOFS	LR LSSVIAADIGIYYCASSI	GITLER BSH	EGPWGQGTLVSVSSPSTK
G6QB3UT02HO603_MS3_CSF/1-128	QLHLQESGPGLVKPSKTL	TLTCSVSGGSITSSDYFWSWIRQPPRE	GAGVDWEYLQS	MIAYYNP 5 L	LT SRVIL SVDT SK SQFSI	LKLNSVAAADTAVYYCARHE	LVQTPATSK	F G P W G Q G T L V T V S S A S T K
G6QB3UT02HRXHV_MS3_CSF/1-128	QLHLRESGPGLVKTSKTL	T L T C T V S G D S I S S N D Y Y W G W I R Q P P	GKGLEWIGSVYK S	G L A Y Y N P S L	LSSRAIVSLDTSKSQFS	L K L N S V A A A D T A V Y Y C A R H E	<u> </u>	F G P W G Q G T L V T V S S A S T K
G6QB3UT02JD1AB_MS3_CSF/1-128 C6OD3UT03WTUB_MS3_CSF/1-127	Q L H L Q E S G P G L V K P S K T L	T L T C S V S G G S I A S S D Y FWSR I R Q P P	GKGLEWIGSIYK S	MIAYYNPSL	LT SR <mark>VILSVDT SK</mark> SQFSI	L K L N S V A A A D T A V Y Y C A R H E	LVQTPATSK	F G P W G Q G T L V T V S S A S T K
G60B3UT02F2AMC_MS3_CSF/1-127 G60B3UT02F2AMC_MS3_CSF/1-128	OI HIOFSGPGIVKPSKTL	TITCSVSGGSITSSDYYWSWIRQPP	GKGLEWIGTITKS	MIATTNF3L	T SRV I V SVDT SK SQFS	LK LN SVAAADTAVTTCARHE	I VOTPATSK	FGPWG0GTIVTVSSASTK
G6QB3UT02F5Z4X_MS3_CSF/1-128	QLHLQESGPGLVKPSKTL	T L T C S V S G G S V T S S D Y Y W S W I R Q P P	GKGLEWIGSIYK S	GIAYYNP 5 L	L T S R V I V S V D T S E S Q F S I	L K L S S V A A A D T A V Y Y C A R H E	LVQTPTTSK	F G P W G Q G T L V T V S S A S T K
G6QB3UT02JZ4CE_MS3_CSF/1-128	Q L H L Q Q S G P G L V K P S K T L	T L T C S V S G G S I T S S H Y F W S W I R Q P P	GKGLEWIGSIYK S	G I A Y Y N P S L	LT SRVIVSVDT SK SQFSI	L K L N S V A A A D T A V Y Y C A R H E	LVQTPTTSK	F G P W G Q G T L V T V S S A S T K
G6QB3U102H647D_MS3_CSF/1-128 G6QB3UT02GCAPL_MS3_CSF/1-128		T L T C S V S G G S L T S S D Y Y W S W I R Q P P T L T C S V S G G S L T S S R Y Y W S W I R Q P P	GKGLEWIGSIYK N	G I A Y HNP S L	T SRVIVSVDT SK SQFSI	LK LN SVAAADTAVYHCARHE	AVQIPIISK	FGPWGQGTLVTVSSASTK
G6QB3UT02UHI3_MS3_CSF/1-128	Q L H L Q E S G P G L A K P S K T L	T L T C S V S G G S I T S S R Y Y W S W I R Q P P	GKGLEWIGTIYR S	G I A Y H N P S L	LT SRVIVSVDT SK SQFSI	LKLNSVAAADTAVYYCARHE	LVQTPATSK	F G P W G Q G T L V T V S S A S T K
G6QB3UT02FX7IG_MS3_CSF/1-128	QLHLQESGPGLVKPSKTL	T L T C S V S G G S I T S S R Y Y W S W I R Q P P	GKGLEWIETIYR S	G I A Y Y N P S L	L T S R V I V S V D T S K S Q F S I	L K L N S V A A A D T A V Y Y C A R H E	L V Q T P A T S K	F G P W G Q G T L V T V S S A S T K
G6QB3UT02FWUTZ_MS3_CSF/1-128	Q L H L Q E S G P G L V K P S K T L	T L T C S V S G G S I T S S R Y Y W S W I R Q P P	GKGLEWIGTIYG S	GIAYYNPSL	LT SRVIVSVDT SK SQFSI	L K L N S V A A A D T A V Y Y C A R H E	LVQTPATSK	F G P W G Q G T L V T V S S A S T K
G6QB3UT02HQ21_M35_C3F/1-128 G6QB3UT02HKY3C_MS3_C3F/1-128	QLHLQESGPGLVKPSKTL	TLTCSVSGGSITSSAYYWSWIRQPP	GKGLEWIGSIYK N	GIAYYNP SL	T SRVIV SVDT SK SQFSI	LK LN SVAAADTA VII CARHE	LVQTPTTSK	FGPGGQGTLVTVSSASTK
G6QB3UT02FS9PL_MS3_CSF/1-128	QLHLQESGPGLVKPSKTL	T L T C S V S G G S I T S S D Y N W S W I R Q P P	GKGLEWIGSIYK S	G I A F Y N P S L	LT SR <mark>VIVSVDT SK SQFSI</mark>	L K L N S V A A A D T A V Y Y C A R <mark>H E</mark>	L V Q R P T I S K	F G P W G Q G T L V T V S S A S T K
G6QB3UT02IMN17_MS3_CSF/1-125	LQESGPGLVKPSKTL	T L T C S V S G G S I T S S D Y Y W S W I R Q P P	GKGLEWIGSISK S	G I A Y Y N P S L	LTTR LIVSVDTSK SQFSI	L K L N S V A A A D T A V Y Y C A R H E	FLQTPTTSK	F G P W G Q G T L V T V S S A S T K
G6QB3UT02G95GB_M53_CSF/1-128 G6QB3UT02IZ8ZH_MS3_CSE/1-128	Q L H L Q E S G P G L V K P S K T L	T L T C S V S G G S T T S S D Y Y W S W I R Q P P T L T C S V S G G S I T S S D Y Y W S W I R Q P P	GKGLEWIGSISK N	G A YYNPSI	TTRLIVSVDTSK SQFS	L K L N S V A A A D T A V Y Y C V R H E	LLQIPIISK	
G6QB3UT02J31X9_MS3_CSF/1-128	Q L H L Q E S G P G L V K P S K T L	TLTCSVSGGSITSSDYYWSWIRQPP	GKGLEWIGSISK S	G VAYYNP S L	TTRLIVSVDTSK SQFSI	LKLNSVAAADTAVYYCARHE	LLQTPTTSK	F D P W G Q G T L V T V S S A S T K
G6QB3UT02I3O34_MS3_CSF/1-128	Q L H L Q E S G P G L V K P S K T L	T L T C S V S G G S I T S S D Y Y W G W I R Q P P	G K G L E W I G S I S K S	G I A Y Y N P S L	LTTR <mark>LIVSVDTSKGQFS</mark> I	L K L N S V A A A D T A I Y Y C A R <mark>H E</mark>	LLQTPTTSK	F G P W G Q G T L V T V S S A S T K
G6QB3UT02G1M1M_MS3_CSF/1-128	Q L H L Q E S G P G L V K P S K T L	T L T C S V S G G S I T S S D Y Y W S W I R Q P P	GKGLEWIGSTSKS		TTRLIVSVDT SK SQFSI	LKLNSVAAADTAVYYGARHE	LLQTPSTSK	FGPWGQGTLVTVASASTK
G60B3UT02F4TF0_M55_C5F/1-125 G60B3UT02I251X_MS3_C5F/1-119	G3GPGLVKP3KTL	T L T C S V S G G S I T S SA TT W S W I R Q P P T L T C S V S G G S I T N S D Y Y W S W I R O P P	GKGLEWIGSISK S	GIAYYNP SL	TTRLIVSVDTSK SQFSI	K LNSVAAADTAFTTCARHE	LLOTPTTSK	FGPWGQGTLVTV55A5TK
G6QB3UT02HK9YT_MS3_CSF/1-121	GP G L V K P S K T L	T L T C S V S G G S I T S S D Y Y W S W I R Q P P	GKGLEWIGSISK S	G VAYYNP S L	LTTR LIVSVDT SK SQFSI	L K L N S V A A A D T A V Y Y C A R H E	LLQTPSTSK	F G P W G Q G T L V T V S S A S T K
G6QB3UT02HE789_MS3_CSF/1-121	GP G L V K P S K T L	T L T C S V S G G S I T S S A Y Y W S W I R Q P P	GKGLEWIGSISK S	<u>G</u> V A Y Y N P S L	TTRLIVSVDTSK SQFS	L K L N S V A A A DM A V Y Y C A R H E	LLQTPTTSK	F G P W G Q G T L V T V S S A S T K
G6QB3U102F6M10_MS3_CSF/1-124 G6QB3U102F6M10_MS3_CSF/1-124	VCPCLVKPSKIL	ILICSVSGGSIISSDYYWSWVRQPP	GKGLEWIGSIYKS	GSTYK SVTAYYNPSL	LIGRVIVSVDISK SQFS	LKLNSVAAADTAVYYCARHE	LVQTPTTSK	MDVWGQGTLVTVSSASTK
G57NQVN02G9Q5T_MS2_CSF/1-128	Q V Q L Q E S G P G L V K P S E T L	SLTCTVSGGSIG TYYWNWIRQPP	GKGLEWIGHIYY S	G STNYNP SL	LESRVTISVDTSNNHFSI	K LR SVTAADTAVYYCARGS	DILTGYSLGGW	FDPWGQGTLVTVSSASTK
G6QB3UT02I9C92_MS3_CSF/1-129	QVQLQESGPGLVKPSETL	S L T C T V S G G P I S T Y Y W S W I R Q P P	G K G L E W I G Y I Y Y S	G S T D Y N P S L	LKNR <mark>VT I SVDT SK</mark> NQFSI	LK LR SVTAADTAMYFCAR	T Y G S G T Y S -	- R D Y Y Y G M D V W G Q G T T V T V S S A S T K
G57NQVN02IIHBO_MS2_CSF/1-128	Q V Q L Q E S G P G L V K P S E T L	SLTCTVSGASIS TYDWSWIRQPP	GKGLEWVGYIYY S	G ST NY NP S L	LKSR <mark>VTISVVPSK</mark> NQFSI	LKLTSVTAADTAVYYCAKRA	T Y C D G K R C -	- SRA FDYWGQGTPVIVSSASTK
G0QB30102JQD2P_M53_C5F/1-132 G50A0Cl02H5IOQ_MS5_PRMC/1-127	Q V Q L Q E S G P G L V K P S Q T L Q V Q L Q E S G P G L V K P S Q T L	SLICIVSGDSISSGGYYWNWIRQHP SLTCTVSGGSISSGSYYWSWTRPPA	GKGLEWIGTIYN I	G ST NY NP SL	K SRVTMSVDTSKNQFS	LKLSSVTAADTAVYYCVRS-	KYDILÍGY-	 TDKGHAFHTWGQGTKVTVSSASTK SPYYYYMDAWGKGTTVTVSSASTK
G57NQVN02J36GA_MS2_CSF/1-125	QVQLQESGPGLVKPSQTL	SLTCTVSGGSFNSADYYWSWIRQHP	GKGLEWIGYIHY S	<u>G</u> STYYNP SL	LKSRLTISLDTSKNQLS	LKLSSVTAADTAVYHCAR-	VD-	- RTAGYYFDNWGQGTLVTVSSASTK
G6QB3UT02F4CAN_MS3_CSF/1-124	Q L Q E S G P G L V R P S E T L	SLICTVSGGSLSGSTYYWGWIRQPP	GKGLEWIGSIHS G	G ST Y Y N P V V	K SRVIISVDT SKNHFSI	L N L S S V T A S D T A V Y Y C A S P -	R A -	- I G A T G P F D Y W G Q G T L V A V S S A S T K
G6QB3UT02GS7NF_MS3_CSF/1-137	Q L Q L Q E S G P G L V K P S E T L	S L S C T V S G G S N S S D N Y YWGW I RQAP	GKELEWIGTIYE S	G ST YYNP SL	LK SR <mark>VT I SVDTAK</mark> NQFSI	LNLSSVTAADTAVYYCARHI	ALPARAMYYHDT -	- IGTPGPLDFWGQGTLVTVSSASTK
G57NQVN02G88TV_MS2_CSF/1-125 G57NQVN02G88TV_MS2_CSF/1-129	O L O F S G P G L V K P S F T L	SET CTVSGDSTTSSAY - WAWEROPP	GKGLEWIGSIYYS	0STEYNPSI	L N S K V A L S A D A P K N H F F I L K G R V T L S V D T S R N H F S I	LNLISVIAIDIAMYYCAR LELISVIAADTAVYYCARH-		- PRELSPHSDWGQGTLVTVSSASTK - RAFENPEDYWGOGALVTVSSASTK
G57NQVN02I0UJB_MS2_CSF/1-119	GLVKPSETL	SLTCTVSGGSIASSTYYWGWIRQPP	GKGLEWIGFVYY T	ESTYYKSSL	LKSRVTISVDTSKNQFSI	LKLSSVTAADTSVYYCVA	VR YFA-	- WSAGK LFDYWGQGTLVTVSSASTK
GYUR81E01CCVMB_MS1_CSF/1-117	P G L V K P S E T L	S L T C N V S G G S L S R Y Y W S W I R Q P P	G K G L E W I G Y I Y Y G	G T T K Y N P S F	EKRR <mark>VAMSIDT SRN</mark> QESI	L K L T S V T A A D T A K Y Y C A R S G	P G -	- G E P V Y Y F D P W G Q G T L V S V S S A S T K
G50A0Cl02l2QUX_MS5_PBMC/1-128	Q V Q L V Q S G A E V K K P G S S V	KVSCKVSGDTFSNYAISWVRQAP	GEGLEWMGNVIP L	FGSRHYAQKF	FQGR <mark>VTITADESTR</mark> TGY'	ELSSPTSEDTAVYYCAPGI	- YIAGAGGKTY	FDYWGQGTLVAVSSASTK
G3718Q21023023F_m32_C3F/1-129	LVQLOQJOACOENAGESL	KIJCKVJOTDED- NDWIOWVKQKP	OQUEEWWOMITPG	De construction de la constructi	QUQUIT SAUK SISTAT	L STRUCE KAST AMELICAR BE	ALCHOILDMICA	

identical or very similar colors do not necessarily indicate identical OCB peptides. For additional information refer to Table S3.