A	CDRH1	CDRH2	CDRH3
1023	ESGAELVKPGASVKLSCKASGYTFTSY	YWMQWVKQRPGQGLEWIGEIDPSDSYTNYNQKFKGKATLTVDISSSTAYMQ	LSSLTSEDSAVYYCARGLRRYFDVWGTGTTVTVSS
1005		YWMDWVKQRPGQGLEWIGNIYPSDSETHYNQKFKDKATLTVDKSSSTAYMQ	
1012	ESGAELVKPGASVKLSCKASGYTFTSY	YWMHWVKQRPGQGLEWIGMIHPNSGSSNYNEKFKSKATLTVDKSSSTAYMQ	2LSSLTSEDSAVYYCAREAWGTVYAMDYWGQGTSVTVSS
1021	ESGAELVKPGASVKLSYKASGYTFTSY	YWMHWVKQRPGQGLEWIGMIHPNSGSSNYNEKFKSKATLTVDKSSSTAYMQ	2LSSLTSEDSAVYYCAREAWGTVYAMDYWGQGTSVTVSS
1014	ESGPELVKPGASVKISCKASGYTFTDY	YYMNWVKQSHGKSLEWIGDINPNNGGTSYNQKFKGKATLTVDKSSSTAYME	LRSLTSEDSAVYYCARELRPPDYAMDYWGQGTSVTVSS
1002	ESGPELVKPGASVKISCKASGYAFSSS	SWMNWVKQRPGKGLEWIGRIYPGDGDTNYNGKFKGKATLTADKSSSTAYMQ	LSSLTSEDSAVYFCANAVVADYWGQGTTLTVSS
1003	ESGPELVKPGASVKISCKASGYAFSSS	SWMNWVKQRPGKGLEWIGRIYPGDGDTNYNGKFKGKATLTADKSSSTAYMQ	LSSLTSEDSAVYFCARYEYFDYWGQGTTLTVSS
1011	ESGPELVKPGASVKISCKASGYAFSSS	SWMNWVKQRPGKGLEWIGRIYPGDGDTNYNGKFKGKATLTADKSSSTAYMQ	LSSLTSEDSAVYFCARSLGYFDYWGQGTTLTVSS
1004	ESGPELVKPGASVKISCKASGYSFTSY	YYIHWVKQRPGQGLEWIGWIYPGSGNTKYNEKFKGKATLTADTSSSTAYMQ	LSSLTSEDSAVYYCGGAQATDYWGQGTTLTVSS
8-18C	5 ESGAGLVKPGASVEISCKATGYTFSSF	FWIEWVKQRPGHGLEWIGEILPGRGRTNYNEKFKGKATFTAETSSNTAYMQ	LSSLTSEDSAVYYCATGNTMVNMPYWGQGTTVTVSS
1013	ESGAELVRPGASVKLSCTASGFNIKDI	DYMHWVKQRPEQGLEWIGWIDPENGDTEYASKFQGKATITADTSSNTAYLQ	2LSSLTSEDTAVYYCTTGGNYEVDYFDYWGQGTTLTVSS
1009	ESGGGLVQPKGSLKLSCAASGFSFNTY	YAMNWVRQAPGKGLEWVARIRSKSNNYATYYADSVKDRFTISRDDSESMLYLQ	MNNLKTEDTAMYYCVSYYYGSSYAMDYWGQGTSVTVSS
1010	ESGGGLVQPKGSLKLSCAASGFSFNTY	YAMNWVRQAPGKGLEWVARIRSKSNNYATYYADSVKDRFTISRDDSESMLYLQ	MNNLKTEDTAMYYCVSYYYGSAWYFDVWGTGTTVTVSS
1019	ESGGGLVQPGGSMKLSCAASGFTFSDA	AWMDWVRQSPEKGLEWVAEIRKKANNHATCYAESVKGRFTISRDDSKSSVYLQ	MNSLRAEDTGIYYCTLSFYAMDYWGQGTSVTVSS
1022	ESGGGLVKPGGSLKLSCAASGFTFSSY	YAMSWVRQSPEKRLEWVATISNGGVYTYYPDNVKDRFTISRDNAKNSLFLQ	MSHLRSEDTAMYYCARDNGINFYYFDYWGQGTALTVSS
1001	ESGPALVKPSQTVSLTCTVTGYSITNGNH	HWWNWIRQVSGSRLEWIGFISSSGSTDSNPSLKSRISITRDTSKNQLFLQ	LNSVTTEDIATYYCARDDYDGLDYWGQGTSVTVSS
	*** **:* ::.:: .: <mark>*: :.</mark>	*::* ***:. * ::.:: :::: ::::	: : :*: . *:* ***::****

В	V CDRL1	CDRL2	CDRL3
1003	K5M5M5VGERVTLSCKASENVGTYV	WYQQKPEQSPKLLIYGASNRYIGVPDRFIGSGSATDFTLI	IISSVQAEDLADYHCGQSYSYPYTFGGGTKLEIKR
1012	KSMSMSVGERVTLSCKASENVGTYV	WYQQKPEQSPKLLIYGASNRYTGVPDRFTGSGSATDFTLI	ISSVQAEDLADYHCGQSYSYPYTFGGGTKLEIKR
1011	KSMSMSVGERVTLSCKASENVGTYV	WYQQKPEQSPKLLIYGASNRYTGVPDRFTGSGSATDFTLT	ISSVQAEDLADYHCGQSYSYPFTFGSGTKLEIKR
1019	SSLAVSVGEKVTMSCKSSQSLLYSSIQKNYL	WYQQKPGQSPKLLIYWASIRESGVPDRFIGSGSEIDFILI	ISSVKAEDLAVYYCQQYYSYPYIFGGGTKLEIKR
8-18C	5 SSLAVSAGEKVTMSCKSSQSLLNSGNQKNYL	WYQQKPGLPPKLLIYGASTRESGVPDRFTGSGSGTDFTLT	ISSVQAEDLAVYYCQNDHSYPLTFGAGTKLEIKR
1023	AIMSASPGEKVTMTCSASSSVTYI	WYQQKPGSSPRLLIYDTSNLASGVPVRFSGSGSGTSYSLT	ISRMEAEDAATYYCQQWNNYPPTFGAGTKLELKR
1004	AILSVSPGERVSFSCRASQSIGTSI	WYQQRINGSPRLLIMYASESISGIPSRFSGSGSGIDFILS	SINSVESEDIADYYCQQSNSWPFIFGSGIKLEIKR
1001	ASLSVSVGETVTITCRASENIYSNL	WYQQKQGKSPQLLVYAATNLADGVPSRFSGSGSGSGTQYSLF	KINSLQSEDFGSYYCQHFWGTPWTFGGGTKLEIKR
1021	ASLSVSVGETVTITCRASENIYSNL	WYQQKQGKSPQLLVYAATNLADGVPSRFSGSGSGSGTQYSLF	KINSLQSEDFGSYYCQHFWGTPYTFGGGTKLEIKR
1014	ASLSVSVGETVTITCRASENIYSNL	WYQQKQGKSPQLLVYAATNLADGVPSRFSGSGSGSGIQYSLK	KINSLQSEDFGSYYCQHFWGIRIFGGGIKLEIKR
1002	SSLSASLGERVSLTCRASQDIGSSL	WLQQEPDGTIKRLIYAISSLDSGVPKRFSGSRSGSDYSLI	ISSLESEDFVDYYCLQYASSPWTFGGGTKLEIKR
1013	SSLSASLGERVSLTCRASQDIGSSL	WLQQEPDGTIKRLIYATSSLDSGVPKRFSGSRSGSDYSLI	ISSLESEDFVDYYCLQYASSPWIFGGGTKLEIKR
1022	SSMYASLGERVTITCKASQDINSYL	WFQQKPGKSPKTLIYRANRLVDGVPSRFSGSGSGQDYSLI	ISSLECEDMGIYYCLQYDEFPLTFGAGTKLELKR
1010	SYLAASPGETITINGRASKSISKYL	WYQEKPGKTNKLLIYSGSTLQSGIPSRFSGSGSGTDFTLI	ISSLEPEDFAMYYCQQHNEYPFGSGTKLEIKR
1005	ASLAVSLGQRATISCRASKSVSTSGYSYM	WYQQKPGQPPKLLIYLASNLESGVPARFSGSGSGTDFTLN	VIHPVEEEDAATYYCQHSRELPWIFGGGTKLEIKR
1009	ASLAVSLGQRATISYRASKSVSTSGYSYM	WNQQKPGQPPRLLIYLVSGVPARFSGSGSGIDFILN	VIHPVEEEDAATYYCQHIRELIRSEGGPSWSFGGGTKLEIKR
	1 * *1 11. 1*1	* *: : *: . *:* **:** * .::*.	* :: ** *: *: * * ***::**

Figure S1. Sequence alignment of the V_H (A) and V_L (B) domain sequences of the mAbs indicates a diverse repertoire. Amino acid sequences of V_H and V_L domains of anti hMOG mAbs and 8-18C5 were aligned using the Clustal-W (http://www.ebi.ac.uk/Tools/msa/clustalw2/). The numbering is based on Kabat database (1). Arrowhead indicates sixth and ninth residue from the N-terminus in V_H and V_L , respectively. Primer encoded sequences are not shown. CDRs are shown boxed.

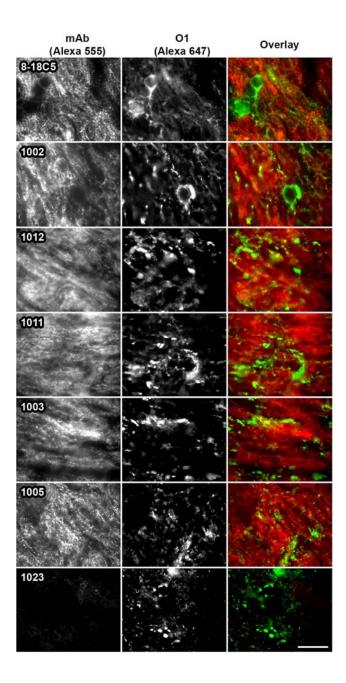


Figure S2. Staining patterns of the anti-MOG mAbs that exacerbate EAE are similar. Spinal cord sections of C57BL/6 mice were co-stained with 50 μ g/ml Alexa 555-labeled anti-MOG antibodies (pseudocolored red in overlay) and Alexa 647-labeled anti-oligodendrocyte marker O1 (pseudocolored green in overlay). Each image for the EAE-exacerbating mAbs was adjusted individually to similar intensity levels. MAb 1023 stains at background levels and was used as control (images for staining by mAb 1005 and mAb 1023 were processed analogously). Scale bar represents 20 μ m.

REFERENCES

1. Kabat, E. A., T. T. Wu, H. M. Perry, K. S. Gottesman, and C. Foeller. 1991. *Sequences of proteins of immunological interest*. U.S. Dept. of Health and Human Services.