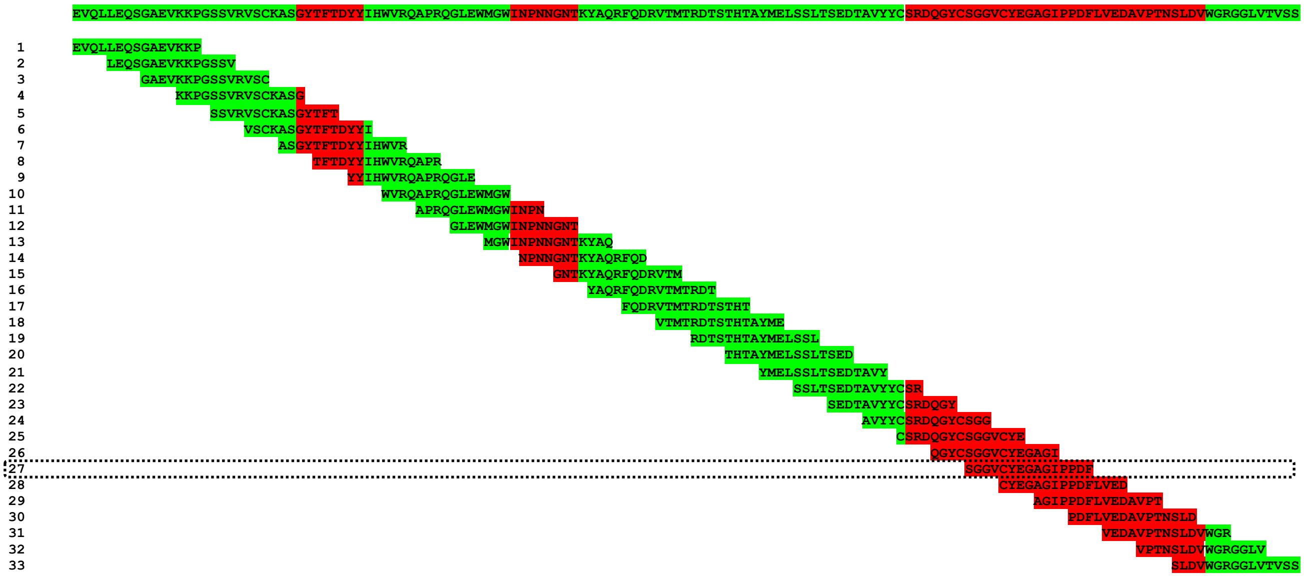
Figure S1

a

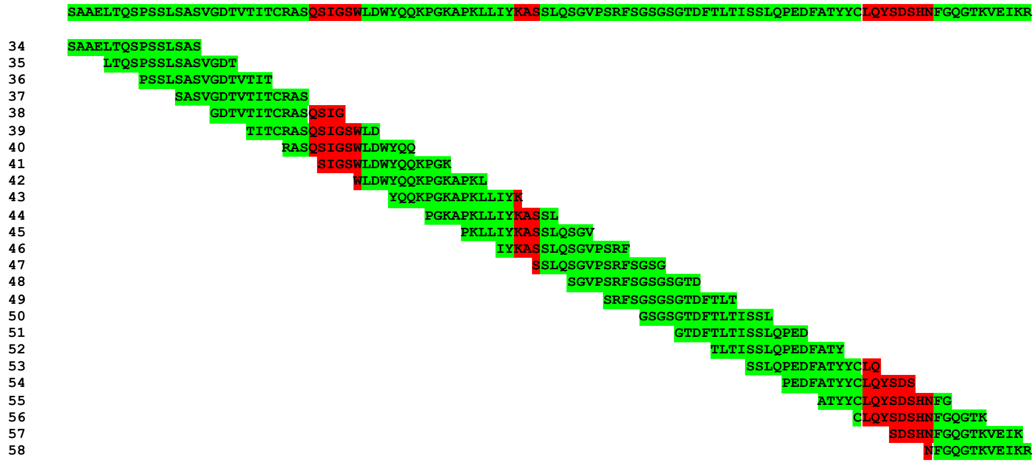
5L7 Heavy chain variable region - overlapping peptides



EVQLLEQSGAEVKKPGSSVRVSCKASGYTFTDYYIHWVRQAPRQGLEWMGWINPNNGNTKYAQRFQDRVTMTRDTSTHTAYMELSSLTSEDTAVYYCSRDQGYCSGGVCYEGAGIPPDFLVEDAVPTNSLDVWGRGGLVTVSS

1 EVQLLEQSGAEVKKP
2 LEQSGAEVKKPGSSV
3 GAEVKKPGSSVRVSC
4 KKPGSSVRVSCKASG
5 SSVRVSCKASGYTFT
6 VSCKASGYTFTDYYI
7 ASGYTFTDYYIHWVR
8 TFTDYYIHWVRQAPR
9 YYIHWVRQAPRQGLE
10 WVRQAPRQGLEWMGW
11 APRQGLEWMGWINPN
12 GLEWMGWINPNNGNT
13 MGWINPNNGNTKYAQ
14 NPNNGNTKYAQRFQD
15 GNTKYAQRFQDRVTM
16 YAQRFQDRVTMTRDT
17 FQDRVTMTRDTSTHT
18 VTMTRDTSTHTAYME
19 RDTSTHTAYMELSSL
20 THTAYMELSSLTSED
21 YMELSSLTSEDTAVY
22 SSLTSEDTAVYYCSR
23 SEDTAVYYCSRDQGY
24 AVYYCSRDQGYCSGG
25 CSRDQGYCSGGVCYE
26 QGYCSGGVCYEGAGI
27 SGGVCYEGAGIPPDF
28 CYEGAGIPPDFLVED
29 AGIPPDFLVEDAVPT
30 PDFLVEDAVPTNSLD
31 VEDAVPTNSLDVWGR
32 VPTNSLDVWGRGGLV
33 SLDVWGRGGLVTVSS

5L7 Light chain variable region - overlapping peptides



SAAELTQSPSSLSASVGDTVTITCRASQSIGSWLDWYQQKPGKAPKLLIYKASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCLQYSDSHNFGQGTKVEIKR

34 SAAELTQSPSSLSAS
35 LTQSPSSLSASVGDT
36 PSSLSASVGDTVTIT
37 SASVGDTVTITCRAS
38 GDTVTITCRASQSIG
39 TITCRASQSIGSWLD
40 RASQSIGSWLDWYQQ
41 SIGSWLDWYQQKPGK
42 WLDWYQQKPGKAPKL
43 YQQKPGKAPKLLIYK
44 PGKAPKLLIYKASSL
45 PKLLIYKASSLQSGV
46 IYKASSLQSGVPSRF
47 SSLQSGVPSRFSGSG
48 SGVPSRFSGSGSGTD
49 SRFSGSGSGTDFTLT
50 GSGSGTDFTLTISSL
51 GTDFTLTISSLQPED
52 TLTISSLQPEDFATY
53 SSLQPEDFATYYCLQ
54 PEDFATYYCLQYSDS
55 ATYYCLQYSDSHNFG
56 CLQYSDSHNFGQGTK
57 SDSHNFGQGTKVEIK
58 NFGQGTKVEIKR

b

Comparison of full length CDR-H3 peptides and peptides 27

```
SRDQGYCSGGVCYEGAGIPPDFLVEDAVPTNSLDV        5L7 full_CDR-H3
ARDLGYCSDGVCYDGAGIPPDFIGIPAVPMNSLDV        4L6 full_CDR-H3
         SGGVCYEGAGIPPDF                  5L7 pep27_CDR-H3
         SDGVCYDGAGIPPDF                  4L6 pep27_CDR-H3
```

Figure S1. Amino acid sequences of the overlapping peptides used in the Pepscans. (a) Oligopeptides spanning both the heavy chain variable region (upper part) and the light chain variable region (lower part) of 5L7 IgG1. Corresponding residues to the CDRs are indicated in red. Peptide 27 is boxed for clarity. Peptides were 15-mer in length and overlapped by 11. **(b)** Alignment of full-length CDR-H3 peptides and corresponding peptides 27 for both 5L7 IgG1 and 4L6 IgG1. Amino acid differences are underlined and colored in blue.