

Table 9.3 Summary of mutants as a result of performing mutations in the complementary determining region (CDR) sequence of mAb1 and mAb2. Bold amino acid residues are charged residues in the CDR sequences of the mAbs

CDR	Light chain 1 ^a	Light chain 3 ^a	Heavy chain 3 ^b	The rest of the CDR	Description
mAb1 mAb2 M1	QSV DY DGDSYMN Q— DV NTAVA Q— DG DSYMN	HED PYT Y TTPPT HED PYT	G S H Y F G H W H F A V W W G G D G F Y A M D Y W G S H Y F G H W H F A V W	mAb1 LC and HC mAb2 LC and HC mAb1 LC and HC	mAb1 WT mAb2 WT mAb1 with SVDY deletion in LC1
M5	QSV DY AGNSYMN	Y TTPYT	G S H Y F G H W H F A V W	mAb1 LC and HC	mAb1 with substitution in LC1 and LC3
M6	QSV DY DGDSYMN	HED PYT	G S G Y F G Y W M F A V W	mAb1 LC and HC	mAb1 with substitution in HC3
M7	QSV DY AGNSYMN	Y TTPYT	G S G Y F G Y W M F A V W	mAb1 LC and HC	mAb1 with substitution in LC1, LC3, and HC3
M10	E — DV DTAVA	HED PPT	W G H D G F H A H D Y W	mAb2 LC and HC	mAb2 with substitution in LC1, LC3, and HC3
M11	QSV DY DGDSYMN	HED PYT	G S H Y F G H W H F A V W	mAb1 LC and HC; made in <i>Escherichia coli</i>	Aglycosylated mAb1

Numbers 1 and 3 correspond to the different loops of the variable regions (LC light chain; HC heavy chain) in the CDR.

^aMutations performed in the variable light (VL) chain sequence.

^bMutations performed in the variable heavy (VH) chain sequence.

From [Yadav, Sreedhara et al. \(2011\)](#).