

Table S1. Sequence alignment of 1F1 and 1I20 heavy chains (GenBank GI: 309753504 and GI:163931316, respectively). The amino-acid residue numbering follows the Kabat scheme to be consistent with the numbering in other crystal structures in the PDB. The framework/loop definitions are based on the international ImMunoGeneTics information system (IMGT).

FR=framework, CDR-H1-3=heavy chain complementarity determining regions 1, 2, or 3

	FR1		CDR-H1		FR2		CDR-H2		
	10	20	30	40	50				
	1234567890123456789012345	67890123	45678901234567890	12A34567					
1F1H	EVQLVQSGGGVVP	RRSLRLS	CAAS	GFTFSSYA	MHWVRQAPGK	GLEWVAV	ISYDGRNK		
1I20HE.....GG.....I..	A.NLGIFGF	.R...GKT					
	FR3			CDR-H3			FR4		
	60	70	80	90	100			110	
	8901234567890123456789012	ABC3456789012	34567890	ABCDEFGHI12	3456789012				
1F1H	YYADSVKGRFTVSR	DNSKNTLYLQ	MNSLRAEDTSVYYC	ARELLMDYYDHIGY	SPGPT-	WGQGLVTVS			
1I20H	F.....I.....T...AL...	..DATA...GPGS	.PNWLDP					