

IgG1f	SEQ ID NO:278	SEQ ID NO:293	SEQ ID NO:280	SEQ ID NO:282	NO:283
IgG1-IgG2-IgG1f2	IgG1 wildtype SEQ ID NO:278	IgG2 wildtype SEQ ID NO:291	IgG1 wildtype SEQ ID NO:280	IgG1 wildtype SEQ ID NO:282	SEQ ID NO:287
IgG1-IgG2CS-IgG1f	IgG1 wildtype SEQ ID NO:278	IgG2C219S/IgG1 SEQ ID NO:294	IgG1 wildtype SEQ ID NO:280	IgG1 wildtype SEQ ID NO:282	SEQ ID NO:284
IgG1-IgG2CS-IgG1f2	IgG1 wildtype SEQ ID NO:278	IgG2 C219S SEQ ID NO:292	IgG1 wildtype SEQ ID NO:280	IgG1 wildtype SEQ ID NO:282	SEQ ID NO:288
IgG2-IgG1f	IgG2 wildtype SEQ ID NO:279	IgG2/IgG1 SEQ ID NO:293	IgG1 wildtype SEQ ID NO:280	IgG1 wildtype SEQ ID NO:282	SEQ ID NO:223
IgG2-IgG1f2	IgG2 wildtype SEQ ID NO:279	IgG2 wildtype SEQ ID NO:291	IgG1 wildtype SEQ ID NO:280	IgG1 wildtype SEQ ID NO:282	SEQ ID NO:289
IgG2CS-IgG1f	IgG2 wildtype SEQ ID NO:279	IgG2C219S/IgG1 SEQ ID NO:294	IgG1 wildtype SEQ ID NO:280	IgG1 wildtype SEQ ID NO:282	SEQ ID NO:225
IgG2CS-IgG1f2	IgG2 wildtype SEQ ID NO:279	IgG2 C219S SEQ ID NO:292	IgG1 wildtype SEQ ID NO:280	IgG1 wildtype SEQ ID NO:282	SEQ ID NO:290
IgG1-IgG2-IgG1.1f	IgG1 wildtype SEQ ID NO:278	IgG2 wildtype SEQ ID NO:291	IgG1 A330S/P331S SEQ ID NO:281	IgG1 wildtype SEQ ID NO:282	SEQ ID NO: 285
IgG1-IgG2CS-IgG1.1f	IgG1 wildtype SEQ ID NO:278	IgG2 C219S SEQ ID NO:292	IgG1 A330S/P331S SEQ ID NO:281	IgG1 wildtype SEQ ID NO:282	SEQ ID NO: 286
IgG2-IgG1.1f	IgG2 wildtype SEQ ID NO:279	IgG2 wildtype SEQ ID NO:291	IgG1 A330S/P331S SEQ ID NO:281	IgG1 wildtype SEQ ID NO:282	SEQ ID NO:224
IgG2CS-IgG1.1f	IgG2 wildtype SEQ ID NO:279	IgG2 C219S SEQ ID NO:292	IgG1 A330S/P331S SEQ ID NO:281	IgG1 wildtype SEQ ID NO:282	SEQ ID NO: 226

In certain embodiments, an anti-GITR antibody comprises a modified heavy chain constant region comprising an IgG2 hinge comprising SEQ ID NO: 291, 292, 293, or 294 or a variant thereof, such as an IgG2 hinge comprising an amino acid sequence that (i) differs from SEQ ID NO: 291, 292, 293, or 294 in 1, 2, 3, 4 or 5 amino acids substitutions, additions or deletions; (ii) differs from SEQ ID NO: 291, 292, 293, or 294 in at most 5, 4, 3, 2, or 1 amino acids substitutions, additions or deletions; (iii) differs from SEQ ID NO: 291, 292, 293, or 294 in 1-5, 1-3, 1-2, 2-5 or 3-5 amino acids substitutions, additions or deletions and/or (iv) comprises an amino acid sequence that is at least about 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98% or 99% identical to SEQ ID NO: 291, 292, 293, or 294, wherein in any of (i)-(iv), an amino acid substitution may be a conservative amino acid substitution or a non-conservative amino acid