

325F12H3	-	++	+	IgG
328G2C4	-	+	+	IgG
360F1G1	+	++	+	IgG
382A11H12	na	na	na	IgM
399H6A10	+	++	+	IgG
406D10H7	-	+	+	IgG
420G5E2	-	+	+	IgG
429G1B7	+	+++	+	IgG
409E2C5	-	+++	+	IgG
413B5B4	-	+++	+	IgG
416E8G10	+	++	+	IgG
417H3B1	-	+++	+	IgG
325E8C8	-	+++	+	IgG
350G12E1	-	+++	+	IgG
357B8F8	-	+++	-	IgG
364D1A7	-	+++	++	IgG
408B9D4	-	+++	++	IgG
413H9F8	-	+++	++	IgG

Example 7 - Chimerization

[0303] Murine and rat antibodies were chimerized by expressing murine and rat light chain variable region in the pCDNA3.1(+) plasmid which comprises a DNA sequence encoding amino acids of a signal sequence and a constant region of human IgG1. The sequences of heavy and light chain constant regions (CH and CL) of human IgG1 are shown in Table 4.

[0304] The binding affinities of chimeric antibodies on CHO-CLDN18.2 cell line were determined as described previously. As shown in Fig. 6A-Fig. 6D, chimeric antibodies 282A12F3, 364D1A7, and 413H9F8 specifically bind to CLDN18.2. Chimeric 282A12F3, 364D1A7 and 413H9F8 showed stronger binding affinities as compared with reference antibody 175D10.

Example 8 - Antibody sequence analysis and removal of post-translational modification sites

[0305] The sequences of antibodies produced by hybridoma technology were analyzed for post-translational modifications (PTMs), which sometimes cause problems during the development of a therapeutic protein such as increased heterogeneity, reduced bioactivity, reduced stability, immunogenicity, fragmentation and aggregation. The potential impact of PTMs depends on their location and in some cases on solvent exposure. The CDRs of all sequences were analyzed for asparagine deamination, aspartate isomerization, free cysteine thiol groups, N-glycosylation, oxidation, and fragmentation by potential hydrolysis sites.