

Fig. 1

scFv	Substance added to T2											
	Solvent	Peptide	1F	2M	3A	4A	5A	6L	7F	8A	9A	gp100
	DMSO	NY-ESO										
NYA-0001	<u>1.04</u>	5.75	<u>0.60</u>	7.72	7.88	<u>0.83</u>	<u>0.78</u>	7.97	<u>0.97</u>	6.67	6.56	<u>0.43</u>
NYA-1143	<u>0.98</u>	12.90	<u>1.77</u>	11.89	10.20	<u>5.91</u>	<u>3.15</u>	12.92	<u>4.26</u>	8.74	15.12	<u>0.41</u>
NYA-1154	<u>1.02</u>	9.98	<u>3.98</u>	9.49	8.00	6.63	<u>1.12</u>	9.36	6.08	11.95	11.16	<u>0.46</u>
NYA-1163	<u>0.97</u>	3.67	<u>0.53</u>	1.85	<u>1.70</u>	<u>0.57</u>	<u>0.62</u>	<u>1.74</u>	<u>1.11</u>	6.00	4.01	<u>0.44</u>
NYA-2023	<u>0.94</u>	8.85	<u>0.72</u>	6.74	4.92	<u>2.48</u>	<u>1.21</u>	7.51	4.72	5.40	10.79	<u>0.40</u>
NYA-2027	<u>1.09</u>	5.75	<u>0.57</u>	7.84	9.91	<u>0.99</u>	<u>0.75</u>	7.85	5.41	9.47	6.90	<u>0.41</u>
NYA-2035	<u>1.03</u>	9.94	<u>0.60</u>	8.80	5.81	<u>2.16</u>	<u>2.27</u>	8.95	5.83	6.41	11.46	<u>0.38</u>
NYA-2044	<u>0.91</u>	12.93	<u>0.68</u>	13.53	10.90	<u>3.21</u>	<u>2.20</u>	13.39	<u>3.62</u>	10.04	15.61	<u>0.39</u>
NYA-2045	<u>0.81</u>	9.03	<u>0.53</u>	8.8	7.46	<u>1.17</u>	<u>0.94</u>	8.8	<u>1.99</u>	7.35	9.98	<u>0.39</u>
NYA-2047	<u>0.89</u>	7.99	<u>0.48</u>	7.34	6.09	<u>0.86</u>	<u>1.03</u>	7.07	<u>3.11</u>	6.61	9.54	<u>0.39</u>
NYA-2048	<u>0.90</u>	6.58	<u>0.51</u>	5.36	4.20	<u>0.63</u>	<u>0.67</u>	6.14	<u>1.46</u>	4.11	7.75	<u>0.41</u>
NYA-2060	<u>0.83</u>	8.78	<u>0.52</u>	6.93	5.51	<u>0.73</u>	<u>0.70</u>	7.94	<u>2.51</u>	6.18	9.48	<u>0.41</u>
NYA-2061	<u>0.85</u>	8.62	<u>0.54</u>	7.17	4.73	<u>0.59</u>	<u>0.66</u>	7.13	<u>2.04</u>	5.22	9.16	<u>0.40</u>
NYA-2143	<u>1.04</u>	13.06	<u>2.72</u>	13.19	10.28	7.19	<u>4.30</u>	12.87	<u>5.26</u>	9.69	14.50	<u>0.38</u>
NYC-0003	<u>0.92</u>	3.74	3.28	3.73	4.34	<u>0.76</u>	<u>0.69</u>	4.14	3.99	3.42	4.77	<u>0.39</u>
NYC-0004	<u>0.76</u>	6.02	3.56	5.66	4.75	<u>2.02</u>	<u>0.65</u>	3.78	5.07	3.69	7.99	<u>0.37</u>

Fig. 2A

Gene	Uniprot ID	Start position	Sequence	HLA-A0201 IC50 (nM)
DOLPP1	Q86YN1	104	SQFMWFFSV	2.64
IL20RB	Q6UXL0	14	SLFMWFFYA	2.95
PRKD1	Q15139	763	SLDMWSVG	14.74
PRKD3	O94806	756	SLDMWSVG	14.74
PRKD2	Q9BZL6	731	SLDMWSVG	14.74
CD163	Q86VB7	885	SIPMWVDN	145.66
P2RY8	Q86VZ1	186	SVAMWAVFL	212.86
NY-ESO-1	P78358	157	SLLMWITQC	363.83

Fig. 2B

scFv	Substance added to T2							
	Solvent	Peptide	DOLPP1	IL20RB	PRKD2	CD163	P2RY8	gp100
	DMSO	NY-ESO						
NYA-0001	0.92	<u>5.12</u>	0.37	0.42	0.33	0.48	0.73	0.31
NYA-1143	0.94	<u>13.44</u>	0.37	0.42	0.32	0.46	0.69	0.30
NYA-1154	1.01	<u>13.76</u>	0.46	0.51	<u>2.72</u>	0.54	0.65	0.31
NYA-1163	0.88	<u>4.21</u>	0.36	0.41	0.31	0.46	0.69	0.30
NYA-2023	0.88	<u>10.11</u>	0.42	0.42	0.42	0.48	0.70	0.30
NYA-2027	0.96	<u>7.25</u>	0.39	0.42	0.32	0.51	0.70	0.31
NYA-2035	0.97	<u>11.14</u>	0.38	0.41	0.33	0.48	0.69	0.29
NYA-2044	0.95	<u>14.28</u>	0.38	0.43	0.33	0.47	0.72	0.32
NYA-2045	0.96	<u>13.84</u>	0.43	0.47	0.34	0.48	0.58	0.30
NYA-2047	0.98	<u>10.25</u>	0.40	0.43	0.35	0.47	0.72	0.30
NYA-2048	0.90	<u>8.82</u>	0.44	0.48	0.35	0.52	0.69	0.34
NYA-2060	0.85	<u>11.17</u>	0.42	0.45	0.33	0.47	0.62	0.32
NYA-2061	0.82	<u>10.37</u>	0.40	0.46	0.33	0.48	0.57	0.32
NYA-2143	0.90	<u>13.48</u>	0.38	0.42	0.32	0.46	0.69	0.31
NYC-0003	1.00	<u>5.22</u>	0.38	0.43	<u>1.53</u>	<u>1.08</u>	<u>2.01</u>	0.32
NYC-0004	1.01	<u>9.19</u>	0.39	0.43	<u>3.41</u>	0.49	<u>1.98</u>	0.32

Fig. 3

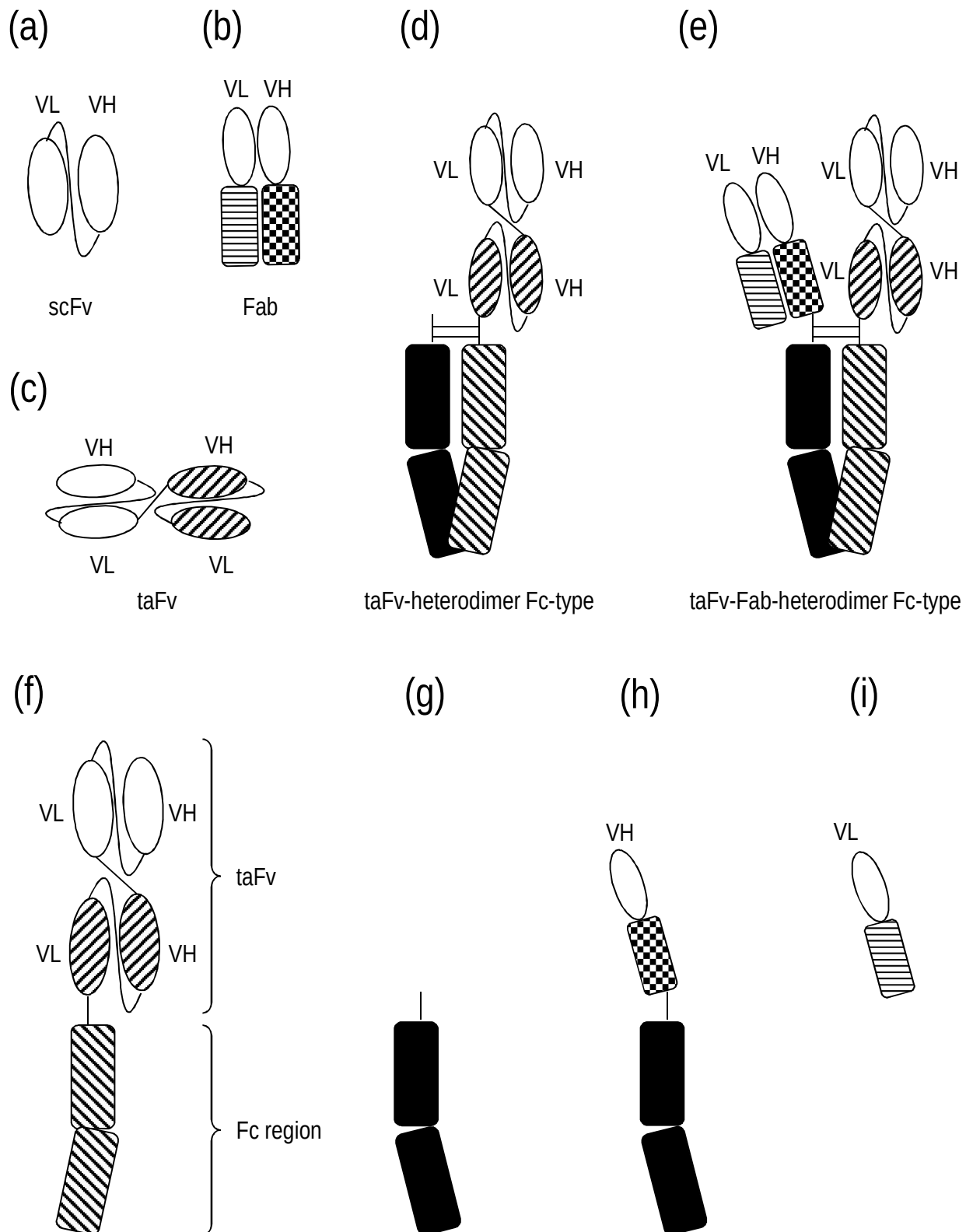


Fig. 4A

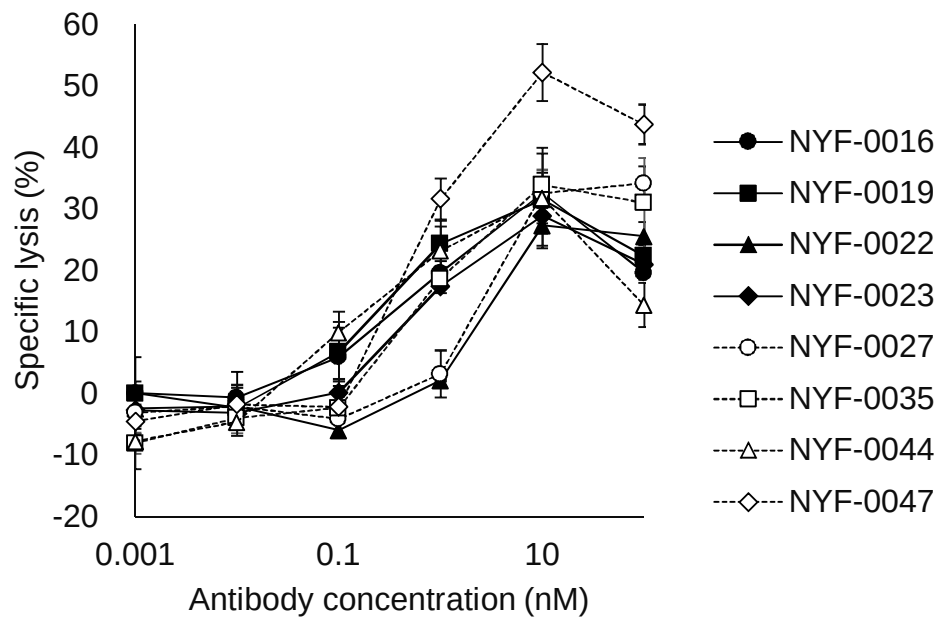


Fig. 4B

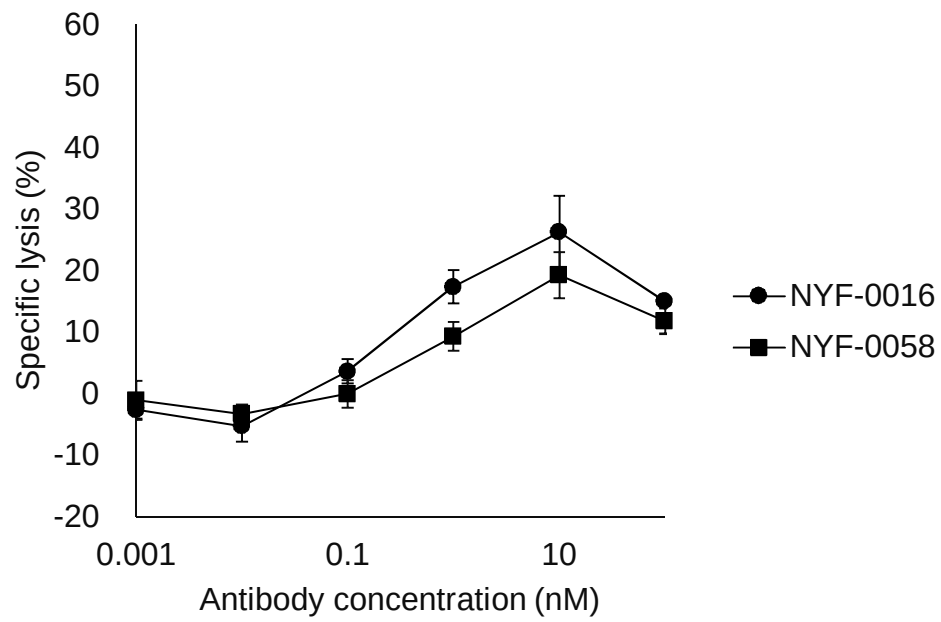


Fig. 4C

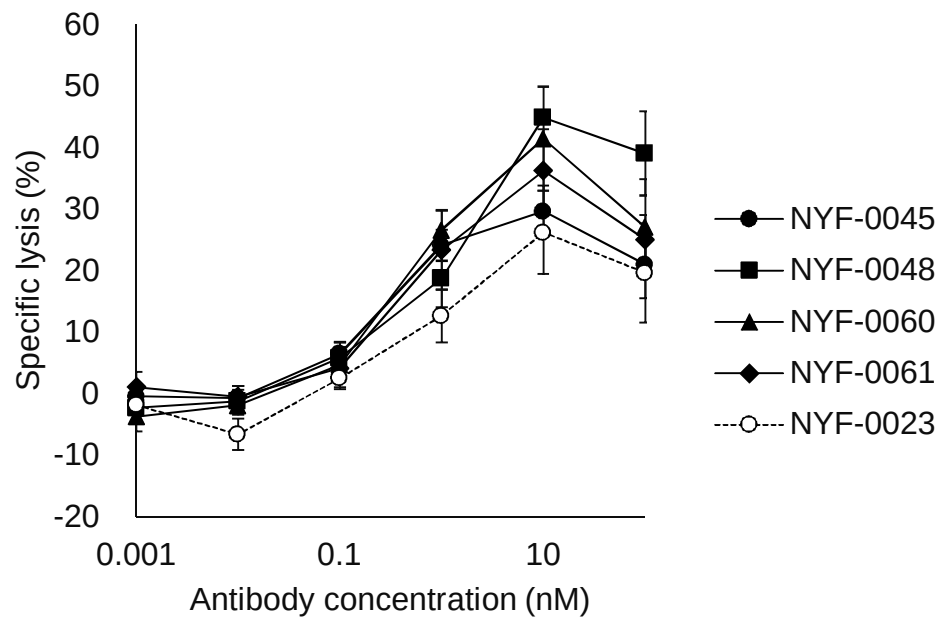


Fig. 4D

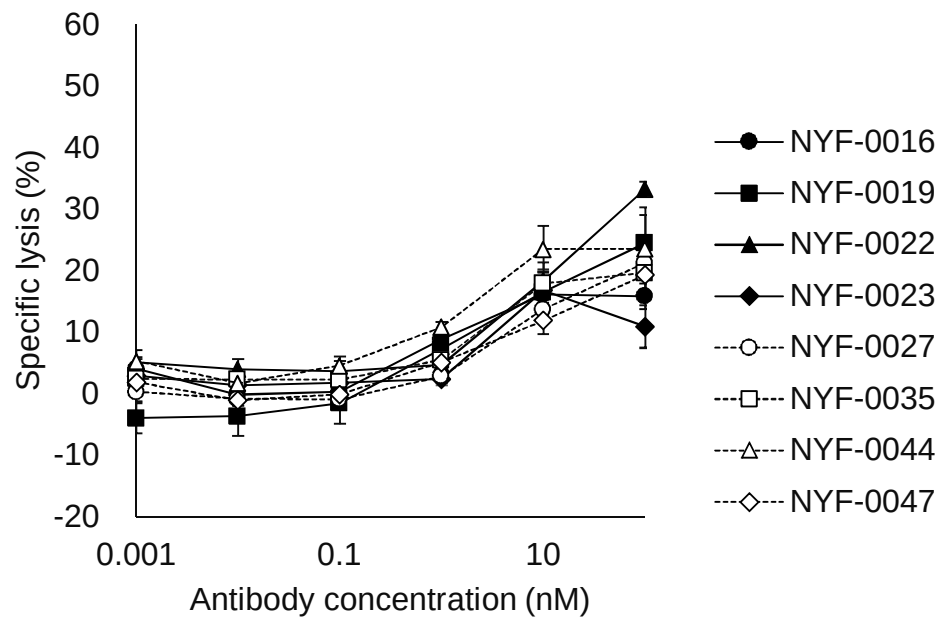


Fig. 4E

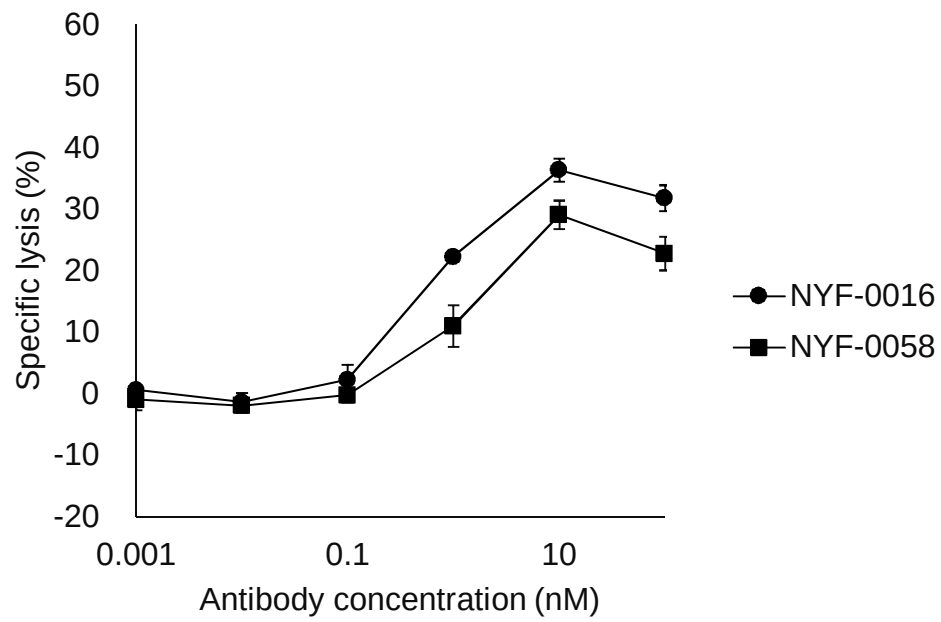


Fig. 4F

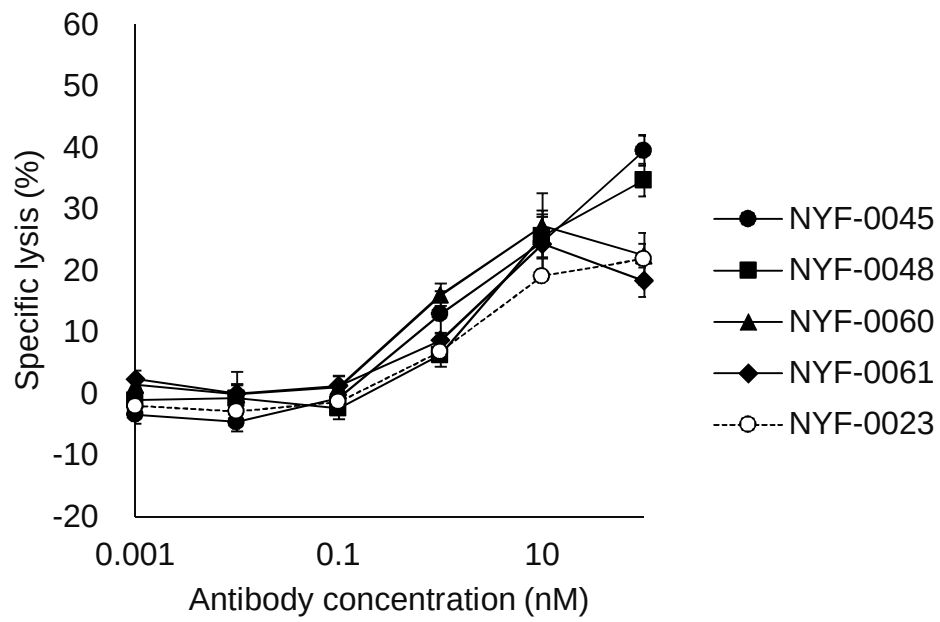


Fig. 4G

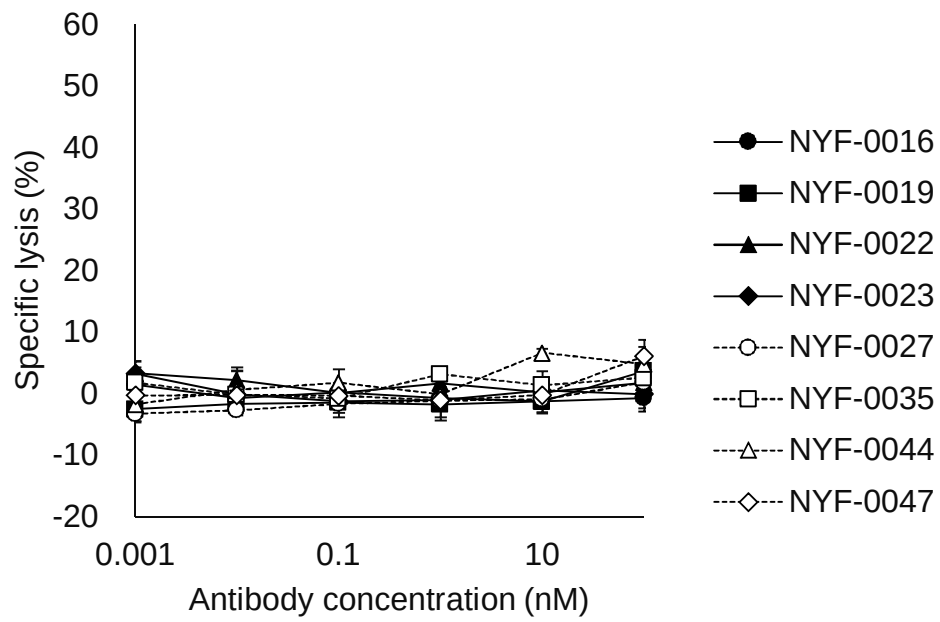


Fig. 4H

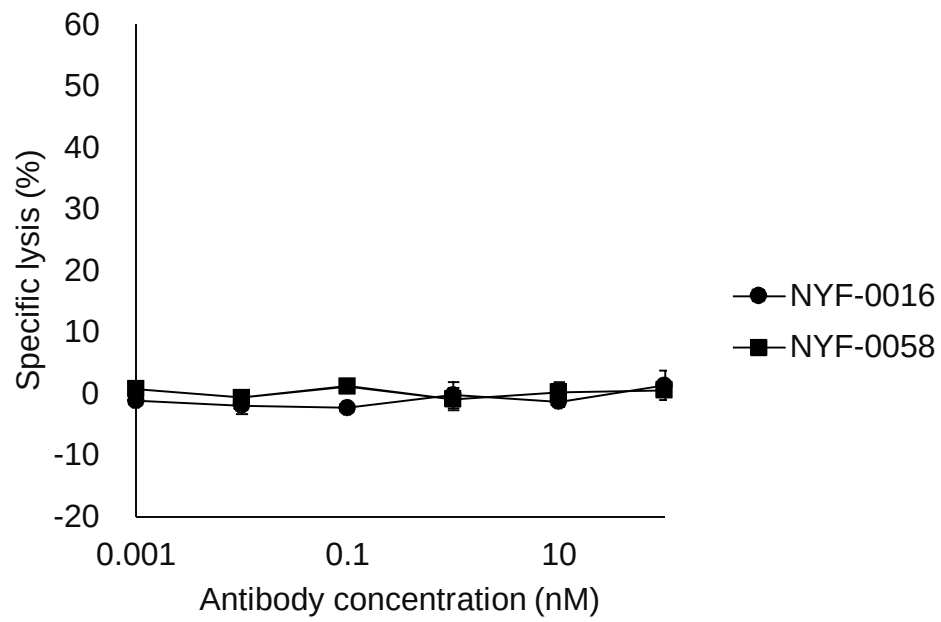


Fig. 4I

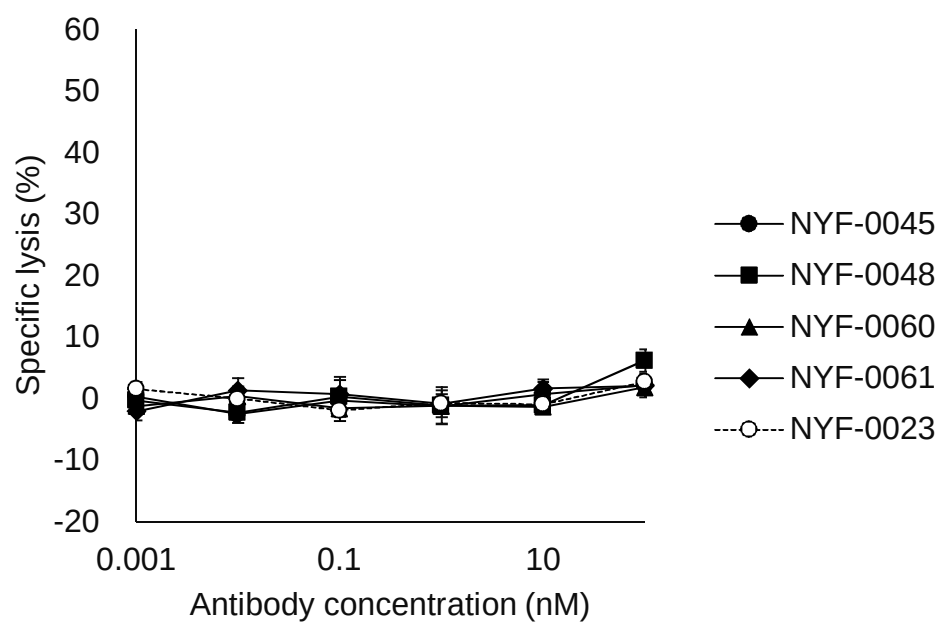


Fig. 4J

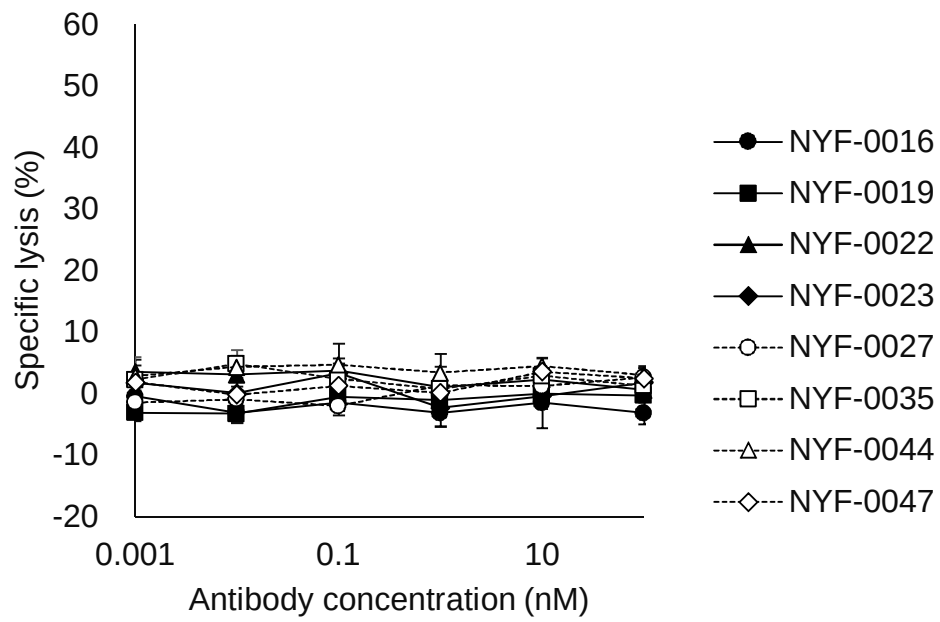


Fig. 4K

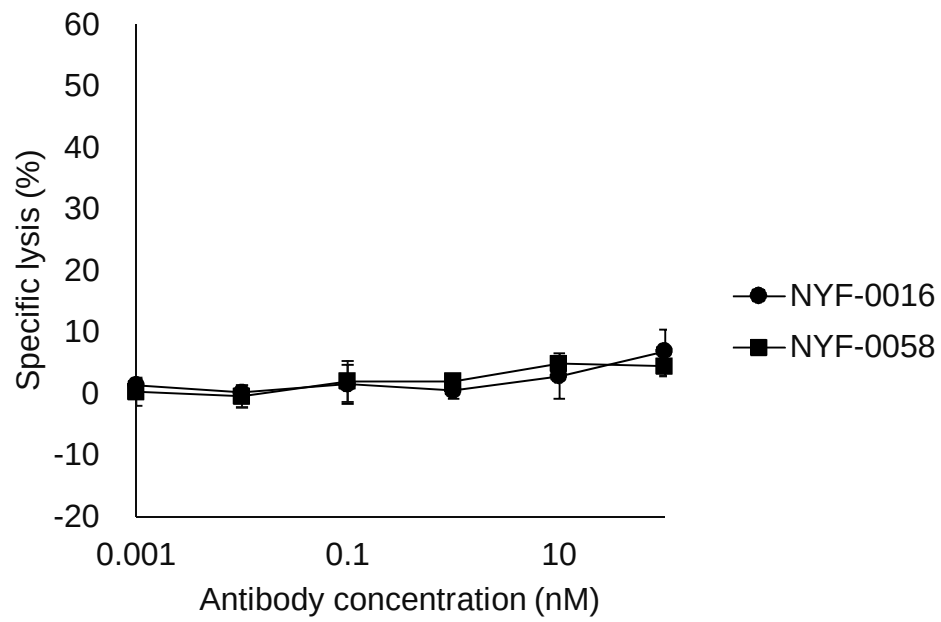


Fig. 4L

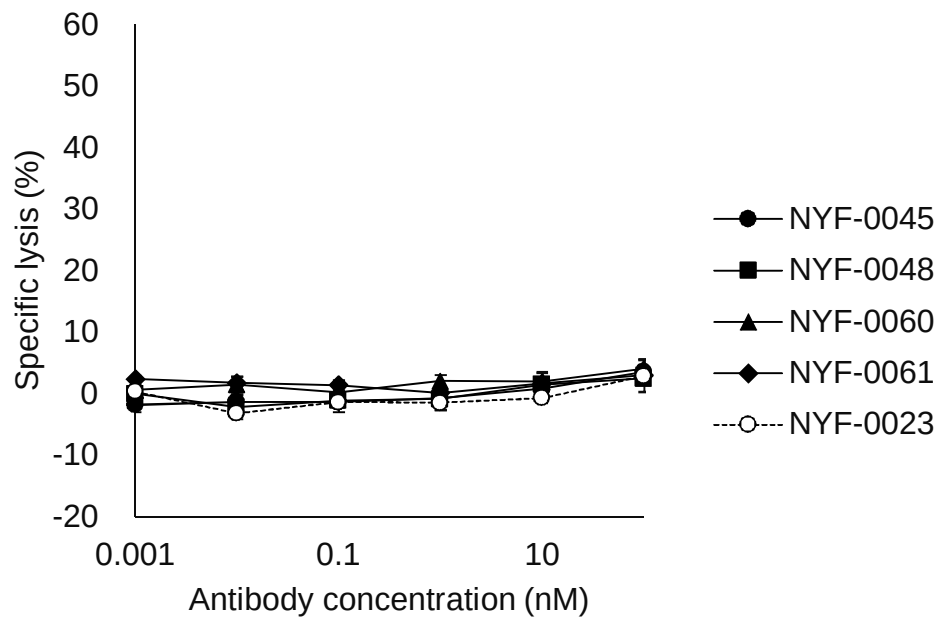


Fig. 5A

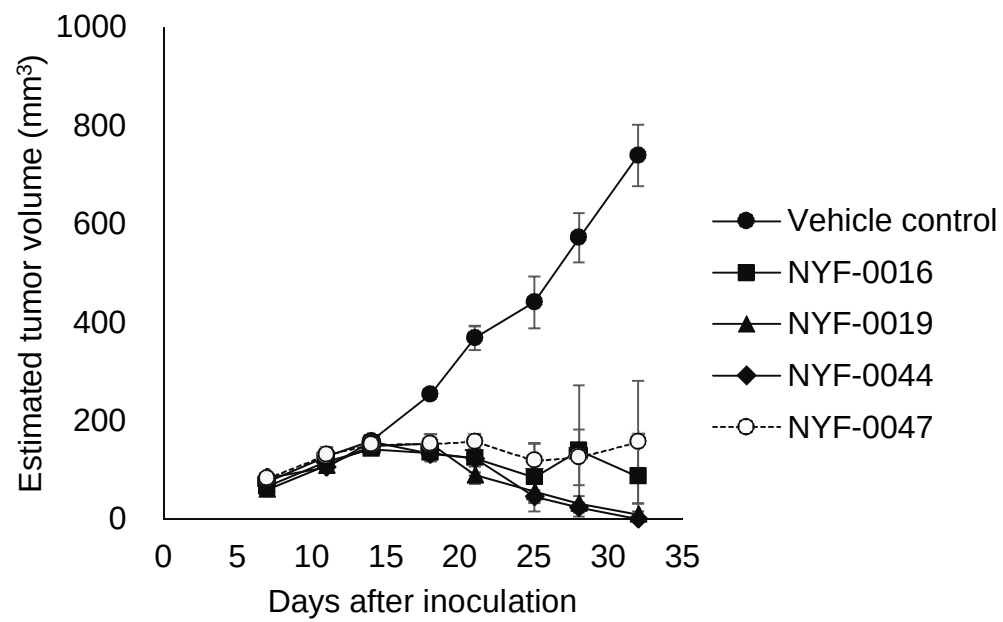


Fig. 5B

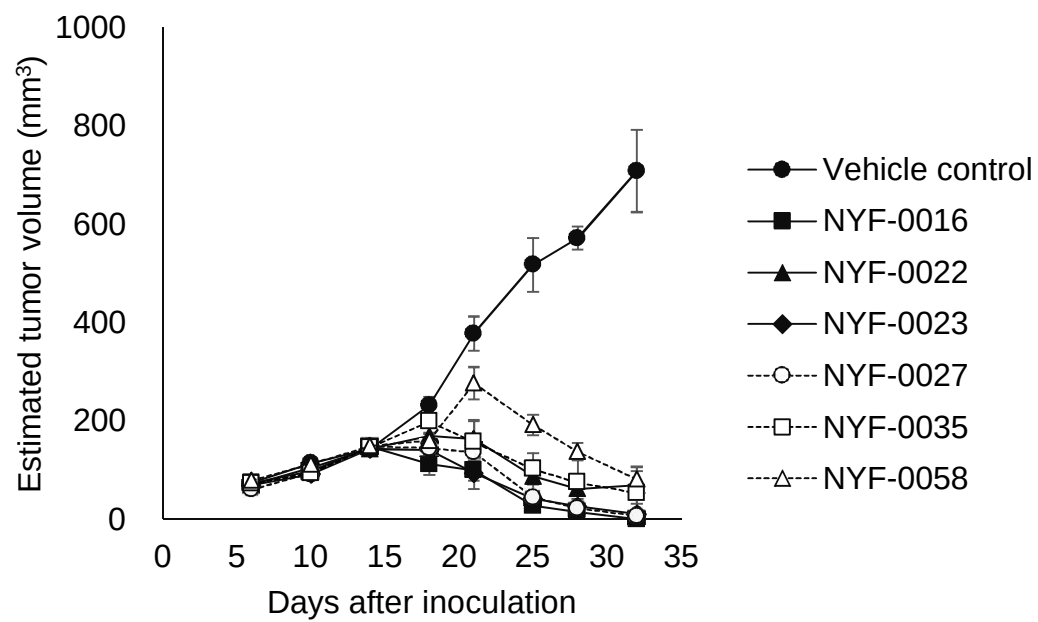


Fig. 5C

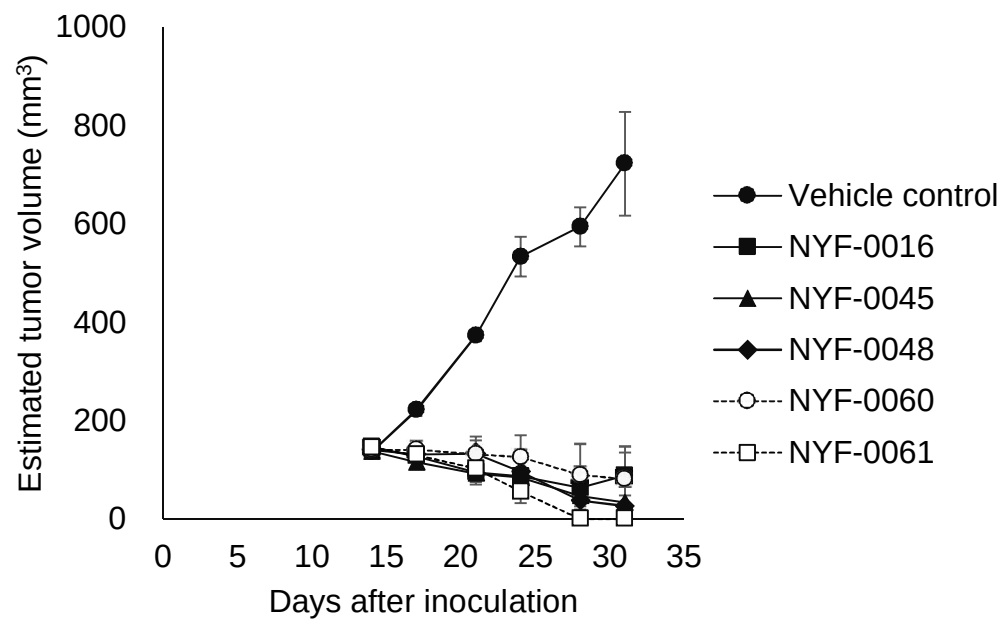
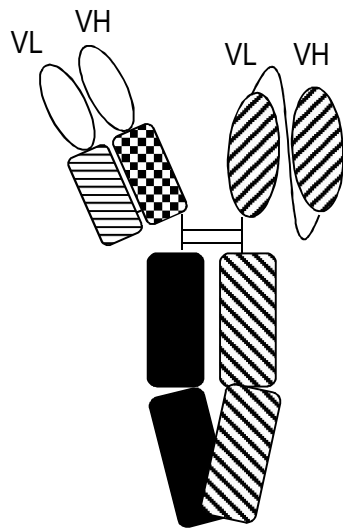


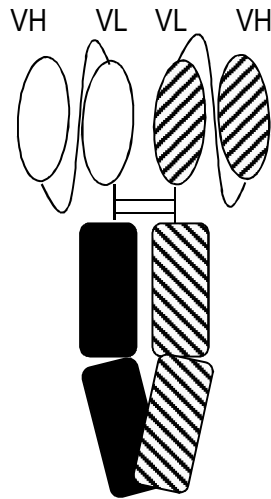
Fig. 6A

(a)



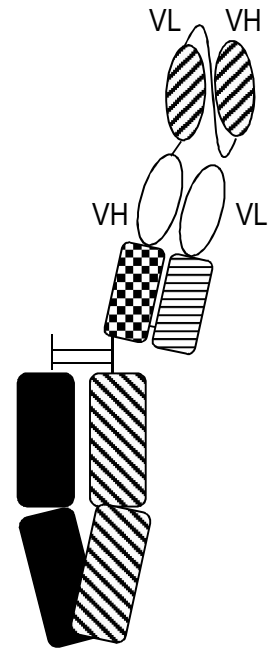
Hybrid-type

(b)



Dual-type

(c)



scFv-Fab-heterodimer Fc-type

Fig. 6B

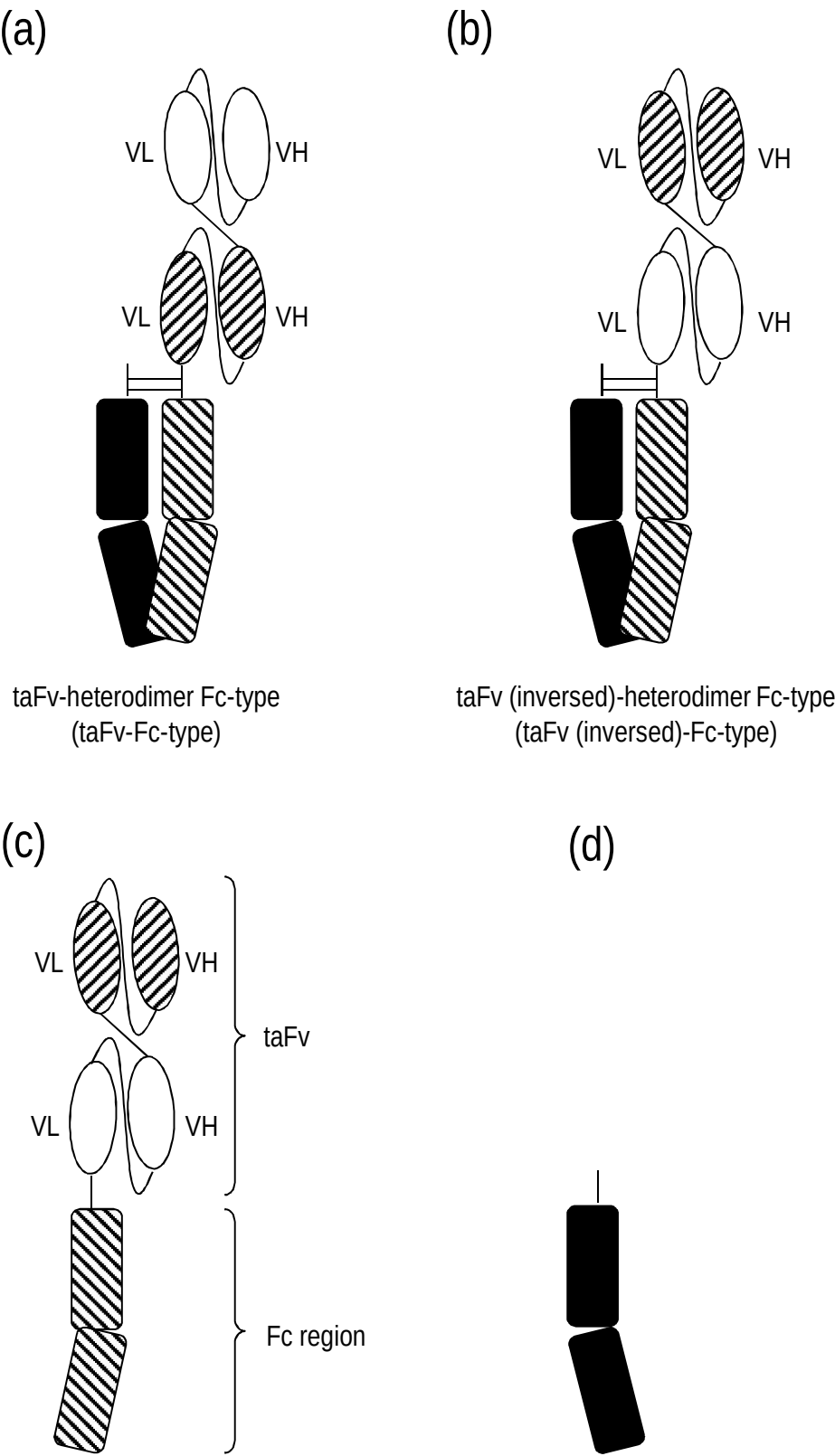


Fig. 7A

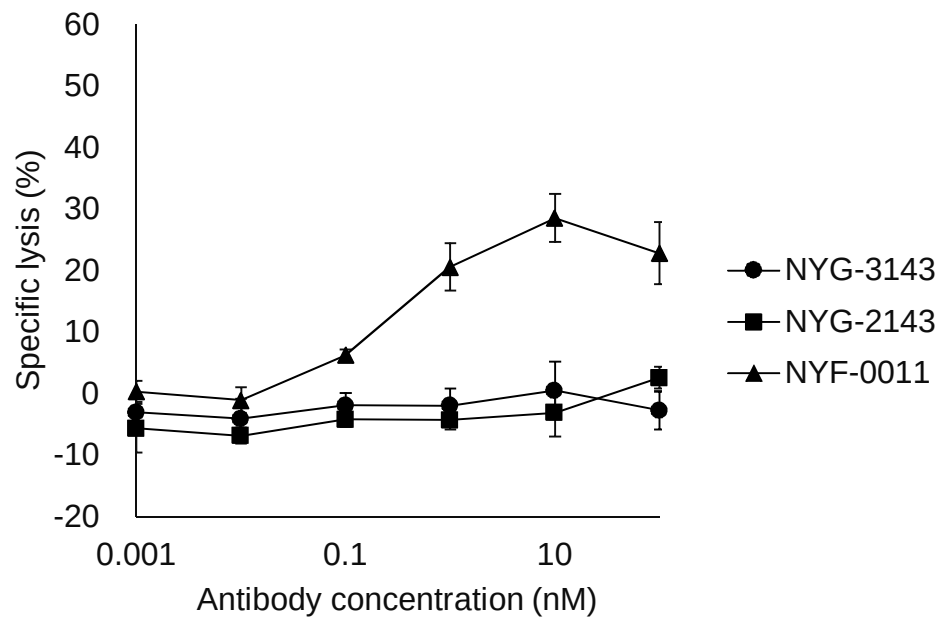


Fig. 7B

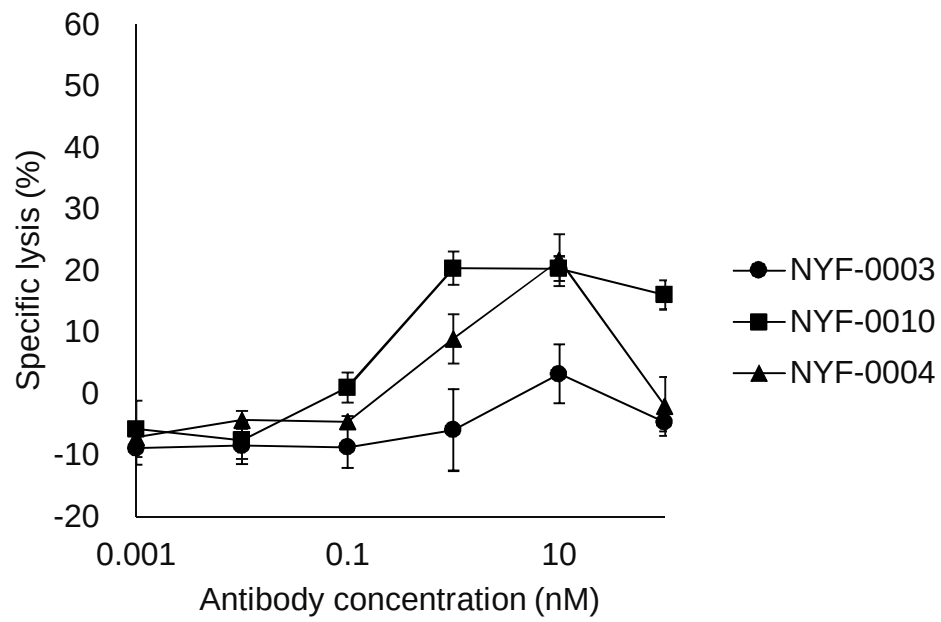


Fig. 8

NY-ESO Peptide
SLLMWITQC
(SEQ ID NO: 1)

Fig. 9

MAGEC-1 Peptide
ILFGISLREV
(SEQ ID NO: 2)

Fig. 10

scFv sequence analysis primer 1
CTCTTCGCTATTACGCCAGCTGGCGA
(SEQ ID NO: 3)

Fig. 11

scFv sequence analysis primer 2
ATAACAATTTACACAGGAAACAGCTATGA
(SEQ ID NO: 4)

Fig. 12

NYA-0001 heavy chain variable region

**GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAC
ACCCTCCTGTTTCAGCGTCTGGATTCTCCATCCGTAGTTATGATATACACTGGGTCC
GCCAGGCTCCAGGCAAGGGGCTAGAGTGGGTGGCCACTATATCATATGATGGAAGT
CAGAAGTACTTCGCAGACTCCGTGAAGGGCCGATTTACCATCTTCAGAGACGAATC
GGAGAACATGGTGTATCTGCAAATGAGCGGCCTGAGAGTTGAGGACACGGCTGTTT
ATCACTGTGCGAGAGGGAGTAGTGGTCATTATGAGGCTTTTGATATCTGGGGCCAA
GGGACAATGGTCACCGTCTCTTCA**

(SEQ ID NO: 5)

Fig. 13

NYA-0001 heavy chain variable region
EVQLVESGGGVVQPGRSLTPSCSASGFSIRSYDIHWVRQAPGKGLEWVATISYDGS
QKYFADSVKGRFTIFRDESENMVYLQMSGLRVEDTAVYHCARGSSGHYEAFDIWGQ
GTMVTVSS
(SEQ ID NO: 6)

Fig. 14

NYA-0001 light chain variable region

**CAGTCTGTGTTGACGCAGCCGCCCTCAGTGTCTGCGGCCCCAGGACAGAAGGTCAC
CATCTCCTGCTCTGGAAGCAGCTCCAACATTGGGAATAATTATGTATCCTGGTACC
AGCAGCTCCCAGGAACAGCCCCAAACTCCTCATTTATGACAATAATAAGCGACCC
TCAGGGATTCCTGACCGATTCTCTGGCTCCAAGTCTGGCACGTCAGCCACCCTGGG
CATCACCGGACTCCAGACTGGGGACGAGGCCGATTATTACTGCGGAACATGGGATA
GCAGCCTGAGTGCCCCTTGGGTGTTCTGGCGGAGGGACCAAGGTCACCGTCCTA
(SEQ ID NO: 7)**

Fig. 15

NYA-0001 light chain variable region
QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSWYQQLPGTAPKLLIYDNNKRP
SGIPDRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSLAPWVFGGGTKVTVL
(SEQ ID NO: 8)

Fig. 16

NYA-0060 heavy chain variable region

**GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAC
ACCCTCCTGTTTCAGCGTCTGGATTCTCCATCCGTAGCTATGATATACACTGGGTCC
GCCTGGCTCCAGGCAAGGGGCTAGAGTGGGTGGCCACTATATCATATGATGGAAGT
CAGAAGTACTTCGCAGACTCCGTGAAGGGCCGATTTACCATCTTCAGAGACGAATC
GGAGAACATGGTGTATCTGCAAATGAGCGGCCTGAGAGTTGAGGACACGGCTGTTT
ATCACTGTGCGAGAGGGAGTAGTGGTCATTATGAGGCTTTTGATATCTGGGGCCAA
GGGACAATGGTCACCGTCTCTTCA**

(SEQ ID NO: 9)

Fig. 17

NYA-0060 heavy chain variable region
EVQLVESGGGVVQPGRSLTPSCSASGFSIRSYDIHWVRLAPGKGLEWVATISYDGS
QKYFADSVKGRFTIFRDESENMVYLQMSGLRVEDTAVYHCARGSSGHYEAFDIWGQ
GTMVTVSS
(SEQ ID NO: 10)

Fig. 18

NYA-0060 light chain variable region

**CAGTCTGTGTTGACGCAGCCGCCCTCAGTGTCTGCGGCCCCAGGACAGAAGGTCAC
CATCTCCTGCTCTGGAAGCAGCTCCAACATTGGGAATAATTATGTATCCTGGTACC
AGCAGCTCCCAGGAACAGCCCCAAACTCCTCATTTATGACAATAATAAGCGACCC
TCAGGGATTCCTGACCGATTCTCTGGCTCCAAGTCTGGCACGTCAGCCACCCTGGG
CATCACCGGACTCCAGACTGGGGACGAGGCCGATTATTACTGCGGAACATGGGATA
GCAGCCTGAGTGCCCCTTGGGTGTTGCGCGGAGGGACCAAGGTCACCGTCCTA
(SEQ ID NO: 11)**

Fig. 19

NYA-0060 light chain variable region
QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSWYQQLPGTAPKLLIYDNNKRP
SGIPDRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSLAPWVFGGGTKVTVL
(SEQ ID NO: 12)

Fig. 20

NYA-0068 heavy chain variable region

**GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAC
ACCCTCCTGTTTCAGCGTCTGGATTCTCCATCCGTAGTTATGATATACACTGGGTCC
GCCAGGCTCCAGGCAAGGGGCTAGAGTGGGTGGCCACTATATCATATGATGGAAGT
CAGAAGTACTTCGCAGACTCCGTGAAGGGCCGATTTACCATCTTCAGAGACGAATC
GGAGAACATGGTGTATCTGCAAATGAGCGGCCTGAGAGTTGAGGACACGGCTGTTT
ATCACTGTGCGAGAGGGAGTAGTGGTCATTATGAGGCTTTTGATATCTGGGGCCAA
GGGACAATGGTCACCGTCTCTTCA**

(SEQ ID NO: 13)

Fig. 21

NYA-0068 heavy chain variable region
EVQLVESGGGVVQPGRSLTPSCSASGFSIRSYDIHWVRQAPGKGLEWVATISYDGS
QKYFADSVKGRFTIFRDESENMVYLQMSGLRVEDTAVYHCARGSSGHYEAFDIWGQ
GTMVTVSS
(SEQ ID NO: 14)

Fig. 22

NYA-0068 light chain variable region

**CAGTCTGTGTTGACGCAGCCGCCCTCAGTGTCTGCGGCCCCAGGACAGAAGGTCAC
CATCTCCTGCTCTGGAAGCAGCTCCAACATTGGGAATTGGTATGTATCCTGGTACC
AGCAGCTCCCAGGAACAGCCCCAAACTCCTCATTTATGACAATAATAAGCGACCC
TCAGGGATTCCTGACCGATTCTCTGGCTCCAAGTCTGGCACGTCAGCCACCCTGGG
CATCACCGGACTCCAGACTGGGGACGAGGCCGATTATTACTGCGGAACATGGGATA
GCAGCCTGAGTGCCCCTTGGGTGTTGCGCGGAGGGACCAAGGTCACCGTCCTA
(SEQ ID NO: 15)**

Fig. 23

NYA-0068 light chain variable region

**QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNWYVSWYQQLPGTAPKLLIYDNNKRP
SGIPDRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSLSAPWVFGGGTKVTVL
(SEQ ID NO: 16)**

Fig. 24

NYA-0082 heavy chain variable region

**GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAC
ACCCTCCTGTTTCAGCGTCTGGATTCTCCATCCGTAGTTATGATATACACTGGGTCC
GCCAGGCTCCAGGCAAGGGGCTAGAGTGGGTGGCCACTATATCATATGATGGAAGT
CAGAAGTACTTCGCAGACTCCGTGAAGGGCCGATTTACCATCTTCAGAGACGAATC
GGAGAACATGGTGTATCTGCAAATGAGCGGCCTGAGAGTTGAGGACACGGCTGTTT
ATCACTGTGCGAGAGGGAGTAGTGGTCATTATGAGGCTTTTGATATCTGGGGCCAA
GGGACAATGGTCACCGTCTCTTCA**

(SEQ ID NO: 17)

Fig. 25

NYA-0082 heavy chain variable region

**EVQLVESGGGVVQPGRSLTPSCSASGFSIRSYDIHWVRQAPGKGLEWVATISYDGS
QKYFADSVKGRFTIFRDESENMVYLQMSGLRVEDTAVYHCARGSSGHYEAFDIWGQ
GTMVTVSS**

(SEQ ID NO: 18)

Fig. 26

NYA-0082 light chain variable region

**CAGTCTGTGTTGACGCAGCCGCCCTCAGTGTCTGCGGCCCCAGGACAGAAGGTCAC
CATCTCCTGCTCTGGAAGCAGCTCCAACATTGGGAATAATTATGTATCCTGGTACC
AGCGGCTCCCAGGAACAGCCCCAAACTCCTCATTTATGACAATAATAAGCGACCC
TCAGGGATTCCTGACCGATTCTCTGGCTCCAAGTCTGGCACGTCAGCCACCCTGGG
CATCACCGGACTCCAGACTGGGGACGAGGCCGATTATTACTGCGGATCATGGGATA
GCAGCCTGAGTGCCCCTTGGGTGTTCTGGCGGAGGGACCAAGGTCACCGTCCTA
(SEQ ID NO: 19)**

Fig. 27

NYA-0082 light chain variable region
QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSWYQRLPGTAPKLLIYDNNKRP
SGIPDRFSGSKSGTSATLGITGLQTGDEADYYCGSWDSSLAPWVFGGGTKVTVL
(SEQ ID NO: 20)

Fig. 28

NYA-1163 tag adduct

**ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGGCAGCTCCCAGATGGGTGCTGAG
CGGAGAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCC
TGACACCCTCCTGTTCAAGCTCTGGATTCTCCATCCGTAGCTATGATATACACTGG
GTCCGCCTGGCTCCAGGCAAGGGGCTAGAGTGGGTGGCCACTATATCATATGATGG
AAGTCAGAAGTACTTCGCAGACTCCGTGAAGGGCCGATTTACCATCTTCAGAGACG
AATCGGAGAACATGGTGTATCTGCAAATGAGCGGCCTGAGAGTTGAGGACACGGCT
GTTTATCACTGTGCGAGAGGGAGTAGTGGTCATTATGAGGCTTTTGATATCTGGGG
CCAAGGGACAATGGTCACCGTCTCTTCAGGTGGAGGCGGTTTCAGGCGGAGGTGGCA
GCGGCGGTGGCGGGAGTCAGTCTGTGTTGACGCAGCCGCCCTCAGTGTCTGCGGCC
CCAGGACAGAAGGTCACCATCTCCTGCTCTGGAAGCAGCTCCAACATTGGGAATAA
TTATGTATCCTGGTACCAGCAGCTCCCAGGAACAGCCCCAACTCCTCATTTATG
ACAATAATAAGCGACCCTCAGGGATTCTTGACCGATTCTCTGGCTCCAAGTCTGGC
ACGTCAGCCACCCTGGGCATCACCGGACTCCAGACTGGGGACGAGGCCGATTATTA
CTGCGGAACATGGGATAGCAGCCTGAGTGCCCTTGGGTGTTGCGCGGAGGGACCA
AGGTCACCGTCCTAGGCGCGGCCGCAGGTGCAGGTGGTGATTACAAAGATGATGAC
GATAAAGGTGCAGCGGCGCATCACCATCATCACCAC**

(SEQ ID NO: 21), signal sequence (1-57), NYA-1163 (61-798), FLAG-His tag (799-876)

Fig. 29

NYA-2023 tag adduct

**ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGGCAGCTCCCAGATGGGTGCTGAG
CGGAGAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCC
TGACACCCTCCTGTTCAAGCTCTGGATTCTCCATCCGTAGTTATGATATACACTGG
GTCCGCCAGGCTCCAGGCAAGGGGCTAGAGTGGGTGGCCACTATATCATATGATGG
AAGTCAGAAGTACTTCGCAGACTCCGTGAAGGGCCGATTTACCATCTTCAGAGACG
AATCGGAGAACATGGTGTATCTGCAAATGAGCGGCCTGAGAGTTGAGGACACGGCT
GTTTATCACTGTGCGAGAGGGAGTAGTGGTCATTATGAGGCTTTTGATATCTGGGG
CCAAGGGACAATGGTCACCGTCTCTTCAGGTGGAGGCGGTTTCAGGCGGAGGTGGCA
GCGGCGGTGGCGGGAGTCAGTCTGTGTTGACGCAGCCGCCCTCAGTGTCTGCGGCC
CCAGGACAGAAGGTCACCATCTCCTGCTCTGGAAGCAGCTCCAACATTGGGAATTG
GTATGTATCCTGGTACCAGCAGCTCCCAGGAACAGCCCCAACTCCTCATTTATG
ACAATAATAAGCGACCCTCAGGGATTCTTGACCGATTCTCTGGCTCCAAGTCTGGC
ACGTCAGCCACCCTGGGCATCACCGGACTCCAGACTGGGGACGAGGCCGATTATTA
CTGCGGAACATGGGATAGCAGCCTGAGTGCCCTTGGGTGTTGCGCGGAGGGACCA
AGGTCACCGTCCTAGGCGCGGCCGCAGGTGCAGGTGGTGATTACAAAGATGATGAC
GATAAAGGTGCAGCGGCGCATCACCATCATCACCAC**

(SEQ ID NO: 22), signal sequence (1-57), NYA-2023 (61-798), FLAG-His tag (799-876)

Fig. 30

NYA-2027 tag adduct

**ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGGCAGCTCCCAGATGGGTGCTGAG
CGGAGAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCC
TGACACCCTCCTGTTCAAGCTCTGGATTCTCCATCCGTAGTTATGATATACACTGG
GTCCGCCAGGCTCCAGGCAAGGGGCTAGAGTGGGTGGCCACTATATCATATGATGG
AAGTCAGAAGTACTTCGCAGACTCCGTGAAGGGCCGATTTACCATCTTCAGAGACG
AATCGGAGAACATGGTGTATCTGCAAATGAGCGGCCTGAGAGTTGAGGACACGGCT
GTTTATCACTGTGCGAGAGGGAGTAGTGGTCATTATGAGGCTTTTGATATCTGGGG
CCAAGGGACAATGGTCACCGTCTCTTCAGGTGGAGGCGGTTTCAGGCGGAGGTGGCA
GCGGCGGTGGCGGGAGTCAGTCTGTGTTGACGCAGCCGCCCTCAGTGTCTGCGGCC
CCAGGACAGAAGGTCACCATCTCCTGCTCTGGAAGCAGCTCCAACATTGGGAATAA
TTATGTATCCTGGTACCAGCAGCTCCCAGGAACAGCCCCAACTCCTCATTTATG
ACAATAATAAGCGACCCTCAGGGATTCTTGACCGATTCTCTGGCTCCAAGTCTGGC
ACGTCAGCCACCCTGGGCATCACCGGACTCCAGACTGGGGACGAGGCCGATTATTA
CTGCGGATCATGGGATAGCAGCCTGAGTGCCCTTGGGTGTTTCGGCGGAGGGACCA
AGGTCACCGTCCTAGGCGCGGCCGCAGGTGCAGGTGGTGATTACAAAGATGATGAC
GATAAAGGTGCAGCGGCGCATCACCATCATCACCAC**

**(SEQ ID NO: 23), signal sequence (1-57), NYA-2027(61-
798), FLAG-His tag (799-876)**

Fig. 31

NYA-1143 tag adduct

**ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGGCAGCTCCCAGATGGGTGCTGAG
CGGAGAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCC
TGACACCCTCCTGTTCAAGCTCTGGATTCTCCATCCGTAGCTATGATATACACTGG
GTCCGCCTGGCTCCAGGCAAGGGGCTAGAGTGGGTGGCCACTATATCATATGATGG
AAGTCAGAAGTACTTCGCAGACTCCGTGAAGGGCCGATTTACCATCTTCAGAGACG
AATCGGAGAACATGGTGTATCTGCAAATGAGCGGCCTGAGAGTTGAGGACACGGCT
GTTTATCACTGTGCGAGAGGGAGTAGTGGTCATTATGAGGCTTTTGATATCTGGGG
CCAAGGGACAATGGTCACCGTCTCTTCAGGTGGAGGCGGTTTCAGGCGGAGGTGGCA
GCGGCGGTGGCGGGAGTCAGTCTGTGTTGACGCAGCCGCCCTCAGTGTCTGCGGCC
CCAGGACAGAAGGTCACCATCTCCTGCTCTGGAAGCAGCTCCAACATTGGGAATTG
GTATGTATCCTGGTACCAGCAGCTCCCAGGAACAGCCCCAACTCCTCATTTATG
ACAATAATAAGCGACCCTCAGGGATTCTTGACCGATTCTCTGGCTCCAAGTCTGGC
ACGTCAGCCACCCTGGGCATCACCGGACTCCAGACTGGGGACGAGGCCGATTATTA
CTGCGGAACATGGGATAGCAGCCTGAGTGCCCTTGGGTGTTGCGCGGAGGGACCA
AGGTCACCGTCCTAGGCGCGGCCGCAGGTGCAGGTGGTGATTACAAAGATGATGAC
GATAAAGGTGCAGCGGCGCATCACCATCATCACCAC**

**(SEQ ID NO: 24), signal sequence (1-57), NYA-1143 (61-
798), FLAG-His tag (799-876)**

Fig. 32

NYA-2143 tag adduct

**ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGGCAGCTCCCAGATGGGTGCTGAG
CGGAGAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCC
TGACACCCTCCTGTTCAAGCTCTGGATTCTCCATCCGTAGCTATGATATACACTGG
GTCCGCCTGGCTCCAGGCAAGGGGCTAGAGTGGGTGGCCACTATATCATATGATGG
AAGTCAGAAGTACTTCGCAGACTCCGTGAAGGGCCGATTTACCATCTTCAGAGACG
AATCGGAGAACATGGTGTATCTGCAAATGAGCGGCCTGAGAGTTGAGGACACGGCT
GTTTATCACTGTGCGAGAGGGAGTAGTGGTCATTATGAGGCTTTTGATATCTGGGG
CCAAGGGACAATGGTCACCGTCTCTTCAGGTGGAGGCGGTTTCAGGCGGAGGTGGCA
GCGGCGGTGGCGGGAGTCAGTCTGTGTTGACGCAGCCGCCCTCAGTGTCTGCGGCC
CCAGGACAGAAGGTCACCATCTCCTGCTCTGGAAGCAGCTCCAACATTGGGAATTG
GTATGTATCCTGGTACCAGCGGCTCCCAGGAACAGCCCCAACTCCTCATTTATG
ACAATAATAAGCGACCCTCAGGGATTCTTGACCGATTCTCTGGCTCCAAGTCTGGC
ACGTCAGCCACCCTGGGCATCACCGGACTCCAGACTGGGGACGAGGCCGATTATTA
CTGCGGAACATGGGATAGCAGCCTGAGTGCCCTTGGGTGTTGCGCGGAGGGACCA
AGGTCACCGTCCTAGGCGCGGCCGCAGGTGCAGGTGGTGATTACAAAGATGATGAC
GATAAAGGTGCAGCGGCGCATCACCATCATCACCAC**

**(SEQ ID NO: 25), signal sequence (1-57), NYA-2143 (61-
798), FLAG-His tag (799-876)**

Fig. 33

NYA-1163 tag adduct

**MKHLWFFLLLVAAPRWVLSGEVQLVESGGGVVQPGRSLTPSCSASGFSIRSYDIHW
VRLAPGKGLEWVATISYDGSQKYFADSVKGRFTIFRDESENMVYLQMSGLRVEDTA
VYHCARGSSGHYEAFDIWGQGTMTVSSGGGGSGGGGSGGGGSQSVLTQPPSVSAA
PGQKVTISCSGSSSNIGNNYVSWYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSG
TSATLGITGLQTGDEADYYCGTWDSSLSAPWVFGGGTKVTVLGAAAGAGGDYKDDD
DKGAAAHHHHHH**

(SEQ ID NO: 26), signal sequence (1-19), NYA-1163 (21-266), FLAG-His tag (267-292)

Fig. 34

NYA-2023 tag adduct

**MKHLWFFLLLVAAPRWVLSGEVQLVESGGGVVQPGRSLTPSCSASGFSIRSYDIHW
VRQAPGKGLEWVATISYDGSQKYFADSVKGRFTIFRDESENMVYLQMSGLRVEDTA
VYHCARGSSGHYEAFDIWGQGTMTVSSGGGGSGGGGSGGGGSQSVLTQPPSVSAA
PGQKVTISCSGSSSNIGNWYVSWYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSG
TSATLGITGLQTGDEADYYCGTWDSSLSAPWVFGGGTKVTVLGAAAGAGGDYKDDD
DKGAAAHHHHHH**

(SEQ ID NO: 27), signal sequence (1-19), NYA-2023 (21-266), FLAG-His tag (267-292)

Fig. 35

NYA-2027 tag adduct

**MKHLWFFLLLVAAPRWVLSGEVQLVESGGGVVQPGRSLTPSCSASGFSIRSYDIHW
VRQAPGKGLEWVATISYDGSQKYFADSVKGRFTIFRDESENMVYLQMSGLRVEDTA
VYHCARGSSGHYEAFDIWGQGTMTVSSGGGGSGGGGSGGGGSQSVLTQPPSVSAA
PGQKVTISCSGSSSNIGNNYVSWYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSG
TSATLGITGLQTGDEADYYCGSWDSSLSAPWVFGGGTKVTVLGAAAGAGGDYKDDD
DKGAAAHHHHHH**

**(SEQ ID NO: 28), signal sequence (1-19), NYA-2027(21-
266), FLAG-His tag (267-292)**

Fig. 36

NYA-1143 tag adduct

**MKHLWFFLLLVAAPRWVLSGEVQLVESGGGVVQPGRSLTPSCSASGFSIRSYDIHW
VRLAPGKGLEWVATISYDGSQKYFADSVKGRFTIFRDESENMVYLQMSGLRVEDTA
VYHCARGSSGHYEAFDIWGQGTMTVSSGGGGSGGGGSGGGGSQSVLTQPPSVSAA
PGQKVTISCSGSSSNIGNWYVSWYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSG
TSATLGITGLQTGDEADYYCGTWDSSLSAPWVFGGGTKVTVLGAAAGAGGDYKDDD
DKGAAAHHHHHH**

(SEQ ID NO: 29), signal sequence (1-19), NYA-1143 (21-266), FLAG-His tag (267-292)

Fig. 37

NYA-2143 tag adduct

**MKHLWFFLLLVAAPRWVLSGEVQLVESGGGVVQPGRSLTPSCSASGFSIRSYDIHW
VRLAPGKGLEWVATISYDGSQKYFADSVKGRFTIFRDESENMVYLQMSGLRVEDTA
VYHCARGSSGHYEAFDIWGQGTMTVSSGGGGSGGGGSGGGGSQSVLTQPPSVSAA
PGQKVTISCSGSSSNIGNWYVSWYQRLPGTAPKLLIYDNNKRPSGIPDRFSGSKSG
TSATLGITGLQTGDEADYYCGTWDSSLSAPWVFGGGTKVTVLGAAAGAGGDYKDDD
DKGAAAHHHHHH**

(SEQ ID NO: 30), signal sequence (1-19), NYA-2143 (21-266), FLAG-His tag (267-292)

Fig. 38

NYA-1154 tag adduct

ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGGCAGCTCCCAGATGGGTGCTGAG
CGGAGAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCC
TGACACCCTCCTGTTCAAGCTCTGGATTCTCCATCCGTAGTTATGATATGCACTGG
GTCCGCCAGGCTCCAGGCAAGGGGCTAGAGTGGGTGGCCACTATATCATATGATGG
AAGTCAGAAGTACTTCGCAGACTCCGTGAAGGGCCGATTTACCATCTTCAGAGACG
AATCGGAGAACATGGTGTATCTGCAAATGAGCGGCCTGAGAGTTGAGGACACGGCC
GTTTATCACTGTGCGAGAGGGAGTAGTAATCATTATGAGGCTTTTGATATCTGGGG
CCAAGGGACAATGGTCACCGTCTCTTCAGGTGGAGGCGGTTTCAGGCGGAGGTGGCA
GCGGCGGTGGCGGGAGTCAGTCTGTGTTGACGCAGCCGCCCTCAGTGTCTGCGGCC
CCAGGACAGAAGGTCACCATCTCCTGCTCTGGAAGCAGCTCCAACATTGGGAATAA
TTATGTATCCTGGTACCAGCGGCTCCCAGGAACAGCCCCAACTCCTCATTTATG
ACAATAATAAGCGACCCTCAGGGATTCTTGACCGATTCTCTGGCTCCAAGTCTGGC
ACGTCAGCCACCCTGGGCATCACCGGACTCCAGACTGGGGACGAGGCCGATTACTA
CTGCGGAGCATGGGATAGCAGCCTGAGTGCCCTTGGGTGTTGCGCGGAGGGACCA
AGGTCACCGTCCTAGGCGCGGCCGCAGGTGCAGGTGGTGATTACAAAGATGATGAC
GATAAAGGTGCAGCGGCGCATCACCATCATCACCAC

(SEQ ID NO: 31), signal sequence (1-57), NYA-1154(61-798), FLAG-His tag (799-876)

Fig. 39

NYA-1154 tag adduct

**MKHLWFFLLLVAAPRWVLSGEVQLVESGGGVVQPGRSLTPSCSASGFSIRSYDMHW
VRQAPGKGLEWVATISYDGSQKYFADSVKGRFTIFRDESENMVYLQMSGLRVEDTA
VYHCARGSSNHYEAFDIWGQGTMTVSSGGGGSGGGGSGGGGSQSVLTQPPSVSAA
PGQKVTISCSGSSSNIGNNYVSWYQRLPGTAPKLLIYDNNKRPSGIPDRFSGSKSG
TSATLGITGLQTGDEADYYCGAWDSSLSAPWVFGGGTKVTVLGAAAGAGGDYKDDD
DKGAAAHHHHHH**

(SEQ ID NO: 32), signal sequence (1-19), NYA-1154(21-266), FLAG-His tag (267-292)

Fig. 40

HLA-A*0201 (GenBank:ASA47534.1) truncate
MSHSMRYFFTSVSRPGRGEPRIAVGYVDDTQFVRFDSDAASQRMEPRAPWIEQEG
PEYWDGETRKVKAHSQTHRVDLGTLRGYYNQSEAGSHTVQRMYGCDVGSDWRFLRG
YHQYAYDGKDYIALKEDLRSWTAADMAAQTTKHKWEAAHVAEQLRAYLEGTCVEWL
RRYLENGKETLQRTDAPKTHMTHHAVSDHEATLRCWALSFYPAEITLTWQRDGEDQ
TQDTELVETRPAGDGTFFQKWAAVVPSGQEQRYTCHVQHEGLPKPLTLRWEGLNDI
FEAQKIEWHE
(SEQ ID NO: 33)

Fig. 41

β 2-microglobulin

MIQRTPKIQVYSRHPAENGKSNFLNCYVSGFHPSDIEVDLLKNGERIEKVEHSDLS

FSKDWSFYLLYYTEFTPTEKDEYACRVNHVTLSPKIVKWDRDM

(SEQ ID NO: 34)

Fig. 42

NYA-2035 tag adduct

**ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGGCAGCTCCCAGATGGGTGCTGAG
CGGAGAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCC
TGACACCCTCCTGTTCAAGCTCTGGATTCTCCATCCGTAGCTATGATATACACTGG
GTCCGCCTGGCTCCAGGCAAGGGGCTAGAGTGGGTGGCCACTATATCATATGATGG
AAGTCAGAAGTACTTCGCAGACTCCGTGAAGGGCCGATTTACCATCTTCAGAGACG
AATCGGAGAACATGGTGTATCTGCAAATGAGCGGCCTGAGAGTTGAGGACACGGCT
GTTTATCACTGTGCGAGAGGGAGTAGTGGTCATTATGAGGCTTTTGATATCTGGGG
CCAAGGGACAATGGTCACCGTCTCTTCAGGTGGAGGCGGTTTCAGGCGGAGGTGGCA
GCGGCGGTGGCGGGAGTCAGTCTGTGTTGACGCAGCCGCCCTCAGTGTCTGCGGCC
CCAGGACAGAAGGTCACCATCTCCTGCTCTGGAAGCAGCTCCAACATTGGGAATTG
GAAGGTATCCTGGTACCAGCAGCTCCCAGGAACAGCCCCAACTCCTCATTTATG
ACAATAATAAGCGACCCTCAGGGATTCTTGACCGATTCTCTGGCTCCAAGTCTGGC
ACGTCAGCCACCCTGGGCATCACCGGACTCCAGACTGGGGACGAGGCCGATTATTA
CTGCGGAACATGGGATAGCAGCCTGAGTGCCCTTGGGTGTTGCGCGGAGGGACCA
AGGTCACCGTCCTAGGCGCGGCCGCAGGTGCAGGTGGTGATTACAAAGATGATGAC
GATAAAGGTGCAGCGGCGCATCACCATCATCACCAC**

(SEQ ID NO: 35), signal sequence (1-57), NYA-2035 (61-798), FLAG-His tag (799-876)

Fig. 43

NYA-2035 tag adduct

**MKHLWFFLLLVAAPRWVLSGEVQLVESGGGVVQPGRSLTPSCSASGFSIRSYDIHW
VRLAPGKGLEWVATISYDGSQKYFADSVKGRFTIFRDESENMVYLQMSGLRVEDTA
VYHCARGSSGHYEAFDIWGQGTMTVSSGGGGSGGGGSGGGGSQSVLTQPPSVSAA
PGQKVTISCSGSSSNIGNWKVSWYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSG
TSATLGITGLQTGDEADYYCGTWDSSLSAPWVFGGGTKVTVLGAAAGAGGDYKDDD
DKGAAAHHHHHH**

(SEQ ID NO: 36), signal sequence (1-19), NYA-2035 (21-266), FLAG-His tag (267-292)

Fig. 44

NYA-1143-VH01

**EVQLVESGGGLVQPGGSLRLSCAASGFSIRSYDIHWVRLAPGKGLEWVATISYDGS
QKYYADSVKGRFTISRDESKNTLYLQMNSLRAEDTAVYHCARGSSGHYEAFDIWGQ
GTLVTVSS**

(SEQ ID NO: 37)

Fig. 45

NYA-1143-VH02

**QVQLVESGGGVVQPGRSLRLSCAASGFSIRSYDMHWVRQAPGKGLEWVATISYDGS
QKYYADSVKGRFTISRDN SKNTLYLQMSSLRAEDTAVYHCARGSSGHYEAFDIWGQ
GTLVTVSS**

(SEQ ID NO: 38)

Fig. 46

NYA-1143-VH03

**EVQLVESGGGLVQPGGSLRLSCAASGFSIRSYDIHWVRQAPGKGLEWVATISYDGS
QKYYADSVKGRFTISRDESKNTLYLQMNSLRAEDTAVYHCARGSSGHYEAFDIWGQ
GTLVTVSS**

(SEQ ID NO: 39)

Fig. 47

NYA-1143-VL01

QSVLTQPPSASGTPGQRTISCSGSSSNIGNWYVSWYQQLPGTAPKLLIYDNNKRP
SGVPDRFSGSKSGTSASLAISGLQSEDEADYYCGTWDSLSAPWVFGGGTKLTVL
(SEQ ID NO: 40)

Fig. 48

NYA-2044 tag adduct

**ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGGCAGCTCCCAGATGGGTGCTGAG
CGGTGAGGTACAGCTGGTGGAATCCGGTGGAGGCCTTGTGCAACCGGGAGGCTCCC
TGC GACTCTCTTGCGCCGCATCTGGCTTTTCCATACGATCCTACGATATTCATTGG
GTCCGACTCGCCCCTGGCAAAGGTCTTGAATGGGTTGCCACTATCTCCTACGACGG
GTCTCAGAAATATTATGCGGATTCAGTGAAGGGGCGGTTTACAATTTACGAGACG
AGTCAAAGAATACACTGTACCTCCAAATGAATTCAGTGAAGAGCCGAGGATACTGCA
GTCTATCATTGTGCAAGAGGGTCTCAGGCCACTACGAGGCCTTTGATATATGGGG
CCAAGGCACCTTGGTAACCGTTAGTAGCGGAGGTGGAGGAAGCGGAGGCGGCGGTT
CCGGAGGAGGTGGAAGTCAATCCGTTCTGACTCAGCCACCCTCCGTGAGTGCAGCG
CCTGGACAGAAGGTCACAATATCATGTTCTGGCTCTTCAAGCAACATCGGAAACTG
GTACGTGAGCTGGTACCAGCAGCTCCCCGGCACGGCGCCCAAGCTTCTGATATATG
ACAACAACAAACGGCCCAGTGAATCCCTGACAGATTCAGTGGGTCTAAAAGTGGT
ACAAGCGCTACCCTGGGTATCACCGGATTGCAGACCGGAGATGAGGCGGACTATTA
TTGCGGAACCTGGGACTCCAGCCTGAGCGCTCCCTGGGTTTTTCGGCGGAGGTACTA
AGGTTACCGTCTTGGGCGCGGCCGCAGGTGCAGGTGGTGATTACAAAGATGATGAC
GATAAAGGTGCAGCGGCGCATCACCATCATCACCAC**

(SEQ ID NO: 41), signal sequence (1-57), NYA-2044(61-798), FLAG-His tag (799-876)

Fig. 49

NYA-2045 tag adduct

**ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGGCAGCTCCCAGATGGGTGCTGAG
CGGTGAGGTACAGCTGGTGGAATCCGGTGGAGGCCTTGTGCAACCGGGAGGCTCCC
TGC GACTCTCTTGCGCCGCATCTGGCTTTTCCATACGATCCTACGATATTCATTGG
GTCCGACTCGCCCCCTGGCAAAGGTCTTGAATGGGTTGCCACTATCTCCTACGACGG
GTCTCAGAAATATTATGCGGATTCAGTGAAGGGGCGGTTTACAATTTACGAGACG
AGTCAAAGAATACACTGTACCTCCAAATGAATTCAGTGAAGAGCCGAGGATACTGCA
GTCTATCATTGTGCAAGAGGGTCTCAGGCCACTACGAGGCCTTTGATATATGGGG
CCAAGGCACCTTGGTAACCGTTAGTAGCGGAGGTGGAGGAAGCGGAGGCGGCGGTT
CCGGAGGAGGTGGAAGTCAATCCGTTCTGACTCAGCCACCCTCCGCCTCTGGCACC
CCGGGCCAACGGGTCACAATATCATGTTCTGGCTCTTCAAGCAACATCGGAAACTG
GTACGTGAGCTGGTACCAGCAGCTCCCCGGCACGGCGCCCAAGCTTCTGATATATG
ACAACAACAAACGGCCCAGTGGAGTTCCTGACAGATTCAGTGGGTCTAAAAGTGGT
ACAAGCGCTAGCCTGGCCATAAGTGGTCTGCAGAGTGAAGATGAGGCGGACTATTA
TTGCGGAACCTGGGACTCCAGCCTGAGCGCTCCCTGGGTTTTTCGGCGGAGGTACTA
AGCTGACCGTCTTGGGCGCGGCCGCAGGTGCAGGTGGTGATTACAAAGATGATGAC
GATAAAGGTGCAGCGGCGCATCACCATCATCACCAC**

**(SEQ ID NO: 42), signal sequence (1-57), NYA-2045 (61-
798), FLAG-His tag (799-876)**

Fig. 50

NYA-2047 tag adduct

**ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGGCAGCTCCCAGATGGGTGCTGAG
CGGTCAAGTACAGCTGGTGGAATCCGGTGGAGGCGTGGTCCAGCCGGGACGCAGCT
TGAGACTGTCCTGCGCTGCATCTGGCTTTTCCATACGATCCTACGATATGCACTGG
GTTCCGCAAGCCCCCTGGCAAAGGTCTTGAATGGGTTGCCACTATCTCCTACGACGG
GTCTCAGAAATATTACGCGGATTTCAGTGAAGGGGCGGTTTACAATTTACGGGACA
ATTCAAAGAATACCTTGTATCTCCAGATGTCTTCACTGAGAGCCGAGGATACTGCA
GTCTATCATTGTGCAAGAGGGTCTCAGGCCACTACGAGGCCTTTGATATATGGGG
CCAAGGCACCTTGGTAACCGTTAGTAGCGGAGGTGGAGGAAGCGGAGGCGGCGGTT
CCGGAGGAGGTGGAAGTCAATCCGTTCTGACTCAGCCACCCTCCGTGAGTGCAGCG
CCTGGACAGAAGGTCACAATATCATGTTCTGGCTCTTCAAGCAACATCGGAAACTG
GTACGTGAGCTGGTACCAGCAGCTCCCCGGCACGGCGCCCAAGCTTCTGATATATG
ACAACAACAAACGGCCCAGTGGAATCCCTGACAGATTTCAGTGGGTCTAAAAGTGGT
ACAAGCGCTACCCTGGGTATCACCGGATTGCAGACCGGAGATGAGGCGGACTATTA
TTGCGGAACCTGGGACTCCAGCCTGAGCGCTCCCTGGGTTTTTCGGCGGAGGTACTA
AGGTTACCGTCTTGGGCGCGGCCGCAGGTGCAGGTGGTGATTACAAAGATGATGAC
GATAAAGGTGCAGCGGCGCATCACCATCATCACCAC**

(SEQ ID NO: 43), signal sequence (1-57), NYA-2047(61-798), FLAG-His tag (799-876)

Fig. 51

NYA-2048 tag adduct

**ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGGCAGCTCCCAGATGGGTGCTGAG
CGGACAAGTTCAACTCGTGGAATCTGGTGGAGGGGTGGTACAACCAGGCCGGTCAC
TTAGACTGTCCTGCGCTGCGAGTGGATTTTCCATCAGATCTTACGACATGCACTGG
GTTCGCCAAGCACCCGGAAAGGGTTTGGAATGGGTGGCTACGATCTCCTACGATGG
ATCCCAGAAGTATTACGCCGACAGCGTCAAGGGCCGATTTACAATATCACGGGACA
ATTCAAAGAATACCTTGTATCTCCAGATGTCTTCACTGAGAGCCGAGGATACTGCA
GTCTATCATTGTGCAAGAGGGTCCTCAGGCCACTACGAGGCCTTTGATATATGGGG
CCAAGGCACCTTGGTAACCGTTAGTAGCGGAGGTGGAGGAAGCGGAGGCGGCGGTT
CCGGAGGAGGTGGAAGTCAATCCGTTCTGACTCAGCCACCCTCCGCCTCTGGCACC
CCGGGCCAACGGGTCACAATATCATGTTCTGGCTCTTCAAGCAACATCGGAAACTG
GTACGTGAGCTGGTACCAGCAGCTCCCCGGCACGGCGCCCAAGCTTCTGATATATG
ACAACAACAAACGGCCCAGTGGAGTTCCTGACAGATTCAGTGGGTCTAAAAGTGGT
ACAAGCGCTAGCCTGGCCATAAGTGGTCTGCAGAGTGAAGATGAGGCGGACTATTA
TTGCGGAACCTGGGACTCCAGCCTGAGCGCTCCCTGGGTTTTTCGGCGGAGGTACTA
AGCTGACCGTCTTGGGCGCGGCCGCAGGTGCAGGTGGTGATTACAAAGATGATGAC
GATAAAGGTGCAGCGGCGCATCACCATCATCACCAC**

(SEQ ID NO: 44), signal sequence (1-57), NYA-2048(61-798), FLAG-His tag (799-876)

Fig. 52

NYA-2060 tag adduct

**ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGGCAGCTCCCAGATGGGTGCTGAG
CGGTGAGGTACAGCTGGTGGAATCCGGTGGAGGCCTTGTGCAACCGGGAGGCTCCC
TGC GACTCTCTTGCGCCGCATCTGGCTTTTCCATACGATCCTACGATATTCATTGG
GTCCGACAAGCCCCCTGGCAAAGGTCTTGAATGGGTTGCCACTATCTCCTACGACGG
GTCTCAGAAATATTATGCGGATTCAGTGAAGGGGCGGTTTACAATTTACGAGACG
AGTCAAAGAATACACTGTACCTCCAAATGAATTCAGTGAAGAGCCGAGGATACTGCA
GTCTATCATTGTGCAAGAGGGTCTCAGGCCACTACGAGGCCTTTGATATATGGGG
CCAAGGCACCTTGGTAACCGTTAGTAGCGGAGGTGGAGGAAGCGGAGGCGGCGGTT
CCGGAGGAGGTGGAAGTCAATCCGTTCTGACTCAGCCACCCTCCGTGAGTGCAGCG
CCTGGACAGAAGGTCACAATATCATGTTCTGGCTCTTCAAGCAACATCGGAAACTG
GTACGTGAGCTGGTACCAGCAGCTCCCCGGCACGGCGCCCAAGCTTCTGATATATG
ACAACAACAAACGGCCCAGTGAATCCCTGACAGATTCAGTGGGTCTAAAAGTGGT
ACAAGCGCTACCCTGGGTATCACCGGATTGCAGACCGGAGATGAGGCGGACTATTA
TTGCGGAACCTGGGACTCCAGCCTGAGCGCTCCCTGGGTTTTTCGGCGGAGGTACTA
AGGTTACCGTCTTGGGCGCGGCCGCAGGTGCAGGTGGTGATTACAAAGATGATGAC
GATAAAGGTGCAGCGGCGCATCACCATCATCACCAC**

(SEQ ID NO: 45), signal sequence (1-57), NYA-2060(61-798), FLAG-His tag (799-876)

Fig. 53

NYA-2061 tag adduct

**ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGGCAGCTCCCAGATGGGTGCTGAG
CGGTGAGGTACAGCTGGTGGAATCCGGTGGAGGCCTTGTGCAACCGGGAGGCTCCC
TGC GACTCTCTTGCGCCGCATCTGGCTTTTCCATACGATCCTACGATATTCATTGG
GTCCGACAAGCCCCCTGGCAAAGGTCTTGAATGGGTTGCCACTATCTCCTACGACGG
GTCTCAGAAATATTATGCGGATTCAGTGAAGGGGCGGTTTACAATTTACGAGACG
AGTCAAAGAATACACTGTACCTCCAAATGAATTCAGTGAAGAGCCGAGGATACTGCA
GTCTATCATTGTGCAAGAGGGTCTCAGGCCACTACGAGGCCTTTGATATATGGGG
CCAAGGCACCTTGGTAACCGTTAGTAGCGGAGGTGGAGGAAGCGGAGGCGGCGGTT
CCGGAGGAGGTGGAAGTCAATCCGTTCTGACTCAGCCACCCTCCGCCTCTGGCACC
CCGGGCCAACGGGTCACAATATCATGTTCTGGCTCTTCAAGCAACATCGGAAACTG
GTACGTGAGCTGGTACCAGCAGCTCCCCGGCACGGCGCCCAAGCTTCTGATATATG
ACAACAACAAACGGCCCAGTGGAGTTCCTGACAGATTCAGTGGGTCTAAAAGTGGT
ACAAGCGCTAGCCTGGCCATAAGTGGTCTGCAGAGTGAAGATGAGGCGGACTATTA
TTGCGGAACCTGGGACTCCAGCCTGAGCGCTCCCTGGGTTTTTCGGCGGAGGTACTA
AGCTGACCGTCTTGGGCGCGGCCGCAGGTGCAGGTGGTGATTACAAAGATGATGAC
GATAAAGGTGCAGCGGCGCATCACCATCATCACCAC**

(SEQ ID NO: 46), signal sequence (1-57), NYA-2061 (61-798), FLAG-His tag (799-876)

Fig. 54

NYA-2044 tag adduct

**MKHLWFFLLLVAAPRWVLSGEVQLVESGGGLVQPGGSLRLSCAASGFSIRSYDIHW
VRLAPGKGLEWVATISYDGSQKYYADSVKGRFTISRDESKNTLYLQMNSLRAEDTA
VYHCARGSSGHYEAFDIWGQGTTLVTVSSGGGGSGGGGSGGGGSQSVLTQPPSVSAA
PGQKVTISCSGSSSNIGNWYVSWYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSG
TSATLGITGLQTGDEADYYCGTWDSSLSAPWVFGGGTKVTVLGAAAGAGGDYKDDD
DKGAAAHHHHHH**

(SEQ ID NO: 47), signal sequence (1-19), NYA-2044(21-266), FLAG-His tag (267-292)

Fig. 55

NYA-2045 tag adduct

**MKHLWFFLLLVAAPRWVLSGEVQLVESGGGLVQPGGSLRLSCAASGFSIRSYDIHW
VRLAPGKGLEWVATISYDGSQKYYADSVKGRFTISRDESKNTLYLQMNSLRAEDTA
VYHCARGSSGHYEAFDIWGGTTLVTVSSGGGGSGGGGSGGGGSQSVLTQPPSASGT
PGQRTVISCSSSSNIGNWYVSWYQQLPGTAPKLLIYDNNKRPSGVPDRFSGSKSG
TSASLAISGLQSEDEADYYCGTWDSSLSAPWVFGGGTKLTVLGAAAGAGGDYKDDD
DKGAAAHHHHHH**

(SEQ ID NO: 48), signal sequence (1-19), NYA-2045 (21-266), FLAG-His tag (267-292)

Fig. 56

NYA - 0082

**EVQLVESGGGVVQPGRSLTPSCSASGFSIRSYDIHWVRQAPGKGLEWVATISYDGS
QKYFADSVKGRFTIFRDESENMVYLQMSGLRVEDTAVYHCARGSSGHYEAFDIWGQ
GTMVTVSSGGGGSGGGGSGGGGSQSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNY
VSWYQRLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGTSATLGITGLQTGDEADYYC
GSWDSSLSAPWVFGGGTKVTVL
(SEQ ID NO: 49)**

Fig. 57

NYA-2047 tag adduct

**MKHLWFFLLLVAAPRWVLSGQVQLVESGGGVVQPGRSLRLSCAASGFSIRSYDMHW
VRQAPGKGLEWVATISYDGSQKYYADSVKGRFTISRDN SKNTLYLQMSSLRAEDTA
VYHCARGSSGHYEAFDIWGQGT LVTVSSGGGGSGGGGSGGGGSQSVLTQPPSVSAA
PGQKVTISCSGSSSNIGNWYVSWYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSG
TSATLGITGLQTGDEADYYCGTWDSSLSAPWVFGGGTKVTVLGAAAGAGGDYKDDD
DKGAAAHHHHHH**

**(SEQ ID NO: 50), signal sequence (1-19), NYA-2047(21-
266), FLAG-His tag (267-292)**

Fig. 58

NYA-2048 tag adduct

**MKHLWFFLLLVAAPRWVLSGQVQLVESGGGVVQPGRSLRLSCAASGFSIRSYDMHW
VRQAPGKGLEWVATISYDGSQKYYADSVKGRFTISRDN SKNTLYLQMSSLRAEDTA
VYHCARGSSGHYEAFDIWGQGT LVTVSSGGGGSGGGGSGGGGSQSVLTQPPSASGT
PGQRTISCSGSSSNIGNWYVSWYQQLPGTAPKLLIYDNNKRPSGVPDRFSGSKSG
TSASLAISGLQSEDEADYYCGTWDSSLSAPWVFGGGTKLTVLGAAAGAGGDYKDDD
DKGAAAHHHHHH**

**(SEQ ID NO: 51), signal sequence (1-19), NYA-2048 (21-
266), FLAG-His tag (267-292)**

Fig. 59

NYA-2060 tag adduct

**MKHLWFFLLLVAAPRWVLSGEVQLVESGGGLVQPGGSLRLSCAASGFSIRSYDIHW
VRQAPGKGLEWVATISYDGSQKYYADSVKGRFTISRDESKNTLYLQMNSLRAEDTA
VYHCARGSSGHYEAFDIWGQGTTLTVSSGGGGSGGGGSGGGGSQSVLTQPPSVSAA
PGQKVTISCSGSSSNIGNWYVSWYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSG
TSATLGITGLQTGDEADYYCGTWDSSLSAPWVFGGGTKVTVLGAAAGAGGDYKDDD
DKGAAAHHHHHH**

**(SEQ ID NO: 52), signal sequence (1-19), NYA-2060(21-
266), FLAG-His tag (267-292)**

Fig. 60

NYA-2061 tag adduct

**MKHLWFFLLLVAAPRWVLSGEVQLVESGGGLVQPGGSLRLSCAASGFSIRSYDIHW
VRQAPGKGLEWVATISYDGSQKYYADSVKGRFTISRDESKNTLYLQMNSLRAEDTA
VYHCARGSSGHYEAFDIWGGTTLVTVSSGGGGSGGGGSGGGGSQSVLTQPPSASGT
PGQRTVISCSSSSNIGNWYVSWYQQLPGTAPKLLIYDNNKRPSGVPDRFSGSKSG
TSASLAISGLQSEDEADYYCGTWDSSLSAPWVFGGGTKLTVLGAAAGAGGDYKDDD
DKGAAAHHHHHH**

**(SEQ ID NO: 53), signal sequence (1-19), NYA-2061 (21-
266), FLAG-His tag (267-292)**

Fig. 61

NYA-0001-CDRH1	GFSIRSYD
NYA-0001-CDRH2	ISYDGSQK
NYA-0001-CDRH3	ARGSSGHYEAFDI
NYA-0001-CDRL1	SSNIGNNY
NYA-0001-CDRL2	DNN
NYA-0001-CDRL3	GTWDSSLAPWV

(SEQ ID NOs: 54 to 59)

Fig. 62

NYA-2023-CDRL1
SSNIGNWY
(SEQ ID NO: 60)

Fig. 63

**NYA-2027-CDRL3
GSWDSSLAPWV
(SEQ ID NO: 61)**

Fig. 64

NYA-1154-CDRH3	ARGSSNHYEAFDI
NYA-1154-CDRL3	GAWDSSLAPWV
(SEQ ID NOS: 62 and 63)	

Fig. 65

NYA-0035-CDRL1
SSNIGNWK
(SEQ ID NO: 64)

Fig. 66

NYC-0003 tag adduct

ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGGCAGCTCCCAGATGGGTGCTGAG
CGGCGAAGTCCAGCTGTTGGAGTCAGGTGGCGGATTGGTGCAACCTGGCGGGTCAC
TGAGGCTGAGTTGTGCAGCTAGCGGCTTCACATTCTCTACGTATCAGATGAGCTGG
GTGAGACAGGCTCCAGGAAAGGGTCTGGAATGGGTGAGCGGGATTGTGTCTAGCGG
TGGCTCCACTGCCTATGCCGATAGCGTAAAAGGCCGCTTTACGATCTCTCGGGACA
ACTCTAAGAACACACTCTATCTGCAGATGAATTCCTTAGAGCCGAAGATACCGCC
GTGTACTACTGTGCTGGGGAAGTCTCCCGTATTACGGTATGGACGTTTGGGGCCA
AGGCACCACTGTCACAGTGAGTTCCGGTGGAGGCGGGTCAGGCGGAGGCGGTAGTG
GAGGTGGAGGATCACAAAGCGAGCTGACACAGCCTAGGTCCGTATCCGGAAGTCCA
GGGCAGAGCGTCACCATCAGCTGCACTGGCACCTCTCGAGATGTCGGCGGATACAA
CTACGTGTCTTGGTATCAGCAGCATCCCGGCAAAGCGCCCAAACATCATACACG
ACGTGATTGAGCGGTCCAGTGGGGTTCCCGATCGTTTCAGCGGGTCAAAGTCCGGA
AATACGCAAGCCTGACCATTTCTGGGCTTCAGGCAGAGGATGAGGCTGACTACTA
CTGCTGGTCCTTTGCCGGGAGCTATTACGTGTTTGGGACAGGGACTGACGTGACTG
TTCTGGGCGCGGCCGAGGTGCAGGTGGTGATTACAAAGATGATGACGATAAAGGT
GCAGCGGCGCATCACCATCATCACCAC

(SEQ ID NO: 65), signal sequence (1-57), NYC-0003 (61-789), FLAG-His tag (789-867)

Fig. 67

NYC-0004 tag adduct

ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGGCAGCTCCCAGATGGGTGCTGAG
CGGCGAAGTCCAGCTGTTGGAGTCAGGTGGCGGATTGGTGCAACCTGGCGGGTCAC
TGAGGCTGAGTTGTGCAGCTAGCGGCTTCACATTCTCTACGTATCAGATGAGCTGG
GTGAGACAGGCTCCAGGAAAGGGTCTGGAATGGGTGAGCGGGATTGTGTCTAGCGG
TGGCTCCACTGCCTATGCCGATAGCGTAAAAGGCCGCTTTACGATCTCTCGGGACA
ACTCTAAGAACACACTCTATCTGCAGATGAATTCCTTAGAGCCGAAGATACCGCC
GTGTACTACTGTGCTGGGGAAGTCTCCCGTATTACGGTATGGACGTTTGGGGCCA
AGGCACCACTGTCACAGTGAGTTCCGGTGGAGGCGGGTCAGGCGGAGGCGGTAGTG
GAGGTGGAGGATCACAAAGCGAGCTGACACAGCCTAGGTCCGTATCCGGAAGTCCA
GGGCAGAGCGTCACCATCAGCTGCACTGGCACCGAGCGAGATGTCGGCGGATACAA
CTACGTGTCTTGGTATCAGCAGCATCCCGGCAAAGCGCCCAAACATCATACACG
ACGTGATTGAGCGGTCCAGTGGGGTTCCCGATCGTTTCAGCGGGTCAAAGTCCGGA
AATACCGCAAGCCTGACCATTTCTGGGCTTCAGGCAGAGGATGAGGCTGACTACTA
CTGCTGGTCCTTTGCCGGGGGCTATTACGTGTTTGGGACAGGGACTGACGTGACTG
TTCTGGGCGCGGCCGCAGGTGCAGGTGGTGATTACAAAGATGATGACGATAAAGGT
GCAGCGGCGCATCACCATCATCACCAC

(SEQ ID NO: 66), signal sequence (1-57), NYC-0004(61-789), FLAG-His tag (789-867)

Fig. 68

NYC-0003 tag adduct

**MKHLWFFLLLVAAPRWVLSGEVQLLES GGGLVQP GGSLRLSCAASGFTFSTYQMSW
VRQAPGKGLEWVSGIVSSGGSTAYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTA
VYYCAGELL PYYGMDVWGQTTTVTVSSGGGGSGGGGSGGGGSQSELTQPRSVSGSP
GQSVTISCTGTSRDVGGYNYVSWYQQHPGKAPKLI IHDVIERSSGVPDRFSGSKSG
NTASLTISGLQAEDEADYYCWSFAGSY YVFGTGTDTV LGAAAGAGGDYKDDDDKG
AAAHHHHHH**

**(SEQ ID NO: 67), signal sequence (1-19), NYC-0003 (21-
263), FLAG-His tag (264-289)**

Fig. 69

NYC-0004 tag adduct

**MKHLWFFLLLVAAPRWVLSGEVQLLESGGGLVQPGGSLRLSCAASGFTFSTYQMSW
VRQAPGKGLEWVSGIVSSGGSTAYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTA
VYYCAGELL PYYGMDVWGQTTTVTVSSGGGGSGGGGSGGGGSQSELTQPRSVSGSP
GQSVTISCTGTERDVGGYNYVSWYQQHPGKAPKLIHDVIERSSGVPDRFSGSKSG
NTASLTISGLQAEDEADYYCWSFAGGYVFGTGTDTV LGAAAGAGGDYKDDDDKG
AAAHHHHHH**

**(SEQ ID NO: 68), signal sequence (1-19), NYC-0004(21-
263), FLAG-His tag (264-289)**

Fig. 70

NYA-0001 tag adduct

**ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGGCAGCTCCCAGATGGGTGCTGAG
CGGAGAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCC
TGACACCCTCCTGTTCAAGCTCTGGATTCTCCATCCGTAGTTATGATATACACTGG
GTCCGCCAGGCTCCAGGCAAGGGGCTAGAGTGGGTGGCCACTATATCATATGATGG
AAGTCAGAAGTACTTCGCAGACTCCGTGAAGGGCCGATTTACCATCTTCAGAGACG
AATCGGAGAACATGGTGTATCTGCAAATGAGCGGCCTGAGAGTTGAGGACACGGCT
GTTTATCACTGTGCGAGAGGGAGTAGTGGTCATTATGAGGCTTTTGATATCTGGGG
CCAAGGGACAATGGTCACCGTCTCTTCAGGTGGAGGCGGTTTCAGGCGGAGGTGGCA
GCGGCGGTGGCGGGAGTCAGTCTGTGTTGACGCAGCCGCCCTCAGTGTCTGCGGCC
CCAGGACAGAAGGTCACCATCTCCTGCTCTGGAAGCAGCTCCAACATTGGGAATAA
TTATGTATCCTGGTACCAGCAGCTCCCAGGAACAGCCCCAACTCCTCATTTATG
ACAATAATAAGCGACCCTCAGGGATTCTTGACCGATTCTCTGGCTCCAAGTCTGGC
ACGTCAGCCACCCTGGGCATCACCGGACTCCAGACTGGGGACGAGGCCGATTATTA
CTGCGGAACATGGGATAGCAGCCTGAGTGCCCTTGGGTGTTTCGGCGGAGGGACCA
AGGTCACCGTCCTAGGCGCGGCCGCAGGTGCAGGTGGTGATTACAAAGATGATGAC
GATAAAGGTGCAGCGGCGCATCACCATCATCACCAC**

**(SEQ ID NO: 69), signal sequence (1-57), NYA-0001 (61-
798), FLAG-His tag (799-876)**

Fig. 71

NYA-0001 tag adduct

**MKHLWFFLLLVAAPRWVLSGEVQLVESGGGVVQPGRSLTPSCSASGFSIRSYDIHW
VRQAPGKGLEWVATISYDGSQKYFADSVKGRFTIFRDESENMVYLQMSGLRVEDTA
VYHCARGSSGHYEAFDIWGQGTMTVSSGGGGSGGGGSGGGGSQSVLTQPPSVSAA
PGQKVTISCSGSSSNIGNNYVSWYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSG
TSATLGITGLQTGDEADYYCGTWDSSLSAPWVFGGGTKVTVLGAAAGAGGDYKDDD
DKGAAAHHHHHH**

**(SEQ ID NO: 70), signal sequence (1-19), NYA-0001 (21-
266), FLAG-His tag (267-292)**

Fig. 72

HC1

ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGGCAGCTCCCAGATGGGTGCTGAG
CGACAAAACCTCACACATGCCACCCTGCCAGCACCTGAAGCCGCAGGGGGACCCT
CAGTCTTCCTCTTCCCCCAAACCAAGGACACCCTCATGATCTCCCGGACCCCT
GAGGTCACATGCGTGGTGGTGTCAGTGAGCCACGAAGACCCTGAGGTCAAGTTCAA
CTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCCCGGGAGGAGC
AGTACAACAGCACGTACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGG
CTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCAT
CGAGAAAACCATCTCAAAGCCAAAGGCCAGCCCCGGGAACCACAGGTGTACGTGC
TGCCCCCATCCCGGGACGAGCTGACCAAGAACCAGGTCAGCCTGCTGTGCCTGGTC
AAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGCCAGCCCGA
GAACAACTACCTGACCTGGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCT
ACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGCAACGTCTTCTCATGC
TCCGTGATGCATGAGGCTCTGCACAACCACTACACCCAGAAGAGCCTCTCCCTGTC
TCCCGGCAAG

(SEQ ID NO: 71), signal sequence (1-57), hinge (58-87),
CH2 (88-417), CH3 (418-738)

Fig. 73

NYF - 0016 - HC2

ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGGCAGCTCCCAGATGGGTGCTGAG
CGGAGAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCC
TGACACCCTCCTGTTTCAGCGTCTGGATTCTCCATCCGTAGCTATGATATACACTGG
GTCCGCCTGGCTCCAGGCAAGGGGCTAGAGTGGGTGGCCACTATATCATATGATGG
AAGTCAGAACTACTTCGCAGACTCCGTGAAGGGCCGATTTACCATCTTCAGAGACG
AATCGGAGAACATGGTGTATCTGCAAATGAGCGGCCTGAGAGTTGAGGACACGGCT
GTTTATCACTGTGCGAGAGGGAGTAGTGGTCATTATGAGGCTTTTGATATCTGGGG
CCAAGGGACAATGGTCACCGTCTCTTCAGGTGGAGGCGGTTTCAGGCGGAGGTGGCA
GCGGCGGTGGCGGGAGTCAGTCTGTGTTGACGCGAGCCGCCCTCAGTGTCTGCGGCC
CCAGGACAGAAGGTCACCATCTCCTGCTCTGGAAGCAGCTCCAACATTGGGAATTG
GTATGTATCCTGGTACCAGCAGCTCCCAGGAACAGCCCCAACTCCTCATTTATG
ACAATAATAAGCGACCCTCAGGGATTCTGACCGATTCTCTGGCTCCAAGTCTGGC
ACGTCAGCCACCCTGGGCATCACCGGACTCCAGACTGGGGACGAGGCCGATTATTA
CTGCGGAACATGGGATAGCAGCCTGAGTGCCCTTTGGGTGTTGGGCGGAGGGACCA
AGGTCACCGTCTAGGGGGAGGCGGTTTCAGAAAGTGCAGCTGGTGGAATCCGGGGGG
GGCCTGGTGCAGCCTGGGGGGAGCCTGAGACTGAGTTGTGCCGCCTCTGGGGTGAC
ATTTAACTACTATGGCATGTCTTGATCCGCCAGGCACCTGGAAAGGGCCTGGAGT
GGGTGGCCAGCATCACTAGGTCCGGCGGGCGAATCTACTATCCCGACAGCGTCAAG
GGCAGGTTTACAATTTCCCGCGAGAACACACAGAAAACCTCTGTACCTGCAGATGAA
TAGCCTGAGAGCCGAAGATACAGCTGTGTACTATTGCACTCTGGACGGCAGGGATG
GGTGGGTGCGCTATTGGGGGCAGGGAACCCTGGTGACAGTCAGCTCCGGAGGAGGA
GGATCTGGCGGAGGAGGCAGTGGGGGAGGCGGGTCAAACCTTTATGCTCACTCAGCC
GTCCTCTGTTTCTGGCGTACCTGGCCAACGGGTGACCATTAGCTGTACGGGTAATA
CCGGGAATATCGGGTCTAACTACGTGAACTGGTATCAGCAGCTTCCAGGGACAGCT
CCCAAGTTGCTGATCTATCGCGACGACAAAAGACCCTCAGGGGTCCCTGACCGATT
TAGTGGCAGCAAAAGCGGTACTTCCGCTTCCCTGGCGATAACCGGCTTTCAGGCCG
AAGATGAGGCAGACTACTATTGCCAGTCATATTCCAGCGGCTTCATCTTCGGAGGC
GGAACATAAGCTGACAGTGTTGGCAGCCGAGCCCAAATCTTCTGACAAAACCTCACAC
ATGCCACACCCTGCCAGCACCTGAAGCCGCAGGGGGACCCTCAGTCTTCTCTTCC
CCCCAAAACCAAGGACACCCTCATGATCTCCCGGACCCTGAGGTCACATGCGTG
GTGGTGTCAGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGG
CGTGGAGGTGCATAATGCCAAGACAAAGCCCCGGGAGGAGCAGTACAACAGCACGT
ACCGGGTGGTCAGCGTCTCACCGTCTGCACCAGGACTGGCTGAATGGCAAGGAG
TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTC
CAAAGCCAAAGGCCAGCCCCGGGAACCACAGGTGTACGTGTACCCCCCATCCGGG
ACGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC
AGCGACATCGCCGTGGAGTGGGAGAGCAATGGCCAGCCCGAGAACAACTACAAGAC
CACCCCTCCCGTGCTGGACTCCGACGGCTCCTTCGCCCTCGTGAGCAAGCTCACCG
TGGACAAGAGCAGGTGGCAGCAGGGCAACGTCTTCTCATGCTCCGTGATGCATGAG
GCTCTGCACAACCACTACACCCAGAAGAGCCTCTCCCTGTCTCCCGGCAAG
(SEQ ID NO: 72), signal sequence (1-57), NYA-1143 (61-
798), linker (799-813), C3E-7085 (814-1533), linker
(1534-1539), hinge (1540-1584), CH2 (1585-1914), CH3
(1915-2235)

Fig. 74

NYF - 0019 - HC2

ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGGCAGCTCCCAGATGGGTGCTGAG
CGGAGAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCC
TGACACCCTCCTGTTTCAGCGTCTGGATTCTCCATCCGTAGCTATGATATACACTGG
GTCCGCCTGGCTCCAGGCAAGGGGCTAGAGTGGGTGGCCACTATATCATATGATGG
AAGTCAGAACTACTTCGCAGACTCCGTGAAGGGCCGATTTACCATCTTCAGAGACG
AATCGGAGAACATGGTGTATCTGCAAATGAGCGGCCTGAGAGTTGAGGACACGGCT
GTTTATCACTGTGCGAGAGGGAGTAGTGGTCATTATGAGGCTTTTGATATCTGGGG
CCAAGGGACAATGGTCACCGTCTCTTCAGGTGGAGGCGGTTTCAGGCGGAGGTGGCA
GCGGCGGTGGCGGGAGTCAGTCTGTGTTGACGCGAGCCGCCCTCAGTGTCTGCGGCC
CCAGGACAGAAGGTCACCATCTCCTGCTCTGGAAGCAGCTCCAACATTGGGAATTG
GTATGTATCCTGGTACCAGCGGCTCCCAGGAACAGCCCCAACTCCTCATTTATG
ACAATAATAAGCGACCCTCAGGGATTCTGACCGATTCTCTGGCTCCAAGTCTGGC
ACGTCAGCCACCCTGGGCATCACCGGACTCCAGACTGGGGACGAGGCCGATTATTA
CTGCGGAACATGGGATAGCAGCCTGAGTGCCCCTTGGGTGTTGGGCGGAGGGACCA
AGGTCACCGTCCTAGGGGGAGGCGGTTTCAGAAGTGCAGCTGGTGGAATCCGGGGGG
GGCCTGGTGCAGCCTGGGGGGAGCCTGAGACTGAGTTGTGCCGCCTCTGGGGTGAC
ATTTAACTACTATGGCATGTCTTGATCCGCCAGGCACCTGGAAAGGGCCTGGAGT
GGGTGGCCAGCATCACTAGGTCCGGCGGGCGAATCTACTATCCCGACAGCGTCAAG
GGCAGGTTTACAATTTCCCGCGAGAACACACAGAAAACCTCTGTACCTGCAGATGAA
TAGCCTGAGAGCCGAAGATACAGCTGTGTACTATTGCACTCTGGACGGCAGGGATG
GGTGGGTGCGCTATTGGGGGCAGGGAACCCTGGTGACAGTCAGCTCCGGAGGAGGA
GGATCTGGCGGAGGAGGCAGTGGGGGAGGCGGGTCAAACCTTTATGCTCACTCAGCC
GTCCTCTGTTTCTGGCGTACCTGGCCAACGGGTGACCATTAGCTGTACGGGTAATA
CCGGGAATATCGGGTCTAACTACGTGAACTGGTATCAGCAGCTTCCAGGGACAGCT
CCCAAGTTGCTGATCTATCGCGACGACAAAAGACCCTCAGGGGTCCCTGACCGATT
TAGTGGCAGCAAAAGCGGTACTTCCGCTTCCCTGGCGATAACCGGCTTTCAGGCCG
AAGATGAGGCAGACTACTATTGCCAGTCATATTCCAGCGGCTTCATCTTCGGAGGC
GGAACCTAAGCTGACAGTGTTGGCAGCCGAGCCCAAATCTTCTGACAAAACCTCACAC
ATGCCCACCCTGCCAGCACCTGAAGCCGCAGGGGGACCCTCAGTCTTCTCTTCC
CCCCAAAACCAAGGACACCCTCATGATCTCCCGGACCCTGAGGTCACATGCGTG
GTGGTGTCAGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGG
CGTGGAGGTGCATAATGCCAAGACAAAGCCCCGGGAGGAGCAGTACAACAGCACGT
ACCGGGTGGTCAGCGTCCTACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG
TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTC
CAAAGCCAAAGGCCAGCCCCGGGAACCACAGGTGTACGTGTACCCCCCATCCGGG
ACGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC
AGCGACATCGCCGTGGAGTGGGAGAGCAATGGCCAGCCCGAGAACAACTACAAGAC
CACCCCTCCCGTGCTGGACTCCGACGGCTCCTTCGCCCTCGTGAGCAAGCTCACCG
TGGACAAGAGCAGGTGGCAGCAGGGCAACGTCTTCTCATGCTCCGTGATGCATGAG
GCTCTGCACAACCACTACACCCAGAAGAGCCTCTCCCTGTCTCCCGGCAAG
(SEQ ID NO: 73), signal sequence (1-57), NYA-2143 (61-
798), linker (799-813), C3E-7085 (814-1533), linker
(1534-1539), hinge (1540-1584), CH2 (1585-1914), CH3
(1915-2235)

Fig. 75

NYF - 0022 - HC2

ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGGCAGCTCCCAGATGGGTGCTGAG
CGGAGAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCC
TGACACCCTCCTGTTTCAGCGTCTGGATTCTCCATCCGTAGCTATGATATACACTGG
GTCCGCCTGGCTCCAGGCAAGGGGCTAGAGTGGGTGGCCACTATATCATATGATGG
AAGTCAGAACTACTTCGCAGACTCCGTGAAGGGCCGATTTACCATCTTCAGAGACG
AATCGGAGAACATGGTGTATCTGCAAATGAGCGGCCTGAGAGTTGAGGACACGGCT
GTTTATCACTGTGCGAGAGGGAGTAGTGGTCATTATGAGGCTTTTGATATCTGGGG
CCAAGGGACAATGGTCACCGTCTCTTCAGGTGGAGGCGGTTTCAGGCGGAGGTGGCA
GCGGCGGTGGCGGGAGTCAGTCTGTGTTGACGCGAGCCGCCCTCAGTGTCTGCGGCC
CCAGGACAGAAGGTCACCATCTCCTGCTCTGGAAGCAGCTCCAACATTGGGAATAA
TTATGTATCCTGGTACCAGCAGCTCCCAGGAACAGCCCCAACTCCTCATTTATG
ACAATAATAAGCGACCCTCAGGGATTCTGACCGATTCTCTGGCTCCAAGTCTGGC
ACGTCAGCCACCCTGGGCATCACCGGACTCCAGACTGGGGACGAGGCCGATTATTA
CTGCGGAACATGGGATAGCAGCCTGAGTGCCCTTTGGGTGTTGGGCGGAGGGACCA
AGGTCACCGTCTAGGGGGAGGCGGTTTCAGAAGTGCAGCTGGTGGAATCCGGGGGG
GGCCTGGTGCAGCCTGGGGGGAGCCTGAGACTGAGTTGTGCCGCCTCTGGGGTGAC
ATTTAACTACTATGGCATGTCTTGATCCGCCAGGCACCTGGAAAGGGCCTGGAGT
GGGTGGCCAGCATCACTAGGTCCGGCGGGCGAATCTACTATCCCGACAGCGTCAAG
GGCAGGTTTACAATTTCCCGCGAGAACACACAGAAAACCTCTGTACCTGCAGATGAA
TAGCCTGAGAGCCGAAGATACAGCTGTGTACTATTGCACTCTGGACGGCAGGGATG
GGTGGGTGCGCTATTGGGGGCAGGGAACCCTGGTGACAGTCAGCTCCGGAGGAGGA
GGATCTGGCGGAGGAGGCAGTGGGGGAGGCGGGTCAAACCTTTATGCTCACTCAGCC
GTCCTCTGTTTCTGGCGTACCTGGCCAACGGGTGACCATTAGCTGTACGGGTAATA
CCGGGAATATCGGGTCTAACTACGTGAACTGGTATCAGCAGCTTCCAGGGACAGCT
CCCAAGTTGCTGATCTATCGCGACGACAAAAGACCCTCAGGGGTCCCTGACCGATT
TAGTGGCAGCAAAAGCGGTACTTCCGCTTCCCTGGCGATAACCGGCTTTCAGGCCG
AAGATGAGGCAGACTACTATTGCCAGTCATATTCCAGCGGCTTCATCTTCGGAGGC
GGAATAAGCTGACAGTGTTGGCAGCCGAGCCCAAATCTTCTGACAAAACCTCACAC
ATGCCACACCCTGCCAGCACCTGAAGCCGCAGGGGGACCCTCAGTCTTCTCTTCC
CCCCAAAACCAAGGACACCCTCATGATCTCCCGGACCCTGAGGTCACATGCGTG
GTGGTGTCAGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGG
CGTGGAGGTGCATAATGCCAAGACAAAGCCCCGGGAGGAGCAGTACAACAGCACGT
ACCGGGTGGTCAGCGTCTCACCGTCTGCACCAGGACTGGCTGAATGGCAAGGAG
TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTC
CAAAGCCAAAGGCCAGCCCCGGGAACCACAGGTGTACGTGTACCCCCCATCCGGG
ACGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC
AGCGACATCGCCGTGGAGTGGGAGAGCAATGGCCAGCCCGAGAACAACTACAAGAC
CACCCCTCCCGTGCTGGACTCCGACGGCTCCTTCGCCCTCGTGAGCAAGCTCACCG
TGGACAAGAGCAGGTGGCAGCAGGGCAACGTCTTCTCATGCTCCGTGATGCATGAG
GCTCTGCACAACCACTACACCCAGAAGAGCCTCTCCCTGTCTCCCGGCAAG
(SEQ ID NO: 74), signal sequence (1-57), NYA-1163 (61-
798), linker (799-813), C3E-7085 (814-1533), linker
(1534-1539), hinge (1540-1584), CH2 (1585-1914), CH3
(1915-2235)

Fig. 76

NYF - 0023 - HC2

ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGGCAGCTCCCAGATGGGTGCTGAG
CGGAGAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCC
TGACACCCTCCTGTTTCAGCGTCTGGATTCTCCATCCGTAGTTATGATATACACTGG
GTCCGCCAGGCTCCAGGCAAGGGGCTAGAGTGGGTGGCCACTATATCATATGATGG
AAGTCAGAACTACTTCGCAGACTCCGTGAAGGGCCGATTTACCATCTTCAGAGACG
AATCGGAGAACATGGTGTATCTGCAAATGAGCGGCCTGAGAGTTGAGGACACGGCT
GTTTATCACTGTGCGAGAGGGAGTAGTGGTCATTATGAGGCTTTTGATATCTGGGG
CCAAGGGACAATGGTCACCGTCTCTTCAGGTGGAGGCGGTTTCAGGCGGAGGTGGCA
GCGGCGGTGGCGGGAGTCAGTCTGTGTTGACGCGAGCCGCCCTCAGTGTCTGCGGCC
CCAGGACAGAAGGTCACCATCTCCTGCTCTGGAAGCAGCTCCAACATTGGGAATTG
GTATGTATCCTGGTACCAGCAGCTCCCAGGAACAGCCCCAACTCCTCATTTATG
ACAATAATAAGCGACCCTCAGGGATTCTGACCGATTCTCTGGCTCCAAGTCTGGC
ACGTCAGCCACCCTGGGCATCACCGGACTCCAGACTGGGGACGAGGCCGATTATTA
CTGCGGAACATGGGATAGCAGCCTGAGTGCCCCTTGGGTGTTGCGCGGAGGGACCA
AGGTCACCGTCTAGGGGGAGGCGGTTGAGAAAGTGCAGCTGGTGGAAATCCGGGGGG
GGCCTGGTGCAGCCTGGGGGGAGCCTGAGACTGAGTTGTGCCGCCTCTGGGGTGAC
ATTTAACTACTATGGCATGTCTTGGATCCGCCAGGCACCTGGAAAGGGCCTGGAGT
GGGTGGCCAGCATCACTAGGTCCGGCGGGCGAATCTACTATCCCGACAGCGTCAAG
GGCAGGTTTACAATTTCCCGCGAGAACACACAGAAAACCTCTGTACCTGCAGATGAA
TAGCCTGAGAGCCGAAGATACAGCTGTGTACTATTGCACTCTGGACGGCAGGGATG
GGTGGGTGCGCTATTGGGGGCAGGGAACCCTGGTGACAGTCAGCTCCGGAGGAGGA
GGATCTGGCGGAGGAGGCAGTGGGGGAGGCGGGTCAAACCTTTATGCTCACTCAGCC
GTCCTCTGTTTCTGGCGTACCTGGCCAACGGGTGACCATTAGCTGTACGGGTAATA
CCGGGAATATCGGGTCTAACTACGTGAACTGGTATCAGCAGCTTCCAGGGACAGCT
CCCAAGTTGCTGATCTATCGCGACGACAAAAGACCCTCAGGGGTCCCTGACCGATT
TAGTGGCAGCAAAAGCGGTACTTCCGCTTCCCTGGCGATAACCGGCTTTCAGGCCG
AAGATGAGGCAGACTACTATTGCCAGTCATATTCCAGCGGCTTCATCTTCGGAGGC
GGAACCTAAGCTGACAGTGTTGGCAGCCGAGCCCAAATCTTCTGACAAAACCTCACAC
ATGCCACACCCTGCCAGCACCTGAAGCCGCAGGGGGACCCTCAGTCTTCTCTTCC
CCCCAAAACCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTG
GTGGTGTCAGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGG
CGTGGAGGTGCATAATGCCAAGACAAAGCCCCGGGAGGAGCAGTACAACAGCACGT
ACCGGGTGGTCAGCGTCTCACCGTCTGCACCAGGACTGGCTGAATGGCAAGGAG
TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTC
CAAAGCCAAAGGCCAGCCCCGGGAACCACAGGTGTACGTGTACCCCCCATCCGGG
ACGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC
AGCGACATCGCCGTGGAGTGGGAGAGCAATGGCCAGCCCGAGAACAACTACAAGAC
CACCCCTCCCGTGCTGGACTCCGACGGCTCCTTCGCCCTCGTGAGCAAGCTCACCG
TGGACAAGAGCAGGTGGCAGCAGGGCAACGTCTTCTCATGCTCCGTGATGCATGAG
GCTCTGCACAACCACTACACCCAGAAGAGCCTCTCCCTGTCTCCCGGCAAG
(SEQ ID NO: 75), signal sequence (1-57), NYA-2023 (61-
798), linker (799-813), C3E-7085 (814-1533), linker
(1534-1539), hinge (1540-1584), CH2 (1585-1914), CH3
(1915-2235)

Fig. 77

NYF - 0027 - HC2

ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGGCAGCTCCCAGATGGGTGCTGAG
CGGAGAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCC
TGACACCCTCCTGTTTCAGCGTCTGGATTCTCCATCCGTAGTTATGATATACACTGG
GTCCGCCAGGCTCCAGGCAAGGGGCTAGAGTGGGTGGCCACTATATCATATGATGG
AAGTCAGAACTACTTCGCAGACTCCGTGAAGGGCCGATTTACCATCTTCAGAGACG
AATCGGAGAACATGGTGTATCTGCAAATGAGCGGCCTGAGAGTTGAGGACACGGCT
GTTTATCACTGTGCGAGAGGGAGTAGTGGTCATTATGAGGCTTTTGATATCTGGGG
CCAAGGGACAATGGTCACCGTCTCTTCAGGTGGAGGCGGTTTCAGGCGGAGGTGGCA
GCGGCGGTGGCGGGAGTCAGTCTGTGTTGACGCGAGCCGCCCTCAGTGTCTGCGGCC
CCAGGACAGAAGGTCACCATCTCCTGCTCTGGAAGCAGCTCCAACATTGGGAATAA
TTATGTATCCTGGTACCAGCAGCTCCCAGGAACAGCCCCCAAACCTCCTCATTTATG
ACAATAATAAGCGACCCTCAGGGATTCTGACCGATTCTCTGGCTCCAAGTCTGGC
ACGTCAGCCACCCTGGGCATCACCGGACTCCAGACTGGGGACGAGGCCGATTATTA
CTGCGGATCATGGGATAGCAGCCTGAGTGCCCCTTGGGTGTTGGGCGGAGGGACCA
AGGTCACCGTCTAGGGGGAGGCGGTTTCAGAAGTGCAGCTGGTGGAATCCGGGGGG
GGCCTGGTGCAGCCTGGGGGGAGCCTGAGACTGAGTTGTGCCGCCTCTGGGGTGAC
ATTTAACTACTATGGCATGTCTTGATCCGCCAGGCACCTGGAAAGGGCCTGGAGT
GGGTGGCCAGCATCACTAGGTCCGGCGGGCGAATCTACTATCCCGACAGCGTCAAG
GGCAGGTTTACAATTTCCCGCGAGAACACACAGAAAACCTCTGTACCTGCAGATGAA
TAGCCTGAGAGCCGAAGATACAGCTGTGTACTATTGCACTCTGGACGGCAGGGATG
GGTGGGTGCGCTATTGGGGGCAGGGAACCCTGGTGACAGTCAGCTCCGGAGGAGGA
GGATCTGGCGGAGGAGGCAGTGGGGGAGGCGGGTCAAACCTTTATGCTCACTCAGCC
GTCCTCTGTTTCTGGCGTACCTGGCCAACGGGTGACCATTAGCTGTACGGGTAATA
CCGGGAATATCGGGTCTAACTACGTGAACTGGTATCAGCAGCTTCCAGGGACAGCT
CCCAAGTTGCTGATCTATCGCGACGACAAAAGACCCTCAGGGGTCCCTGACCGATT
TAGTGGCAGCAAAAGCGGTACTTCCGCTTCCCTGGCGATAACCGGCTTTCAGGCCG
AAGATGAGGCAGACTACTATTGCCAGTCATATTCCAGCGGCTTCATCTTCGGAGGC
GGAACCTAAGCTGACAGTGTTGGCAGCCGAGCCCAAATCTTCTGACAAAACCTCACAC
ATGCCACACCCTGCCAGCACCTGAAGCCGCAGGGGGACCCTCAGTCTTCTCTTCC
CCCCAAAACCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTG
GTGGTGTCAGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGG
CGTGGAGGTGCATAATGCCAAGACAAAGCCCCGGGAGGAGCAGTACAACAGCACGT
ACCGGGTGGTCAGCGTCTCACCGTCTGCACCAGGACTGGCTGAATGGCAAGGAG
TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTC
CAAAGCCAAAGGCCAGCCCCGGGAACCACAGGTGTACGTGTACCCCCCATCCGGG
ACGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC
AGCGACATCGCCGTGGAGTGGGAGAGCAATGGCCAGCCCGAGAACAACCTACAAGAC
CACCCCTCCCGTGCTGGACTCCGACGGCTCCTTCGCCCTCGTGAGCAAGCTCACCG
TGGACAAGAGCAGGTGGCAGCAGGGCAACGTCTTCTCATGCTCCGTGATGCATGAG
GCTCTGCACAACCACTACACCCAGAAGAGCCTCTCCCTGTCTCCCGGCAAG
(SEQ ID NO: 76), signal sequence (1-57), NYA-2027(61-
798), linker (799-813), C3E-7085 (814-1533), linker
(1534-1539), hinge (1540-1584), CH2 (1585-1914), CH3
(1915-2235)

Fig. 78

NYF - 0035 - HC2

ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGGCAGCTCCCAGATGGGTGCTGAG
CGGAGAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCC
TGACACCCTCCTGTTTCAGCGTCTGGATTCTCCATCCGTAGCTATGATATACACTGG
GTCCGCCTGGCTCCAGGCAAGGGGCTAGAGTGGGTGGCCACTATATCATATGATGG
AAGTCAGAACTACTTCGCAGACTCCGTGAAGGGCCGATTTACCATCTTCAGAGACG
AATCGGAGAACATGGTGTATCTGCAAATGAGCGGCCTGAGAGTTGAGGACACGGCT
GTTTATCACTGTGCGAGAGGGAGTAGTGGTCATTATGAGGCTTTTGATATCTGGGG
CCAAGGGACAATGGTCACCGTCTCTTCAGGTGGAGGCGGTTTCAGGCGGAGGTGGCA
GCGGCGGTGGCGGGAGTCAGTCTGTGTTGACGCGAGCCGCCCTCAGTGTCTGCGGCC
CCAGGACAGAAGGTCACCATCTCCTGCTCTGGAAGCAGCTCCAACATTGGGAATTG
GAAGGTATCCTGGTACCAGCAGCTCCCAGGAACAGCCCCAACTCCTCATTTATG
ACAATAATAAGCGACCCTCAGGGATTCTGACCGATTCTCTGGCTCCAAGTCTGGC
ACGTCAGCCACCCTGGGCATCACCGGACTCCAGACTGGGGACGAGGCCGATTATTA
CTGCGGAACATGGGATAGCAGCCTGAGTGCCCTTTGGGTGTTGCGCGGAGGGACCA
AGGTCACCGTCTAGGGGGAGGCGGTTTCAGAAGTGCAGCTGGTGGAATCCGGGGGG
GGCCTGGTGCAGCCTGGGGGGAGCCTGAGACTGAGTTGTGCCGCTCTGGGGTGAC
ATTTAACTACTATGGCATGTCTTGATCCGCCAGGCACCTGGAAAGGGCCTGGAGT
GGGTGGCCAGCATCACTAGGTCCGGCGGGCGAATCTACTATCCCGACAGCGTCAAG
GGCAGGTTTACAATTTCCCGCGAGAACACACAGAAAACCTCTGTACCTGCAGATGAA
TAGCCTGAGAGCCGAAGATACAGCTGTGTACTATTGCACTCTGGACGGCAGGGATG
GGTGGGTGCGCTATTGGGGGCAGGGAACCCTGGTGACAGTCAGCTCCGGAGGAGGA
GGATCTGGCGGAGGAGGCAGTGGGGGAGGCGGGTCAAACCTTTATGCTCACTCAGCC
GTCCTCTGTTTCTGGCGTACCTGGCCAACGGGTGACCATTAGCTGTACGGGTAATA
CCGGGAATATCGGGTCTAACTACGTGAACTGGTATCAGCAGCTTCCAGGGACAGCT
CCCAAGTTGCTGATCTATCGCGACGACAAAAGACCCTCAGGGGTCCCTGACCGATT
TAGTGGCAGCAAAAGCGGTACTTCCGCTTCCCTGGCGATAACCGGCTTTCAGGCCG
AAGATGAGGCAGACTACTATTGCCAGTCATATTCCAGCGGCTTCATCTTCGGAGGC
GGAACCTAAGCTGACAGTGTTGGCAGCCGAGCCCAAATCTTCTGACAAAACCTCACAC
ATGCCACCCCTGCCAGCACCTGAAGCCGCAGGGGGACCCTCAGTCTTCTCTTCC
CCCCAAAACCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTG
GTGGTGTCAGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGG
CGTGGAGGTGCATAATGCCAAGACAAAGCCCCGGGAGGAGCAGTACAACAGCACGT
ACCGGGTGGTCAGCGTCTCACCGTCTGCACCAGGACTGGCTGAATGGCAAGGAG
TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTC
CAAAGCCAAAGGCCAGCCCCGGGAACCACAGGTGTACGTGTACCCCCCATCCGGG
ACGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC
AGCGACATCGCCGTGGAGTGGGAGAGCAATGGCCAGCCCGAGAACAACTACAAGAC
CACCCCTCCCGTGCTGGACTCCGACGGCTCCTTCGCCCTCGTGAGCAAGCTCACCG
TGGACAAGAGCAGGTGGCAGCAGGGCAACGTCTTCTCATGCTCCGTGATGCATGAG
GCTCTGCACAACCACTACACCCAGAAGAGCCTCTCCCTGTCTCCCGGCAAG
(SEQ ID NO: 77), signal sequence (1-57), NYA-2035 (61-
798), linker (799-813), C3E-7085 (814-1533), linker
(1534-1539), hinge (1540-1584), CH2 (1585-1914), CH3
(1915-2235)

Fig. 79

NYF - 0044 - HC2

ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGGCAGCTCCCAGATGGGTGCTGAG
CGGTGAGGTACAGCTGGTGGGAATCCGGTGGAGGCCTTGTGCAACCGGGAGGCTCCC
TGCGACTCTCTTGCGCCGCATCTGGCTTTTCCATACGATCCTACGATATTCATTGG
GTCCGACTCGCCCCTGGCAAAGGTCTTGAATGGGTTGCCACTATCTCCTACGACGG
GTCTCAGAAATATTATGCGGATTCAGTGAAGGGGCGGTTTACAATTTACGAGACG
AGTCAAAGAATACACTGTACCTCCAAATGAATTCAGTGAAGGCCGAGGATACTGCA
GTCTATCATTGTGCAAGAGGGTCCTCAGGCCACTACGAGGCCTTTGATATATGGGG
CCAAGGCACCTTGGTAACCGTTAGTAGCGGAGGTGGAGGAAGCGGAGGCGGCGGTT
CCGGAGGAGGTGGAAGTCAATCCGTTCTGACTCAGCCACCCTCCGTGAGTGCAGCG
CCTGGACAGAAGGTCACAATATCATGTTCTGGCTCTTCAAGCAACATCGGAAACTG
GTACGTGAGCTGGTACCAGCAGCTCCCCGGCACGGCGCCCAAGCTTCTGATATATG
ACAACAACAAACGGCCCAGTGGGAATCCCTGACAGATTCAGTGGGTCTAAAAGTGGT
ACAAGCGCTACCCTGGGTATCACCGGATTGCAGACCGGAGATGAGGCGGACTATTA
TTGCGGAACCTGGGACTCCAGCCTGAGCGCTCCCTGGGTTTTTCGGCGGAGGTACTA
AGGTTACCGTCTTGGGAGGAGGCGGTTTCAAGTGCAGCTGGTGGGAATCCGGGGGG
GGCCTGGTGCAGCTGGGGGGAGCCTGAGACTGAGTTGTGCCGCCTCTGGGGTGAC
ATTTAACTACTATGGCATGTCTTGGATCCGCCAGGCACCTGGAAAGGGCCTGGAGT
GGGTGGCCAGCATCACTAGGTCCGGCGGGCGAATCTACTATCCCGACAGCGTCAAG
GGCAGGTTTACAATTTCCCGCGAGAACACACAGAAAACCTCTGTACCTGCAGATGAA
TAGCCTGAGAGCCGAAGATACAGCTGTGTACTATTGCACTCTGGACGGCAGGGATG
GGTGGGTGCGCTATTGGGGGCAGGGAACCCTGGTGACAGTCAGCTCCGGAGGAGGA
GGATCTGGCGGAGGAGGCAGTGGGGGAGGCGGGTCAAACCTTTATGCTCACTCAGCC
GTCCTCTGTTTCTGGCGTACCTGGCCAACGGGTGACCATTAGCTGTACGGGTAATA
CCGGGAATATCGGGTCTAACTACGTGAACTGGTATCAGCAGCTTCCAGGGACAGCT
CCCAAGTTGCTGATCTATCGCGACGACAAAAGACCCTCAGGGGTCCCTGACCGATT
TAGTGGCAGCAAAAGCGGTACTTCCGCTTCCCTGGCGATAACCGGCTTTCAGGCCG
AAGATGAGGCAGACTACTATTGCCAGTCATATTCCAGCGGCTTCATCTTCGGAGGC
GGAATAAGCTGACAGTGTTGGCAGCCGAGCCCAAATCTTCTGACAAAACCTCACAC
ATGCCACCCTGCCAGCACCTGAAGCCGCAGGGGGACCCTCAGTCTTCTCTTCC
CCCCAAAACCAAGGACACCCTCATGATCTCCCGGACCCTGAGGTCACATGCGTG
GTGGTGTCAGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGG
CGTGGAGGTGCATAATGCCAAGACAAAGCCCCGGGAGGAGCAGTACAACAGCACGT
ACCGGGTGGTCAGCGTCCTACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG
TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTC
CAAAGCCAAAGGCCAGCCCCGGGAACCACAGGTGTACGTGTACCCCCCATCCGGG
ACGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC
AGCGACATCGCCGTGGAGTGGGAGAGCAATGGCCAGCCCGAGAACAACCTACAAGAC
CACCCCTCCCGTGCTGGACTCCGACGGCTCCTTCGCCCTCGTGAGCAAGCTCACCG
TGGACAAGAGCAGGTGGCAGCAGGGCAACGTCTTCTCATGCTCCGTGATGCATGAG
GCTCTGCACAACCACTACACCCAGAAGAGCCTCTCCCTGTCTCCCGGCAAG
(SEQ ID NO: 78), signal sequence (1-57), NYA-2044 (61-
798), linker (799-813), C3E-7085 (814-1533), linker
(1534-1539), hinge (1540-1584), CH2 (1585-1914), CH3
(1915-2235)

Fig. 80

NYF - 0045 - HC2

ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGGCAGCTCCCAGATGGGTGCTGAG
CGGTGAGGTACAGCTGGTGGGAATCCGGTGGAGGCCTTGTGCAACCGGGAGGCTCCC
TGCGACTCTCTTGCGCCGCATCTGGCTTTTCCATACGATCCTACGATATTCATTGG
GTCCGACTCGCCCCTGGCAAAGGTCTTGAATGGGTTGCCACTATCTCCTACGACGG
GTCTCAGAAATATTATGCGGATTCAGTGAAGGGGCGGTTTACAATTTACGAGACG
AGTCAAAGAATACACTGTACCTCCAAATGAATTCAGTGAAGGCCGAGGATACTGCA
GTCTATCATTGTGCAAGAGGGTCCTCAGGCCACTACGAGGCCTTTGATATATGGGG
CCAAGGCACCTTGGTAACCGTTAGTAGCGGAGGTGGAGGAAGCGGAGGCGGCGGTT
CCGGAGGAGGTGGAAGTCAATCCGTTCTGACTCAGCCACCCTCCGCCTCTGGCACC
CCGGGCCAACGGGTCACAATATCATGTTCTGGCTCTTCAAGCAACATCGGAAACTG
GTACGTGAGCTGGTACCAGCAGCTCCCCGGCACGGCGCCCAAGCTTCTGATATATG
ACAACAACAAACGGCCCAGTGGAGTTCCTGACAGATTCAGTGGGTCTAAAAGTGGT
ACAAGCGCTAGCCTGGCCATAAGTGGTCTGCAGAGTGAAGATGAGGCGGACTATTA
TTGCGGAACCTGGGACTCCAGCCTGAGCGCTCCCTGGGTTTTTCGGCGGAGGTACTA
AGCTGACCGTCTTGGGAGGAGGCGGTTTCAAGAGTGCAGCTGGTGAATCCGGGGGG
GGCCTGGTGCAGCTGGGGGGAGCCTGAGACTGAGTTGTGCCGCCTCTGGGGTGAC
ATTTAACTACTATGGCATGTCTTGGATCCGCCAGGCACCTGGAAAGGGCCTGGAGT
GGGTGGCCAGCATCACTAGGTCCGGCGGGCGAATCTACTATCCCGACAGCGTCAAG
GGCAGTTTACAATTTCCCGCGAGAACACACAGAAAACCTCTGTACCTGCAGATGAA
TAGCCTGAGAGCCGAAGATACAGCTGTGTACTATTGCACTCTGGACGGCAGGGATG
GGTGGGTGCGCTATTGGGGGCAGGGAACCCTGGTGACAGTCAGCTCCGGAGGAGGA
GGATCTGGCGGAGGAGGCAGTGGGGGAGGCGGGTCAAACCTTTATGCTCACTCAGCC
GTCCTCTGTTTCTGGCGTACCTGGCCAACGGGTGACCATTAGCTGTACGGGTAATA
CCGGGAATATCGGGTCTAACTACGTGAACTGGTATCAGCAGCTTCCAGGGACAGCT
CCCAAGTTGCTGATCTATCGCGACGACAAAAGACCCTCAGGGGTCCCTGACCGATT
TAGTGGCAGCAAAAGCGGTACTTCCGCTTCCCTGGCGATAACCGGCTTTCAGGCCG
AAGATGAGGCAGACTACTATTGCCAGTCATATTCCAGCGGCTTCATCTTCGGAGGC
GGAACCTAAGCTGACAGTGTTGGCAGCCGAGCCCAAATCTTCTGACAAAACCTCACAC
ATGCCACCCTGCCAGCACCTGAAGCCGCAGGGGGACCCTCAGTCTTCTCTTCC
CCCCAAAACCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTG
GTGGTGTCAGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGG
CGTGGAGGTGCATAATGCCAAGACAAAGCCCCGGGAGGAGCAGTACAACAGCACGT
ACCGGGTGGTCAGCGTCCTACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG
TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTC
CAAAGCCAAAGGCCAGCCCCGGGAACCACAGGTGTACGTGTACCCCCCATCCGGG
ACGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC
AGCGACATCGCCGTGGAGTGGGAGAGCAATGGCCAGCCCGAGAACAACTACAAGAC
CACCCCTCCCGTGCTGGACTCCGACGGCTCCTTCGCCCTCGTGAGCAAGCTCACCG
TGGACAAGAGCAGGTGGCAGCAGGGCAACGTCTTCTCATGCTCCGTGATGCATGAG
GCTCTGCACAACCACTACACCCAGAAGAGCCTCTCCCTGTCTCCCGGCAAG
(SEQ ID NO: 79), signal sequence (1-57), NYA-2045 (61-
798), linker (799-813), C3E-7085 (814-1533), linker
(1534-1539), hinge (1540-1584), CH2 (1585-1914), CH3
(1915-2235)

Fig. 81

NYF - 0047 - HC2

ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGGCAGCTCCCAGATGGGTGCTGAG
CGGTCAAGTACAGCTGGTGGGAATCCGGTGGAGGCGTGGTCCAGCCGGGACGCAGCT
TGAGACTGTCCTGCGCTGCATCTGGCTTTTCCATACGATCCTACGATATGCACTGG
GTTTCGCCAAGCCCCCTGGCAAAGGTCTTGAATGGGTTGCCACTATCTCCTACGACGG
GTCTCAGAAATATTACGCGGATTCAGTGAAGGGGCGGTTTACAATTTACGGGACA
ATTCAAAGAATACCTTGTATCTCCAGATGTCTTCACTGAGAGCCGAGGATACTGCA
GTCTATCATTGTGCAAGAGGGTCCTCAGGCCACTACGAGGCCTTTGATATATGGGG
CCAAGGCACCTTGGTAACCGTTAGTAGCGGAGGTGGAGGAAGCGGAGGCGGCGGTT
CCGGAGGAGGTGGAAGTCAATCCGTTCTGACTCAGCCACCCTCCGTGAGTGCAGCG
CCTGGACAGAAGGTCACAATATCATGTTCTGGCTCTTCAAGCAACATCGGAAACTG
GTACGTGAGCTGGTACCAGCAGCTCCCCGGCACGGCGCCCAAGCTTCTGATATATG
ACAACAACAAACGGCCCAGTGGGAATCCCTGACAGATTCAGTGGGTCTAAAAGTGGT
ACAAGCGCTACCCTGGGTATCACCGGATTGCAGACCGGAGATGAGGCGGACTATTA
TTGCGGAACCTGGGACTCCAGCCTGAGCGCTCCCTGGGTTTTTCGGCGGAGGTACTA
AGGTTACCGTCTTGGGAGGAGGCGGTTTCAAGTGCAGCTGGTGGGAATCCGGGGGG
GGCCTGGTGCAGCCTGGGGGGAGCCTGAGACTGAGTTGTGCCGCCTCTGGGGTGAC
ATTTAACTACTATGGCATGTCTTGGATCCGCCAGGCACCTGGAAAGGGCCTGGAGT
GGGTGGCCAGCATCACTAGGTCCGGCGGGCGAATCTACTATCCCGACAGCGTCAAG
GGCAGGTTTACAATTTCCCGCGAGAACACACAGAAAACCTCTGTACCTGCAGATGAA
TAGCCTGAGAGCCGAAGATACAGCTGTGTACTATTGCACTCTGGACGGCAGGGATG
GGTGGGTGCGCTATTGGGGGCAGGGAACCCTGGTGACAGTCAGCTCCGGAGGAGGA
GGATCTGGCGGAGGAGGCAGTGGGGGAGGCGGGTCAAACCTTTATGCTCACTCAGCC
GTCCTCTGTTTCTGGCGTACCTGGCCAACGGGTGACCATTAGCTGTACGGGTAATA
CCGGGAATATCGGGTCTAACTACGTGAACTGGTATCAGCAGCTTCCAGGGACAGCT
CCCAAGTTGCTGATCTATCGCGACGACAAAAGACCCTCAGGGGTCCCTGACCGATT
TAGTGGCAGCAAAAGCGGTACTTCCGCTTCCCTGGCGATAACCGGCTTTCAGGCCG
AAGATGAGGCAGACTACTATTGCCAGTCATATTCCAGCGGCTTCATCTTCGGAGGC
GGAATAAGCTGACAGTGTTGGCAGCCGAGCCCAAATCTTCTGACAAAACCTCACAC
ATGCCACCCTGCCAGCACCTGAAGCCGCAGGGGGACCCTCAGTCTTCTCTTCC
CCCCAAAACCAAGGACACCCTCATGATCTCCCGGACCCTGAGGTCACATGCGTG
GTGGTGTCAGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGG
CGTGGAGGTGCATAATGCCAAGACAAAGCCCCGGGAGGAGCAGTACAACAGCACGT
ACCGGGTGGTCAGCGTCCTACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG
TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTC
CAAAGCCAAAGGCCAGCCCCGGGAACCACAGGTGTACGTGTACCCCCCATCCGGG
ACGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC
AGCGACATCGCCGTGGAGTGGGAGAGCAATGGCCAGCCCGAGAACAACCTACAAGAC
CACCCCTCCCGTGCTGGACTCCGACGGCTCCTTCGCCCTCGTGAGCAAGCTCACCG
TGGACAAGAGCAGGTGGCAGCAGGGCAACGTCTTCTCATGCTCCGTGATGCATGAG
GCTCTGCACAACCACTACACCCAGAAGAGCCTCTCCCTGTCTCCCGGCAAG
(SEQ ID NO: 80), signal sequence (1-57), NYA-2047(61-
798), linker (799-813), C3E-7085 (814-1533), linker
(1534-1539), hinge (1540-1584), CH2 (1585-1914), CH3
(1915-2235)

Fig. 82

NYF - 0048 - HC2

ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGGCAGCTCCCAGATGGGTGCTGAG
CGGACAAGTTCAACTCGTGGAATCTGGTGGAGGGGTGGTACAACCAGGCCGGTCAC
TTAGACTGTCCTGCGCTGCGAGTGGATTTTCCATCAGATCTTACGACATGCACTGG
GTTTCGCCAAGCACCCGGAAAGGGTTTGAATGGGTGGCTACGATCTCCTACGATGG
ATCCCAGAAGTATTACGCCGACAGCGTCAAGGGCCGATTTACAATATCACGGGACA
ATTCAAAGAATACCTTGTATCTCCAGATGTCTTCACTGAGAGCCGAGGATACTGCA
GTCTATCATTGTGCAAGAGGGTCCTCAGGCCACTACGAGGCCCTTTGATATATGGGG
CCAAGGCACCTTGGTAACCGTTAGTAGCGGAGGTGGAGGAAGCGGAGGCCGGCGGTT
CCGGAGGAGGTGGAAGTCAATCCGTTCTGACTCAGCCACCCTCCGCCTCTGGCACC
CCGGGCCAACGGGTCACAATATCATGTTCTGGCTCTTCAAGCAACATCGGAAACTG
GTACGTGAGCTGGTACCAGCAGCTCCCCGGCACGGCGCCCAAGCTTCTGATATATG
ACAACAACAAACGGCCCAGTGGAGTTCCTGACAGATTCAGTGGGTCTAAAAGTGGT
ACAAGCGCTAGCCTGGCCATAAGTGGTCTGCAGAGTGAAGATGAGGCGGACTATTA
TTGCGGAACCTGGGACTCCAGCCTGAGCGCTCCCTGGGTTTTTCGGCGGAGGTACTA
AGCTGACCGTCTTGGGAGGAGGCGGTTTCAAGAGTGCAGCTGGTGAATCCGGGGGG
GGCCTGGTGCAGCCTGGGGGGAGCCTGAGACTGAGTTGTGCCGCCTCTGGGGTGAC
ATTTAACTACTATGGCATGTCTTGGATCCGCCAGGCACCTGGAAAGGGCCTGGAGT
GGGTGGCCAGCATCACTAGGTCCGGCGGGCGAATCTACTATCCCGACAGCGTCAAG
GGCAGTTTCACAATTTCCCGCGAGAACACACAGAAAACCTCTGTACCTGCAGATGAA
TAGCCTGAGAGCCGAAGATACAGCTGTGTACTATTGCACTCTGGACGGCAGGGATG
GGTGGGTGCGCTATTGGGGGCAGGGAACCCTGGTGACAGTCAGCTCCGGAGGAGGA
GGATCTGGCGGAGGAGGCAGTGGGGGAGGCGGGTCAAACCTTTATGCTCACTCAGCC
GTCCTCTGTTTCTGGCGTACCTGGCCAACGGGTGACCATTAGCTGTACGGGTAATA
CCGGGAATATCGGGTCTAACTACGTGAACTGGTATCAGCAGCTTCCAGGGACAGCT
CCCAAGTTGCTGATCTATCGCGACGACAAAAGACCCTCAGGGGTCCCTGACCGATT
TAGTGGCAGCAAAAGCGGTACTTCCGCTTCCCTGGCGATAACCGGCTTTCAGGCCG
AAGATGAGGCAGACTACTATTGCCAGTCATATTCCAGCGGCTTCATCTTCGGAGGC
GGAACCTAAGCTGACAGTGTGGCAGCCGAGCCCAAATCTTCTGACAAAACCTCACAC
ATGCCACCCTGCCAGCACCTGAAGCCGCAGGGGGACCCTCAGTCTTCTCTTCC
CCCCAAAACCAAGGACACCCTCATGATCTCCCGGACCCTGAGGTCACATGCGTG
GTGGTGTCAGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGG
CGTGGAGGTGCATAATGCCAAGACAAAGCCCCGGGAGGAGCAGTACAACAGCACGT
ACCGGGTGGTCAGCGTCCTACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG
TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTC
CAAAGCCAAAGGCCAGCCCCGGGAACCACAGGTGTACGTGTACCCCCCATCCGGG
ACGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC
AGCGACATCGCCGTGGAGTGGGAGAGCAATGGCCAGCCCGAGAACAACCTACAAGAC
CACCCCTCCCGTGCTGGACTCCGACGGCTCCTTCGCCCTCGTGAGCAAGCTCACCG
TGGACAAGAGCAGGTGGCAGCAGGGCAACGTCTTCTCATGCTCCGTGATGCATGAG
GCTCTGCACAACCACTACACCCAGAAGAGCCTCTCCCTGTCTCCCGGCAAG
(SEQ ID NO: 81), signal sequence (1-57), NYA-2048(61-
798), linker (799-813), C3E-7085 (814-1533), linker
(1534-1539), hinge (1540-1584), CH2 (1585-1914), CH3
(1915-2235)

Fig. 83

NYF - 0060 - HC2

ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGGCAGCTCCCAGATGGGTGCTGAG
CGGTGAGGTACAGCTGGTGGGAATCCGGTGGAGGCCTTGTGCAACCGGGAGGCTCCC
TGCGACTCTCTTGCGCCGCATCTGGCTTTTCCATACGATCCTACGATATTCATTGG
GTCCGACAAGCCCCTGGCAAAGGTCTTGAATGGGTTGCCACTATCTCCTACGACGG
GTCTCAGAAATATTATGCGGATTCAGTGAAGGGGCGGTTTACAATTTACGAGACG
AGTCAAAGAATACACTGTACCTCCAAATGAATTCAGTGAAGGCCGAGGATACTGCA
GTCTATCATTGTGCAAGAGGGTCCTCAGGCCACTACGAGGCCTTTGATATATGGGG
CCAAGGCACCTTGGTAACCGTTAGTAGCGGAGGTGGAGGAAGCGGAGGCGGCGGTT
CCGGAGGAGGTGGAAGTCAATCCGTTCTGACTCAGCCACCCTCCGTGAGTGCAGCG
CCTGGACAGAAGGTCACAATATCATGTTCTGGCTCTTCAAGCAACATCGGAAACTG
GTACGTGAGCTGGTACCAGCAGCTCCCCGGCACGGCGCCCAAGCTTCTGATATATG
ACAACAACAAACGGCCCAGTGGGAATCCCTGACAGATTCAGTGGGTCTAAAAGTGGT
ACAAGCGCTACCCTGGGTATCACCGGATTGCAGACCGGAGATGAGGCGGACTATTA
TTGCGGAACCTGGGACTCCAGCCTGAGCGCTCCCTGGGTTTTTCGGCGGAGGTACTA
AGGTTACCGTCTTGGGAGGAGGCGGTTTCAAGTGCAGCTGGTGGGAATCCGGGGGG
GGCCTGGTGCAGCTGGGGGGAGCCTGAGACTGAGTTGTGCCGCCTCTGGGGTGAC
ATTTAACTACTATGGCATGTCTTGGATCCGCCAGGCACCTGGAAAGGGCCTGGAGT
GGGTGGCCAGCATCACTAGGTCCGGCGGGCGAATCTACTATCCCGACAGCGTCAAG
GGCAGGTTTACAATTTCCCGCGAGAACACACAGAAAACCTCTGTACCTGCAGATGAA
TAGCCTGAGAGCCGAAGATACAGCTGTGTACTATTGCACTCTGGACGGCAGGGATG
GGTGGGTGCGCTATTGGGGGCAGGGAACCCTGGTGACAGTCAGCTCCGGAGGAGGA
GGATCTGGCGGAGGAGGCAGTGGGGGAGGCGGGTCAAACCTTTATGCTCACTCAGCC
GTCCTCTGTTTCTGGCGTACCTGGCCAACGGGTGACCATTAGCTGTACGGGTAATA
CCGGGAATATCGGGTCTAACTACGTGAACTGGTATCAGCAGCTTCCAGGGACAGCT
CCCAAGTTGCTGATCTATCGCGACGACAAAAGACCCTCAGGGGTCCCTGACCGATT
TAGTGGCAGCAAAAGCGGTACTTCCGCTTCCCTGGCGATAACCGGCTTTCAGGCCG
AAGATGAGGCAGACTACTATTGCCAGTCATATTCCAGCGGCTTCATCTTCGGAGGC
GGAATAAGCTGACAGTGTTGGCAGCCGAGCCCAAATCTTCTGACAAAACCTCACAC
ATGCCACCCTGCCAGCACCTGAAGCCGCAGGGGGACCCTCAGTCTTCTCTTCC
CCCCAAAACCAAGGACACCCTCATGATCTCCCGGACCCTGAGGTCACATGCGTG
GTGGTGTCAGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGG
CGTGGAGGTGCATAATGCCAAGACAAAGCCCCGGGAGGAGCAGTACAACAGCACGT
ACCGGGTGGTCAGCGTCCTACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG
TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTC
CAAAGCCAAAGGCCAGCCCCGGGAACCACAGGTGTACGTGTACCCCCCATCCGGG
ACGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC
AGCGACATCGCCGTGGAGTGGGAGAGCAATGGCCAGCCCGAGAACAACCTACAAGAC
CACCCCTCCCGTGCTGGACTCCGACGGCTCCTTCGCCCTCGTGAGCAAGCTCACCG
TGGACAAGAGCAGGTGGCAGCAGGGCAACGTCTTCTCATGCTCCGTGATGCATGAG
GCTCTGCACAACCACTACACCCAGAAGAGCCTCTCCCTGTCTCCCGGCAAG
(SEQ ID NO: 82), signal sequence (1-57), NYA-2060(61-
798), linker (799-813), C3E-7085 (814-1533), linker
(1534-1539), hinge (1540-1584), CH2 (1585-1914), CH3
(1915-2235)

Fig. 84

NYF - 0061 - HC2

ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGGCAGCTCCCAGATGGGTGCTGAG
CGGTGAGGTACAGCTGGTGGGAATCCGGTGGAGGCCTTGTGCAACCGGGAGGCTCCC
TGCGACTCTCTTGCGCCGCATCTGGCTTTTCCATACGATCCTACGATATTCATTGG
GTCCGACAAGCCCCTGGCAAAGGTCTTGAATGGGTTGCCACTATCTCCTACGACGG
GTCTCAGAAATATTATGCGGATTCAGTGAAGGGGCGGTTTACAATTTACGAGACG
AGTCAAAGAATACACTGTACCTCCAAATGAATTCAGTGAAGGCCGAGGATACTGCA
GTCTATCATTGTGCAAGAGGGTCCTCAGGCCACTACGAGGCCTTTGATATATGGGG
CCAAGGCACCTTGGTAACCGTTAGTAGCGGAGGTGGAGGAAGCGGAGGCGGCGGTT
CCGGAGGAGGTGGAAGTCAATCCGTTCTGACTCAGCCACCCTCCGCCTCTGGCACC
CCGGGCCAACGGGTCACAATATCATGTTCTGGCTCTTCAAGCAACATCGGAAACTG
GTACGTGAGCTGGTACCAGCAGCTCCCCGGCACGGCGCCCAAGCTTCTGATATATG
ACAACAACAAACGGCCCAGTGGAGTTCCTGACAGATTCAGTGGGTCTAAAAGTGGT
ACAAGCGCTAGCCTGGCCATAAGTGGTCTGCAGAGTGAAGATGAGGCGGACTATTA
TTGCGGAACCTGGGACTCCAGCCTGAGCGCTCCCTGGGTTTTTCGGCGGAGGTACTA
AGCTGACCGTCTTGGGAGGAGGCGGTTTCAAGAGTGCAGCTGGTGAATCCGGGGGG
GGCCTGGTGCAGCTGGGGGGAGCCTGAGACTGAGTTGTGCCGCCTCTGGGGTGAC
ATTTAACTACTATGGCATGTCTTGGATCCGCCAGGCACCTGGAAAGGGCCTGGAGT
GGGTGGCCAGCATCACTAGGTCCGGCGGGCGAATCTACTATCCCGACAGCGTCAAG
GGCAGTTTACAATTTCCCGCGAGAACACACAGAAAACCTCTGTACCTGCAGATGAA
TAGCCTGAGAGCCGAAGATACAGCTGTGTACTATTGCACTCTGGACGGCAGGGATG
GGTGGGTGCGCTATTGGGGGCAGGGAACCCTGGTGACAGTCAGCTCCGGAGGAGGA
GGATCTGGCGGAGGAGGCAGTGGGGGAGGCGGGTCAAACCTTTATGCTCACTCAGCC
GTCCTCTGTTTCTGGCGTACCTGGCCAACGGGTGACCATTAGCTGTACGGGTAATA
CCGGGAATATCGGGTCTAACTACGTGAACTGGTATCAGCAGCTTCCAGGGACAGCT
CCCAAGTTGCTGATCTATCGCGACGACAAAAGACCCTCAGGGGTCCCTGACCGATT
TAGTGGCAGCAAAAGCGGTACTTCCGCTTCCCTGGCGATAACCGGCTTTCAGGCCG
AAGATGAGGCAGACTACTATTGCCAGTCATATTCCAGCGGCTTCATCTTCGGAGGC
GGAACCTAAGCTGACAGTGTGGCAGCCGAGCCCAAATCTTCTGACAAAACCTCACAC
ATGCCACCCTGCCAGCACCTGAAGCCGCAGGGGGACCCTCAGTCTTCTCTTCC
CCCCAAAACCAAGGACACCCTCATGATCTCCCGGACCCTGAGGTCACATGCGTG
GTGGTGTCAGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGG
CGTGGAGGTGCATAATGCCAAGACAAAGCCCCGGGAGGAGCAGTACAACAGCACGT
ACCGGGTGGTCAGCGTCTCACCGTCTGCACCAGGACTGGCTGAATGGCAAGGAG
TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTC
CAAAGCCAAAGGCCAGCCCCGGGAACCACAGGTGTACGTGTACCCCCCATCCGGG
ACGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC
AGCGACATCGCCGTGGAGTGGGAGAGCAATGGCCAGCCCGAGAACAACCTACAAGAC
CACCCCTCCCGTGCTGGACTCCGACGGCTCCTTCGCCCTCGTGAGCAAGCTCACCG
TGGACAAGAGCAGGTGGCAGCAGGGCAACGTCTTCTCATGCTCCGTGATGCATGAG
GCTCTGCACAACCACTACACCCAGAAGAGCCTCTCCCTGTCTCCCGGCAAG
(SEQ ID NO: 83), signal sequence (1-57), NYA-2061 (61-
798), linker (799-813), C3E-7085 (814-1533), linker
(1534-1539), hinge (1540-1584), CH2 (1585-1914), CH3
(1915-2235)

Fig. 85

HC1

MKHLWFFLLLVAAPRWVLSDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVSVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYVLPISRDELTKNQVSLCCLVKGFYPSDIAVEWESNGQPENNYLTWPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

(SEQ ID NO: 84), signal sequence (1-19), hinge (20-29), CH2 (30-139), CH3 (140-246)

Fig. 86

NYF-0016-HC

**MKHLWFFLLLVAAPRWVLSGEVQLVESGGGVVQPGRSLTPSCSASGFSIRSYDIHW
VRLAPGKGLEWVATISYDGSQKYFADSVKGRFTIFRDESENMVYLMMSGRLRVEDTA
VYHCARGSSGHYEAFDIWGQGTMTVSSGGGGSGGGGSGGGGSQSVLTQPPSVSAA
PGQKVTISCSGSSSNIGNWYVSWYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSG
TSATLGITGLQTGDEADYYCGTWDSSLSAPWVFGGGTKVTVLGGGGSEVQLVESGG
GLVQPGGSLRLSCAASGVTFNYYGMSWIRQAPGKGLEWVASITRSGGRIYYPDVSK
GRFTISRENTQKTLYLQMNSLRAEDTAVYYCTLDGRDGVVAYWGQGTLVTVSSGGG
GSGGGGSGGGGSGNFMLTQPSSVSGVPGQRTISCTGNTGNIGSNYVNWYQQLPGTA
PKLLIYRDDKRPSGVPDRFSGSKSGTSASLAITGFQAEDEADYYCQSYSSGFIFGG
GTKLTVLAAEPKSSDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCV
VVSVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE
YKCKVSNKALPAPIEKTISKAKGQPREPQVYVPPSRDELTKNQVSLTCLVKGFYP
SDIAVEWESNGQPENNYKTTPPVLDSDGSFALVSKLTVDKSRWQQGNVFSQSVMHE
ALHNHYTQKSLSLSPGK**

(SEQ ID NO: 85), signal sequence (1-19), NYA-1143 (21-266), linker (267-271), C3E-7085 (272-511), linker (512-513), hinge (514-528), CH2 (529-638), CH3 (639-745)

Fig. 87

NYF-0019-HC2

**MKHLWFFLLLVAAPRWVLSGEVQLVESGGGVVQPGRSLTPSCSASGFSIRSYDIHW
VRLAPGKGLEWVATISYDGSQKYFADSVKGRFTIFRDESENMVYLMQMSGLRVEDTA
VYHCARGSSGHYEAFDIWGQGTMTVSSGGGGSGGGGSGGGGSQSVLTQPPSVSAA
PGQKVTISCSGSSSNIGNWYVSWYQRLPGTAPKLLIYDNNKRPSGIPDRFSGSKSG
TSATLGITGLQTGDEADYYCGTWDSSLSAPWVFGGGTKVTVLGGGGSEVQLVESGG
GLVQPGGSLRLSCAASGVTFNYYGMSWIRQAPGKGLEWVASITRSGGRIYYPDVSK
GRFTISRENTQKTLYLQMNSLRAEDTAVYYCTLDGRDGVVAYWGQGTLVTVSSGGG
GSGGGGSGGGGSGNFMLTQPSSVSGVPGQRTISCTGNTGNIGSNYVNWYQLPGTA
PKLLIYRDDKRPSGVPDRFSGSKSGTSASLAITGFQAEDEADYYCQSYSSGFIFGG
GTKLTVLAAEPKSSDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCV
VVSVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE
YKCKVSNKALPAPIEKTISKAKGQPREPQVYVPPSRDELTKNQVSLTCLVKGFYP
SDIAVEWESNGQPENNYKTTPPVLDSDGSFALVSKLTVDKSRWQQGNVFSCSVMHE
ALHNHYTQKSLSLSPGK**

(SEQ ID NO: 86), signal sequence (1-19), NYA-2143 (21-266), linker (267-271), C3E-7085 (272-511), linker (512-513), hinge (514-528), CH2 (529-638), CH3 (639-745)

Fig. 88

NYF - 0022 - HC2

**MKHLWFFLLLVAAPRWVLSGEVQLVESGGGVVQPGRSLTPSCSASGFSIRSYDIHW
VRLAPGKGLEWVATISYDGSQKYFADSVKGRFTIFRDESENMVYLMQMSGLRVEDTA
VYHCARGSSGHYEAFDIWGQGTMTVSSGGGGSGGGGSGGGGSQSVLTQPPSVSAA
PGQKVTISCSGSSSNIGNNYVSWYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSG
TSATLGITGLQTGDEADYYCGTWDSSLSAPWVFGGGTKVTVLGGGGSEVQLVESGG
GLVQPGGSLRLSCAASGVTFNYYGMSWIRQAPGKGLEWVASITRSGGRIYYPDVSK
GRFTISRENTQKTLYLQMNSLRAEDTAVYYCTLDGRDGVVAYWGQGTLVTVSSGGG
GSGGGGSGGGGSGNFMLTQPSSVSGVPQQRVTISCTGNTGNIGSNYVNWYQQLPGTA
PKLLIYRDDKRPSGVPDRFSGSKSGTSASLAITGFQAEDEADYYCQSYSSGFIFGG
GTKLTVLAAEPKSSDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCV
VVSVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE
YKCKVSNKALPAPIEKTISKAKGQPREPQVYVPPSRDELTKNQVSLTCLVKGFYP
SDIAVEWESNGQPENNYKTTPPVLDSDGSFALVSKLTVDKSRWQQGNVFSQSVMHE
ALHNHYTQKSLSLSPGK**

(SEQ ID NO: 87), signal sequence (1-19), NYA-1163 (21-266), linker (267-271), C3E-7085 (272-511), linker (512-513), hinge (514-528), CH2 (529-638), CH3 (639-745)

Fig. 89

NYF - 0023 - HC2

**MKHLWFFLLLVAAPRWVLSGEVQLVESGGGVVQPGRSLTPSCSASGFSIRSYDIHW
VRQAPGKGLEWVATISYDGSQKYFADSVKGRFTIFRDESENMVYLMMSGLRVEDTA
VYHCARGSSGHYEAFDIWGQGTMTVSSGGGGSGGGGSGGGGSQSVLTQPPSVSAA
PGQKVTISCSGSSSNIGNWYVSWYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSG
TSATLGITGLQTGDEADYYCGTWDSSLSAPWVFGGGTKVTVLGGGGSEVQLVESGG
GLVQPGGSLRLSCAASGVTFNYYGMSWIRQAPGKGLEWVASITRSGGRIYYPDVSK
GRFTISRENTQKTLYLQMNSLRAEDTAVYYCTLDGRDGVVAYWGQGTLLTVSSGGG
GSGGGGSGGGGSGNFMLTQPSSVSGVPGQRTISCTGNTGNIGSNYVNWYQQLPGTA
PKLLIYRDDKRPSGVPDRFSGSKSGTSASLAITGFQAEDEADYYCQSYSSGFIFGG
GTKLTVLAAEPKSSDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCV
VVSVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE
YKCKVSNKALPAPIEKTISKAKGQPREPQVYVPPSRDELTKNQVSLTCLVKGFYP
SDIAVEWESNGQPENNYKTTPPVLDSDGSFALVSKLTVDKSRWQQGNVFSQSVMHE
ALHNHYTQKSLSLSPGK**

(SEQ ID NO: 88), signal sequence (1-19), NYA-2023 (21-266), linker (267-271), C3E-7085 (272-511), linker (512-513), hinge (514-528), CH2 (529-638), CH3 (639-745)

Fig. 90

NYF - 0027 - HC2

**MKHLWFFLLLVAAPRWVLSGEVQLVESGGGVVQPGRSLTPSCSASGFSIRSYDIHW
VRQAPGKGLEWVATISYDGSQKYFADSVKGRFTIFRDESENMVYLMMSGLRVEDTA
VYHCARGSSGHYEAFDIWGQGTMTVSSGGGGSGGGGSGGGGSQSVLTQPPSVSAA
PGQKVTISCSGSSSNIGNNYVSWYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSG
TSATLGITGLQTGDEADYYCGSWDSSLSAPWVFGGGTKVTVLGGGGSEVQLVESGG
GLVQPGGSLRLSCAASGVTFNYYGMSWIRQAPGKGLEWVASITRSGGRIYYPSVK
GRFTISRENTQKTLYLQMNSLRAEDTAVYYCTLDGRDGVVAYWGQGTLVTVSSGGG
GSGGGGSGGGGSGNFMLTQPSSVSGVPGQRTISCTGNTGNIGSNYVNWYQQLPGTA
PKLLIYRDDKRPSGVPDRFSGSKSGTSASLAITGFQAEDEADYYCQSYSSGFIFGG
GTKLTVLAAEPKSSDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCV
VVSVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE
YKCKVSNKALPAPIEKTISKAKGQPREPQVYVPPSRDELTKNQVSLTCLVKGFYP
SDIAVEWESNGQPENNYKTTPPVLDSDGSFALVSKLTVDKSRWQQGNVFSQSVMHE
ALHNHYTQKSLSLSPGK**

(SEQ ID NO: 89), signal sequence (1-19), NYA-2027(21-266), linker (267-271), C3E-7085 (272-511), linker (512-513), hinge (514-528), CH2 (529-638), CH3 (639-745)

Fig. 91

NYF - 0035 - HC2

**MKHLWFFLLLVAAPRWVLSGEVQLVESGGGVVQPGRSLTPSCSASGFSIRSYDIHW
VRLAPGKGLEWVATISYDGSQKYFADSVKGRFTIFRDESENMVYLMMSGLRVEDTA
VYHCARGSSGHYEAFDIWGQGTMTVSSGGGGSGGGGSGGGGSQSVLTQPPSVSAA
PGQKVTISCSGSSSNIGNWKVSWYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSG
TSATLGITGLQTGDEADYYCGTWDSSLSAPWVFGGGTKVTVLGGGGSEVQLVESGG
GLVQPGGSLRLSCAASGVTFNYYGMSWIRQAPGKGLEWVASITRSGGRIYYPDVSK
GRFTISRENTQKTLYLQMNSLRAEDTAVYYCTLDGRDGVVAYWGQGTLVTVSSGGG
GSGGGGSGGGGSGNFMLTQPSSVSGVPGQRTISCTGNTGNIGSNYVNWYQQLPGTA
PKLLIYRDDKRPSGVPDRFSGSKSGTSASLAITGFQAEDEADYYCQSYSSGFIFGG
GTKLTVLAAEPKSSDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCV
VVSVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE
YKCKVSNKALPAPIEKTISKAKGQPREPQVYVPPSRDELTKNQVSLTCLVKGFYP
SDIAVEWESNGQPENNYKTTPPVLDSDGSFALVSKLTVDKSRWQQGNVFSCSVMHE
ALHNHYTQKSLSLSPGK**

(SEQ ID NO: 90), signal sequence (1-19), NYA-2035 (21-266), linker (267-271), C3E-7085 (272-511), linker (512-513), hinge (514-528), CH2 (529-638), CH3 (639-745)

Fig. 92

NYF - 0044 - HC2

**MKHLWFFLLLVAAPRWVLSGEVQLVESGGGLVQPGGSLRLSCAASGFSIRSYDIHW
VRLAPGKGLEWVATISYDGSQKYADSVKGRFTISRDESKNTLYLQMNSLRAEDTA
VYHCARGSSGHYEAFDIWGQGT LVT VSSGGGGSGGGGSGGGGSQSVLTQPPSVSAA
PGQKVTISCSGSSSNIGNWYVSWYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSG
TSATLGITGLQTGDEADYYCGTWDSSLSAPWVFGGGTKVTVLGGGGSEVQLVESGG
GLVQPGGSLRLSCAASGVTFNYYGMSWIRQAPGKGLEWVASITRSGGRIYYPSVK
GRFTISRENTQKTLYLQMNSLRAEDTAVYYCTLDGRDGVVAYWGQGT LVT VSSGGG
SGGGGGSGGGGSGNFMLTQPSSVSGVPGQRTISCTGNTGNIGSNYVNWYQQLPGTA
PKLLIYRDDKRPSGVPDRFSGSKSGTSASLAITGFQAEDEADYYCQSYSSGFIFGG
GTKLTVLAAEPKSSDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCV
VVSVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE
YKCKVSNKALPAPIEKTISKAKGQPREPQVYVPPSRDELTKNQVSLTCLVKGFYP
SDIAVEWESNGQPENNYKTTPPVLDSDGSFALVSKLTVDKSRWQQGNVFSCSVMHE
ALHNHYTQKSLSLSPGK**

**(SEQ ID NO: 91), signal sequence (1-19), NYA-2044(21-
266), linker (267-271), C3E-7085 (272-511), linker (512-
513), hinge (514-528), CH2 (529-638), CH3 (639-745)**

Fig. 93

NYF - 0045 - HC2

**MKHLWFFLLLVAAPRWVLSGEVQLVESGGGLVQPGGSLRLSCAASGFSIRSYDIHW
VRLAPGKGLEWVATISYDGSQKYADSVKGRFTISRDESKNTLYLQMNSLRAEDTA
VYHCARGSSGHYEAFDIWGQGT LVT VSSGGGGSGGGGSGGGGSQSVLTQPPSASGT
PGQRTVISCSSSNIGNWYVSWYQQLPGTAPKLLIYDNNKRPSGVPDRFSGSKSG
TSASLAISGLQSEDEADYYCGTWDSSLSAPWVFGGGTKLTVLGGGGSEVQLVESGG
GLVQPGGSLRLSCAASGVTFNYYGMSWIRQAPGKGLEWVASITRSGGRIYYPD SVK
GRFTISRENTQKTLYLQMNSLRAEDTAVYYCTLDGRDGVVAYWGQGT LVT VSSGGG
SGGGGGSGGGGSGNFMLTQPSSVSGVPGQRTVISC TGN TGNIGSNYVNWYQQLPGTA
PKLLIYRDDKRPSGVPDRFSGSKSGTSASLAITGFQAEDEADYYCQSYSSGFIFGG
GTKLTVLAAEPKSSDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCV
VVSVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE
YKCKVSNKALPAPIEKTISKAKGQPREPQVYVPPSRDELTKNQVSLTCLVKGFYP
SDIAVEWESNGQPENNYKTTPPVLDSDGSFALVSKLTVDKSRWQQGNVFSCSVMHE
ALHNHYTQKSLSLSPGK**

(SEQ ID NO: 92), signal sequence (1-19), NYA-2045 (21-266), linker (267-271), C3E-7085 (272-511), linker (512-513), hinge (514-528), CH2 (529-638), CH3 (639-745)

Fig. 94

NYF - 0047 - HC2

**MKHLWFFLLLVAAPRWVLSGQVQLVESGGGVVQPGRSLRLSCAASGFSIRSYDMHW
VRQAPGKGLEWVATISYDGSQKYADSVKGRFTISRDN SKNTLYLQMSSLRAEDTA
VYHCARGSSGHYEAFDIWGQGT LVTVSSGGGGSGGGGSGGGGSQSVLTQPPSVSAA
PGQKVTISCSGSSSNIGNWYVSWYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSG
TSATLGITGLQTGDEADYYCGTWDSSLSAPWVFGGGTKVTVLGGGGSEVQLVESGG
GLVQPGGSLRLSCAASGVTFNYYGMSWIRQAPGKGLEWVASITRSGGRIYYPSVK
GRFTISRENTQKTLYLQMNSLRAEDTAVYYCTLDGRDGVVAYWGQGT LVTVSSGGG
SGGGGGSGGGG SNFMLTQPSSVSGVP GQRTISCTGNTGNIGSNYVNWYQQLPGTA
PKLLIYRDDKRPSGVPDRFSGSKSGTSASLAITGFQAEDEADYYCQSYSSGFIFGG
GTKLTVLAAEPKSSDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCV
VVSVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE
YKCKVSNKALPAPIEKTISKAKGQPREPQVYVPPSRDELTKNQVSLTCLVKGFYP
SDIAVEWESNGQPENNYKTTPPVLDSDGSFALVSKLTVDKSRWQQGNVFSCSVMHE
ALHNHYTQKSLSLSPGK**

(SEQ ID NO: 93), signal sequence (1-19), NYA-2047(21-266), linker (267-271), C3E-7085 (272-511), linker (512-513), hinge (514-528), CH2 (529-638), CH3 (639-745)

Fig. 95

NYF - 0048 - HC2

**MKHLWFFLLLVAAPRWVLSGQVQLVESGGGVVQPGRSLRLSCAASGFSIRSYDMHW
VRQAPGKGLEWVATISYDGSQKYADSVKGRFTISRDN SKNTLYLQMSSLRAEDTA
VYHCARGSSGHYEAFDIWGQGT LVTVSSGGGGSGGGGSGGGGSQSVLTQPPSASGT
PGQRTVISCSSSNIGNWYVSWYQQLPGTAPKLLIYDNNKRPSGVPDRFSGSKSG
TSASLAISGLQSEDEADYYCGTWDSSLSAPWVFGGGTKLTVLGGGGSEVQLVESGG
GLVQPGGSLRLSCAASGVTFNYYGMSWIRQAPGKGLEWVASITRSGGRIYYPD SVK
GRFTISRENTQKTLYLQMNSLRAEDTAVYYCTLDGRD GWVAYWGQGT LVTVSSGGG
SGGGGSGGGGSGNFMLTQPSSVSGVPGQRTVISC TGNIGSNYVNWYQQLPGTA
PKLLIYRDDKRPSGVPDRFSGSKSGTSASLAITGFQAEDEADYYCQSYSSGFIFGG
GTKLTVLAAEPKSSDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCV
VVSVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE
YKCKVSNKALPAPIEKTISKAKGQPREPQVYVPPSRDELTKNQVSLTCLVKGFYP
SDIAVEWESNGQPENNYKTTPPVLDSDGSFALVSKLTVDKSRWQQGNVFSCSVMHE
ALHNHYTQKSLSLSPGK**

**(SEQ ID NO: 94), signal sequence (1-19), NYA-2048(21-
266), linker (267-271), C3E-7085 (272-511), linker (512-
513), hinge (514-528), CH2 (529-638), CH3 (639-745)**

Fig. 96

NYF-0060-HC2

**MKHLWFFLLLVAAPRWVLSGEVQLVESGGGLVQPGGSLRLSCAASGFSIRSYDIHW
VRQAPGKGLEWVATISYDGSQKYYADSVKGRFTISRDESKNTLYLQMNSLRAEDTA
VYHCARGSSGHYEAFDIWGQGT LVT VSSGGGGSGGGGSGGGGSQSVLTQPPSVSAA
PGQKVTISCSGSSSNIGNWYVSWYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSG
TSATLGITGLQTGDEADYYCGTWDSSLSAPWVFGGGTKVTVLGGGGSEVQLVESGG
GLVQPGGSLRLSCAASGVTFNYYGMSWIRQAPGKGLEWVASITRSGGRIYYPD SVK
GRFTISRENTQKTLYLQMNSLRAEDTAVYYCTLDGRDGVVAYWGQGT LVT VSSGGG
GSGGGGSGGGGSGNFMLTQPSSVSGVPGQRTISCTGNTGNIGSNYVNWYQQLPGTA
PKLLIYRDDKRPSGVPDRFSGSKSGTSASLAITGFQAEDEADYYCQSYSSGFIFGG
GTKLTVLAAEPKSSDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCV
VVSVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE
YKCKVSNKALPAPIEKTISKAKGQPREPQVYVPPSRDELTKNQVSLTCLVKGFYP
SDIAVEWESNGQPENNYKTTPPVLDSDGSFALVSKLTVDKSRWQQGNVFSCSVMHE
ALHNHYTQKSLSLSPGK**

(SEQ ID NO: 95), signal sequence (1-19), NYA-2060(21-266), linker (267-271), C3E-7085 (272-511), linker (512-513), hinge (514-528), CH2 (529-638), CH3 (639-745)

Fig. 97

NYF - 0061 - HC2

**MKHLWFFLLLVAAPRWVLSGEVQLVESGGGLVQPGGSLRLSCAASGFSIRSYDIHW
VRQAPGKGLEWVATISYDGSQKYADSVKGRFTISRDESKNTLYLQMNSLRAEDTA
VYHCARGSSGHYEAFDIWGQGT LVT VSSGGGGSGGGGSGGGGSQSVLTQPPSASGT
PGQRTISCSGSSSNIGNWYVSWYQQLPGTAPKLLIYDNNKRPSGVPDRFSGSKSG
TSASLAISGLQSEDEADYYCGTWDSSLSAPWVFGGGTKLTVLGGGGSEVQLVESGG
GLVQPGGSLRLSCAASGVTFNYYGMSWIRQAPGKGLEWVASITRSGGRIYYPD SVK
GRFTISRENTQKTLYLQMNSLRAEDTAVYYCTLDGRDGVVAYWGQGT LVT VSSGGG
SGGGGSGGGGSGNFMLTQPSSVSGVPGQRTISCTGNTGNIGSNYVNWYQQLPGTA
PKLLIYRDDKRPSGVPDRFSGSKSGTSASLAITGFQAEDEADYYCQSYSSGFIFGG
GTKLTVLAAEPKSSDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCV
VVSVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE
YKCKVSNKALPAPIEKTISKAKGQPREPQVYVPPSRDELTKNQVSLTCLVKGFYP
SDIAVEWESNGQPENNYKTTPPVLDSDGSFALVSKLTVDKSRWQQGNVFSCSVMHE
ALHNHYTQKSLSLSPGK**

(SEQ ID NO: 96), signal sequence (1-19), NYA-2061 (21-266), linker (267-271), C3E-7085 (272-511), linker (512-513), hinge (514-528), CH2 (529-638), CH3 (639-745)

Fig. 98

NYA-0001-Fab-HC1-k delete

ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGGCAGCTCCCAGATGGGTGCTGAG
CGAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGA
CACCTCCTGTTTCAGCGTCTGGATTCTCCATCCGTAGTTATGATATACACTGGGTC
CGCCAGGCTCCAGGCAAGGGGCTAGAGTGGGTGGCCACTATATCATATGATGGAAG
TCAGAAAGTACTTCGCAGACTCCGTGAAGGGCCGATTTACCATCTTCAGAGACGAAT
CGGAGAACATGGTGTATCTGCAAATGAGCGGCCTGAGAGTTGAGGACACGGCTGTT
TATCACTGTGCGAGAGGGAGTAGTGGTCATTATGAGGCTTTTGATATCTGGGGCCA
AGGGACAATGGTCACCGTCTCTTCAGCCTCCACCAAGGGCCCAAGCGTCTTCCCC
TGGCACCTCCTCCAAGAGCACCTCTGGCGGCACAGCCGCCCTGGGCTGCCTGGTC
AAGGACTACTTCCCCGAACCCGTGACCGTGAGCTGGAACCTCAGGCGCCCTGACCAG
CGGCGTGACACCTTCCCCGCTGTCCTGCAGTCCTCAGGACTCTACTCCCTCAGCA
GCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTG
AATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGA
CAAACTCACACATGCCACCCCTGCCAGCACCTGAAGCCGCAGGGGGACCCCTCAG
TCTTCCTCTTCCCCCAAACCCAAAGGACACCCTCATGATCTCCCGGACCCCTGAG
GTCACATGCGTGGTGGTGTGTCAGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTG
GTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCCCGGGAGGAGCAGT
ACAACAGCACGTACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTG
AATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGA
GAAAACCATCTCCAAAGCCAAAGGCCAGCCCCGGGAACCAAGGTGTACGTGCTGC
CCCCATCCCGGGACGAGCTGACCAAGAACCAGGTGAGCCTGCTGTGCCTGGTCAAA
GGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGCCAGCCCGAGAA
CAACTACCTGACCTGGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCTCTACA
GCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGCAACGTCTTCTCATGCTCC
GTGATGCATGAGGCTCTGCACAACCACTACACCCAGAAGAGCCTCTCCCTGTCTCC
CGGC

(SEQ ID NO: 97), signal sequence (1-57), NYA-0001_VH
(58-417), CH1 (418-711), hinge (712-756), CH2 (757-1086),
CH3 (1087-1404)

Fig. 99

NYA-0001-LC

**ATGGTGCTGCAGACCCAGGTGTTTCATCTCCCTGCTGCTGTGGATCTCCGGCGCGTA
CGGCCAGTCTGTGTTGACGCAGCCGCCCTCAGTGTCTGCGGCCCCAGGACAGAAGG
TCACCATCTCCTGCTCTGGAAGCAGCTCCAACATTGGGAATAATTATGTATCCTGG
TACCAGCAGCTCCCAGGAACAGCCCCAACTCCTCATTTATGACAATAATAAGCG
ACCCTCAGGGATTCTGACCGATTCTCTGGCTCCAAGTCTGGCACGTCAGCCACCC
TGGGCATCACCGGACTCCAGACTGGGGACGAGGCCGATTATTACTGCGGAACATGG
GATAGCAGCCTGAGTGCCCCCTTGCGGTGTTTCGGCGGAGGGACCAAGGTCACCGTCCT
AGGCCAGCCTAAGGCTGCCCCTAGCGTGACCCTGTTCCCTCCTTCCAGCGAGGAGC
TTCAAGCTAACAAGGCCACCCTGGTGTGTCTTATCTCTGACTTCTACCCTGGCGCT
GTGACCGTGGCCTGGAAGGCTGACAGCTCCCCTGTGAAGGCCGGAGTGGAGACCAC
CACACCTAGCAAGCAGTCTAACAACAAGTACGCTGCCAGCTCCTACCTGAGCCTTA
CCCCTGAGCAGTGGAAGTCTCACAGAAGCTACTCCTGTCAAGTGACCCACGAGGGC
AGCACCGTGGAGAAGACCGTGGCTCCTACCGAGTGTTCC**

**(SEQ ID NO: 98), signal sequence (1-60), NYA-0001_VL
(61-393), CL (394-711)**

Fig. 100

NYA-0001-Fab-HC1-k delete

**MKHLWFFLLLVAAPRWVLSEVQLVESGGGVVQPGRSLTPSCSASGFSIRSYDIHWV
RQAPGKGLEWVATISYDGSQKYFADSVKGRFTIFRDESENMVYLQMSGLRVEDTAV
YHCARGSSGHYEAFDIWGQGTMTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNV
NHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPE
VTCVVVSVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL
NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYVLPSPRDELTKNQVSLCLVK
GFYPSDIAVEWESNGQPENNYLTWPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS
VMHEALHNHYTQKSLSLSPG**

**(SEQ ID NO: 99), signal sequence (1-19), NYA-0001_VH
(20-139), CH1 (140-237), hinge (238-252), CH2 (253-362),
CH3 (363-468)**

Fig. 101

NYA-0001-LC

**MVLQTQVFISLLLWISGAYGQSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSW
YQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGTSATLGITGLQTGDEADYYCGTW
DSSLAPWVFGGGTKVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGA
VTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEG
STVEKTVAPTECS**

**(SEQ ID NO: 100), signal sequence (1-20), NYA-0001_VL
(21-131), CL (132-237)**

Fig. 102

NYA-1143-Fab-HC1-k delete

ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGGCAGCTCCCAGATGGGTGCTGAG
CGAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGA
CACCTCCTGTTTCAGCGTCTGGATTCTCCATCCGTAGCTATGATATACACTGGGTC
CGCCTGGCTCCAGGCAAGGGGCTAGAGTGGGTGGCCACTATATCATATGATGGAAG
TCAGAAAGTACTTCGCAGACTCCGTGAAGGGCCGATTTACCATCTTCAGAGACGAAT
CGGAGAACATGGTGTATCTGCAAATGAGCGGCCTGAGAGTTGAGGACACGGCTGTT
TATCACTGTGCGAGAGGGAGTAGTGGTCATTATGAGGCTTTTGATATCTGGGGCCA
AGGGACAATGGTCACCGTCTCTTCAGCCTCCACCAAGGGGCCAAGCGTCTTCCCC
TGGCACCTCCTCCAAGAGCACCTCTGGCGGCACAGCCGCCCTGGGCTGCCTGGTC
AAGGACTACTTCCCCGAACCCGTGACCGTGAGCTGGAACCTCAGGCGCCCTGACCAG
CGGCGTGACACCTTCCCCGCTGTCTGTCAGTCCTCAGGACTCTACTCCCTCAGCA
GCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTG
AATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGA
CAAACTCACACATGCCACCCCTGCCCAGCACCTGAAGCCGCAGGGGGACCCCTCAG
TCTTCCTCTTCCCCCAAACCCAAAGGACACCCTCATGATCTCCCGGACCCCTGAG
GTCACATGCGTGGTGGTGTGTCAGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTG
GTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCCCGGGAGGAGCAGT
ACAACAGCACGTACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTG
AATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGA
GAAAACCATCTCCAAAGCCAAAGGCCAGCCCCGGGAACACAGGTGTACGTGCTGC
CCCCATCCCGGGACGAGCTGACCAAGAACCAGGTGAGCCTGCTGTGCCTGGTCAAA
GGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGCCAGCCCGAGAA
CAACTACCTGACCTGGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCTCTACA
GCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGCAACGTCTTCTCATGCTCC
GTGATGCATGAGGCTCTGCACAACCACTACACCCAGAAGAGCCTCTCCCTGTCTCC
CGGC

(SEQ ID NO: 101), signal sequence (1-57), NYA-1143_VH
(58-417), CH1 (418-711), hinge (712-756), CH2 (757-1086),
CH3 (1087-1404)

Fig. 103

NYA-1143-LC

**ATGGTGCTGCAGACCCAGGTGTTTCATCTCCCTGCTGCTGTGGATCTCCGGCGCGTA
CGGCCAGTCTGTGTTGACGCAGCCGCCCTCAGTGTCTGCGGCCCCAGGACAGAAGG
TCACCATCTCCTGCTCTGGAAGCAGCTCCAACATTGGGAATTGGTATGTATCCTGG
TACCAGCAGCTCCCAGGAACAGCCCCAACTCCTCATTTATGACAATAATAAGCG
ACCCTCAGGGATTCTGACCGATTCTCTGGCTCCAAGTCTGGCACGTCAGCCACCC
TGGGCATCACCGGACTCCAGACTGGGGACGAGGCCGATTATTACTGCGGAACATGG
GATAGCAGCCTGAGTGCCCCCTTGCGGTGTTTCGGCGGAGGGACCAAGGTCACCGTCCT
AGGCCAGCCTAAGGCTGCCCCTAGCGTGACCCTGTTCCCTCCTTCCAGCGAGGAGC
TTCAAGCTAACAAGGCCACCCTGGTGTGTCTTATCTCTGACTTCTACCCTGGCGCT
GTGACCGTGGCCTGGAAGGCTGACAGCTCCCCTGTGAAGGCCGGAGTGGAGACCAC
CACACCTAGCAAGCAGTCTAACAACAAGTACGCTGCCAGCTCCTACCTGAGCCTTA
CCCCTGAGCAGTGGAAGTCTCACAGAAGCTACTCCTGTCAAGTGACCCACGAGGGC
AGCACCGTGGAGAAGACCGTGGCTCCTACCGAGTGTTCC**

**(SEQ ID NO: 102), signal sequence (1-60), NYA-1143_VL
(61-393), CL (394-711)**

Fig. 104

C3E-7085-HC2-k delete

ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGGCAGCTCCCAGATGGGTGCTGAG
CGGAGAAGTGCAGCTGGTGGAATCCGGGGGGGGCCTGGTGCAGCCTGGGGGGAGCC
TGAGACTGAGTTGTGCCGCCTCTGGGGTGACATTTAACTACTATGGCATGTCTTGG
ATCCGCCAGGCACCTGGAAAGGGCCTGGAGTGGGTGGCCAGCATCACTAGGTCCGG
CGGGCGAATCTACTATCCCGACAGCGTCAAGGGCAGGTTTACAATTTCCCGCGAGA
ACACACAGAAAACCTCTGTACCTGCAGATGAATAGCCTGAGAGCCGAAGATACAGCT
GTGTACTATTGCACTCTGGACGGCAGGGATGGGTGGGTGCGCTATTGGGGGCAGGG
AACCCTGGTGACAGTCAGCTCCGGAGGAGGAGGATCTGGCGGAGGAGGCAGTGGGG
GAGGCGGGTCAAACTTTATGCTCACTCAGCCGTCCTCTGTTTCTGGCGTACCTGGC
CAACGGGTGACCATTAGCTGTACGGGTAATACCGGGAATATCGGGTCTAACTACGT
GAACTGGTATCAGCAGCTTCCAGGGACAGCTCCCAAGTTGCTGATCTATCGCGACG
ACAAAAGACCCTCAGGGGTCCCTGACCGATTTAGTGGCAGCAAAAGCGGTACTTCC
GCTTCCCTGGCGATAACCGGCTTTCAGGCCGAAGATGAGGCAGACTACTATTGCCA
GTCATATTCCAGCGGCTTCATCTTCGGAGGCGGAACCTAAGCTGACAGTGTTGGCAG
CCGAGCCCAAATCTTCTGACAAAACCTCACACATGCCACCCCTGCCCAGCACCTGAA
GCCGCAGGGGGACCCTCAGTCTTCTCTTCCCCCAAACCCAAGGACACCCTCAT
GATCTCCCGGACCCCTGAGGTACATGCGTGGTGGTGTGAGTGAGCCACGAAGACC
CTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACA
AAGCCCCGGGAGGAGCAGTACAACAGCACGTACCGGGTGGTCAGCGTCCTCACCGT
CCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAG
CCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGCCAGCCCCGGGAA
CCACAGGTGTACGTGTACCCCCCATCCCGGGACGAGCTGACCAAGAACCAGGTGAG
CCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGA
GCAATGGCCAGCCCGAGAACAACTACAAGACCACCCCTCCCGTGCTGGACTCCGAC
GGCTCCTTCGCCCTCGTGAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGG
CAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACCCAGA
AGAGCCTCTCCCTGTCTCCC

(SEQ ID NO: 103), signal sequence (1-57), C3E-7085 (61-780), linker (781-786), hinge (787-831), CH2 (832-1161), CH3 (1162-1479)

Fig. 105

NYA-1143-Fab-HC1-k delete

**MKHLWFFLLLVAAPRWVLSEVQLVESGGGVVQPGRSLTPSCSASGFSIRSYDIHWV
RLAPGKGLEWVATISYDGSQKYFADSVKGRFTIFRDESENMVYLQMSGLRVEDTAV
YHCARGSSGHYEAFDIWGQGTMTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNV
NHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPE
VTCVVVSVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL
NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYVLPSPRDELTKNQVSLCLVK
GFYPSDIAVEWESNGQPENNYLTWPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS
VMHEALHNHYTQKSLSLSPG**

**(SEQ ID NO: 104), signal sequence (1-19), NYA-1143_VH
(20-139), CH1 (140-237), hinge (238-252), CH2 (253-362),
CH3 (363-468)**

Fig. 106

NYA-1143-LC

**MVLQTQVFISLLLWISGAYGQSVLTQPPSVSAAPGQKVTISCSGSSSNIGNWYVSW
YQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGTSATLGITGLQTGDEADYYCGTW
DSSLAPWVFGGGTKVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGA
VTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEG
STVEKTVAPTECS**

**(SEQ ID NO: 105), signal sequence (1-20), NYA-1143_VL
(21-131), CL (132-237)**

Fig. 107

C3E-7085-HC2-k delete

**MKHLWFFLLLVAAPRWVLSGEVQLVESGGGLVQPGGSLRLSCAASGVTFNYYGMSW
IRQAPGKGLEWVASITRSGGRIYYPDSVKGRFTISRENTQKTLYLQMNSLRAEDTA
VYYCTLDGRDGWVAYWGQGLTVTVSSGGGGSGGGGSGGGGSNFMLTQPSSVSGVPG
QVRTISCTGNTGNIGSNYVNWYQQLPGTAPKLLIYRDDKRPSGVPDRFSGSKSGTS
ASLAITGFQAEDEADYYCQSYSSGFIFGGGTKLTVLAAEPKSSDKTHTCPPCPAPE
AAGGPSVFLFPPKPKDTLMISRTPEVTCVVVSVSHEDPEVKFNWYVDGVEVHNAKT
KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE
PQVYVYPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDS
GSFALVSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG**

(SEQ ID NO: 106), signal sequence (1-19), C3E-7085 (21-260), linker (261-262), hinge (263-277), CH2 (278-387), CH3 (388-493)

Fig. 108

NYA-1143-HC1-k delete

ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGGCAGCTCCCAGATGGGTGCTGAG
CGGAGAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCC
TGACACCCTCCTGTTCAAGCTCTGGATTCTCCATCCGTAGCTATGATATACACTGG
GTCCGCCTGGCTCCAGGCAAGGGGCTAGAGTGGGTGGCCACTATATCATATGATGG
AAGTCAGAAGTACTTCGCAGACTCCGTGAAGGGCCGATTTACCATCTTCAGAGACG
AATCGGAGAACATGGTGTATCTGCAAATGAGCGGCCTGAGAGTTGAGGACACGGCT
GTTTATCACTGTGCGAGAGGGAGTAGTGGTCATTATGAGGCTTTTGATATCTGGGG
CCAAGGGACAATGGTCACCGTCTCTTCAGGTGGAGGCGGTTTCAGGCGGAGGTGGCA
GCGGCGGTGGCGGGAGTCAGTCTGTGTTGACGCAGCCGCCCTCAGTGTCTGCGGCC
CCAGGACAGAAGGTCACCATCTCCTGCTCTGGAAGCAGCTCCAACATTGGGAATTG
GTATGTATCCTGGTACCAGCAGCTCCCAGGAACAGCCCCAACTCCTCATTTATG
ACAATAATAAGCGACCCTCAGGGATTCTTGACCGATTCTCTGGCTCCAAGTCTGGC
ACGTCAGCCACCCTGGGCATCACCGGACTCCAGACTGGGGACGAGGCCGATTATTA
CTGCGGAACATGGGATAGCAGCCTGAGTGCCCCCTTGGGTGTTGGGCGGAGGGACCA
AGGTCACCGTCCTAGCAGCCGAGCCCAAATCTTCTGACAAAACCTCACACATGCCCA
CCCTGCCCAGCACCTGAAGCCGCAGGGGGACCCTCAGTCTTCCTCTTCCCCCAA
ACCCAAGGACACCCTCATGATCTCCCGGACCCTGAGGTCACATGCGTGGTGGTGT
CAGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAG
GTGCATAATGCCAAGACAAAGCCCCGGGAGGAGCAGTACAACAGCACGTACCGGGT
GGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGT
GCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCAAAGCC
AAAGGCCAGCCCCGGGAACCACAGGTGTACGTGCTGCCCCCATCCCGGGACGAGCT
GACCAAGAACCAGGTCAGCCTGCTGTGCCTGGTCAAAGGCTTCTATCCCAGCGACA
TCGCCGTGGAGTGGGAGAGCAATGGCCAGCCCGAGAACAACTACCTGACCTGGCCT
CCCGTGCTGGACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAA
GAGCAGGTGGCAGCAGGGCAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGC
ACAACCACTACACCCAGAAGAGCCTCTCCCTGTCTCCCGGC

(SEQ ID NO: 107), signal sequence (1-57), NYA-1143 (61-798), linker799-800), hinge (801-849), CH2 (850-1179), CH3 (1180-1497)

Fig. 109

NYA-1143-HC1-k delete

**MKHLWFFLLLVAAPRWVLSGEVQLVESGGGVVQPGRSLTPSCSASGFSIRSYDIHW
VRLAPGKGLEWVATISYDGSQKYFADSVKGRFTIFRDESENMVYLQMSGLRVEDTA
VYHCARGSSGHYEAFDIWGQGTMTVSSGGGGSGGGGSGGGGSQSVLTQPPSVSAA
PGQKVTISCSGSSSNIGNWYVSWYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSG
TSATLGITGLQTGDEADYYCGTWDSSLSAPWVFGGGTKVTVLAAEPKSSDKTHTCP
PCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVTVSVSHEDPEVKFNWYVDGVE
VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
KGQPREPQVYVLPISRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYLTWP
PVLDSGDGSFFLYSKLTVDKSRWQQGNVFSQVMHEALHNHYTQKSLSLSPG
(SEQ ID NO: 108), signal sequence (1-19), NYA-1143 (21-
266), linker (267-268), hinge (269-283), CH2 (284-393),
CH3 (394-499)**

Fig. 110

C3E-7085-NYA-1154-Fab-HC2-k delete

ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGGCAGCTCCCAGATGGGTGCTGAG
CGGAGAAGTGCAGCTGGTGGAAATCCGGGGGGGGCCTGGTGCAGCCTGGGGGGAGCC
TGAGACTGAGTTGTGCCGCCTCTGGGGTGACATTTAACTACTATGGCATGTCTTGG
ATCCGCCAGGCACCTGGAAAGGGCCTGGAGTGGGTGGCCAGCATCACTAGGTCCGG
CGGGCGAATCTACTATCCCGACAGCGTCAAGGGCAGGTTACAATTTCCCGCGAGA
ACACACAGAAAACCTCTGTACCTGCAGATGAATAGCCTGAGAGCCGAAGATACAGCT
GTGTACTATTGCACTCTGGACGGCAGGGATGGGTGGGTGCGCTATTGGGGGCAGGG
AACCTGGTGCAGTCAGCTCCGGAGGAGGAGGATCTGGCGGAGGAGGCAGTGGGG
GAGGCGGGTCAAACTTTATGCTCACTCAGCCGTCCTCTGTTTCTGGCGTACCTGGC
CAACGGGTGACCATTAGCTGTACGGGTAATACCGGGAATATCGGGTCTAACTACGT
GAACTGGTATCAGCAGCTTCCAGGGACAGCTCCCAAGTTGCTGATCTATCGCGACG
ACAAAAGACCCTCAGGGGTCCCTGACCGATTTAGTGGCAGCAAAAGCGGTACTTCC
GCTTCCCTGGCGATAACCGGCTTTCAGGCCGAAGATGAGGCAGACTACTATTGCCA
GTCATATTCCAGCGGCTTCATCTTCGGAGGCGGAACCTAAGCTGACAGTGTTGGGGG
GAGGCGGTTTCAGAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGG
AGGTCCCTGACACCCTCCTGTTACGCGTCTGGATTCTCCATCCGTAGTTATGATAT
GCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTAGAGTGGGTGGCCACTATATCAT
ATGATGGAAGTCAGAAAGTACTTCGCAGACTCCGTGAAGGGCCGATTTACCATCTTC
AGAGACGAATCGGAGAACATGGTGTATCTGCAAATGAGCGGCCTGAGAGTTGAGGA
CACGGCCGTTTATCACTGTGCGAGAGGGAGTAGTAATCATTATGAGGCTTTTGATA
TCTGGGGCCAAGGGACAATGGTCACCGTCTCTTCAGCCTCCACCAAGGGCCCAAGC
GTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGCGGCACAGCCGCCCTGGG
CTGCCTGGTCAAGGACTACTTCCCCGAACCCGTGACCGTGAGCTGGAACCTCAGGCG
CCCTGACCAGCGGCGTGACACCTTCCCCGCTGTCTGCACTCCTCAGGACTCTAC
TCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACAT
CTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCA
AATCTTGTGACAAAACCTCACACATGCCCACCCTGCCCAGCACCTGAAGCCGCAGGG
GGACCCTCAGTCTTCTCTTCCCCCAAAACCCAAGGACACCCTCATGATCTCCCG
GACCCCTGAGGTCACATGCGTGGTGGTGTGAGTGAGCCACGAAGACCCTGAGGTCA
AGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCCCGG
GAGGAGCAGTACAACAGCACGTACCGGGTGGTCAGCGTCCTCACCGTCTGACCA
GGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAG
CCCCATCGAGAAAACCATCTCAAAGCCAAAGGCCAGCCCCGGGAACCACAGGTG
TACGTGTACCCCCCATCCCGGGACGAGCTGACCAAGAACCAGGTGAGCCTGACCTG
CCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGCC
AGCCCGAGAACAACCTACAAGACCACCCTCCCGTGCTGGACTCCGACGGCTCCTTC
GCCCTCGTGAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGCAACGTCTT
CTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACCCAGAAGAGCCTCT
CCCTGTCTCCCGGC

(SEQ ID NO: 109), signal sequence (1-57), C3E-7085 (61-780), linker (781-795), NYA-1154-VH (796-1155), CH1 (1156-1470), hinge (1471-1500), CH2 (1501-1830), CH3 (1831-2142)

Fig. 111

NYA-1154-LC

**ATGGTGCTGCAGACCCAGGTGTTTCATCTCCCTGCTGCTGTGGATCTCCGGCGCGTA
CGGCCAGTCTGTGTTGACGCAGCCGCCCTCAGTGTCTGCGGCCCCAGGACAGAAGG
TCACCATCTCCTGCTCTGGAAGCAGCTCCAACATTGGGAATAATTATGTATCCTGG
TACCAGCGGCTCCCAGGAACAGCCCCAACTCCTCATTTATGACAATAATAAGCG
ACCCTCAGGGATTCTGACCGATTCTCTGGCTCCAAGTCTGGCACGTCAGCCACCC
TGGGCATCACCGGACTCCAGACTGGGGACGAGGCCGATTACTACTGCGGAGCATGG
GATAGCAGCCTGAGTGCCCCCTTGCGGTGTTTCGGCGGAGGGACCAAGGTCACCGTCCT
AGGCCAGCCTAAGGCTGCCCCTAGCGTGACCCTGTTCCCTCCTTCCAGCGAGGAGC
TTCAAGCTAACAAGGCCACCCTGGTGTGTCTTATCTCTGACTTCTACCCTGGCGCT
GTGACCGTGGCCTGGAAGGCTGACAGCTCCCCTGTGAAGGCCGGAGTGGAGACCAC
CACACCTAGCAAGCAGTCTAACAACAAGTACGCTGCCAGCTCCTACCTGAGCCTTA
CCCCTGAGCAGTGGAAGTCTCACAGAAGCTACTCCTGTCAAGTGACCCACGAGGGC
AGCACCGTGGAGAAGACCGTGGCTCCTACCGAGTGTTCC**

**(SEQ ID NO: 110), signal sequence (1-60), NYA-1154_VL
(61-393), CL (394-711)**

Fig. 112

OAA-HC1-k delete

ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGGCAGCTCCCAGATGGGTGCTGAG
CGACAAAACCTCACACATGCCACCCCTGCCAGCACCTGAAGCCGCAGGGGGACCCT
CAGTCTTCCTCTTCCCCCAAACCCAAGGACACCCTCATGATCTCCCGGACCCCT
GAGGTCACATGCGTGGTGGTGTGTCAGTGAGCCACGAAGACCCTGAGGTCAAGTTCAA
CTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCCCGGGAGGAGC
AGTACAACAGCACGTACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGG
CTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCAT
CGAGAAAACCATCTCCAAAGCCAAAGGCCAGCCCCGGGAACCACAGGTGTACGTGC
TGCCCCCATCCCGGGACGAGCTGACCAAGAACCAGGTCAGCCTGCTGTGCCTGGTC
AAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGCCAGCCCGA
GAACAACTACCTGACCTGGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCT
ACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGCAACGTCTTCTCATGC
TCCGTGATGCATGAGGCTCTGCACAACCACTACACCCAGAAGAGCCTCTCCCTGTC
TCCCGGC

(SEQ ID NO: 111), signal sequence (1-57), hinge (58-87),
CH2 (88-417), CH3 (418-735)

Fig. 113

C3E-7085-NYA-1154-Fab-HC2-k delete

**MKHLWFFLLLVAAPRWVLSGEVQLVESGGGLVQPGGSLRLSCAASGVTFNYYGMSW
IRQAPGKGLEWVASITRSGGRIYYPDSVKGRFTISRENTQKTLYLQMNSLRAEDTA
VYYCTLDGRDGWVAYWGQGLTVTVSSGGGGSGGGGSGGGGSNFMLTQPSSVSGVPG
QRTISCTGNTGNIGSNYVNWYQQLPGTAPKLLIYRDDKRPSGVPDRFSGSKSGTS
ASLAITGFQAEDEADYYCQSYSSGFIFGGGTKLTVLGGGGSEVQLVESGGGVVQPG
RSLTPSCSASGFSIRSYDMHWVRQAPGKGLEWVATISYDGSQKYFADSVKGRFTIF
RDESENMVYLLQMSGLRVEDTAVYHCARGSSNHYEAFDIWGQGTMTVTSSASTKGPS
VFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY
SLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEAAG
GPSVFLFPPKPKDTLMISRTPEVTCVIVSVSHEDPEVKFNWYVDGVEVHNAKTKPR
EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV
YVYPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSF
ALVSKLTVDKSRWQQGNVFSQSVSMHEALHNHYTQKSLSLSPG**

(SEQ ID NO: 112), signal sequence (1-19), C3E-7085 (21-260), linker (261-265), NYA-1154-VH (266-385), CH1 (386-490), hinge (491-500), CH2 (501-610), CH3 (611-714)

Fig. 114

NYA-1154-LC

**MVLQTQVFISLLLWISGAYGQSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSW
YQRLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGTSATLGITGLQTGDEADYYCGAW
DSSLAPWVFGGGTKVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGA
VTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEG
STVEKTVAPTECS**

**(SEQ ID NO: 113), signal sequence (1-20), NYA-1154_VL
(21-131), CL (132-237)**

Fig. 115

OAA-HC1-k delete

MKHLWFFLLLVAAPRWVLSDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMIS RTP
EVTCTVVSVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW
LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYVLPISRDELTKNQVSLCLV
KGFYPSDIAVEWESNGQPENNYLTWPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSC
SVMHEALHNHYTQKSLSLSPG

(SEQ ID NO: 114), signal sequence (1-19), hinge (20-29),
CH2 (30-139), CH3 (140-245)

Fig. 116

NYF-0010-HC2-k delete

ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGGCAGCTCCCAGATGGGTGCTGAG
CGGAGAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCC
TGACACCCTCCTGTTTCAGCGTCTGGATTCTCCATCCGTAGTTATGATATGCACTGG
GTCCGCCAGGCTCCAGGCAAGGGGCTAGAGTGGGTGGCCACTATATCATATGATGG
AAGTCAGAACTACTTCGCAGACTCCGTGAAGGGCCGATTTACCATCTTCAGAGACG
AATCGGAGAACATGGTGTATCTGCAAATGAGCGGCCTGAGAGTTGAGGACACGGCC
GTTTATCACTGTGCGAGAGGGAGTAGTAATCATTATGAGGCTTTTGATATCTGGGG
CCAAGGGACAATGGTCACCGTCTCTTCAGGTGGAGGCGGTTTCAGGCGGAGGTGGCA
GCGGCGGTGGCGGGAGTCAGTCTGTGTTGACGCGAGCCGCCCTCAGTGTCTGCGGCC
CCAGGACAGAAGGTCACCATCTCCTGCTCTGGAAGCAGCTCCAACATTGGGAATAA
TTATGTATCCTGGTACCAGCGGCTCCCAGGAACAGCCCCCAAACCTCCTCATTTATG
ACAATAATAAGCGACCCTCAGGGATTCTGACCGATTCTCTGGCTCCAAGTCTGGC
ACGTCAGCCACCCTGGGCATCACCGGACTCCAGACTGGGGACGAGGCCGATTACTA
CTGCGGAGCATGGGATAGCAGCCTGAGTGCCCTTTGGGTGTTGCGCGGAGGGACCA
AGGTCACCGTCTAGGGGGAGGCGGTTTCAGAAGTGCAGCTGGTGGAATCCGGGGGG
GGCCTGGTGCAGCCTGGGGGGAGCCTGAGACTGAGTTGTGCCGCCTCTGGGGTGAC
ATTTAACTACTATGGCATGTCTTGATCCGCCAGGCACCTGGAAAGGGCCTGGAGT
GGGTGGCCAGCATCACTAGGTCCGGCGGGCGAATCTACTATCCCGACAGCGTCAAG
GGCAGGTTTACAATTTCCCGCGAGAACACACAGAAAACCTCTGTACCTGCAGATGAA
TAGCCTGAGAGCCGAAGATACAGCTGTGTACTATTGCACTCTGGACGGCAGGGATG
GGTGGGTGCGCTATTGGGGGCAGGGAACCCTGGTGACAGTCAGCTCCGGAGGAGGA
GGATCTGGCGGAGGAGGCAGTGGGGGAGGCGGGTCAAACCTTTATGCTCACTCAGCC
GTCCTCTGTTTCTGGCGTACCTGGCCAACGGGTGACCATTAGCTGTACGGGTAATA
CCGGGAATATCGGGTCTAACTACGTGAACTGGTATCAGCAGCTTCCAGGGACAGCT
CCCAAGTTGCTGATCTATCGCGACGACAAAAGACCCTCAGGGGTCCCTGACCGATT
TAGTGGCAGCAAAAGCGGTACTTCCGCTTCCCTGGCGATAACCGGCTTTCAGGCCG
AAGATGAGGCAGACTACTATTGCCAGTCATATTCCAGCGGCTTCATCTTCGGAGGC
GGAACCTAAGCTGACAGTGTTGGCAGCCGAGCCCAAATCTTCTGACAAAACCTCACAC
ATGCCACACCCTGCCAGCACCTGAAGCCGCAGGGGGACCCTCAGTCTTCTCTTCC
CCCCAAAACCAAGGACACCCTCATGATCTCCCGGACCCTGAGGTCACATGCGTG
GTGGTGTCAGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGG
CGTGGAGGTGCATAATGCCAAGACAAAGCCCCGGGAGGAGCAGTACAACAGCACGT
ACCGGGTGGTCAGCGTCTCACCGTCTGCACCAGGACTGGCTGAATGGCAAGGAG
TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTC
CAAAGCCAAAGGCCAGCCCCGGGAACCACAGGTGTACGTGTACCCCCCATCCGGG
ACGAGCTGACCAAGAACCAGGTGACCTGACCTGCCTGGTCAAAGGCTTCTATCCC
AGCGACATCGCCGTGGAGTGGGAGAGCAATGGCCAGCCCGAGAACAACTACAAGAC
CACCCCTCCCGTGCTGGACTCCGACGGCTCCTTCGCCCTCGTGAGCAAGCTCACCG
TGGACAAGAGCAGGTGGCAGCAGGGCAACGTCTTCTCATGCTCCGTGATGCATGAG
GCTCTGCACAACCACTACACCCAGAAGAGCCTCTCCCTGTCTCCCGG
(SEQ ID NO: 115), signal sequence (1-57), NYA-1154(61-
798), linker (799-813), C3E-7085 (814-1533), linker
(1534-1539), hinge (1540-1584), CH2 (1585-1914), CH3
(1915-2232)

Fig. 117

NYF-0004-HC2-k delete

ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGGCAGCTCCCAGATGGGTGCTGAG
CGGAGAAGTGCAGCTGGTGGGAATCCGGGGGGGGCCTGGTGCAGCCTGGGGGGAGCC
TGAGACTGAGTTGTGCCGCCTCTGGGGTGACATTTAACTACTATGGCATGTCTTGG
ATCCGCCAGGCACCTGGAAAGGGCCTGGAGTGGGTGGCCAGCATCACTAGGTCCGG
CGGGCGAATCTACTATCCCGACAGCGTCAAGGGCAGGTTACAATTTCCCGCGAGA
ACACACAGAAAACCTCTGTACCTGCAGATGAATAGCCTGAGAGCCGAAGATACAGCT
GTGTACTATTGCACTCTGGACGGCAGGGATGGGTGGGTCGCCTATTGGGGGCAGGG
AACCCTGGTGACAGTCAGCTCCGGAGGAGGAGGATCTGGCGGAGGAGGCAGTGGGG
GAGGCGGGTCAAACTTTATGCTCACTCAGCCGTCCTCTGTTTCTGGCGTACCTGGC
CAACGGGTGACCATTAGCTGTACGGGTAATACCGGGAATATCGGGTCTAACTACGT
GAACTGGTATCAGCAGCTTCCAGGGACAGCTCCCAAGTTGCTGATCTATCGCGACG
ACAAAAGACCCTCAGGGGTCCCTGACCGATTTAGTGGCAGCAAAAGCGGTACTTCC
GCTTCCCTGGCGATAACCGGCTTTCAGGCCGAAGATGAGGCAGACTACTATTGCCA
GTCATATTCCAGCGGCTTCATCTTCGGAGGCGGAACCTAAGCTGACAGTGTTGGGGG
GAGGCGGTTTCAGAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGG
AGGTCCCTGACACCCTCCTGTTACGCGTCTGGATTCTCCATCCGTAGTTATGATAT
GCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTAGAGTGGGTGGCCACTATATCAT
ATGATGGAAGTCAGAAAGTACTTCGCAGACTCCGTGAAGGGCCGATTTACCATCTTC
AGAGACGAATCGGAGAACATGGTGTATCTGCAAATGAGCGGCCTGAGAGTTGAGGA
CACGGCCGTTTATCACTGTGCGAGAGGGAGTAGTAATCATTATGAGGCTTTTGATA
TCTGGGGCCAAGGGACAATGGTCACCGTCTCTTCAGGTGGAGGCGGTTCAGGCGGA
GGTGGCAGCGGCGGTGGCGGGAGTCAGTCTGTGTTGACGCAGCCGCCCTCAGTGTC
TGCGGCCCCAGGACAGAAGGTACCATCTCCTGCTCTGGAAGCAGCTCCAACATTG
GGAATAATTATGTATCCTGGTACCAGCGGCTCCCAGGAACAGCCCCCAAACCTCCTC
ATTTATGACAATAATAAGCGACCCTCAGGGATTCTGACCGATTCTCTGGCTCCAA
GTCTGGCACGTACGCCACCCTGGGCATCACCGGACTCCAGACTGGGGACGAGGCCG
ATTACTACTGCGGAGCATGGGATAGCAGCCTGAGTGCCCTTGGGTGTTTCGGCGGA
GGGACCAAGGTACCGTCTTAGCAGCCGAGCCCAAATCTTCTGACAAAACCTCACAC
ATGCCACACCCTGCCAGCACCTGAAGCCGCAGGGGGACCCTCAGTCTTCTCTTCC
CCCCAAAACCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTG
GTGGTGTCAGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGG
CGTGGAGGTGCATAATGCCAAGACAAAGCCCCGGGAGGAGCAGTACAACAGCACGT
ACCGGGTGGTCAGCGTCTCACCGTCTGCACCAGGACTGGCTGAATGGCAAGGAG
TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTC
CAAAGCCAAAGGCCAGCCCCGGGAACCACAGGTGTACGTGTACCCCCCATCCCGGG
ACGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC
AGCGACATCGCCGTGGAGTGGGAGAGCAATGGCCAGCCCGAGAACAACCTACAAGAC
CACCCCTCCCGTGCTGGACTCCGACGGCTCCTTCGCCCTCGTGAGCAAGCTCACCG
TGGACAAGAGCAGGTGGCAGCAGGGCAACGTCTTCTCATGCTCCGTGATGCATGAG
GCTCTGCACAACCACTACACCCAGAAGAGCCTCTCCCTGTCTCCCGGC
(SEQ ID NO: 116), signal sequence (1-57), C3E-7085 (61-
780), linker (781-795), NYA-1154(796-1533), linker
(1534-1539), hinge (1540-1584), CH2 (1585-1914), CH3
(1915-2232)

Fig. 118

NYF-0011-HC2-k delete

ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGGCAGCTCCCAGATGGGTGCTGAG
CGGAGAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCC
TGACACCCTCCTGTTTCAGCGTCTGGATTCTCCATCCGTAGCTATGATATACACTGG
GTCCGCCTGGCTCCAGGCAAGGGGCTAGAGTGGGTGGCCACTATATCATATGATGG
AAGTCAGAAGTACTTCGCAGACTCCGTGAAGGGCCGATTTACCATCTTCAGAGACG
AATCGGAGAACATGGTGTATCTGCAAATGAGCGGCCTGAGAGTTGAGGACACGGCT
GTTTATCACTGTGCGAGAGGGAGTAGTGGTCATTATGAGGCTTTTGATATCTGGGG
CCAAGGGACAATGGTCACCGTCTCTTCAGGTGGAGGCGGTTTCAGGCGGAGGTGGCA
GCGGCGGTGGCGGGAGTCAGTCTGTGTTGACGCGAGCCGCCCTCAGTGTCTGCGGCC
CCAGGACAGAAGGTCACCATCTCCTGCTCTGGAAGCAGCTCCAACATTGGGAATTG
GTATGTATCCTGGTACCAGCAGCTCCCAGGAACAGCCCCCAAACCTCCTCATTTATG
ACAATAATAAGCGACCCTCAGGGATTCTGACCGATTCTCTGGCTCCAAGTCTGGC
ACGTCAGCCACCCTGGGCATCACCGGACTCCAGACTGGGGACGAGGCCGATTATTA
CTGCGGAACATGGGATAGCAGCCTGAGTGCCCCCTTGGGTGTTGGGCGGAGGGACCA
AGGTCACCGTCCTAGGGGGAGGCGGTTCAGAAGTGCAGCTGGTGGAATCCGGGGGG
GGCCTGGTGCAGCCTGGGGGGAGCCTGAGACTGAGTTGTGCCGCCTCTGGGGTGAC
ATTTAACTACTATGGCATGTCTTGATCCGCCAGGCACCTGGAAAGGGCCTGGAGT
GGGTGGCCAGCATCACTAGGTCCGGCGGGCGAATCTACTATCCCGACAGCGTCAAG
GGCAGGTTTACAATTTCCCGCGAGAACACACAGAAAACCTCTGTACCTGCAGATGAA
TAGCCTGAGAGCCGAAGATACAGCTGTGTACTATTGCACTCTGGACGGCAGGGATG
GGTGGGTGCGCTATTGGGGGCAGGGAACCCTGGTGACAGTCAGCTCCGGAGGAGGA
GGATCTGGCGGAGGAGGCAGTGGGGGAGGCGGGTCAAACCTTTATGCTCACTCAGCC
GTCCTCTGTTTCTGGCGTACCTGGCCAACGGGTGACCATTAGCTGTACGGGTAATA
CCGGGAATATCGGGTCTAACTACGTGAACTGGTATCAGCAGCTTCCAGGGACAGCT
CCCAAGTTGCTGATCTATCGCGACGACAAAAGACCCTCAGGGGTCCCTGACCGATT
TAGTGGCAGCAAAAGCGGTACTTCCGCTTCCCTGGCGATAACCGGCTTTCAGGCCG
AAGATGAGGCAGACTACTATTGCCAGTCATATTCCAGCGGCTTCATCTTCGGAGGC
GGAACATAAGCTGACAGTGTTGGCAGCCGAGCCCAAATCTTCTGACAAAACCTCACAC
ATGCCACACCCTGCCAGCACCTGAAGCCGCAGGGGGACCCTCAGTCTTCTCTTCC
CCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCTGAGGTCACATGCGTG
GTGGTGTCAGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGG
CGTGGAGGTGCATAATGCCAAGACAAAGCCCCGGGAGGAGCAGTACAACAGCACGT
ACCGGGTGGTCAGCGTCTCACCGTCTGCACCAGGACTGGCTGAATGGCAAGGAG
TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTC
CAAAGCCAAAGGCCAGCCCCGGGAACCACAGGTGTACGTGTACCCCCCATCCCGGG
ACGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC
AGCGACATCGCCGTGGAGTGGGAGAGCAATGGCCAGCCCGAGAACAACTACAAGAC
CACCCCTCCCGTGCTGGACTCCGACGGCTCCTTCGCCCTCGTGAGCAAGCTCACCG
TGGACAAGAGCAGGTGGCAGCAGGGCAACGTCTTCTCATGCTCCGTGATGCATGAG
GCTCTGCACAACCACTACACCCAGAAGAGCCTCTCCCTGTCTCCCGGC
(SEQ ID NO: 117), signal sequence (1-57), NYA-1143 (61-
798), linker (799-813), C3E-7085 (814-1533), linker
(1534-1539), hinge (1540-1584), CH2 (1585-1914), CH3
(1915-2232)

Fig. 119

NYF-0010-HC2-k delete

MKHLWFFLLLVAAPRWVLSGEVQLVESGGGVVQPGRSLTPSCSASGFSIRSYDMHW
VRQAPGKGLEWVATISYDGSQKYFADSVKGRFTIFRDESENMVYLQMSGLRVEDTA
VYHCARGSSNHYEAFDIWGQGTMTVSSGGGGSGGGGSGGGGSQSVLTQPPSVSAA
PGQKVTISCSGSSSNIGNNYVSWYQRLPGTAPKLLIYDNNKRPSGIPDRFSGSKSG
TSATLGITGLQTGDEADYYCGAWDSSLSAPWVFGGGTKVTVLGGGGSEVQLVESGG
GLVQPGGSLRLSCAASGVTFNYYGMSWIRQAPGKGLEWVASITRSGGRIYYPDVSK
GRFTISRENTQKTLYLQMNSLRAEDTAVYYCTLDGRDGVVAYWGQGTLVTVSSGGG
GSGGGGSGGGGSGNFMLTQPSSVSGVPQQRVTISCTGNTGNIGSNYVNWYQQLPGTA
PKLLIYRDDKRPSGVPDRFSGSKSGTSASLAITGFQAEDEADYYCQSYSSGFIFGG
GTKLTVLAAEPKSSDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCV
VVSVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE
YKCKVSNKALPAPIEKTISKAKGQPREPQVYVPPSRDELTKNQVSLTCLVKGFYP
SDIAVEWESNGQPENNYKTTPPVLDSDGSFALVSKLTVDKSRWQQGNVFSCSVMHE
ALHNHYTQKSLSLSPG

(SEQ ID NO: 118), signal sequence (1-19), NYA-1154(21-266), linker (267-271), C3E-7085 (272-511), linker (512-513), hinge (514-528), CH2 (529-638), CH3 (639-744)

Fig. 120

NYF-0004-HC2-k delete

MKHLWFFLLLVAAPRWVLSGEVQLVESGGGLVQPGGSLRLSCAASGVTFNYYGMSW
IRQAPGKGLEWVASITRSGGRIYYPDSVKGRFTISRENTQKTLYLQMNSLRAEDTA
VYYCTLDGRDGWVAYWGQGLTVTVSSGGGGSGGGGSGGGGSGNFMLTQPSSVSGVPG
QRTISCTGNTGNIGSNYVNWYQQLPGTAPKLLIYRDDKRPSGVPDRFSGSKSGTS
ASLAITGFQAEDADYYCQSYSSGFIFGGGTKLTVLGGGGSEVQLVESGGGVVQPG
RSLTPSCSASGFSIRSYDMHWVRQAPGKGLEWVATISYDGSQKYFADSVKGRFTIF
RDESENMVYLQMSGLRVEDTAVYHCARGSSNHYEAFDIWGQGTMTVTVSSGGGGSGG
GGSGGGGSQSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSWYQRLPGTAPKLL
IYDNNKRPSGIPDRFSGSKSGTSATLGITGLQTGDEADYYCGAWDSSLSAPWVFGG
GTKVTVLAAEPKSSDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCV
VVSVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE
YKCKVSNKALPAPIEKTISKAKGQPREPQVYVPPSRDELTKNQVSLTCLVKGFYP
SDIAVEWESNGQPENNYKTTPPVLDSDGSFALVSKLTVDKSRWQQGNVFSQSVNHE
ALHNHYTQKSLSLSPG

(SEQ ID NO: 119), signal sequence (1-19), C3E-7085 (21-260), linker (261-265), NYA-1154 (272-511), linker (512-513), hinge (514-528), CH2 (529-638), CH3 (639-744)

Fig. 121

NYF-0011-HC2-k delete

MKHLWFFLLLVAAPRWVLSGEVQLVESGGGVVQPGRSLTPSCSASGFSIRSYDIHW
VRLAPGKGLEWVATISYDGSQKYFADSVKGRFTIFRDESENMVYLQMSGLRVEDTA
VYHCARGSSGHYEAFDIWGQGTMTVSSGGGGSGGGGSGGGGSQSVLTQPPSVSAA
PGQKVTISCSGSSSNIGNWYVSWYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSG
TSATLGITGLQTGDEADYYCGTWDSSLSAPWVFGGGTKVTVLGGGGSEVQLVESGG
GLVQPGGSLRLSCAASGVTFNYYGMSWIRQAPGKGLEWVASITRSGGRIYYPDVSK
GRFTISRENTQKTLYLQMNSLRAEDTAVYYCTLDGRDGWVAYWGQGT LVT VSSGGG
GSGGGGSGGGGSGNFMLTQPSSVSGVPGQRTISCTGNTGNIGSNYVNWYQQLPGTA
PKLLIYRDDKRPSGVPDRFSGSKSGTSASLAITGFQAEDEADYYCQSYSSGFIFGG
GTKLTVLAAEPKSSDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCV
VVSVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE
YKCKVSNKALPAPIEKTISKAKGQPREPQVYVPPSRDELTKNQVSLTCLVKGFYP
SDIAVEWESNGQPENNYKTTPPVLDSDGSFALVSKLTVDKSRWQQGNVFSCSVMHE
ALHNHYTQKSLSLSPG

(SEQ ID NO: 120), signal sequence (1-19), NYA-1143 (21-266), linker (267-271), C3E-7085 (272-511), linker (512-513), hinge (514-528), CH2 (529-638), CH3 (639-744)

Fig. 122

Point mutant NY-ES0 peptide 1F
FLLMWITQC
(SEQ ID NO: 121)

Fig. 123

Point mutant NY-ES0 peptide 2M
SMLMWITQC
(SEQ ID NO: 122)

Fig. 124

Point mutant NY-ES0 peptide 3A
SLAMWITQC
(SEQ ID NO: 123)

Fig. 125

Point mutant NY-ES0 peptide 4A
SLLAWITQC
(SEQ ID NO: 124)

Fig. 126

Point mutant NY-ES0 peptide 5A
SLLMAITQC
(SEQ ID NO: 125)

Fig. 127

Point mutant NY-ES0 peptide 6L
SLLMWLTQC
(SEQ ID NO: 126)

Fig. 128

Point mutant NY-ES0 peptide 7F
SLLMWIFQC
(SEQ ID NO: 127)

Fig. 129

Point mutant NY-ES0 peptide 8A
SLLMWITAC
(SEQ ID NO: 128)

Fig. 130

Point mutant NY-ES0 peptide 9A
SLLMWITQA
(SEQ ID NO: 129)

Fig. 131

gp100 Peptide
IMDQVPFSV
(SEQ ID NO: 130)

Fig. 132

Homologous peptide DOLPP1
SQFMWFFSV
(SEQ ID NO: 131)

Fig. 133

Homologous peptide IL20RB
SLFMWFFYA
(SEQ ID NO: 132)

Fig. 134

Homologous peptide PRKD2
SLDMWSVG
(SEQ ID NO: 133)

Fig. 135

Homologous peptide CD163
SIPMWVDNV
(SEQ ID NO: 134)

Fig. 136

Homologous peptide P2RY8
SVAMWAVFL
(SEQ ID NO: 135)

Fig. 137

C3E-7034

**GEVQLVESGGGLVQPGGSLRLSCAASGVTFNYYGMSWIRQAPGKGLEWVASITNSG
GRIYYPDSVKGRFTISRENTQKTLYLQMNSLRAEDTAVYYCTLDGRDGVVAYWGQG
TLVTVSSGGGGSGGGGSGGGGSNFMLTQPHSVSESPGKTVTISCKRNTGNIGSNYV
NWYQQHEGSSPTTIIYRDDKRPDGVSDRFSGSIDRSSKSASLTISNLKTEDEADYF
CQSYSSGFIFGGGTKLTVLGAAAGAGGDYKDDDDKGAAAHHHHHH**

(SEQ ID NO: 136), C3E-7034 (1-269), C3E-7034 scFv (2-243), FLAG-His tag (244-269)

Fig. 138

C3E-7036

**GEVQLVESGGGLVQPGGSLRLSCAASGVTFNYYGMSWIRQAPGKGLEWVASITNSG
GRIYYPDSVKGRFTISRENTQKTLYLQMNSLRAEDTAVYYCTLDGRDGVVAYWGQG
TLVTVSSGGGGSGGGGSGGGGSNFMLTQPSSVSGVPGQRTISCTGNTGNIGSNYV
NWYQQLPGTAPKLLIYRDDKRPSGVPDRFSGSKSGTSASLAITGFQAEDEADYYCQ
SYSSGFIFGGGTKLTVLGAAAGAGGDYKDDDDKGAHHHHHHH**

**(SEQ ID NO: 137), C3E-7036 (1-267), C3E-7036 scFv (2-
241), FLAG-His tag (242-267)**

Fig. 139

C3E-7085

**GEVQLVESGGGLVQPGGSLRLSCAASGVTFNYYGMSWIRQAPGKGLEWVASITRSG
GRIYYPDSVKGRFTISRENTQKTLYLQMNSLRAEDTAVYYCTLDGRDGVVAYWGQG
TLVTVSSGGGGSGGGGSGGGGSNFMLTQPSSVSGVPGQRTISCTGNTGNIGSNYV
NWYQQLPGTAPKLLIYRDDKRPSGVPDRFSGSKSGTSASLAITGFQAEDEADYYCQ
SYSSGFIFGGGTKLTVLGAAAGAGGDYKDDDDKGAHHHHHHH**

(SEQ ID NO: 138), C3E-7085 (1-267), C3E-7085 scFv (2-241), FLAG-His tag (242-267)

Fig. 140

C3E-7088

**GEVQLVESGGGLVQPGGSLRLSCAASGVTFNYYGMSWIRQAPGKGLEWVASITRSG
GRIYYPDSVKGRFTISRENTQKTLYLQMNSLRAEDTAVYYCTLDGRDGVVAYWGQG
TLVTVSSGGGGSGGGGSGGGGSNFMLTQPHSVSESPGKTVTISCKRNTGNIGSNYV
NWYQQHEGSSPTTIIYRNDKRPDGVSDRFSGSIDRSSKSASLTISNLKTEDEADYF
CQSYSSGFIFGGGTKLTVLGAAAGAGGDYKDDDDKGAAAHHHHHH**

**(SEQ ID NO: 139), C3E-7088(1-269), C3E-7088 scFv (2-243),
FLAG-His tag (244-269)**

Fig. 141

C3E-7093

**GEVQLVESGGGLVQPGGSLRLSCAASGVTFNYYGMSWIRQAPGKGLEWVASITSSG
GRIYYPDSVKGRFTISRENTQKTLYLQMNSLRAEDTAVYYCTLDGRDGVVAYWGQG
TLVTVSSGGGGSGGGGSGGGGSNFMLTQPHSVSESPGKTVTISCKRNTGNIGSNYV
NWYQQHEGSSPTTIIYRNDKRPDGVSDRFSGSIDRSSKSASLTISNLKTEDEADYF
CQSYSSGFIFGGGTKLTVLGAAAGAGGDYKDDDDKGAAAHHHHHH**

(SEQ ID NO: 140), C3E-7093 (1-269), C3E-7093 scFv (2-243), FLAG-His tag (244-269)

Fig. 142

C3E-7085 heavy chain CDRH1	GVTFNYYG
C3E-7085 heavy chain CDRH2	ITRSGGRI
C3E-7085 heavy chain CDRH3	TLDGRDGWVAY
C3E-7085 light chain CDRL1	TGNIGSNY
C3E-7085 light chain CDRL2	RDD
C3E-7085 light chain CDRL3	QSYSSGFI

(SEQ ID NOs: 141 to 146)

Fig. 143

C3E-7078

**GEVQLVESGGGLVQPGGSLRLSCAASGVTFNYYGMSWIRQAPGKGLEWVASITRSG
GRIYYPDSVKGRFTISRENTQKTLYLQMNSLRAEDTAVYYCTLDGRDGVVAYWGQG
TLVTVSSGGGGSGGGGSGGGGSNFMLTQPHSVSESPGKTVTISCKRNTGNIGSNYV
NWYQQHEGSSPTTIIYRDDKRPDGVSDRFSGSIDRSSKSASLTISNLKTEDEADYF
CQSYSSGFIFGGGTKLTVLGAAAGAGGDYKDDDDKGAAHHHHHH**

**(SEQ ID NO: 147), C3E-7078(1-269), C3E-7078 scFv (2-243),
FLAG-His tag (244-269)**

Fig. 144

NYF-0014-HC2

ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGGCAGCTCCCAGATGGGTGCTGAG
CGGAGAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCC
TGACACCCTCCTGTTCAAGCTCTGGATTCTCCATCCGTAGTTATGATATACACTGG
GTCCGCCAGGCTCCAGGCAAGGGGCTAGAGTGGGTGGCCACTATATCATATGATGG
AAGTCAGAAGTACTTCGCAGACTCCGTGAAGGGCCGATTTACCATCTTCAGAGACG
AATCGGAGAACATGGTGTATCTGCAAATGAGCGGCCTGAGAGTTGAGGACACGGCT
GTTTATCACTGTGCGAGAGGGAGTAGTGGTCATTATGAGGCTTTTGATATCTGGGG
CCAAGGGACAATGGTCACCGTCTCTTCAGGTGGAGGCGGTTTCAGGCGGAGGTGGCA
GCGGCGGTGGCGGGAGTCAGTCTGTGTTGACGCAGCCGCCCTCAGTGTCTGCGGCC
CCAGGACAGAAGGTCACCATCTCCTGCTCTGGAAGCAGCTCCAACATTGGGAATAA
TTATGTATCCTGGTACCAGCAGCTCCCAGGAACAGCCCCAAACTCCTCATTTATG
ACAATAATAAGCGACCCTCAGGGATTCTGACCGATTCTCTGGCTCCAAGTCTGGC
ACGTCAGCCACCCTGGGCATCACCGGACTCCAGACTGGGGACGAGGCCGATTATTA
CTGCGGAACATGGGATAGCAGCCTGAGTGCCCCCTTGGGTGTTGCGCGGAGGGACCA
AGGTCACCGTCCTAGGGGGAGGCGGTTGAGAAGTGCAGCTGGTGGAATCCGGGGGG
GGCCTGGTGCAGCCTGGGGGGAGCCTGAGACTGAGTTGTGCCGCTCTGGGGTGAC
ATTTAACTACTATGGCATGTCTTGATCCGCCAGGCACCTGGAAAGGGCCTGGAGT
GGGTGGCCAGCATCACTAGGTCCGGCGGGCGAATCTACTATCCCGACAGCGTCAAG
GGCAGGTTACAATTTCCCGCGAGAACACACAGAAAACCTCTGTACCTGCAGATGAA
TAGCCTGAGAGCCGAAGATACAGCTGTGTACTATTGCACTCTGGACGGCAGGGATG
GGTGGGTGCGCTATTGGGGGCAGGGAACCCTGGTGACAGTCAGCTCCGGAGGAGGA
GGATCTGGCGGAGGAGGCAGTGGGGGAGGCGGGTCAAACCTTTATGCTCACTCAGCC
GTCCTCTGTTTCTGGCGTACCTGGCCAACGGGTGACCATTAGCTGTACGGGTAATA
CCGGGAATATCGGGTCTAACTACGTGAACTGGTATCAGCAGCTTCCAGGGACAGCT
CCCAAGTTGCTGATCTATCGCGACGACAAAAGACCCTCAGGGGTCCCTGACCGATT
TAGTGGCAGCAAAAGCGGTACTTCCGCTTCCCTGGCGATAACCGGCTTTTCAGGCCG
AAGATGAGGCAGACTACTATTGCCAGTCATATTCCAGCGGCTTCATCTTCGGAGGC
GGAATAAGCTGACAGTGTTGGCAGCCGAGCCCAAATCTTCTGACAAAACCTCACAC
ATGCCCACCCTGCCCAGCACCTGAAGCCGAGGGGGACCCTCAGTCTTCTCTTCC
CCCCAAAACCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTACATGCGTG
GTGGTGTCAGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGG
CGTGGAGGTGCATAATGCCAAGACAAAGCCCCGGGAGGAGCAGTACAACAGCACGT
ACCGGGTGGTCAGCGTCCTACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG
TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCATCGAGAAAACCATCTC
CAAAGCCAAAGGCCAGCCCCGGGAACCACAGGTGTACGTGTACCCCCATCCCGGG
ACGAGCTGACCAAGAACCAGGTGAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC
AGCGACATCGCCGTGGAGTGGGAGAGCAATGGCCAGCCGAGAACAACTACAAGAC
CACCCCTCCCGTGCTGGACTCCGACGGCTCCTTCGCCCTCGTGAGCAAGCTCACCG
TGGACAAGAGCAGGTGGCAGCAGGGCAACGTCTTCTCATGCTCCGTGATGCATGAG
GCTCTGCACAACCACTACACCCAGAAGAGCCTCTCCCTGTCTCCCGGCAAG
(SEQ ID NO: 148), signal sequence (1-57), NYA-0001 (61-
798), linker (799-813), C3E-7085 (814-1533), linker
(1534-1539), hinge (1540-1584), CH2 (1585-1914), CH3
(1915-2235)

Fig. 145

NYF-0014-HC2

**MKHLWFFLLLVAAPRWVLSGEVQLVESGGGVVQPGRSLTPSCSASGFSIRSYDIHW
VRQAPGKGLEWVATISYDGSQKYFADSVKGRFTIFRDESENMVYLQMSGLRVEDTA
VYHCARGSSGHYEAFDIWGQGTMTVSSGGGGSGGGGSGGGGSQSVLTQPPSVSAA
PGQKVTISCSGSSSNIGNNYVSWYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSG
TSATLGITGLQTGDEADYYCGTWDSSLSAPWVFGGGTKVTVLGGGGSEVQLVESGG
GLVQPGGSLRLSCAASGVTFNYYGMSWIRQAPGKGLEWVASITRSGGRIYYPDVSK
GRFTISRENTQKTLYLQMNSLRAEDTAVYYCTLDGRDGWVAYWGQGT LVT VSSGGG
GSGGGGSGGGGSGNFMLTQPSSVSGVPGQRTISCTGNTGNIGSNYVNWYQQLPGTA
PKLLIYRDDKRPSGVPDRFSGSKSGTSASLAITGFQAEDEADYYCQSYSSGFIFGG
GTKLTVLAAEPKSSDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCV
VVSVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE
YKCKVSNKALPAPIEKTISKAKGQPREPQVYVPPSRDELTKNQVSLTCLVKGFYP
SDIAVEWESNGQPENNYKTTPPVLDSDGSFALVSKLTVDKSRWQQGNVFSCSVMHE
ALHNHYTQKSLSLSPGK**

(SEQ ID NO: 149), signal sequence (1-19), NYA-0001 (21-266), linker (267-271), C3E-7085 (272-511), linker (512-513), hinge (514-528), CH2 (529-638), CH3 (639-745)

Fig. 146

NYF-0082-HC2

**MKHLWFFLLLVAAPRWVLSGEVQLVESGGGVVQPGRSLTPSCSASGFSIRSYDIHW
VRQAPGKGLEWVATISYDGSQKYFADSVKGRFTIFRDESENMVYLQMSGLRVEDTA
VYHCARGSSGHYEAFDIWGQGTMTVSSGGGGSGGGGSGGGGSQSVLTQPPSVSAA
PGQKVTISCSGSSSNIGNNYVSWYQRLPGTAPKLLIYDNNKRPSGIPDRFSGSKSG
TSATLGITGLQTGDEADYYCGSWDSSLSAPWVFGGGTKVTVLGGGGSEVQLVESGG
GLVQPGGSLRLSCAASGVTFNYYGMSWIRQAPGKGLEWVASITRSGGRIYYPDsvK
GRFTISRENTQKTLYLQMNSLRAEDTAVYYCTLDGRDGWVAYWGQGTlVTVSSGGG
GSGGGGSGGGGsnfMLTQPSSVSGVPGQRVTISCTGNTGNIGSNYVNWYQQLPGTA
PKLLIYRDDKRPSGVPDRFSGSKSGTSASLAITGFQAEDEADYYCQSYSSGFIFGG
GTKLTVLAAEPKSSDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCV
VVSVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE
YKCKVSNKALPAPIEKTISKAKGQPREPQVYVPPSRDELTKNQVSLTCLVKGFYP
SDIAVEWESNGQPENNYKTTPPVLDSDGSFALVSKLTVDKSRWQQGNVfSCSVMHE
ALHNHYTQKSLSLSPGK**

(SEQ ID NO: 150), signal sequence (1-19), NYA-0082 (21-266), linker (267-271), C3E-7085 (272-511), linker (512-513), hinge (514-528), CH2 (529-638), CH3 (639-745)

Fig. 147

Human CD3 ϵ amino acid sequence

MQSGTHWRVLGLCLLSVGWVGQDGNEEMGGITQTPYKVSISGTTVILTCPQYPGSE
ILWQHNDKNIGGDEDDKNIGSDEDHLSLKEFSELEQSGYYVCYPRGSKPEDANFYL
YLRARVCENCMEMDVMSVATIVIVDICITGGLLLVYYWSKNRKAKAKPVTRGAGA
GGRQRGQNKERPPPVPNPDYEPKRGQRDLYSGLNQRR
(SEQ ID NO: 151: NCBI Reference Sequence: NP_000724.1)

Fig. 148

NYZ - 0038 - HC2

ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGGCAGCTCCCAGATGGGTGCTGAG
CGGTGAGGTACAGCTGGTGGAATCCGGTGGAGGCCTTGTGCAACCGGGAGGCTCCC
TGCGACTCTCTTGCGCCGCATCTGGCTTTTCCATACGATCCTACGATATTCATTGG
GTCCGACAAGCCCCTGGCAAAGGTCTTGAATGGGTTGCCACTATCTCCTACGACGG
GTCTCAGAAATATTATGCGGATTCAGTGAAGGGGCGGTTTACAATTTACGAGACG
AGTCAAAGAATACACTGTACCTCCAAATGAATTCAGTGAAGAGCCGAGGATACTGCA
GTCTATCATTGTGCAAGAGGGTCTCAGGCCACTACGAGGCCTTTGATATATGGGG
CCAAGGCACCTTGTAACCGTTAGTAGCGGAGGTGGAGGAAGCGGAGGCGGCGGTT
CCGGAGGAGGTGGAAGTCAATCCGTTCTGACTCAGCCACCCTCCGCCTCTGGCACC
CCGGGCCAACGGGTCACAATATCATGTTCTGGCTCTTCAAGCAACATCGGAAACTG
GTACGTGAGCTGGTACCAGCAGCTCCCCGGCACGGCGCCCAAGCTTCTGATATATG
ACAACAACAAACGGCCCAAGTGGAGTTCCTGACAGATTCAGTGGGTCTAAAAGTGGT
ACAAGCGCTAGCCTGGCCATAAGTGGTCTGCAGAGTGAAGATGAGGCGGACTATTA
TTGCGGAACCTGGGACTCCAGCCTGAGCGCTCCCTGGGTTTTTCGGCGGAGGTAATA
AGCTGACCGTCTTGGGAGGAGGCGGTTTCAAGTGCAGCTGGTGGAAATCCGGGGGG
GGCCTGGTGCAGCCTGGGGGGAGCCTGAGACTGAGTTGTGCCGCTCTGGGGTGAC
ATTTAACTACTATGGCATGTCTTGGATCCGCCAGGCACCTGGAAAGGGCCTGGAGT
GGGTGGCCAGCATCACTAGGTCCGGCGGGCGAATCTACTATCCCGACAGCGTCAAG
GGCAGGTTTACAATTTCCCGCGAGAACACACAGAAAACCTCTGTACCTGCAGATGAA
TAGCCTGAGAGCCGAAGATACAGCTGTGTACTATTGCACTCTGGACGGCAGGGATG
GGTGGGTGCGCTATTGGGGGTGTGGAACCCTGGTGCAGTCAGCTCCGGAGGAGGA
GGATCTGGCGGAGGAGGCAGTGGGGGAGGCGGGTCAAACCTTTATGCTCACTCAGCC
GTCCTCTGTTTCTGGCGTACCTGGCCAACGGGTGACCATTAGCTGTACGGGTAATA
CCGGGAATATCGGGTCTAACTACGTGAACTGGTATCAGCAGCTTCCAGGGACATGT
CCCAAGTTGCTGATCTATCGCGACGACAAAAGACCCTCAGGGGTCCCTGACCGATT
TAGTGGCAGCAAAAGCGGTACTTCCGCTTCCCTGGCGATAACCGGCTTTCAGGCCG
AAGATGAGGCAGACTACTATTGCCAGTCATATTCCAGCGGCTTCATCTTCGGAGGC
GGAATAAGCTGACAGTGTTGGCAGCCGAGCCCAAATCTTCTGACAAAACCTCACAC
ATGCCCACCCTGCCCAGCACCTGAAGCCGAGGGGGACCCTCAGTCTTCTCTTCC
CCCCAAAACCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTACATGCGTG
GTGGTGTCAGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGG
CGTGGAGGTGCATAATGCCAAGACAAAGCCCCGGGAGGAGCAGTACAACAGCACGT
ACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG
TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCATCGAGAAAACCATCTC
CAAAGCCAAAGGCCAGCCCCGGGAACCACAGGTGTACGTGTACCCCCATCCCGGG
ACGAGCTGACCAAGAACCAGGTGAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC
AGCGACATCGCCGTGGAGTGGGAGAGCAATGGCCAGCCGAGAACAACTACAAGAC
CACCCCTCCCGTGCTGGACTCCGACGGCTCCTTCGCCCTCGTGAGCAAGCTCACCG
TGGACAAGAGCAGGTGGCAGCAGGGCAACGTCTTCTCATGCTCCGTGATGCATGAG
GCTCTGCACAACCACTACACCCAGAAGAGCCTCTCCCTGTCTCCCGGCAAG
(SEQ ID NO: 152), signal sequence (1-57), NYA-2061 (61-
798), linker (799-813), C3E-7096(814-1533), linker
(1534-1539), hinge (1540-1584), CH2 (1585-1914), CH3
(1915-2235)

Fig. 149

NYZ - 0082 - HC2

ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGGCAGCTCCCAGATGGGTGCTGAG
CGGTGAGGTACAGCTGGTGGAATCCGGTGGAGGCCTTGTGCAACCGGGAGGCTCCC
TGCGACTCTCTTGCGCCGCATCTGGCTTTTCCATACGATCCTACGATATTCATTGG
GTCCGACAAGCCCCTGGCAAAGGTCTTGAATGGGTTGCCACTATCTCCTACGACGG
GTCTCAGAAATATTATGCGGATTCAGTGAAGGGGCGGTTTACAATTTACGAGACG
AGTCAAAGAATACACTGTACCTCCAAATGAATTCAGTGAAGAGCCGAGGATACTGCA
GTCTATCATTGTGCAAGAGGGTCTCAGGCCACTACGAGGCCTTTGATATATGGGG
CCAAGGCACCTTGGTAACCGTTAGTAGCGGAGGTGGAGGAAGCGGAGGCGGCGGTT
CCGGAGGAGGTGGAAGTGGAGGAGGTGGATCTCAATCCGTTCTGACTCAGCCACCC
TCCGCTCTGGCACCCCGGGCCAACGGGTACAAATATCATGTTCTGGCTCTTCAAG
CAACATCGGAAACTGGTACGTGAGCTGGTACCAGCAGCTCCCCGGCACGGCGCCCA
AGCTTCTGATATATGACAACAACAAACGGCCCAAGTGGAGTTCCTGACAGATTCACT
GGGTCTAAAAGTGGTACAAGCGCTAGCCTGGCCATAAGTGGTCTGCAGAGTGAAGA
TGAGGCGGACTATTATTGCGGAACCTGGGACTCCAGCCTGAGCGCTCCCTGGGTTT
TCGGCGGAGGTACTAAGCTGACCGTCTTGGGAGGAGGCGGTTTCAAGTGCAGCTG
GTGGAATCCGGGGGGGGCCTGGTGCAGCCTGGGGGGAGCCTGAGACTGAGTTGTGC
CGCTCTGGGGTGACATTTAACTACTATGGCATGTCTTGGATCCGCCAGGCACCTG
GAAAGGGCCTGGAGTGGGTGGCCAGCATCACTAGGTCCGGCGGGCGAATCTACTAT
CCCGACAGCGTCAAGGGCAGGTTTACAATTTCCCGCGAGAACACACAGAAAACCTCT
GTACCTGCAGATGAATAGCCTGAGAGCCGAAGATACAGCTGTGTACTATTGCACTC
TGGACGGCAGGGATGGGTGGGTGCGCTATTGGGGGTGTGGAACCCTGGTGACAGTC
AGCTCCGGAGGAGGAGGATCTGGCGGAGGAGGCAGTGGGGGAGGCGGGTCAAACCT
TATGCTCACTCAGCCGTCTCTGTTTCTGGCGTACCTGGCCAACGGGTGACCATT
GCTGTACGGGTAATACCGGGAATATCGGGTCTAACTACGTGAACTGGTATCAGCAG
CTTCCAGGGACATGTCCCAAGTTGCTGATCTATCGCGACGACAAAAGACCCTCAGG
GGTCCCTGACCGATTTAGTGGCAGCAAAAGCGGTACTTCCGCTTCCCTGGCGATAA
CCGGCTTTCAGGCCGAAGATGAGGCAGACTACTATTGCCAGTCATATTCCAGCGGC
TTCATCTTTCGGAGGCGGAACCTAAGCTGACAGTGTTGGCAGCCGAGCCCAAATCTTC
TGACAAAACCTCACACATGCCACCCTGCCAGCACCTGAAGCCGACGGGGGACCCT
CAGTCTTCTCTTCCCCCAAAACCAAGGACACCCTCATGATCTCCCGGACCCCT
GAGGTCACATGCGTGGTGGTGTGTCAGTGAGCCACGAAGACCCTGAGGTCAAGTTCAA
CTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCCCGGGAGGAGC
AGTACAACAGCACGTACCGGGTGGTCAGCGTCCTCACCGTCTGACCAAGGACTGG
CTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCAGCCCCCAT
CGAGAAAACCATCTCCAAAGCCAAAGGCCAGCCCCGGGAACCACAGGTGTACGTGT
ACCCCCCATCCCGGGACGAGCTGACCAAGAACCAGGTGAGCTGACCTGCCTGGTC
AAAGGCTTCTATCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGCCAGCCCGA
GAACAACCTACAAGACCACCCCTCCCGTGCTGGACTCCGACGGCTCCTTCGCCCTCG
TGAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGCAACGTCTTCTCATGC
TCCGTGATGCATGAGGCTCTGCACAACCACTACACCCAGAAGAGCCTCTCCCTGTC
TCCCGGCAAG

(SEQ ID NO: 153), signal sequence (1-57), NYA-3061 (61-813), linker (814-828), C3E-7096(829-1548), linker (1549-1554), hinge (1555-1599), CH2 (1600-1929), CH3 (1930-2250)

Fig. 150

NYZ - 0083 - HC2

ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGGCAGCTCCCAGATGGGTGCTGAG
CGGTGAGGTACAGCTGGTGGAATCCGGTGGAGGCCTTGTGCAACCGGGAGGCTCCC
TGCGACTCTCTTGCGCCGCATCTGGCTTTTCCATACGATCCTACGATATTCATTGG
GTCCGACAAGCCCCTGGCAAAGGTCTTGAATGGGTTGCCACTATCTCCTACGACGG
GTCTCAGAAATATTATGCGGATTCAGTGAAGGGGCGGTTTACAATTTACGAGACG
AGTCAAAGAATACACTGTACCTCCAAATGAATTCAGTGAAGAGCCGAGGATACTGCA
GTCTATCATTGTGCAAGAGGGTCTCAGGCCACTACGAGGCCTTTGATATATGGGG
CCAAGGCACCTTGTAACCGTTAGTAGCGGAGGTGGAGGAAGCGGAGGCGGCGGTT
CCGGAGGAGGTGGAAGTGGAGGAGGTGGATCTCAATCCGTTCTGACTCAGCCACCC
TCCGCTCTGGCACCCCGGGCCAACGGGTACAAATATCATGTTCTGGCTCTTCAAG
CAACATCGGAAACTGGTACGTGAGCTGGTACCAGCAGCTCCCCGGCACGGCGCCCA
AGCTTCTGATATATGACAACAACAACGGCCCAAGTGGAGTTCCTGACAGATTCACT
GGGTCTAAAAGTGGTACAAGCGCTAGCCTGGCCATAAGTGGTCTGCAGAGTGAAGA
TGAGGCGGACTATTATTGCGGAACCTGGGACTCCAGCCTGAGCGCTCCCTGGGTTT
TCGGCGGAGGTACTAAGCTGACCGTCTTGGGAGGAGGCGGTTTCAAGTGCAGCTG
GTGGAATCCGGGGGGGGCCTGGTGCAGCCTGGGGGGAGCCTGAGACTGAGTTGTGC
CGCTCTGGGGTGACATTTAACTACTATGGCATGTCTTGGATCCGCCAGGCACCTG
GAAAGTGTCTGGAGTGGGTGGCCAGCATCACTAGGTCCGGCGGGCGAATCTACTAT
CCCGACAGCGTCAAGGGCAGGTTTACAATTTCCCGCGAGAACACACAGAAAACCTCT
GTACCTGCAGATGAATAGCCTGAGAGCCGAAGATACAGCTGTGTACTATTGCACTC
TGGACGGCAGGGATGGGTGGGTGCGCTATTGGGGGCAGGGAACCCTGGTGACAGTC
AGCTCCGGAGGAGGAGGATCTGGCGGAGGAGGCAGTGGGGGAGGCGGGTCAAACCT
TATGCTCACTCAGCCGTCTCTGTTTCTGGCGTACCTGGCCAACGGGTGACCATT
GCTGTACGGGTAATACCGGGAATATCGGGTCTAACTACGTGAACTGGTATCAGCAG
CTTCCAGGGACAGCTCCCAAGTTGCTGATCTATCGCGACGACAAAAGACCCTCAGG
GGTCCCTGACCGATTTAGTGGCAGCAAAAGCGGTACTTCCGCTTCCCTGGCGATAA
CCGGCTTTCAGGCCGAAGATGAGGCAGACTACTATTGCCAGTCATATTCCAGCGGC
TTCATCTTTCGGATGTGGAACCTAAGCTGACAGTGTTGGCAGCCGAGCCCAAATCTTC
TGACAAAACCTCACACATGCCACCCTGCCAGCACCTGAAGCCGCAGGGGGACCCT
CAGTCTTCTCTTCCCCCAAAACCAAGGACACCCTCATGATCTCCCGGACCCCT
GAGGTCACATGCGTGGTGGTGTGAGTGAAGACCCCTGAGGTCAAGTTCAA
CTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCCCGGGAGGAGC
AGTACAACAGCACGTACCGGGTGGTCAAGCTCCTCACCGTCTGACCAAGGACTGG
CTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCAGCCCCAT
CGAGAAAACCATCTCCAAAGCCAAAGGCCAGCCCCGGGAACCACAGGTGTACGTGT
ACCCCCCATCCCGGGACGAGCTGACCAAGAACCAGGTGAGCTGACCTGCCTGGTC
AAAGGCTTCTATCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGCCAGCCCGA
GAACAACCTACAAGACCACCCCTCCCGTGCTGGACTCCGACGGCTCCTTCGCCCTCG
TGAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGCAACGTCTTCTCATGC
TCCGTGATGCATGAGGCTCTGCACAACCACTACACCCAGAAGAGCCTCTCCCTGTC
TCCCGGCAAG

(SEQ ID NO: 154), signal sequence (1-57), NYA-3061 (61-813), linker (814-828), C3E-7097(829-1548), linker (1549-1554), hinge (1555-1599), CH2 (1600-1929), CH3 (1930-2250)

Fig. 151

NYZ - 0038 - HC2

**MKHLWFFLLLVAAPRWVLSGEVQLVESGGGLVQPGGSLRLSCAASGFSIRSYDIHW
VRQAPGKGLEWVATISYDGSQKYADSVKGRFTISRDESKNTLYLQMNSLRAEDTA
VYHCARGSSGHYEAFDIWGQGLTVTVSSGGGGSGGGGSGGGGSQSVLTQPPSASGT
PGQRTVISCSSSNIGNWYVSWYQQLPGTAPKLLIYDNNKRPSGVPDRFSGSKSG
TSASLAISGLQSEDEADYYCGTWDSSLSAPWVFGGGTKLTVLGGGGSEVQLVESGG
GLVQPGGSLRLSCAASGVTFNYYGMSWIRQAPGKGLEWVASITRSGGRIYYPDVSK
GRFTISRENTQKTLYLQMNSLRAEDTAVYYCTLDGRDGWVAYWCGTLTVTVSSGGG
SGGGGGSGGGGSNFMLTQPSSVSGVPQQRVTISCTGNTGNIGSNYVNWYQQLPGTC
PKLLIYRDDKRPSGVPDRFSGSKSGTSASLAITGFQAEDEADYYCQSYSSGFIFGG
GTKLTVLAAEPKSSDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCV
VVSVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE
YKCKVSNKALPAPIEKTISKAKGQPREPQVYVPPSRDELTKNQVSLTCLVKGFYP
SDIAVEWESNGQPENNYKTTPPVLDSDGSFALVSKLTVDKSRWQQGNVFSCSVMHE
ALHNHYTQKSLSLSPGK**

(SEQ ID NO: 155), signal sequence (1-19), NYA-2061 (21-266), linker (267-271), C3E-7096(272-511), linker (512-513), hinge (514-528), CH2 (529-638), CH3 (639-745)

Fig. 152

NYZ - 0082 - HC2

**MKHLWFFLLLVAAPRWVLSGEVQLVESGGGLVQPGGSLRLSCAASGFSIRSYDIHW
VRQAPGKGLEWVATISYDGSQKYYADSVKGRFTISRDESKNTLYLQMNSLRAEDTA
VYHCARGSSGHYEAFDIWGQGT LVT VSSGGGGSGGGGSGGGGSGGGGSQSVLTQPP
SASGTPGQRTISCSGSSSNIGNWYVSWYQQLPGTAPKLLIYDNNKRPSGVPDRFS
GSKSGTSASLAISGLQSEDEADYYCGTWDSSLSAPWVFGGGTKLTVLGGGGSEVQL
VESGGGLVQPGGSLRLSCAASGVTFNYYGMSWIRQAPGKGLEWVASITRSGGRIYY
PDSVKGRFTISRENTQKTLYLQMNSLRAEDTAVYYCTLDGRDGVVAYWCGTLVTV
SSGGGGSGGGGSGGGGSGNFMLTQPSSVSGVPQRTISCTGNTGNIGSNYVNWYQQ
LPGTCPKLLIYRDDKRPSGVPDRFSGSKSGTSASLAITGFQAEDEADYYCQSYSSG
FIFGGGTKLTVLAAEPKSSDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTP
EVTCTVVSVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW
LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYVPPSRDELTKNQVSLTCLV
KGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFALVSKLTVDKSRWQQGNVFSC
SVMHEALHNHYTQKSLSLSPGK**

(SEQ ID NO: 156), signal sequence (1-19), NYA-3061 (21-271), linker (272-276), C3E-7096(277-516), linker (517-518), hinge (519-533), CH2 (534-643), CH3 (644-750)

Fig. 153

NYZ - 0083 - HC2

**MKHLWFFLLLVAAPRWVLSGEVQLVESGGGLVQPGGSLRLSCAASGFSIRSYDIHW
VRQAPGKGLEWVATISYDGSQKYYADSVKGRFTISRDESKNTLYLQMNSLRAEDTA
VYHCARGSSGHYEAFDIWGQGT LVT VSSGGGGSGGGGSGGGGSGGGGSQSVLTQPP
SASGTPGQRTISCSGSSSNIGNWYVSWYQQLPGTAPKLLIYDNNKRPSGVPDRFS
GSKSGTSASLAISGLQSEDEADYYCGTWDSSLSAPWVFGGGTKLTVLGGGGSEVQL
VESGGGLVQPGGSLRLSCAASGVTFNYYGMSWIRQAPGKCLEWVASITRSGGRIYY
PDSVKGRFTISRENTQKTLYLQMNSLRAEDTAVYYCTLDGRDGVVAYWGQGT LVT V
SSGGGGSGGGGSGGGGSGNFMLTQPSSVSGVPQRTISCTGNTGNIGSNYVNWYQQ
LPGTAPKLLIYRDDKRPSGVPDRFSGSKSGTSASLAITGFQAEDEADYYCQSYSSG
FIFGCGTKLTVLAAEPKSSDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTP
EVTCTVVSVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW
LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYVPPSRDELTKNQVSLTCLV
KGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFALVSKLTVDKSRWQQGNVFSC
SVMHEALHNHYTQKSLSLSPGK**

(SEQ ID NO: 157), signal sequence (1-19), NYA-3061 (21-271), linker (272-276), C3E-7097(277-516), linker (517-518), hinge (519-533), CH2 (534-643), CH3 (644-750)

Fig. 154

NYZ-1010-HC2

ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGGCAGCTCCCAGATGGGTGCTGAG
CGGTGAGGTACAGCTGGTGGAATCCGGTGGAGGCCTTGTGCAACCGGGAGGCTCCC
TGCGACTCTCTTGCGCCGCATCTGGCTTTTCCATACGATCCTACGATATTCATTGG
GTCCGACAAGCCCCTGGCAAAGGTCTTGAATGGGTTGCCACTATCTCCTACGACGG
GTCTCAGAAATATTATGCGGATTCAGTGAAGGGGCGGTTTACAATTTACGAGACG
AGTCAAAGAATACACTGTACCTCCAAATGAATTCAGTGAAGAGCCGAGGATACTGCA
GTCTATCATTGTGCAAGAGGGTCTCAGGCCACTACGAGGCCTTTGATATATGGGG
CCAAGGCACCTTGTAACCGTTAGTAGCGGAGGTGGAGGAAGCGGAGGCGGCGGTT
CCGGAGGAGGTGGAAGTGGAGGAGGTGGATCTCAATCCGTTCTGACTCAGCCACCC
TCCGCTCTGGCACCCCGGGCCAACGGGTACAAATATCATGTTCTGGCTCTTCAAG
CAACATCGGAACTGGTACGTGAGCTGGTACCAGCAGCTCCCCGGCACGGCGCCCA
AGCTTCTGATATATGACAACAACAAACGGCCCAAGTGGAGTTCCTGACAGATTCACT
GGGTCTAAAAGTGGTACAAGCGCTAGCCTGGCCATAAGTGGTCTGCAGAGTGAAGA
TGAGGCGGACTATTATTGCGGAACCTGGGACTCCAGCCTGAGCGCTCCCTGGGTTT
TCGGCGGAGGTACTAAGCTGACCGTCTTGGGAGGAGGCGGTTTCAAGTGCAGCTG
GTGGAATCCGGGGGGGGCCTGGTGCAGCCTGGGGGGAGCCTGAGACTGAGTTGTGC
CGCTCTGGGGTGACATTTAACTACTATGGCATGTCTTGGATCCGCCAGGCACCTG
GAAAGGGCCTGGAGTGGGTGGCCAGCATCACTAGGTCCGGCGGGCGAATCTACTAT
CCCGACAGCGTCAAGGGCAGGTTTACAATTTCCCGCGAGAACACACAGAAAACCTCT
GTACCTGCAGATGAATAGCCTGAGAGCCGAAGATACAGCTGTGTACTATTGCACTC
TGGACGGCAGGGATGGGTGGGTGCGCTATTGGGGTCAGGGAACCCTGGTGACAGTC
AGCTCCGCTCCACCAAGGGCCCAAGCGTCTTCCCCCTGGCACCCCTCCTCCAAGAG
CACCTCTGGCGGCACAGCCGCCCTGGGCTGCTGGTCAAGGACTACTTCCCCGAAC
CCGTGACCGTGAGCTGGAACCTCAGGCGCCCTGACCAGCGGCGTGACACCTTCCCC
GCTGTCTGCACTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTC
CAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACA
CCAAGGTGGACAAGAGAGTTGAGCCCAAGTCTTGGGACAAAACCTCACACATGCCCA
CCCTGCCCAGCACCTGAAGCCGCAGGGGGACCCTCAGTCTTCTCTTCCCCCAAA
ACCCAAGGACACCCCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGTGGTGT
CAGTGAGCCACGAAGACCCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAG
GTGCATAATGCCAAGACAAAGCCCCGGGAGGAGCAGTACAACAGCACGTACCGGGT
GGTCAGCGTCTCACTGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGT
GCAAGGTCTCCAACAAAGCCCTCCAGCCCCCATCGAGAAAACCATCTCCAAAGCC
AAAGGCCAGCCCCGGGAACCAAGGTGTACGTGTACCCCCCATCCCGGGACGAGCT
GACCAAGAACCAGGTGAGCCTGACCTGCTGGTCAAAGGCTTCTATCCAGCGACA
TCGCCGTGGAGTGGGAGAGCAATGGCCAGCCCGAGAACAACTACAAGACCACCCCT
CCCGTGCTGGACTCCGACGGCTCCTTCGCCCTCGTGAGCAAGCTCACCGTGGACAA
GAGCAGGTGGCAGCAGGGCAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGC
ACAACCACTACACCCAGAAGAGCCTCTCCCTGTCTCCCGGCAAG

(SEQ ID NO: 158), signal sequence (1-57), NYA-3061 (61-813), linker (814-828), C3E-7085-VH (829-1182), CH1 (1183-1476), hinge (1477-1521), CH2 (1522-1851), CH3 (1831-2172)

Fig. 155

C3E-7085-LC

**ATGGTGCTGCAGACCCAGGTGTTTCATCTCCCTGCTGCTGTGGATCTCCGGCGCGTA
CGGCAACTTTATGCTCACTCAGCCGTCCTCTGTTTCTGGCGTACCTGGCCAACGGG
TGACCATTAGCTGTACGGGTAATACCGGGAATATCGGGTCTAACTACGTGAACTGG
TATCAGCAGCTTCCAGGGACAGCTCCCAAGTTGCTGATCTATCGCGACGACAAAAG
ACCCTCAGGGGTCCCTGACCGATTTAGTGGCAGCAAAAGCGGTACTTCCGCTTCCC
TGGCGATAACCGGCTTTCAGGCCGAAGATGAGGCAGACTACTATTGCCAGTCATAT
TCCAGCGGCTTCATCTTCGGAGGCGGAACCTAAGCTGACAGTGCTGGGCCAGCCTAA
GGCTGCCCCTAGCGTGACCCTGTTCCCTCCTTCCAGCGAGGAGCTTCAAGCTAACA
AGGCCACCCTGGTGTGTCTTATCTCTGACTTCTACCCTGGCGCTGTGACCGTGGCC
TGGGAAGGCTGACAGCTCCCCTGTGAAGGCCGGAGTGGAGACCACCACACCTAGCAA
GCAGTCTAACAACAAGTACGCTGCCAGCTCCTACCTGAGCCTTACCCCTGAGCAGT
GGAAGTCTCACAGAAGCTACTCCTGTCAAGTGACCCACGAGGGCAGCACCGTGGAG
AAGACCGTGGCTCCTACCGAGTGTTCC**

**(SEQ ID NO: 159), signal sequence (1-60), C3E-7085_VL
(61-381), CL (382-699)**

Fig. 156

NYZ - 1010 - HC2

**MKHLWFFLLLVAAPRWVLSGEVQLVESGGGLVQPGGSLRLSCAASGFSIRSYDIHW
VRQAPGKGLEWVATISYDGSQKYADSVKGRFTISRDESKNTLYLQMNSLRAEDTA
VYHCARGSSGHYEAFDIWGGQGLTVTVSSGGGGSGGGGSGGGGSGGGGSQSVLTQPP
SASGTPGQRTISCSGSSSNIGNWYVSWYQQLPGTAPKLLIYDNNKRPSGVPDRFS
GSKSGTSASLAISGLQSEDEADYYCGTWDSSLSAPWVFGGGTKLTVLGGGGSEVQL
VESGGGLVQPGGSLRLSCAASGVTFNYYGMSWIRQAPGKGLEWVASITRSGGRIYY
PDSVKGRFTISRENTQKTLYLQMNSLRAEDTAVYYCTLDGRDGVVAYWGQGLTVTV
SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFP
AVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCP
PCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVTVSVSHEDPEVKFNWYVDGVE
VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
KGQPREPQVYVYPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP
PVLDSGGSFALVSKLTVDKSRWQQGNVFSVMSHEALHNHYTQKSLSLSPGK
(SEQ ID NO: 160), signal sequence (1-19), NYA-3061 (21-
271), linker (272-276), C3E-7085-VH (277-394), CH1 (395-
492), hinge (493-507), CH2 (508-617), CH3 (618-724)**

Fig. 157

C3E-7085-LC

**MVLQTQVFISLLLWISGAYGNFMLTQPSSVSGVPGQRTISCTGNTGNIGSNYVNW
YQQLPGTAPKLLIYRDDKRPSGVPDRFSGSKSGTSASLAITGFQAEDEADYYCQSY
SSGFIFGGGKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVA
WKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVE
KTVAPTECS**

**(SEQ ID NO: 161), signal sequence (1-20), C3E-7085_VL
(21-127), CL (128-233)**

Fig. 158A

Antibody	Substance added to T2											
	Solvent	Peptide										
	DMSO	NY-ESO	1F	2M	3A	4A	5A	6L	7F	8A	9A	gp100
NYZ-0038	<u>1.02</u>	57.13	<u>0.66</u>	45.71	29.72	<u>1.39</u>	<u>1.13</u>	47.00	<u>5.56</u>	<u>19.15</u>	58.37	<u>0.37</u>
NYZ-0082	<u>1.02</u>	54.49	<u>0.79</u>	41.13	<u>27.09</u>	<u>2.26</u>	<u>1.74</u>	45.35	<u>10.08</u>	<u>19.93</u>	58.10	<u>0.36</u>
NYZ-0083	<u>1.01</u>	53.60	<u>0.96</u>	41.34	28.94	<u>3.05</u>	<u>2.15</u>	45.85	<u>12.76</u>	<u>22.46</u>	56.72	<u>0.34</u>
NYZ-1010	<u>1.15</u>	43.32	<u>0.86</u>	39.52	<u>21.30</u>	<u>1.05</u>	<u>1.02</u>	37.59	<u>3.86</u>	<u>17.38</u>	51.90	<u>0.53</u>

Fig. 158B

Antibody	Substance added to T2							
	Solvent	Peptide						
	DMSO	NY-ESO	DOLPP1	IL20RB	PRKD2	CD163	P2RY8	gp100
NYZ-0038	1.07	<u>51.65</u>	0.71	0.70	0.41	0.66	0.89	0.44
NYZ-0082	1.11	<u>47.54</u>	0.69	0.69	0.40	0.62	0.87	0.42
NYZ-0083	1.01	<u>47.17</u>	0.63	0.62	0.37	0.55	0.76	0.38
NYZ-1010	1.19	<u>44.35</u>	0.70	0.88	0.54	0.67	0.95	0.54

Fig. 159A

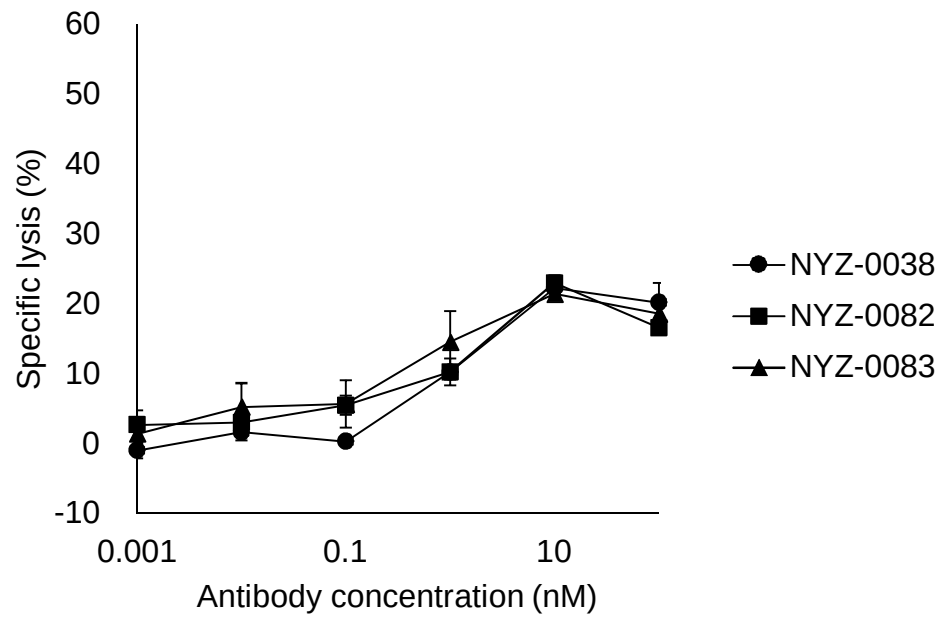


Fig. 159B

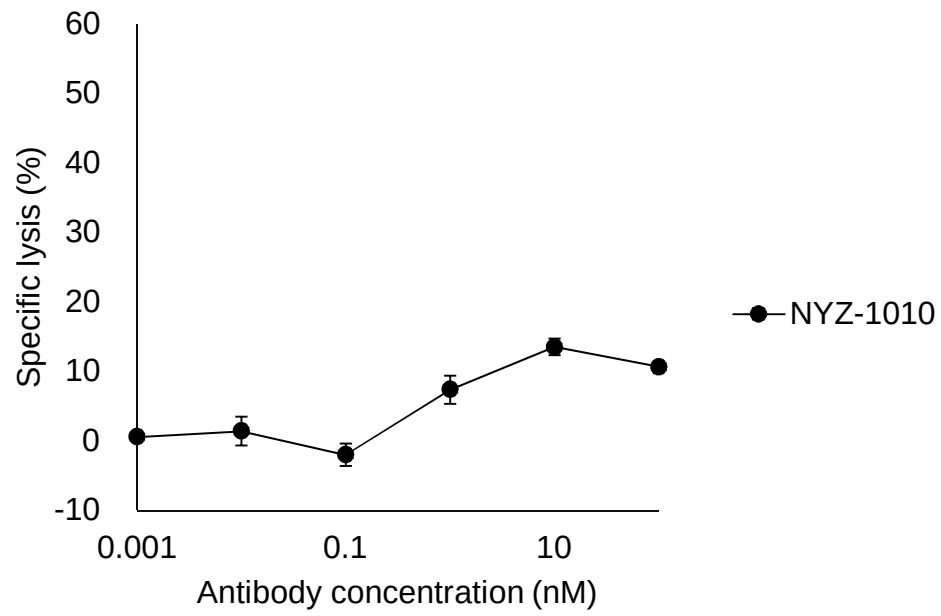


Fig. 159C

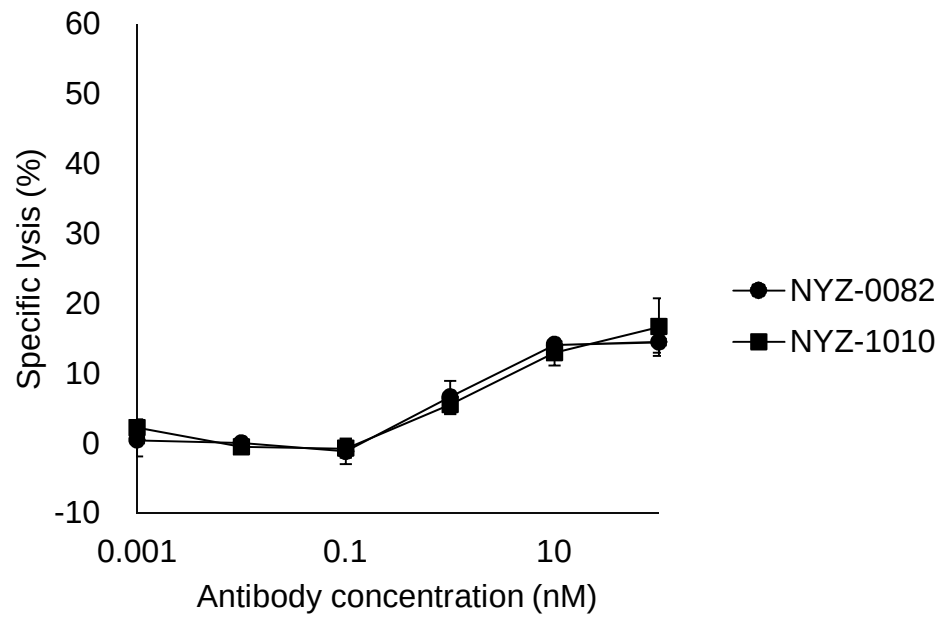


Fig. 159D

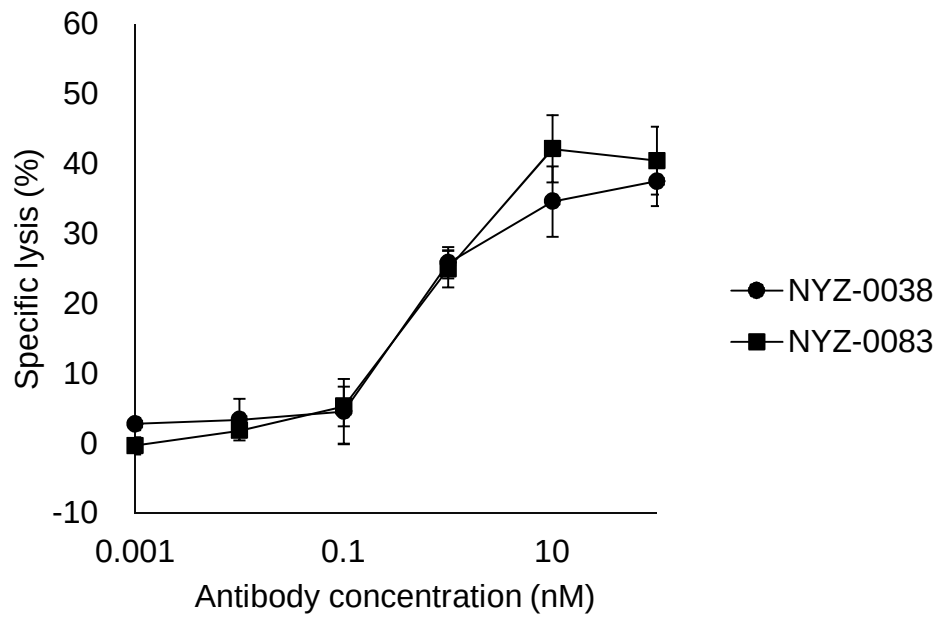


Fig. 159E

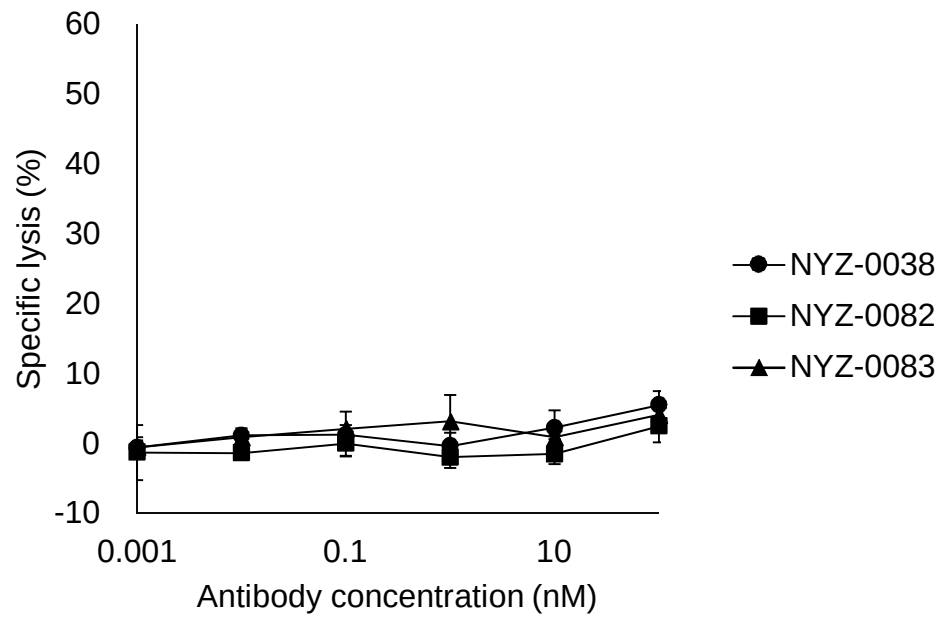


Fig. 159F

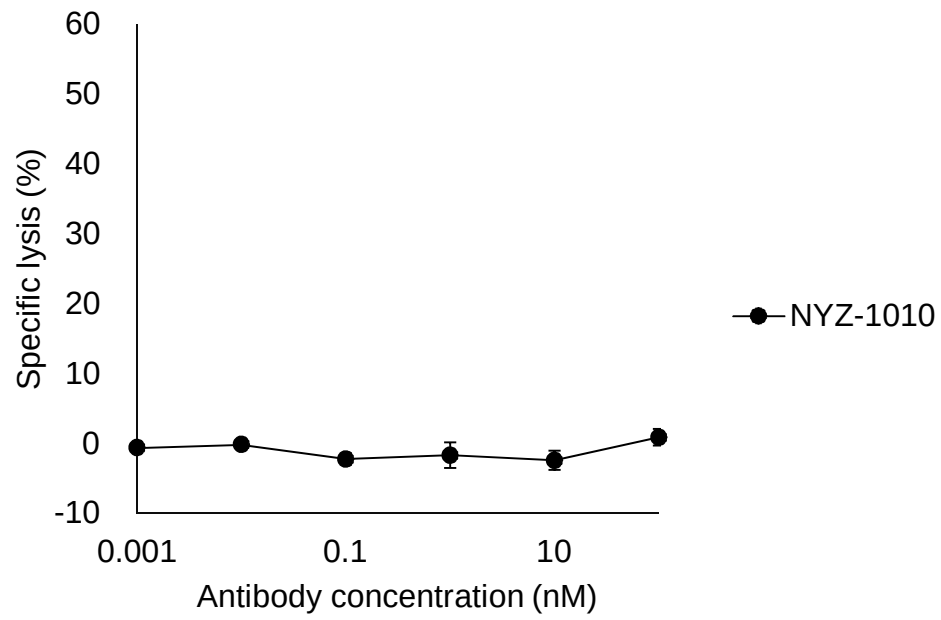


Fig. 159G

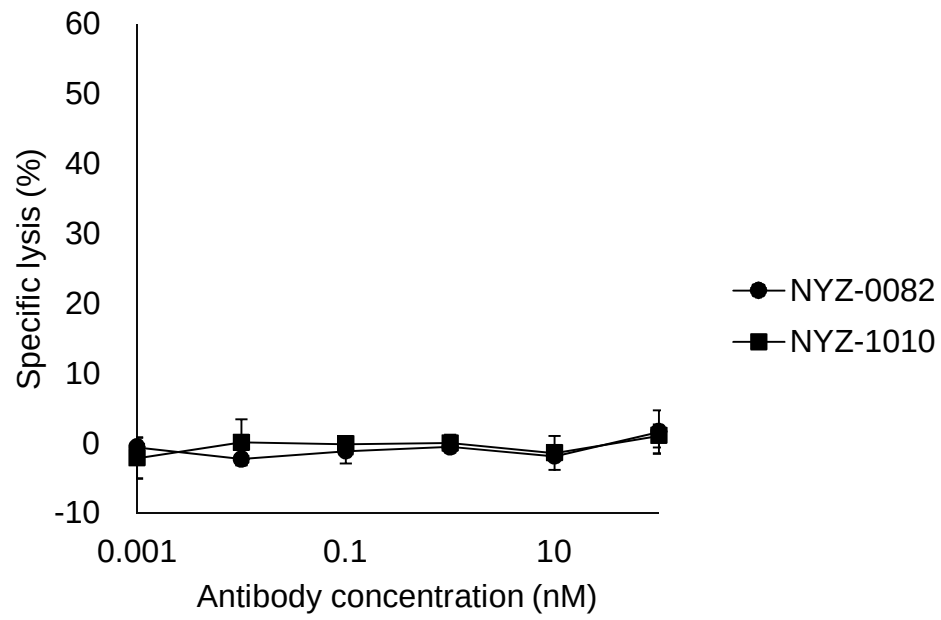


Fig. 159H

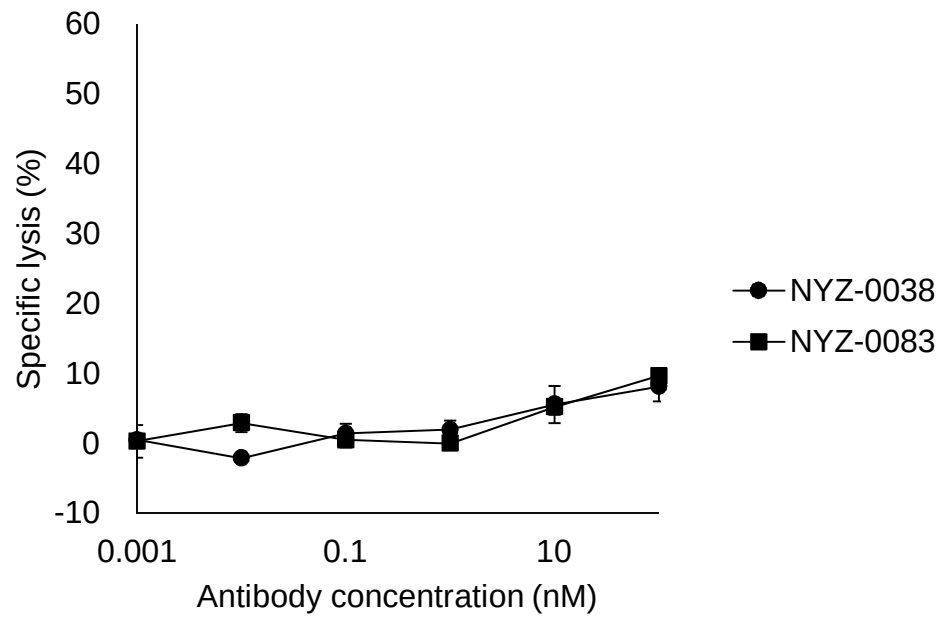


Fig. 160A

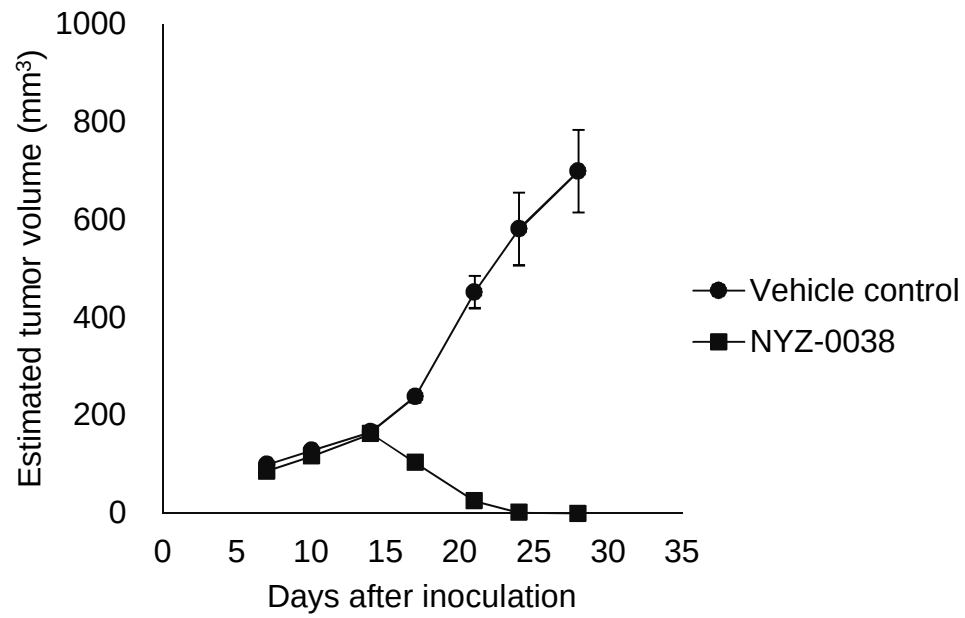


Fig. 160B

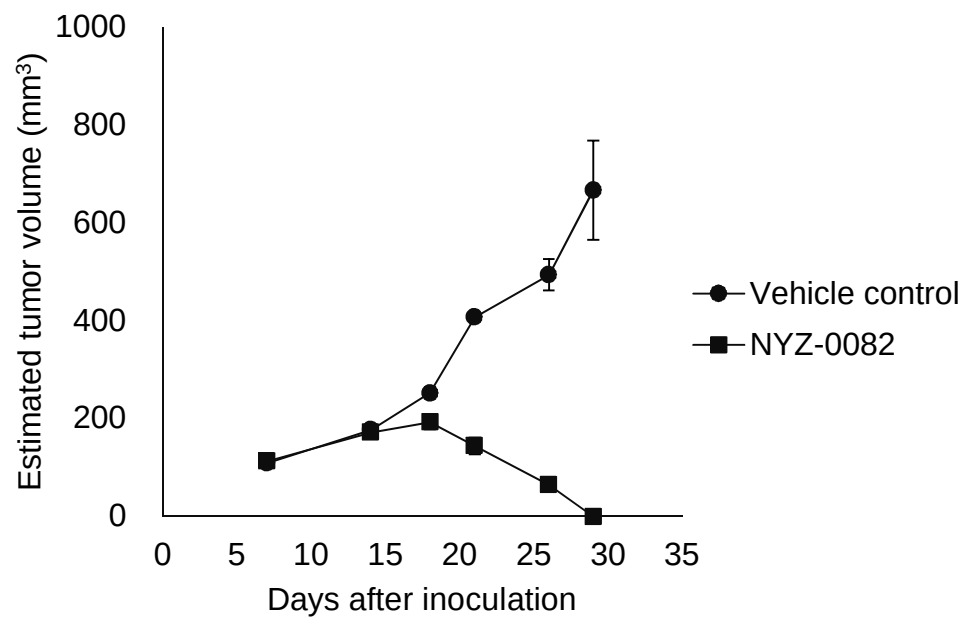


Fig. 160C

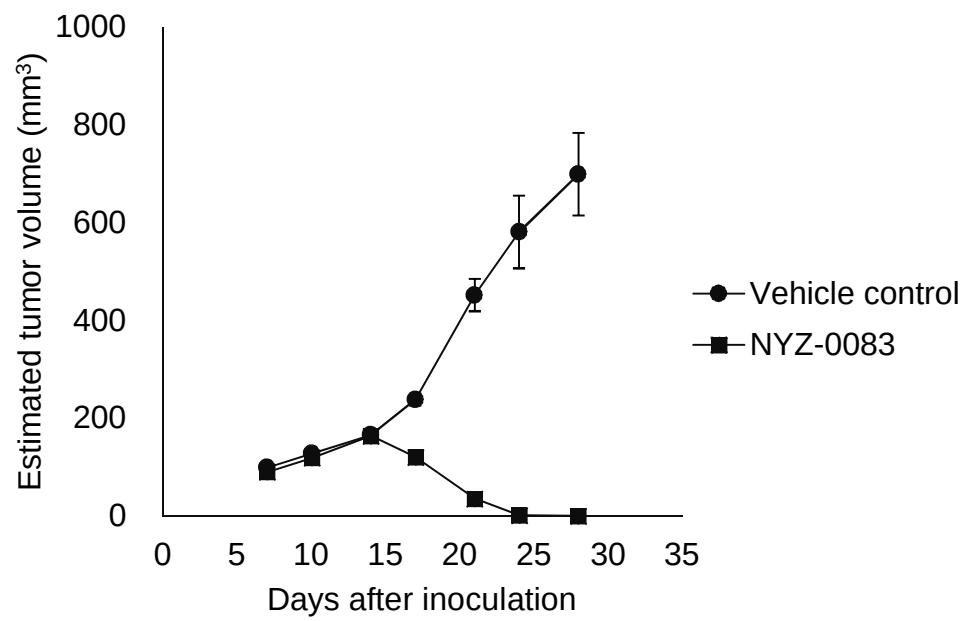


Fig. 160D

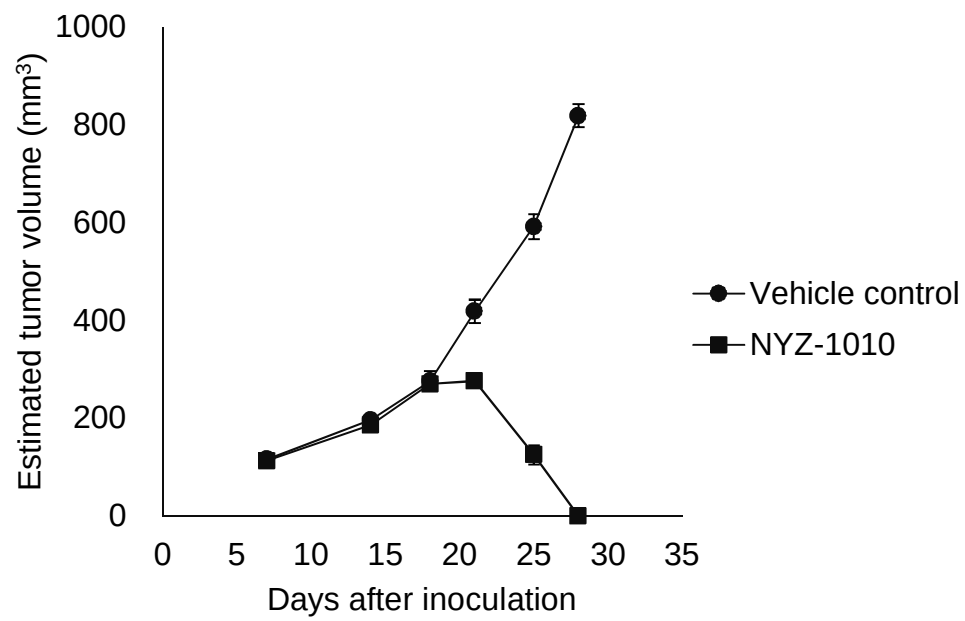


Fig. 161

GGGGS linker
GGGGS
(SEQ ID NO: 162)

Fig. 162

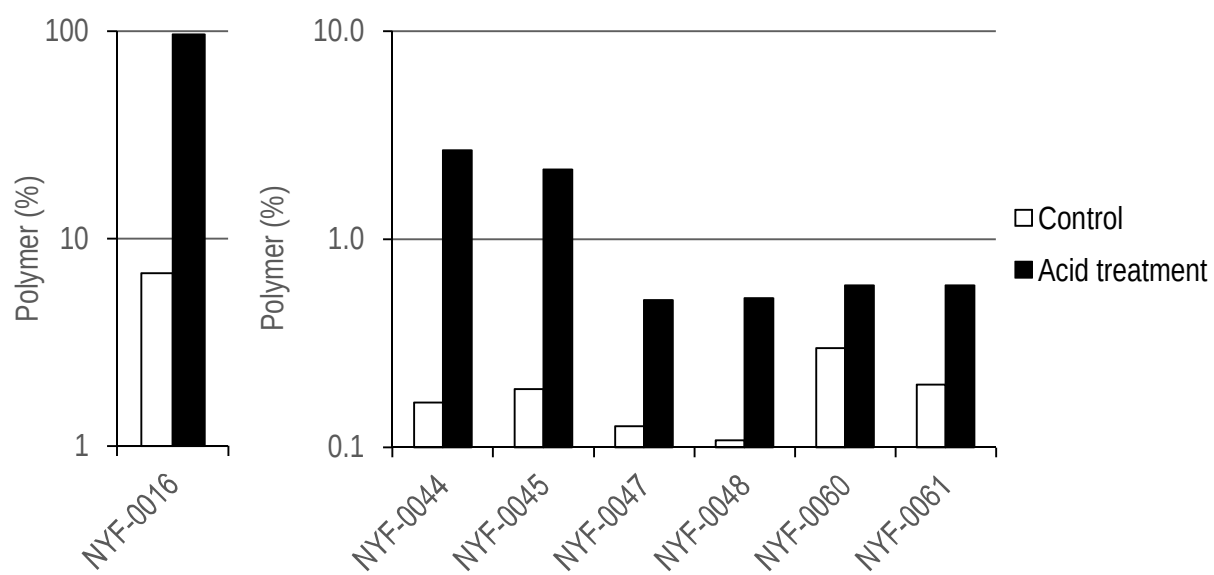


Fig. 163

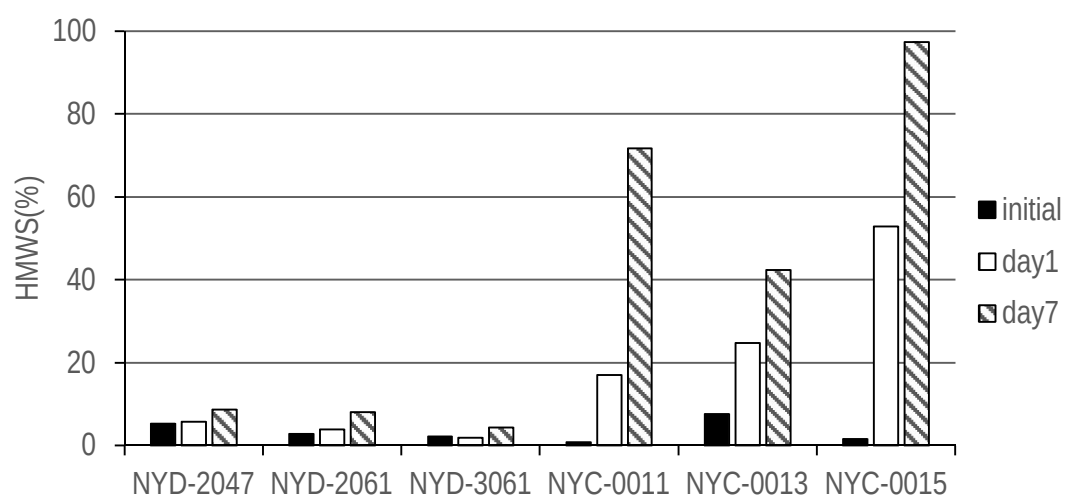


Fig. 164

NYA - 3061

**ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGGCAGCTCCCAGATGGGTGCTGAG
CGGTGAGGTACAGCTGGTGGAATCCGGTGGAGGCCTTGTGCAACCGGGAGGCTCCC
TGC GACTCTCTTGCGCCGCATCTGGCTTTTCCATACGATCCTACGATATTCATTGG
GTCCGAc aaGCCCCCTGGCAAAGGTCTTGAATGGGTTGCCACTATCTCCTACGACGG
GTCTCAGAAATATTATGCGGATTCAGTGAAGGGGCGGTT CACAATTTACGAGACG
AGTCAAAGAATACACTGTACCTCCAAATGAATTCAGTGAAGAGCCGAGGATACTGCA
GTCTATCATTGTGCAAGAGGGTCTCAGGCCACTACGAGGCCTTTGATATATGGGG
CCAAGGCACCTTGGTAAACGTTAGTAGCGGAGGTGGAGGAAGCGGAGGCGGCGGTT
CCGGAGGAGGTGGAAGTGGAGGAGGTGGATCTCAATCCGTTCTGACTCAGCCACCC
TCCGCCTCTGGCACCCCGGGCCAACGGGT CACAATATCATGTTCTGGCTCTTCAAG
CAACATCGGAAACTGGTACGTGAGCTGGTACCAGCAGCTCCCCGGCACGGCGCCCA
AGCTTCTGATATATGACAACAACAAACGGCCCAGTGGAGTTCCTGACAGATT CAGT
GGGTCTAAAAGTGGTACAAGCGCTAGCCTGGCCATAAGTGGTCTGCAGAGTGAAGA
TGAGGCGGACTATTATTGCGGAACCTGGGACTCCAGCCTGAGCGCTCCCTGGGTTT
TCGGCGGAGGTACTAAGCTGACCGTCTTGGGCGCGGCCGCAGGTGCAGGTGGTGAT
TACAAAGATGATGACGATAAAGGTGCAGCGGCGCATCACCATCATCACCAC
(SEQ ID NO: 163), signal sequence (1-57), NYA-3061 (61-
813), FLAG-His tag (814-891)**

Fig. 165

NYA-3061

**MKHLWFFLLLVAAPRWVLSGEVQLVESGGGLVQPGGSLRLSCAASGFSIRSYDIHW
VRQAPGKGLEWVATISYDGSQKYADSVKGRFTISRDESKNTLYLQMNSLRAEDTA
VYHCARGSSGHYEAFDIWGGTTLVTVSSGGGGSGGGGSGGGGSGGGGSQSVLTQPP
SASGTPGQRTISCSGSSSNIGNWYVSWYQQLPGTAPKLLIYDNNKRPSGVPDRFS
GSKSGTSASLAISGLQSEDEADYYCGTWDSSLSAPWVFGGGTKLTVLGAAAGAGGD
YKDDDDKGAAHHHHHHH**

**(SEQ ID NO: 164), signal sequence (1-19), NYA-3061 (21-
271), FLAG-His tag (272-297)**

Fig. 166

NYC-0005

**ATGAAGCACCTGTGGTTCTTTCTGCTGCTGGTGGCCGCTCCTAGATGGGTGTTGTC
TGGCGAAGTGCAGCTGGTGGAATCTGGTGGCGGAGTTGTTCAGCCTGGCGGCTCTC
TGAGACTGAGCTGTGTGGCCAGCGGCTTCACCTTCGACGACTACGCCATGTACTGG
GTCCGACAGGTGCCAGGCAAGGACCTGGAATGGGTGTCCCTGATTTCTGGCGACGG
CGACATCACCTACTACGTGGACTCTGTGAAGGGCAGATTACCGTGTCCAGAGACA
ACAACAAGAACAGCCTGTACCTGCAGATGAAGTCCCTGCGCGTGGAAGATACAGCC
CTGTACTACTGCGCCAAGGACATGATCTACTACGCCTCTTGGAGCGGCTACGGCAG
CAGCGATTACTACTACTATGTGATGGACGTGTGGGGCCAGGGCACCACCGTTACAG
TTTCTAGCGGAGGCGGAGGAAGTGGCGGCGGAGGATCTGGCGGTGGTGGTTCTGAT
ATCCAGATGACACAGAGCCCCAGCAGCCTGTCTGCCTCTGTGGGAGACAGAGTGAC
CATCACCTGTAGAGCCAGCCAGAGCATCAGCAGCTACCTGAACTGGTATCAGCAGA
AGCCCGGCAAGGCCCTAAACTGCTGATCTATGCCGCCTCCAGTCTGCAGAGCGGA
GTGCCTAGCAGATTTTCTGGCAGCGGCTCCGGCACCGATTTACCCTGACCATATC
TAGCCTGCAGCCTGAGGACTTCGCCACCTACTATTGCCAGCAGAGCTACAGCACCC
CTCCTATCACCTTTGGCCAGGGAACCAGACTGGAAATCAAAGGCGCTGCTGCAGGC
GCTGGCGGCGACTACAAAGACGATGATGATAAGGGCGCTGCCGCTCACCACCACCA
TCACCAT**

(SEQ ID NO: 165), signal sequence (1-57), NYC-0005 (61-825), FLAG-His tag (826-903)

Fig. 167

NYC-0005

**MKHLWFFLLLVAAPRWVLSGEVQLVESGGGVVQPGGSLRLSCVASGFTFDDYAMYW
VRQVPKDLWVSLISGDGDITYYVDSVKGRFTVSRDNNKNSLYLQMKSLRVEDTA
LYYCAKDMIYYASWSGYGSSDYVVMDVWGQGTTVTVSSGGGGSGGGGSGGGGSD
IQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSG
VPSRFSGSGSGTDFTLTISLQPEDFATYYCQQSYSTPPITFGQGTRLEIKGAAAG
AGGDYKDDDDKGAAAHHHHHH**

(SEQ ID NO: 166), signal sequence (1-19), NYC-0005 (21-275), FLAG-His tag (276-301)

Fig. 168

NYC-0006

**ATGAAGCACCTGTGGTTCTTTCTGCTGCTGGTGGCCGCTCCTAGATGGGTGTTGTC
TGGCGAAGTGCAGCTGGTGGAATCTGGTGGCGGAGTTGTTCAGCCTGGCGGCTCTC
TGAGACTGTCTTGTGCCGCCAGCGGCTTCACCTTCGACGACTACGCCATGTACTGG
GTCCGACAGGCCCTGGCAAAGGCCTTGAATGGGTGTCCCTGATCAGCGGAGATGG
CGGCAGCATGTACTACGCCGATAGCGTGAAGGGCAGATTACCATCAGCCGGGACA
ACAGCAAGAACAGCCTGTACCTGCAGATGAACTCCCTGCGGACCGAGGACACAGCC
CTGTACTACTGCGCCAAGGATATGATCTTCTACGCCTTTTGGAGCGGCTACGGCAG
CAGCGATTACTACTACTACGTGATGGACGTGTGGGGCCAGGGCACCACAGTGACAG
TTTATTCTGGCGGCGGAGGATCTGGCGGAGGTGGAAGCGGAGGCGGTGGATCTGAT
ATCCAGATGACACAGAGCCCCAGCAGCCTGTCTGCCTCTGTGGGAGACAGAGTGAC
CATCACCTGTCGGGCCAGCCAGAGAATCAGCACCTACCTGAACTGGTATCAGCAGA
AGCCCGGCAAGGCCCTAAGCTGCTGATCTATGCTGCCTCCAGTCTGCAGAGCGGC
GTGCCAAGCAGATTTTCTGGCAGCGGCTCTGGCACCGACTTCACCCTGACCATATC
TAGCCTGCAGCCTGAGGACTTCGCCACCTACTACTGCCAGCAGAGCTACAGCACCC
CTCCTATCACCTTTGGCCAGGGAACCAGACTGGAAATCAAAGGCGCTGCTGCAGGC
GCAGGCGGCGACTACAAAGACGATGATGATAAGGGCGCTGCCGCTCACCACCACCA
TCACCAT**

(SEQ ID NO: 167), signal sequence (1-57), NYC-0006(61-825), FLAG-His tag (826-903)

Fig. 169

NYC-0006

**MKHLWFFLLLVAAPRWVLSGEVQLVESGGGVVQPGGSLRLSCAASGFTFDDYAMYW
VRQAPGKGLEWVSLISGDGGSYYYADSVKGRFTISRDN SKNSLYLQMNSLRTE
DTA LYYCAKDMIFYAFWSGYGSSDYVVVMDVWGQGTTVTVYSGGGSGGGGSGGGGSD
IQMTQSPSSLSASVGRVTITCRASQRISTYLNWYQQKPKAPKLLIYAASSLQSG
VPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPPITFGQGRLEIKGAAAG
AGGDYKDDDDKGAAAHHHHHH**

(SEQ ID NO: 168), signal sequence (1-19), NYC-0006(21-275), FLAG-His tag (276-301)

Fig. 170

NYC-0007

**ATGAAGCACCTGTGGTTCTTTCTGCTGCTGGTGGCCGCTCCTAGATGGGTGTTGTC
TGGCGAAGTGCAGCTGGTGGAATCTGGTGGCGGAGTTGTTCAGCCTGGCGGCTCTC
TGAGACTGTCTTGTGCCGCCAGCGGCTTCACCTTCGACGATTATGCCATGCACTGG
GTCCGACAGGCCCTGGCAAAGGACTTGAATGGGTGTCCCTGATCAGCGGCGACGG
CGACAATACCTACTACGCCGATAGCGTGAAGGGCAGATTACCATCAGCCGGGACA
ACAACAAGAACAGCCTGTACCTGCAGATGAACTCCCTGCGGACCGAGGACACCGCC
TTCTACTACTGTGCCAAAGAGCTGATCTTCGGCAAGGTGCTGCACGACTTTTACTA
CTACGTGATGGACGTGTGGGGCCAGGGCACCACAGTGACAGTTTCTAGCGGAGGCG
GAGGAAGTGGCGGCGGAGGATCTGGCGGTGGTGGTTCTGATATCCAGATGACACAG
AGCCCCAGCAGCCTGTCTGCCTCTGTGGGAGACAGAGTGACCATCACCTGTAGAGC
CAGCCAGAGCATCAGCAGCTACCTGAACTGGTATCAGCAGAAGCCCGGCAAGGCC
CTAAACTGCTGATCTATGCCGCCTCCAGTCTGCAGAGCGGAGTGCCTAGCAGATTT
TCTGGCAGCGGCTCCGGCACCGATTTACCCTGACCATATCTAGCCTGCAGCCTGA
GGAATTCGCCACCTACTACTGCCAGCAGAGCTACAGCACCCCTCCTATCACCTTTG
GCCAGGGAACCAGACTGGAAATCAAAGGCGCTGCTGCAGGCGCAGGCGGCGACTAC
AAAGACGATGATGATAAGGGCGCTGCCGCTCACCACCACCATCACCAT**

(SEQ ID NO: 169), signal sequence (1-57), NYC-0007(61-810), FLAG-His tag (811-888)

Fig. 171

NYC-0007

**MKHLWFFLLLVAAPRWVLSGEVQLVESGGGVVQPGGSLRLSCAASGFTFDDYAMHW
VRQAPGKGLEWVSLISGDGNTYYADSVKGRFTISRDNKNSLYLQMNSLRTE
DYA
FYCAKELIFGKVLHDFYYYVMDVWGQGT
TVTVSSGGGGSGGGGSGGGGSDIQMTQ
SPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRF
SGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPPITFGQGTRLEIKGAAAGAGGDY
KDDDDKGAAAHHHHHH**

(SEQ ID NO: 170), signal sequence (1-19), NYC-0007(21-270), FLAG-His tag (271-296)

Fig. 172

NYC-0008

ATGAAGCACCTGTGGTTCTTTCTGCTGCTGGTGGCCGCTCCTAGATGGGTGTTGTC
TGGCGAAGTGCAGCTGGTGGAAATCTGGTGGCGGAGTTGTTCAGCCTGGCGGCTCTC
TGAGACTGAGCTGTGAAGCCTCCGGCTTCATCTTCGACGACTACGCCATGCACTGG
GTCCGACAGGCACCTGGCAAAGGCCTTGAATGGGTGTCCCTGATCTCTGGCGACGG
CGACATCATCTACTACGCCGACTCTGTGAAGGGCAGATTACCATCAGCCGGGACA
ACAGCAAGAACAGCCTGTACCTGCAGATGAACTCCCTGATCATCGAGGACACAGCC
CTGTACTACTGCGCCAAGGATTGGGTGTTTCGGCGTCGTGATGACCCACTACTGGTA
CTTCGGCCTGGATGTGTGGGGCCAGGGAACCACAGTGACAGTTTCTAGCGGAGGCG
GAGGAAGTGGCGGCGGAGGATCTGGCGGTGGTGGTTCTGATATCCAGATGACACAG
AGCCCCAGCAGCCTGTCTGCCTCTGAAGGCGACAGAGTGACCATCACCTGTAGAGC
CAGCCAGAGCATCAGCACCTACCTGAACTGGTATCAGCAGAAGCCCGGCAAGGCCC
CTAAGCTGCTGATCTATGGTGCCTCCAGTCTGCAGAGCGGCGTGCCAAGCAGATTT
TCTGGCAGCGGCTCTGGCACCGACTTCACCCTGACCATATCTAGCCTGCAGCCTGA
GGACTTCGCCACCTACTACTGCCAGCAGTCCTACAGCACCCCTCCTATCACATTTG
GCCAGGGCACCAAGGTGGAAATCAAAGGCGCTGCTGCAGGCGCTGGCGGCGACTAC
AAAGACGATGATGATAAGGGCGCTGCCGCTCACCACCACCATCACCAT

(SEQ ID NO: 171), signal sequence (1-57), NYC-0008(61-810), FLAG-His tag (811-888)

Fig. 173

NYC-0008

**MKHLWFFLLLVAAPRWVLSGEVQLVESGGGVVQPGGSLRLSCEASGFIFDDYAMHW
VRQAPGKGLEWVSLISGDGDIIYYADSVKGRFTISRDNKNSLYLQMNSLIIEDTA
LYYCAKDWVFGVVMTHYWYFGLDVWGQGTTVTVSSGGGGSGGGGSGGGGSDIQMTQ
SPSSLSASEGDRVITICRASQSISTYLNWYQQKPGKAPKLLIYGASSLQSGVPSRF
SGSGSGTDFTLTISLQPEDFATYYCQQSYSTPPITFGQGTKVEIKGAAAGAGGDY
KDDDDKGAAAHHHHHH**

(SEQ ID NO: 172), signal sequence (1-19), NYC-0008(21-270), FLAG-His tag (271-296)

Fig. 174

NYC-0009

**ATGAAGCACCTGTGGTTCTTTCTGCTGCTGGTGGCCGCTCCTAGATGGGTGTTGTC
TGGCGAAGTGCAGCTGGTGGAATCTGGTGGCGGAGTTGTTCAGCCTGGCGGCTCTC
TGAGACTGTCTTGTGCCGCCAGCGGCTTCACCTTCGACGATTATGCCATGCACTGG
GTCCGACAGGCCCCCTGGCAAAGGACTTGAATGGGTGTCCCTGATCTCTGGCGGAGG
CGGCGGAACCTACTACAGCGATTCTGTGAAGGGCAGATTACCATCAGCCGGGACA
CCAGCAAGGACAGCCTGTACCTGCAGATGAACAGCCTGCGGACCGAGGACACAGCC
CTGTACTACTGCGCCAAGGACATGGTGTTCGGCGTGGTCACCCCTTACTACTT
CGCCCTGGATGTGTGGGGCCAGGGCACAACAGTGACAGTCTCTTCTGGCGGCGGAG
GAAGCGGAGGCGGAGGATCCGGTGGTGGTGGATCTGACATCCAGATGACACAGAGC
CCCAGCAGCCTGTCTGCCTCTGTGGGAGACAGAGTGACCATCACCTGTAGAGCCAG
CCAGAGCATCAACAGCTACCTGAACTGGTATCAGCAGAAGCCCGGCAAGGCCCTA
AGCTGCTGATCTATGCTGCCTCCAGTCTGCAGAGCGGCGTGCCAAGCAGATTTTCT
GGCAGCGGCTCTGGCACCGACTTCACCCTGACCATATCTAGCCTGCAGCCTGAGGA
CTTCGCCACCTACTACTGCCAGCAGAGCTACAGCGCCCCTCCTATCACATTTGGCC
AGGGAACCAGACTGGAAATCAAAGGCGCTGCTGCAGGCGCAGGCGGCGACTACAAA
GACGATGATGATAAGGGCGCTGCCGCTCACCACCATCACCATCAT**

(SEQ ID NO: 173), signal sequence (1-57), NYC-0009(61-807), FLAG-His tag (808-885)

Fig. 175

NYC-0009

**MKHLWFFLLLVAAPRWVLSGEVQLVESGGGVVQPGGSLRLSCAASGFTFDDYAMHW
VRQAPGKGLEWVSLISGGGGGTYYSDSVKGRFTISRDTSKDSLYLQMNSLRTE
D
TALYYCAKDMVFGVVTPYFFALDVWGQGT
TVTVSSGGGGSGGGGSGGGGSDIQMTQS
PSSLSASVGDRVTITCRASQSINSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFS
GSGSGTDFTLTISSLQPEDFATYYCQQSYSA
PPITFGQGTRLEIKGAAAGAGGDYK
DDDDKGA
AAHHHHHH**

(SEQ ID NO: 174), signal sequence (1-19), NYC-0009(21-269), FLAG-His tag (270-295)

Fig. 176

NYC-0010

**ATGAAGCACCTGTGGTTCTTTCTGCTGCTGGTGGCCGCTCCTAGATGGGTGTTGTC
TGGCGAAGTGCAGCTGGTGGAATCTGGTGGCGGAGTTGTTACGCCTGGCGGCTCTC
TGAGACTGAGCTGTGCTGTGTCCGGCTTCACCTTCGACGACTACGCCATGCACTGG
GTCCGACAGGCACCTGGCAAAGGCCTTGAATGGGTGTCCCTGATCAGCGGAGATGG
CGGCAGCACACACTACGCCGATTCTGTGAAGGGCAGATTACCATCAGCCGGGACA
ACAGCAAGAACAGCCTGTACCTGCAGATGAACTCCCTGCGGACAGGCGACACAGCC
CTGTACTACTGCGCCAAGGACATGATCTTCGCCGTGGTCATCACCGACTACCACTA
CTACGGCATGGACGTGTGGGGCCAGGGAACCACAGTGACAGTTTCTAGCGGAGGCG
GAGGAAGTGGCGGCGGAGGATCTGGCGGTGGTGGTTCTGATATCCAGATGACACAG
AGCCCCAGCAGCCTGTCTGCCTCTGTGGGAGACAGAGTGACCATCACCTGTAGAGC
CAGCCAGAGCATCAGCAGCTACCTGAACTGGTATCAGCAGAAGCCCGGCAAGGCCC
CTAAACTGCTGATCTATGCCGCCTCCAGTCTGCAGAGCGGAGTGCCTAGCAGATTT
TCTGGCAGCGGCTCCGGCACCGATTTACCCTGACCATATCTAGCCTGCAGCCTGA
GGAATTCGCCACCTACTACTGCCAGCAGAGCTACAGCACCCCTCCTATCACCTTTG
GCCAGGGCACCACTGAGTGGAAATCAAAGGCGCTGCTGCAGGCGCTGGCGGCGACTAC
AAAGACGATGATGATAAGGGCGCTGCCGCTCACCACCACCATCACCAT**

(SEQ ID NO: 175), signal sequence (1-57), NYC-0010(61-810), FLAG-His tag (811-888)

Fig. 177

NYC-0010

**MKHLWFFLLLVAAPRWVLSGEVQLVESGGGVVQPGGSLRLSCAVSGFTFDDYAMHW
VRQAPGKGLEWVSLISGDGGSTHYADSVKGRFTISRDNKNSLYLQMNSLRTGDTA
LYYCAKDMIFAVVITDYHYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSDIQMTQ
SPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRF
SGSGSGTDFTLTISLQPEDFATYYCQQSYSTPPITFGQGTRLEIKGAAAGAGGDY
KDDDDKGAAAHHHHHH**

**(SEQ ID NO: 176), signal sequence (1-19), NYC-0010(21-
270), FLAG-His tag (271-296)**

Fig. 178

HC-h

ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGGCAGCTCCCAGATGGGTGCTGAG
CGACAAAACCTCACACATGCCACCCTGCCAGCACCTGAAGCCGCCGGCGGACCCT
CAGTCTTCCTCTTCCCCCAAACCAAGGACACCCTCATGATCTCCCGGACCCCT
GAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAA
CTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACCAAGCCTAGAGAGGAAC
AGTACAACAGCACCTACCGGGTGGTGTCCGTGCTGACAGTGCTGCACCAGGACTGG
CTGAACGGCAAAGAGTACAAGTGCAAGGTGTCCAACAAGGCCCTGCCTGCCCCCAT
CGAGAAAACCATCAGCAAGGCCAAGGGCCAGCCCCGCGAACCTCAAGTGTGCACCC
TGCCACCCTCCCGGGATGAGCTGACCAAGAACCAGGTGTCCCTGAGCTGTGCCGTG
AAGGGCTTCTACCCCTCCGATATCGCCGTGGAATGGGAGAGCAACGGCCAGCCCGA
GAACAACTACAAGACCACCCCCCTGTGCTGGACAGCGACGGCTCATTCTTCCTGG
TGTCCAAGCTGACCGTGGACAAGTCCAGATGGCAGCAGGGCAACGTCTTCTCATGC
TCCGTGATGCATGAGGCTCTGCACAACCACTACACCCAGAAGAGCCTCTCCCTGTC
TCCCGGCAAA

(SEQ ID NO: 177), signal sequence (1-57), constant
region (58-738)

Fig. 179

HC-h

MKHLWFFLLLVAAPRWVLSDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVCTLPSSRDELTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGSSFFLVSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

(SEQ ID NO: 178), signal sequence (1-19), constant region (20-246)

Fig. 180

NYD-2047-HC-k

ATGAAGCACCTGTGGTTCTTTCTGCTGCTGGTGGCCGCTCCTAGATGGGTGCTGTC
TGGTCAAGTACAGCTGGTGGGAATCCGGTGGAGGCGTGGTCCAGCCGGGACGCAGCT
TGAGACTGTCCTGCGCTGCATCTGGCTTTTCCATACGATCCTACGATATGCACTGG
GTTTCGCCAAGCCCCCTGGCAAAGGTCTTGAATGGGTTGCCACTATCTCCTACGACGG
GTCTCAGAAATATTACGCGGATTCACTGAAGGGGCGGTTTACAATTTACGCGGACA
ATTCAAAGAATACCTTGTATCTCCAGATGTCTTCACTGAGAGCCGAGGATACTGCA
GTCTATCATTGTGCAAGAGGGTCTCTCAGGCCACTACGAGGCCTTTGATATATGGGG
CCAAGGCACCTTGGTAACCGTTAGTAGCGGAGGTGGAGGAAGCGGAGGCGGCGGTT
CCGGAGGAGGTGGAAGTCAATCCGTTCTGACTCAGCCACCCTCCGTGAGTGCAGCG
CCTGGACAGAAGGTCACAATATCATGTTCTGGCTCTTCAAGCAACATCGGAAACTG
GTACGTGAGCTGGTACCAGCAGCTCCCCGGCACGGCGCCCAAGCTTCTGATATATG
ACAACAACAACGGCCCAGTGGGAATCCCTGACAGATTCACTGGGTCTAAAAGTGGT
ACAAGCGCTACCCTGGGTATCACCGGATTGCAGACCGGAGATGAGGCGGACTATTA
TTGCGGAACCTGGGACTCCAGCCTGAGCGCTCCCTGGGTTTTTCGGCGGAGGTACTA
AGGTTACCGTCTTGGGCGGAGAACCCAAGAGCgcaGACAAGACCCACACCTGTCTCT
CCATGTCTCTGCTCCAGAAGCTGCAGGCGGCCCTTCCGTGTTTCTGTTCCCTCCAAA
GCCTAAGGACACCCTGATGATCAGCCGGACACCTGAAGTGACCTGCGTGGTGGTGG
ATGTGTCCCACGAGGATCCCGAAGTGAAGTTCAATTGGTACGTGGACGGCGTGGAA
GTGCACAACGCCAAGACCAAGCCTAGAGAGGAACAGTACAACAGCACCTACAGAGT
GGTGTCTGTGCTGACAGTGCTGCACCAGGACTGGCTGAACGGCAAAGAGTACAAGT
GCAAGGTGTCCAACAAGGCCCTGCCTGCTCCTATCGAGAAAACCATCAGCAAGGCC
AAGGGCCAGCCTAGGGAACCCCAGGTTTACACCCTGCCTCCATGCAGGGATGAGCT
GACCAAGAACCAGGTGTCCCTGTGGTGCCTGGTTAAGGGCTTCTACCCCTCCGATA
TCGCCGTGGAATGGGAGAGCAATGGCCAGCCAGAGAACAACTACAAGACAACCCCT
CCTGTGCTGGACTCCGACGGCTCATTCTTCTGTACAGCAAGCTGACCGTGGACAA
GAGCAGATGGCAGCAGGGCAACGTGTTCACTGTCAGCGTGATGCACGAGGCCCTGC
ACAACCACTACACACAGAAGTCCCTGTCTCTGAGCCCCGGCAAA

(SEQ ID NO: 179), signal sequence (1-57), NYA-2047(61-798), linker (799-804), constant region (805-1500)

Fig. 181

NYD-2047-HC-k

MKHLWFFLLLVAAPRWVLSGQVQLVESGGGVVQPGRSLRLSCAASGFSIRSYDMHW
VRQAPGKGLEWVATISYDGSQKYYADSVKGRFTISRDN SKNTLYLQMSSLRAEDTA
VYHCARGSSGHYEAFDIWGQGT LVT VSSGGGGSGGGGSGGGGSQSVLTQPPSVSAA
PGQKVTISCSGSSSNIGNWYVSWYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSG
TSATLGITGLQTGDEADYYCGTWDSSLSAPWVFGGGTKVTVLGGEPKSADKTHTCP
PCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE
VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
KGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTP
PVLDS DGSFFLYSKLTVDKSRWQQGNV FSCSVMHEALHNHYTQKSLSLSPGK
(SEQ ID NO: 180), signal sequence (1-19), NYA-2047(21-
266), linker (267-268), constant region (269-500)

Fig. 182

NYD-2061-HC-k

ATGAAGCACCTGTGGTTCTTTCTGCTGCTGGTGGCCGCTCCTAGATGGGTGCTGTC
TGGTGAGGTACAGCTGGTGGAATCCGGTGGAGGCCTTGTGCAACCGGGAGGCTCCC
TGC GACTCTCTTGCGCCGCATCTGGCTTTTCCATACGATCCTACGATATTCATTGG
GTCCGAc aaGCCCCCTGGCAAAGGTCTTGAATGGGTTGCCACTATCTCCTACGACGG
GTCTCAGAAATATTATGCGGATTCAGTGAAGGGGCGGTTTACAATTTACGAGACG
AGTCAAAGAATACACTGTACCTCCAAATGAATTCAGTGAAGAGCCGAGGATACTGCA
GTCTATCATTGTGCAAGAGGGTCTCTCAGGCCACTACGAGGCCTTTGATATATGGGG
CCAAGGCACCTTGGTAACCGTTAGTAGCGGAGGTGGAGGAAGCGGAGGCGGCGGTT
CCGGAGGAGGTGGAAGTCAATCCGTTCTGACTCAGCCACCCTCCGCTCTGGCACC
CCGGGCCAACGGGTACAATATCATGTTCTGGCTCTTCAAGCAACATCGGAAACTG
GTACGTGAGCTGGTACCAGCAGCTCCCCGGCACGGCGCCCAAGCTTCTGATATATG
ACAACAACAACGGCCCAGTGGAGTTCCTGACAGATTCAGTGGGTCTAAAAGTGGT
ACAAGCGCTAGCCTGGCCATAAGTGGTCTGCAGAGTGAAGATGAGGCGGACTATTA
TTGCGGAACCTGGGACTCCAGCCTGAGCGCTCCCTGGGTTTTTCGGCGGAGGTACTA
AGCTGACCGTCTTGGGCGGAGAACCCAAGAGCgcaGACAAGACCCACACCTGTCTCT
CCATGTCTCTGCTCCAGAAGCTGCAGGCGGCCCTTCCGTGTTTCTGTTCCCTCCAAA
GCCTAAGGACACCCTGATGATCAGCCGGACACCTGAAGTGACCTGCGTGGTGGTGG
ATGTGTCCCACGAGGATCCCGAAGTGAAGTTCAATTGGTACGTGGACGGCGTGGAA
GTGCACAACGCCAAGACCAAGCCTAGAGAGGAACAGTACAACAGCACCTACAGAGT
GGTGTCTGTGCTGACAGTGTGTCACCAGGACTGGCTGAACGGCAAAGAGTACAAGT
GCAAGGTGTCCAACAAGGCCCTGCCTGCTCCTATCGAGAAAACCATCAGCAAGGCC
AAGGGCCAGCCTAGGGAACCCAGGTTTACACCCTGCCTCCATGCAGGGATGAGCT
GACCAAGAACCAGGTGTCCCTGTGGTGCCTGGTTAAGGGCTTCTACCCCTCCGATA
TCGCCGTGGAATGGGAGAGCAATGGCCAGCCAGAGAACAACTACAAGACAACCCCT
CCTGTGCTGGACTCCGACGGCTCATTCTTCTGTACAGCAAGCTGACCGTGGACAA
GAGCAGATGGCAGCAGGGCAACGTGTTTCACTGTCAGCGTGATGCACGAGGCCCTGC
ACAACCACTACACACAGAAGTCCCTGTCTCTGAGCCCCGGCAA

(SEQ ID NO: 181), signal sequence (1-57), NYA-2061 (61-798), linker (799-804), constant region (805-1500)

Fig. 183

NYD-2061-HC-k

**MKHLWFFLLLVAAPRWVLSGEVQLVESGGGLVQPGGSLRLSCAASGFSIRSYDIHW
VRQAPGKGLEWVATISYDGSQKYADSVKGRFTISRDESKNTLYLQMNSLRAEDTA
VYHCARGSSGHYEAFDIWGGTLVTVSSGGGGSGGGGSGGGGSQSVLTQPPSASGT
PGQRTVISCSSSSNIGNWYVSWYQQLPGTAPKLLIYDNNKRPSGVPDRFSGSKSG
TSASLAISGLQSEDEADYYCGTWDSSLSAPWVFGGGTKLTVLGGEPKSADKTHTCP
PCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE
VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
KGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTP
PVLDSGDGSFFLYSKLTVDKSRWQQGNVFSQVMHEALHNHYTQKSLSLSPGK
(SEQ ID NO: 182), signal sequence (1-19), NYA-2061 (21-
266), linker (267-268), constant region (269-500)**

Fig. 184

NYD-3061-HC-k

ATGAAGCACCTGTGGTTCTTTCTGCTGCTGGTGGCCGCTCCTAGATGGGTGCTGTC
TGGTGAGGTACAGCTGGTGGAATCCGGTGGAGGCCTTGTGCAACCGGGAGGCTCCC
TGC GACTCTCTTGCGCCGCATCTGGCTTTTCCATACGATCCTACGATATTCATTGG
GTCCGAc aaGCCCCCTGGCAAAGGTCTTGAATGGGTTGCCACTATCTCCTACGACGG
GTCTCAGAAATATTATGCGGATTCAGTGAAGGGGCGGTTTCACAATTTACGAGACG
AGTCAAAGAATACACTGTACCTCCAAATGAATTCAGTGAAGAGCCGAGGATACTGCA
GTCTATCATTGTGCAAGAGGGTCTCTCAGGCCACTACGAGGCCTTTGATATATGGGG
CCAAGGCACCTTGGTAACCGTTAGTAGCGGAGGTGGAGGAAGCGGAGGCGGCGGTT
CCGGAGGAGGTGGAAGTGGAGGAGGTGGATCTCAATCCGTTCTGACTCAGCCACCC
TCCGCCTCTGGCACCCCGGGCCAACGGGTACAAATATCATGTTCTGGCTCTTCAAG
CAACATCGGAAACTGGTACGTGAGCTGGTACCAGCAGCTCCCCGGCACGGCGCCCA
AGCTTCTGATATATGACAACAACAAACGGCCCAGTGGAGTTCCTGACAGATTCAGT
GGGTCTAAAAGTGGTACAAGCGCTAGCCTGGCCATAAGTGGTCTGCAGAGTGAAGA
TGAGGCGGACTATTATTGCGGAACCTGGGACTCCAGCCTGAGCGCTCCCTGGGTTT
TCGGCGGAGGTACTAAGCTGACCGTCTTGGGCGGAGAACCCAAGAGCGCAGACAAG
ACCCACACCTGTCTCCATGTCTGCTCCAGAAGCTGCAGGCGGCCCTTCCGTGTT
TCTGTTCCCTCCAAAGCCTAAGGACACCCTGATGATCAGCCGGACACCTGAAGTGA
CCTGCGTGGTGGTGGATGTGTCCCACGAGGATCCCGAAGTGAAGTTCAATTGGTAC
GTGGACGGCGTGGAAGTGCACAACGCCAAGACCAAGCCTAGAGAGGAACAGTACAA
CAGCACCTACAGAGTGGTGTCTGTGCTGACAGTGTGCAACAGGACTGGCTGAACG
GCAAAGAGTACAAGTGCAAGGTGTCCAACAAGGCCCTGCCTGCTCCTATCGAGAAA
ACCATCAGCAAGGCCAAGGGCCAGCCTAGGGAACCCCAGGTTTACACCCTGCCTCC
ATGCAGGGATGAGCTGACCAAGAACCAGGTGTCCCTGTGGTGCCTGGTTAAGGGCT
TCTACCCCTCCGATATCGCCGTGGAATGGGAGAGCAATGGCCAGCCAGAGAACAAAC
TACAAGACAACCCCTCCTGTGCTGGACTCCGACGGCTCATTCTTCTGTACAGCAA
GCTGACCGTGGACAAGAGCAGATGGCAGCAGGGCAACGTGTTCACTGTCAGCGTGA
TGCACGAGGCCCTGCACAACCACTACACACAGAAGTCCCTGTCTCTGAGCCCCGGC
AAA

(SEQ ID NO: 183), signal sequence (1-57), NYA-3061 (61-813), linker (814-819), constant region (820-1515)

Fig. 185

NYD-3061-HC-k

**MKHLWFFLLLVAAPRWVLSGEVQLVESGGGLVQPGGSLRLSCAASGFSIRSYDIHW
VRQAPGKGLEWVATISYDGSQKYADSVKGRFTISRDESKNTLYLQMNSLRAEDTA
VYHCARGSSGHYEAFDIWGGTTLTVSSGGGGSGGGGSGGGGSGGGGSQSVLTQPP
SASGTPGQRVTISCSGSSSNIGNWYVSWYQQLPGTAPKLLIYDNNKRPSGVPDRFS
GSKSGTSASLAISGLQSEDEADYYCGTWDSSLSAPWVFGGGTKLTVLGGEPKSADK
THTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWY
VDGVEVHNAKTKPREEQYNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEK
TISKAKGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENN
YKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVVFSCSVMHEALHNHYTQKSLSLSPG
K**

(SEQ ID NO: 184), signal sequence (1-19), NYA-3061 (21-271), linker (272-273), constant region (274-505)

Fig. 186

NYC-0011-HC-k

ATGAAGCACCTGTGGTTCTTTCTGCTGCTGGTGGCCGCTCCTAGATGGGTGCTGTC
TGGCGAAGTGCAGCTGGTGGGAATCTGGTGGCGGAGTTGTTACGCCTGGCGGCTCTC
TGAGACTGAGCTGTGTGGCCAGCGGCTTCACCTTCGACGACTACGCCATGTACTGG
GTCCGACAGGTGCCAGGCAAGGACCTGGAATGGGTGTCCCTGATTTCTGGCGACGG
CGACATCACCTACTACGTGGACTCTGTGAAGGGCAGATTACCGTGTCCAGAGACA
ACAACAAGAACAGCCTGTACCTGCAGATGAAGTCCCTGCGCGTGGAAGATACAGCC
CTGTACTACTGCGCCAAGGACATGATCTACTACGCCTCTTGGAGCGGCTACGGCAG
CAGCGATTACTACTACTATGTGATGGACGTGTGGGGCCAGGGCACCACCGTTACAG
TTTCTAGCGGAGGCGGAGGAAGTGGCGGCGGAGGATCTGGCGGTGGTGGTTCTGAT
ATCCAGATGACACAGAGCCCCAGCAGCCTGTCTGCCTCTGTGGGAGACAGAGTGAC
CATCACCTGTAGAGCCAGCCAGAGCATCAGCAGCTACCTGAACTGGTATCAGCAGA
AGCCCGGCAAGGCCCTAAACTGCTGATCTATGCCGCCTCCAGTCTGCAGAGCGGA
GTGCCTAGCAGATTTTCTGGCAGCGGCTCCGGCACCGATTTACCCCTGACCATATC
TAGCCTGCAGCCTGAGGACTTCGCCACCTACTATTGCCAGCAGAGCTACAGCACCC
CTCCTATCACCTTTGGCCAGGGAACCAGACTGGAAATCAAAGGCGGAGAACCCAAG
AGCgcaGACAAGACCCACACCTGTCTCTCCATGTCTCTGCTCCAGAAGCTGCAGGCGG
CCCTTCCGTGTTTCTGTTCCCTCCAAAGCCTAAGGACACCCTGATGATCAGCCGGA
CACCTGAAGTGACCTGCGTGGTGGTGGATGTGTCCACGAGGATCCCGAAGTGAAG
TTCAATTGGTACGTGGACGGCGTGGAAGTGACAACGCCAAGACCAAGCCTAGAGA
GGAACAGTACAACAGCACCTACAGAGTGGTGTCTGTGCTGACAGTGCTGCACCAGG
ACTGGCTGAACGGCAAAGAGTACAAGTGCAAGGTGTCCAACAAGGCCCTGCCTGCT
CCTATCGAGAAAACCATCAGCAAGGCCAAGGGCCAGCCTAGGGAACCCAGGTTTA
CACCTGCCTCCATGCAGGGATGAGCTGACCAAGAACCAGGTGTCCCTGTGGTGCC
TGGTTAAGGGCTTCTACCCCTCCGATATCGCCGTGGAATGGGAGAGCAATGGCCAG
CCAGAGAACAACCTACAAGACAACCCCTCCTGTGCTGGACTCCGACGGCTCATTCTT
CCTGTACAGCAAGCTGACCGTGGACAAGAGCAGATGGCAGCAGGGCAACGTGTTCA
GCTGCAGCGTGATGCACGAGGCCCTGCACAACCACTACACACAGAAGTCCCTGTCT
CTGAGCCCCGGCAAA

(SEQ ID NO: 185), signal sequence (1-57), NYC-0005 (61-825), linker (826-831), constant region (832-1527)

Fig. 187

NYC-0011-HC-k

**MKHLWFFLLLVAAPRWVLSGEVQLVESGGGVVQPGGSLRLSCVASGFTFDDYAMYW
VRQVPGKDLEWVSLISGDGDITYYVDSVKGRFTVSRDNNKNSLYLQMKSLRVEDTA
LYYCAKDMIYYASWSGYGSSDYYYYVMDVWGQGTTVTVSSGGGGSGGGGSGGGGSD
IQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSG
VPSRFSGSGSGTDFTLTISLQPEDFATYYCQQSYSTPPITFGQGTRLEIKGGEPK
SADKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK
FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA
PIEKTISKAKGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQ
PENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFSQVMHEALHNHYTQKSLS
LSPGK**

(SEQ ID NO: 186), signal sequence (1-19), NYC-0005 (21-275), linker (276-277), constant region (278-509)

Fig. 188

NYC-0012-HC-k

ATGAAGCACCTGTGGTTCTTTCTGCTGCTGGTGGCCGCTCCTAGATGGGTGCTGTC
TGGCGAAGTGCAGCTGGTGGGAATCTGGTGGCGGAGTTGTTGAGCCTGGCGGCTCTC
TGAGACTGTCTTGTGCCGCCAGCGGCTTCACCTTCGACGACTACGCCATGTACTGG
GTCCGACAGGCCCCCTGGCAAAGGCCTTGAATGGGTGTCCCTGATCAGCGGAGATGG
CGGCAGCATGTACTACGCCGATAGCGTGAAGGGCAGATTACCATCAGCCGGGACA
ACAGCAAGAACAGCCTGTACCTGCAGATGAACTCCCTGCGGACCGAGGACACAGCC
CTGTACTACTGCGCCAAGGATATGATCTTCTACGCCTTTTGGAGCGGCTACGGCAG
CAGCGATTACTACTACTACGTGATGGACGTGTGGGGCCAGGGCACCACAGTGACAG
TTTATTCTGGCGGCGGAGGATCTGGCGGAGGTGGAAGCGGAGGCGGTGGATCTGAT
ATCCAGATGACACAGAGCCCCAGCAGCCTGTCTGCCTCTGTGGGAGACAGAGTGAC
CATCACCTGTCGGGCCAGCCAGAGAATCAGCACCTACCTGAACTGGTATCAGCAGA
AGCCCGGCAAGGCCCTAAGCTGCTGATCTATGCTGCCTCCAGTCTGCAGAGCGGC
GTGCCAAGCAGATTTTCTGGCAGCGGCTCTGGCACCGACTTCACCCTGACCATATC
TAGCCTGCAGCCTGAGGACTTCGCCACCTACTACTGCCAGCAGAGCTACAGCACCC
CTCCTATCACCTTTGGCCAGGGAACCAGACTGGAAATCAAAGGCGGAGAACCCAAG
AGCgcaGACAAGACCCACACCTGTCCTCCATGTCCTGCTCCAGAAGCTGCAGGCGG
CCCTTCCGTGTTTCTGTTCCCTCCAAAGCCTAAGGACACCCTGATGATCAGCCGGA
CACCTGAAGTGACCTGCGTGGTGGTGGATGTGTCCACGAGGATCCCGAAGTGAAG
TTCAATTGGTACGTGGACGGCGTGGAAGTGACAACGCCAAGACCAAGCCTAGAGA
GGAACAGTACAACAGCACCTACAGAGTGGTGTCTGTGCTGACAGTGCTGCACCAGG
ACTGGCTGAACGGCAAAGAGTACAAGTGCAAGGTGTCCAACAAGGCCCTGCCTGCT
CCTATCGAGAAAACCATCAGCAAGGCCAAGGGCCAGCCTAGGGAACCCAGGTTTA
CACCTGCCTCCATGCAGGGATGAGCTGACCAAGAACCAGGTGTCCCTGTGGTGCC
TGGTTAAGGGCTTCTACCCCTCCGATATCGCCGTGGAATGGGAGAGCAATGGCCAG
CCAGAGAACAACCTACAAGACAACCCCTCCTGTGCTGGACTCCGACGGCTCATTCTT
CCTGTACAGCAAGCTGACCGTGGACAAGAGCAGATGGCAGCAGGGCAACGTGTTCA
GCTGCAGCGTGATGCACGAGGCCCTGCACAACCACTACACACAGAAGTCCCTGTCT
CTGAGCCCCGGCAAA

(SEQ ID NO: 187), signal sequence (1-57), NYC-0006 (61-825), linker (826-831), constant region (832-1527)

Fig. 189

NYC-0012-HC-k

MKHLWFFLLLVAAPRWVLSGEVQLVESGGGVVQPGGSLRLSCAASGFTFDDYAMYW
VRQAPGKGLEWVSLISGDGGSMYYADSVKGRFTISRDNKNSLYLQMNSLRTE
D
T
A
L
Y
Y
C
A
K
D
M
I
F
Y
A
F
W
S
G
Y
G
S
D
Y
Y
Y
Y
V
M
D
V
W
G
Q
G
T
T
V
T
V
Y
S
G
G
G
S
G
G
G
S
G
G
G
S
D
I
Q
M
T
Q
S
P
S
S
L
S
A
S
V
G
D
R
V
T
I
T
C
R
A
S
Q
R
I
S
T
Y
L
N
W
Y
Q
Q
K
P
G
K
A
P
K
L
L
I
Y
A
A
S
S
L
Q
S
G
V
P
S
R
F
S
G
S
G
S
G
T
D
F
T
L
T
I
S
S
L
Q
P
E
D
F
A
T
Y
Y
C
Q
Q
S
Y
S
T
P
P
I
T
F
G
Q
G
T
R
L
E
I
K
G
G
E
P
K
S
A
D
K
T
H
T
C
P
P
C
A
P
E
A
A
G
G
P
S
V
F
L
F
P
P
K
P
K
D
T
L
M
I
S
R
T
P
E
V
T
C
V
V
D
V
S
H
E
D
P
E
V
K
F
N
W
Y
V
D
G
V
E
V
H
N
A
K
T
K
P
R
E
E
Q
Y
N
S
T
Y
R
V
S
V
L
T
V
L
H
Q
D
W
L
N
G
K
E
Y
K
C
K
V
S
N
K
A
L
P
A
P
I
E
K
T
I
S
K
A
K
G
Q
P
R
E
P
Q
V
Y
T
L
P
P
C
R
D
E
L
T
K
N
Q
V
S
L
W
C
L
V
K
G
F
Y
P
S
D
I
A
V
E
W
E
S
N
G
Q
P
E
N
N
Y
K
T
T
P
P
V
L
D
S
D
G
S
F
F
L
Y
S
K
L
T
V
D
K
S
R
W
Q
Q
G
N
V
F
S
C
S
V
M
H
E
A
L
H
N
H
Y
T
Q
K
S
L
S
L
S
P
G
K

(SEQ ID NO: 188), signal sequence (1-19), NYC-0006 (21-275), linker (276-277), constant region (278-509)

Fig. 190

NYC-0013-HC-k

ATGAAGCACCTGTGGTTCTTTCTGCTGCTGGTGGCCGCTCCTAGATGGGTGCTGTC
TGGCGAAGTGCAGCTGGTGAATCTGGTGGCGGAGTTGTTACGCCTGGCGGCTCTC
TGAGACTGTCTTGTGCCGCCAGCGGCTTCACCTTCGACGATTATGCCATGCACTGG
GTCCGACAGGCCCCCTGGCAAAGGACTTGAATGGGTGTCCCTGATCAGCGGCGACGG
CGACAATACCTACTACGCCGATAGCGTGAAGGGCAGATTACCATCAGCCGGGACA
ACAACAAGAACAGCCTGTACCTGCAGATGAACTCCCTGCGGACCGAGGACACCGCC
TTCTACTACTGTGCCAAAGAGCTGATCTTCGGCAAGGTGCTGCACGACTTTTACTA
CTACGTGATGGACGTGTGGGGCCAGGGCACCACAGTGACAGTTTCTAGCGGAGGCG
GAGGAAGTGGCGGCGGAGGATCTGGCGGTGGTGGTTCTGATATCCAGATGACACAG
AGCCCCAGCAGCCTGTCTGCCTCTGTGGGAGACAGAGTGACCATCACCTGTAGAGC
CAGCCAGAGCATCAGCAGCTACCTGAACTGGTATCAGCAGAAGCCCGGCAAGGCC
CTAAACTGCTGATCTATGCCGCCTCCAGTCTGCAGAGCGGAGTGCCTAGCAGATTT
TCTGGCAGCGGCTCCGGCACCGATTTACCCCTGACCATATCTAGCCTGCAGCCTGA
GGACTTCGCCACCTACTACTGCCAGCAGAGCTACAGCACCCCTCCTATCACCTTTG
GCCAGGGAACCAGACTGGAAATCAAAGGCGGAGAACCCAAGAGCgcaGACAAGACC
CACACCTGTCCTCCATGTCCTGCTCCAGAAGCTGCAGGCGGCCCTTCCGTGTTTCT
GTTCCCTCCAAAGCCTAAGGACACCCTGATGATCAGCCGGACACCTGAAGTGACCT
GCGTGGTGGTGGATGTGTCCCACGAGGATCCCGAAGTGAAGTTCAATTGGTACGTG
GACGGCGTGGAAGTGCAACGCCAAGACCAAGCCTAGAGAGGAACAGTACAACAG
CACCTACAGAGTGGTGTCTGTGCTGACAGTGCTGCACCAGGACTGGCTGAACGGCA
AAGAGTACAAGTGCAAGGTGTCCAACAAGGCCCTGCCTGCTCCTATCGAGAAAACC
ATCAGCAAGGCCAAGGGCCAGCCTAGGGAACCCCAGGTTTACACCCTGCCTCCATG
CAGGGATGAGCTGACCAAGAACCAGGTGTCCCTGTGGTGCCTGGTTAAGGGCTTCT
ACCCCTCCGATATCGCCGTGGAATGGGAGAGCAATGGCCAGCCAGAGAACAACCTAC
AAGACAACCCCTCCTGTGCTGGACTCCGACGGCTCATTCTTCTGTACAGCAAGCT
GACCGTGGACAAGAGCAGATGGCAGCAGGGCAACGTGTTTCAGCTGCAGCGTGATGC
ACGAGGCCCTGCACAACCACTACACACAGAAGTCCCTGTCTCTGAGCCCCGGCAAA
(SEQ ID NO: 189), signal sequence (1-57), NYC-0007 (61-
810), linker (811-816), constant region (817-1512)

Fig. 191

NYC-0013-HC-k

**MKHLWFFLLLVAAPRWVLSGEVQLVESGGGVVQPGGSLRLSCAASGFTFDDYAMHW
VRQAPGKGLEWVSLISGDGDNITYYADSVKGRFTISRDNKNSLYLQMNSLRTE
DYA
FYCAKELIFGKVLHDFYYYVMDVWGQGTITVTVSSGGGGSGGGGSGGGGSDIQMTQ
SPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRF
SGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPPITFGQGTRLEIKGGEPKSADKT
HTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV
DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
ISKAKGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNY
KTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
(SEQ ID NO: 190), signal sequence (1-19), NYC-0007 (21-
270), linker (271-272), constant region (273-504)**

Fig. 192

NYC-0014-HC-k

ATGAAGCACCTGTGGTTCTTTCTGCTGCTGGTGGCCGCTCCTAGATGGGTGCTGTC
TGGCGAAGTGCAGCTGGTGAATCTGGTGGCGGAGTTGTTGAGCCTGGCGGCTCTC
TGAGACTGAGCTGTGAAGCCTCCGGCTTCATCTTCGACGACTACGCCATGCACTGG
GTCCGACAGGCACCTGGCAAAGGCCTTGAATGGGTGTCCCTGATCTCTGGCGACGG
CGACATCATCTACTACGCCGACTCTGTGAAGGGCAGATTACCATCAGCCGGGACA
ACAGCAAGAACAGCCTGTACCTGCAGATGAACTCCCTGATCATCGAGGACACAGCC
CTGTACTACTGCGCCAAGGATTGGGTGTTGCGCGTCGTGATGACCCACTACTGGTA
CTTCGGCCTGGATGTGTGGGGCCAGGGAACCACAGTGACAGTTTCTAGCGGAGGCG
GAGGAAGTGGCGGCGGAGGATCTGGCGGTGGTGGTTCTGATATCCAGATGACACAG
AGCCCCAGCAGCCTGTCTGCCTCTGAAGGCGACAGAGTGACCATCACCTGTAGAGC
CAGCCAGAGCATCAGCACCTACCTGAACTGGTATCAGCAGAAGCCCGGCAAGGCC
CTAAGCTGCTGATCTATGGTGCCTCCAGTCTGCAGAGCGGCGTGCCAAGCAGATTT
TCTGGCAGCGGCTCTGGCACCGACTTCACCCTGACCATATCTAGCCTGCAGCCTGA
GGACTTCGCCACCTACTACTGCCAGCAGTCTACAGCACCCCTCCTATCACATTTG
GCCAGGGCACCAAGGTGGAAATCAAAGGCGGAGAACCCAAGAGCgcaGACAAGACC
CACACCTGTCCTCCATGTCCTGCTCCAGAAGCTGCAGGCGGCCCTTCCGTGTTTCT
GTTCCCTCCAAAGCCTAAGGACACCCTGATGATCAGCCGGACACCTGAAGTGACCT
GCGTGGTGGTGGATGTGTCCCACGAGGATCCCGAAGTGAAGTTCAATTGGTACGTG
GACGGCGTGGAAGTGCACAACGCCAAGACCAAGCCTAGAGAGGAACAGTACAACAG
CACCTACAGAGTGGTGTCTGTGCTGACAGTGCTGCACCAGGACTGGCTGAACGGCA
AAGAGTACAAGTGCAAGGTGTCCAACAAGGCCCTGCCTGCTCCTATCGAGAAAACC
ATCAGCAAGGCCAAGGGCCAGCCTAGGGAACCCCAGGTTTACACCCTGCCTCCATG
CAGGGATGAGCTGACCAAGAACCAGGTGTCCCTGTGGTGCCTGGTTAAGGGCTTCT
ACCCCTCCGATATCGCCGTGGAATGGGAGAGCAATGGCCAGCCAGAGAACAACCTAC
AAGACAACCCCTCCTGTGCTGGACTCCGACGGCTCATTCTTCTGTACAGCAAGCT
GACCGTGGACAAGAGCAGATGGCAGCAGGGCAACGTGTTTCAGCTGCAGCGTGATGC
ACGAGGCCCTGCACAACCACTACACACAGAAGTCCCTGTCTCTGAGCCCCGGCAAA
(SEQ ID NO: 191), signal sequence (1-57), NYC-0008 (61-
810), linker (811-816), constant region (817-1512)

Fig. 193

NYC-0014-HC-k

MKHLWFFLLLVAAPRWVLSGEVQLVESGGGVVQPGGSLRLSCEASGFIFDDYAMHW
VRQAPGKGLEWVSLISGDGDIIYYADSVKGRFTISRDNKNSLYLQMNSLIIEDTA
LYYCAKDWVFGVVMTHYWYFGLDVWGQGTTVTVSSGGGGSGGGGSGGGGSDIQMTQ
SPSSLSASEGDRVTITCRASQSISTYLNWYQQKPGKAPKLLIYGASSLQSGVPSRF
SGSGSGTDFTLTISLQPEDFATYYCQQSYSTPPITFGQGTKVEIKGGEPKSADKT
HTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV
DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
ISKAKGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNY
KTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVVFSCSVMHEALHNHYTQKSLSLSPGK
(SEQ ID NO: 192), signal sequence (1-19), NYC-0008 (21-
270), linker (271-272), constant region (273-504)

Fig. 194

NYC-0015-HC-k

ATGAAGCACCTGTGGTTCTTTCTGCTGCTGGTGGCCGCTCCTAGATGGGTGCTGTC
TGGCGAAGTGCAGCTGGTGGAATCTGGTGGCGGAGTTGTTCAGCCTGGCGGCTCTC
TGAGACTGTCTTGTGCCGCCAGCGGCTTCACCTTCGACGATTATGCCATGCACTGG
GTCCGACAGGCCCCCTGGCAAAGGACTTGAATGGGTGTCCCTGATCTCTGGCGGAGG
CGGCGGAACCTACTACAGCGATTCTGTGAAGGGCAGATTACCATCAGCCGGGACA
CCAGCAAGGACAGCCTGTACCTGCAGATGAACAGCCTGCGGACCGAGGACACAGCC
CTGTACTACTGCGCCAAGGACATGGTGTTCGGCGTGGTCACCCCTTACTACTACTT
CGCCCTGGATGTGTGGGGCCAGGGCACAAACAGTGACAGTCTCTTCTGGCGGCGGAG
GAAGCGGAGGCGGAGGATCCGGTGGTGGTGGATCTGACATCCAGATGACACAGAGC
CCCAGCAGCCTGTCTGCCTCTGTGGGAGACAGAGTGACCATCACCTGTAGAGCCAG
CCAGAGCATCAACAGCTACCTGAACTGGTATCAGCAGAAGCCCGGCAAGGCCCTA
AGCTGCTGATCTATGCTGCCTCCAGTCTGCAGAGCGGCGTGCCAAGCAGATTTTCT
GGCAGCGGCTCTGGCACCGACTTCACCCTGACCATATCTAGCCTGCAGCCTGAGGA
CTTCGCCACCTACTACTGCCAGCAGAGCTACAGCGCCCCTCCTATCACATTTGGCC
AGGGAACCAGACTGGAAATCAAAGGCGGAGAACCCAAGAGCgcaGACAAGACCCAC
ACCTGTCTCTCCATGTCCTGCTCCAGAAGCTGCAGGCGGCCCTTCCGTGTTTCTGTT
CCCTCCAAAGCCTAAGGACACCCTGATGATCAGCCGGACACCTGAAGTGACCTGCG
TGGTGGTGGATGTGTCCACGAGGATCCCGAAGTGAAGTTCAATTGGTACGTGGAC
GGCGTGGAAGTGACAACGCCAAGACCAAGCCTAGAGAGGAACAGTACAACAGCAC
CTACAGAGTGGTGTCTGTGCTGACAGTGCTGCACCAGGACTGGCTGAACGGCAAAG
AGTACAAGTGCAAGGTGTCCAACAAGGCCCTGCCTGCTCCTATCGAGAAAACCATC
AGCAAGGCCAAGGGCCAGCCTAGGGAACCCAGGTTTACACCCTGCCTCCATGCAG
GGATGAGCTGACCAAGAACCAGGTGTCCCTGTGGTGCCTGGTTAAGGGCTTCTACC
CCTCCGATATCGCCGTGGAATGGGAGAGCAATGGCCAGCCAGAGAACAACCTACAAG
ACAACCCCTCCTGTGCTGGACTCCGACGGCTCATTCTTCTGTACAGCAAGCTGAC
CGTGGACAAGAGCAGATGGCAGCAGGGCAACGTGTTTCAGCTGCAGCGTGATGCACG
AGGCCCTGCACAACCACTACACACAGAAGTCCCTGTCTCTGAGCCCCGGCAAA
(SEQ ID NO: 193), signal sequence (1-57), NYC-0009 (61-
807), linker (808-813), constant region (814-1509)

Fig. 195

NYC-0015-HC-k

MKHLWFFLLLVAAPRWVLSGEVQLVESGGGVVQPGGSLRLSCAASGFTFDDYAMHW
VRQAPGKGLEWVSLISGGGGGTYYSDSVKGRFTISRDTSKDSLYLQMNSLRTE
D
TALYYCAKDMVFGVVTPYFFALDVWGQGTITVTVSSGGGGSGGGGSGGGGSDIQMTQS
PSSLSASVGDRVTITCRASQSINSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFS
GSGSGTDFTLTISSLQPEDFATYYCQQSYSAAPPITFGQGTRLEIKGGEPKSA
DKTH
TCTPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD
GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI
SKAKGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYK
TTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
(SEQ ID NO: 194), signal sequence (1-19), NYC-0009 (21-269), linker (270-271), constant region (272-503)

Fig. 196

NYC-0016-HC-k

ATGAAGCACCTGTGGTTCTTTCTGCTGCTGGTGGCCGCTCCTAGATGGGTGCTGTC
TGGCGAAGTGCAGCTGGTGAATCTGGTGGCGGAGTTGTTACGCCTGGCGGCTCTC
TGAGACTGAGCTGTGCTGTGTCCGGCTTCACCTTCGACGACTACGCCATGCACTGG
GTCCGACAGGCACCTGGCAAAGGCCTTGAATGGGTGTCCCTGATCAGCGGAGATGG
CGGCAGCACACACTACGCCGATTCTGTGAAGGGCAGATTACCATCAGCCGGGACA
ACAGCAAGAACAGCCTGTACCTGCAGATGAACTCCCTGCGGACAGGCGACACAGCC
CTGTACTACTGCGCCAAGGACATGATCTTCGCCGTGGTCATCACCGACTACCACTA
CTACGGCATGGACGTGTGGGGCCAGGGAACCACAGTGACAGTTTCTAGCGGAGGCG
GAGGAAGTGGCGGCGGAGGATCTGGCGGTGGTGGTTCTGATATCCAGATGACACAG
AGCCCCAGCAGCCTGTCTGCCTCTGTGGGAGACAGAGTGACCATCACCTGTAGAGC
CAGCCAGAGCATCAGCAGCTACCTGAACTGGTATCAGCAGAAGCCCGGCAAGGCC
CTAAACTGCTGATCTATGCCGCCTCCAGTCTGCAGAGCGGAGTGCCTAGCAGATTT
TCTGGCAGCGGCTCCGGCACCGATTTACCCCTGACCATATCTAGCCTGCAGCCTGA
GGACTTCGCCACCTACTACTGCCAGCAGAGCTACAGCACCCCTCCTATCACCTTTG
GCCAGGGCACCAAGACTGGAAATCAAAGGCGGAGAACCCAAGAGCgcaGACAAGACC
CACACCTGTCCTCCATGTCCTGCTCCAGAAGCTGCAGGCGGCCCTTCCGTGTTTCT
GTTCCCTCCAAAGCCTAAGGACACCCTGATGATCAGCCGGACACCTGAAGTGACCT
GCGTGGTGGTGGATGTGTCCACGAGGATCCCGAAGTGAAGTTCAATTGGTACGTG
GACGGCGTGGAAGTGCACAACGCCAAGACCAAGCCTAGAGAGGAACAGTACAACAG
CACCTACAGAGTGGTGTCTGTGCTGACAGTGCTGCACCAGGACTGGCTGAACGGCA
AAGAGTACAAGTGCAAGGTGTCCAACAAGGCCCTGCCTGCTCCTATCGAGAAAACC
ATCAGCAAGGCCAAGGGCCAGCCTAGGGAACCCCAGGTTTACACCCTGCCTCCATG
CAGGGATGAGCTGACCAAGAACCAGGTGTCCCTGTGGTGCCTGGTTAAGGGCTTCT
ACCCCTCCGATATCGCCGTGGAATGGGAGAGCAATGGCCAGCCAGAGAACAACCTAC
AAGACAACCCCTCCTGTGCTGGACTCCGACGGCTCATTCTTCTGTACAGCAAGCT
GACCGTGGACAAGAGCAGATGGCAGCAGGGCAACGTGTTTCAGCTGCAGCGTGATGC
ACGAGGCCCTGCACAACCACTACACACAGAAGTCCCTGTCTCTGAGCCCCGGCAAA
(SEQ ID NO: 195), signal sequence (1-57), NYC-0010 (61-
810), linker (811-816), constant region (817-1512)

Fig. 197

NYC-0016-HC-k

**MKHLWFFLLLVAAPRWVLSGEVQLVESGGGVVQPGGSLRLSCAVSGFTFDDYAMHW
VRQAPGKGLEWVSLISGDGGSTHYADSVKGRFTISRDNKNSLYLQMNSLRTGDTA
LYYCAKDMIFAVVITDYHYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSDIQMTQ
SPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRF
SGSGSGTDFTLTISLQPEDFATYYCQQSYSTPPITFGQGTRLEIKGGEPKSADKT
HTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV
DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
ISKAKGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNY
KTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVVFSCSVMHEALHNHYTQKSLSLSPGK
(SEQ ID NO: 196), signal sequence (1-19), NYC-0010 (21-
270), linker (271-272), constant region (273-504)**

Fig. 198

NYZ - 1007 - HC2

**MKHLWFFLLLVAAPRWVLSGEVQLVESGGGLVQPGGSLRLSCAASGFSIRSYDIHW
VRQAPGKGLEWVATISYDGSQKYYADSVKGRFTISRDESKNTLYLQMNSLRAEDTA
VYHCARGSSGHYEAFDIWGGQTLTVTVSSGGGGSGGGGSGGGGSQSVLTQPPSASGT
PGQRTVISCSSSSNIGNWYVSWYQQLPGTAPKLLIYDNNKRPSGVPDRFSGSKSG
TSASLAISGLQSEDEADYYCGTWDSSLSAPWVFGGGTKLTVLGGGGSEVQLVESGG
GLVQPGGSLRLSCAASGVTFNYYGMSWIRQAPGKGLEWVASITRSGGRIYYPDVSK
GRFTISRENTQKTLYLQMNSLRAEDTAVYYCTLDGRDGVVAYWGQGTLLTVTVSSAST
KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS
SGLYSLSVTVPSSSLGTQTYICNVNHKPSNTKVDKRVKPKSCDKTHTCPPCPAP
EAAGGPSVFLFPPKPKDTLMISRTPEVTCVTVSVSHEDPEVKFNWYVDGVEVHNAK
TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR
EPQVYVYPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSD
DGSFALVSKLTVDKSRWQQGNVFSVMHEALHNHYTQKSLSLSPGK**

(SEQ ID NO: 197), signal sequence (1-19), NYA-2061 (21-266), linker (267-271), C3E-7085-VH (272-389), CH1 (390-487), hinge (488-502), CH2 (503-612), CH3 (613-719)

Fig. 199

NYZ - 1017 - HC2

**MKHLWFFLLLVAAPRWVLSGQVQLVESGGGVVQPGRSLRLSCAASGFSIRSYDMHW
VRQAPGKGLEWVATISYDGSQKYYADSVKGRFTISRDN SKNTLYLQMSSLRAEDTA
VYHCARGSSGHYEAFDIWGQGT LVTVSSGGGGSGGGGSGGGGSQSVLTQPPSVSAA
PGQKVTISCSGSSSNIGNWYVSWYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSG
TSATLGITGLQTGDEADYYCGTWDSSLSAPWVFGGGTKVTVLGGGGSEVQLVESGG
GLVQPGGSLRLSCAASGVTFNYYGMSWIRQAPGKGLEWVASITRSGGRIYYPD SVK
GRFTISRENTQKTLYLQMNSLRAEDTAVYYCTLDGRDGVVAYWGQGT LVTVSSAST
KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS
SGLYSLSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAP
EAAGGPSVFLFPPKPKDTLMISRTPEVTCVTVSVSHEDPEVKFNWYVDGVEVHNAK
TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR
EPQVYVYPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDS
DGSFALVSKLTVDKSRWQQGNV FSCSVMHEALHNHYTQKSLSLSPGK**

(SEQ ID NO: 198), signal sequence (1-19), NYA-2047 (21-266), linker (267-271), C3E-7085-VH (272-389) , CH1 (390-487), hinge (488-502), CH2 (503-612), CH3 (613-719)