

[Fig. 1]

[illegible]

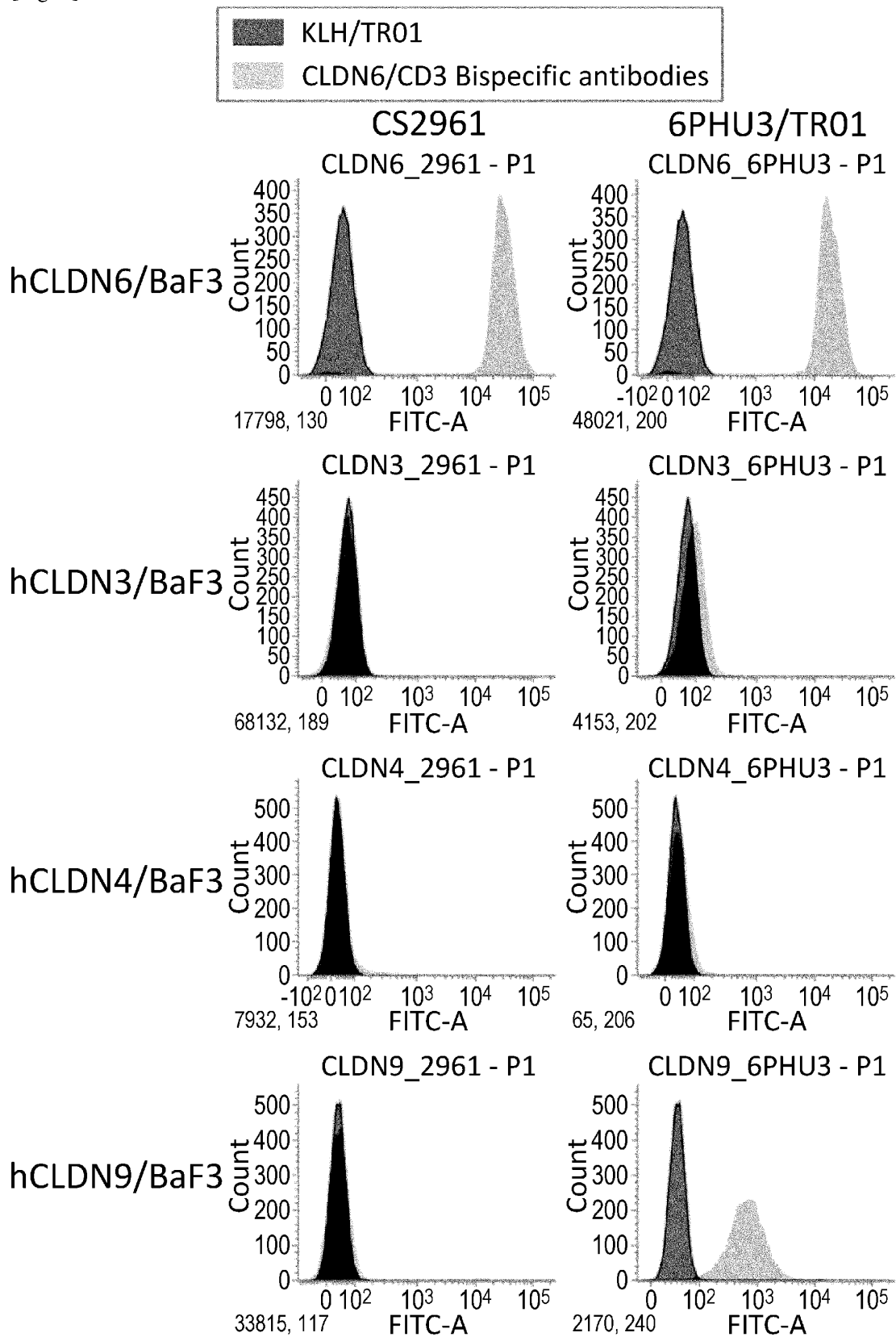
Figure 2 Structural analysis of the CD137-CD137L interaction. The top panel shows the CD137-CD137L complex in a front view, with the heavy chain (thick) and light chain (thin) of CD137L. The CD137 molecule is shown as a thick ribbon. The CD137L molecule is shown as a thin ribbon. The CD137L heavy chain is labeled with H_CDR1, H_CDR2, and H_CDR3. The CD137L light chain is labeled with L_CDR1, L_CDR2, and L_CDR3. The CD137 molecule is labeled with CD137. The bottom panel shows the same complex rotated 180 degrees, with the heavy chain (thick) and light chain (thin) of CD137L. The CD137 molecule is shown as a thick ribbon. The CD137L molecule is shown as a thin ribbon. The CD137L heavy chain is labeled with H_CDR1, H_CDR2, and H_CDR3. The CD137L light chain is labeled with L_CDR1, L_CDR2, and L_CDR3. The CD137 molecule is labeled with CD137. A 180-degree rotation arrow is shown between the two panels.

(a) Tri-specific Ab (1+1)Ig FAST-Ig structure. The diagram shows a Y-shaped antibody molecule composed of four chains: Chain 1, Chain 2, Chain 3, and Chain 4. Chain 1 and Chain 2 form the Fc region, while Chain 3 and Chain 4 form the FvB region. The Fc region is labeled 'Fc region' and the FvB region is labeled 'FvB'. The structure is also labeled 'Tri-specific Ab (1+1)Ig FAST-Ig'.

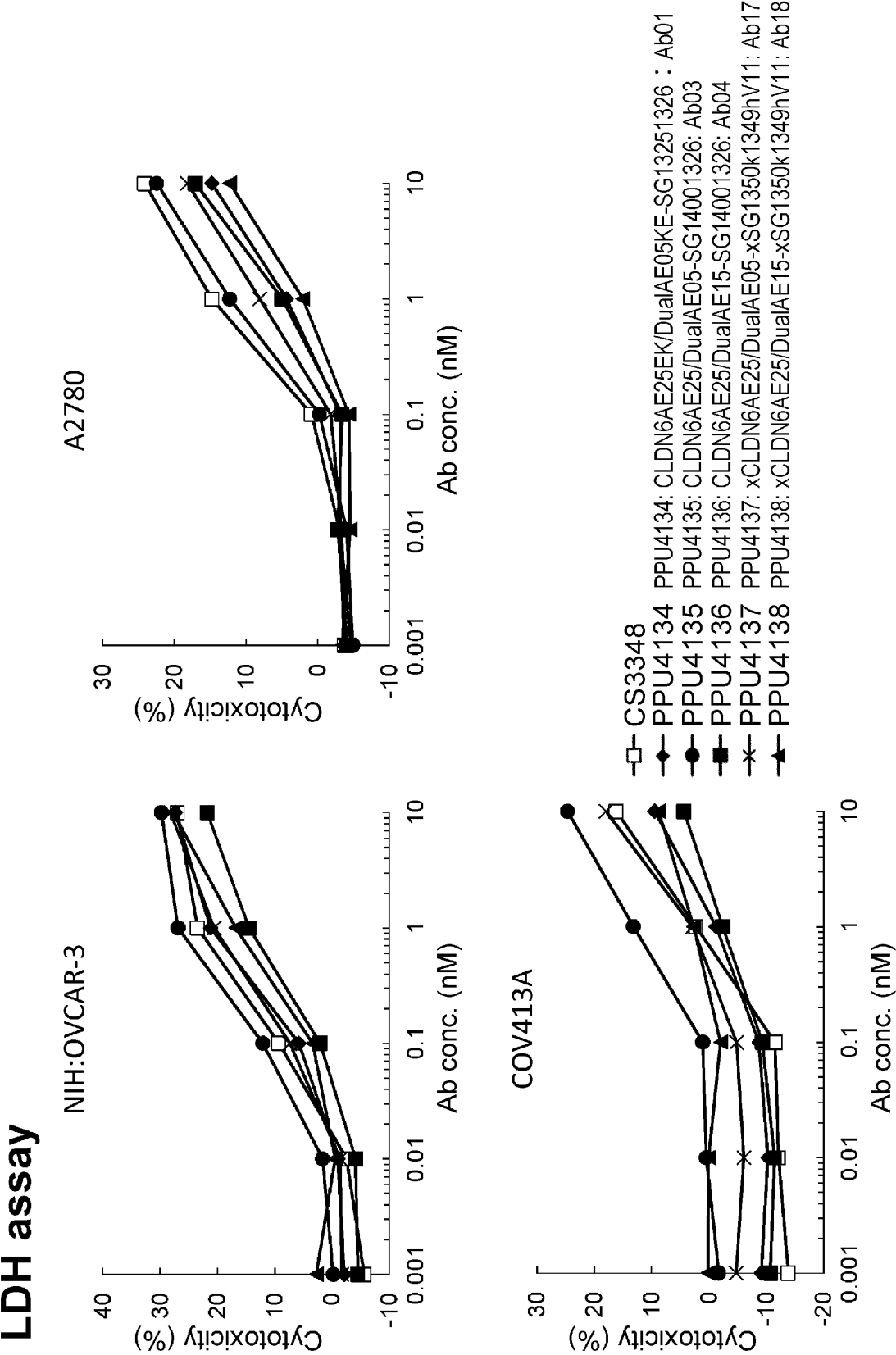
(b) Tri-specific Ab (1+1) CrossMab structure. The diagram shows a Y-shaped antibody molecule composed of four chains: Chain 1, Chain 2, Chain 3, and Chain 4. Chain 1 and Chain 2 form the Fc region, while Chain 3 and Chain 4 form the FvB region. The Fc region is labeled 'Fc region' and the FvB region is labeled 'FvB'. The structure is also labeled 'Tri-specific Ab (1+1) CrossMab'.

Variable heavy chain domain (VH)
Variable light chain domain (VL)
Constant heavy chain domain 1 (CH1)
Constant light chain domain (CL)

[Fig. 4]



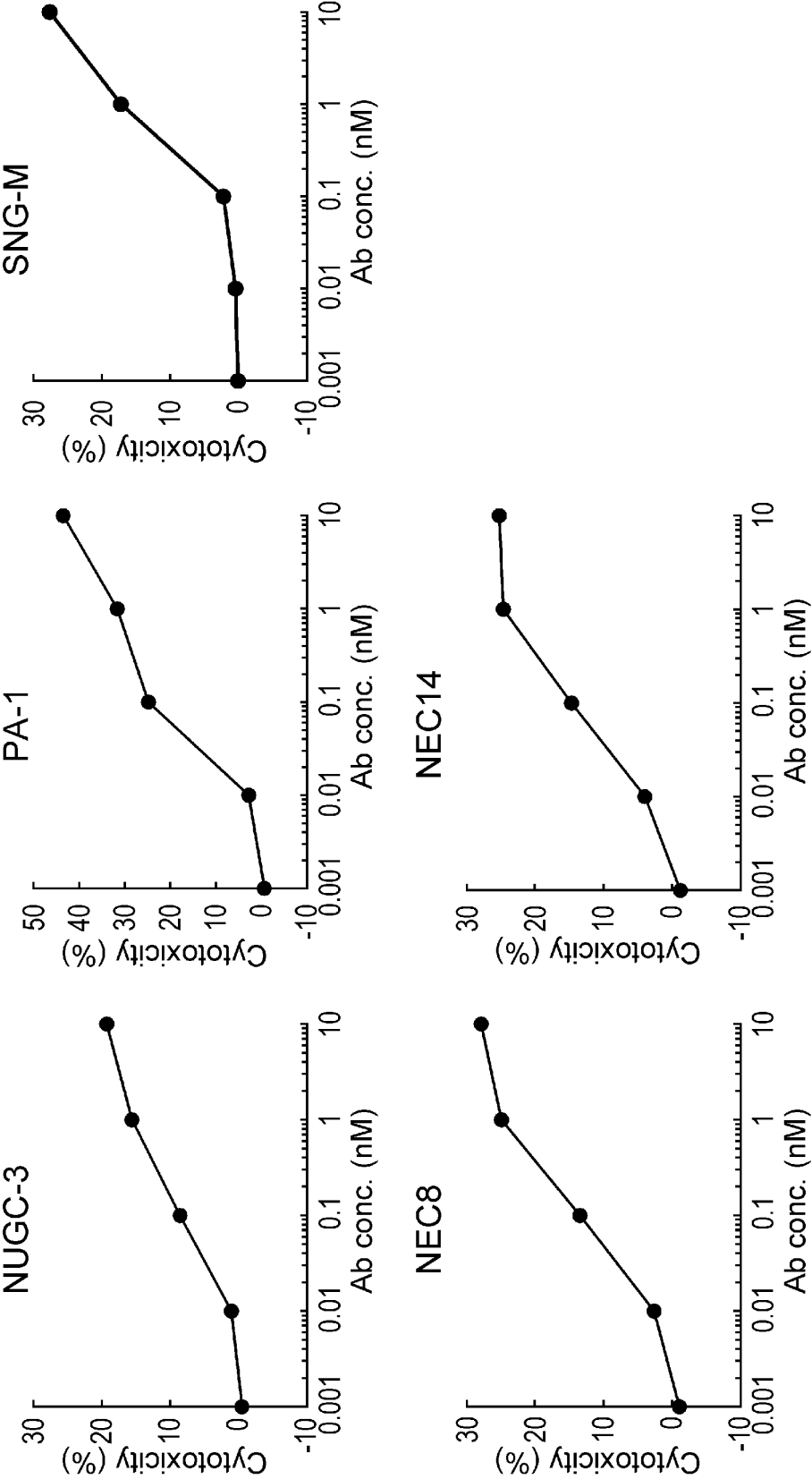
[Fig. 5]



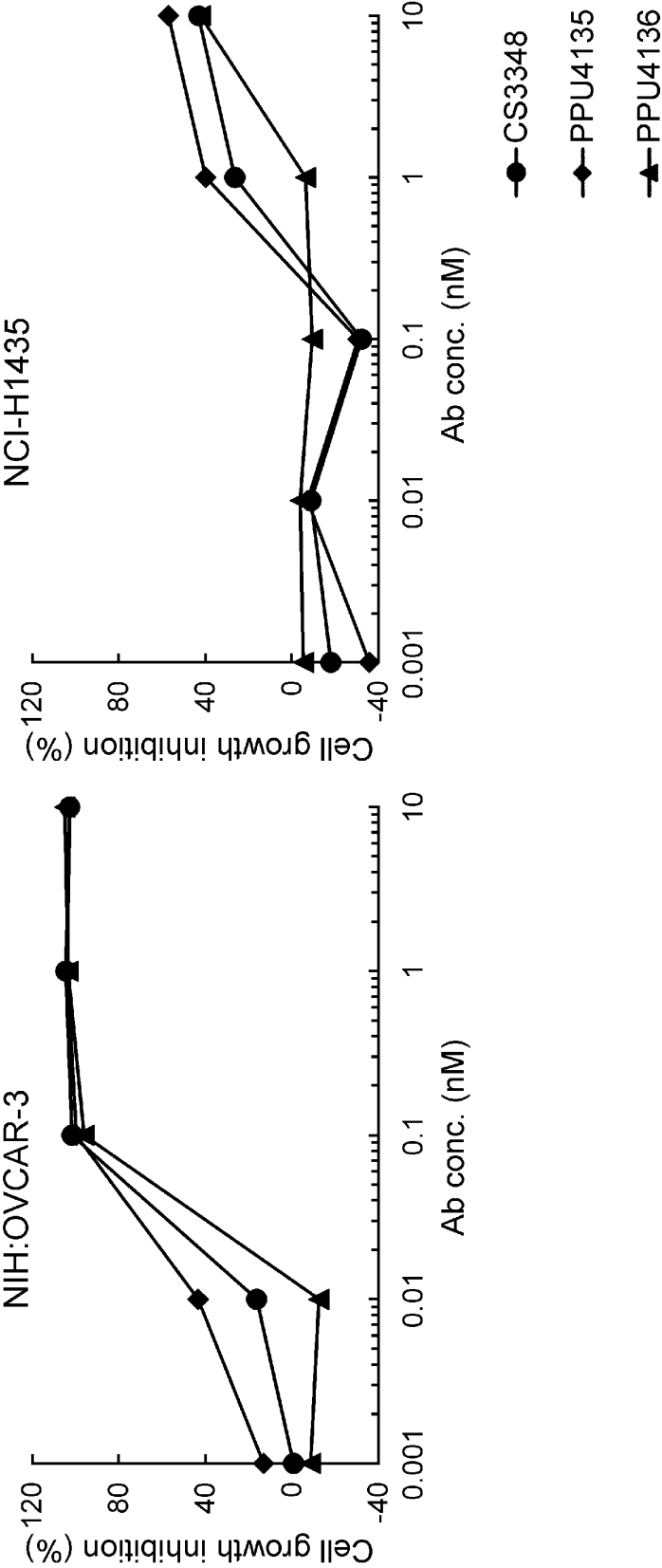
[Fig. 6]

	Extracellular domain 1		Extracellular domain 2	
hCLDN6	1	MASAGMQLGAVLTLLGWNVGLVSCALPMKVKTAFIGNSIVVAQVVWEGLMWSCVVQSTGQMCKVYDSLLALPQDLQAARALCVTALLV	90	
hCLDN9	1	MASITGLEILGMTLAVLGNLGTLVSCALPMKVKTAFIGNSIVVAQVVWEGLMWSCVVQSTGQMCKVYDSLLALPQDLQAARALCVTALLL	90	
hCLDN6	91	ALFGLLVYLAGAKCTTCVEFEKDSKARLVLTSGIVFVISGMLTLPVPCWTAAHAIIRDFYNPLVAEATKRELGASLYLGWAAASGLILGGGGL	180	
hCLDN9	91	ALLGLLVAIIGAQCCTTCVEDEGAKARLVLTNGVLLLSGLTLPVPCWTAAHAIIRDFYNPLVAEATKRELGASLYLGWAAATALLMLGGGL	180	
hCLDN6	181	LCCTCPGSGSQGPSPHYMARYSTAPAISSRGSPSEYPTKNYV*	221	
hCLDN9	181	LCCTCPSPSHFERPRGPRLGYSIPSRSGASGLDKRDYV*	218	

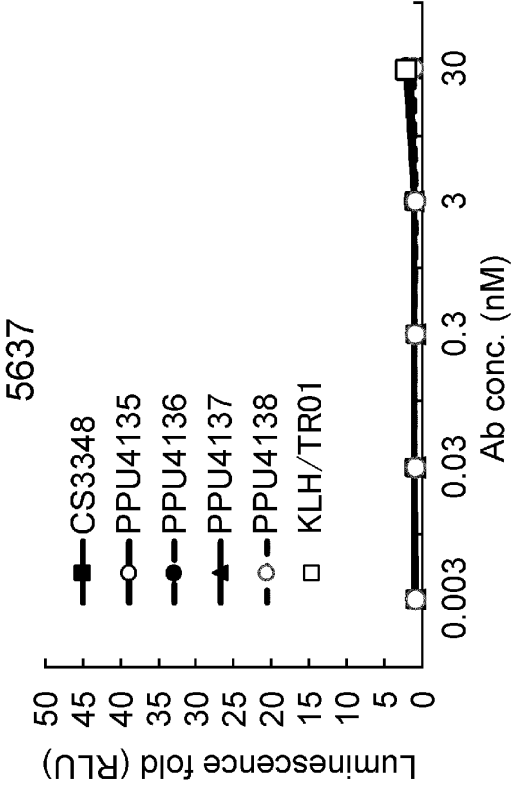
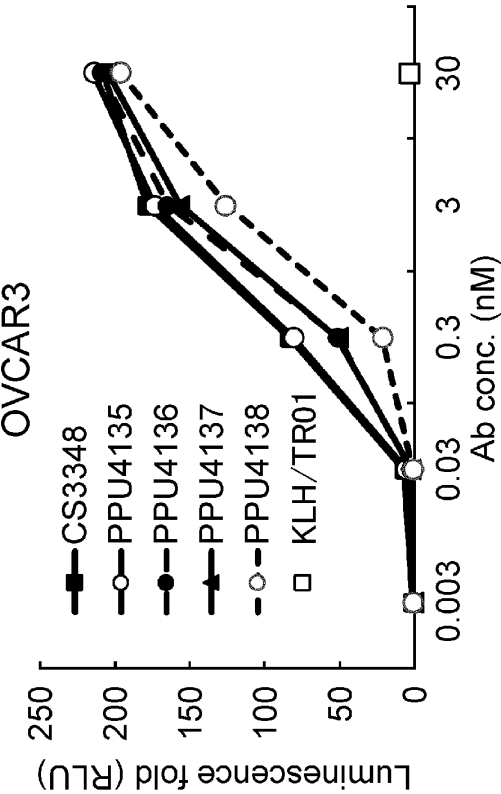
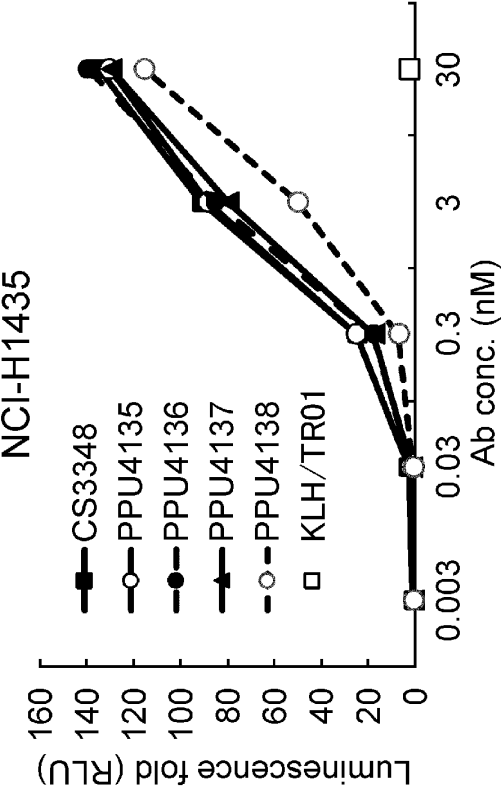
[Fig. 7]



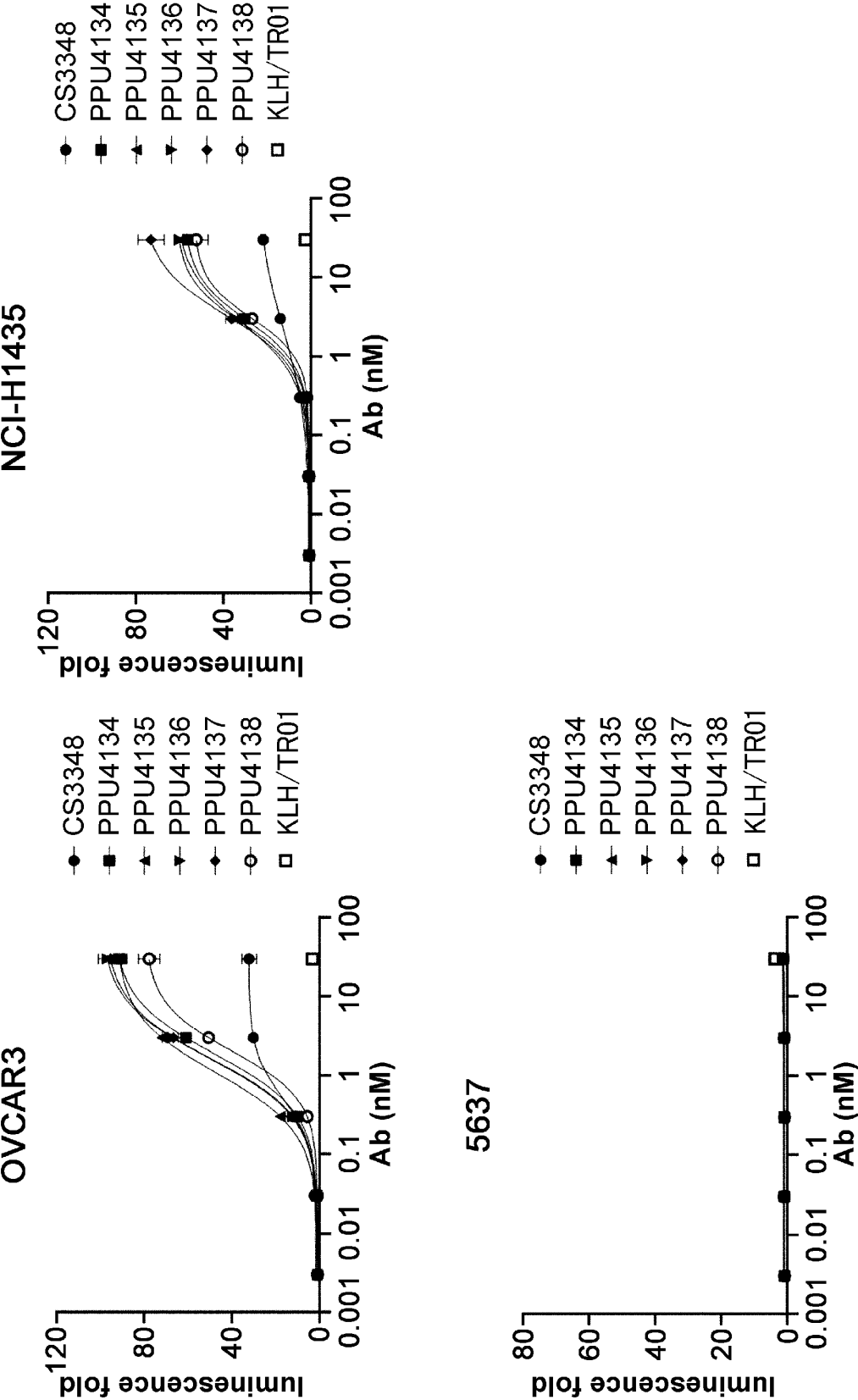
[Fig. 8]



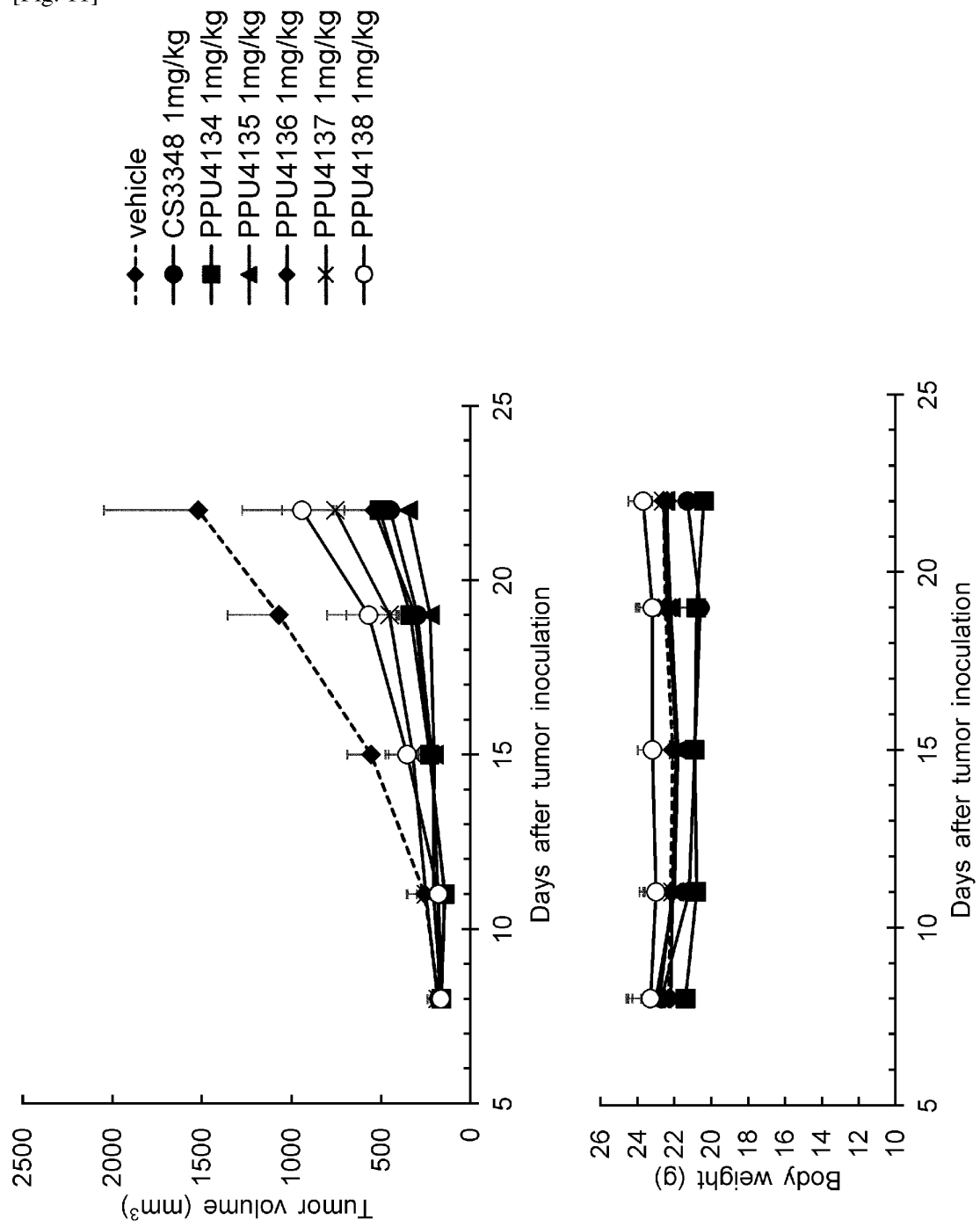
[Fig. 9]



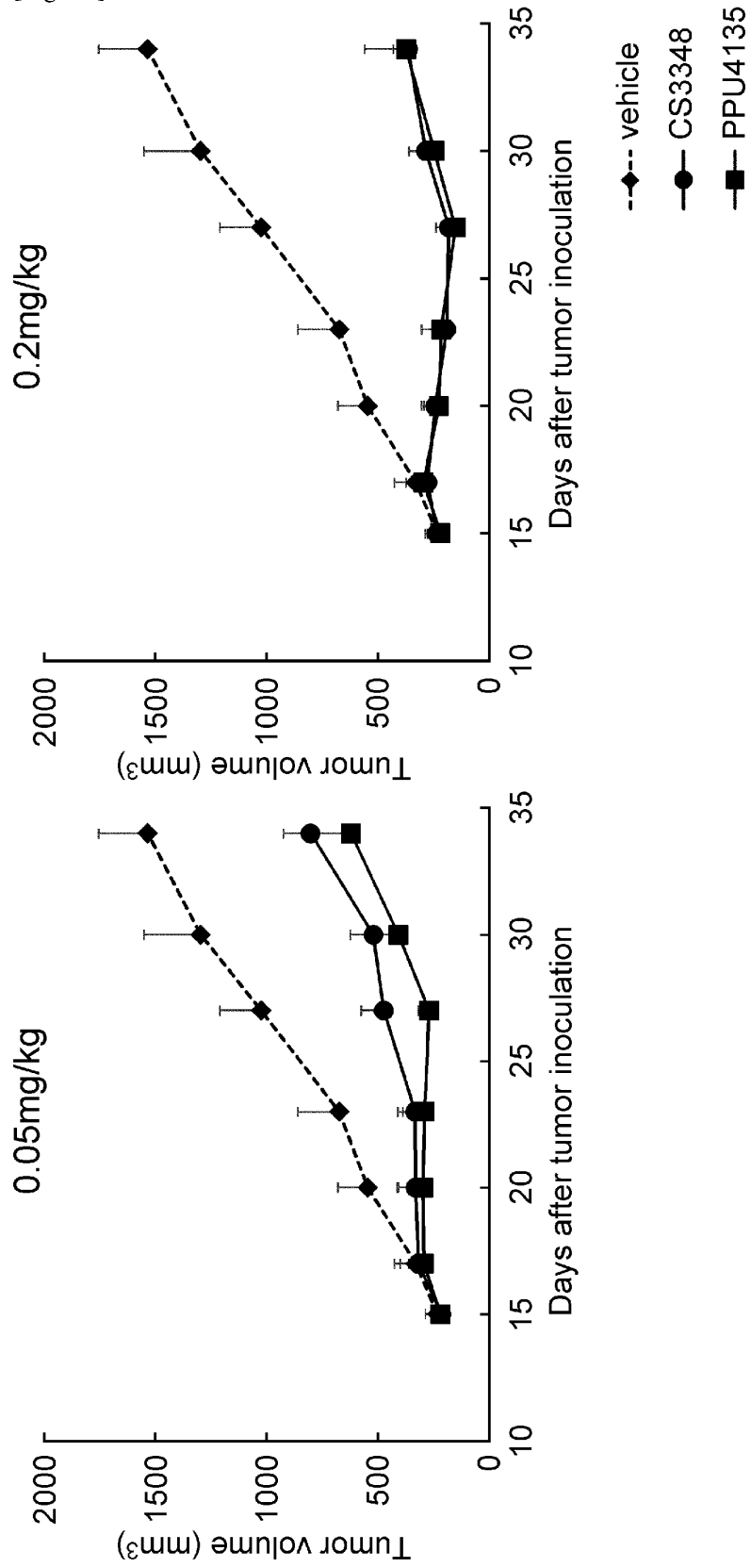
[Fig. 10]



[Fig. 11]



[Fig. 12]



[Fig. 13]

