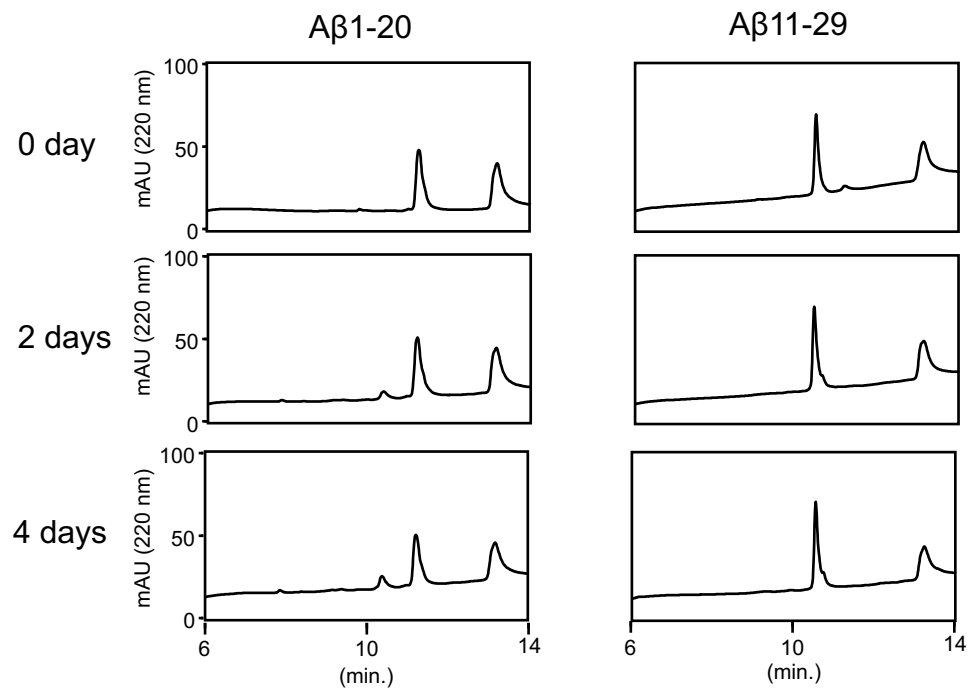


BOX A		
Tob 1	HWYPEKPYK GSGFRC IHI	GSGFR
Tob 2	HWYPEKPLK GSGFRC VHI	GSGFR
BTG 1	HWFPEK PCKGSGYRC IRI	GSGYR
BTG 2	HWFPEK PSKGSGYRC IRI	GSGYR
BTG 3	HWYPEK PSKGQAYRC IRV	GQAYR
BTG 4	HWHSDC PSKGQAFRC IRI	GQAFR

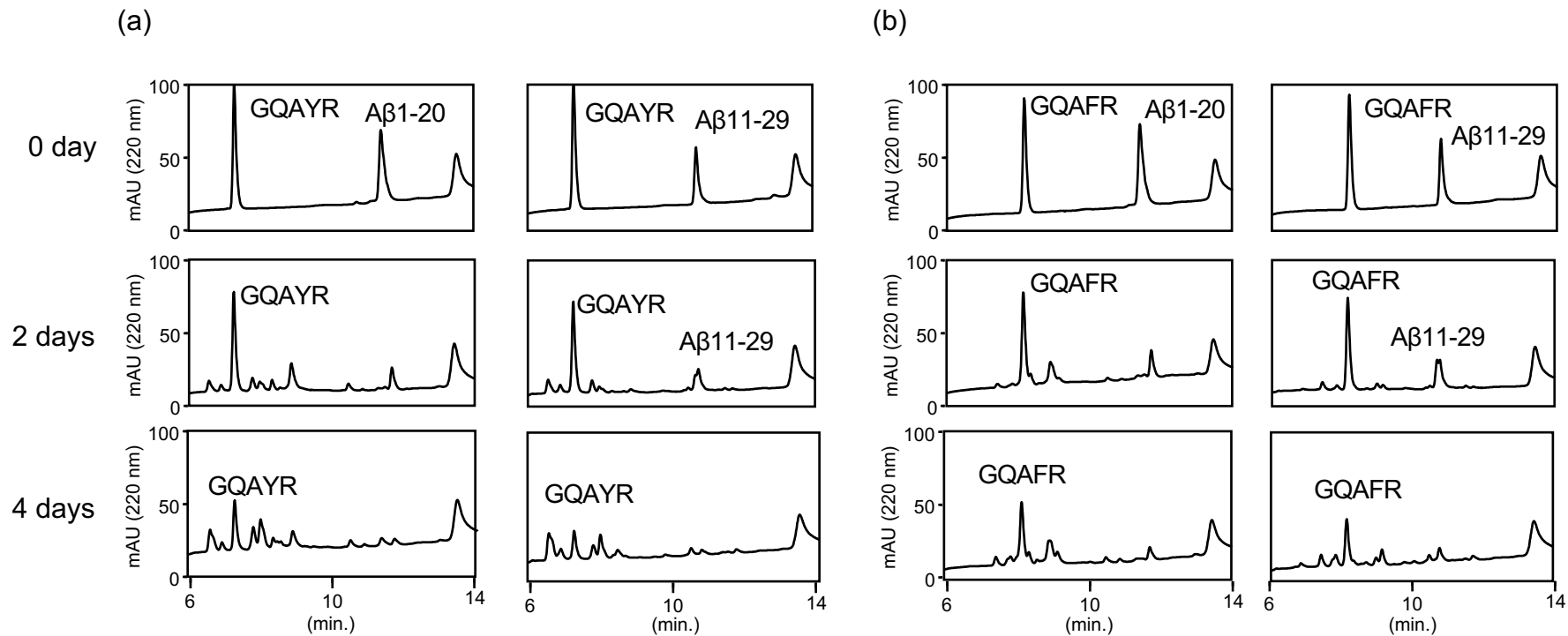
SFig. 1 Amino acid sequences of the Box A region of Tob/BTG family proteins. The red square describes the position of 5-mer peptides.

Origin	Sequence	Detected ion m/z	Experimental Mass	Theoretical Mass
Tob1, Tob2	GSGFR	[M + 1H] ¹⁺	522.11	522.6
BTG1, BTG2	GSGYR	[M + 1H] ¹⁺	539.12	538.6
BTG3	GQAYR	[M + 1H] ¹⁺	593.16	593.6
BTG4	GQAFR	[M + 1H] ¹⁺	577.19	577.6

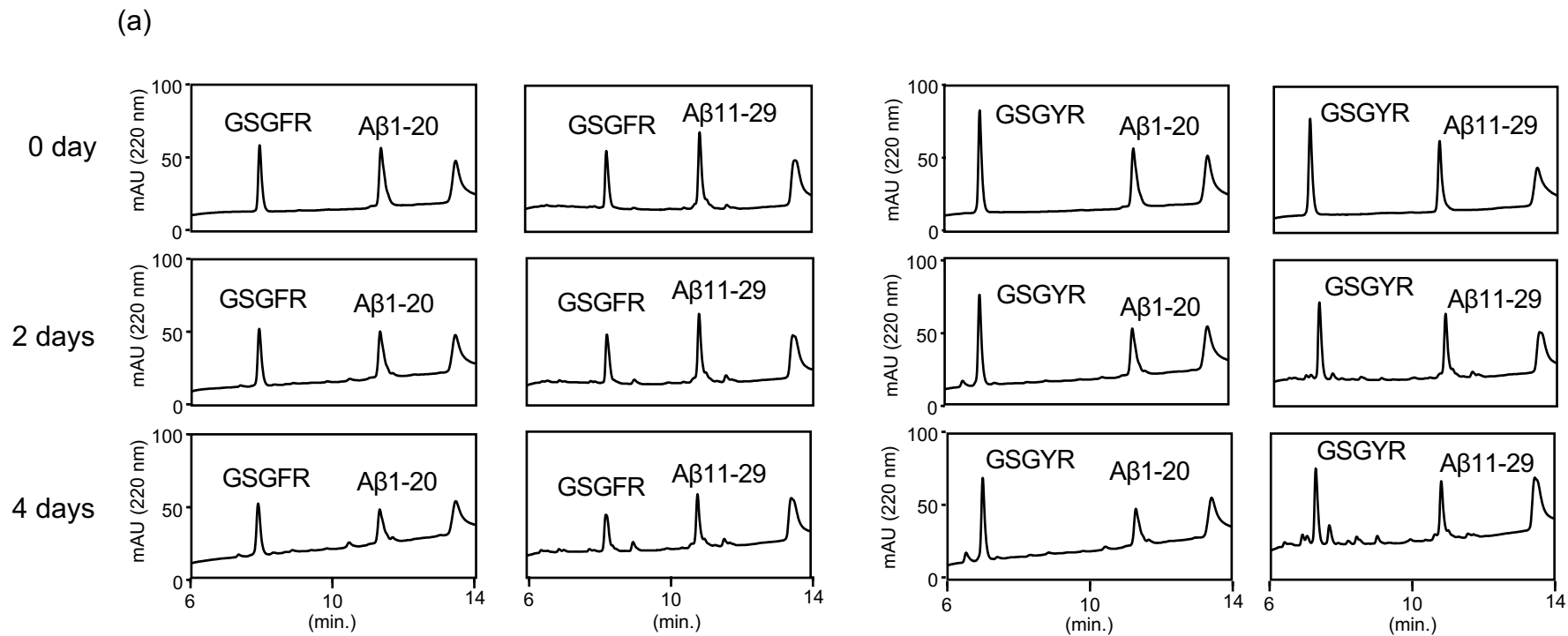
SFig. 2 Amino acid sequences of each 5-mer peptides with the corresponding molecular weight.



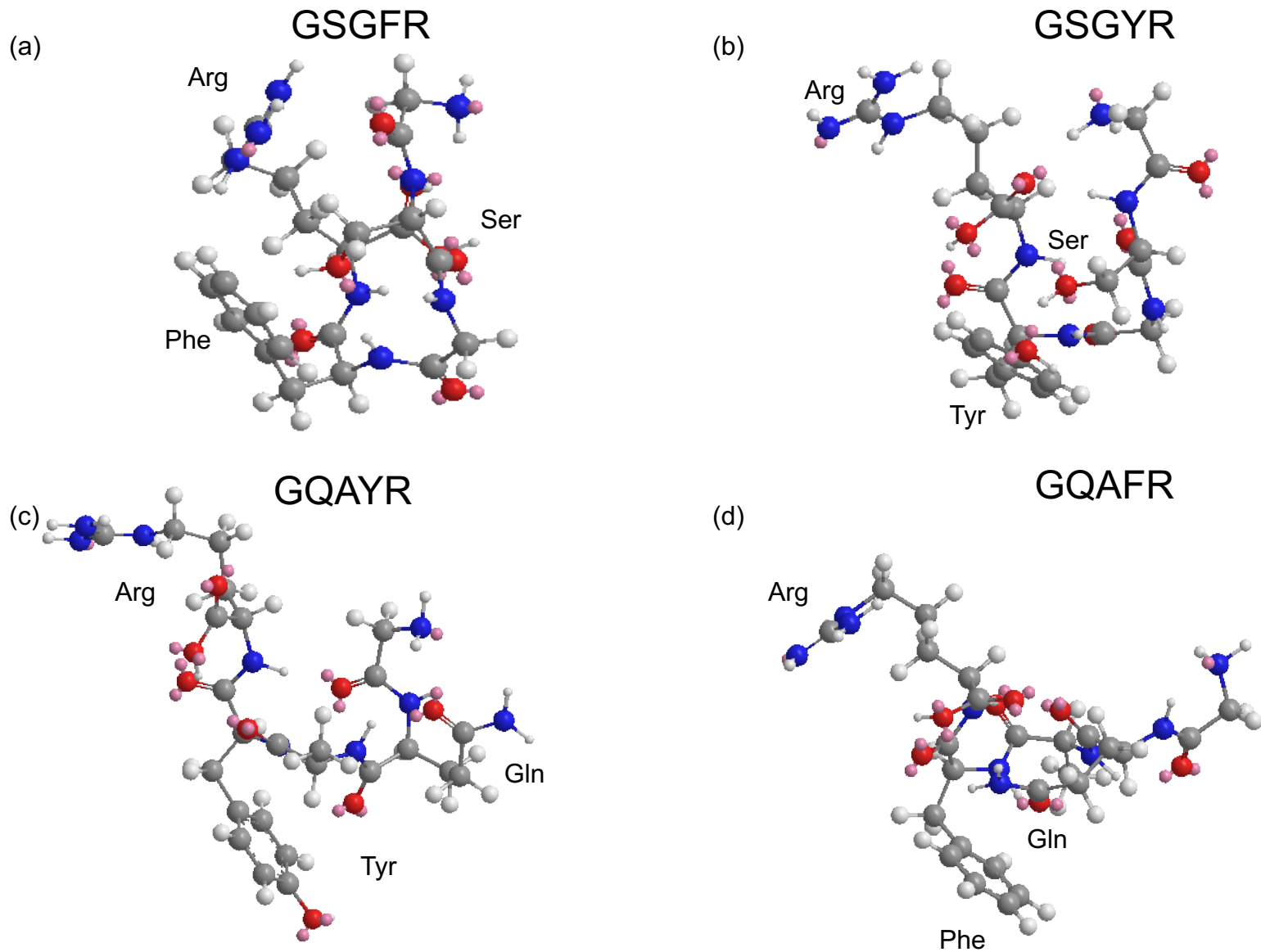
SFig. 3 Chromatogram of each substrate. Each substrate was incubated in PBS containing HSA, and 10 μ L of reaction mixture was analyzed by HPLC. Left: A β 1-20 Right: A β 11-29.



SFig. 4 Proteolytic cleavage of A β 1-20 and A β 11-29 by GQAYR and GQAFR.
 (a) GQAYR with A β 1-20 or A β 11-29 (b) GQAFR with A β 1-20 or A β 11-29



SFig. 5 Proteolytic cleavage of A β 1-20 and A β 11-29 by GSGFR and GSGYR.
(a) GSGFR with A β 1-20 or A β 11-29 (b) GSGYR with A β 1-20 or A β 11-29



SFig. 6 Computer modeling of JAL-TA9. (a) GSGFR (b) GSGYR (c) GQAYR (d) GQAFR