

Biophysical Journal, Volume 96

Supporting Material

Functional and Structural Characterization of Factor Xa Dimer In Solution

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Supplemental Material

Table S1

Residue changes 3 mM Ca ⁺² to 3 mM Ca ⁺² + C6PS	Residue changes 5 mM Ca ⁺² to 5 mM Ca ⁺² + C6PS	Residue changes due to dimerization
9 → 9	9 → 9	
62 → 62	62 → 62	
79 → 79	79 → 79	
242 → 242 (62)	242 → 242	
270 → 270 (90)	270 → 270	270
276 → 276 (96)	276 → 276	
289 → 289 (109)	289 → 289	
317 → 317 (134)	317 → 317	
330 → 330 (147)	330 → 330	
338 → 338 (156)	338 → 338	
351 → 351 (169)	351 → 351	
388 → 388 (204)	388 → 388	
406 → 406 (223)	406 → 406	
408 → 408 (224)	408 → 408	
414 → 414 (230)	414 → 414	414
420 → 420 (236)	420 → 420	
427 → 427 (243)	427 → 427	

Table S2

Residue changes 3 mM Ca ⁺² TO mM 5 Ca ⁺²	Residue changes 3 mM Ca ⁺² + C6PS TO 5 mM Ca ⁺² + C6PS	Residue changes due to dimerization
9 → 9	9 → 9	
62 → 62	62 → 62	
79 → 79	79 → 79	
242 → 242 (62)	242 → 242	
270 → 270 (90)	270 → 270	270
276 → 276 (96)	221 → 221	
289 → 289 (109)	289 → 289	
317 → 317 (134)	317 → 317	
330 → 330 (147)	330 → 330	
338 → 338 (156)	338 → 338	
351 → 351 (169)	351 → 351	
388 → 388 (204)	388 → 388	
406 → 406 (223)	406 → 406	
408 → 408 (224)	408 → 408	
414 → 414 (230)	414 → 414	414
420 → 420 (236)	420 → 420	
427 → 427 (243)	427 → 427	

Table S: Change in Lys residues upon addition of C6PS and Calcium determined from Lys acetylation followed by mass spectrometry. S1) Columns 1 and 2 show Lys residues that change upon addition of C6PS at 3 mM and 5 mM Ca^{+2} , respectively, S2) Columns 1 and 2 show Lys residues that change upon increase from 3 mM to 5 mM Ca^{+2} in the absence and presence of 400 μM C6PS, respectively. **Blue** = residues accessible to both acetylation and enzymatic digestion, **Green** = residues not accessible to acetylation but observed after enzymatic digestion, **Red** = residues not observed at all. Numberings of the Lysine residues are according to Fung et al., Proceedings of the National Academy of Sciences, 1985, 82, 3591-3595. Parenthesis shows the chymotrypsin numbering for the amino acid residues in the catalytic domain. In Pedersen model Fung Numbering system is followed.