

u	HK1																	R2			
	Helix a1				Helix a2			Helix a3				Helix a4									
Layers	а	d	е	g	а	b	d	е	а	С	d	е	g	а	b	d	е	g			
1 2	Q9	112	A13	N8	Q141	K142	1144	Y138	Q9	L11	112	A13	N8	Q141	K142	1144	A145	N140	Layers	s a	d
3 4 5	F16	A19	120	K22	F148	N149	A151	1152	F16	S18	A19	120	K22	F148	N149	A151	I152	K154	1 2 3	A110	L113
6 7	т30	S26	L27	S29	1155 T162	Q156	S158	L159	Т30	S32	S26	L27	S29	T162	A163	S158	L159	S161	4 5	1103	L106
9 10	L37	V40	L34	K36	L169	Q170	A165	L166	L37	D39	V40	V41	K36	L169	Q170	V172	V173	K168		-	
11 12 13	N44	A47	L48	T50	N176	A177	A179	L180	N44	Q46	A47	L48	T50	N176	A177	A179	L180	T182			
14 15	L55	N58	F59	A61	L187	S188	N190	F191	L55	S57	N58	F59	A61	L187	S188	N190	F191	A193			
10	102	V65	L66	D68	1194	S195			102	S64	V65	L66	D68	1194	S195	V197	L198	D200			

Supplementary information, Fig. S1: Interhelical packing interactions in HR121. a Schematic representation of HR121. The corresponding sequences of HR1, HR2 and the linker are shown in diagram. The "e" and "g" positions in HR1 and "a" and "d" residues in HR2 are colored in red. The residues involved in interaction between HR1 and HR2 are marked with a grey background. b Left: formation of HR121 between HR1 and HR2. The inner HR1 trimer (α 1, α 3, and α 4) is formed through the interaction of residues located at the "a" and "d" positions, and two HR2s depend on the residues located at the "a" and "d" positions to interact with the residues in "e" and "g" positions in the inner HR1 trimer. Another HR1 (a2) depend on the residues at "e" positions to bind with the residues at "g" positions in HR1 (α 3), and the residues at "a" positions to bind with the residues at "e" positions in HR1 (α 4). Right: formation of the post-fusion structure of SARS-CoV-2 6-HB (PDB code: 6LXT). The HR1 trimer is formed through the interaction of residues located at "a" and "d" positions, and the HR2 depend on the residue located at the "a" and "d" position to interact with the residues in "e" and "g" positions in HR1. c A cartoon representation showing superimposition of the inner HR1 trimer (α 1, α 3, and α 4) of HR121 with the central HR1 trimer of SARS-CoV2 6-HB (PDB code: 6LXT). The figures below are diagrams of the superimposed helices in top view. **d** List of interacting residues between HR121 helical bundles. The helical fusion core regions are marked with dark blue box.