Probing the Molecular Mechanism of Human Soluble Guanylate Cyclase Activation by NO in *vitro* and in *vivo*

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Fig.S1 Conformational change of FlAsH-labeled sGC β1(1-385)H105A-^{243}TC^{248} (a), and sGC β1(1-385)H105A-^{386}TC^{391} (b) upon NO binding or CO binding. The protein was 2 μM in 20 mM HEPES, 150 mM KCl, pH 7.4.

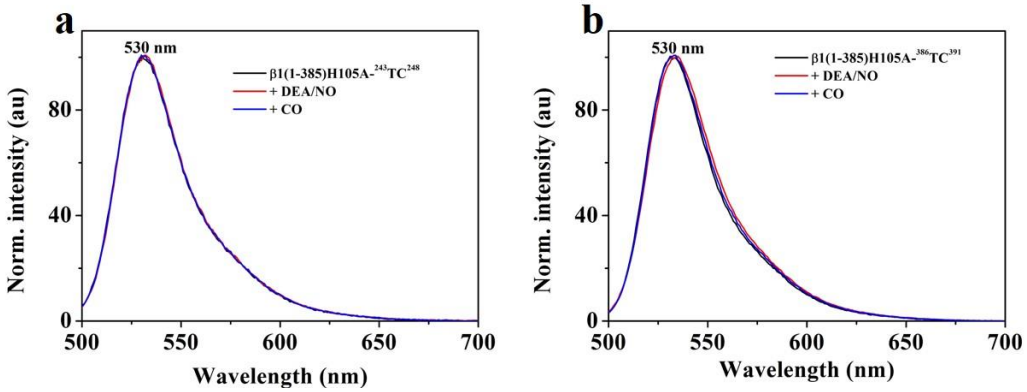

Fig.S2 Conformational change of FlAsH-labeled sGC β1(1-619)H105A-^{243}TC^{248} (a), and sGC β1(1-619)H105A-^{386}TC^{391} (b) upon NO binding or CO binding. The protein was 3 μM in 20 mM HEPES, 150 mM KCl, pH 7.4.

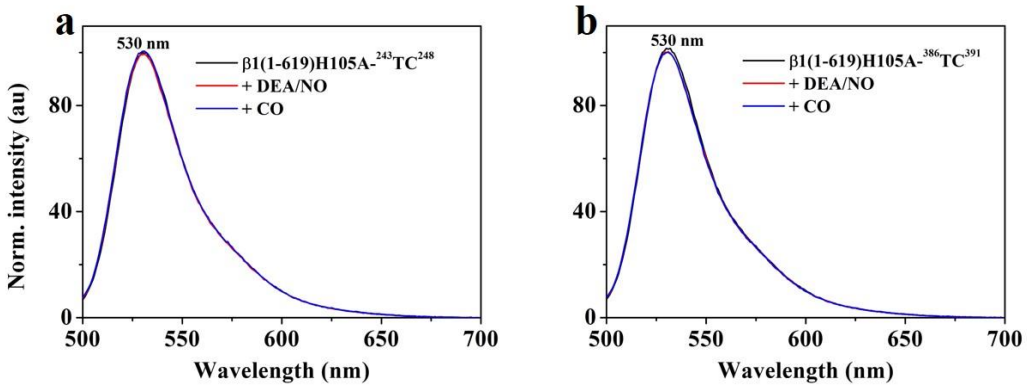

Fig.S3 The full-length gel of the western-blot shown in Figure 7.

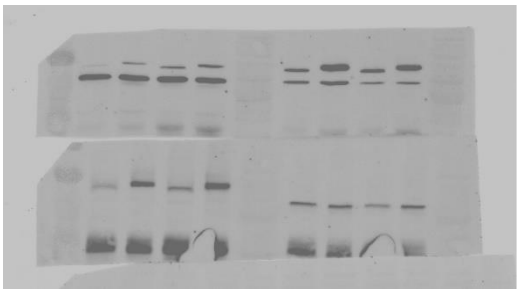

Fig.S4 The model summarizing various labeled proteins in relation to the sGC three dimensional models. FlAsH-EDT_2 labeled to the PAS domain (A) and coil-coiled domain (B); CFP and YFP fused to C-terminus of α1subunit and β1subunit (C); CFP fused to the N-terminus of α1subunit and YFP fused to the C-terminus of β1subunit (D).