## **Electronic Supplementary Information (ESI)**



Fig. S1 The 15% SDS-PAGE of sGC  $\beta$ 1 (1-194) (Lane 1), Marker (Lane 6) and *Ns* H-NOX (Lane 8)



**Fig. S2** Resonance Raman spectrum of the reduced form of *Ns* H-NOX using an excitation wavelength of 413.1 nm.



Fig. S3 High-frequency Raman spectra of *Ns* H-NOX, with  ${}^{12}C^{16}O$  complex colored blue and  ${}^{13}C^{18}O$  complex colored red. (A) *Ns* H-NOX; (B) sGC  $\beta 1_{(1-194)}$ .



Backbone RMSD

**Fig. S4** Backbone root-mean-square deviation (RMSD) of the two H-NOX proteins during MD simulations (blue for sGC H-NOX; red for *Ns* H-NOX).



Fig. S5 Hydrogen bond formed between Y112 and Y83 in sGC H-NOX, which leads to the bending of  $\alpha$ F that subsequently affects the heme position.

	Ns H-NOX		sGC β1 (1-194)	
nm	before	after	before	after
Soret	423	423	422	422
β	538	538	540	540
α	566	566	570	570

**Tabel S1** Comparison of the UV-visual spectra of the *Ns* H-NOX and sGC  $\beta$ 1 (1-194) proteins before and after the Raman measurement.

**Table S2**. Selected DFT-optimized parameters of (ImH)FeP(CO) in the absence or presence of water.

	Absence of water	Presence of water
$R_{\rm H \ bonding}({\rm \AA})$		2.237
$R_{C\equiv O}(\text{\AA})$	1.151	1.154
$R_{Fe-CO}(\text{\AA})$	1.797	1.784
$R_{Fe-N}(Å)$	2.079	2.078

## Sequence aligment file used for homology modelling

>P1;2o09

structureX:2009\_A: 1 :A:+184 :A:::-1.00:-1.00

MYGLVNKAIQDMISKHHGEDTWEAIKQKAGLEDIDFFVGMEAYSDDVTYHLVGAASEVLGKPAEELLIAFGEYWV TYTSEEGYGELLASAGDSLPEFMENLDNLHARVGLSFPQLRPPAFECQHTSS-KSMELHYQSTRCGLAPMVLGLL HGLGKRFQTKVEVTQTAFRETGEDHDIFSIKYEhb\*

>P1;rat\_sgc

sequence:rat\_sgc: : : : ::: 0.00: 0.00

MYGFVNHALELLVIRNYGPEVWEDIKKEAQLDEEGQFLVRIIYDDSKTYDLVAAASKVLNLNAGEILQMFGKMFF VFCQESGYDTILRVLGSNVREFLHNLDALHDHLATIYPGMRAPSFRCTDAEKGKGLILHYYSEREGLQDIVIGII KTVAQQIHGTEIDMKVIQQRSEECDHTQFLIEEhb\*