# Comperative study of bacterial homologs of β1 H-NOX domain of human soluble guanylyl cyclase (sGC)

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Soluble guanylate cyclase (sGC) is considered as the primary NO receptor across several known eukaryotes. The main interest regarding the biological role and its function, focuses on the H-NOX domain of the β1 subunit. This domain in its active form bears a ferrous b type heme as prosthetic group, which facilitates the binding of NO and other diatomic gases. The key point that still needs to be answered is how the redox state of heme determines H-NOX active state and coordination upon binding of diatomic gases. H-NOX domain is present in the genomes of both prokaryotes and eukaryotes, either as a stand-alone protein domain or as a partner of a larger polypeptide. The biological functions of these signaling modules for a wide range of genomes, diverge considerably along with their ligand binding properties [1]. In this direction, we examine five prokaryotic H-NOX proteins from *Nostoc punctiforme* (*Npun* H-NOX), *Vibrio Cholerae* (*Vb* H-NOX), *Caldanaerobacter subterraneus* (*Cs* H-NOX), *Shewanella oneidensis* (*So* H-NOX) and *Shewanella woodyi* (*Sw* H-NOX). These domains share some common amino acids in their sequence that may explain to an extent the organism-specific ligand preference. Since Fe-heme as a substrate can bind diatomic gases with binding affinities of the order NO>>CO>>$O_2$, we aim to address the perception of the redox state switch mechanism of heme [2]. Based on physicochemical and spectroscopical properties we intend to highlight the significant structural induced alterations in common key-regions of the selected H-NOX domains.

*References*

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*[2] Chasapi, S.A., Argyriou, A.I. and Spyroulias, G.A. (2022), Biomol NMR Assign.*

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