**Supplementary Material**

**Supplementary Table S1.** Characteristic features of bacterial hemerythrin domain-containing sensors.
The canonical non-heme diiron site is H-HxxxE-HxxxH-HxxxxD, whereas the non-canonical motif is H-HxxxE-HxE-HxxxxD in *A. cellulolyticus* P1B-5-ATPase.

| Source         | Location of Hr domain | Non-heme diiron site | Function | Active form | Inactive form       |
|----------------|------------------------|----------------------|----------|-------------|---------------------|
| DcrH           | C                      | canonical            | MCP      |             | not reported        |
| Bhr-DGC        | N                      | canonical            | DGC      | deoxy       | met, azidomet       |
| Bhr-HD-GYP     | N                      | canonical            | PDE      | deoxy       | met, azidomet       |
| P1B-5-ATPase   | C                      | non-canonical        | ATPase   |             | not reported        |

*Source Location of Hr domain Non-heme diiron site Function Active form Inactive form*

*Source Location of Hr domain Non-heme diiron site Function Active form Inactive form*

*Source Location of Hr domain Non-heme diiron site Function Active form Inactive form*
DcrH     826  DTGDADVKVWSEDLAN--LPSIDTQHKLVDYINDLYRAARRR-----DMDKAREVFDAL 879
Bhr-DGC  1 ------MQSFKWDQYFTGELLEVDQHQLVNNVRSSLLAENH----VSLDEIRLALFEL 52
Bhr-HD-GYP 14 NTKKSVDFIPWNEYFKGIEEIDIKQHEKLVGILNEVATHVSFN----SKLPELQDIIEKL 69
P_1B-5-ATPase  619 LLPTRHTVGLATADQAAERLRAEHDVRSVGQRVVADALAPCREDFALEDLVGEL 678
Hr       1 MGFPIPDPYVWDPSFRTFYSIIIDDEHKTLFNGIFHLA----------IDDNADNLGEL 48

*:      *:     :               . *  :   :   .
826  DTGDADVKVWSEDLAN--LPSIDTQHKLVDYINDLYRAARRR-----DMDKAREVFDAL 879
886 890 895 900

DcrH     880  KNYAVEHFGYEE----LFADYAYP--EATRHKEIHRRFVETVLKWEKQLAAGDPE---- 929
Bhr-DGC  53  SRYSEYHFKEEEK----LMREVGISALHLEHIHQVHTFMSEVSMQAFIHVDDDR---- 104
Bhr-HD-GYP  70 VDYTQYHFTEES----LWEYKLKMDSSAILHKSHDRIKINAIKLADNTPTEN---- 122
P_1B-5-ATPase  679 EAVLPPEHERAEEQQLLPIVARALSSDVDGVLSSLRAAHEIEHYVVRLLQLTTMVGGEPSD 738
Hr       49 RRCTGKHFLNEQV----LMQASQYQ--FYDEHKKEHETFIHALDWNKG---------- 90
*:      *:     :               . *  :   :   .
930 945 950

DcrH     930  ---VVMTTTLRLGVLQWLNHIMKED--KKYEAYLRERGS 963
Bhr-DGC  105  ---SAVQLLEFIHWLAYHILGDQNMARQVIAIRSGMS 140
Bhr-HD-GYP  123  ---IIINDLLGYLTVWILEHDEXSYIVYGIQCGLT 158
P_1B-5-ATPase  739 DVIEARRLLYLHSLALHLNAAEDEIDAFAIPPGDQRTNT 777
Hr       91  ------------DVKWAKSLVNHIKTIDFKYKGKI---------- 114
*:      *:     :               . *  :   :   .

**Supplementary Figure S2.** Shown is the amino acid sequence alignment of the hemerythrin domain of bacterial hemerythrin domain-containing oxygen/redox sensor proteins, *D. vulgaris* DcrH (residues 826-963) (UniProt ID: Q726F3), *V. cholerae* Bhr-DGC (residues 1-140) (UniProt ID: Q9KSP0), *Ferrovum* sp. PN-J185 Bhr-HD-GYP (residues 14-158) (UniProt ID: A0A149VUS3), and *A. cellulolyticus* P_1B-5-ATPase (residues 619-777) (UniProt ID: A0LQU2), and *P. gouldii* hemerythrin (Hr) (UniProt ID: P02244). Iron ligand residues are shown in red.