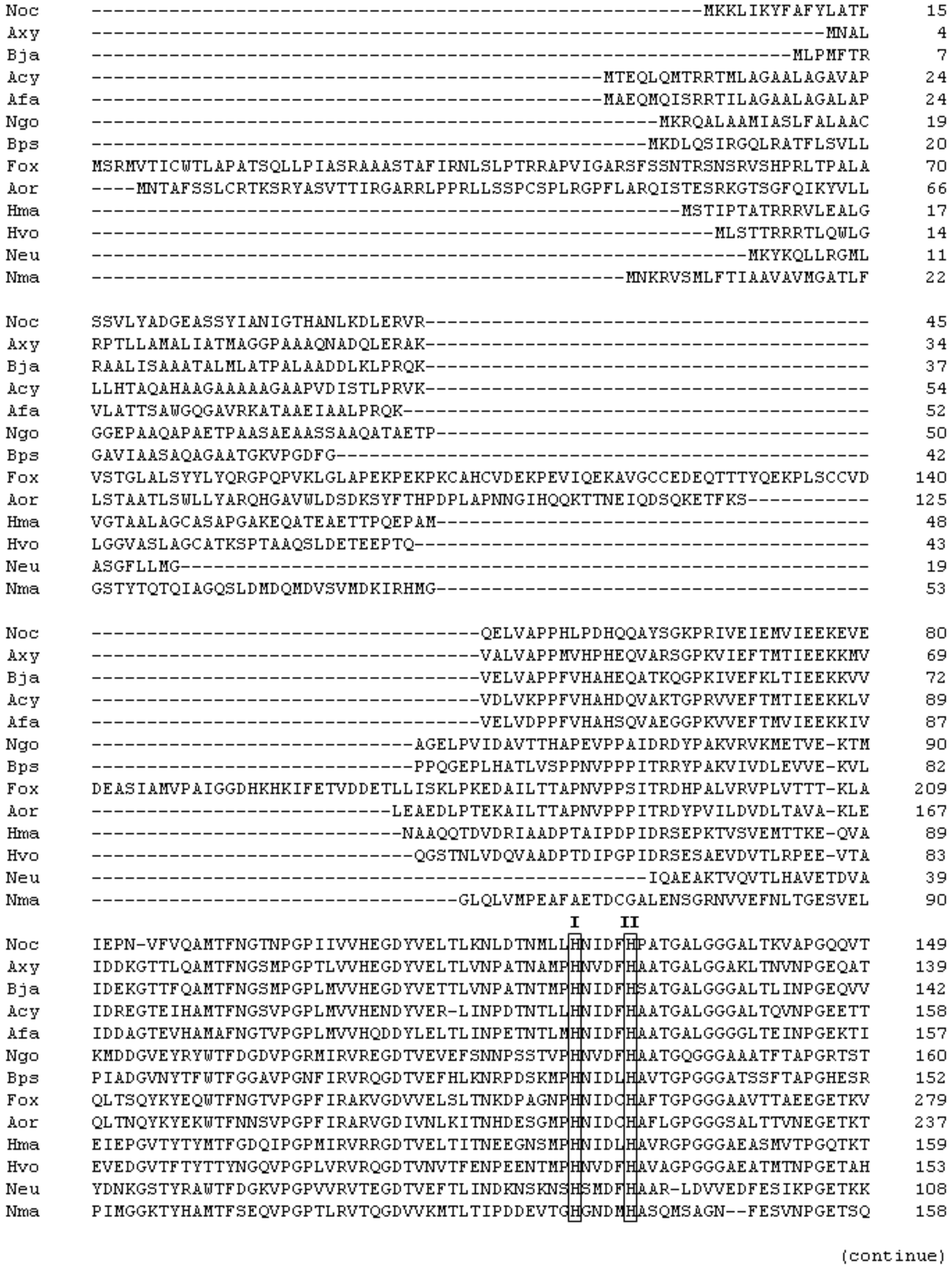
Supplemental Fig. 1. Sequence alignment of Cu-containing nitrite reductases. Amino acid sequence of the enzyme from *N. oceani* (Nco) is aligned with those from *A. xylosoxidans* (Axy), *B. japonicum* (Bja), *A. cycloclastes* (Acy), *A. faecalis* (Afa), *N. gonorrhoeae* (Ngo), *B. pseudomallei* (Bps), *F. oxysporum* (Fox), *A. oryzae* (Aor), *H. marismortui* (Hma), *H. volcanii* (Hvo), *N. europaea* (Neu), and *N. maritimus* (Nma). Amino acids are numbered at the right margin. Putative Cu-binding residues for type 1 and type 2 Cu are indicated by I and II, respectively. Insertions and deletions of the sequence that are common in the class 1 or class 2 enzymes are boxed. Accession numbers of the sequences are indicated in Figure 1.

Supplemental Figure 1_1



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Noc         -------------------------------------------------------MKKLIKYFAFYLATF     15
Axy         ------------------------------------------------------------------MNAL      4
Bja         ---------------------------------------------------------------MLPMFTR      7
Acy         ----------------------------------------------MTEQLQMTRRTMLAGAALAGAVAP     24
Afa         ----------------------------------------------MAEQMQISRRTILAGAALAGALAP     24
Ngo         ---------------------------------------------------MKRQALAAMIASLFALAAC     19
Bps         --------------------------------------------------MKDLQSIRGQLRATFLSVLL     20
Fox         MSRMVTICWTLAPATSQLLPIASRAAASTAFIRNLSLPTRRAPVIGARSFSSNTRSNSRVSHPRLTPALA     70
Aor         ----MNTAFSSLCRTKSRYASVTTIRGARRLPPRLLSSPCSPLRGPFLARQISTESRKGTSGFQIKYVLL     66
Hma         -----------------------------------------------------MSTIPTATRRRVLEALG     17
Hvo         --------------------------------------------------------MLSTTRRRTLQWLG     14
Neu         -----------------------------------------------------------MKYKQLLRGML     11
Nma         ------------------------------------------------MNKRVSMLFTIAAVAVMGATLF     22

Noc         SSVLYADGEASSYIANIGTHANLKDLERVR----------------------------------------     45
Axy         RPTLLAMALIATMAGGPAAAQNADQLERAK----------------------------------------     34
Bja         RAALISAAATALMLATPALAADDLKLPRQK----------------------------------------     37
Acy         LLHTAQAHAAGAAAAAGAAPVDISTLPRVK----------------------------------------     54
Afa         VLATTSAWGQGAVRKATAAEIAALPRQK------------------------------------------     52
Ngo         GGEPAAQAPAETPAASAEAASSAAQATAETP---------------------------------------     50
Bps         GAVIAASAQAGAATGKVPGDFG------------------------------------------------     42
Fox         VSTGLALSYYLYQRGPQPVKLGLAPEKPEKPKCAHCVDEKPEVIQEKAVGCCEDEQTTTYQEKPLSCCVD    140
Aor         LSTAATLSWLLYARQHGAVWLDSDKSYFTHPDPLAPNNGIHQQKTTNEIQDSQKETFKS-----------    125
Hma         VGTAALAGCASAPGAKEQATEAETTPQEPAM---------------------------------------     48
Hvo         LGGVASLAGCATKSPTAAQSLDETEEPTQ-----------------------------------------     43
Neu         ASGFLLMG--------------------------------------------------------------     19
Nma         GSTYTQTQIAGQSLDMDQMDVSVMDKIRHMG---------------------------------------     53

Noc         -----------------------------------QELVAPPHLPDHQQAYSGKPRIVEIEMVIEEKEVE     80
Axy         -----------------------------------VALVAPPMVHPHEQVARSGPKVIEFTMTIEEKKMV     69
Bja         -----------------------------------VELVAPPFVHAHEQATKQGPKIVEFKLTIEEKKVV     72
Acy         -----------------------------------VDLVKPPFVHAHDQVAKTGPRVVEFTMTIEEKKLV     89
Afa         -----------------------------------VELVDPPFVHAHSQVAEGGPKVVEFTMVIEEKKIV     87
Ngo         -----------------------------AGELPVIDAVTTHAPEVPPAIDRDYPAKVRVKMETVE-KTM     90
Bps         -----------------------------PPQGEPLHATLVSPPNVPPPITRRYPAKVIVDLEVVE-KVL     82
Fox         DEASIAMVPAIGGDHKHKIFETVDDETLLISKLPKEDAILTTAPNVPPSITRDHPALVRVPLVTTT-KLA    209
Aor         ---------------------------LEAEDLPTEKAILTTAPNVPPPITRDYPVILDVDLTAVA-KLE    167
Hma         ----------------------------NAAQQTDVDRIAADPTAIPDPIDRSEPKTVSVEMTTKE-QVA     89
Hvo         -----------------------------QGSTNLVDQVAADPTDIPGPIDRSESAEVDVTLRPEE-VTA     83
Neu         --------------------------------------------------IQAEAKTVQVTLHAVETDVA     39
Nma         ---------------------------------GLQLVMPEAFAETDCGALENSGRNVVEFNLTGESVEL     90
                                                       I   II
Noc         IEPN-VFVQAMTFNGTNPGPIIVVHEGDYVELTLKNLDTNMLLHNIDFHPATGALGGGALTKVAPGQQVT    149
Axy         IDDKGTTLQAMTFNGSMPGPTLVVHEGDYVELTLVNPATNAMPHNVDFHAATGALGGAKLTNVNPGEQAT    139
Bja         IDEKGTTFQAMTFNGSMPGPLMVVHEGDYVETTLVNPATNTMPHNIDFHSATGALGGGALTLINPGEQVV    142
Acy         IDREGTEIHAMTFNGSVPGPLMVVHENDYVER-LINPDTNTLLHNIDFHAATGALGGGALTQVNPGEETT    158
Afa         IDDAGTEVHAMAFNGTVPGPLMVVHQDDYLELTLINPETNTLMHNIDFHAATGALGGGGLTEINPGEKTI    157
Ngo         KMDDGVEYRYWTFDGDVPGRMIRVREGDTVEVEFSNNPSSTVPHNVDFHAATGQGGGAAATFTAPGRTST    160
Bps         PIADGVNYTFWTFGGAVPGNFIRVRQGDTVEFHLKNRPDSKMPHNIDLHAVTGPGGGATSSFTAPGHESR    152
Fox         QLTSQYKYEQWTFNGTVPGPFIRAKVGDVVELSLTNKDPAGNPHNIDCHAFTGPGGGAAVTTAEEGETKV    279
Aor         QLTNQYKYEKWTFNNSVPGPFIRARVGDIVNLKITNHDESGMPHNIDCHAFLGPGGGSALTTVNEGETKT    237
Hma         EIEPGVTYTYMTFGDQIPGPMIRVRRGDTVELTITNEEGNSMPHNIDLHAVRGPGGGAEASMVTPGQTKT    159
Hvo         EVEDGVTFTYTTYNGQVPGPLVRVRQGDTVNVTFENPEENTMPHNVDFHAVAGPGGGAEATMTNPGETAH    153
Neu         YDNKGSTYRAWTFDGKVPGPVVRVTEGDTVEFTLINDKNSKNSHSMDFHAAR-LDVVEDFESIKPGETKK    108
Nma         PIMGGKTYHAMTFSEQVPGPTLRVTQGDVVKMTLTIPDDEVTGHGNDMHASQMSAGN--FESVNPGETSQ    158

                                                                         (continue)
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Supplemental Figure 1_2

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                       II I          I    I
Noc         LRFKADKAGTYVYHCAPGGL-MTPYHVVSGMYGAIMIFPKKGLRDQNGKKVTYDKAYYVGEQGWYIPKDK    218
Axy         LRFKADRSGTFVYHCAPEG--MVPWHVVAGMSGTLMVLPRDGLKDPQGKPLRYDRAYTIGEFDLYIPKDA    207
Bja         LRWKATKTGVFVYHCAPGGP-MIPWHVVSGMNGAVMVLPRDGLNDGKGHALKYDKVYYVGEQDMYVPRDE    211
Acy         LRFKATKPGVFVYHCAPEG--MVPWHVTSGMNGAIMVLPRDGLKDEKGQPLTYDKIYYVGEQDFYVPKDE    226
Afa         LRFKATKPGVFVYHCAPPG--MVPWHVVSGMNGAIMVLPREGLHDGKGKALTYDKIYYVGEQDFYVPRDE    225
Ngo         FSFKALQPGLYIYHCAVAP---VGMHIANGMYGLILVEPK-------EGLPKVDKEFYIVQGDFYTK---    217
Bps         FTFKALNEGLFVYHCATAP---VGMHVANGMYGLILVEPP-------EGLPKVDREYYVMQGDFYTN---    209
Fox         GRFKLLYPGLYVYHCAAAP---VPVHIANGMYGLMYVQPEG------NDLPPVDKEYYVMQSEFYHEPPE    340
Aor         ARFRLQNPGLYIYHCAVGP---VGVHIANGMYGLLYVQPE-------QDLPPVDKEYYVMQSEFYHEPPE    297
Hma         FRFKATYPGAFIYHCAVPN---LDMHISSGMFGMILVEPK-------EGLPEVDHEFYFGQHELYTT---    216
Hvo         LRFKATYPGAYIYHCAVPN---MDMHISAGMFGLILVEPP-------EGMPEVDHEIYLGQHELYTD---    210
Neu         YTFTADNPGVFFYHCGSDP---MIQHIARGMYGVIIVDPKD-----ANALPKADREYVLIQAEHYEN---    167
Nma         YCYIAESAGMFKYHCSGVKLIGMDQHVLSGMYGITIVDPANG--YKKLMVEKTSGSGELDRKFYDADALE    226

Noc         NGKYKRYANAIEPYGDTLEVMRGLVPTHVTYNGSKGALTG------------------------------    258
Axy         NGKYKDYPTLAESYGDTVAVMRTLTPSHIVFNGKVGALTG------------------------------    247
Bja         KGNFKSYDSPGEAFTDTEEMMKKLIPSHVVFNGKVGALTG------------------------------    251
Acy         AGNYKKYETPGEAYEDAVKAMRTLTPTHIVFNGAVGALTG------------------------------    266
Afa         NGKYKKYEAPGDAYEDTVKVMRTLTPTHVVFNGAVGALTG------------------------------    265
Ngo         -----GKKGAQGLQPFDMDKAVAEQPEYVVFNGHVGAIAG------------------------------    252
Bps         -----GKYREKGLQSFDMDKAIDERPTYVVFNGAEGALTG------------------------------    244
Fox         ---VDDDGRRSEIVEFSYPNGLREEPQVVAFNGSESALTR------------------------------    377
Aor         ---PDDNGQMSSTVEFSWPHALREAADVVVFNGSEAALT-------------------------------    333
Hma         -----GDTGEKGHHDFDMEAMAAEEPTYVLMNGEKYAITPDRH---------------------------    254
Hvo         -----KDAGEEGQHAFDYEAMRNEEPTYVLMNGEKYAWTPNGR---------------------------    248
Neu         --------------PDDKTAMMQNKWSNVVFNGGVFKYDPVHDS------------------------EA    199
Nma         FQLQYNQLYLTPEGNYDAGAMFKHQNTATVVNGMQFGYVPNMAHNLLVNGDVNKNIFVAQPWNGLEHKQY    296

Noc         DNAMKAKVGDSVLFIHS--QANEDSRIHLIGGHGDLVWPGGSFKNTPMVDKETWHVNGGESVAALYTFKQ    326
Axy         ANALTAKVGETVLLIHS--QANRDTRPHLIGGHGDWVWETGKFANPPQKDLETWFIRGGSAGAALYTFKQ    315
Bja         KNALTANVGENVLIVHS--QANRDSRPHLIGGHGDYVWETGKFGNAPEVGLETWFIRGGSAGAAMYKFMQ    319
Acy         DHALTAAVGERVLVVHS--QANRDTRPHLIGGHGDYVWATGKFRNPPDLDQETWLIPGGTAGAAFYTFRQ    334
Afa         DKAMTAAVGEKVLIVHS--QANRDTRPHLIGGHGDYVWATGKFNTPPDVDQETWFIPGGAAGAAFYTFQQ    333
Ngo         DNALKAKAGETVRMYVGNGGPNLVSSFHVIGEIFDKVYVEGGKLINEN--VQSTIVPAGGSAIVEFKVDI    320
Bps         ERAMRARTDETVRLFVGNGGPNLVSSFHVIGAVFDKVRADGSNVTQND--VQTTLIPAGGAATIEFHTRV    312
Fox         DHPLKAHVGDDVRIFFGNAGPNLTSSFHIIGTHFKNVYRDGGVTSNPSKGIQTVSVPCGGSTIVDLKMAV    447
Aor         EKPLKATLDDTVRIFFGNGGPNLTSSFHVIGTCFNKVYRDSDVLSPPGQCVQTVSVPPGGSTIVDMKMVV    403
Hma         G-SPSMQVGETARVYFVTGGPNLDSSFHPIGSVWDEVWQQGSIAGPPNRYVQTTPVKPGSCAIATLHAEV    323
Hvo         GPAATVGLDETVRVYFVDGGPNLSSSFHPIGSVWETLYPEGSLTTEPQTHIQTRQVPPGSTTIATMSSPV    318
Neu         TSWLQAKPGERVRIYFVNAGPNELSSLHPIAGIWDRVYPSGN-PKNVQYALQSYLIGAGDAATLDLISPV    268
Nma         QSQLLFVENDQHVRLFVENQGNEPVFFHIVGEILDRVTQGNRVQSAAT---ETWLLGGSQGMIVDLVFDE    363
                    II
Noc         PGLYAYLNHNLIQAFMLGGAAHVKVDGE-WNNDLMEQVVKPSPINAD.                          372
Axy         PGVYAYLNHNLIEAFELGAAGHIKVEGK-WNDDLMKQIKAPGPIPR.                           360
Bja         PGIYAYVTHNLIEAADLGATAHFKVEGK-WNDDLMTQVKAPAEIPANTN.                        367
Acy         PGVYAYVNHNLIEAFELGAAGHFKVTGE-WNDDLMTSVVKPASM.                             377
Afa         PGIYAYVNHNLIEAFELGAAAHFKVTGE-WNDDLMTSVLAPSGT.                             376
Ngo         PGNYTLVDHSIFRAFNKGALGQLKVEGA-ENPEIMTQKLSDTAYAGSGAAS(+22aa).               392
Bps         PGNYTFVDHSIFRAFNKGALAILKVDGP-ENKAIYSGKELDAPYSG-DAVT(+159aa).              520
Fox         PGTYTLVDHSIFR-LDKGAVGFLNVSGP-QNPGVYQSSQPPRPCVGCKLHS.                      496
Aor         PGTYTIVDHAIFR-LEKGAKGFLNVSGE-PRPMLYYSTLPPQPCEGFNLKY(+107aa).              559
Hma         PGPIKLVDHALSRVARKGTMAIINREGA-ANPDVFEPEA.                                  361
Hvo         PGDFKLVDHSLSRVVRKGCMAVVRAEGA-EDPEIFDPDPDPQ.                               359
Neu         EGANAIVDHSMRHAHSGAIAVIMFTNDA-DPEAGRGENILIR.                               309
Nma         PGAYAAVNHDYAAIYTGAATVFVAGDPFGLNPVLVEKGVIPAPVASYAYAL(+56aa).               470
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