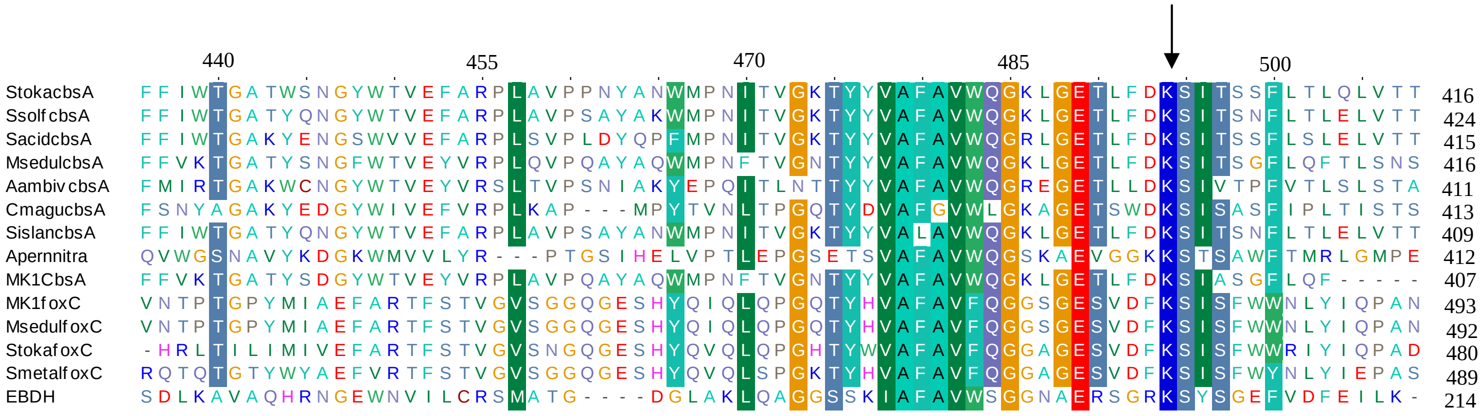
SUPPLEMENTAL FIGURE 1. Protein alignment of FoxC, CbsA and the cytochrome *b* subunit of the ethylbenzene dehydrogenase from *Azoarcus* sp. EbN1. The conserved lysine (K484 from Figure 5 alignment) is indicated by an arrow. Stokoda- (*S. tokodaii*), Ssolf- (*S. solfataricus*), Sacido- (*S. acidocaldarius*), Msedul- (*M. sedula*), Silan- (*S. islandicus*), Apernnitra (*Aeropyrum pernix* nitrate reductase), MK1- (Strain MK1), EBDH (*Azoarcus* sp. EbN1 EBDH gamma subunit), Cmagu- (*C. maquilingensis*), Smetal- (*S. metallicus*). Dark shaded amino acids are based on a shade threshold of 85%.



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                 440            455            470            485            500
StokacbsA    FFIWTGATWSNGYWTVEFARPLAVPPNYANWMPNITVGKTYYVAFAVWQGKLGETLFDKSITSSFLTLQLVTT  416
SsolfcbsA    FFIWTGATYQNGYWTVEFARPLAVPSAYAKWMPNITVGKTYYVAFAVWQGKLGETLFDKSITSNFLTLELVTT  424
SacidcbsA    FFIWTGAKYENGSWVVEFARPLSVPLDYQPFMPNITVGKTYYVAFAVWQGRLGETLFDKSITSSFLSLELVTT  415
MsedulcbsA   FFVKTGATYSNGFWTVEYVRPLQVPQAYAQWMPNFTVGNTYYVAFAVWQGKLGETLFDKSITSGFLQFTLSNS  416
AambivcbsA   FMIRTGAKWCNGYWTVEYVRSLTVPSNIAKYEPQITLNTTYYVAFAVWQGREGETLLDKSIVTPFVTLSLSTA  411
CmagucbsA    FSNYAGAKYEDGYWIVEFVRPLKAP---MPYTVNLTPGQTYDVAFGVWLGKAGETSWDKSISASFIPLTISTS  413
SislancbsA   FFIWTGATYQNGYWTVEFARPLAVPSAYANWMPNITVGKTYYVALAVWQGKLGETLFDKSITSNFLTLELVTT  409
Apernnitra   QVWGSNAVYKDGKWMVVLYR---PTGSIHELVPTLEPGSETSVAFAVWQGSKAEVGGKKSTSAWFTMRLGMPE  412
MK1CbsA      FFVKTGATYSDGYWTVEYVRPLAVPQAYAQWMPNFTVGNTYYVAFAVWQGKLGETLFDKSIASGFLQF-----  407
MK1foxC      VNTPTGPYMIAEFARTFSTVGVSGGQGESHYQIQLQPGQTYHVAFAVFQGGSGESVDFKSISFWWNLYIQPAN  493
MsedulfoxC   VNTPTGPYMIAEFARTFSTVGVSGGQGESHYQIQLQPGQTYHVAFAVFQGGSGESVDFKSISFWWNLYIQPAN  492
StokafoxC    -HRLTILIMIVEFARTFSTVGVSNGQGESHYQVQLQPGHTYWVAFAVFQGGAGESVDFKSISFWWRIYIQPAD  480
SmetalfoxC   RQTQTGTYWYAEFVRTFSTVGVSGGQGESHYQVQLSPGKTYHVAFAVFQGGAGESVDFKSISFWYNLYIEPAS  489
EBDH         SDLKAVAQHRNGEWNVILCRSMATG----DGLAKLQAGGSSKIAFAVWSGGNAERSGRKSYSGEFVDFEILK-  214
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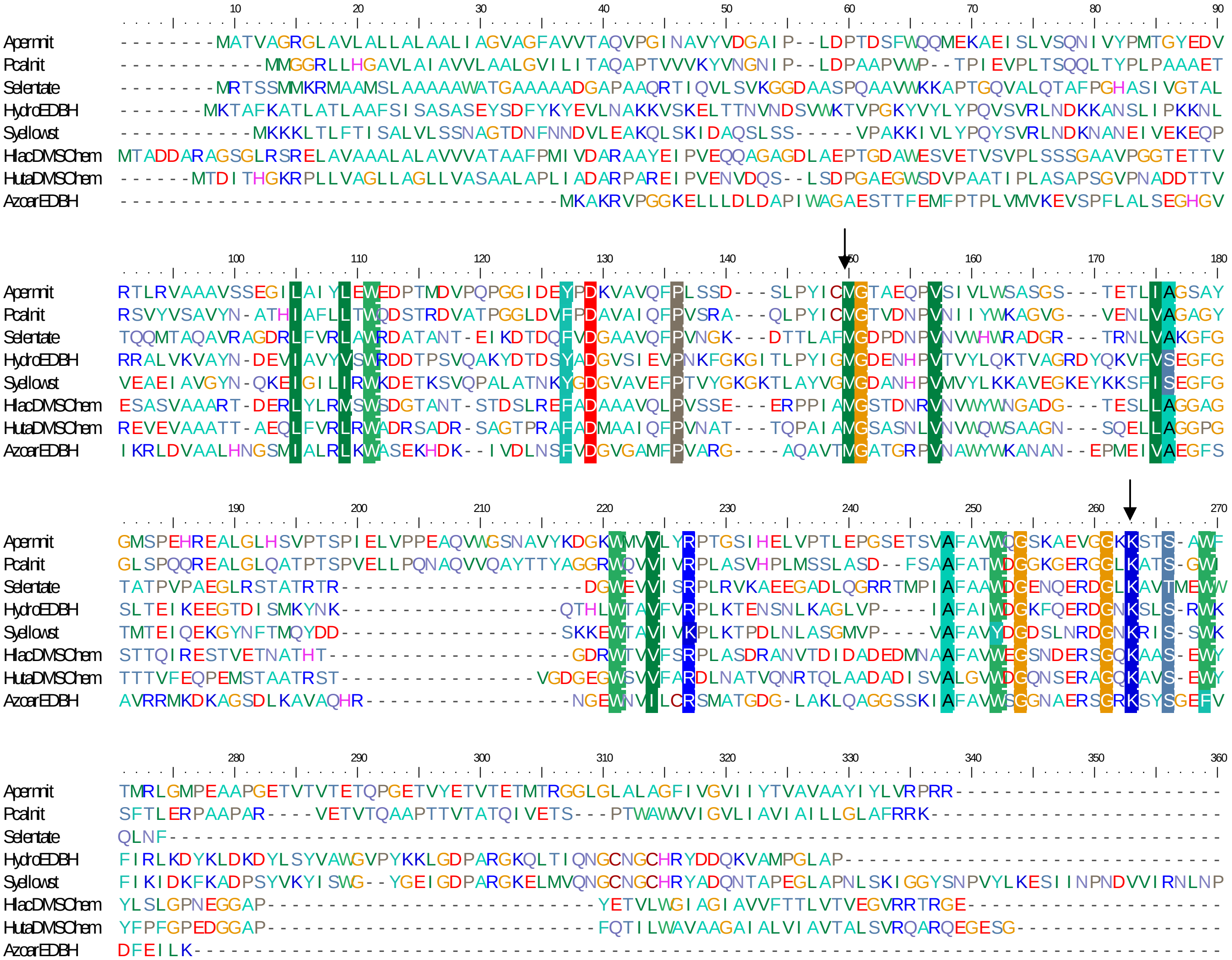
SUPPLEMENTAL FIGURE 2. Alignment of homologous sequences to the *Azoarcus* sp. EbN1 gamma EBDH Lys-Met axially coordinated heme B (alignment id: AzoarEBDH) which include: the EBDH from *Hydrogenivirga* sp. 128-5-R1-1 (HydroEBDH); nitrate reductases from *Aeropyrum pernix* (Apernnit) and *Pyrobaculum calidifontis* (Pcalnit); selenate reductase from *Thauera selenatis* (Selenate); DMSO reductase heme B subunit from *Halorubrum lacusprofundi* (HlacDMSOhem) and *Halorhabdus utahensis* (HutaDMSOhem); and hypothetical cytochromes from *Sulfurihydrogenibium yellowstonense* (Syellowst). The conserved methionine and lysine responsible for heme B coordination are indicated with arrows.



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                     10        20        30        40        50        60        70        80        90
             ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Apernnit     --------MATVAGRGLAVLALLALAALIAGVAGFAVVTAQVPGINAVYVDGAIP--LDPTDSFWQQMEKAEISLVSQNIVYPMTGYEDV
Pcalnit      ------------MMGGRLLHGAVLAIAVVLAALGVILITAQAPTVVVKYVNGNIP--LDPAAPVWP--TPIEVPLTSQQLTYPLPAAAET
Selentate    --------MRTSSMMKRMAAMSLAAAAAWATGAAAAADGAPAAQRTIQVLSVKGGDAASPQAAVWKKAPTGQVALQTAFPGHASIVGTAL
HydroEDBH    -------MKTAFKATLATLAAFSISASASEYSDFYKYEVLNAKKVSKELTTNVNDSVWKTVPGKYVYLYPQVSVRLNDKKANSLIPKKNL
Syellowst    -----------MKKKLTLFTISALVLSSNAGTDNFNNDVLEAKQLSKIDAQSLSS-----VPAKKIVLYPQYSVRLNDKNANEIVEKEQP
HlacDMSOhem  MTADDARAGSGLRSRELAVAAALALAVVVATAAFPMIVDARAAYEIPVEQQAGAGDLAEPTGDAWESVETVSVPLSSSGAAVPGGTETTV
HutaDMSOhem  ------MTDITHGKRPLLVAGLLAGLLVASAALAPLIADARPAREIPVENVDQS--LSDPGAEGWSDVPAATIPLASAPSGVPNADDTTV
AzoarEDBH    ------------------------------------MKAKRVPGGKELLLDLDAPIWAGAESTTFEMFPTPLVMVKEVSPFLALSEGHGV

                                                                        ↓
                    100       110       120       130       140       150       160       170       180
             ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Apernnit     RTLRVAAAVSSEGILAIYLEWEDPTMDVPQPGGIDEYPDKVAVQFPLSSD---SLPYICMGTAEQPVSIVLWSASGS---TETLIAGSAY
Pcalnit      RSVYVSAVYN-ATHIAFLLTWQDSTRDVATPGGLDVFPDAVAIQFPVSRA---QLPYICMGTVDNPVNIIYWKAGVG---VENLVAGAGY
Selentate    TQQMTAQAVRAGDRLFVRLAWRDATANT-EIKDTDQFVDGAAVQFPVNGK---DTTLAFMGDPDNPVNVWHWRADGR---TRNLVAKGFG
HydroEDBH    RRALVKVAYN-DEVIAVYVSWRDDTPSVQAKYDTDSYADGVSIEVPNKFGKGITLPYIGMGDENHPVTVYLQKTVAGRDYQKVFVSEGFG
Syellowst    VEAEIAVGYN-QKEIGILIRWKDETKSVQPALATNKYGDGVAVEFPTVYGKGKTLAYVGMGDANHPVMVYLKKAVEGKEYKKSFISEGFG
HlacDMSOhem  ESASVAAART-DERLYLRMSWSDGTANT-STDSLREFADAAAVQLPVSSE---ERPPIAMGSTDNRVNVWYWNGADG---TESLLAGGAG
HutaDMSOhem  REVEVAAATT-AEQLFVRLRWADRSADR-SAGTPRAFADMAAIQFPVNAT---TQPAIAMGSASNLVNVWQWSAAGN---SQELLAGGPG
AzoarEDBH    IKRLDVAALHNGSMIALRLKWASEKHDK--IVDLNSFVDGVGAMFPVARG----AQAVTMGATGRPVNAWYWKANAN--EPMEIVAEGFS

                                                                                               ↓
                    190       200       210       220       230       240       250       260       270
             ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Apernnit     GMSPEHREALGLHSVPTSPIELVPPEAQVWGSNAVYKDGKWMVVLYRPTGSIHELVPTLEPGSETSVAFAVWQGSKAEVGGKKSTS-AWF
Pcalnit      GLSPQQREALGLQATPTSPVELLPQNAQVVQAYTTYAGGRWQVVIVRPLASVHPLMSSLASD--FSAAFATWDGGKGERGGLKATS-GWI
Selentate    TATPVPAEGLRSTATRTR--------------------DGWEVVISRPLRVKAEEGADLQGRRTMPIAFAAWDGENQERDGLKAVTMEWW
HydroEDBH    SLTEIKEEGTDISMKYNK------------------QTHLWTAVFVRPLKTENSNLKAGLVP----IAFAIWDGKFQERDGNKSLS-RWK
Syellowst    TMTEIQEKGYNFTMQYDD------------------SKKEWTAVIVKPLKTPDLNLASGMVP----VAFAVYDGDSLNRDGNKRIS-SWK
HlacDMSOhem  STTQIRESTVETNATHT--------------------GDRWTVVFSRPLASDRANVTDIDADEDMNAAFAVWEGSNDERSGQKAAS-EWY
HutaDMSOhem  TTTVFEQPEMSTAATRST----------------VGDGEGWSVVFARDLNATVQNRTQLAADADISVALGVWDGQNSERAGQKAVS-EWY
AzoarEDBH    AVRRMKDKAGSDLKAVAQHR-----------------NGEWNVILCRSMATGDG-LAKLQAGGSSKIAFAVWSGGNAERSGRKSYSGEFV

                    280       290       300       310       320       330       340       350       360
             ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Apernnit     TMRLGMPEAAPGETVTVTETQPGETVYETVTETMTRGGLGLALAGFIVGVIIYTVAVAAYIYLVRPRR----------------------
Pcalnit      SFTLERPAAPAR----VETVTQAAPTTVTATQIVETS---PTWAWVVIGVLIAVIAILLGLAFRRK------------------------
Selentate    QLNF--------------------------------------------------------------------------------------
HydroEDBH    FIRLKDYKLDKDYLSYVAWGVPYKKLGDPARGKQLTIQNGCNGCHRYDDQKVAMPGLAP-------------------------------
Syellowst    FIKIDKFKADPSYVKYISWG--YGEIGDPARGKELMVQNGCNGCHRYADQNTAPEGLAPNLSKIGGYSNPVYLKESIINPNDVVIRNLNP
HlacDMSOhem  YLSLGPNEGGAP---------------------------YETVLWGIAGIAVVFTTLVTVEGVRRTRGE---------------------
HutaDMSOhem  YFPFGPEDGGAP---------------------------FQTILWAVAAGAIALVIAVTALSVRQARQEGESG-----------------
AzoarEDBH    DFEILK------------------------------------------------------------------------------------
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SUPPLEMENTAL TABLE 1. Primers utilized in this study with melting temperatures and product length (bp).

Primer ID	**Sequence 5'-3'**	**Melting Temp**	**Product length**
SoxBF	TGGGGCGCTCTACTACTATG	58.0	
SoxBR	TGTTAGACCTGAACCCGAAG	57.8	202
SoxMF	CTTCGGTCCCATAAACACTG	58.1	
SoxMR	CCAAGTGAAGAGCGACATCT	58.0	202
FoxAF	CCAGGACGAAGAGTACTGGA	57.9	
FoxAR	GTGGGCTCAACATCTACCTG	58.2	201
FoxCF	GGAGTAGCCTATGGTGCTGA	57.9	
FoxCR	CACTGTTGTGTGCCCTGATA	58.1	202
FoxGF	CCTGTCCACACGACAACATA	58.0	
FoxGR	GGTACCAGCAACTTGGAGAA	57.8	217
DoxB2F	GGCATGCTAGGCGTAATAGA	58.0	
DoxB2R	CCACTTTGCTCTAGGTTCCA	58.0	213
DoxBF	AAACCGAACAGATCCCTTTC	58.1	
DoxBR	TTTGTGACAGCTTTGTTCCA	57.9	218
SoxE1F	ACCTGCAGGCTACAGCATAG	58.2	
SoxE1R	ACTTCAGTGGCTGACTGACC	57.8	198
SoxE2F	TATCCATTGGCGGATGTAAC	58.3	
SoxE2R	ACACTCAACACCACCAAACC	58.3	212
TqodF	CTCTCAGGTTCGCTGTAGGA	58.2	
TqodR	GTAAGGAACGCTACGTCCAA	57.9	196
McoF	TGCAGGCTGGTACATAAACA	57.8	
McoR	AAGGACTTCCGAACTCTGGT	57.8	212
16SF	CCGTAAAGTCACCGTTTAAAGAC	59.2	
16SR	GTATCTAATCCCTTTTGCTACCC	57.4	206
SoxBF	TTACCTATCCCGCAAACAGC	55.1	
SoxBR	TACACCACTGGGTGACCGTA	57.7	580

SoxMF	CACCTTTCTTCGGTCCCATA	54.2	
SoxMR	GCTATCTCTCTGGCCACGTC	57.3	565
DoxBF	GCCATGTAAACCACAGCGTG	57.0	
DoxBR	GGTCTCAGGCGTACTTGTGT	56.9	600
DoxB2F	CATCAGTGCGGCTATCCTAGC	57.6	
DoxB2R	TCCTCCAGTTTCATACTCACCTCC	57.8	700
FoxAF	CTGGCCAACATATCCGTCTT	54.8	
FoxAR	CCGAATATCCAGCCTGTGTT	54.8	550
FoxBF	GAAGAACAGAGCTATTACAGTACC	52.7	
FoxBR	GGTACTGTAATAGCTCTGTTCTTC	52.7	520
FoxCF	ATCCTAATGAAGGCCCCAGT	55.8	
FoxCR	GGGGAGTGTAGGCAACTTGA	56.8	566
FoxDF	TGTTTCTTTAGTCTACGTTTTCG	51.1	
FoxDR	TGTCTTTTTTGTACTCTAACATCG	51.2	750
FoxEF	CCTGGCCATGGTGCTGGTGAC	63.3	
FoxER	TGGCAGGAGTTAAGTTCTCAAGG	56.7	520
FoxGF	GAGTGGGTGCACAGACTTCA	57.2	
FoxGR	AATAGGACGACACCGGTCAG	56.5	600
FoxJF	GGAAGATATTAACGCCAGTAAGGA	54.3	
FoxJR	TGTAGGATGGACCCTCATAATGC	56.3	710
SoxE1F	GACGGTGCAGATAACACTGG	55.7	
SoxE1R	CCACATTCCAGACTCAGCG	55.8	350
SoxE2F	CGAGAATCCAGTCGGGATGT	55.6	
SoxE2R	CAGCTGAGTCACAAGACTTCC	55.4	450
TqodF	CCTCTCAGGTTCGCTGTAGG	57.0	
TqodR	CCAGTAGGCTGGAGCGAAGC	60.5	250
McoF	CGCCTGGATTAATGAAAGTGA	52.9	
McoR	TTCCTGCCATCCCCATATTA	53.2	584
RcbfF	ATCCCAGCTGGATGTAAACG	54.8	
RcbfR	GGCCACATTTACATGGCTTT	53.9	460
CbsAF	GGTCGCAGCTCTCGTAATGG	58.0	
CbsAR	CCACTCGCGGGAGGATACAAC	59.9	300