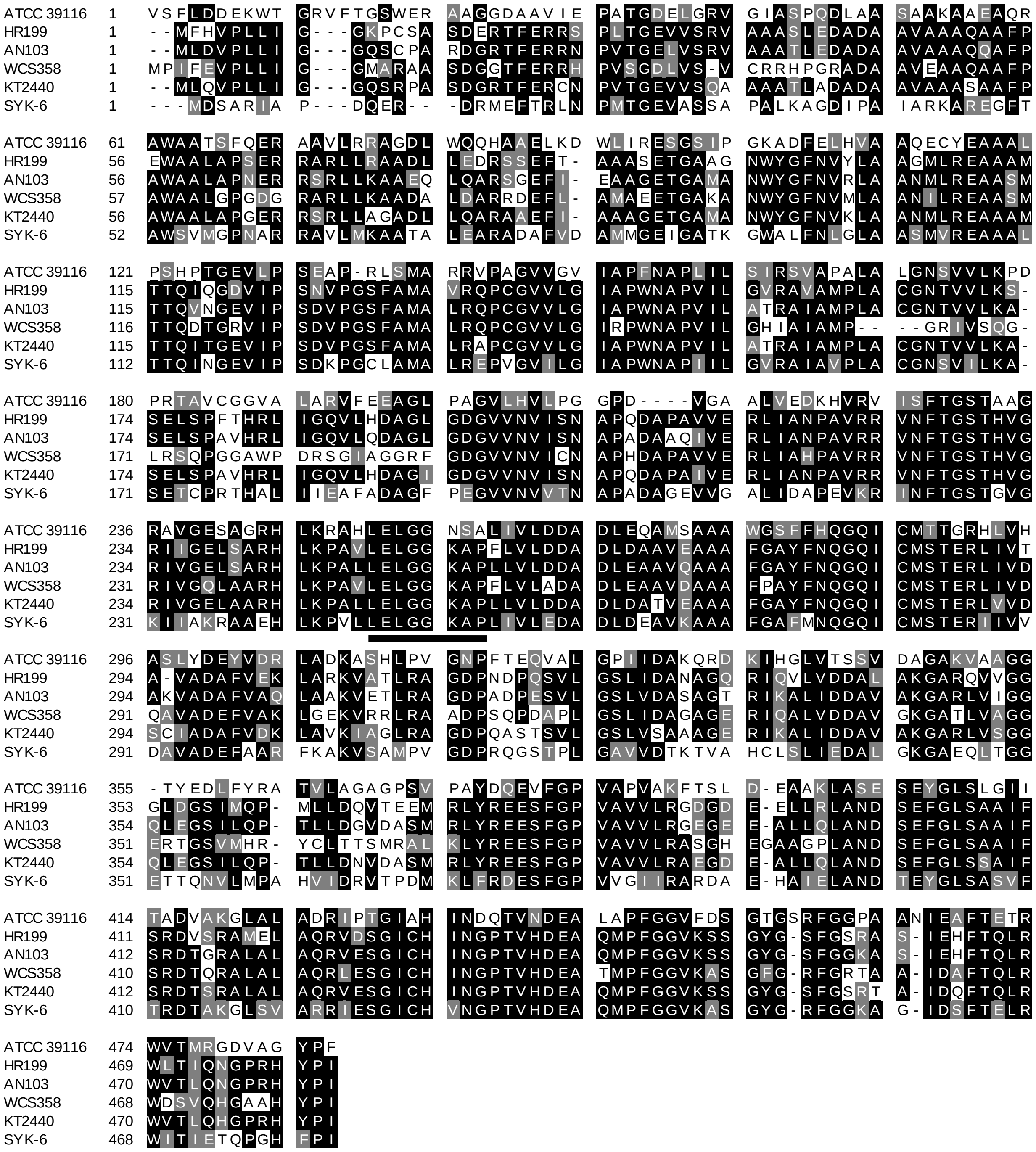

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ATCC 39116   1    VSFLDDEKWT GRVFTGSWER AAGGDAAVIE PATGDELGRV GIASPQDLAA SAAKAAEAQR
HR199        1    --MFHVPLLI G---GKPCSA SDERTFERRS PLTGEVVSRV AAASLEDADA AVAAAQAAFP
AN103        1    --MLDVPLLI G---GQSCPA RDGRTFERRN PVTGELVSRV AAATLEDADA AVAAAQQAFP
WCS358       1    MPIFEVPLLI G---GMARAA SDGGTFERRH PVSGDLVS-V CRRHPGRADA AVEAAQAAFP
KT2440       1    --MLQVPLLI G---GQSRPA SDGRTFERCN PVTGEVVSQA AAATLADADA AVAAASAAFP
SYK-6        1    ---MDSARIA P---DQER-- -DRMEFTRLN PMTGEVASSA PALKAGDIPA IARKAREGFT

ATCC 39116   61   AWAATSFQER AAVLRRAGDL WQQHAAELKD WLIRESGSIP GKADFELHVA AQECYEAAAL
HR199        56   EWAALAPSER RARLLRAADL LEDRSSEFT- AAASETGAAG NWYGFNVYLA AGMLREAAAM
AN103        56   AWAALAPNER RSRLLKAAEQ LQARSGEFI- EAAGETGAMA NWYGFNVRLA ANMLREAASM
WCS358       57   AWAALGPGDG RARLLKAADA LDARRDEFL- AMAEETGAKA NWYGFNVMLA ANILREAASM
KT2440       56   AWAALAPGER RSRLLAGADL LQARAAEFI- AAAGETGAMA NWYGFNVKLA ANMLREAAAM
SYK-6        52   AWSVMGPNAR RAVLMKAATA LEARADAFVD AMMGEIGATK GWALFNLGLA ASMVREAAAL

ATCC 39116   121  PSHPTGEVLP SEAP-RLSMA RRVPAGVVGV IAPFNAPLIL SIRSVAPALA LGNSVVLKPD
HR199        115  TTQIQGDVIP SNVPGSFAMA VRQPCGVVLG IAPWNAPVIL GVRAVAMPLA CGNTVVLKS-
AN103        115  TTQVNGEVIP SDVPGSFAMA LRQPCGVVLG IAPWNAPVIL ATRAIAMPLA CGNTVVLKA-
WCS358       116  TTQDTGRVIP SDVPGSFAMA LRQPCGVVLG IRPWNAPVIL GHIAIAMP-- --GRIVSQG-
KT2440       115  TTQITGEVIP SDVPGSFAMA LRAPCGVVLG IAPWNAPVIL ATRAIAMPLA CGNTVVLKA-
SYK-6        112  TTQINGEVIP SDKPGCLAMA LREPVGVILG IAPWNAPIIL GVRAIAVPLA CGNSVILKA-

ATCC 39116   180  PRTAVCGGVA LARVFEEAGL PAGVLHVLPG GPD----VGA ALVEDKHVRV ISFTGSTAAG
HR199        174  SELSPFTHRL IGQVLHDAGL GDGVVNVISN APQDAPAVVE RLIANPAVRR VNFTGSTHVG
AN103        174  SELSPAVHRL IGQVLQDAGL GDGVVNVISN APADAAQIVE RLIANPAVRR VNFTGSTHVG
WCS358       171  LRSQPGGAWP DRSGIAGGRF GDGVVNVICN APHDAPAVVE RLIAHPAVRR VNFTGSTHVG
KT2440       174  SELSPAVHRL IGQVLHDAGI GDGVVNVISN APQDAPAIVE RLIANPAVRR VNFTGSTHVG
SYK-6        171  SETCPRTHAL IIEAFADAGF PEGVVNVVTN APADAGEVVG ALIDAPEVKR INFTGSTGVG

ATCC 39116   236  RAVGESAGRH LKRAHLELGG NSALIVLDDA DLEQAMSAAA WGSFFHQGQI CMTTGRHLVH
HR199        234  RIIGELSARH LKPAVLELGG KAPFLVLDDA DLDAAVEAAA FGAYFNQGQI CMSTERLIVT
AN103        234  RIVGELSARH LKPALLELGG KAPLLVLDDA DLEAAVQAAA FGAYFNQGQI CMSTERLIVD
WCS358       231  RIVGQLAARH LKPAVLELGG KAPFLVLADA DLEAAVDAAA FPAYFNQGQI CMSTERLIVD
KT2440       234  RIVGELAARH LKPALLELGG KAPLLVLDDA DLDATVEAAA FGAYFNQGQI CMSTERLVVD
SYK-6        231  KIIAKRAAEH LKPVLLELGG KAPLIVLEDA DLDEAVKAAA FGAFMNQGQI CMSTERIIVV

ATCC 39116   296  ASLYDEYVDR LADKASHLPV GNPFTEQVAL GPIIDAKQRD KIHGLVTSSV DAGAKVAAGG
HR199        294  A-VADAFVEK LARKVATLRA GDPNDPQSVL GSLIDANAGQ RIQVLVDDAL AKGARQVVGG
AN103        294  AKVADAFVAQ LAAKVETLRA GDPADPESVL GSLVDASAGT RIKALIDDAV AKGARLVIGG
WCS358       291  QAVADEFVAK LGEKVRRLRA ADPSQPDAPL GSLIDAGAGE RIQALVDDAV GKGATLVAGG
KT2440       294  SCIADAFVDK LAVKIAGLRA GDPQASTSVL GSLVSAAAGE RIKALIDDAV AKGARLVSGG
SYK-6        291  DAVADEFAAR FKAKVSAMPV GDPRQGSTPL GAVVDTKTVA HCLSLIEDAL GKGAEQLTGG

ATCC 39116   355  -TYEDLFYRA TVLAGAGPSV PAYDQEVFGP VAPVAKFTSL D-EAAKLASE SEYGLSLGII
HR199        353  GLDGSIMQP- MLLDQVTEEM RLYREESFGP VAVVLRGDGD E-ELLRLAND SEFGLSAAIF
AN103        354  QLEGSILQP- TLLDGVDASM RLYREESFGP VAVVLRGEGE E-ALLQLAND SEFGLSAAIF
WCS358       351  ERTGSVMHR- YCLTTSMRAL KLYREESFGP VAVVLRASGH EGAAGPLAND SEFGLSAAIF
KT2440       354  QLEGSILQP- TLLDNVDASM RLYREESFGP VAVVLRAEGD E-ALLQLAND SEFGLSSAIF
SYK-6        351  ETTQNVLMPA HVIDRVTPDM KLFRDESFGP VVGIIRARDA E-HAIELAND TEYGLSASVF

ATCC 39116   414  TADVAKGLAL ADRIPTGIAH INDQTVNDEA LAPFGGVFDS GTGSRFGGPA ANIEAFTETR
HR199        411  SRDVSRAMEL AQRVDSGICH INGPTVHDEA QMPFGGVKSS GYG-SFGSRA S-IEHFTQLR
AN103        412  SRDTGRALAL AQRVESGICH INGPTVHDEA QMPFGGVKSS GYG-SFGGKA S-IEHFTQLR
WCS358       410  SRDTQRALAL AQRLESGICH INGPTVHDEA TMPFGGVKAS GFG-RFGRTA A-IDAFTQLR
KT2440       412  SRDTSRALAL AQRVESGICH INGPTVHDEA QMPFGGVKSS GYG-SFGSRT A-IDQFTQLR
SYK-6        410  TRDTAKGLSV ARRIESGICH VNGPTVHDEA QMPFGGVKAS GYG-RFGGKA G-IDSFTELR

ATCC 39116   474  WVTMRGDVAG YPF
HR199        469  WLTIQNGPRH YPI
AN103        470  WVTLQNGPRH YPI
WCS358       468  WDSVQHGAAH YPI
KT2440       470  WVTLQHGPRH YPI
SYK-6        468  WITIETQPGH FPI
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FIG. S1. Homology at amino acid level of the putative VDH$_{\text{ATCC 39116}}$ of *Amycolatopsis* sp. ATCC 39116 to different enzymes with VDH activity. The amino acid sequence of the VDH$_{\text{ATCC 39116}}$ of *Amycolatopsis* sp. ATCC 39116 was compared to sequences of a VDH of *Pseudomonas* sp. HR199 (36); a VDH of *P. fluorescens* AN103 (12); a VDH of *P. putida* WCS358 (46); a VDH of *P. putida* KT2440 (28) and a VDH of *S. paucimobilis* SYK-6 (22). Identical amino acids are labeled in black, while similar amino acids are shaded in grey. The characteristic motif of aldehyde dehydrogenases with glutamic acid in the catalytic center is underlined in black (amino acids 251 to 258).