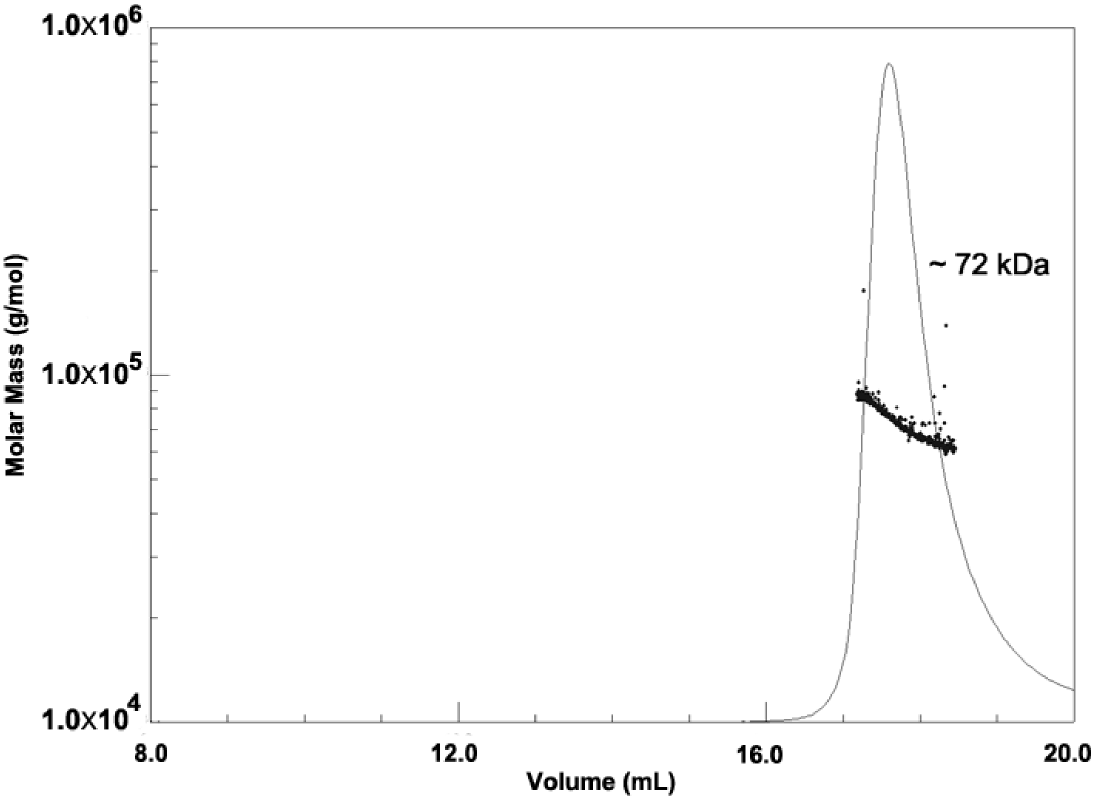
SUPPLEMENTARY FIGURE LEGENDS

Supplementary Fig. 1. Multiangle light scattering analysis of purified OatWY. OatWY forms a trimer in solution.

Supplementary Fig. 2. Multiple sequence alignment of OatWY with other bacterial *O*-acetyltransferases. Conserved catalytic residues (His121 and Trp145') are highlighted in *grey.* The numbering of the *N. meningitidis* sequence is shown. Residues involved in the protruding loop region are italicized, underlined, and highlighted in *grey*. Sequence alignments were calculated using the program ClustalW (55). Sequences from the following bacterial species are shown (TrEMBL accession code: OatWY–*N. meningitidis* serogroup Y (Q93S40), NeuO–*E. coli* K1 (Q58WP5), VatD–*E. faecium* (P50870), MAT–*E. coli* K1 (P77791), PaXAT–*P. aeruginosa* (Q02HJ8), GAT–*E. coli* K1 (P07464)).

Supplementary Figure 1



Supplementary Figure 2

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OatWY-N.mening  ----------MGTHMYSEQGINNTINISTTSLTNATQLTVIGNNNSVYIGNNCKIVSSNI 50
MAT-E.coli      -------------------STEKEKMIAGELYRSADETLSRDRLRARQLIHRYNHSLAEE 41
GAT-E.coli      -----------------MNMPMTERIRAGKLFTDMCEGLPEKRLRGKTLMYEFNHSHPSE 43
VatD-E.faecium  ----------------MGPNPMKMYPIEGNKSVQFIKPILEKLENVEVGEYSYYD-SKNG 43
PaXAT-P.aerug   ----------------MG--NYFESPFRGKLLSEQVS-----NPNIRVGRYSYYSGYYHG 37
NeuO-E.coli K1  MLRLKTQDSRLKTQDSRLKTQDSRLKTQDSRLKTQDSRLKTQDSRLKTQDSRLKTQDSRL 60

OatWY-N.mening  RLKGNNITLFIADDVENMG--------------------------------LVCSLHSDC 78
MAT-E.coli      HTLRQQILADLFGQVTE----------------------------AYIEPTFRCDYGYNI 73
GAT-E.coli      VEKRESLIKEMFATVGEN---------------------------AWVEPPVYFSYGSNI 76
VatD-E.faecium  ETFDKQILYHYPILN------------------------------------------DKL 61
PaXAT-P.aerug   HSFDDCARYLMPDRDDV----------------------------------------DKL 57
NeuO-E.coli K1  KTQDSRLKTQDSFSVDDNGSGNVFVCGDLVNSKENKVQFNGNNNKLIIEDDVECRWLTVI 120

OatWY-N.mening  SLQIQAKTTMGN--------------------------GEITIAEKGKISIGKDCMLAHG 112
MAT-E.coli      FLGNNFFANFD-----------------------------CVMLDVCPIRIGDNCMLAPG 104
GAT-E.coli      HIGRNFYANFN-----------------------------LTIVDDYTVTIGDNVLIAPN 107
VatD-E.faecium  KIGK--FCSIG-----------------------------PGVTIIMNG-ANHRMDGSTY 89
PaXAT-P.aerug   VIGS--FCSIG-----------------------------SGAAFIMAGNQGHRAEWAST 86
NeuO-E.coli K1  FRGDNNYVRIHKNSKIKGDIVATKGSKVIIGRRTTIGAGFEVVTDKCNVTIGHDCMIARD 180

                       121                     145                       171
OatWY-N.mening  YEIRNTDMHPIYSLENGERINHGKDVIIGNHVWLGRNVTILKGVCIPNNVVVGSHTVLYK 172
MAT-E.coli      VHIYTAT-HPIDPVARNSGAELGKPVTIGNNVWIGGRAVINPGVTIGDNVVVASGAVVTK 163
GAT-E.coli      VTLSVTG-HPVHHELRKNGEMYSFPITIGNNVWIGSHVVINPGVTIGDNSVIGAGSIVTK 166
VatD-E.faecium  PFNLFGN-GWEKHMPKLDQLPIKGDTIIGNDVWIGKDVVIMPGVKIGDGAIVAANSVVVK 148
PaXAT-P.aerug   FPFHFMH-EEPAFAGAVNGYQPAGDTLIGHEVWIGTEAMFMPGVRVGHGAIIGSRALVTG 145
NeuO-E.coli K1  VILRASDGHPIFDIHSKKRINWAKDIIISSYVWVGRNVSIMKGVSVGSGSVIGYGSIVTK 240

OatWY-N.mening  SFKEPNCVIAGSPAKIVKENIVWGRKMYHSTMYDDPTLNEFYK----------------- 215
MAT-E.coli      DVP-DNVVVGGNPARIIKKL---------------------------------------- 182
GAT-E.coli      DIP-PNVVAAGVPCRVIREINDRDKHYYFKDYKVESSV---------------------- 203
VatD-E.faecium  DIA-PYMLAGGNPANEIKQRFDQDTINQLLDIKWWNWPIDIINENIDKILDNSIIREVIW 207
PaXAT-P.aerug   DVE-PYAIVGGNPARTIRKRFSDGDIQNLLEMAWWDWPLADIEAAMPLLCTGDIPALYQH 204
NeuO-E.coli K1  DVP-SMCAAAGNPAKIIKRNIIWARTDKAELISDDKRCSSYHAKLTQ------------- 286

OatWY-N.mening  --------
MAT-E.coli      --------
GAT-E.coli      --------
VatD-E.faecium  KK------ 209
PaXAT-P.aerug   WKQRQATA 212
NeuO-E.coli K1  --------
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