Supplementary information

Characterization of two VAO-type flavoprotein oxidases from *Myceliophthora thermophile*

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n712		β16 η4	α12	β1	7 α13
P/15 P615			000000000000000000000000000000000000000	000	
	430	440	450 46	50 470	480
P713 P615 EncM 6HDNO GOOX LaO GilR TamL AknOx	DPVGSTS GNAAYFP AVVPDRI FEDGMSN ADLNITYNYDVHEYF DHVDFI.TPQPVENF GDVMGARS. GDMTGRA TGGFDRT	IITSRLTNPEALT FTNSRIIPRSLVT YTKSGYLN LWIDREIA YANSLTAP YAKSLTLK ASKSAYHRA KIKAAYARR KSKGAYLRK	DYNKVREAIEVVA. DPSSNAVVTDLFRNTS. .ELSDEATDTVLEHAA. .MPNARFAEATAGNLD. .RLSDEAIQAFVDYKFI .SIKGDAVKNFVDYYFI .APTDEQLSVLHHLH. .SFDDRQIGTLYRLT. .PWTAAQAATLYRHLS.	GKPEEVSSNVU .QVPAFSPFYC .DIASPFTQLEI KFVSEPASGGSVKLEI NS.SVR.PGRGWWIQW VSNKV.KDRFWFYQI ADHPGQASVMM STDYDNPAGVVAI ADSQVWGEVSI	VLLVSGGQÜFK CDS.FSVAD JLY.LGGAVAR EG.MPFGN IDF.HGGKNSALAA DV.HGGKNSQVTK 'NS.YGGEINR JA.YGGEVNA YS.YGGKVNS
	4				
P713 P615	η5 η6 200 TT 2000 2000 490	β18 500	al4 200.200000000 TT <u>200.200000000</u> 510 520	α15 12 20202022 12 2020202 530	۳۱ ۵۵ ۲۲ TT 540
P713 P615 EncM 6HDNO GOOX LaO GilR TamL AknOx	DKADTSSGLHPAWRV K.PHPANSLHPAWRT V.PDDATAYP.NRQ P.KRTPAR.HRD V.SNDETAYA.HRD V.TNAETAYP.HRD R.GPSDAAVP.QRD V.PADRTAVA.QRD V.PETATATA.QRD	SFFVMISGQGIP. GMLLCAPAGSMO. SFFVTNLAAAMM. AMGVLALAEWS. QLWLWQFYDSIYD KLWLIQFYDRYD. SVVKSSWFSAMQ. SILKIVYVTTWE. SLIKVWMSATWM.	KVASREI.RDYVQHQV WDASPEE.MAARDRYAA DTTEDARHTAWA GAAPGSEKYPELA YENNTSPYPESGFEFM NNQTYPETSFKFL DAELDELHLGWL DPAQDPVHVRWI DPAHDDANLAWI	HVKGAALKK. LA ETLQPMMDA. AT REGYRALAG. HL RELDAALLRAGVT QGFVATIED. TL DGWVNSVTK. AL RGLYEEFFA. GTGG RELYRDVYA. DTGGV RELYRELFA. TTGGV	PNTGGYMN PGGSYYIN ISGGYVN TSGFGLIN PEDRKGKYFN PKSDWGMYIN PVIGGRIDGGYIN PVVGGAADGAYVN PVVPDDRTEGTFIN
4					
P713 P615	2 TT TT 5	α16 η8 202020 2020 20200 2020 50 560	α17 2000000000 TT 2000000000 570	η9 β19 TT 202→ TT 202→ TT 580 590	β20 →
P713 P615 EncM 6HDNO GOOX LaO GilR TamL AknOx	EGDGSD. PANHLY. FMNPGE. YADTTLTK. YADTRMDR. YPDADLLDPARNRSG YPDVDLADEEWNTSG YPDVDLVDERWNTSG	PEYIDAFY.GKNY ANWKESFY.GDNY ADRTREAYGAAKF AEMVAEVYKPEVY EEAQKLYW.RCNL DYATKVYY.GENL EPWHHLYY.KDNY VPWSELYY.KDAY VPWYTLYY.KGNY	AQHLAARRKYDDDNIB ARLLRWKKKYDDDSVBY ERLQGWKAKYDDDNIB SRLAAWKREYDDENNBF EKLQAIXAKYDDEDVB ARLQXIKAKYDDEDVB ARLQXIKAKYDDEDVB RRLQAWKARMDENVBF PRLQAWKARMDERVBF PRLQAWKARMDERVBF	CRTCVGAEDFIERPDC VKTGVGSEVWDVDATC LINONIPP HNYNIDPE NVVSVEPIAY YPQAVREVK HASIGL HALSVRVPPA HALSVRVPP	SPLCRK SRLCRA

Figure S1: Multiple sequence alignment. Structure–based alignment of MtVAO713 and MtVAO615, EncM (PDB code 3w8w) [22], 6-hydroxy-D-nicotine oxidase (6HDNO, PDB code 2bvf) [23], glucooligosaccharide oxidase (GOOX, PDB code 1ZR6) [4], lactose oxidase (LaO, PDB code 3rj8), oxidoreductase GilR (PDB code 3POP) [25], S. sp. 307-9 tirandamycin oxidase (TamL, PDB code 2Y08) [24] and aclacinomycin oxidoreductase (AckOx, PDB code 2IPI) [8]. The structural alignment was made with Promals3D [38]. The indicated secondary structure elements are those obtained from the crystal structure of MtVAO713 and MtVAO615. Residues involved in FAD binding have a cyan background color, identical residues have a red background color and similar residues have a red color. Residues with orange background are likely to be involved in catalysis. Disulfide linkages are indicated in green italics below the sequences. The figure was created with ESPript [39].



Fig S2: Spectrum of 5 μ M MtVAO713 in the redox potential determination experiment with xanthine oxidase. The collected spectra are shown between time point 0 and time point at 34 minutes.



Fig S3: Spectrum of 10 μ M MtVAO615 in the redox potential determination experiment with xanthine oxidase. The collected spectra are shown between time point 0 and time point at 88 minutes.



Fig S4: Deconvoluted absorption spectra of reduced (A), intermediate (B) and oxidized (C) MtVAO713 during reoxidation by molecular oxygen as measured by double-mixing stopped-flow spectrophotometry, after a delay time of 1.0 s.



Fig S5: Deconvoluted absorption spectra of reduced (A), intermediate 1 (B), intermediate 2 (C) and oxidized (D) MtVAO615 during reoxidation by molecular oxygen as measured by double-mixing stopped-flow spectrophotometry, after a delay time of 1.0 s.



Fig S6: GC spectra of ricinoleic acid conversion by MtVAO713. A) Negative control without MtVAO713. B) Conversion with MtVAO713 present.



Figure S7: MS spectrum of the selected peak corresponding to 12-ketooleic acid.