Table S1: Proteins identified via reverse-phase LC-MS/MS proteomics analysis of Fraction V post mono-Q enrichment.

Main Accession	Putative Function via UniProtKB	Gene Name	MW [kDa]	Coverage [%]	Spectrum Counting	#Validated Peptides	#Unique	#PSMs
A2RAL4	Probable beta-glucosidase A	bglA	93.1714703	28.14	560.7119284	18	27	186
A2QF78	Chitinase activity	An02g13580	43.05643604	33.16	2624.656217	14	24	220
A2R709	Lipase activity	An16g01880	31.67435762	44.11	5598.194305	13	17	354
A2RAR6	Probable glucan 1,3-beta-glucosidase A	exgA	45.49696318	35.1	935.8460255	g	17	89
A2QP93	Hydrolase activity, acting on glycosyl bonds	An07g08640	54.526728	23.81	567.4089795	g	16	65
A2R252	Amine oxidase	An13g03560	51.01335399	23.71	453.1621704	8	11	66
A2QEK4	Extracellular serine-rich protein	An02g11390	86.15441258	16.17	1480.208666	8	15	83
A5ABL2	Extracellular endo-inulinase inuA	inuA	55.84709725	24.61	1232.679493	7	13	65
A2QE24	Aldose 1-epimerase activity	An02g09090	44.11192073	20.35	1047.322436	7	11	129
A2QTI6	Beta-hexosaminidase	An09g02240	67.69893747	16.89	531.6271719	7	11	49
A2QUQ2	Endochitinase A	ctcA	122.0205431	6.84	1241.566454	7	7	97
A2QRM5	Spermidine synthase activity	An08g06560	33.24053717	28.42	456.5385883	6	10	58
A2QWD1	Prolyl aminopeptidase papA	papA	57.7372705	20.16	344.5448481	6	15	46
A2QAS2	Probable mannosyl-oligosaccharide alpha-1,2-mannosidase 1B	mns1B	55.89411029	17.93	381.6086824	6	7	15
A2QF94	Metallocarboxypeptidase activity	An02g13740	63.60141568	16.44	365.3948524	6	11	45
A2QHE1	Glucan 1,4-alpha-glucosidase activity	glaA	68.26665479	14.06	356.6182785	6	10	27
A2QYN8	Phosphatase activity	An12g01910	53.8413057	13.31	1167.103748	6	9	50
A2R0K1	Oxidoreductase / uncharacterized	An12g08890	33.87158216	20.32	1371.868422	5	14	55
A2QAI7	Probable 1,4-beta-D-glucan cellobiohydrolase B	cbhB	56.16899525	11.57	1625.370314	5	15	49
A2R0E0	Extracellular exo-inulinase inuE	inuE	59.11351636	10.99	575.1785503	5	8	42
A2QGH4	PNGaseA	An03g03300	60.89483848	9.8	827.4761912	5	8	49
A2QVI4	Hydrolase activity, hydrolyzing O-glycosyl compounds	An11g01540	37.12356116	22.64	551.0582584	4	5	30
A2R7J0	Lysophospholipase activity	An16g03700	53.89451422	10.49	355.3355148	4	11	25
A2QW02	Acid alpha-amylase	An11g03340	55.20334347	10.3	343.3572843	4	8	22
A2QM62	Aspartic-type endopeptidase activity	An07g00950	40.04297772	8.89	3652.982971	4	7	62
A2R140	Cupin domain protein	An12g10830	31.67117242	17.77	326.6353386	3	6	16
A2QYU7	Probable feruloyl esterase C	faeC	28.56966793	13.33	1907.359642	3	5	54
A2R738	Epoxide hydrolase hyl1	hyl1	44.3253009	10.8	672.4845207	3	6	22
A2QZS1	Serine-type peptidase activity	An12g05960	62.88940732	8.61	156.2461826	3	4	8
A5AAX1	Glycoside Hydrolase Family 76	An07g07700	66.89819093	6.45	154.5010342	3	9	12
A2QAR3	Glucan exo-1,3-beta-glucosidase activity	An01g12450	98.73606787	6.27	255.8262792	3	6	27
A2Q7Q3	Glycoside Hydrolase Family 65	An01g01540	116.0968684	5.97	93.12873387	3	5	13
A2Q7Q4	Catalase	An01g01550	80.16702912	4.4	94.0131233	3	5	17
A2QT52	Cell_wall_mannoprotein_1	An09g00840	21.33298726	20	1003.42376	2	4	20
A2Q8J2	Phosphoric diester hydrolase activity	An01g04530	32.55377751	16.56	971.8076191	2	4	18
A2R5D5	Hydrolase activity, hydrolyzing O-glycosyl compounds	An15g03550	27.33062556	14.74	181.464077	2	2	4
A2QVZ0	Endo-1,4-beta-xylanase activity	An11g03120	35.40598031	11.01	895.9140717	2	7	19
A5AAV4	Hydrolase activity, hydrolyzing O-glycosyl compounds	An07g07530	45.58120023	5.66	313.5699251	2	4	8
A5AA94	Chitinase activity	An02g07020	45.32111952	5.06	97.99060159	2	3	8
A2QS62	Hydroquinone:oxygen oxidoreductase activity	An08g08450	66.54517198	4.88	322.6028036	2	9	17
A2QJY8	Glycoside hydrolase family 125 protein	An04g08730	58.94021328	4.85	303.8468266	2	8	22
A2QMJ7	(R)-6-hydroxynicotine oxidase activity	An07g02360	59.72490928	4.54	304.0151628	2	10	27
A5ABC7	Uncharacterized protein	An08g09840	22.85275197	4.29	5947.015821	2	2	39
A2QQM7	Alpha mannosidase activity	An08g03060	87.72783487	3.38	59.05271659	2	5	8
A2QIL3	Metalloaminopeptidase activity	apsA	97.71208942	2.72	54.5149383	2	12	21
A2QF38	Glucan exo-1,3-beta-glucosidase activity	An02g13180	101.0430797	2.54	63.73372461	2	5	8
A2QY74	RidA protein	An12g00240	10.40940401	12.63	330.0736054	1	1	2
A2QEI1	Necrosis inducing protein	An02g11180	32.56964541	6.48	83.39625667	1	3	4
A2QIK3	Ubiquitin binding protein	An04g03830	52.9293525	4.36	96.78084108	1	1	1
A2R2Y1	Pyridoxamine 5'-phosphate oxidase	An14g02350	29.2357174	4.25	70.30715809	1	3	4
A2QP32	Serine-type carboypeptidase activity	pepF	59.49807019	3.77	55.20597273	1	7	9
A2QQS9	1,3-beta-glucanosyltransferase activity	An08g03580	32.0715527	3.65	62.21625498	1	4	5
A2QEJ9	Probable alpha-galactosidase B	aglB	48.79584661	3.16	67.2896835	1	1	4
A2QM68	Sulfuric ester hydrolase activity	An07g01010	55.83325634	2.44	68.91646705	1	4	6
A2QGK8	Glutathione reductase	An03g03660	51.61933507	2.33	36.12556741	1	4	5
A2QV29	Purine nucleoside permease	An10g00800	43.49473207	2.21	89.59140717	1	2	2
A2QG29	Aminopeptidase activity	An03g01660	59.31236453	2.19	109.639834	1	3	7
A2QAC1	Glycoside Hydrolase Family 31	An01g10930	96.87374122	1.73	109.8318477	1	4	8
A2QH12	Serine-type carboxypeptidase activity	An03g05200	62.55988748	1.59	92.77216719	1	2	3

Legend accession

accession

ccession

eliminated as candidate via clearly defined unrelated biological function

eliminated as candidate due to its presence in inactive peak III

potential candidate enzyme due to putative function, greater abundance in peak V compared to IV, and absence in inactive peak III

candidate capable of oxidatively deaminating fumonisins



Figure S1. Fumonisin deamination activity from *A. niger* **culture supernatant is temperature and pH-dependent. A**) Relative fumonisin deamination activity as a function of temperature. **B**) Relative fumonisin deamination activity as a function of pH. Activity measured via reverse phase LC-MS analysis of partially-enriched culture supernatants of *A. niger*. Error bars represent standard deviation (n=3).



Figure S2. Enrichment of fumonisin deamination activity from culture supernatants of *A. niger*. **A**) *A. niger* culture supernatant applied to Q-Sepharose anion exchange column post 75% (*w:v*) ammonium sulfate precipitation. Fumonisin deamination activity bound to the column and was batch eluted at 250 mM NaCl (Fraction 2). These elution conditions also removed significant amounts of contaminating black pigment and nucleic acids that bound to the resin. **B**) Phenyl Sepharose enrichment of fumonisin deamination activity following anion exchange. Black curve

represents absorbance at 280nm. Dashed line represents conductivity (mS/cm). Grey bars represent % conversion of intact FB₁ into FPy₁. Active fractions spanning areas i and ii (black underline) were pooled and separately applied to a Bio-Rad SEC650 gel permeation column. **C**, **D**) Gel permeation chromatography enrichment of pooled samples (i and ii) from Phenyl-Sepharose run. Black curves represent absorbance at 280nm. Grey bars represent % conversion of intact FB₁ into FPy₁. **E**, **F**) Mono-Q anion exchange chromatography of pooled active samples following gel permeation analysis. Black curves represent absorbance at 280nm. Grey bars represent % conversion of intact FB₁ into FPy₁. Dashed line represents conductivity (mS/cm). Numbers above individual fractions (I, II, III, IV, V) represent those subjected to proteomics analysis.



atgtctgtatccaacgatcctactacaaagctctacgatgcggtgatcgtggggggccgga - 60 M S V S N D P T T K L Y D A V I V G A G cttagcggccttcaagccgcgcattccatccaggcagcaggattcagcgtgtgtatcctg - 120 S G L Q A A H S I Q A A G F S V C I L L gaagctacggaccgaatgggtgggaagacgttgaccgtaaaatccagcgagaaaggatac - 180 E A T D R M G G K T L T V K S S E K G Y aacgatctaggagcggcttgggtgaatgatacgaaccagacggagattttcaaacttcat - 240 Τ K L H Α W Ν D Ν Q Α cagcggtatggactggatgggtggttcagtatacttgtggagatgatatcctcgagtca - 300 Q R Y G L D G V V Q Y T C G D D I L E S ggcgagggggtgatccgcaagataccgtatggattgccattgactgggcttccgaagaaa - 360 G E G V I R K I P Y G L Ρ K K G ttgttggatattctccgaattgagtcctcacggttagacttggacgatcctacgagtttt - 420 L L D I L R I E S S R L D L D D P F ccaggggccacagaagtggataatctgacgttcagggacttttgcgtcgagaagactgga- 480 P G A T E V D N L T F R D F C V E K T G tcggaggatgttattcacattacagatgctatttcaacggcgctgcttggattgaatagt - 540 S E D V I H I T D A I S T A L L G L N S aacgaactcagtgctttgtatatgctctactacttcaaaagtgggagtgggatcgacaat - 600 N E L S A L Y M L Y Y F K S Ν G D ctgctgtcagatgagagagaggagcacagtacctgcggacaagacaaggtacccaaacc - 660 R D G A Q Y L R T R Q G T Q T atcgcccggaagatggcagatgagctcacccaatcggacatttttctgggcatgcccgtc - 720 I A R K M A D E L T Q S D I F L G M P V acttcaatcaatcagactgacgctgatgctcactgcgtggtccagacacttgatggaagt - 780 T S I N Q T D A D A H C V V Q T L D G S tcttttcgctgtcgacgcgttatcgtgtctatccctaccaccttataccggagtgtctcc - 840 S F R C R R V I V S Ι Ρ Т Т L Y RSVS ttccacccccacttccacatgcaaaacaggtattaagtgaccatacgatcatgggatac - 900 F H P P L P H A K Q V L S D Η Τ Ι M G Y tacagtaaagtgatcttcatcttcaaagaaccatggtggcgcgacgctggacttaccgga - 960 Y S K V I F I F K E P W W R D A G L T G atcgtcaactgtgcgggtggccccataacctttacacgggacacgagtgtacccaccgac - 1020 I V N C A G G P I T F T R D T S V P T D gaccaatggtctatcacatgcttcatggtgggcagtcgcggacgagcgtggtctaagctg - 1080 D Q W S I T C F M V G S R G R A W S K L tcaaaggatgatcgatacagccaagtgtgggagcagtttcgccgatgttttgaagagttc - 1140 SKDDR<mark>YSQVWEQFR</mark>RCFEEF gtggaaaacatccccgagccagtaaataccctggagatggaatggagtaaagagccttat - 1200 V E N I P E P V N T L E M E W S K E P Y ttccttggagcaccttgtccggctatgatacccggcttactgactactgccgggagtgat - 1260 F L G A P C P A M I P G L L T T A G S D ctagctgcaccgcacggcaaagtgcattttatcggaacagaaacgtccacagtgtggcgt - 1320 LAAPHGKVHFIGTE TSTVWR gggtacatggaaggggctattagagccgggcagcgaggaggagccgaggttgtgacggca - 1380 GYMEGAIRAGQRGGAEVVTA ctgcaggaagactag - 1395 LQED*

Figure S3. MS/MS sequencing and amino acid sequence of AnFAO_seq1. A) MS/MS spectrum of tryptic peptide corresponding to AnFAO_seq1 sequence (K)SGSGIDNLLSDER. **B**) Amino acid sequence of AnFAO_seq1. Peptides identified via MS/MS sequencing are boxed in light grey. The additional peptide identified following PCR amplification and DNA sequencing of AnFAO_seq1 is highlighted in red.

AnFAO_seq3	MSVSNDPTTKLYDAVIVGAGLSGLQAAHSIQAAGFSVCILEATDRVGGKTLTVKSSEKGY	60
AnFAO seq2	MSVSNDPTTKLYDAVIVGAGLSGLQAAHSIQAAGFSVCILEATDRVGGKTLTVKSSEKGY	60
AnFAO seq1	MSVSNDPTTKLYDAVIVGAGLSGLQAAHSIQAAGFSVCILEATDEMGGKTLTVKSSEKGY	60
AnFAO seq5	MSVSNDPTTKLYDAVIVGAGLSGLOAAHSIOAAGFSVCILEATDRVGGKTLTVKSSEKGY	60
AnFAO seq6	MSVSNDPTTKLYDAVIVGAGLSGLQAAHSIQAAGFSVCILEATDRVGGKTLTVKSSEKGY	60
AnFAO seq4	MSVSNDPTTKLYDAVIVGAGLSGLOAAHSIOAAGFSVCILEATDRVGGKTLTVKSSEKGY	60

AnFAO sea3	NDLGAAWVNDTNOTETEKLHOOYGLDGVVOYTCGDDTLESGEGVTRKTPYGLPLTGLPKK	120
AnFAO seg2	NDLGAAWVNDTNOTEIEKLHOOYGLDGVVOYTCGDDILESGEGVIRKIPYGLPLTGLPKK	120
AnFAO segi		120
ApFAO seg5		120
AnFAO segé	NDLGAAWVNDTNOTETEKLHORYCLDCVVOYDCODDILESGEGVIRKIPYCLDITGLPKK	120
AnrAO_Seq0		120
AIIFAO_SEQ4		120
	•	
		100
AnrAO_seq3		100
AnrAO_seq2		100
AnFAO_seq1		100
AnFAO_seq5		180
AnFAO_seq6		180
AnFAO_seq4	LLDILRIESSRLDLDDHMGFPGATEVDNLTFRDFCVEKTGSEDVIHITDAISTALLGLNS	180

AnFAO_seq3	NELSALYMLYYFKSGSGIDNLLSDERDGAQYLRTRQGTQTIARKMADELTQSDIFLGMPV	240
AnFAO_seq2	NELSALYMLYYFKSGSGIDNLLSDERDGAQYLRTRQGTQTIARKMADELTQSDIFLGMPV	240
AnFAO_seq1	NELSALYMLYYFKSGSGIDNLLSDERDGAQYLRTRQGTQTIARKMADEITQSDIFLGMPV	240
AnFAO_seq5	NELSALYMLYYFKSGSGIDNLLSDERDGAQYLRTRQGTQTIARKMADELSQSDIFLGMPV	240
AnFAO_seq6	NELSALYMLYYFKSGSGIDNLLSDERDGAQYLRTRQGTQTIARKMADELSQSDIFLGMPV	240
AnFAO_seq4	NELSALYMLYYFKSGSGIDNLLSDERDGAQYLRTRQGTQTIARKMADEISDSDIFLGMPV	240

AnFAO_seq3	TSINQTDADAHCVVQTLDGSSFRCRRVIVSIPTTLYRSVSFHPPLPHAKQVLSDHTIMGY	300
AnFAO_seq2	TSINQTDADAHCVVQTLDGSSFRCRRLIVSIPTTLYRSVSFHPPLPHAKQVLSDHTIMGY	300
AnFAO_seq1	TSINQTDADAHCVVQTLDGSSFRCRRVIVSIPTTLYRSVSFHPPLPHAKQVLSDHTIMGY	300
AnFAO_seq5	TSINQTDADAHCVVKTLDGSSFRCRRVIVSIPTTLYRSVSFHPPLPHAKQVLSDHTIMGY	300
AnFAO_seq6	TSINQTDADAHCVVQTLDGSSFRCRRVIVSIPTTLYRSVSFHPPLPHAKQVLSDHTIMGY	300
AnFAO_seq4	TSINQTDADAHCVVQTLDGSSFRCRRVIVSIPTTLYRSVSFHPPLPHAKQVLSDHTIMGY	300

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AnFAO_seq3	YSKVIFIFKEPWWRDAGLTGIVDCAGGPITFTRDTSVPTDDQWSITCFMVGSRGRAWSKL	360
AnFAO_seq2	YSKVIFIFKEPWWRDAGLTGIVNCAGGPITFTRDTSVPTDDQWSITCFMVGSRGRAWSKL	360
AnFAO_seq1	YSKVIFIFKEPWWRDAGLTGIVNCAGGPITFTRDTSVPTDDQWSITCFMVGSRGRAWSKL	360
AnFAO_seq5	YSKVIFIFKEPWWRDAGLTGIVDCAGGPITFTRDTSVPTDDQWSITCFMVGSRGRAWSKL	360
AnFAO_seq6	YSKVIFIFKEPWWRDAGLTGIVDCAGGPITFTRDTSVPTDDQWSITCFMVGSRGRAWSKL	360
AnFAO_seq4	YSKVIFIFKEPWWRDAGLTGIV <mark>D</mark> CAGGPITFTRDTSVPTDDQWSITCFMVGSRGRAWSKL	360

AnFAO_seq3	SKDDRYSQVWEQFRRCLEGFVENIPEHANTLEMEWSKEPYFLGAPCPAMIPGLLTTTGSD	420
AnFAO_seq2	SKDDRYSQVWEQFRRCFEEFVENIPEFVNTLEMEWSKEPYFLGAPCPAMIPGLLTTAGSD	420
AnFAO_seq1	SKDDRYSQVWEQFRRCFEEFVENIPEPVNTLEMEWSKEPYFLGAPCPAMIPGLLTTAGSD	420
AnFAO_seq5	SKDDRYSQVWEQFRRFFEEFVENIPEPANTLEMEWSKEPYFLGAPCPAMIPGLLTTAGSD	420
AnFAO_seq6	SKDDRYSQVWEQFRRCFEDFVENIPEFANTLEMEWSKEPYFLGAPCPAMIPGLLTTAGSD	420
AnFAO_seq4	SKDDRYSQVWEQFRRCFEDFVENIPEPANTLEMEWSKEPYFLGAPCPAMIPGLLTTAGSD	420

AnFAO_seq3	LAAPHGKVHFIGTETSTVWRGYMEGAIRAGQRGGAEVVTALQED 464	
AnFAO_seq2	LAAPHGKVHFIGTETSTVWRGYME <mark>G</mark> AIRAGQRGGAEVVTALQED 464	
AnFAO_seq1	LAAPHGKVHFIGTETSTVWRGYME <mark>G</mark> AIRAGQRGGAEVVTALQED 464	
AnFAO_seq5	LAAPHGKVHFIGTETSTVWRGYME <mark>G</mark> AIRAGQRGGAEVVTALQED 464	
AnFAO seq6	VAAPHGKVHFIGTETSTVWRGYMEEAIRAGQRGGAEVVTALQED 464	
AnFAO seq4	VAAPHGKVHFIGTETSTVWRGYMEGAIRAGQRGGAEVVTALQED 464	
_ *		

Figure S4. Multiple sequence alignment of AnFAO homologs identified in this study. Aligned are the amino acid sequences of clones AnFAO_seq1-6. * represents 100% conservation, while : represents a strongly conserved substitution, and a . represents a conserved substitution. Boxed in red are amino acid positions that show variation between homologs. Alignment was generated in Clustal Omega.



Figure S5. Fumonisin deamination activity of MBP-tagged AnFAO. A) Relative activity of MBP-tagged AnFAO_seq1 compared to the affinity tag free version as measured via AmplexTM red assay using FB₁ as substrate. Error bars represent standard error of the mean (n=3). **B)** Coomassie-stained SDS-PAGE analysis of MBP-tagged AnFAO following gel permeation chromatography. PM represents protein markers. Numbers represent the molecular weight of the protein markers.

MAON MAOA		0
MAOB		0
EsAO	MALAPSYINPPNVASPAGYSHVGVGPDGGRYVTIAGQIGQDASGVTDPAYEKQVAQAFAN	60
AIITAO_Seq1		0
MAON MAOA	MTSRDGYQWTPETGLTQG	18
MAOB		0
EsAO	$\label{eq:label} LRACLAAVGATSNDVTKLNYYIVDYAPSKLTAIGDGLKATFALDRLPPCTLVPVSALSSP$	120
AnFAO_seq1		0
MAON	VPSLGVISPPTNIEDTDKDGPWDVIVIGGGYCGLTATRDLT-AGFKTLLLEARDRIGGRS	77
MAOA MAOB	MENQEKASIAGHMFDVVVIGGGISGLSAAKLLHDSGLNVVVLEARDRVGGRT	52 43
EsAO	EYLFEVDATALVPGHTTPDNVADVVVVGAGLSGLETARKVQAAGLSCLVLEAMDRVGGKT	180
AnFAO_seq1	MSVSNDPTTKLYDAVIVGAGLSGLQAAHSIQAAGFSVCILEATDRMGGKT	50
	**.*.*.	
MAON	WSSNIDGYPYEMGGTWVHWH-QSHVWREITRYKMHNALSPSFNFSRGVNHFQLR	130
MAOA	YTIRNEHVDYVDVGGAYVGPT-QNRILRLSKELGIETYKVNVSERLVQY-VKGK	104
MAOB Esao	YTLRNQKVKYVDLGGSYVGPT-QNRILRLAKELGLETYKVNEVERLIHH-VKGK LSVOSGPGRTTINDLGAAWINDSNOSEVSRLFERFHLEGELORTTGNSIHOAODGTTT	95 238
AnFAO_seq1	LTVKSSEKGYNDLGAAWVNDTNQTEIFKLHQRYGLDGVVQYTCGDDILESGEGVIR	106
	: ::*.::: *: : . :. :	
MAON	TNPTTSTYMTHEAEDELLRSALHKFTNVDGTNGRTVLPEPHDMFYVPEFRKYDEMSYSER	190
MAOA	TYPFRGAFPPVWNPIAYL-DYNNLWRTIDNMGKEIPTDAPWEAQHADKWDKMTMKEL	160
MAOB	SYPFRGPFPPVWNPITYL-DHNNFWRTMDDMGREIPSDAPWKAPLAEEWDNMTMKEL	151
EsAO AnFAO segi	TAPYGDSLLSEEVASALA-ELLPVWSQLIEEHSLQDLKASPQAKRLDSVSFAHY KIPYGLPLTGLPKKLL-DILRIFSSBLDLDDPTSFPGATEVDNLTERDF	291
mirno_seqr	. *	101
MAON	IDQIRDELSLNERSSLEAFILLCSGGTLENSSFGEFLHWWAMSGYTYQGCMDCLIS IDKICWTKTABBFAXIFVNINVTSEDHE-VSALWELWYVKOCGCTTRIESVTNG	246
MAOB	LDKLCWTESAKQLATLFVNLCVTAETHE-VSALWFLWYVKQCGGTTRIISTING	204
EsAO	CEKELNLPAVLGVANQITRALLGVEAHE-ISMLFLTDYIKSATGLSNIFSDKKD	344
AnFAO_seq1	CVEKTGSEDVIHITDAISTALLGLNSNE-LSALYMLYYFKSGSGIDNLLSDERD	207
MAON	YKFKDGQSAFARRFWEEAAGTGRLGYVFGCPVRSVVNERDAVRVTARDGREFVA	300
MAOA Maob	G-QERKFVGGSGQVSER-IMDLLGDQVKLNHPVTHVDQSSDNIIIETLNHEHYEC G-OERKFVGGSGQVSER-IMDLLGDRVKLERPVIYIDOTRENVLVETLNHEMYEA	266
EsAO	GGQYMRCKTGMQSICHAMSKELVPGSVHLNTPVAEIEQSASGCTVRSASGAVFRS	399
AnFAO_seq1	GAQYLRTRQGTQTIARKMADELTQSDIFLGMPVTSINQTDADAHCVVQTLDGSSFRC	264
	: * : : ** : : : : : : . : .	
MAON	KRVVCTIPLNVLSTIQFSPALSTERISAMQAGHVNMCTKVHAEVDNKDMRSWTGIA	356
MAOA	KYVINAIPPTLTAKIHFRPELPAERNQLIQRLPMGAVIKCMMYYKEAFWKKKDYCGCMII	326
MAOB Esao	KYVISAIPPTLGMKIHFNPPLPMMRNQMITRVPLGSVIKCIVYYKEPFWRKKDYCGTMII KKVVVSLPTTLYPTLTFSPPLPAEKOALAENSILGYYSKIVFVWDKPWWREOGESGVL	317 457
AnFAO_seq1	RRVIVSIPTTLYRSVSFHPPLPHAKQVLSDHTIMGYYSKVIFIFKEPWWRDAGLTGIV	322
	: *: :: * : : * * * : :. * .: . *	
MAON	-YPENKLCYAIGDGTTPAGNTHLVCEGTDANHIOPDEDVRET-LKAVGOLAP	406
MAOA	EDEDAPISITLDDTKPDGSLPAIMGFILARKADRLAKLHKEIRKKKICELYAKVLGSQ	384
MAOB	DGEEAPVAYTLDDTKPEGNYAAIMGFILAHKARKLARLTKEERLKKLCELYAKVLGSL	375
ESAO AnFAO segl	QSSCDPISFARDTSIDVDRQWSITCFMVGDPGRKWSQQSKQVRQKSVWDQLRAAYENAGA NCAGGPITFTRDTSVPTDDOWSITCFMVGSRGRAWSKLSKDDRYSOVWEOFRRCFEEFVE	382
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MAON	CERCURATIVE REPORT OF THE REPORT	4.65
MAON	GTFGVKRLVFHNWVKDEFAKGAWF-FSRPGMVSECLQGLREKHGGVVFANSDWALGWRSF EALHPVHYEEKNWCEEOYSGGCYTAYFPPGIMTOYGRVIROPVGRIFFAGTETATKWSGY	465
MAOB	EALEPVHYEEKNWCEEQYSGCYTTYFPFGILTQYGRVLRQPVDRIYFAGTETATHWSGY	435
EsAO	QVPEPANVLEIEWSKQQYFQCAPSAVYGLNDLITLGSALRTPFKSVHFVGTETSLVWKGY	577
AnrAU_seq1	NIFEFVNILEMEWSKEFIFLGARCPAMIFGLLTTAGSDLAAPHGKVHFIGTETSTVWRGY **::: *. : *. : : : : : : : : : : : : :	44∠
MAON		494
MAOA	<pre>megaveageraareilhamgkipedeiwosepesvdvpaopitttflerhlpsvpgllri</pre>	495
EsAO	MEGAIRSGQRGAAEVVASLVPAA	600
AnFAO_seq1	MEGAIRAGQRGGAEVVTALQED	464
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MAON	494	
MAOA	IGFSTSVTALGFVLYKYKLLPRS 527	
MAUB EsAO	600	
AnFAO seq1	464	

Figure S6. Multiple sequence alignment of select homologous amine oxidase sequences. Amino acid sequence colored blue represents the N-terminal Reactive Intermediate Deaminase (RID) domain found in the *Exophiala spinifera* AO (XP_016238458.1), while sequence colored orange represents the N-terminal addition of *Aspergillus niger* MAO-N (EHA25738.1). Amino acid sequences colored red represent C-terminal extensions found in human MAO-A (NP_000231.1) and human MAO-B (P27338.3). Sequence boxed in red represent the conserved GXGXXG motif characteristic of ADP-binding $\beta\alpha\beta$ -folds, while sequence boxed in green denotes the position of the cysteine residue required for covalent FAD binding in human MAO-A and MAO-B that is absent in AnFAO and the other isoforms. * represents 100% conservation, while : represents a strongly conserved substitution, and a . represents a conserved substitution. Alignment was generated using Clustal omega.