

Comprehensive genome-wide analysis reveals different classes of enigmatic old yellow enzyme in fungi

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Supplementary Table S1. List of previously reported OYEs used as query sequences in this study.

S. No.	OYE	Accession number	Organism
1.	OYE1	Q02899.3	<i>Saccharomyces pastorianus</i>
2.	OYE2	NP_012049.1	<i>Saccharomyces cerevisiae</i>
3.	OYE3	NP_015154.1	-do-
4.	KYE1	XP_451397.1	<i>Kluyveromyces lactis</i>
5.	HYE1	AAN09952.1	<i>Hansenula polymorpha</i>
6.	HYE2	AAN09953.1	-do-
7.	HYE3	AAN09954.1	-do-
8.	PsOYE1	XP_001384055.1	<i>Pichia stipites</i>
9.	SYE1	NP_718044.1	<i>Shewanella oneidensis</i>
10.	SYE2	NP_718043.1	-do-
11.	SYE3	NP_719682.1	-do-
12.	SYE4	NP_718946.1	-do-
13.	AtOPR	CAA71627.1	<i>Arabidopsis thaliana</i>
14.	LeOPR	NP_001234781.1	<i>Solanum lycopersicum</i>
15.	YqjM	NP_390263.1	<i>Bacillus subtilis</i>
16.	GkOYE	YP_148185.1	<i>Geobacillus kaustophilus</i>
17.	TpOYE	YP_001664021.1	<i>Thermoanaerobacter pseudethanolicus</i>
18.	TsOYE	YP_004203660.1	<i>Thermus scotoductus</i>
19.	TtOYE	YP_143423.1	<i>Thermus thermophiles</i>
20.	GmOYE	YP_006721534.1	<i>Geobacter metallireducens</i>
21.	PpOYE	NP_743414.1	<i>Pseudomonas putida</i>

Supplementary Table S2. List of fungal species used in this comparative study.

Species	Class	Order	Lifestyle	Genome size (Mb)	Number of genes
<i>Ascochyta rabiei</i>	<i>Dothideomycetes</i>	<i>Pleosporales</i>	Necrotroph	NA	NA
<i>Ashbya gossypii</i>	<i>Saccharomycetes</i>	<i>Saccharomycetales</i>	Biotroph	9.2	4,718
<i>Aspergillus clavatus</i>	<i>Eurotiomycetes</i>	<i>Eurotiales</i>	Animal pathogen	27.86	9,121
<i>Aspergillus flavus</i>	<i>Eurotiomycetes</i>	<i>Eurotiales</i>	Necrotroph	36.79	12,604
<i>Aspergillus fumigatus</i>	<i>Eurotiomycetes</i>	<i>Eurotiales</i>	Animal pathogen	29.38	9,887
<i>Aspergillus nidulans</i>	<i>Eurotiomycetes</i>	<i>Eurotiales</i>	Saprotroph	30.07	10,560
<i>Aspergillus niger</i>	<i>Eurotiomycetes</i>	<i>Eurotiales</i>	Saprotroph	37.2	11,200
<i>Aspergillus oryzae</i>	<i>Eurotiomycetes</i>	<i>Eurotiales</i>	Saprotroph	37.12	12,063
<i>Aspergillus terreus</i>	<i>Eurotiomycetes</i>	<i>Eurotiales</i>	Saprotroph	29.33	10,406
<i>Baudoinia compniacensis</i>	<i>Dothideomycetes</i>	<i>Capnodiales</i>	Saprotroph	21.88	10,513
<i>Botryotinia fuckeliana</i>	<i>Leotiomycetes</i>	<i>Helotiales</i>	Necrotroph	38.8	13,664
<i>Candida albicans</i>	<i>Saccharomycetes</i>	<i>Saccharomycetales</i>	Animal pathogen	16	6,214
<i>Candida glabrata</i>	<i>Saccharomycetes</i>	<i>Saccharomycetales</i>	Animal pathogen	12.28	5,213
<i>Chaetomium globosum</i>	<i>Sordariomycetes</i>	<i>Sordariales</i>	Saprotroph	34.89	11,124
<i>Claviceps purpurea</i>	<i>Sordariomycetes</i>	<i>Hypocreales</i>	Biotroph	NA	NA
<i>Coccidioides immitis</i>	<i>Eurotiomycetes</i>	<i>Onygenales</i>	Animal pathogen	28.95	9,757
<i>Coccidioides posadasii</i>	<i>Eurotiomycetes</i>	<i>Onygenales</i>	Animal pathogen	27.58	10,225
<i>Cochliobolus heterostrophus</i>	<i>Dothideomycetes</i>	<i>Pleosporales</i>	Necrotroph	36.46	13,336
<i>Cochliobolus sativus</i>	<i>Dothideomycetes</i>	<i>Pleosporales</i>	Hemibiotroph	34.42	12,250
<i>Cryptococcus gattii</i>	<i>Tremellomycetes</i>	<i>Tremellales</i>	Animal pathogen	18.37	6,565
<i>Cryptococcus neoformans</i>	<i>Tremellomycetes</i>	<i>Tremellales</i>	Animal pathogen	18.87	6,967
<i>Dothistroma septosporum</i>	<i>Dothideomycetes</i>	<i>Capnodiales</i>	Hemibiotroph	30.21	12,580
<i>Fusarium graminearum</i>	<i>Sordariomycetes</i>	<i>Hypocreales</i>	Necrotroph	36.45	13,321
<i>Fusarium oxysporum</i>	<i>Sordariomycetes</i>	<i>Hypocreales</i>	Hemibiotroph	61.36	17,708
<i>Fusarium solani</i>	<i>Sordariomycetes</i>	<i>Hypocreales</i>	Necrotroph	51.3	15,706
<i>Fusarium verticillioides</i>	<i>Sordariomycetes</i>	<i>Hypocreales</i>	Hemibiotroph	41.78	15,869
<i>Hansenula polymorpha</i>	<i>Saccharomycetes</i>	<i>Saccharomycetales</i>	Animal pathogen	9.5	5,933
<i>Histoplasma capsulatum</i>	<i>Eurotiomycetes</i>	<i>Onygenales</i>	Animal pathogen	32.99	9,248
<i>Kluyveromyces lactis</i>	<i>Saccharomycetes</i>	<i>Saccharomycetales</i>	Saprotroph	10.6	5,329
<i>Laccaria bicolor</i>	<i>Agaricomycetes</i>	<i>Agaricales</i>	Symbiont	64.9	20,614
<i>Leptosphaeria maculans</i>	<i>Dothideomycetes</i>	<i>Pleosporales</i>	Hemibiotroph	44.89	12,469
<i>Macrophomina phaseolina</i>	<i>Dothideomycetes</i>	<i>Botryosphaerales</i>	Necrotroph	49	14,249
<i>Magnaporthe oryzae</i>	<i>Sordariomycetes</i>	<i>Magnaporthales</i>	Hemibiotroph	39.4	12,841
<i>Mycosphaerella fijiensis</i>	<i>Dothideomycetes</i>	<i>Capnodiales</i>	Hemibiotroph	74.14	13,107
<i>Mycosphaerella graminicola</i>	<i>Dothideomycetes</i>	<i>Capnodiales</i>	Hemibiotroph	39.69	10,933
<i>Mycosphaerella populorum</i>	<i>Dothideomycetes</i>	<i>Capnodiales</i>	Hemibiotroph	29.35	10,233
<i>Neosartorya fischeri</i>	<i>Eurotiomycetes</i>	<i>Eurotiales</i>	Animal pathogen	32.55	10,406
<i>Neurospora crassa</i>	<i>Sordariomycetes</i>	<i>Sordariales</i>	Saprotroph	41.04	9,730
<i>Paracoccidioides brasiliensis</i>	<i>Eurotiomycetes</i>	<i>Onygenales</i>	Animal pathogen	30.0	8,741
<i>Penicillium chrysogenum</i>	<i>Eurotiomycetes</i>	<i>Eurotiales</i>	Saprotroph	32.19	12,943
<i>Penicillium digitatum</i>	<i>Eurotiomycetes</i>	<i>Eurotiales</i>	Necrotroph	26	9,153
<i>Penicillium marneffei</i>	<i>Eurotiomycetes</i>	<i>Eurotiales</i>	Animal pathogen	28.64	10,638
<i>Pichia pastoris</i>	<i>Saccharomycetes</i>	<i>Saccharomycetales</i>	Saprotroph	9.43	5,313
<i>Pichia stipitis</i>	<i>Saccharomycetes</i>	<i>Saccharomycetales</i>	Saprotroph	15.4	5,839
<i>Piriformospora indica</i>	<i>Agaricomycetes</i>	<i>Sebacinales</i>	Symbiont	24.98	11,769
<i>Puccinia graminis f. sp. tritici</i>	<i>Urediniomycetes</i>	<i>Uredinales</i>	Biotroph	88.64	15,800
<i>Pyrenophora teres f. teres</i>	<i>Dothideomycetes</i>	<i>Pleosporales</i>	Necrotroph	33.58	11,799
<i>Pyrenophora tritici-repentis</i>	<i>Dothideomycetes</i>	<i>Pleosporales</i>	Necrotroph	37.84	12,141

<i>Rhizoctonia solani</i>	<i>Agaricomycetes</i>	<i>Cantharellales</i>	Necrotroph	36.94	10,489
<i>Rhodosporidium toruloides</i>	<i>Ustilaginomycetes</i>	<i>Ustilaginales</i>	Saprotroph	20.2	8,171
<i>Saccharomyces cerevisiae</i>	<i>Saccharomycetes</i>	<i>Saccharomycetales</i>	Saprotroph	12.2	6,692
<i>Schizosaccharomyces pombe</i>	<i>Schizosaccharomycetes</i>	<i>Schizosaccharomycetales</i>	Saprotroph	12.5	5,058
<i>Sclerotinia sclerotiorum</i>	<i>Leotiomycetes</i>	<i>Helotiales</i>	Necrotroph	38.0	11,860
<i>Setosphaeria turcica</i>	<i>Dothideomycetes</i>	<i>Pleosporales</i>	Hemibiotroph	43.01	11,702
<i>Stagonospora nodorum</i>	<i>Dothideomycetes</i>	<i>Pleosporales</i>	Necrotroph	37.21	12,380
<i>Trichoderma atroviride</i>	<i>Sordariomycetes</i>	<i>Hypocreales</i>	Saprotroph	36.1	11,100
<i>Trichoderma reesei</i>	<i>Sordariomycetes</i>	<i>Hypocreales</i>	Saprotroph	33.9	9,129
<i>Trichoderma virens</i>	<i>Sordariomycetes</i>	<i>Hypocreales</i>	Saprotroph	38.8	11,643
<i>Ustilago hordei</i>	<i>Ustilaginomycetes</i>	<i>Ustilaginales</i>	Biotroph	26.1	7,113
<i>Ustilago maydis</i>	<i>Ustilaginomycetes</i>	<i>Ustilaginales</i>	Biotroph	19.8	6,786

Supplementary Table S3. List of primers used to amplify genes needed for gene expression analyses.

Primer name	Forward primer (5'-3')	Reverse primer (5'-3')
ArOYE1-RT	CCGACTACCCATTTAGCGAAGA	CTGAACGCCATACTGATGCAA
ArOYE2-RT	GACAGAAGAGGAAGGTTATACGGACTA	ATCCCTCTAATTTATACCGACCTTGA
ArOYE3-RT	ACAACGCAGTCCCCAAGCT	TTCGGCAGGTCTGGATTTG
ArOYE4-RT	CTGTCCGGCTCCATCACCAA	AACATGCGACCGACAAAAGC
ArOYE5-RT	GTGCGGTTCCCGAAGCT	ATCATCGTGTATCTATCCATCTAGCATT
ArOYE6-RT	GCCACCGACGAGGACATT	CTGGGCTGCGTGGACAA
ArEF1 α -RT	GATCACTTTTTTCGGTCGTTTGT	CTTCGTTCCACCAGACCGTAA

ArOYE: *Ascochyta rabiei* Old Yellow Enzyme, ArEF1 α : *Ascochyta rabiei* Elongation factor1- α

Supplementary Table S4. List of OYE genes identified from 60 fungal species along with their corresponding nomenclature, HMM score, protein sequence ID, Class, protein length and sub-cellular localization.

S.No.	Species	OYEs	Score	Sequence ID	OYE Class	Amino acid length	Sub-cellular localization
1.	<i>Ascochyta rabiei</i>	ArOYE1	385.2	KF644454	I	367	Cytoplasm
		ArOYE2	348.6	KF644455	I	384	Mitochondria
		ArOYE3	357.2	KF644456	I	412	Cytoplasm
		ArOYE4	382	KF644457	II	425	Cytoplasm
		ArOYE5	340.5	KF644458	II	473	Cytoplasm
		ArOYE6	728.5	KF644459	III	448	Cytoplasm
2.	<i>Ashbya gossypii</i>	AgOYE1	552.3	NP_986995.1	I	399	Mitochondria
3.	<i>Aspergillus clavatus</i>	AcOYE1	390.7	XP_001272777.1	I	402	Cytoplasm
		AcOYE2	289.2	XP_001274702.1	I	415	Cytoplasm
		AcOYE3	353.9	XP_001276393.1	II	442	Mitochondria
		AcOYE4	362.5	XP_001272755.1	II	421	Cytoplasm
		AcOYE5	374.5	XP_001273480.1	II	422	Cytoskeleton
		AcOYE6	606.9	XP_001269037.1	III	444	Mitochondria
		AcOYE7	460.6	XP_001267752.1	III	427	Mitochondria
4.	<i>Aspergillus flavus</i>	AfiOYE1	388.3	XP_002373681.1	I	370	Mitochondria
		AfiOYE2	348.6	XP_002384860.1	I	377	Mitochondria
		AfiOYE3	339.5	XP_002379104.1	I	385	Mitochondria
		AfiOYE4	232.5	XP_002375082.1	I	340	Mitochondria
		AfiOYE5	288.6	XP_002380161.1	I	408	Cytoplasm
		AfiOYE6	376.6	XP_002375947.1	II	439	Cytoplasm
		AfiOYE7	370.1	XP_002376724.1	II	413	Cytoplasm
		AfiOYE8	386	XP_002372644.1	II	420	Cytoplasm
		AfiOYE9	357.2	XP_002379909.1	II	456	Cytoplasm
		AfiOYE10	372.7	XP_002375111.1	II	421	Cytoplasm
		AfiOYE11	614.6	XP_002384922.1	III	444	Cytoskeleton
		AfiOYE12	435.9	XP_002378137.1	III	393	Cytoplasm
		AfiOYE13	416.3	XP_002375650.1	III	417	Mitochondria
		AfiOYE14	263.1	XP_002379925.1	III	338	Cytoskeleton
5.	<i>Aspergillus fumigatus</i>	AfuOYE1	380.6	XP_749538.1	I	373	Mitochondria
		AfuOYE2	340.6	XP_756133.1	I	376	Mitochondria
		AfuOYE3	299.5	XP_753224.1	I	409	Cytoplasm
		AfuOYE4	365.5	XP_748197.1	II	442	Mitochondria
		AfuOYE5	364.6	XP_749564.1	II	421	Cytoplasm
		AfuOYE6	375.8	XP_748868.1	II	422	Cytoplasm
		AfuOYE7	617.3	XP_752589.1	III	444	Mitochondria
		AfuOYE8	438.6	XP_755160.1	III	421	Mitochondria
6.	<i>Aspergillus nidulans</i>	AndOYE1	369.5	XP_661749.1	I	349	Mitochondria
		AndOYE2	373.4	XP_662832.1	I	379	Mitochondria
		AndOYE3	381.8	XP_682614.1	I	410	Mitochondria

		AndOYE4	341.7	XP_682446.1	I	388	Cytoplasm
		AndOYE5	291.3	CBF84219.1	I	412	Cytoplasm
		AndOYE6	359.9	XP_657934.1	II	435	Cytoplasm
		AndOYE7	375.1	XP_664357.1	II	422	Cytoplasm
		AndOYE8	366.5	XP_659486.1	II	421	Cytoplasm
		AndOYE9	487.8	XP_663771.1	III	369	Cytoskeleton
7.	<i>Aspergillus niger</i>	AngOYE1	365	XP_001394816.2	I	370	Cytoplasm
		AngOYE2	374.4	XP_001393044.1	I	369	Cytoplasm
		AngOYE3	322.5	XP_001390054.1	I	384	Mitochondria
		AngOYE4	283.8	XP_001401198.1	I	421	Cytoplasm
		AngOYE5	377.7	XP_001389993.1	II	420	Cytoplasm
		AngOYE6	366.1	XP_001389551.2	II	419	Cytoplasm
		AngOYE7	365.1	CAK48758.1	II	415	Cytoplasm
		AngOYE8	378	XP_001399273.1	II	421	Cytoplasm
		AngOYE9	353.6	XP_001397404.1	II	443	Cytoplasm
		AngOYE10	361.6	XP_001391174.1	II	422	Cytoplasm
		AngOYE11	450.9	XP_001390672.2	III	412	Mitochondria
		AngOYE12	427.7	XP_001395504.2	III	418	Mitochondria
8.	<i>Aspergillus oryzae</i>	AoOYE1	391.7	XP_001818449.1	I	370	Mitochondria
		AoOYE2	380.8	XP_001817710.1	I	368	Mitochondria
		AoOYE3	343.5	XP_001823674.2	I	385	Cytoplasm
		AoOYE4	291.9	BAE56743.1	I	410	Mitochondria
		AoOYE5	287.6	XP_001819457.2	I	398	Mitochondria
		AoOYE6	288.6	XP_001818745.2	I	408	Cytoplasm
		AoOYE7	376.3	XP_001727650.1	II	439	Cytoplasm
		AoOYE8	386	XP_001817541.1	II	420	Cytoplasm
		AoOYE9	367.9	XP_001820991.1	II	413	Cytoplasm
		AoOYE10	358.6	XP_001821546.2	II	456	Cytoplasm
		AoOYE11	359.3	BAE59544.1	II	478	Mitochondria
		AoOYE12	615.7	XP_001827676.1	III	444	Cytoskeleton
		AoOYE13	466.3	BAE66156.1	III	409	Cytoskeleton
		AoOYE14	446.8	XP_001827289.2	III	412	Cytoskeleton
		AoOYE15	466.2	XP_001826449.2	III	418	Cytoskeleton
		AoOYE16	415.5	XP_001727395.2	III	417	Mitochondria
		AoOYE17	403	XP_001821534.1	III	376	Cytoplasm
9.	<i>Aspergillus terreus</i>	AtOYE1	363	XP_001217695.1	I	367	Cytoplasm
		AtOYE2	355.9	XP_001212002.1	I	370	Cytoplasm
		AtOYE3	330.5	XP_001211883.1	I	365	Mitochondria
		AtOYE4	293.6	XP_001217203.1	I	344	Mitochondria
		AtOYE5	355.5	XP_001218397.1	II	443	Mitochondria
		AtOYE6	352.6	XP_001215108.1	II	425	Nucleus
		AtOYE7	368	XP_001212014.1	III	399	Plasma membrane
10.	<i>Baudoinia compniacensis</i>	BcOYE1	408.1	EMC94206.1	I	375	Cytoplasm
		BcOYE2	342.7	EMC92829.1	I	359	Cytoplasm
		BcOYE3	335.4	EMC93881.1	I	373	Cytoplasm
		BcOYE4	379.7	EMC99563.1	II	424	Cytoplasm
		BcOYE5	687.8	EMC99204.1	III	448	Cytoplasm
		BcOYE6	468.9	EMC98898.1	III	459	Cytoplasm

		BcOYE7	320.7	EMC91925.1	III	481	Cytoskeleton
11.	<i>Botryotinia fuckeliana</i>	BfOYE1	404.4	XP_001558622.1	I	373	Cytoplasm
		BfOYE2	378.5	XP_001556041.1	I	413	Cytoplasm
		BfOYE3	382.1	XP_001558929.1	II	432	Cytoplasm
		BfOYE4	364.8	XP_001554780.1	II	439	Mitochondria
		BfOYE5	327.5	XP_001548368.1	II	365	Cytoplasm
		BfOYE6	726.9	XP_001547575.1	III	443	Cytoplasm
		BfOYE7	325.6	XP_001547383.1	III	335	Cytoskeleton
12.	<i>Candida albicans</i>	CaOYE1	518.5	XP_714056.1	I	406	Cytoplasm
		CaOYE2	536	XP_716750.1	I	402	Cytoplasm
		CaOYE3	502.9	XP_716740.1	I	406	Cytoplasm
		CaOYE4	511.6	XP_716749.1	I	413	Cytoplasm
		CaOYE5	458.8	XP_717925.1	I	392	Cytoplasm
		CaOYE6	454.1	XP_715357.1	I	392	Cytoplasm
		CaOYE7	381.4	XP_718652.1	I	432	Nucleus
		CaOYE8	313.9	XP_715510.1	II	432	Cytoplasm
		CaOYE9	260.9	XP_713846.1	II	369	Nucleus
13.	<i>Candida glabrata</i>	CgOYE1	646.8	XP_447339.1	I	400	Cytoplasm
		CgOYE2	674.5	XP_447364.1	I	401	Cytoplasm
		CgOYE3	611.9	XP_448689.1	I	400	Cytoplasm
		CgOYE4	616.3	XP_449187.1	I	400	Cytoplasm
		CgOYE5	236.5	XP_448473.1	II	388	Cytoplasm
14.	<i>Chaetomium globosum</i>	ChgOYE1	287.7	XP_001223431.1	I	356	Cytoplasm
		ChgOYE2	389.4	XP_001220253.1	II	433	Mitochondria
		ChgOYE3	380.7	XP_001228015.1	II	423	Cytoplasm
15.	<i>Claviceps purpurea</i>	ClpOYE1	335.9	AET79178.1	I	380	Mitochondria
		ClpOYE2	275.9	CCE31526.1	I	432	Cytoplasm
		ClpOYE3	305.8	CCE30765.1	II	424	Cytoplasm
		ClpOYE4	430.7	CCE32902.1	III	410	Cytoplasm
16.	<i>Coccidioides immitis</i>	CiOYE1	285.1	XP_001247988.1	I	422	Mitochondria
		CiOYE2	373.6	XP_001247544.1	II	424	Cytoplasm
17.	<i>Coccidioides posadasii</i>	CpOYE1	251.8	EFW13419.1	I	397	Mitochondria
		CpOYE2	375.4	EFW21715.1	II	424	Cytoplasm
18.	<i>Cochliobolus heterostrophus</i>	ChOYE1	306.9	EMD89016.1	I	365	Cytoplasm
		ChOYE2	344.5	EMD91314.1	I	359	Mitochondria
		ChOYE3	402.8	EMD88631.1	II	434	Peroxisome
		ChOYE4	349.8	EMD91295.1	II	464	Cytoplasm
		ChOYE5	644.4	EMD87349.1	III	446	Cytoplasm
19.	<i>Cochliobolus sativus</i>	CsOYE1	337.8	EMD58472.1	I	369	Mitochondria
		CsOYE2	403.1	EMD64475.1	II	434	Peroxisome
		CsOYE3	349	EMD58448.1	II	464	Cytoplasm
		CsOYE4	650.7	EMD59455.1	III	447	Cytoplasm

20.	<i>Cryptococcus gattii</i>	CrgOYE1	339.1	XP_003195791.1	I	393	Cytoplasm
		CrgOYE2	260.1	XP_003196956.1	I	416	Cytoplasm
		CrgOYE3	238.1	XP_003193576.1	I	383	Cytoplasm
		CrgOYE4	379	XP_003191968.1	II	459	Cytoplasm
21.	<i>Cryptococcus neoformans</i>	CnOYE1	271.1	XP_572706.1	I	393	Cytoplasm
		CnOYE2	335.6	XP_572301.1	I	427	Cytoplasm
		CnOYE3	234.7	XP_570269.1	I	383	Mitochondria
		CnOYE4	376.7	XP_566607.1	II	459	Cytoplasm
22.	<i>Dothistroma septosporum</i>	DsOYE1	397.3	EME41543.1	I	384	Mitochondria
		DsOYE2	333.9	EME43066.1	I	410	Cytoplasm
		DsOYE3	297.5	EME43152.1	I	354	Cytoplasm
		DsOYE4	379.8	EME49641.1	II	436	Cytoplasm
		DsOYE5	346.7	EME40738.1	II	447	Mitochondria
		DsOYE6	306.6	EME43711.1	II	441	Cytoplasm
		DsOYE7	675.3	EME49464.1	III	448	Cytoplasm
		DsOYE8	464.9	EME45535.1	III	453	Cytoplasm
		DsOYE9	326	EME43373.1	III	484	Mitochondria
23.	<i>Fusarium graminearum</i>	FgOYE1	382.3	XP_380241.1	I	366	Cytoskeleton
		FgOYE2	372.2	XP_383438.1	I	369	Mitochondria
		FgOYE3	370.1	XP_383531.1	I	397	Cytoplasm
		FgOYE4	245	XP_389988.1	I	332	Extracellular
		FgOYE5	339	XP_383386.1	I	379	Mitochondria
		FgOYE6	293	XP_388018.1	I	408	Cytoplasm
		FgOYE7	410.9	XP_381422.1	II	413	Mitochondria
		FgOYE8	372.3	XP_388253.1	II	413	Cytoplasm
		FgOYE9	388	XP_389860.1	II	426	Cytoplasm
		FgOYE10	372	XP_380250.1	II	442	Cytoplasm
		FgOYE11	376	XP_386704.1	II	452	Mitochondria
		FgOYE12	631.5	XP_383886.1	III	450	Cytoplasm
		FgOYE13	519.5	XP_384188.1	III	446	Cytoplasm
		FgOYE14	411.6	XP_384931.1	III	411	Cytoplasm
		FgOYE15	417.4	XP_390626.1	III	409	Mitochondria
24.	<i>Fusarium oxysporum</i>	FoOYE1	362.1	EGU88302.1	I	370	Mitochondria
		FoOYE2	354.9	EMT72633.1	I	351	Cytoplasm
		FoOYE3	319.2	EMT71554.1	I	345	Cytoplasm
		FoOYE4	361.9	ENH74399.1	I	383	Mitochondria
		FoOYE5	328.9	ENH65629.1	I	364	Mitochondria
		FoOYE6	321.5	EMT68747.1	I	362	Mitochondria
		FoOYE7	357.4	EMT71362.1	I	397	Mitochondria
		FoOYE8	336.4	EMT62821.1	I	416	Cytoplasm
		FoOYE9	290.6	EMT66576.1	I	408	Cytoplasm
		FoOYE10	413.5	EMT66832.1	II	413	Cytoplasm
		FoOYE11	397.5	EMT60475.1	II	415	Cytoplasm
		FoOYE12	381.9	EMT64308.1	II	451	Cytoplasm
		FoOYE13	376.1	EMT67619.1	II	421	Mitochondria
		FoOYE14	375.2	EMT71732.1	II	458	Cytoplasm

		FoOYE15	630.8	EMT71216.1	III	450	Cytoplasm
		FoOYE16	532.7	EMT70547.1	III	451	Cytoplasm
		FoOYE17	480.6	EMT65783.1	III	436	Cytoplasm
		FoOYE18	376.5	EMT72012.1	III	415	Cytoplasm
		FoOYE19	397.9	EMT74453.1	III	383	Mitochondria
		FoOYE20	423.1	EMT63134.1	III	409	Mitochondria
		FoOYE21	318.7	EMT71670.1	III	403	Mitochondria
25.	<i>Fusarium solani</i>	FsOYE1	390.9	XP_003040617.1	I	367	Mitochondria
		FsOYE2	390.6	XP_003043600.1	I	365	Cytoplasm
		FsOYE3	391.1	XP_003046890.1	I	386	Cytoplasm
		FsOYE4	337.5	XP_003046052.1	I	375	Mitochondria
		FsOYE5	353.9	XP_003047418.1	I	368	Mitochondria
		FsOYE6	343.2	XP_003049050.1	I	361	Mitochondria
		FsOYE7	361.9	XP_003047276.1	I	391	Mitochondria
		FsOYE8	344.4	XP_003043831.1	I	394	Cytoplasm
		FsOYE9	333.5	XP_003040921.1	I	413	Cytoplasm
		FsOYE10	281.9	XP_003047281.1	I	407	Cytoplasm
		FsOYE11	169.1	XP_003043159.1	I	368	Cytoplasm
		FsOYE12	416.3	XP_003053408.1	II	444	Cytoplasm
		FsOYE13	370.5	XP_003043011.1	II	411	Cytoplasm
		FsOYE14	374.5	XP_003049114.1	II	409	Cytoplasm
		FsOYE15	376.2	XP_003045875.1	II	416	Cytoplasm
		FsOYE16	371.4	XP_003040465.1	II	407	Cytoskeleton
		FsOYE17	366.8	XP_003049535.1	II	455	Cytoplasm
		FsOYE18	554.7	XP_003047330.1	III	437	Cytoplasm
		FsOYE19	541.4	XP_003044944.1	III	453	Mitochondria
		FsOYE20	512.4	XP_003042155.1	III	429	Cytoplasm
		FsOYE21	415.4	XP_003043112.1	III	411	Mitochondria
		FsOYE22	421.4	XP_003054679.1	III	412	Mitochondria
26.	<i>Fusarium verticillioides</i>	FvOYE1	371.5	FVEG_10034	I	370	Cytoskeleton
		FvOYE2	390.6	FVEG_00100	I	368	Mitochondria
		FvOYE3	368.3	FVEG_08460	I	386	Mitochondria
		FvOYE4	362.7	FVEG_08535	I	370	Mitochondria
		FvOYE5	340.1	FVEG_06429	I	375	Cytoplasm
		FvOYE6	343.4	FVEG_05741	I	373	Mitochondria
		FvOYE7	288.2	FVEG_10591	I	356	Mitochondria
		FvOYE8	356.9	FVEG_08619	I	398	Mitochondria
		FvOYE9	334.5	FVEG_11005	I	416	Cytoplasm
		FvOYE10	287	FVEG_07175	I	408	Cytoplasm
		FvOYE11	413.8	FVEG_01376	II	413	Cytoplasm
		FvOYE12	396.1	FVEG_06291	II	415	Cytoplasm
		FvOYE13	381.8	FVEG_05618	II	451	Cytoplasm
		FvOYE14	357.2	FVEG_12306	II	421	Cytoplasm
		FvOYE15	324.4	FVEG_11755	II	437	Cytoplasm
		FvOYE16	632.5	FVEG_08742	III	450	Cytoplasm
		FvOYE17	521.4	FVEG_09300	III	452	Cytoplasm
		FvOYE18	522.3	FVEG_10181	III	448	Cytoplasm
		FvOYE19	420.6	FVEG_09981	III	409	Cytoplasm
		FvOYE20	425.5	FVEG_03185	III	409	Mitochondria
		FvOYE21	351.7	FVEG_08332	III	405	Mitochondria

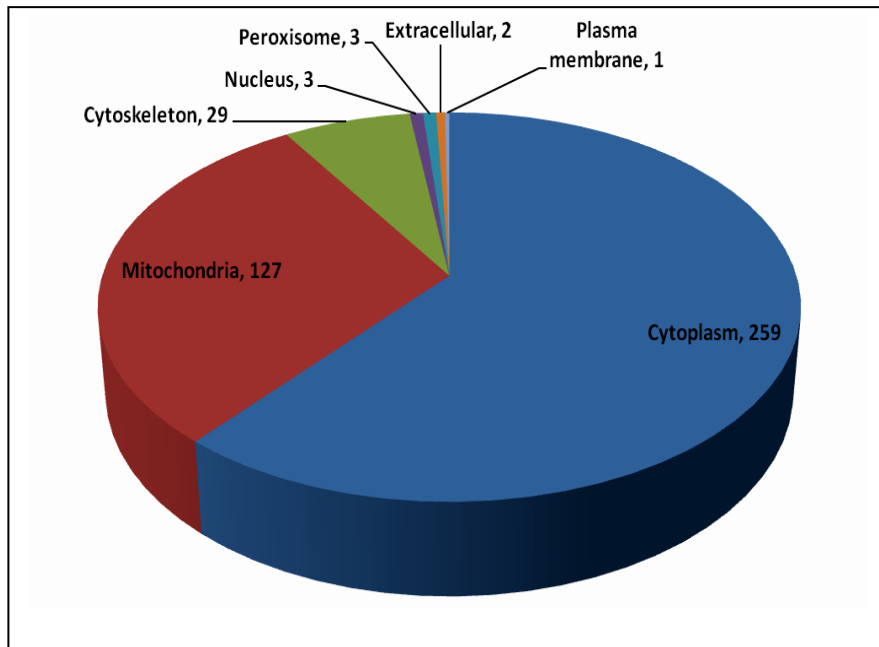
		FvOYE2	115.6	FVEG_08314	III	314	Mitochondria
27.	<i>Hansenula polymorpha</i>	HpOYE1	669.8	AAN09952.1	I	401	Cytoplasm
		HpOYE2	688.4	AAN09954.1	I	402	Cytoplasm
		HpOYE3	688.4	AAN09953.1	I	402	Cytoplasm
28.	<i>Histoplasma capsulatus</i>	HcOYE1	358.3	XP_001538118.1	II	420	Cytoplasm
29.	<i>Kluyveromyces lactis</i>	KIOYE1	678.7	XP_451397.1	I	398	Cytoplasm
		KIOYE2	279.8	XP_452270.1	II	409	Cytoplasm
30.	<i>Laccaria bicolor</i>	LbOYE1	371	XP_001886261.1	I	373	Mitochondria
		LbOYE2	368.7	XP_001886575.1	I	384	Mitochondria
		LbOYE3	228.7	XP_001889520.1	I	374	Cytoplasm
		LbOYE4	218.2	XP_001885579.1	I	378	Cytoplasm
		LbOYE5	408.5	XP_001881077.1	II	415	Cytoplasm
31.	<i>Leptosphaeria maculans</i>	LmOYE1	334	XP_003839270.1	I	444	Mitochondria
		LmOYE2	392.1	XP_003839692.1	II	430	Peroxisome
		LmOYE3	344.3	XP_003835675.1	II	467	Mitochondria
		LmOYE4	659.8	XP_003840432.1	III	449	Cytoplasm
32.	<i>Macrophomina phaseolina</i>	MpOYE1	361.7	EKG18001.1	I	332	Cytoplasm
		MpOYE2	366.1	EKG20624.1	I	370	Cytoplasm
		MpOYE3	376.2	EKG17496.1	I	348	Cytoplasm
		MpOYE4	218.5	EKG17706.1	I	240	Cytoskeleton
		MpOYE5	357.3	EKG21699.1	I	399	Cytoplasm
		MpOYE6	332.9	EKG22108.1	I	416	Mitochondria
		MpOYE7	205.4	EKG13357.1	I	403	Cytoplasm
		MpOYE8	367.1	EKG20918.1	II	416	Cytoplasm
		MpOYE9	358.6	EKG11784.1	II	429	Cytoplasm
		MpOYE10	729.2	EKG20669.1	III	446	Cytoplasm
		MpOYE11	598.8	EKG16952.1	III	453	Cytoplasm
33.	<i>Magnaporthe oryzae</i>	MoOYE1	336.6	XP_003715783.1	I	373	Mitochondria
		MoOYE2	286.4	XP_003721368.1	I	409	Cytoplasm
		MoOYE3	405	XP_003713598.1	II	442	Cytoplasm
		MoOYE4	694.8	XP_003720070.1	III	417	Cytoplasm
34.	<i>Mycosphaerella fijiensis</i>	MfOYE1	377	EME87822.1	I	383	Cytoplasm
		MfOYE2	375.9	EME88727.1	I	391	Mitochondria
		MfOYE3	346.9	EME81724.1	I	406	Cytoplasm
		MfOYE4	375.7	EME89616.1	II	437	Cytoplasm
		MfOYE5	373.3	EME81169.1	II	461	Cytoplasm
		MfOYE6	679.1	EME87367.1	III	448	Cytoplasm
35.	<i>Mycosphaerella graminicola</i>	MgOYE1	365.5	XP_003856408.1	I	375	Mitochondria
		MgOYE2	292.2	XP_003855430.1	I	343	Cytoplasm
		MgOYE3	316.6	XP_003854988.1	I	372	Cytoplasm
		MgOYE4	308.3	XP_003848998.1	I	355	Mitochondria

		MgOYE5	383.5	XP_003853525.1	II	424	Cytoplasm
		MgOYE6	350.3	XP_003849629.1	II	452	Cytoplasm
		MgOYE7	683.6	XP_003856796.1	III	448	Cytoplasm
		MgOYE8	441.1	XP_003854564.1	III	456	Cytoskeleton
		MgOYE9	314.3	XP_003854244.1	III	430	Mitochondria
36.	<i>Mycosphaerella populorum</i>	MypOYE1	341.5	EMF11974.1	I	406	Mitochondria
		MypOYE2	342.3	EMF12018.1	I	400	Cytoplasm
		MypOYE3	388.8	EMF16473.1	II	430	Cytoplasm
		MypOYE4	339.1	EMF09315.1	II	452	Cytoplasm
		MypOYE5	671.8	EMF16976.1	III	445	Cytoplasm
		MypOYE6	322.3	EMF11720.1	III	481	Cytoskeleton
37.	<i>Neosartorya fischeri</i>	NfOYE1	377.7	XP_001260040.1	I	368	Mitochondria
		NfOYE2	302.4	XP_001259238.1	I	408	Cytoplasm
		NfOYE3	369.1	XP_001266387.1	II	442	Mitochondria
		NfOYE4	385.1	XP_001261594.1	II	422	Cytoplasm
		NfOYE5	367.4	XP_001260063.1	II	421	Cytoplasm
		NfOYE6	618.5	XP_001264538.1	III	444	Mitochondria
		NfOYE7	458.3	XP_001260337.1	III	421	Mitochondria
38.	<i>Neurospora crassa</i>	NcOYE1	395.6	XP_955910.1	I	379	Mitochondria
		NcOYE2	414.5	XP_964639.1	II	434	Cytoplasm
		NcOYE3	593	XP_958838.1	III	437	Mitochondria
39.	<i>Paracoccidioides brasiliensis</i>	PbOYE1	352.2	EEH45369.1	I	375	Cytoplasm
		PbOYE2	357.6	EEH16871.1	I	394	Cytoplasm
		PbOYE3	330.1	EEH43640.1	II	415	Cytoplasm
40.	<i>Penicillium chrysogenum</i>	PcOYE1	389.2	XP_002563769.1	I	367	Cytoplasm
		PcOYE2	364.8	XP_002561471.1	I	364	Cytoplasm
		PcOYE3	367.4	XP_002562456.1	I	368	Mitochondria
		PcOYE4	257.6	XP_002564652.1	I	402	Cytoplasm
		PcOYE5	387.7	XP_002560972.1	II	422	Cytoplasm
		PcOYE6	352.1	XP_002568438.1	II	443	Cytoplasm
		PcOYE7	382.6	XP_002556925.1	II	413	Cytoplasm
		PcOYE8	598	XP_002560444.1	III	444	Cytoskeleton
		PcOYE9	540.7	XP_002560103.1	III	458	Cytoplasm
		PcOYE10	426.1	XP_002556645.1	III	413	Mitochondria
		PcOYE11	436.9	XP_002558887.1	III	416	Mitochondria
41.	<i>Penicillium digitatum</i>	PdOYE1	313.5	EKV09666.1	I	365	Mitochondria
		PdOYE2	337.5	EKV16874.1	I	385	Cytoplasm
		PdOYE3	234	EKV04694.1	I	393	Cytoplasm
		PdOYE4	391	EKV18347.1	II	422	Cytoplasm
		PdOYE5	597.6	EKV06611.1	III	444	Cytoplasm
42.	<i>Penicillium marneffei</i>	PmOYE1	379.9	XP_002150574.1	I	376	Mitochondria
		PmOYE2	399.6	XP_002152521.1	I	364	Mitochondria
		PmOYE3	352.6	XP_002144880.1	I	385	Mitochondria

		PmOYE4	283.7	XP_002145688.1	I	409	Cytoplasm
		PmOYE5	360.5	XP_002149480.1	II	454	Cytoplasm
		PmOYE6	346.3	XP_002147920.1	II	423	Cytoplasm
		PmOYE7	373	XP_002144915.1	II	422	Cytoplasm
		PmOYE8	416	XP_002151394.1	III	417	Mitochondria
43.	<i>Pichia pastoris</i>	PpOYE1	544.9	XP_002492601.1	I	409	Cytoplasm
		PpOYE2	541.7	XP_002492600.1	I	409	Cytoplasm
		PpOYE3	331.9	XP_002490248.1	II	402	Cytoplasm
44.	<i>Pichia stipitis</i>	PsOYE1	580.9	XP_001385078.1	I	406	Cytoplasm
		PsOYE2	522.9	XP_001383638.1	I	404	Mitochondria
		PsOYE3	537.2	XP_001382344.1	I	401	Cytoplasm
		PsOYE4	554.2	XP_001385076.2	I	405	Mitochondria
		PsOYE5	637.9	XP_001384054.1	I	406	Cytoplasm
		PsOYE6	628.2	XP_001384056.2	I	407	Cytoplasm
		PsOYE7	510.2	XP_001385077.2	I	403	Mitochondria
		PsOYE8	620.3	XP_001384116.1	I	406	Cytoplasm
		PsOYE9	647.3	XP_001384055.1	I	407	Cytoplasm
		PsOYE10	328.7	XP_001383472.2	II	434	Cytoplasm
		PsOYE11	334	XP_001383637.2	II	422	Cytoplasm
45.	<i>Piriformospora indica</i>	PiOYE1	405.8	CCA71264.1	I	365	Cytoskeleton
		PiOYE2	411.4	CCA71265.1	I	366	Mitochondria
		PiOYE3	413.8	CCA70874.1	II	417	Cytoplasm
46.	<i>Puccinia graminis tritici</i>	PgtOYE1	413.4	XP_003322550.1	III	405	Mitochondria
		PgtOYE2	366.4	XP_003321709.2	III	402	Cytoplasm
47.	<i>Pyrenophora tritici-repentis</i>	PtrOYE1	385.2	XP_001938581.1	I	366	Cytoplasm
		PtrOYE2	297.9	XP_001930843.1	I	345	Mitochondria
		PtrOYE3	337.9	XP_001938029.1	I	408	Cytoplasm
		PtrOYE4	402.4	XP_001936933.1	II	434	Cytoplasm
		PtrOYE5	331.5	XP_001941724.1	II	399	Mitochondria
		PtrOYE6	663.1	XP_001934295.1	III	449	Cytoplasm
48.	<i>Pyrenophora teres teres</i>	PttOYE1	371.7	XP_003295711.1	I	366	Cytoplasm
		PttOYE2	251.4	XP_003304545.1	I	284	Cytoplasm
		PttOYE3	340.3	XP_003297182.1	I	408	Cytoplasm
		PttOYE4	403.4	XP_003301552.1	II	456	Cytoplasm
		PttOYE5	200.3	XP_003296488.1	II	254	Cytoplasm
		PttOYE6	662.5	XP_003296539.1	III	449	Cytoplasm
49.	<i>Rhizoctonia solani</i>	RsOYE1	416.3	ELU42401.1	I	410	Mitochondria
		RsOYE2	350.5	ELU37570.1	I	399	Mitochondria
		RsOYE3	282.1	ELU44178.1	I	355	Mitochondria
		RsOYE4	401	ELU39655.1	II	503	Extracellular
		RsOYE5	465.1	ELU41063.1	III	450	Cytoplasm
		RsOYE6	430	ELU37947.1	III	440	Cytoskeleton
50.	<i>Rhodosporidium</i>	RtOYE1	399.2	EMS24376.1	I	374	Mitochondria

	<i>toruloides</i>						
		RtOYE2	377.9	EMS23446.1	II	452	Cytoplasm
		RtOYE3	423.2	EMS18823.1	III	427	Cytoplasm
		RtOYE4	312.2	EMS18357.1	III	437	Cytoplasm
		RtOYE5	290.1	EMS18551.1	III	515	Cytoplasm
51.	<i>Saccharomyces cerevisiae</i>	ScOYE1	712.7	NP_012049.1	I	400	Cytoplasm
		ScOYE2	690.5	NP_015154.1	I	400	Cytoplasm
52.	<i>Schizosaccharomyces pombe</i>	SpOYE1	296.3	NP_592823.1	I	392	Cytoplasm
		SpOYE2	293.3	NP_592817.1	I	382	Cytoplasm
		SpOYE3	402.7	NP_595868.1	II	395	Cytoskeleton
53.	<i>Sclerotinia sclerotiorum</i>	SsOYE1	415.8	XP_001597795.1	I	373	Mitochondria
		SsOYE2	388.8	XP_001595831.1	II	409	Cytoplasm
		SsOYE3	371.4	XP_001585571.1	II	435	Mitochondria
		SsOYE4	684.6	XP_001598970.1	III	443	Cytoplasm
		SsOYE5	361.5	XP_001586962.1	III	344	Cytoskeleton
54.	<i>Setosphaeria turcica</i>	StOYE1	387.1	EOA82937.1	I	366	Cytoplasm
		StOYE2	302.7	EOA81858.1	I	358	Mitochondria
		StOYE3	338.1	EOA88743.1	I	414	Cytoplasm
		StOYE4	404.5	EOA88147.1	II	455	Cytoplasm
		StOYE5	327.2	EOA81831.1	II	401	Mitochondria
		StOYE6	661.7	EOA86065.1	III	449	Cytoplasm
55.	<i>Stagnospora nodorum</i>	SnOYE1	385.5	XP_001799909.1	I	369	Mitochondria
		SnOYE2	383.4	XP_001792787.1	I	367	Cytoplasm
		SnOYE3	296.5	XP_001793205.1	I	332	Cytoplasm
		SnOYE4	340	XP_001803927.1	I	395	Cytoplasm
		SnOYE5	307	XP_001794614.1	I	392	Cytoplasm
		SnOYE6	388.9	XP_001802700.1	II	425	Cytoplasm
		SnOYE7	236.4	XP_001805280.1	II	489	Cytoplasm
		SnOYE8	659.4	XP_001806580.1	III	449	Cytoplasm
56.	<i>Trichoderma atroviride</i>	TaOYE1	365.5	EHK49303.1	I	362	Mitochondria
		TaOYE2	382.3	EHK43606.1	I	368	Cytoskeleton
		TaOYE3	358.7	EHK49437.1	I	365	Cytoplasm
		TaOYE4	371.3	EHK50809.1	I	371	Cytoskeleton
		TaOYE5	350.8	EHK42252.1	I	384	Mitochondria
		TaOYE6	353.8	EHK50404.1	I	383	Cytoplasm
		TaOYE7	341.4	EHK44334.1	I	374	Cytoplasm
		TaOYE8	306.5	EHK42728.1	I	407	Cytoplasm
		TaOYE9	265.7	EHK41134.1	I	374	Cytoplasm
		TaOYE10	289.8	EHK40486.1	I	411	Cytoplasm
		TaOYE11	409.1	EHK45545.1	II	417	Cytoplasm
		TaOYE12	381.3	EHK42431.1	II	459	Cytoplasm
		TaOYE13	371.8	EHK45467.1	II	458	Mitochondria
		TaOYE14	368.9	EHK41164.1	II	415	Cytoskeleton
		TaOYE15	328	EHK46788.1	II	370	Cytoplasm

		TaOYE16	567.5	EHK49477.1	III	438	Cytoplasm
		TaOYE17	423.4	EHK49302.1	III	405	Cytoskeleton
57.	<i>Trichoderma reesei</i>	TrOYE1	352	EGR52964.1	I	363	Mitochondria
		TrOYE2	295.9	EGR49960.1	I	410	Cytoplasm
		TrOYE3	413.2	EGR47783.1	II	415	Cytoplasm
		TrOYE4	362.5	EGR50387.1	II	456	Mitochondria
		TrOYE5	568.1	EGR44758.1	III	443	Cytoplasm
		TrOYE6	422	EGR52420.1	III	411	Mitochondria
		TrOYE7	358.8	EGR50287.1	III	401	Mitochondria
58.	<i>Trichoderma virens</i>	TvOYE1	365.0	EHK21778.1	I	346	Cytoplasm
		TvOYE2	386.7	EHK18275.1	I	371	Cytoskeleton
		TvOYE3	357.1	EHK24193.1	I	360	Mitochondria
		TvOYE4	347.2	EHK19405.1	I	365	Cytoskeleton
		TvOYE5	362.6	EHK23110.1	I	383	Mitochondria
		TvOYE6	308.3	EHK16730.1	I	406	Mitochondria
		TvOYE7	413.4	EHK26344.1	II	416	Cytoplasm
		TvOYE8	382.7	EHK24541.1	II	457	Mitochondria
		TvOYE9	366.6	EHK19931.1	II	454	Mitochondria
		TvOYE10	371.4	EHK24097.1	II	411	Cytoskeleton
		TvOYE11	556.3	EHK19464.1	III	443	Cytoplasm
		TvOYE12	406.2	EHK20481.1	III	408	Mitochondria
		TvOYE13	431.4	EHK24194.1	III	409	Cytoskeleton
		TvOYE14	357.7	EHK20478.1	III	418	Cytoplasm
59.	<i>Ustilago hordei</i>	UhOYE1	327.6	CCF53752.1	II	466	Cytoplasm
		UhOYE2	431.9	CCF53697.1	III	422	Cytoplasm
		UhOYE3	275.8	CCF53309.1	III	551	Cytoplasm
60.	<i>Ustilago maydis</i>	UmOYE1	345.5	XP_756193.1	II	462	Cytoplasm
		UmOYE2	430.4	XP_756166.1	III	414	Cytoplasm
		UmOYE3	295.5	XP_758016.1	III	540	Mitochondria



Supplementary Figure S1. Sub-cellular localization prediction of 424 fungal OYEs. Majority of the OYEs are predicted to be localized in cytoplasm, mitochondria and cytoskeleton.

A

PLTRFR

GYPNNVPGI



B

HGANG YGGS

Table with columns representing amino acid positions from 180 to 340. The table lists various protein sequences and their corresponding amino acid residues at each position. The residues are color-coded by type: blue for basic, red for acidic, green for polar, orange for non-polar, and grey for glycine. Two regions are highlighted with blue boxes: positions 299-302 and 308-311. The table ends with a color-coded bar at the bottom.

Table with columns representing amino acid positions from 310 to 340. This section continues the sequence data from the previous table, showing the residues for the final 30 positions. It also includes a color-coded bar at the bottom.



D

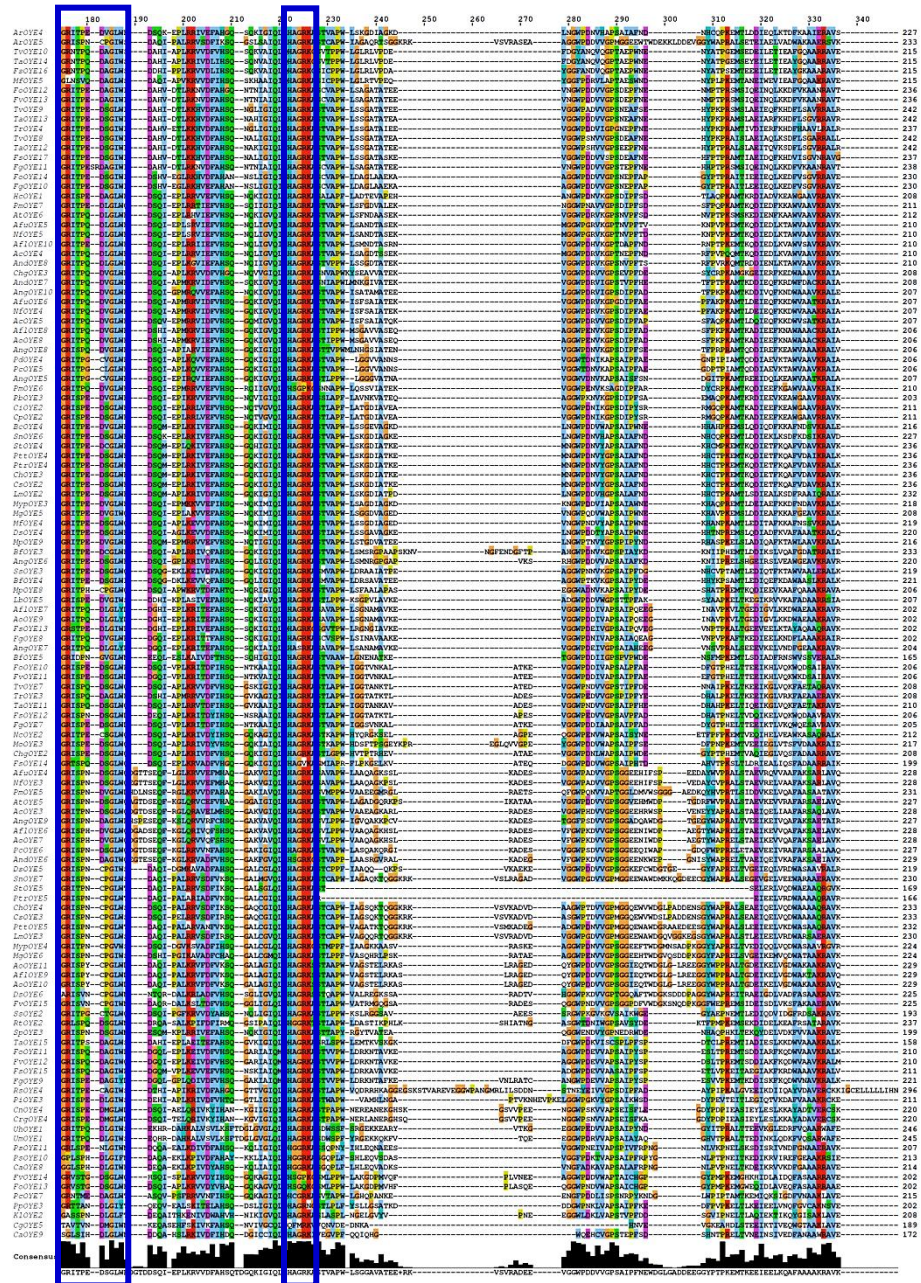
PMCQY



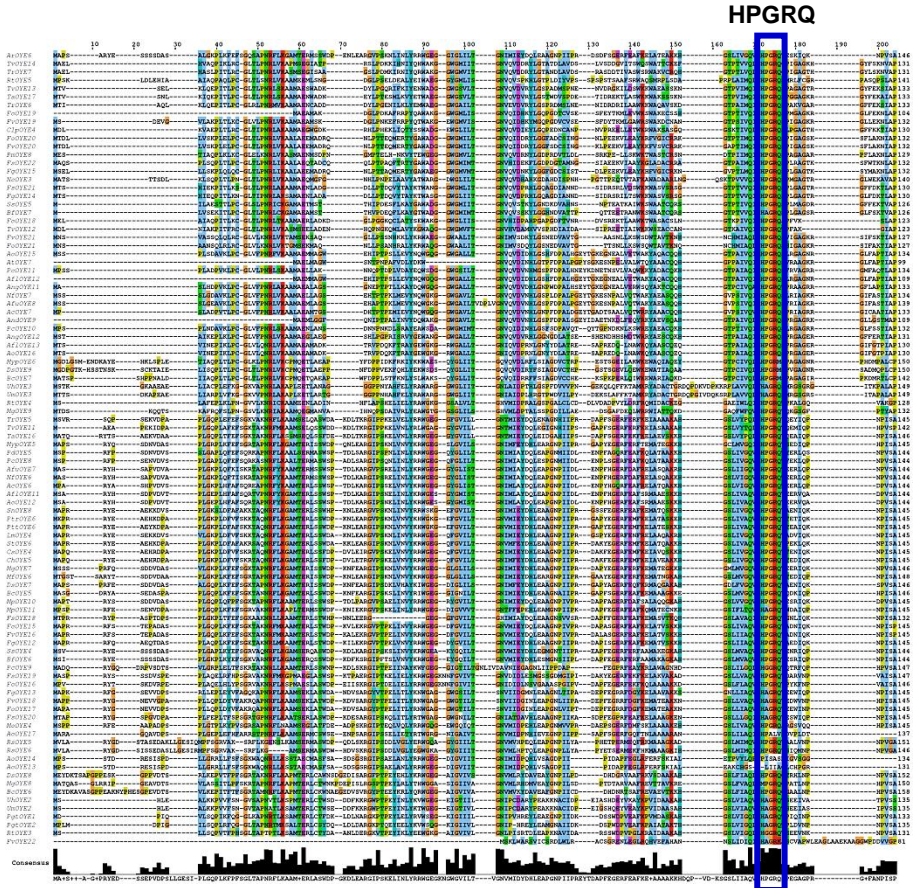
E

GRITPEDSGLW

HAGRK

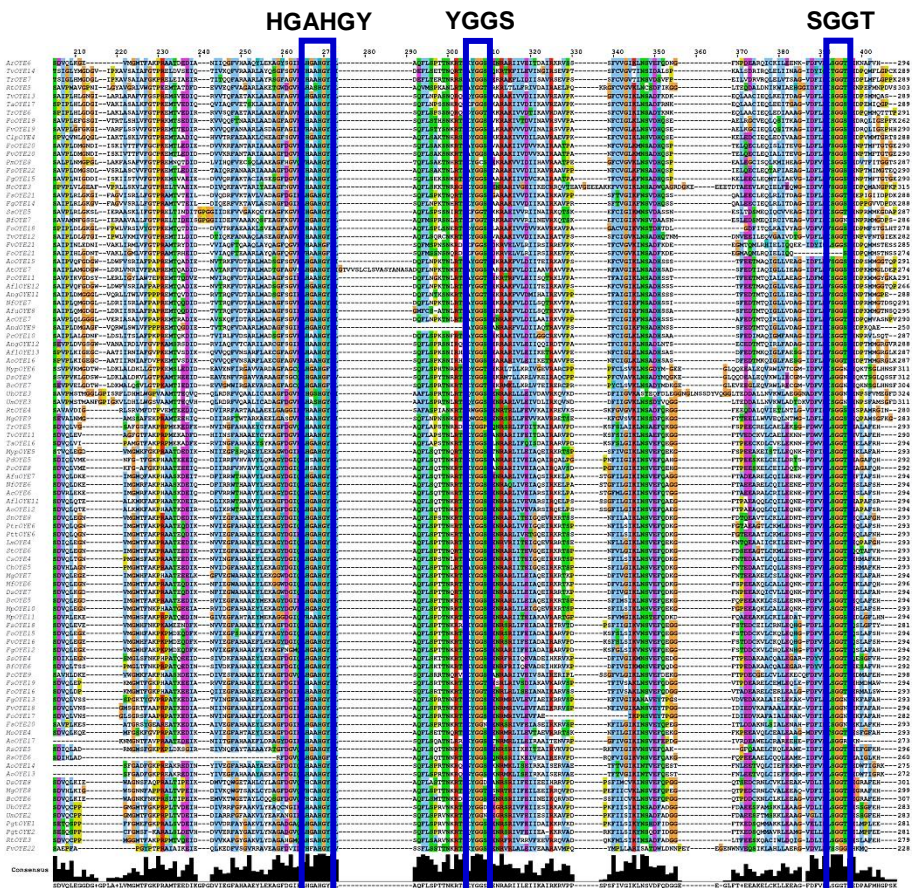


G



HPGRQ

H

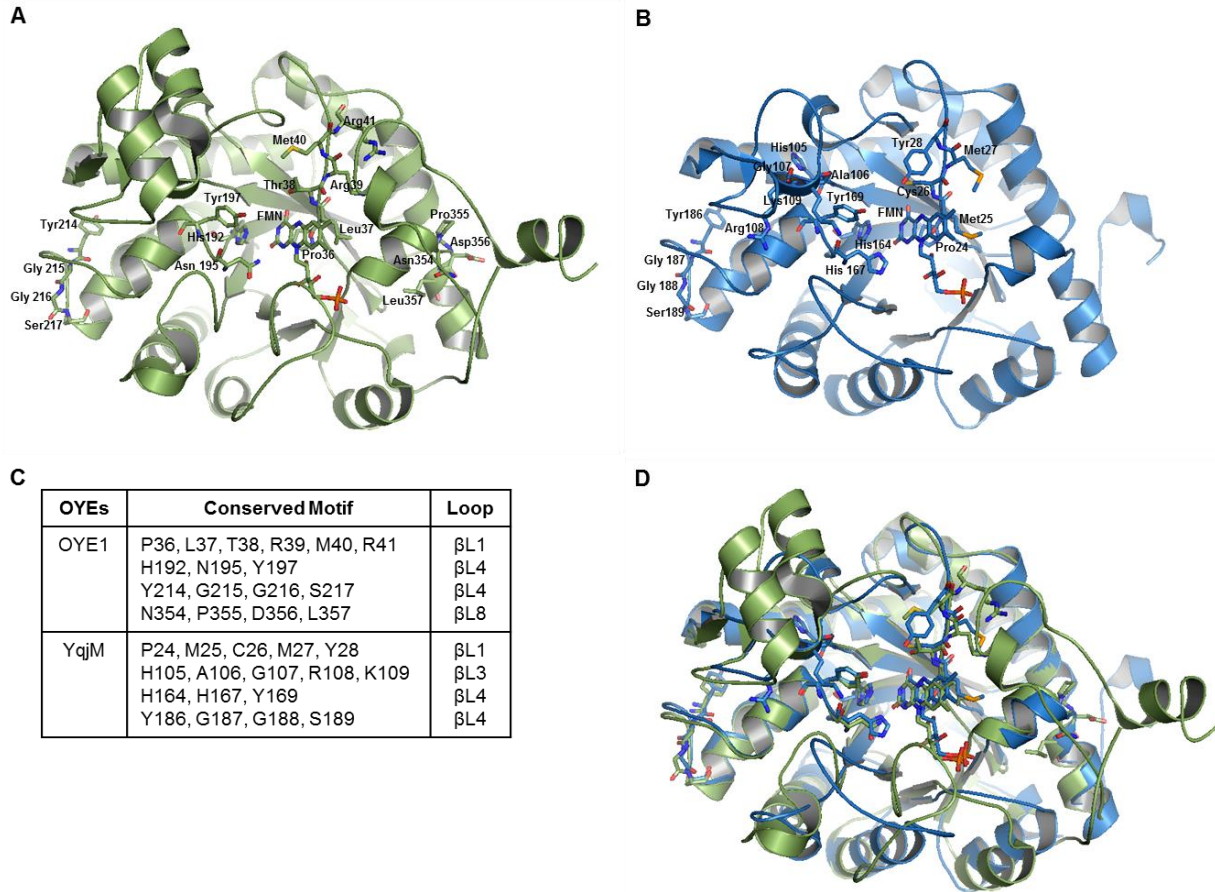


HGAHGY

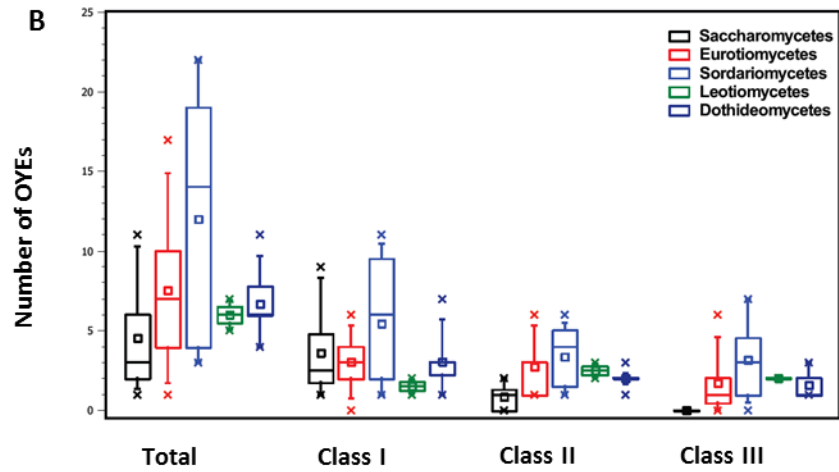
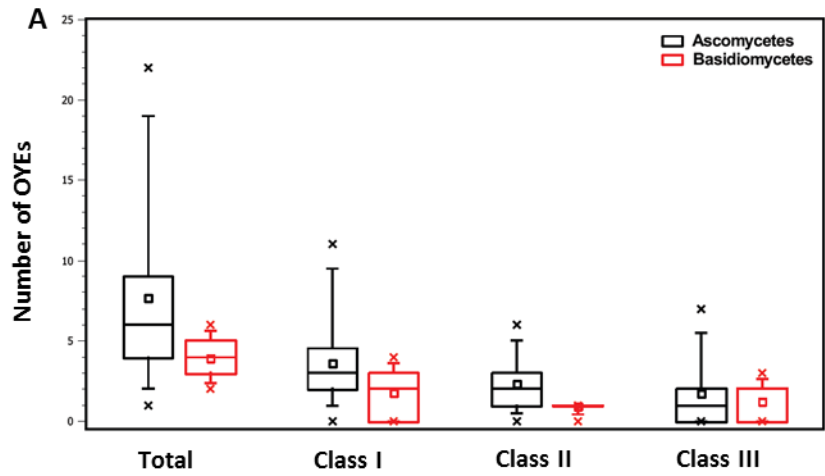
YGGS

SGGT

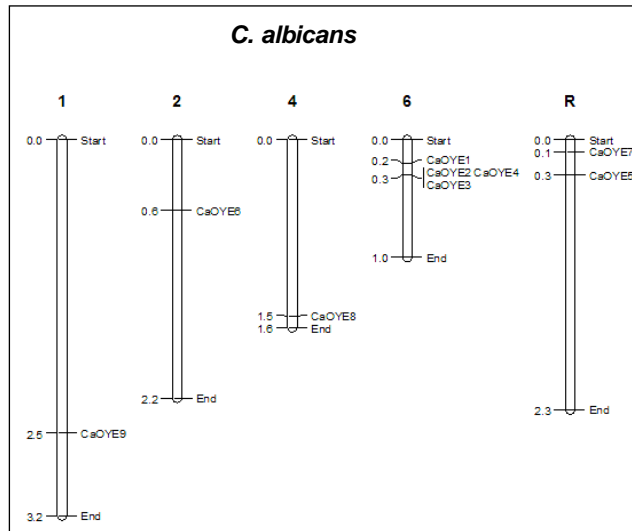
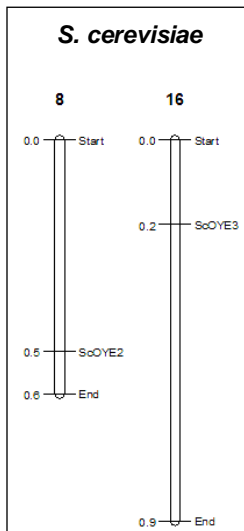
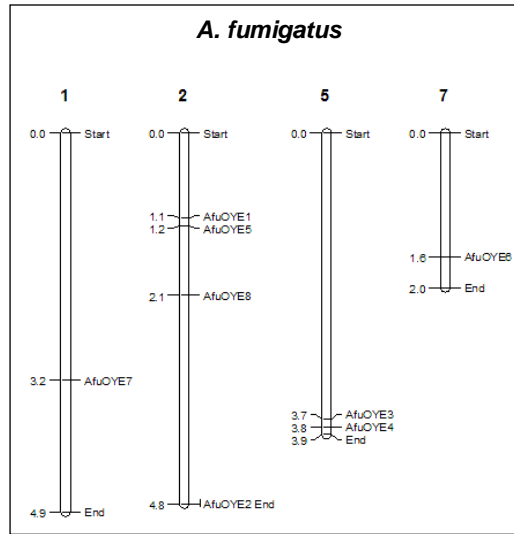
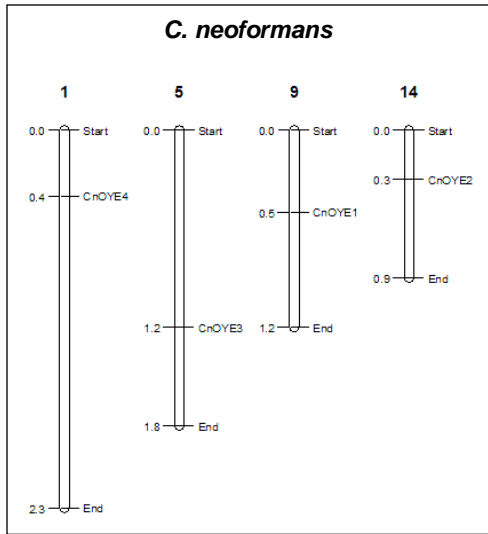
Supplementary Figure S2. Class-wise multiple sequence alignment of full length OYE proteins from fungi. The alignment was generated with the PROMALS3D program using default parameters and visualized by Jalview 2.8 (Supplementary reference 1). (A), (B) and (C) Class I OYEs, (D) (E) and (F) Class II OYEs, and (G) and (H) Class III OYEs. The positions of the conserved active site residues and other class specific conserved motifs as described in text are highlighted with the rectangular boxes. The consensus sequence is displayed below the alignment.

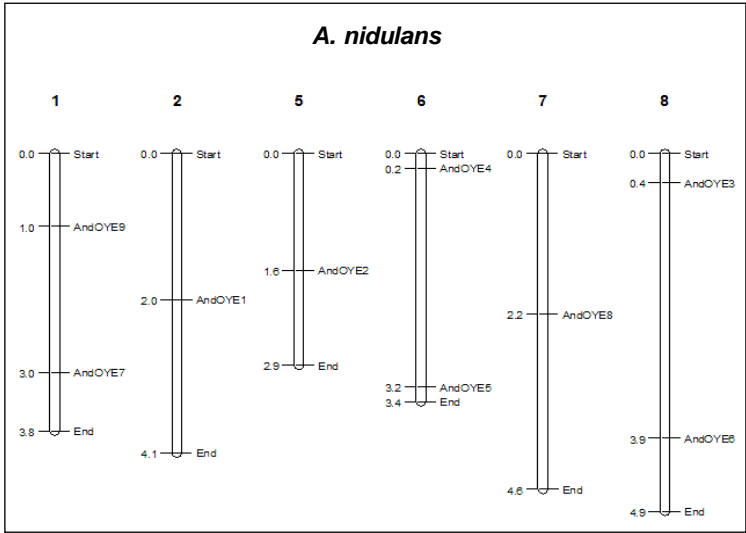
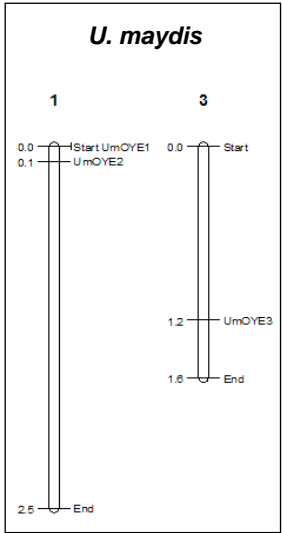
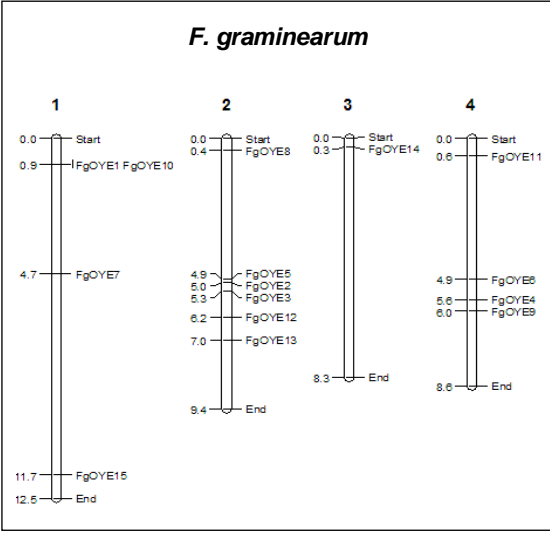
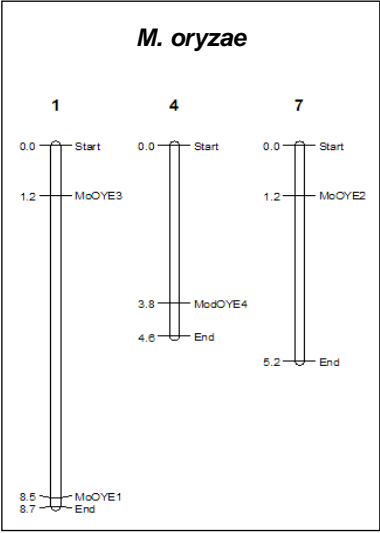


Supplementary Figure S3. Location of conserved motifs in the structures of typical OYEs. 3D structures of (A) yeast OYE1 (PDBID: 1OYB) representing Class I OYE and (B) YqjM (PDBID: 1Z42) representing Class II OYE were retrieved from the Protein Data Bank (PDB) and visualized using PyMOL (www.pymol.org). The cartoon representation shows the backbone of both proteins, whereas conserved amino acid residues along with the cofactor (FMN) are shown as sticks. (C) Table shows the location of these conserved motifs in the loop region of their respective 3D structures. (D) Superposition of the two structures (OYE1 = smudge green and YqjM = sky blue) with their respective conserved motifs.



Supplementary Figure S4. Comparison of OYEs among fungi, (A) between ascomycetes (black) and basidiomycetes (red), and (B) among different classes of ascomycetes.





Supplementary Figure S5. Chromosomal distribution of *OYE* genes in few selected fungi. Physical locations of *OYE*s are represented on the respective chromosomes in eight different fungal species. On the top of each chromosome, the chromosome number is written. Values on the left side of the chromosome represent the position of the corresponding gene on the right side. Chromosomal distances are in Mb.

Supplementary reference

1. Waterhouse, A.M., Procter, J.B., Martin, D.M.A, Clamp, M. & Barton, G. J. Jalview Version 2 – a multiple sequence alignment editor and analysis workbench. *Bioinformatics*. **9**, 1189-1191 (2009).