

Table S1: Predicted physicochemical properties of OePARs, OeCCRs and OeDFRs.

Gene ID	Rename	Amino acid length	Molecular weight(Da)	pI	Subcellular localization	Fat Coefficient	Overall Average Hydroplicity	Number of predicted TMHs
GWHPAOPM001236	OePAR1	328	36162.85	8.10	Chloroplast	91.59	-0.09	0
GWHPAOPM025266	OePAR2	319	34841.41	6.55	Chloroplast	96.33	-0.01	0
GWHPAOPM052601	OePAR3	328	36140.79	7.59	Chloroplast	91.59	-0.08	0
GWHPAOPM034895	OePAR4	325	36025.39	6.34	Chloroplast	92.98	-0.14	0
GWHPAOPM004996	OePAR5	279	30605.31	6.00	Cytosol	100.29	0.08	0
GWHPAOPM048801	OePAR6	287	31724.85	7.00	Chloroplast	100.14	0.10	0
GWHPAOPM004999	OePAR7	263	29201.35	5.30	Cytosol	101.14	-0.04	0
GWHPAOPM005000	OePAR8	284	31474.06	5.69	Chloroplast	97.11	-0.10	0
GWHPAOPM035936	OeCCR1	332	36751.27	6.14	Chloroplast	92.47	-0.20	0
GWHPAOPM004209	OeCCR2	334	36966.56	6.03	Chloroplast	95.12	-0.14	0
GWHPAOPM004206	OeCCR3	306	33723.77	5.50	Chloroplast	95.56	-0.05	0
GWHPAOPM025264	OeCCR4	347	38378.66	6.72	Cytosol	97.75	0.01	0
GWHPAOPM025263	OeCCR5	324	35775.39	5.74	Cytosol	100.22	-0.04	0
GWHPAOPM025262	OeCCR6	352	38657.70	5.62	Cytosol	96.39	-0.02	0
GWHPAOPM018625	OeCCR7	280	30608.28	6.17	Chloroplast	101.25	0.07	0
GWHPAOPM017499	OeCCR8	319	35184.27	6.48	Chloroplast	92.85	-0.25	0
GWHPAOPM039626	OeCCR9	334	36818.20	7.97	Chloroplast	92.99	-0.21	0
GWHPAOPM021895	OeDFR1	320	35557.67	5.57	Chloroplast	92.56	-0.16	0
GWHPAOPM008251	OeDFR2	285	31722.62	5.90	Chloroplast	96.42	-0.09	0
GWHPAOPM052074	OeDFR3	306	33700.10	8.30	Chloroplast	99.93	0.04	0
GWHPAOPM009919	OeDFR4	354	38953.59	5.69	Cytosol	93.02	-0.01	0

Table S2: Accession numbers of genes used for phylogenetic analysis.

Identifier	Gene Bank Accession	Organism
AtCCR1	AT1G15950	<i>Arabidopsis thaliana</i>
AtCCR2	AT1G80820	<i>Arabidopsis thaliana</i>
AtCCR3	AT2G02400	<i>Arabidopsis thaliana</i>
AtCCR4	AT1G68540	<i>Arabidopsis thaliana</i>
AtCCR5	AT5G14700	<i>Arabidopsis thaliana</i>
AtCCR6	AT2G23910	<i>Arabidopsis thaliana</i>
AtCCR7	AT4G30470	<i>Arabidopsis thaliana</i>
AtCCR8	AT2G33590	<i>Arabidopsis thaliana</i>
AtCCR11	AT2G33600	<i>Arabidopsis thaliana</i>
AtCCR12	AT5G58490	<i>Arabidopsis thaliana</i>
PtoCCR1	KP281597	<i>Populus tomentosa</i>
PtoCCR2	KP281606	<i>Populus tomentosa</i>
PtoCCR3	KP281598	<i>Populus tomentosa</i>
PtoCCR4	KP281599	<i>Populus tomentosa</i>
PtoCCR5	KP281600	<i>Populus tomentosa</i>
PtoCCR6	KP281601	<i>Populus tomentosa</i>
PtoCCR7	KF145198	<i>Populus tomentosa</i>
PtoCCR8	KP281602	<i>Populus tomentosa</i>
PtoCCR9	KP281603	<i>Populus tomentosa</i>
PtoCCR10	KP281604	<i>Populus tomentosa</i>
PtoCCR11	KP281605	<i>Populus tomentosa</i>
ZmCCR1	CAA66707.1	<i>Zea mays</i>
ZmCCR2	AAO42621	<i>Zea mays</i>

LpCCR1	KM516130	<i>Lolium perenne</i>
LpCCR2	KM516131	<i>Lolium perenne</i>
LpCCR3	KM516132	<i>Lolium perenne</i>
LpCCR4	KM516133	<i>Lolium perenne</i>
LpCCR5	KM516134	<i>Lolium perenne</i>
LpCCR6	KM516135	<i>Lolium perenne</i>
LpCCR7	KM516136	<i>Lolium perenne</i>
LpCCR8	KM516137	<i>Lolium perenne</i>
LpCCR9	KM516138	<i>Lolium perenne</i>
LpCCR11	KM516142	<i>Lolium perenne</i>
PmCCR	ACE76870	<i>Pinus massoniana</i>
PaCCR	CAK18610	<i>Picea abies</i>
IhDFR	BAF93856.1	<i>Iris × hollandica</i>
ApDFR	AB099529.1	<i>Agapanthus praecox</i>
AtDFR	AB033294	<i>Arabidopsis thaliana</i>
LhDFR	AB058641	<i>Lilium hybrid</i>
PhDFR	AF233639	<i>Petunia hybrida</i>
VvDFR	X75964	<i>Vitis vinifera</i>
AngDFR1	KJ817183	<i>Angelonia angustifolia</i>
AngDFR2	KF285561	<i>Angelonia angustifolia</i>
ZmDFR	Y16040	<i>Zea mays</i>
OsDFR	AB003495	<i>Oryza sativa</i>
PfDFR	AB002817	<i>Perilla frutescens</i>
MdDFR	AAO39816	<i>Malus domestica</i>
SlDFR	CAA79154.1	<i>Solanum lycopersicum</i>
AmDFR	X15536	<i>Antirrhinum majus</i>
FhDFR1	KU132393	<i>Freesia hybrida</i>
FhDFR2	KU132389	<i>Freesia hybrida</i>
FhDFR3	KU132390	<i>Freesia hybrida</i>
GbDFR	AGR34043.1	<i>Ginkgo biloba</i>
OsPAR	XP_015621618.1	<i>Oryza sativa</i>
CsPAR	XP_030489464	<i>Cannabis sativa</i>
VVPAR	XP_010651224.1	<i>Vitis vinifera</i>
LsPAR	XP_023760675.1	<i>Lactuca sativa</i>
GhPAR	XP_016745296.2	<i>Gossypium hirsutum</i>
BnPAR	XP_013698013.1	<i>Brassica napus</i>
PbPAR	XP_018505454.1	<i>Pyrus × bretschneideri</i>
CiPAR	XP_042957787.1	<i>Carya illinoensis</i>

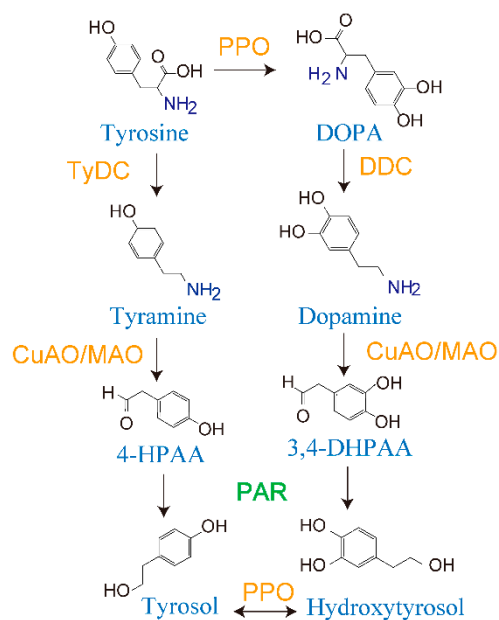


Figure S1: Hydroxytyrosol Biosynthesis Pathway. Blue texts: substrates and products(4-HPAA, 4-hydroxyphenylacetaldehyde; 3,4-DHPAA, 3,4 dihydroxyphenylacetaldehyde); yellow and green texts: catalytic enzymes(PPO, polyphenol oxidase; TyDC, tyrosine decarboxylase; DDC, DOPA decarboxylase; CuAO primary amine (copper-containing) oxidase; MAO, Monoamino oxidase).



Figure S2: TMHMM result of 21 proteins. When "number of predicted TMHs" equals 0, it indicates that no transmembrane domains were predicted for this protein.

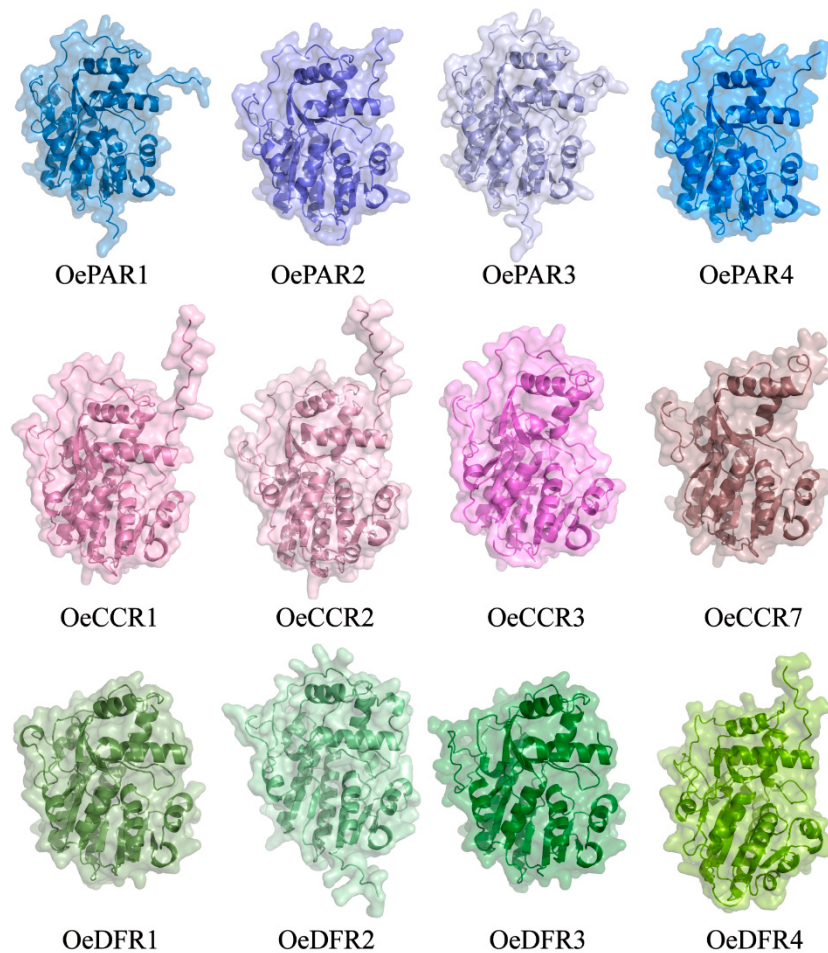


Figure S3: The prediction of the three-dimensional structures of 12 proteins.

OePAR1.1	MSMATKTVCVTGASGYIASWIVKFLLRGYTVKASIRDNDPKKTEHLLALDGAKEHLHLKANLLEQGSFDAVVDGCEG
OePAR1	MSMATKTVCVTGASGYIASWIVKFLLRGYTVKASIRDNDPKKTEHLLALDGAKEHLHLKANLLEQGSFDAVVDGCEG
Consensus	msmatktvcvtgasgyiaswivkfllqrgytkasirdlndpkktehllaldgakerlhllkanlleqgsfdavvdgceg
OePAR1.1	VFHTASPPFFHAVTDPQAEIDPALKGTLNVLESCAKTPSVKRVVLTSSIAAVAYNGKPRTPPEVIVDETWWSNPEFCCKEMK
OePAR1	VFHTASPPFFHAVTDPQAEIDPALKGTLNVLESCAKTPSVKRVVLTSSIAAVAYNGKPRTPPEVIVDETWWSNPEFCCKEMK
Consensus	vfhtasppffhavtdpqaelidpalkgtlnvlescaktpsvkrvvtssiaavayngkprtpevivdetwwsnpefckemk
OePAR1.1	QWYVLSKTLAEDAANKFVKEKGLDMVTINPAMVIGPLLOPTLNTSAAAVLNLIKSPPEYPNATFGWVNVKDVANAHILAF
OePAR1	QWYVLSKTLAEDAANKFVKEKGLDMVTINPAMVIGPLLOPTLNTSAAAVLNLIKSPPEYPNATFGWVNVKDVANAHILAF
Consensus	qwyvlsktdaadaawkfvkekglmdvtnpamvigplloptlntsaavlnlikspeypnatfgwvnnkdvanaahilaf
OePAR1.1	ENPSANGRYCLVERVAHFSEIVQILRELYPSLPLPEKCAADKPFVPKYQVSKEKAKSLGIEFTPLKESIKETVESLKEKN
OePAR1	ENPSANGRYCLVERVAHFSEIVQILRELYPSLPLPEKCAADKPFVPKYQVSKEKAKSLGIEFTPLKESIKETVESLKEKN
Consensus	enpsangryclvervahfseivqilrelypslplpekcaadkpfvpkyqvskekakslgieftplkesiketveslkekn
OePAR1.1	FFGASSA
OePAR1	FFGASSA
Consensus	ffgassa

Figure S4: The alignment of the protein sequences of OePAR1.1 and OePAR1.