AT1G15550 = NP_173008 Q39103 AAC37506 AAF71980 AAO64762 GA4 (GA REQUIRING 4); gibberellin 3-beta-dioxygenase/G3OX1_ARATH Gibberellin 3-beta-dioxygenase 1 (Gibberellin 3 beta-hydroxylase 1) (GA 3-oxidase 1) (AtGA3ox1)/GA4 /GA4 protein /At1g15550

AT1G80340 = NP_178150 Q9ZT84 AAG52442 GA4H; gibberellin 3-beta-dioxygenase/G3OX2_ARATH Gibberellin 3-beta-dioxygenase 2 (Gibberellin 3 beta-hydroxylase 2) (GA 3-oxidase 2) (AtGA3ox2)/gibberellin 3 beta-hydroxylase; 29683-28215

AAC83647 Arabidopsis thaliana gibberellin 3 beta-hydroxylase

AT1G80330 = NP_178149 Q9C971 AAG52440 iron ion binding/isopenicillin-N synthase /G3OX4_ARATH Gibberellin 3-beta-dioxygenase 4 (Gibberellin 3 beta-hydroxylase 4) (GA 3-oxidase 4) (AtGA3ox4) (AtGA3ox3)/putative gibberellin 3 beta-hydroxylase; 27057-25

CAB92914 Cucurbita maxima gibberellin 3-beta-hydroxylase

CAC83089 Cucurbita maxima gibberellin 3-oxidase

AAK91506 Solanum tuberosum gibberellin 3-beta-hydroxylase 2

BAA34125 Lycopersicon esculentum 3b-hydroxylase

AAM12872 Nicotiana sylvestris gibberellin 3-oxidase 1

BAD06943 Ipomoea nil gibberellin 3-oxidase-like protein

AAK91507 Solanum tuberosum gibberellin 3-beta-hydroxylase 1

BAA34124 Lycopersicon esculentum 3b-hydroxylase

AAM12873 Nicotiana sylvestris gibberellin 3-oxidase 2

BAA89316 Nicotiana tabacum gibberellin 3beta-hydroxylase

AAN87570 Spinacia oleracea gibberellin 3-oxidase

BAA37130 Lactuca sativa gibberellin 3beta-hydroxylase

BAA37129 Lactuca sativa gibberellin 3beta-hydroxylase

AAC96017 AAC96015 AAC49794 defective gibberellin 3B-hydroxylase/gibberellin 3B-hydroxylase /gibberellin 3 beta-hydroxylase

AAC86820 Pisum sativum AAC49793 gibberellin 3 beta-hydroxylase/gibberellin 3 beta-hydroxylase

AAB65829 Pisum sativum AAC49792 2-oxoglutarate-dependent dioxygenase/gibberellin 3 beta-hydroxylase

AAR12160 Populus tremula x Populus tremuloides gibberellin 3-oxidase

BAD91162 Prunus subhirtella gibberellin 3-beta hydroxylase

BAD30036 Daucus carota gibberellin 3beta-hydroxylase2

BAD30035 Daucus carota gibberellin 3beta-hydroxylase1

AAB64347 Cucurbita maxima gibberellin 2beta,3beta-hydroxylase

AAF80661 Citrullus lanatus var. lanatus putative gibberellin 3 beta hydroxylase

CAH69705 Phaseolus coccineus gibberellin 3-oxidase

BAB12439 Lactuca sativa gibberellin 3b-hydroxylase No3

BAD30037 Daucus carota gibberellin 3beta-hydroxylase3

AT4G21690 = NP_193900 Q9SVS8 CAB36813 CAB81276 iron ion binding/isopenicillin-N synthase /G3OX3_ARATH Putative gibberellin 3-beta-dioxygenase 3 (Gibberellin 3 beta-hydroxylase 3) (GA 3-oxidase 3) (AtGA3ox3) (AtGA3ox4)/gibberellin 3 beta-hydroxylase-

BAD06944 Ipomoea nil gibberellin 3-oxidase-like protein

BAB62073 Oryza sativa (indica cultivar-group) AAT77356 Oryza sativa (japonica cultivar-group) GA 3beta-hydroxylase/putative gibberellin 3 beta-hydroxylase

AAT49060 Hordeum vulgare subsp. vulgare GA 3-oxidase 1

Q3I410 Triticum aestivum AAZ94378 G3O22_WHEAT Gibberellin 3-beta-dioxygenase 2-2 (Gibberellin 3 beta-hydroxylase 2-2) (Gibberellin 3-oxidase 2-2)/gibberellin 3-oxidase 2-2

Q3I411 Triticum aestivum AAZ94377 G3O21_WHEAT Gibberellin 3-beta-dioxygenase 2-1 (Gibberellin 3 beta-hydroxylase 2-1) (Gibberellin 3-oxidase 2-1)/gibberellin 3-oxidase 2-1

AAT49061 Hordeum vulgare subsp. vulgare GA 3-oxidase 2/gibberellin 3beta-hydroxylase

Q3I409 Triticum aestivum AAZ94379 G3O23_WHEAT Gibberellin 3-beta-dioxygenase 2-3 (Gibberellin 3 beta-hydroxylase 2-3) (Gibberellin 3-oxidase 2-3)/gibberellin 3-oxidase 2-3

BAD62153 Oryza sativa GA 3beta-hydroxylase

BAB62072 Oryza sativa (indica cultivar-group) GA 3beta-hydroxylase3

NP_916509 Oryza sativa (japonica cultivar-group) BAB17075 BAB62154 Oryza sativa BAB62155 Oryza sativa (japonica cultivar-group) GA 3beta-hydroxylase/GA 3beta-hydroxylase /GA 3beta-hydroxylase /GA 3beta-hydroxylase

Smo_GA4_101_2

Ppa_GA4_20_1

AAU93347 Ginkgo biloba flavanone 3-hydroxylase

AT3G19010 = NP_566624 BAB01697 AAM65669 AAO22576 flavonol synthase/iron ion binding /isopenicillin-N synthase /oxidase-like protein /unknown /unknown protein

AT3G13610 = NP_187970 BAB02603 AAS49108 BAD95049 oxidoreductase, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors/leucoanthocyani

AT4G25310 = NP_194261 CAA23072 CAB81342 AAR92265 AAS76252 iron ion binding/isopenicillin-N synthase/oxidoreductase, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one a

NP_914944 Oryza sativa (japonica cultivar-group) BAB64195 putative ethylene-forming enzyme/putative ethylene-forming enzyme

AT3G21420 = NP_566685 BAB03055 AAM61362 AAO64923 oxidoreductase/unnamed protein product /putative ethylene-forming enzyme /At3g21420

Smo_GA4_116_1

Smo_GA4_36_1

Smo_GA4_41_1

NP_910523 Oryza sativa (japonica cultivar-group) BAA81862 putative anthocyanidin synthase/putative anthocyanidin synthase

AAM12973 Arabidopsis thaliana AAM47961 strong similarity to naringenin 3-dioxygenase/strong similarity to naringenin 3-dioxygenase

AT4G10490 = NP_192787 AAD03424 CAB40042 CAB78172 AAO41989 AAO50563 oxidoreductase, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both dono

AT4G10500 = NP_192788 AAD03425 CAB40043 CAB78173 AAQ65160 BAD44441 BAD44674 oxidoreductase, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into

NP_922524 Oryza sativa (japonica cultivar-group) AAL58118 AAM76343 AAP54811 unknown protein/putative flavanone 3-hydroxylase /unknown protein /flavanone 3-hydroxylase, putative

XP_473641 Oryza sativa (japonica cultivar-group) CAD41169 OSJNBa0064M23.14/OSJNBa0064M23.14

AAS21058 Ginkgo biloba flavonol synthase

BAE75810 Vitis vinifera flavonol synthase

XP_467968 Oryza sativa (japonica cultivar-group) BAD17324 putative flavonol synthase/putative flavonol synthase

Q9XHG2 Malus x domestica AAD26261 FLS_MALDO Flavonol synthase/flavanone 3-hydroxylase (FLS)/flavonol synthase

BAC66468 Rosa hybrid cultivar 'Kardinal' flavonol synthase

BAE75809 Vitis vinifera flavonol synthase

BAE75807 Vitis vinifera flavonol synthase

BAE75808 Vitis vinifera flavonol synthase

ABB53382 Antirrhinum majus flavonol synthase

AAT68476 Allium cepa flavonol synthase

Q9ZWQ9 Citrus unshiu BAA36554 FLS_CITUN Flavonol synthase/flavanone 3-hydroxylase (FLS) (CitFLS) /flavonol synthase

Smo_GA4_140_1

Smo_GA4_128_1

XP_475566 Oryza sativa (japonica cultivar-group) AAS90686 putative leucoanthocyanidin dioxygenase (EC 1.14.11.-)/putative leucoanthocyanidin dioxygenase

NP_915344 Oryza sativa (japonica cultivar-group) BAD73770 leucoanthocyanidin dioxygenase-like protein/putative anthocyanidin synthase

AT2G38240 = NP_181359 AAC27173 AAL32721 AAM13301 AAM63604 unknown protein/putative anthocyanidin synthase /putative anthocyanidin synthase /putative anthocyanidin synthase /putative anthocyanidin synthase

AAM61665 Arabidopsis thaliana leucoanthocyanidin dioxygenase-like protein

AT5G05600 = NP_196179 BAB11549 AAK63997 AAM91495 iron ion binding/isopenicillin-N synthase /leucoanthocyanidin dioxygenase-like protein /AT5g05600/MOP10_14 /AT5g05600/MOP10_14

AT3G11180 = NP_187728 AAF01507 AAG50980 iron ion binding/isopenicillin-N synthase /putative leucoanthocyanidin dioxygenase /leucoanthocyanidin dioxygenase, putative; 41415-43854

AT1G30040 = NP_174296 T52578 Q9XFR9 CAB41008 AAG52050 AAO22796 AAO42458 gibberellin 2-beta-dioxygenase/T52578 gibberellin 2beta-dioxygenase (EC 1.14.11.13) 2 /G2O2_ARATH Gibberellin 2-beta-dioxygenase 2 (Gibberellin 2-beta-hydroxylase 2) (Gibberelli

BAD99508 Vigna angularis gibberellin 2-oxidase

Smo_GA4_117_1

Smo_GA4_137_1

AT5G51810 = NP_199994 Q39111 CAA58294 BAB11250 GA20OX2; gibberellin 20-oxidase/GAOX2_ARATH Gibberellin 20 oxidase 2 (Gibberellin C-20 oxidase 2) (GA 20-oxidase 2)/gibberellin 20-oxidase /gibberellin 20-oxidase

Ppa_GA4_9_2

Ppa_GA4_31_1

Smo_GA4_63_1

Ppa_GA4_34_1

Ppa_GA4_3_1

Ppa_GA4_6_1

Ppa_GA4_29_1

Smo_GA4_1_1

Smo_GA4_87_1

0.100