

Table S1. Plasma Analysis of Metabolic Parameters in Male and Female Mice Subjected Either to Standard Diet or to a High-Fat Diet, Related to Figure 3

*, p=0.05; **, p<0.01.

MALES	Standard Diet		High fat diet	
	<i>Rap1^{+/+}</i>	<i>Rap1^{-/-}</i>	<i>Rap1^{+/+}</i>	<i>Rap1^{-/-}</i>
Weight (g)	42.1 ± 3.7	47.6 ± 2.5	44.9 ± 3.0	48.5 ± 1.5
Albumin (g/L)	35.9 ± 1.1	36.1 ± 2.7	35.1 ± 1.0	34.7 ± 0.6
Bilirubin (µmol/L)	2.6 ± 0.4	3.6 ± 1.2	5.9 ± 3.0	2.5 ± 0.2
Calcium (mmol/L)	2.3 ± 0.1	2.1 ± 0	2.2 ± 0.1	2.2 ± 0
Phosphorous (mmol/L)	3.2 ± 0.3	4.0 ± 0.5	2.5 ± 0.1	2.3 ± 0.1
Total proteins (g/dL)	7.2 ± 0.2	6.9 ± 0.2	6.4 ± 0.3	6.3 ± 0.2
Urea (mg/dL)	64.8 ± 9.0	64.0 ± 5.2	56.6 ± 3.1	54.9 ± 4.1
Creatinine (µmol/L)	13.1 ± 4.1	11.3 ± 1.3	10.3 ± 1.6	12.1 ± 1.3
Cholesterol (mg/L)	146.9 ± 6.7	132.4 ± 25.4	194.4 ± 25.9	181.3 ± 8.3
HDL (mg/dL)	53.0 ± 8.0	65.2 ± 2.6	72.3 ± 4.4	68.5 ± 2.9
LDL (mg/dL)	10.0 ± 0.7	12.5 ± 1.3	24.8 ± 4.3	21.8 ± 2.6
Triglycerides (mg/dL)	123.0 ± 13.1	121 ± 9.0	124.3 ± 11.3	114.4 ± 8.4
ALT (U/L)	35.88 ± 3.0	49.64 ± 9.2	195.12 ± 87	111.6 ± 28
Glucose (mmol/L)	5.4 ± 1.5	5.1 ± 0.2	5.4 ± 1.5	4.0 ± 0.8
FEMALES	Standard Diet		High fat diet	
	<i>Rap1^{+/+}</i>	<i>Rap1^{-/-}</i>	<i>Rap1^{+/+}</i>	<i>Rap1^{-/-}</i>
Weight (g)	28.9 ± 3.1	49.5 ± 4.6 **	32.6 ± 3.5	44.0 ± 2.7**
Albumin (g/L)	32.6 ± 2.2	34.2 ± 2.5	34.0 ± 1.9	35.7 ± 1.0
Bilirubin (µmol/L)	4.0 ± 0.9	1.7 ± 0.2	2.6 ± 0.2	2.6 ± 0.2
Calcium (mmol/L)	2.1 ± 0.1	2.3 ± 0	2.3 ± 0.1	2.4 ± 0.1
Phosphorous (mmol/L)	3.2 ± 0.3	2.7 ± 0.2	2.1 ± 0.2	2.5 ± 0.3
Total proteins (g/dL)	6.1 ± 0.6	6.5 ± 0.1	6.5 ± 0.3	6.7 ± 0.2
Urea (mg/dL)	60.9 ± 3.6	57.5 ± 1.8	57.8 ± 2.9	58.8 ± 2.6
Creatinine (µmol/L)	15.8 ± 3.0	7.9 ± 1.2	13.6 ± 1.8	12.1 ± 2.1
Cholesterol (mg/L)	85.6 ± 18.6	118.6 ± 4*	112.4 ± 12	159 ± 10**
HDL (mg/dL)	41.3 ± 8.9	44.3 ± 4.8	51.0 ± 5.1	62.5 ± 1.4
LDL (mg/dL)	9.6 ± 0.8	11.6 ± 1.6	13.3 ± 0.6	18.6 ± 1.3**

Triglycerides (mg/dL)	136.7 ± 10	120.7 ± 7.5	115.5 ± 5.8	111.7 ± 5.6
ALT (U/L)	54.1 ± 14.6	129.53 ± 38**	58.55 ± 20	187 ± 38**
Glucose (mmol/L)	4.1 ± 1.4	5.5 ± 0.2	5.0 ± 0.5	4.3 ± 0.6

Table S2. Significantly Enriched Gene Sets Found in the Livers of 10-Week-Old *Rap1*^{-/-} Females, Related to Figure 6

FDR: False Discovery Rate, NES: Normalized Enrichment Score. FDR<0.25.

Gene Set Name	# Genes	NES	FDR q-val	Source	Rab1 -/- status
BIOSYNTHESIS OF STEROIDS	23	2.5169961	0	KEGG	UP
DRUG METABOLISM - CYTOCHROME P450	75	2.351679	0	KEGG	UP
ANDROGEN AND ESTROGEN METABOLISM	34	2.1567147	0	KEGG	UP
CHOLESTEROL BIOSYNTHESIS	19	2.4279442	0	REACTOME	UP
METABOLISM OF XENOBIOTICS BY CYTOCHROME P450	66	2.1008756	8.69E-04	KEGG	UP
BILE ACID BIOSYNTHESIS	29	2.0114846	9.04E-04	KEGG	UP
TRYPTOPHAN METABOLISM	42	2.0153143	0.001017382	KEGG	UP
PROPANOATE METABOLISM	29	2.0290937	0.001162723	KEGG	UP
DRUG METABOLISM - OTHER ENZYMES	46	2.0367715	0.00135651	KEGG	UP
VALINE, LEUCINE AND ISOLEUCINE DEGRADATION	45	2.0415428	0.001379811	KEGG	UP
BUTANOATE METABOLISM	40	1.9751942	0.001500798	KEGG	UP
RETINOL METABOLISM	62	1.8931497	0.004285994	KEGG	UP
BIOLOGICAL OXIDATIONS	119	2.0317812	0.007228908	REACTOME	UP
ACTIVATION OF THE PRE-REPLICATIVE COMPLEX	29	1.9477711	0.017360628	REACTOME	UP
PYRIMIDINE METABOLISM	89	1.7511019	0.01925754	KEGG	UP
HISTIDINE METABOLISM	27	1.7580942	0.019640766	KEGG	UP
SPHINGOLIPID METABOLISM	36	1.7398285	0.020183748	KEGG	UP
ACTIVATION OF ATR IN RESPONSE TO REPLICATION STRESS	35	1.9065479	0.020955402	REACTOME	UP
PORPHYRIN AND CHLOROPHYLL METABOLISM	32	1.7142601	0.024497299	KEGG	UP
OXIDATIVE PHOSPHORYLATION	110	1.699594	0.025012853	KEGG	UP
FATTY ACID METABOLISM	43	1.703376	0.025527395	KEGG	UP
PYRUVATE METABOLISM	40	1.681831	0.02740653	KEGG	UP
P450 HYDROXYLATIONS	17	1.8235364	0.029125301	REACTOME	UP
P450 DEHYDROGENATION OF ALKANES TO FORM ALKENES	19	1.8323857	0.030639747	REACTOME	UP
DNA REPLICATION	96	1.8384043	0.03243205	REACTOME	UP
DNA REPLICATION PRE-INITIATION	75	1.8597062	0.03294014	REACTOME	UP
PURINE METABOLISM	144	1.6597061	0.0333265	KEGG	UP
FATTY ACIDS	15	1.7806872	0.04325612	REACTOME	UP
M/G1 TRANSITION	61	1.7169871	0.04422614	REACTOME	UP
PHASE 1 - FUNCTIONALIZATION OF COMPOUNDS	71	1.7568594	0.04476819	REACTOME	UP
CELL CYCLE CHECKPOINTS	116	1.7089447	0.045446668	REACTOME	UP
ELECTRON TRANSPORT CHAIN	62	1.7455995	0.046201337	REACTOME	UP
LIPID AND LIPOPROTEIN METABOLISM	180	1.7636501	0.046276826	REACTOME	UP
BRANCHED-CHAIN AMINO ACID CATABOLISM	22	1.7193013	0.046503764	REACTOME	UP
ASSEMBLY OF THE PRE-REPLICATIVE COMPLEX	61	1.7319005	0.04792924	REACTOME	UP
ORC1 REMOVAL FROM CHROMATIN	68	1.6947447	0.048778545	REACTOME	UP
G2/M CHECKPOINTS	45	1.7210207	0.04892913	REACTOME	UP
GLUTATHIONE CONJUGATION	18	1.685878	0.049869407	REACTOME	UP
ATP FORMATION	21	1.6560509	0.050344132	REACTOME	UP
DNA STRAND ELONGATION	29	1.668273	0.05125659	REACTOME	UP

FURTHER PLATELET RELEASATE	37	1.6615132	0.05128681	REACTOME	UP
FORMATION OF PLATELET PLUG	116	1.6639029	0.051657442	REACTOME	UP
EXOCYTOSIS OF ALPHA GRANULE	70	1.6563364	0.052242845	REACTOME	UP
TYROSINE METABOLISM	36	1.601104	0.053438894	KEGG	UP
CYTOCHROME P450	25	1.6686112	0.0535614	REACTOME	UP
HEMOSTASIS	233	1.6699935	0.055531364	REACTOME	UP
DNA REPLICATION	35	1.5892345	0.05606858	KEGG	UP
GLUTATHIONE METABOLISM	53	1.584594	0.05608329	KEGG	UP
COMPLEMENT AND COAGULATION CASCADES	70	1.5644605	0.06346488	KEGG	UP
UREA CYCLE AND METABOLISM OF AMINO GROUPS	27	1.5336365	0.070784725	KEGG	UP
ECM-RECEPTOR INTERACTION	79	1.5421149	0.072123595	KEGG	UP
GLYCINE, SERINE AND THREONINE METABOLISM	44	1.5353991	0.07251592	KEGG	UP
FORMATION OF FIBRIN CLOT (CLOTTING CASCADE)	29	1.6077151	0.07336275	REACTOME	UP
CYTOCHROME P450 - ARRANGED BY SUBSTRATE TYPE	50	1.6014193	0.074300565	REACTOME	UP
LINOLEIC ACID METABOLISM	40	1.5079641	0.084434725	KEGG	UP
G1/S TRANSITION	109	1.5702939	0.0924462	REACTOME	UP
NUCLEOTIDE METABOLISM	82	1.564307	0.09304774	REACTOME	UP
ELEVATION OF CYTOSOLIC CA ⁺⁺ LEVELS	82	1.5488926	0.09932146	REACTOME	UP
GLUCONEOGENESIS	33	1.5512133	0.100048825	REACTOME	UP
CDT1 ASSOCIATION WITH THE CDC6:ORC:ORIGIN COMPLEX	55	1.5378649	0.10466529	REACTOME	UP
NUCLEOTIDE EXCISION REPAIR	40	1.4483975	0.12484158	KEGG	UP
CITRATE CYCLE (TCA CYCLE)	30	1.4495149	0.12825158	KEGG	UP
FGFR4 LIGAND BINDING AND ACTIVATION	15	-1.7794468	0.1311975	REACTOME	DOWN
PENTOSE AND GLUCURONATE INTERCONVERSIONS	18	1.4361193	0.1322497	KEGG	UP
METABOLISM OF NITRIC OXIDE	25	1.4967877	0.1385311	REACTOME	UP
METHIONINE METABOLISM	21	1.4033546	0.16125782	KEGG	UP
INSULIN SYNTHESIS AND SECRETION	54	1.4575654	0.16826625	REACTOME	UP
CELL CYCLE, MITOTIC	317	1.4583124	0.17213766	REACTOME	UP
ORNITHINE METABOLISM	53	1.4614093	0.1739477	REACTOME	UP
NRAGE SIGNALS DEATH THROUGH JNK	15	-1.6779176	0.17573065	REACTOME	DOWN
AMINOACYL-TRNA BIOSYNTHESIS	42	1.383633	0.17774573	KEGG	UP
SELENOAMINO ACID METABOLISM	22	1.3783097	0.1780914	KEGG	UP
APC/C:CDH1 MEDIATED DEGRADATION OF CDC20 AND OTHER APC/C:CDH1 TARGETED PROTEINS IN LATE MITOSIS/EARLY G1	71	1.4450498	0.17934485	REACTOME	UP
COLLAGEN-MEDIATED ACTIVATION CASCADE	16	1.4328508	0.18744712	REACTOME	UP
CYCLIN A:CDK2-ASSOCIATED EVENTS AT S PHASE ENTRY	64	1.4344866	0.18998687	REACTOME	UP
DNA REPAIR	98	1.4264888	0.19095255	REACTOME	UP
PARKINSON'S DISEASE	110	1.3624933	0.1911234	KEGG	UP
AUTODEGRADATION OF CDH1 BY CDH1:APC/C	63	1.4145646	0.19322754	REACTOME	UP
CHYLOMICRON-MEDIATED LIPID TRANSPORT	16	1.4162815	0.19504194	REACTOME	UP
APC/C:CDK20 MEDIATED DEGRADATION OF SECURIN	64	1.4187945	0.19619536	REACTOME	UP
INTEGRIN CELL SURFACE INTERACTIONS	91	1.4010003	0.20655149	REACTOME	UP

CDC20:PHOSPHO-APC/C DEGRADATION OF CYCLIN A	MEDIATED	68	1.3953516	0.20984785	REACTOME	UP
DOUBLE-STRAND BREAK REPAIR		31	1.3887703	0.21332806	REACTOME	UP
G-PROTEIN ACTIVATION		25	1.3749077	0.22127932	REACTOME	UP
G2/M TRANSITION		97	1.3807743	0.22167584	REACTOME	UP
MEMBRANE TRAFFICKING		58	1.3684113	0.2217279	REACTOME	UP
DUAL INCISION REACTION IN GG-NER		21	1.3698521	0.2241191	REACTOME	UP
FORMATION OF INCISION COMPLEX IN GG-NER		21	1.375531	0.22492968	REACTOME	UP
PPAR SIGNALING PATHWAY		74	1.3206327	0.23484382	KEGG	UP
ALANINE AND ASPARTATE METABOLISM		29	1.3252659	0.23598894	KEGG	UP
METABOLISM OF VITAMINS AND COFACTORS		46	1.3481523	0.24488553	REACTOME	UP
MISMATCH REPAIR		22	1.3085029	0.24567536	KEGG	UP

Table S3. Significantly Enriched Gene Sets Found in Gonadal White Fat Tissue of *Rap1*^{-/-} Females, Related to Figure 6

FDR: False Discovery Rate, NES: Normalized Enrichment Score. FDR<0.25.

Gene Set Name	# Genes	NES	FDR q-val	Source	Rab1 -/- status
ECM-RECEPTOR INTERACTION	79	2.004533	0.00552448	KEGG	UP
PYRUVATE METABOLISM	40	-1.9658341	0.009929905	KEGG	DOWN
BLADDER CANCER	42	1.9007902	0.013026089	KEGG	UP
MAPK SIGNALING PATHWAY	257	1.8657416	0.016694758	KEGG	UP
FOCAL ADHESION	190	1.8328364	0.020281324	KEGG	UP
PROPANOATE METABOLISM	29	-1.7186533	0.05040007	KEGG	DOWN
PPAR SIGNALING PATHWAY	74	-1.727355	0.05786784	KEGG	DOWN
CITRATE CYCLE (TCA CYCLE)	30	-1.6800555	0.059602737	KEGG	DOWN
ELECTRON TRANSPORT CHAIN	62	-1.8369874	0.06062995	REACTO ME	DOWN
GLUCOSE METABOLISM	77	-1.7885938	0.061885286	REACTO ME	DOWN
BIOSYNTHESIS OF UNSATURATED FATTY ACIDS	30	-1.6574196	0.06351131	KEGG	DOWN
GLYCOLYSIS	22	-1.8915594	0.06478297	REACTO ME	DOWN
TGF-BETA SIGNALING PATHWAY	85	1.7114409	0.07026618	KEGG	UP
GRAFT-VERSUS-HOST DISEASE	21	-1.6271291	0.07157563	KEGG	DOWN
BASAL CELL CARCINOMA	55	1.6884203	0.07370097	KEGG	UP
OXIDATIVE PHOSPHORYLATION	110	-1.7316537	0.076298594	KEGG	DOWN
HEDGEHOG SIGNALING PATHWAY	53	1.6672674	0.080229335	KEGG	UP
METABOLISM OF CARBOHYDRATES	100	-1.7306147	0.08141958	REACTO ME	DOWN
METABOLISM OF BILE ACIDS AND BILE SALTS	47	-1.6955582	0.08866284	REACTO ME	DOWN
COMPLEMENT AND COAGULATION CASCADES	70	-1.5749704	0.09517886	KEGG	DOWN
GLYCOLYSIS / GLUCONEOGENESIS	53	-1.7444655	0.09906602	KEGG	DOWN
G-PROTEIN ACTIVATION	25	1.8571392	0.10200319	REACTO ME	UP
COLLAGEN ADHESION VIA ALPHA 2 BETA 1 GLYCOPROTEIN	16	1.7720693	0.13963076	REACTO ME	UP
P53 SIGNALING PATHWAY	65	1.562774	0.14037709	KEGG	UP
FGFR1 LIGAND BINDING AND ACTIVATION	20	1.6028283	0.1410056	REACTO ME	UP
ALPHA-LINOLENIC ACID METABOLISM	16	1.5832515	0.14237046	KEGG	UP
FURTHER PLATELET RELEASATE	37	1.6184621	0.1443063	REACTO ME	UP
PROTEASOME	41	-1.5062642	0.14546703	KEGG	DOWN
BASIGIN INTERACTIONS	15	1.5896456	0.1458923	REACTO ME	UP
FGFR2 LIGAND BINDING AND ACTIVATION	19	1.6037223	0.15209194	REACTO ME	UP
WNT SIGNALING PATHWAY	146	1.5635965	0.15346472	KEGG	UP
INTEGRIN CELL SURFACE INTERACTIONS	91	1.6207877	0.15701488	REACTO ME	UP
COLORECTAL CANCER	85	1.5840312	0.15961584	KEGG	UP
ENDOGENOUS STEROLS	18	-1.6016139	0.16369729	REACTO ME	DOWN
EXOCYTOSIS OF ALPHA GRANULE	70	1.5255255	0.17436944	REACTO ME	UP
COLLAGEN-MEDIATED ACTIVATION CASCADE	16	1.6214712	0.1757661	REACTO ME	UP

CELL SURFACE INTERACTIONS AT THE VASCULAR WALL	93	1.5353462	0.17903456	REACTOME	UP
OPIOID SIGNALLING	82	1.5282247	0.17944291	REACTOME	UP
CYCLIN D ASSOCIATED EVENTS IN G1	17	1.5355306	0.18994336	REACTOME	UP
FGFR LIGAND BINDING AND ACTIVATION	23	1.6278551	0.19034383	REACTOME	UP
FORMATION OF PLATELET PLUG	116	1.6787493	0.19109751	REACTOME	UP
FGFR2C LIGAND BINDING AND ACTIVATION	15	1.5422461	0.19196635	REACTOME	UP
PARKINSON'S DISEASE	110	-1.451378	0.19311035	KEGG	DOWN
ARACHIDONIC ACID METABOLISM	69	1.484856	0.19386934	KEGG	UP
CELL ADHESION MOLECULES (CAMS)	110	1.4999945	0.1983287	KEGG	UP
G1 PHASE	17	1.5028735	0.19880383	REACTOME	UP
AMINE-DERIVED HORMONES	16	1.5452377	0.200567	REACTOME	UP
PEPTIDE LIGAND-BINDING RECEPTORS	65	1.6365684	0.20280737	REACTOME	UP
B CELL RECEPTOR SIGNALING PATHWAY	65	1.4876983	0.20352997	KEGG	UP
ELEVATION OF CYTOSOLIC CA ⁺⁺ LEVELS	82	1.4868823	0.2037268	REACTOME	UP
N-GLYCAN DEGRADATION	15	1.5073115	0.20423242	KEGG	UP
NRAGE SIGNALS DEATH THROUGH JNK	15	1.4927717	0.20439309	REACTOME	UP
INTEGRATION OF ENERGY METABOLISM	54	-1.4255652	0.20896266	REACTOME	DOWN
METABOLISM OF NITRIC OXIDE	25	-1.4349115	0.21015264	REACTOME	DOWN
IMMUNOREGULATORY INTERACTIONS BETWEEN A LYMPHOID AND A NON-LYMPHOID CELL	46	1.4764822	0.21061532	REACTOME	UP
MELANOGENESIS	100	1.4620317	0.21549417	KEGG	UP
PHASE 1 - FUNCTIONALIZATION OF COMPOUNDS	71	-1.4004295	0.21579671	REACTOME	DOWN
HEMOSTASIS	233	1.69418	0.21611644	REACTOME	UP
METABOLISM OF WATER-SOLUBLE VITAMINS AND COFACTORS	46	-1.4395648	0.21927734	REACTOME	DOWN
LIPID AND LIPOPROTEIN METABOLISM	180	-1.5230713	0.22054918	REACTOME	DOWN
CITRIC ACID CYCLE (TCA CYCLE)	18	-1.5427071	0.22126439	REACTOME	DOWN
BRANCHED-CHAIN AMINO ACID CATABOLISM	22	-1.4054058	0.22159475	REACTOME	DOWN
CYTOCHROME P450 - ARRANGED BY SUBSTRATE TYPE	50	-1.4619826	0.22325319	REACTOME	DOWN
METABOLISM OF VITAMINS AND COFACTORS	46	-1.4479984	0.22469375	REACTOME	DOWN
DEGRADATION OF BETA-CATENIN BY THE DESTRUCTION COMPLEX	55	-1.4727879	0.22477409	REACTOME	DOWN
CHYLOMICRON-MEDIATED LIPID TRANSPORT	16	-1.484501	0.22968222	REACTOME	DOWN
CLASS A/1 (RHODOPSIN-LIKE RECEPTORS)	65	1.6407377	0.23283313	REACTOME	UP
MEMBRANE TRAFFICKING	58	1.4549385	0.23500216	REACTOME	UP
CYTOKINE-CYTOKINE RECEPTOR INTERACTION	237	1.4410808	0.23852608	KEGG	UP
P450 DEHYDROGENATION OF ALKANES TO FORM ALKENES	19	-1.3733454	0.24052711	REACTOME	DOWN
FORMATION OF FIBRIN CLOT (CLOTTING CASCADE)	29	-1.4933748	0.24174394	REACTOME	DOWN

Table S5. Overrepresentation Analysis of Gene Ontology Terms for the Significantly Deregulated Genes in *Rap1*^{-/-} Liver, Related to Figure 6
FDR: False Discovery Rate. FDR<0.05.

GO BIOLOGICAL PROCESS			
GO term ID	GO term description	FDR	Rap1 ^{-/-} status
GO:0006082	organic acid metabolic process	3.96E-03	UP
GO:0019752	carboxylic acid metabolic process	3.96E-03	UP
GO:0044255	cellular lipid metabolic process	3.96E-03	UP
GO:0008202	steroid metabolic process	1.17E-02	UP
GO:0006631	fatty acid metabolic process	1.23E-02	UP
GO:0006629	lipid metabolic process	1.62E-02	UP
GO:0008203	cholesterol metabolic process	4.30E-02	UP
GO:0007623	circadian rhythm	4.45E-02	DOWN
GO:0010033	response to organic substance	4.45E-02	DOWN
GO CELLULAR COMPONENT			
GO term ID	GO term description	FDR	Rap1 ^{-/-} status
GO:0005783	endoplasmic reticulum	4.73E-05	UP
GO:0019866	organelle inner membrane	1.12E-02	UP
GO:0005792	microsome	2.13E-02	UP
GO:0042175	nuclear outer membrane-endoplasmic reticulum membrane network	2.13E-02	UP
GO:0042598	vesicular fraction	2.20E-02	UP
GO:0000267	cell fraction	2.27E-02	UP
GO:0009986	cell surface	4.29E-02	UP
GO:0044429	mitochondrial part	4.29E-02	UP
GO:0031225	anchored to membrane	4.29E-02	UP
GO:0046658	anchored to plasma membrane	4.29E-02	UP
GO:0005579	membrane attack complex	0.0485849	DOWN
GO:0005783	endoplasmic reticulum	0.0485849	DOWN
GO MOLECULAR FUNCTION			
GO term ID	GO term description	FDR	Rap1 ^{-/-} status
GO:0004497	monooxygenase activity	0.00596968	DOWN
GO:0016705	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen	0.00698089	DOWN
GO:0042802	identical protein binding	1.06E-02	UP
GO:0020037	heme binding	0.0163961	DOWN
GO:0016709	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, NADH or NADPH as one donor, and incorporation of one atom of oxygen	0.0163961	DOWN
GO:0005549	odorant binding	0.0163961	DOWN
GO:0005550	pheromone binding	0.0163961	DOWN
GO:0046906	tetrapyrrole binding	0.0170305	DOWN