Supplementary_table 1									
C. dactylon Phyto constituents	**Plant part**	**PubchemID**	**Canonical smiles**	**MF**	**MW**	**HBD**	**HBA**	**LogP**	**DLS**
phenylmethyl ester	Stem	5461698	CCCCCCN(C(C1=CC(=C(C=C1)OCC(=O)OC)C(=O)OC)C(=O)NCCCC)C(=O)CCCCCN2C(=C(C(NC2=O)C3=CC=C(C=C3)C4=CC=CC=C4)C(=O)OCC5=CC=CC=C5)C	C54 H66	930.48	2	10	9.55	0.78
beta-carotene	Leaves	5280489	CC1=C(C(CCC1)(C)C)C=CC(=CC=CC(=CC=CC=C(C)C=CC=C(C)C=CC2=C(CCCC2(C)C)C)C)C	C40 H56	536.44	0	0	13.93	0.64
Catechin	Leaves	9064	C1C(C(OC2=CC(=CC(=C21)O)O)C3=CC(=C(C=C3)O)O)O	C15H14(	290.27	5	6	0.53	0.64
Vitexin	Leaves	5280441	C1=CC(=CC=C1C2=CC(=O)C3=C(O2)C(=C(C=C3O)O)C4C(C(C(C(O4)CO)O)O)O)O)O	C21 H20	432.11	7	10	0.77	0.6
Orientin	Leaves	5281675	C1=CC(=C(C=C1C2=CC(=O)C3=C(O2)C(=C(C=C3O)O)C4C(C(C(C(O4)CO)O)O)O)O)O)O	C21 H20	448.1	8	11	0.33	0.59
Quercetin	Leaves	5280343	C1=CC(=C(C=C1C2=C(C(=O)C3=C(C=C(C=C3O2)O)O)O)O)O)O	C15H10(	302.23	5	7	1.19	0.52
Kaempferol	Leaves	5280863	C1=CC(=CC=C1C2=C(C(=O)C3=C(C=C(C=C3O2)O)O)O)O	C15H10(	286.24	4	6	1.61	0.5
Luteolin	Leaves	5280445	C1=CC(=C(C=C1C2=CC(=O)C3=C(C=C(C=C3O2)O)O)O)O	C15 H10	286.05	4	6	2.78	0.38
Apigenin	Leaves	5280443	C1=CC(=CC=C1C2=CC(=O)C3=C(C=C(C=C3O2)O)O)O	C15 H15	257.11	1	3	2.68	0.29
diazoprogesterone	Stem	543575	CC(=[N+]=[N-])C1CCC2C1(CCC3C2CCC4=CC(=[N+]=[N-])CCC34C)C	C21H30N	338.5	0	2	4.26	0.18
linolenic acid	Leaves	5280934	CCC=CCC=CCC=CCCCCCCCC(=O)O	C18 H30	278.22	1	2	5.88	0.09
ethyl α-D-glucopyranoside	Leaves	11127487	CCOC1C(C(C(C(O1)CO)O)O)O	C8 H16 (	208.09	4	6	-1.79	0.01
D-mannose	Root	18950	C(C1C(C(C(C(O1)O)O)O)O)O	C6 H12 (	180.06	5	6	-3.02	-0.12
benzoic acid, 2-hydroxy-, methyl ester	Root	4133	COC(=O)C1=CC=CC=C1O	C8 H8 O:	152.05	1	3	2.62	-0.16
vanillic acid	Leaves	8468	COC1=C(C=CC(=C1)C(=O)O)O	C8 H8 O	168.04	2	4	1.2	-0.18

3H-pyrazol-3-one,		11513733	CC1=NN(C(=O)C1N=NC2=CC=CC=C2)C3=CC=CC=C3	C16 H14	278.12	0	4	2.83	-0.24
tricyclo[6.3.0.0(1,5)]undec-2-en-4-one, 2,3,5,9-tetramethyl	Leaves	585747	CC1CCC23C1CCC2(C(=O)C(=C3C)C)C	C15 H22	218.17	0	1	3.42	-0.24
Myricetin	Leaves	5281672	=O)C3=C(C=C(C=C3O2)O)O)O	C15H10(	318.23	6	8	0.97	-0.24
vioxanthin	Leaves	119072	CC1CC2=C(C(=C3C(=C2)C=C(C(=C3O)C4=C(C5=C(C6=C(CC(OC6=O)C)C=C5C=C4OC)O)O)OC)O)C(=O)O1	C30H26(	546.5	4	10	6.6	-0.29
9,12-octadecadienoic acid (Z,Z)-,	Leaves	5280450	CCCCCC=CCC=CCCCCCCCC(=O)O	C18 H32	280.24	1	2	6.6	-0.3
Lutein	Leaves	5281243	CC1=C(C(CC(C1)O)(C)C)C=CC(=CC=CC(=CC=CC=C(C)C=CC=C(C)C=CC2C(=CC(CC2(C)C)O)C)C)C	C40H56(	568.9	2	2	11.81	-0.33
didodecyl phthalate	Stem	17082	CCCCCCCCCCCCOC(=O)C1=CC=CC=C1C(=O)OCCCCCCCCCCCC	C32 H54	502.4	0	4	12.52	-0.43
pyrrolidin-2-one, N-(2,4-dimethylcyclopent-3-enoyl)-, cis	Stem	578892	CC1C=C(CC1C(=O)N2CCCC2=O)C	C12 H17	207.13	0	2	1.81	-0.47
ethanone, 1-(4-hydroxy-3-methoxyphenyl)-	Stem	2214	CC(=O)C1=CC(=C(C=C1)O)OC	C9 H10 (	166.06	1	3	0.9	-0.5
5- methyl propanedioic acid, phenyl	Leaves	254137	CC1=CC(=CC(=C1OC)C)CC(C(=O)O)(C(=O)O)NC(=O)C	C15 H19	309.12	3	6	0.92	-0.51
hexadecanoic acid	Leaves	985	CCCCCCCCCCCCCCCC(=O)O	C16 H32	256.24	1	2	6.64	-0.54
hexanediamide	Leaves	12364	C(CCC(=O)N)CC(=O)N	C6 H12 N	144.09	4	2	-1.79	-0.54
thymol	Leaves	6989	CC1=CC(=C(C=C1)C(C)C)O	C10 H14	150.1	1	1	3.43	-0.54
n-hexadecanoic acid	Leaves	985	CCCCCCCCCCCCCCCC(=O)O	C16 H32	256.24	1	2	6.64	-0.54
pentanoic acid, 4-oxo	Leaves	11579	CC(=O)CCC(=O)O	C5 H8 O3	116.05	1	3	-0.71	-0.59
Ar-tumerone	Leaves	558221	CC1=CC=C(C=C1)C(C)CC(=O)C=C(C)C	C15 H20	216.15	0	1	4.7	-0.67
3-hydroxy-1-methylpyridinium hydroxide	Leaves	572850	C[N+]1([CH-]C=CC(=C1)O)O	C6 H9 N	127.06	2	2	-0.26	-0.67
linolenic acid ethyl ester	Leaves	5367460	CCC=CCC=CCC=CCCCCCCCC(=O)OCC	C20 H34	306.26	0	2	7.08	-0.76

neoxanthin	Leaves	5281247	CC(=CC=CC=C(C)C=CC=C(C)C=C=C1C(CC(CC1(C)O)O)(C)C)C=CC=C(C)C=CC23C(CC(CC2(O3)C)O)(C)C	C40 H56	600.42	3	4	9.95	-0.78
hexadecanoic acid, 2-hydroxy-1-(hydroxymethyl) ethyl ester	Leaves	123409	CCCCCCCCCCCCCCCC(=O)OC(CO)CO	C19 H38	330.28	2	4	6	-0.79
Syringic acid	Leaves	10742	COC1=CC(=CC(=C1O)OC)C(=O)O	C9 H10 O	198.05	2	5	0.82	-0.81
ethyl ester linoleic acid	Leaves	5282184	CCCCCC=CCC=CCCCCCCCC(=O)OCC	C20 H36	308.27	0	2	7.8	-0.84
9,12-octadecadienoic acid ethyl ester	Leaves	5282184	CCCCCC=CCC=CCCCCCCCC(=O)OCC	C20 H36	308.27	0	2	7.8	-0.84
phytol	Leaves	5280435	CC(C)CCCC(C)CCCC(C)CCCC(=CCO)C	C20 H40	296.31	1	1	7.72	-0.87
3,7,11,15-Tetramethyl-2-hexadecen-1-ol	Leaves	5366244	CC(C)CCCC(C)CCCC(C)CCCC(=CCO)C	C20 H40	296.31	1	1	7.72	-0.87
4H-pyran-4-one, 2,3-dihydro-3,5-dihydroxy-6-methyl	Leaves	119838	CC1=C(C(=O)C(CO1)O)O	C6 H8 O4	144.04	2	4	-0.77	-0.96
4H-pyran-4-one, 2,3-dihydro-3,5-dihydroxy-6-methyl-	Leaves	119838	CC1=C(C(=O)C(CO1)O)O	C6 H8 O	144.04	2	4	-0.77	-0.96
benzaldehyde, 3-(chloroacetoxy)- 4-methoxy	Leaves	592476	COC1=C(C=C(C=C1)C=O)OC(=O)CCl	C10 H9 O	228.02	0	4	1.7	-0.97
2,4-dihydro-2,4,5-trimethyl-	Leaves	143499	CC1=NN(C(=O)N1C)C	C5 H9 N3	127.07	0	2	0.08	-0.98
tumerone	Leaves	558173	CC1=CC=C(CC1)C(C)CC(=O)C=C(C)C	C15 H22	218.17	0	1	4.73	-0.98
glycerin	Leaves	753	C(C(CO)O)O	C3 H8 O3	92.05	3	3	-1.49	-0.99
1, 2-propanediol	Leaves	1030	CC(CO)O	C3 H8 O2	76.05	2	2	-0.77	-1.03
levoglucosenone	Leaves	699486	C1C2C=CC(=O)C(O1)O2	C6 H6 O3	126.03	3	0	-0.32	-1.03
curlone	Leaves	196216	CC(CC(=O)C=C(C)C)C1CCC(=C)C=C1	C15 H22	218.17	0	1	4.4	-1.03
levoglucosenone	Leaves	699486	C1C2C=CC(=O)C(O1)O2	C6 H6 O3	126.03	0	3	-0.32	-1.03
10- undecyn-1-ol	Leaves	76015	C#CCCCCCCCCCO	C11 H20	168.15	1	1	3.23	-1.05
propanoic acid, 2-oxo	Leaves	1060	CC(=O)C(=O)O	C3 H4 O3	88.02	1	3	-0.59	-1.08
1-(2-Hydroxy-4,5-dimethoxyphenyl)-ethanone	Leaves	706870	CC(=O)C1=CC(=C(C=C1O)OC)OC	C10 H12	196.07	1	4	1.58	-1.08
decanoic acid, ethyl ester	Leaves	8048	CCCCCCCCCC(=O)OCC	C12 H24	200.18	0	2	4.81	-1.09
hexadecanoic acid ethyl ester	Leaves	12366	CCCCCCCCCCCCCCCC(=O)OCC	C18 H36	284.27	0	2	7.84	-1.09

octadecanoic acid ethyl ester	Leaves	8122	CCCCCCCCCCCCCCCCCC(=O)OCC	C20 H40	312.3	0	2	8.85	-1.09
3-Tert-butyl-4-hydroxyanisole	Leaves	8456	CC(C)(C)C1=C(C=CC(=C1)OC)O	C11 H16	180.12	1	2	3.63	-1.1
2-methoxy-4-vinylphenol	Leaves	332	COC1=C(C=CC(=C1)C=C)O	C9 H10	150.07	1	2	2.11	-1.13
hydroquinone	Leaves	785	C1=CC(=CC=C1O)O	C6 H6 O	110.04	2	2	1.06	-1.16
1,2-cyclopentanediol, 3-methyl-	Leaves	33945	CC1CCC(C1O)O	C6 H12	116.08	2	2	0.35	-1.16
1,6-anhydro-á-D-glucopyranose (levoglucosan)	Leaves	2724705	C1C2C(C(C(C(O1)O2)O)O)O	C6 H10	162.05	3	5	-1.53	-1.17
9, 12-octadecadienoyl chloride, (Z, Z)-	Leaves	98987	CCCCCC=CCC=CCCCCCCCC(=O)Cl	C18 H31	298.21	0	1	7.79	-1.18
pentanal, 2-methyl-	Leaves	31245	CCCC(C)C=O	C6 H12	100.09	0	1	1.77	-1.21
13-tetradece-11-yn-1-ol	Leaves	543337	C=CC#CCCCCCCCCCO	C14 H24	208.18	1	1	4.42	-1.28
2H-pyran-2-one, 5,6-dihydro	Leaves	520660	C1COC(=O)C=C1	C5 H6 O	98.04	0	2	1.02	-1.29
menthol	Leaves	1254	CC1CCC(C(C1)O)C(C)C	C10 H20	156.15	1	1	3.47	-1.33
Pantolactone	Leaves	989	CC1(COC(=O)C1O)C	C6 H10	130.06	1	3	0.39	-1.41
violaxanthin	Leaves	448438	CC(=CC=CC=C(C)C=CC=C(C)C=CC12C(CC(CC1(O2)C)O)(C)C)C=CC=C(C)C=CC34C(CC(CC3(O4)C)O)(C)C	C40 H56	600.42	2	4	10.75	-1.49
1,3-benzenediol, 5-chloro	Leaves	94554	C1=C(C=C(C=C1O)Cl)O	C6 H5 Cl	144	2	2	2.01	-1.5
5-Hydroxymethylfurfural	Leaves	237332	C1=C(OC(=C1)C=O)CO	C6 H6 O	126.03	1	3	0.23	-1.64
phthalic anhydride	Leaves	6811	C1=CC=C2C(=C1)C(=O)OC2=O	C8 H4 O	148.02	0	3	1.2	-1.67
furfural	Leaves	7362	C1=COC(=C1)C=O	C5 H4 O	96.02	0	2	0.68	-1.82
2-furancarbox-aldehyde	Leaves	7362	C1=COC(=C1)C=O	C5 H4 O	96.02	0	2	0.68	-1.82

Supplementary_table 2			
C. dactylon Phyto constituent	**PubchemID**	**Canonical smiles**	**DLS**
Catechin	9064	C1C(C(OC2=CC(=CC(=C21)O)O)C3=CC(=C(C=C3)O)O)O	0.64
Vitexin	5280441	C1=CC(=CC=C1C2=CC(=O)C3=C(O2)C(=C(C=C3O)O)C4C(C(C(C(O4)CO)O)O)O)O	0.6
Orientin	5281675	C1=CC(=C(C=C1C2=CC(=O)C3=C(O2)C(=C(C=C3O)O)C4C(C(C(C(O4)CO)O)O)O)O)O	0.59
Quercetin	5280343	C1=CC(=C(C=C1C2=C(C(=O)C3=C(C=C(C=C3O2)O)O)O)O)O	0.52
Kaempferol	5280863	C1=CC(=CC=C1C2=C(C(=O)C3=C(C=C(C=C3O2)O)O)O)O	0.5
Luteolin	5280445	C1=CC(=C(C=C1C2=CC(=O)C3=C(C=C(C=C3O2)O)O)O)O	0.38
Apigenin	5280443	C1=CC(=CC=C1C2=CC(=O)C3=C(C=C(C=C3O2)O)O)O	0.29
ethyl α-D-glucopyranoside	11127487	CCOC1C(C(C(C(O1)CO)O)O)O	0.01

Supplementary_table 3		
SR No	**Gene name**	**annotation**
1	ABCB1	Multidrug resistance protein 1; Energy-dependent efflux pump responsible for decreased drug accumulation in multidrug-resistant cells; ATP binding cassette subfamily B
2	ABCB5	ATP-binding cassette sub-family B member 5; Drug efflux transporter present in a number of stem cells that acts as a regulator of cellular differentiation. Able to mediate efflux from cells of the rhodamine dye and of the therapeutic drug doxorubicin. Specifically present in limbal stem cells, where it plays a key role in corneal development and repair; ATP binding cassette subfamily B
3	ABCC1	Multidrug resistance-associated protein 1; Mediates export of organic anions and drugs from the cytoplasm. Mediates ATP-dependent transport of glutathione and glutathione conjugates, leukotriene C4, estradiol-17-beta-o- glucuronide, methotrexate, antiviral drugs and other xenobiotics. Confers resistance to anticancer drugs. Hydrolyzes ATP with low efficiency; Belongs to the ABC transporter superfamily. ABCC family. Conjugate transporter (TC 3.A.1.208) subfamily
4	ABCG2	ATP-binding cassette sub-family G member 2; High-capacity urate exporter functioning in both renal and extrarenal urate excretion. Plays a role in porphyrin homeostasis as it is able to mediates the export of protoporhyrin IX (PPIX) both from mitochondria to cytosol and from cytosol to extracellular space, and cellular export of hemin, and heme. Xenobiotic transporter that may play an important role in the exclusion of xenobiotics from the brain. Appears to play a major role in the multidrug resistance phenotype of several cancer cell lines. Implicated in the efflux of numerous drugs a [...]
5	ABL2	Abelson tyrosine-protein kinase 2; Non-receptor tyrosine-protein kinase that plays an ABL1- overlapping role in key processes linked to cell growth and survival such as cytoskeleton remodeling in response to extracellular stimuli, cell motility and adhesion and receptor endocytosis. Coordinates actin remodeling through tyrosine phosphorylation of proteins controlling cytoskeleton dynamics like MYH10 (involved in movement); CTTN (involved in signaling); or TUBA1 and TUBB (microtubule subunits). Binds directly F-actin and regulates actin cytoskeletal structure through its F-actin- bundli [...]
6	ACHE	Acetylcholinesterase; Terminates signal transduction at the neuromuscular junction by rapid hydrolysis of the acetylcholine released into the synaptic cleft. Role in neuronal apoptosis; Belongs to the type-B carboxylesterase/lipase family
7	ADORA1	Adenosine receptor A1; Receptor for adenosine. The activity of this receptor is mediated by G proteins which inhibit adenylyl cyclase; Belongs to the G-protein coupled receptor 1 family
8	ADORA2A	Adenosine A2a receptor; Receptor for adenosine. The activity of this receptor is mediated by G proteins which activate adenylyl cyclase; Belongs to the G-protein coupled receptor 1 family
9	ADORA3	Transmembrane domain-containing protein TMIGD3; Isoform 1: Plays a suppressive role in osteosarcoma malignancy by inhibiting NF-kappa-B activity; Adenosine receptors
10	AHR	Aryl hydrocarbon receptor; Ligand-activated transcriptional activator. Binds to the XRE promoter region of genes it activates. Activates the expression of multiple phase I and II xenobiotic chemical metabolizing enzyme genes (such as the CYP1A1 gene). Mediates biochemical and toxic effects of halogenated aromatic hydrocarbons. Involved in cell-cycle regulation. Likely to play an important role in the development and maturation of many tissues. Regulates the circadian clock by inhibiting the basal and circadian expression of the core circadian component PER1. Inhibits PER1 by repressing [...]
11	AKR1B1	Aldose reductase; Catalyzes the NADPH-dependent reduction of a wide variety of carbonyl-containing compounds to their corresponding alcohols with a broad range of catalytic efficiencies; Belongs to the aldo/keto reductase family

12	AKR1B10	Aldo-keto reductase family 1 member B10; Acts as all-trans-retinaldehyde reductase. Can efficiently reduce aliphatic and aromatic aldehydes, and is less active on hexoses (in vitro). May be responsible for detoxification of reactive aldehydes in the digested food before the nutrients are passed on to other organs
13	ALOX12	Arachidonate 12-lipoxygenase, 12S-type; Non-heme iron-containing dioxygenase that catalyzes the stereo-specific peroxidation of free and esterified polyunsaturated fatty acids generating a spectrum of bioactive lipid mediators. Mainly converts arachidonic acid to (12S)- hydroperoxyeicosatetraenoic acid/(12S)-HPETE but can also metabolize linoleic acid. Has a dual activity since it also converts leukotriene A4/LTA4 into both the bioactive lipoxin A4/LXA4 and lipoxin B4/LXB4. Through the production of specific bioactive lipids like (12S)-HPETE it regulates different biological processes [...]
14	ALOX12B	Arachidonate 12-lipoxygenase, 12R-type; Non-heme iron-containing dioxygenase that catalyzes the stereo-specific peroxidation of free and esterified polyunsaturated fatty acids generating a spectrum of bioactive lipid mediators. Mainly converts arachidonic acid to (12R)- hydroperoxyeicosatetraenoic acid/(12R)-HPETE and minor stereoisomers. In the skin, acts upstream of ALOXE3 on the lineolate moiety of esterified omega-hydroxyacyl-sphingosine (EOS) ceramides to produce an epoxy-ketone derivative, a crucial step in the conjugation of omega-hydroxyceramide to membrane proteins. Therefore [...]
15	ALOX15	Arachidonate 15-lipoxygenase; Non-heme iron-containing dioxygenase that catalyzes the stereo-specific peroxidation of free and esterified polyunsaturated fatty acids generating a spectrum of bioactive lipid mediators. Converts arachidonic acid into 12- hydroperoxyeicosatetraenoic acid/12-HPETE and 15-hydroperoxyeicosatetraenoic acid/15-HPETE. Also converts linoleic acid to 13-hydroperoxyoctadecadienoic acid. May also act on (12S)-hydroperoxyeicosatetraenoic acid/(12S)-HPETE to produce hepoxilin A3. Probably plays an important role in the immune and inflammatory responses. Through the [...]
16	ALOX15B	Arachidonate 15-lipoxygenase B; Non-heme iron-containing dioxygenase that catalyzes the stereo-specific peroxidation of free and esterified polyunsaturated fatty acids generating a spectrum of bioactive lipid mediators. Converts arachidonic acid to 15S- hydroperoxyeicosatetraenoic acid/(15S)-HPETE. Also acts on linoleic acid to produce 13-hydroxyoctadecadienoic acid/13-HPODE. Has no detectable 8S-lipoxygenase activity but reacts with (8S)-HPETE to produce (8S,15S)-diHPETE. May regulate progression through the cell cycle and cell proliferation. May also regulate cytokine secretion by m [...]
17	ALOX5	Arachidonate 5-lipoxygenase; Catalyzes the first step in leukotriene biosynthesis, and thereby plays a role in inflammatory processes; Belongs to the lipoxygenase family
18	ALPL	Alkaline phosphatase, tissue-nonspecific isozyme; This isozyme may play a role in skeletal mineralization; Belongs to the alkaline phosphatase family
19	APEX1	DNA-(apurinic or apyrimidinic site) lyase; Multifunctional protein that plays a central role in the cellular response to oxidative stress. The two major activities of APEX1 in DNA repair and redox regulation of transcriptional factors. Functions as a apurinic/apyrimidinic (AP) endodeoxyribonuclease in the DNA base excision repair (BER) pathway of DNA lesions induced by oxidative and alkylating agents. Initiates repair of AP sites in DNA by catalyzing hydrolytic incision of the phosphodiester backbone immediately adjacent to the damage, generating a single-strand break with 5'-deoxyribo [...]
20	AR	Androgen receptor; Steroid hormone receptors are ligand-activated transcription factors that regulate eukaryotic gene expression and affect cellular proliferation and differentiation in target tissues. Transcription factor activity is modulated by bound coactivator and corepressor proteins. Transcription activation is down-regulated by NR0B2. Activated, but not phosphorylated, by HIPK3 and ZIPK/DAPK3

21	ARG2	Arginase-2, mitochondrial; May play a role in the regulation of extra-urea cycle arginine metabolism and also in down-regulation of nitric oxide synthesis. Extrahepatic arginase functions to regulate L-arginine bioavailability to nitric oxid synthase (NOS). Arginine metabolism is a critical regulator of innate and adaptive immune responses. Seems to be involved in negative regulation of the survival capacity of activated CD4(+) and CD8(+) T cells. May suppress inflammation-related signaling in asthmatic airway epithelium. May contribute to the immune evasion of H.pylori by restricting [...]
22	AURKB	Aurora kinase B; Serine/threonine-protein kinase component of the chromosomal passenger complex (CPC), a complex that acts as a key regulator of mitosis. The CPC complex has essential functions at the centromere in ensuring correct chromosome alignment and segregation and is required for chromatin-induced microtubule stabilization and spindle assembly. Involved in the bipolar attachment of spindle microtubules to kinetochores and is a key regulator for the onset of cytokinesis during mitosis. Required for central/midzone spindle assembly and cleavage furrow formation. Key component of [...]
23	AXL	Tyrosine-protein kinase receptor UFO; Receptor tyrosine kinase that transduces signals from the extracellular matrix into the cytoplasm by binding growth factor GAS6 and which is thus regulating many physiological processes including cell survival, cell proliferation, migration and differentiation. Ligand binding at the cell surface induces dimerization and autophosphorylation of AXL. Following activation by ligand, ALX binds and induces tyrosine phosphorylation of PI3- kinase subunits PIK3R1, PIK3R2 and PIK3R3; but also GRB2, PLCG1, LCK and PTPN11. Other downstream substrate candidate [...]
24	AXL UFO	Tyrosine-protein kinase receptor UFO; Receptor tyrosine kinase that transduces signals from the extracellular matrix into the cytoplasm by binding growth factor GAS6 and which is thus regulating many physiological processes including cell survival, cell proliferation, migration and differentiation. Ligand binding at the cell surface induces dimerization and autophosphorylation of AXL. Following activation by ligand, ALX binds and induces tyrosine phosphorylation of PI3- kinase subunits PIK3R1, PIK3R2 and PIK3R3; but also GRB2, PLCG1, LCK and PTPN11. Other downstream substrate candidate [...]
25	BCHE	Cholinesterase; Esterase with broad substrate specificity. Contributes to the inactivation of the neurotransmitter acetylcholine. Can degrade neurotoxic organophosphate esters; Belongs to the type-B carboxylesterase/lipase family
26	BCR	Breakpoint cluster region protein; GTPase-activating protein for RAC1 and CDC42. Promotes the exchange of RAC or CDC42-bound GDP by GTP, thereby activating them. Displays serine/threonine kinase activity; C2 domain containing
27	CA12	Carbonic anhydrase 12; Reversible hydration of carbon dioxide; Belongs to the alpha-carbonic anhydrase family
28	CA2	Carbonic anhydrase 2; Essential for bone resorption and osteoclast differentiation (By similarity). Reversible hydration of carbon dioxide. Can hydrate cyanamide to urea. Involved in the regulation of fluid secretion into the anterior chamber of the eye. Contributes to intracellular pH regulation in the duodenal upper villous epithelium during proton-coupled peptide absorption. Stimulates the chloride-bicarbonate exchange activity of SLC26A6; Carbonic anhydrases
29	CA4	Carbonic anhydrase 4; Reversible hydration of carbon dioxide. May stimulate the sodium/bicarbonate transporter activity of SLC4A4 that acts in pH homeostasis. It is essential for acid overload removal from the retina and retina epithelium, and acid release in the choriocapillaris in the choroid; Belongs to the alpha-carbonic anhydrase family
30	CA7	Carbonic anhydrase 7; Reversible hydration of carbon dioxide; Belongs to the alpha-carbonic anhydrase family

31	CBR1	Carbonyl reductase [NADPH] 1; NADPH-dependent reductase with broad substrate specificity. Catalyzes the reduction of a wide variety of carbonyl compounds including quinones, prostaglandins, menadione, plus various xenobiotics. Catalyzes the reduction of the antitumor anthracyclines doxorubicin and daunorubicin to the cardiotoxic compounds doxorubicinol and daunorubicinol. Can convert prostaglandin E2 to prostaglandin F2-alpha. Can bind glutathione, which explains its higher affinity for glutathione-conjugated substrates. Catalyzes the reduction of S-nitrosoglutathione; Short chain dehy [...]
32	CCNA1	Cyclin-A1; May be involved in the control of the cell cycle at the G1/S (start) and G2/M (mitosis) transitions. May primarily function in the control of the germline meiotic cell cycle and additionally in the control of mitotic cell cycle in some somatic cells; Belongs to the cyclin family. Cyclin AB subfamily
33	CDK1	Cyclin-dependent kinase 1; Plays a key role in the control of the eukaryotic cell cycle by modulating the centrosome cycle as well as mitotic onset; promotes G2-M transition, and regulates G1 progress and G1-S transition via association with multiple interphase cyclins. Required in higher cells for entry into S-phase and mitosis. Phosphorylates PARVA/actopaxin, APC, AMPH, APC, BARD1, Bcl- xL/BCL2L1, BRCA2, CALD1, CASP8, CDC7, CDC20, CDC25A, CDC25C, CC2D1A, CENPA, CSNK2 proteins/CKII, FZR1/CDH1, CDK7, CEBPB, CHAMP1, DMD/dystrophin, EEF1 proteins/EF-1, EZH2, KIF11/EG5, EGFR, FANCG, FOS, [...]
34	CDK5	Cyclin-dependent-like kinase 5; Proline-directed serine/threonine-protein kinase essential for neuronal cell cycle arrest and differentiation and may be involved in apoptotic cell death in neuronal diseases by triggering abortive cell cycle re-entry. Interacts with D1 and D3- type G1 cyclins. Phosphorylates SRC, NOS3, VIM/vimentin, p35/CDK5R1, MEF2A, SIPA1L1, SH3GLB1, PXN, PAK1, MCAM/MUC18, SEPT5, SYN1, DNM1, AMPH, SYNJ1, CDK16, RAC1, RHOA, CDC42, TONEBP/NFAT5, MAPT/TAU, MAP1B, histone H1, p53/TP53, HDAC1, APEX1, PTK2/FAK1, huntingtin/HTT, ATM, MAP2, NEFH and NEFM. Regulates several ne [...]
35	CDK6	Cyclin-dependent kinase 6; Serine/threonine-protein kinase involved in the control of the cell cycle and differentiation; promotes G1/S transition. Phosphorylates pRB/RB1 and NPM1. Interacts with D-type G1 cyclins during interphase at G1 to form a pRB/RB1 kinase and controls the entrance into the cell cycle. Involved in initiation and maintenance of cell cycle exit during cell differentiation; prevents cell proliferation and regulates negatively cell differentiation, but is required for the proliferation of specific cell types (e.g. erythroid and hematopoietic cells). Essential for cel [...]
36	CELF3	CUGBP Elav-like family member 3; RNA-binding protein involved in the regulation of pre- mRNA alternative splicing. Mediates exon inclusion and/or exclusion in pre-mRNA that are subject to tissue-specific and developmentally regulated alternative splicing. Specifically activates exon 5 inclusion of cardiac isoforms of TNNT2 during heart remodeling at the juvenile to adult transition. Activates the splicing of MAPT/Tau exon 10. Binds to muscle-specific splicing enhancer (MSE) intronic sites flanking the alternative exon 5 of TNNT2 pre-mRNA
37	CFTR	Cystic fibrosis transmembrane conductance regulator; Epithelial ion channel that plays an important role in the regulation of epithelial ion and water transport and fluid homeostasis. Mediates the transport of chloride ions across the cell membrane. Channel activity is coupled to ATP hydrolysis. The ion channel is also permeable to HCO(3-); selectivity depends on the extracellular chloride concentration. Exerts its function also by modulating the activity of other ion channels and transporters. Plays an important role in airway fluid homeostasis. Contributes to the regulation of the pH [...]
38	CISD1	CDGSH iron-sulfur domain-containing protein 1; Plays a key role in regulating maximal capacity for electron transport and oxidative phosphorylation (By similarity). May be involved in Fe-S cluster shuttling and/or in redox reactions; Belongs to the CISD protein family

39	Cisd2	CDGSH iron-sulfur domain-containing protein 2; Regulator of autophagy that contributes to antagonize BECN1-mediated cellular autophagy at the endoplasmic reticulum. Participates in the interaction of BCL2 with BECN1 and is required for BCL2-mediated depression of endoplasmic reticulum Ca(2+) stores during autophagy. Contributes to BIK-initiated autophagy, while it is not involved in BIK-dependent activation of caspases. Involved in life span control, probably via its function as regulator of autophagy; CDGSH iron sulfur domain containing
40	COX	Cytochrome c oxidase subunit 5A, mitochondrial; This is the heme A-containing chain of cytochrome c oxidase, the terminal oxidase in mitochondrial electron transport
41	CSNK2A1	Casein kinase II subunit alpha; Catalytic subunit of a constitutively active serine/threonine-protein kinase complex that phosphorylates a large number of substrates containing acidic residues C-terminal to the phosphorylated serine or threonine. Regulates numerous cellular processes, such as cell cycle progression, apoptosis and transcription, as well as viral infection. May act as a regulatory node which integrates and coordinates numerous signals leading to an appropriate cellular response. During mitosis, functions as a component of the p53/TP53-dependent spindle assembly checkpoin [...]
42	CSNK2A2	Casein kinase II subunit alpha; Catalytic subunit of a constitutively active serine/threonine-protein kinase complex that phosphorylates a large number of substrates containing acidic residues C-terminal to the phosphorylated serine or threonine. Regulates numerous cellular processes, such as cell cycle progression, apoptosis and transcription, as well as viral infection. May act as a regulatory node which integrates and coordinates numerous signals leading to an appropriate cellular response. During mitosis, functions as a component of the p53/TP53-dependent spindle assembly checkpoin [...]
43	CSNK2A3	Casein kinase II subunit alpha 3; Probable catalytic subunit of a constitutively active serine/threonine-protein kinase complex that phosphorylates a large number of substrates containing acidic residues C-terminal to the phosphorylated serine or threonine. Amplification-dependent oncogene; promotes cell proliferation and tumorigenesis by down- regulating expression of the tumor suppressor protein, PML. May play a role in the pathogenesis of the lung cancer development and progression
44	CYP19A1	Aromatase; Catalyzes the formation of aromatic C18 estrogens from C19 androgens; Cytochrome P450 family 19
45	CYP1A1	Cytochrome P450 1A1; Cytochromes P450 are a group of heme-thiolate monooxygenases. In liver microsomes, this enzyme is involved in an NADPH-dependent electron transport pathway. It oxidizes a variety of structurally unrelated compounds, including steroids, fatty acids, and xenobiotics
46	DNPEP	Aspartyl aminopeptidase; Aminopeptidase with specificity towards an acidic amino acid at the N-terminus. Likely to play an important role in intracellular protein and peptide metabolism
47	DPP4	Dipeptidyl peptidase 4; Cell surface glycoprotein receptor involved in the costimulatory signal essential for T-cell receptor (TCR)-mediated T-cell activation. Acts as a positive regulator of T-cell coactivation, by binding at least ADA, CAV1, IGF2R, and PTPRC. Its binding to CAV1 and CARD11 induces T-cell proliferation and NF- kappa-B activation in a T-cell receptor/CD3-dependent manner. Its interaction with ADA also regulates lymphocyte-epithelial cell adhesion. In association with FAP is involved in the pericellular proteolysis of the extracellular matrix (ECM), the migration and in [...]

48	EGFR	Epidermal growth factor receptor; Receptor tyrosine kinase binding ligands of the EGF family and activating several signaling cascades to convert extracellular cues into appropriate cellular responses. Known ligands include EGF, TGFA/TGF-alpha, amphiregulin, epigen/EPGN, BTC/betacellulin, epiregulin/EREG and HBEGF/heparin-binding EGF. Ligand binding triggers receptor homo- and/or heterodimerization and autophosphorylation on key cytoplasmic residues. The phosphorylated receptor recruits adapter proteins like GRB2 which in turn activates complex downstream signaling cascades. Activates [...]
49	ELAVL3	ELAV-like protein 3; Binds to AU-rich sequences (AREs) of target mRNAs, including VEGF mRNA. May also bind poly-A tracts via RRM 3 (By similarity). May be involved in neuronal differentiation and maintenance; Belongs to the RRM elav family
50	ESR1	Estrogen receptor; Nuclear hormone receptor. The steroid hormones and their receptors are involved in the regulation of eukaryotic gene expression and affect cellular proliferation and differentiation in target tissues. Ligand-dependent nuclear transactivation involves either direct homodimer binding to a palindromic estrogen response element (ERE) sequence or association with other DNA- binding transcription factors, such as AP-1/c-Jun, c-Fos, ATF-2, Sp1 and Sp3, to mediate ERE-independent signaling. Ligand binding induces a conformational change allowing subsequent or combinatorial a [...]
51	ESR2	Estrogen receptor beta; Nuclear hormone receptor. Binds estrogens with an affinity similar to that of ESR1, and activates expression of reporter genes containing estrogen response elements (ERE) in an estrogen-dependent manner. Isoform beta-cx lacks ligand binding ability and has no or only very low ere binding activity resulting in the loss of ligand-dependent transactivation ability. DNA-binding by ESR1 and ESR2 is rapidly lost at 37 degrees Celsius in the absence of ligand while in the presence of 17 beta-estradiol and 4-hydroxy-tamoxifen loss in DNA-binding at elevated temperature [...]
52	ESRRB	Steroid hormone receptor ERR2; Isoform 3: Transcription factor that binds a canonical ESRRB recognition (ERRE) sequence 5'TCAAGGTCA-3' localized on promoter and enhancer of targets genes regulating their expression or their transcription activity. Plays a role, in a LIF-independent manner, in maintainance of self-renewal and pluripotency of embryonic and trophoblast stem cells through different signaling pathways including FGF signaling pathway and Wnt signaling pathways. Upon FGF signaling pathway activation, interacts with KDM1A by directly binding to enhancer site of ELF5 and EOMES [...]
53	F10	Coagulation factor X; Factor Xa is a vitamin K-dependent glycoprotein that converts prothrombin to thrombin in the presence of factor Va, calcium and phospholipid during blood clotting; Gla domain containing
54	F2	Prothrombin; Thrombin, which cleaves bonds after Arg and Lys, converts fibrinogen to fibrin and activates factors V, VII, VIII, XIII, and, in complex with thrombomodulin, protein C. Functions in blood homeostasis, inflammation and wound healing; Belongs to the peptidase S1 family
55	FASN	Fatty acid synthase; Fatty acid synthetase catalyzes the formation of long- chain fatty acids from acetyl-CoA, malonyl-CoA and NADPH. This multifunctional protein has 7 catalytic activities and an acyl carrier protein; Seven-beta-strand methyltransferase motif containing
56	FGF1	Fibroblast growth factor 1; Plays an important role in the regulation of cell survival, cell division, angiogenesis, cell differentiation and cell migration. Functions as potent mitogen in vitro. Acts as a ligand for FGFR1 and integrins. Binds to FGFR1 in the presence of heparin leading to FGFR1 dimerization and activation via sequential autophosphorylation on tyrosine residues which act as docking sites for interacting proteins, leading to the activation of several signaling cascades. Binds to integrin ITGAV:ITGB3. Its binding to integrin, subsequent ternary complex formation with int [...]

57	FGF2	Fibroblast growth factor 2; Plays an important role in the regulation of cell survival, cell division, angiogenesis, cell differentiation and cell migration. Functions as potent mitogen in vitro. Can induce angiogenesis; Belongs to the heparin-binding growth factors family
58	FLT3	Receptor-type tyrosine-protein kinase FLT3; Tyrosine-protein kinase that acts as cell-surface receptor for the cytokine FLT3LG and regulates differentiation, proliferation and survival of hematopoietic progenitor cells and of dendritic cells. Promotes phosphorylation of SHC1 and AKT1, and activation of the downstream effector MTOR. Promotes activation of RAS signaling and phosphorylation of downstream kinases, including MAPK1/ERK2 and/or MAPK3/ERK1. Promotes phosphorylation of FES, FER, PTPN6/SHP, PTPN11/SHP-2, PLCG1, and STAT5A and/or STAT5B. Activation of wild-type FLT3 causes only m [...]
59	GAA	Lysosomal alpha-glucosidase; Essential for the degradation of glycogen in lysosomes. Has highest activity on alpha-1,4-linked glycosidic linkages, but can also hydrolyze alpha-1,6-linked glucans
60	gag-pol	E3 ubiquitin-protein ligase SH3RF1; Acts as a scaffold protein, contributes to Rac-induced signal transduction such as JNKs (MAPK8 and MAPK9) activation and induces apoptosis. Within a signaling complex, it probably recruits protein kinases such as MAP3K10 or MAP3K11 which are in turn activated leading to the sequential activation of MAP2K4, MAP2K7 and JNKs (MAPK8 and MAPK9) (By similarity). May be involved in targeting of HIV-1 GAG and GAG-POL polyproteins to the plasma membrane; Belongs to the SH3RF family
61	GANAB	Neutral alpha-glucosidase AB; Cleaves sequentially the 2 innermost alpha-1,3-linked glucose residues from the Glc(2)Man(9)GlcNAc(2) oligosaccharide precursor of immature glycoproteins. Required for PKD1/Polycystin-1 and PKD2/Polycystin-2 maturation and localization to the cell surface and cilia; Belongs to the glycosyl hydrolase 31 family
62	GLO1	Lactoylglutathione lyase; Catalyzes the conversion of hemimercaptal, formed from methylglyoxal and glutathione, to S-lactoylglutathione. Involved in the regulation of TNF-induced transcriptional activity of NF- kappa-B. Required for normal osteoclastogenesis
63	GSK3B	Glycogen synthase kinase-3 beta; Constitutively active protein kinase that acts as a negative regulator in the hormonal control of glucose homeostasis, Wnt signaling and regulation of transcription factors and microtubules, by phosphorylating and inactivating glycogen synthase (GYS1 or GYS2), EIF2B, CTNNB1/beta-catenin, APC, AXIN1, DPYSL2/CRMP2, JUN, NFATC1/NFATC, MAPT/TAU and MACF1. Requires primed phosphorylation of the majority of its substrates. In skeletal muscle, contributes to insulin regulation of glycogen synthesis by phosphorylating and inhibiting GYS1 activity and hence glyc [...]
64	HDAC1	Histone deacetylase 1; Responsible for the deacetylation of lysine residues on the N-terminal part of the core histones (H2A, H2B, H3 and H4). Histone deacetylation gives a tag for epigenetic repression and plays an important role in transcriptional regulation, cell cycle progression and developmental events. Histone deacetylases act via the formation of large multiprotein complexes. Deacetylates SP proteins, SP1 and SP3, and regulates their function. Component of the BRG1-RB1-HDAC1 complex, which negatively regulates the CREST- mediated transcription in resting neurons. Upon calcium s [...]
65	HDAC10	Histone deacetylase 10; Responsible for the deacetylation of lysine residues on the N-terminal part of the core histones (H2A, H2B, H3 and H4). Histone deacetylation gives a tag for epigenetic repression and plays an important role in transcriptional regulation, cell cycle progression and developmental events. Histone deacetylases act via the formation of large multiprotein complexes

66	HDAC2	Histone deacetylase 2; Responsible for the deacetylation of lysine residues on the N-terminal part of the core histones (H2A, H2B, H3 and H4). Histone deacetylation gives a tag for epigenetic repression and plays an important role in transcriptional regulation, cell cycle progression and developmental events. Histone deacetylases act via the formation of large multiprotein complexes. Forms transcriptional repressor complexes by associating with MAD, SIN3, YY1 and N-COR. Interacts in the late S-phase of DNA-replication with DNMT1 in the other transcriptional repressor complex composed o [...]
67	HDAC3	Histone deacetylase 3; Responsible for the deacetylation of lysine residues on the N-terminal part of the core histones (H2A, H2B, H3 and H4), and some other non-histone substrates. Histone deacetylation gives a tag for epigenetic repression and plays an important role in transcriptional regulation, cell cycle progression and developmental events. Histone deacetylases act via the formation of large multiprotein complexes. Participates in the BCL6 transcriptional repressor activity by deacetylating the H3 'Lys- 27' (H3K27) on enhancer elements, antagonizing EP300 acetyltransferase activ [...]
68	HDAC4	Histone deacetylase 4; Responsible for the deacetylation of lysine residues on the N-terminal part of the core histones (H2A, H2B, H3 and H4). Histone deacetylation gives a tag for epigenetic repression and plays an important role in transcriptional regulation, cell cycle progression and developmental events. Histone deacetylases act via the formation of large multiprotein complexes. Involved in muscle maturation via its interaction with the myocyte enhancer factors such as MEF2A, MEF2C and MEF2D. Involved in the MTA1-mediated epigenetic regulation of ESR1 expression in breast cancer. [...]
69	HDAC5	Histone deacetylase 5; Responsible for the deacetylation of lysine residues on the N-terminal part of the core histones (H2A, H2B, H3 and H4). Histone deacetylation gives a tag for epigenetic repression and plays an important role in transcriptional regulation, cell cycle progression and developmental events. Histone deacetylases act via the formation of large multiprotein complexes. Involved in muscle maturation by repressing transcription of myocyte enhancer MEF2C. During muscle differentiation, it shuttles into the cytoplasm, allowing the expression of myocyte enhancer factors. Invo [...]
70	HDAC6	Histone deacetylase 6; Responsible for the deacetylation of lysine residues on the N-terminal part of the core histones (H2A, H2B, H3 and H4). Histone deacetylation gives a tag for epigenetic repression and plays an important role in transcriptional regulation, cell cycle progression and developmental events. Histone deacetylases act via the formation of large multiprotein complexes (By similarity). Plays a central role in microtubule-dependent cell motility via deacetylation of tubulin. Involved in the MTA1-mediated epigenetic regulation of ESR1 expression in breast cancer
71	HDAC8	Histone deacetylase 8; Responsible for the deacetylation of lysine residues on the N-terminal part of the core histones (H2A, H2B, H3 and H4). Histone deacetylation gives a tag for epigenetic repression and plays an important role in transcriptional regulation, cell cycle progression and developmental events. Histone deacetylases act via the formation of large multiprotein complexes. Also involved in the deacetylation of cohesin complex protein SMC3 regulating release of cohesin complexes from chromatin. May play a role in smooth muscle cell contractility
72	HDAC9	Histone deacetylase 9; Responsible for the deacetylation of lysine residues on the N-terminal part of the core histones (H2A, H2B, H3 and H4). Histone deacetylation gives a tag for epigenetic repression and plays an important role in transcriptional regulation, cell cycle progression and developmental events. Represses MEF2-dependent transcription; Belongs to the histone deacetylase family. HD type 2 subfamily
73	HSD17B1	Estradiol 17-beta-dehydrogenase 1; Favors the reduction of estrogens and androgens. Also has 20-alpha-HSD activity. Uses preferentially NADH; Short chain dehydrogenase/reductase superfamily

74	HSD17B2	Estradiol 17-beta-dehydrogenase 2; Capable of catalyzing the interconversion of testosterone and androstenedione, as well as estradiol and estrone. Also has 20-alpha-HSD activity. Uses NADH while EDH17B3 uses NADPH; Short chain dehydrogenase/reductase superfamily
75	HSPE1	10 kDa heat shock protein, mitochondrial; Co-chaperonin implicated in mitochondrial protein import and macromolecular assembly. Together with Hsp60, facilitates the correct folding of imported proteins. May also prevent misfolding and promote the refolding and proper assembly of unfolded polypeptides generated under stress conditions in the mitochondrial matrix. The functional units of these chaperonins consist of heptameric rings of the large subunit Hsp60, which function as a back-to-back double ring. In a cyclic reaction, Hsp60 ring complexes bind one unfolded substrate protein per [...]
76	IGF1R	Insulin-like growth factor 1 receptor; Receptor tyrosine kinase which mediates actions of insulin-like growth factor 1 (IGF1). Binds IGF1 with high affinity and IGF2 and insulin (INS) with a lower affinity. The activated IGF1R is involved in cell growth and survival control. IGF1R is crucial for tumor transformation and survival of malignant cell. Ligand binding activates the receptor kinase, leading to receptor autophosphorylation, and tyrosines phosphorylation of multiple substrates, that function as signaling adapter proteins including, the insulin-receptor substrates (IRS1/2), Shc [...]
77	IP6K2	Inositol hexakisphosphate kinase 2; Converts inositol hexakisphosphate (InsP6) to diphosphoinositol pentakisphosphate (InsP7/PP-InsP5). Converts 1,3,4,5,6-pentakisphosphate (InsP5) to PP-InsP4; Belongs to the inositol phosphokinase (IPK) family
78	KDR	Vascular endothelial growth factor receptor 2; Tyrosine-protein kinase that acts as a cell-surface receptor for VEGFA, VEGFC and VEGFD. Plays an essential role in the regulation of angiogenesis, vascular development, vascular permeability, and embryonic hematopoiesis. Promotes proliferation, survival, migration and differentiation of endothelial cells. Promotes reorganization of the actin cytoskeleton. Isoforms lacking a transmembrane domain, such as isoform 2 and isoform 3, may function as decoy receptors for VEGFA, VEGFC and/or VEGFD. Isoform 2 plays an important role as negative reg [...]
79	KIT	Mast/stem cell growth factor receptor Kit; Tyrosine-protein kinase that acts as cell-surface receptor for the cytokine KITLG/SCF and plays an essential role in the regulation of cell survival and proliferation, hematopoiesis, stem cell maintenance, gametogenesis, mast cell development, migration and function, and in melanogenesis. In response to KITLG/SCF binding, KIT can activate several signaling pathways. Phosphorylates PIK3R1, PLCG1, SH2B2/APS and CBL. Activates the AKT1 signaling pathway by phosphorylation of PIK3R1, the regulatory subunit of phosphatidylinositol 3-kinase. Activat [...]
80	LCK	Tyrosine-protein kinase Lck; Non-receptor tyrosine-protein kinase that plays an essential role in the selection and maturation of developing T- cells in the thymus and in the function of mature T-cells. Plays a key role in T-cell antigen receptor (TCR)-linked signal transduction pathways. Constitutively associated with the cytoplasmic portions of the CD4 and CD8 surface receptors. Association of the TCR with a peptide antigen-bound MHC complex facilitates the interaction of CD4 and CD8 with MHC class II and class I molecules, respectively, thereby recruiting the associated LCK protein.
81	LGALS3	Galectin-3; Galactose-specific lectin which binds IgE. May mediate with the alpha-3, beta-1 integrin the stimulation by CSPG4 of endothelial cells migration. Together with DMBT1, required for terminal differentiation of columnar epithelial cells during early embryogenesis (By similarity). In the nucleus: acts as a pre-mRNA splicing factor. Involved in acute inflammatory responses including neutrophil activation and adhesion, chemoattraction of monocytes macrophages, opsonization of apoptotic neutrophils, and activation of mast cells; Endogenous ligands

82	LGALS4	Galectin-4; Galectin that binds lactose and a related range of sugars. May be involved in the assembly of adherens junctions; Galectins
83	LGALS8	Galectin 8; Galectins
84	LIG1	DNA ligase 1; DNA ligase that seals nicks in double-stranded DNA during DNA replication, DNA recombination and DNA repair; Belongs to the ATP-dependent DNA ligase family
85	MAOA	Amine oxidase [flavin-containing] A; Catalyzes the oxidative deamination of biogenic and xenobiotic amines and has important functions in the metabolism of neuroactive and vasoactive amines in the central nervous system and peripheral tissues. MAOA preferentially oxidizes biogenic amines such as 5-hydroxytryptamine (5-HT), norepinephrine and epinephrine; Belongs to the flavin monoamine oxidase family
86	MAOB	Amine oxidase [flavin-containing] B; Catalyzes the oxidative deamination of biogenic and xenobiotic amines and has important functions in the metabolism of neuroactive and vasoactive amines in the central nervous system and peripheral tissues. MAOB preferentially degrades benzylamine and phenylethylamine
87	MECR	Enoyl-[acyl-carrier-protein] reductase, mitochondrial; Catalyzes the NADPH-dependent reduction of trans-2-enoyl thioesters in mitochondrial fatty acid synthesis (fatty acid synthesis type II). Fatty acid chain elongation in mitochondria uses acyl carrier protein (ACP) as an acyl group carrier, but the enzyme accepts both ACP and CoA thioesters as substrates in vitro. Has a preference for short and medium chain substrates, including trans-2-hexenoyl-CoA (C6), trans-2-decenoyl-CoA (C10), and trans- 2-hexadecenoyl-CoA (C16)
88	MET	Hepatocyte growth factor receptor; Receptor tyrosine kinase that transduces signals from the extracellular matrix into the cytoplasm by binding to hepatocyte growth factor/HGF ligand. Regulates many physiological processes including proliferation, scattering, morphogenesis and survival. Ligand binding at the cell surface induces autophosphorylation of MET on its intracellular domain that provides docking sites for downstream signaling molecules. Following activation by ligand, interacts with the PI3-kinase subunit PIK3R1, PLCG1, SRC, GRB2, STAT3 or the adapter GAB1. Recruitment of thes [...]
89	MGAM	Maltase-glucoamylase, intestinal; May serve as an alternate pathway for starch digestion when luminal alpha-amylase activity is reduced because of immaturity or malnutrition. May play a unique role in the digestion of malted dietary oligosaccharides used in food manufacturing
90	MMP12	Macrophage metalloelastase; May be involved in tissue injury and remodeling. Has significant elastolytic activity. Can accept large and small amino acids at the P1' site, but has a preference for leucine. Aromatic or hydrophobic residues are preferred at the P1 site, with small hydrophobic residues (preferably alanine) occupying P3; Belongs to the peptidase M10A family
91	NCOA4	Nuclear receptor coactivator 4; Enhances the androgen receptor transcriptional activity in prostate cancer cells. Ligand-independent coactivator of the peroxisome proliferator-activated receptor (PPAR) gamma
92	NEU1	Sialidase-1; Catalyzes the removal of sialic acid (N-acetylneuraminic acid) moities from glycoproteins and glycolipids. To be active, it is strictly dependent on its presence in the multienzyme complex. Appears to have a preference for alpha 2-3 and alpha 2-6 sialyl linkage
93	NOS3	Nitric oxide synthase, endothelial; Produces nitric oxide (NO) which is implicated in vascular smooth muscle relaxation through a cGMP-mediated signal transduction pathway. NO mediates vascular endothelial growth factor (VEGF)-induced angiogenesis in coronary vessels and promotes blood clotting through the activation of platelets

94	NOX4	NADPH oxidase 4; Constitutive NADPH oxidase which generates superoxide intracellularly upon formation of a complex with CYBA/p22phox. Regulates signaling cascades probably through phosphatases inhibition. May function as an oxygen sensor regulating the KCNK3/TASK-1 potassium channel and HIF1A activity. May regulate insulin signaling cascade. May play a role in apoptosis, bone resorption and lipolysaccharide-mediated activation of NFKB. May produce superoxide in the nucleus and play a role in regulating gene expression upon cell stimulation. Isoform 3 is not functional. Isoform 5 and is [...]
95	NT5E	5'-nucleotidase; Hydrolyzes extracellular nucleotides into membrane permeable nucleosides. Exhibits AMP-, NAD-, and NMN-nucleosidase activities; Belongs to the 5'-nucleotidase family
96	PIK3CG	Phosphatidylinositol 4,5-bisphosphate 3-kinase catalytic subunit gamma isoform; Phosphoinositide-3-kinase (PI3K) that phosphorylates PtdIns(4,5)P2 (Phosphatidylinositol 4,5-bisphosphate) to generate phosphatidylinositol 3,4,5-trisphosphate (PIP3). PIP3 plays a key role by recruiting PH domain-containing proteins to the membrane, including AKT1 and PDPK1, activating signaling cascades involved in cell growth, survival, proliferation, motility and morphology. Links G-protein coupled receptor activation to PIP3 production. Involved in immune, inflammatory and allergic responses. Modulates [...]
97	PIM1	Serine/threonine-protein kinase pim-1; Proto-oncogene with serine/threonine kinase activity involved in cell survival and cell proliferation and thus providing a selective advantage in tumorigenesis. Exerts its oncogenic activity through: the regulation of MYC transcriptional activity, the regulation of cell cycle progression and by phosphorylation and inhibition of proapoptotic proteins (BAD, MAP3K5, FOXO3). Phosphorylation of MYC leads to an increase of MYC protein stability and thereby an increase of transcriptional activity. The stabilization of MYC exerted by PIM1 might explain pa [...]
98	PNLIP	Pancreatic lipase; Belongs to the AB hydrolase superfamily. Lipase family
99	PPIP5K2	Inositol hexakisphosphate and diphosphoinositol-pentakisphosphate kinase 2; Bifunctional inositol kinase that acts in concert with the IP6K kinases IP6K1, IP6K2 and IP6K3 to synthesize the diphosphate group-containing inositol pyrophosphates diphosphoinositol pentakisphosphate, PP-InsP5, and bis-diphosphoinositol tetrakisphosphate, (PP)2-InsP4. PP-InsP5 and (PP)2-InsP4, also respectively called InsP7 and InsP8, regulate a variety of cellular processes, including apoptosis, vesicle trafficking, cytoskeletal dynamics, exocytosis, insulin signaling and neutrophil activation. Phosphorylat [...]
100	PSIP1	PC4 and SFRS1-interacting protein; Transcriptional coactivator involved in neuroepithelial stem cell differentiation and neurogenesis. Involved in particular in lens epithelial cell gene regulation and stress responses. May play an important role in lens epithelial to fiber cell terminal differentiation. May play a protective role during stress-induced apoptosis. Isoform 2 is a more general and stronger transcriptional coactivator. Isoform 2 may also act as an adapter to coordinate pre-mRNA splicing. Cellular cofactor for lentiviral integration; Heparin binding growth factor family
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102	PSIP1	PC4 and SFRS1-interacting protein; Transcriptional coactivator involved in neuroepithelial stem cell differentiation and neurogenesis. Involved in particular in lens epithelial cell gene regulation and stress responses. May play an important role in lens epithelial to fiber cell terminal differentiation. May play a protective role during stress-induced apoptosis. Isoform 2 is a more general and stronger transcriptional coactivator. Isoform 2 may also act as an adapter to coordinate pre-mRNA splicing. Cellular cofactor for lentiviral integration; Heparin binding growth factor family
103	PSMB1	Proteasome subunit beta type-1; Component of the 20S core proteasome complex involved in the proteolytic degradation of most intracellular proteins. This complex plays numerous essential roles within the cell by associating with different regulatory particles. Associated with two 19S regulatory particles, forms the 26S proteasome and thus participates in the ATP-dependent degradation of ubiquitinated proteins. The 26S proteasome plays a key role in the maintenance of protein homeostasis by removing misfolded or damaged proteins that could impair cellular functions, and by removing prot [...]
104	PTGS1	Prostaglandin G/H synthase 1; Converts arachidonate to prostaglandin H2 (PGH2), a committed step in prostanoid synthesis. Involved in the constitutive production of prostanoids in particular in the stomach and platelets. In gastric epithelial cells, it is a key step in the generation of prostaglandins, such as prostaglandin E2 (PGE2), which plays an important role in cytoprotection. In platelets, it is involved in the generation of thromboxane A2 (TXA2), which promotes platelet activation and aggregation, vasoconstriction and proliferation of vascular smooth muscle cells; Belongs to th [...]
105	PTPRS	Receptor-type tyrosine-protein phosphatase S; Cell surface receptor that binds to glycosaminoglycans, including chondroitin sulfate proteoglycans and heparan sulfate proteoglycan. Binding to chondroitin sulfate and heparan sulfate proteoglycans has opposite effects on PTPRS oligomerization and regulation of neurite outgrowth. Contributes to the inhibition of neurite and axonal outgrowth by chondroitin sulfate proteoglycans, also after nerve transection. Plays a role in stimulating neurite outgrowth in response to the heparan sulfate proteoglycan GPC2. Required for normal brain developm [...]
106	rep	Fanconi anemia group D2 protein; Required for maintenance of chromosomal stability. Promotes accurate and efficient pairing of homologs during meiosis. Involved in the repair of DNA double-strand breaks, both by homologous recombination and single-strand annealing. May participate in S phase and G2 phase checkpoint activation upon DNA damage. Plays a role in preventing breakage and loss of missegregating chromatin at the end of cell division, particularly after replication stress. Required for the targeting, or stabilization, of BLM to non-centromeric abnormal structures induced by rep [...]
108	SI	Sucrase-isomaltase, intestinal; Plays an important role in the final stage of carbohydrate digestion. Isomaltase activity is specific for both alpha-1,4- and alpha-1,6-oligosaccharides; Belongs to the glycosyl hydrolase 31 family
109	SMARCB1	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily B member 1; Core component of the BAF (hSWI/SNF) complex. This ATP- dependent chromatin-remodeling complex plays important roles in cell proliferation and differentiation, in cellular antiviral activities and inhibition of tumor formation. The BAF complex is able to create a stable, altered form of chromatin that constrains fewer negative supercoils than normal. This change in supercoiling would be due to the conversion of up to one-half of the nucleosomes on polynucleosomal arrays into asymmetric struct [...]
110	SYN1	Synapsin-1; Neuronal phosphoprotein that coats synaptic vesicles, binds to the cytoskeleton, and is believed to function in the regulation of neurotransmitter release. The complex formed with NOS1 and CAPON proteins is necessary for specific nitric-oxid functions at a presynaptic level; Synapsins

111	TERT	Telomerase reverse transcriptase; Telomerase is a ribonucleoprotein enzyme essential for the replication of chromosome termini in most eukaryotes. Active in progenitor and cancer cells. Inactive, or very low activity, in normal somatic cells. Catalytic component of the teleromerase holoenzyme complex whose main activity is the elongation of telomeres by acting as a reverse transcriptase that adds simple sequence repeats to chromosome ends by copying a template sequence within the RNA component of the enzyme. Catalyzes the RNA- dependent extension of 3'-chromosomal termini with the 6- n [...]
112	TNKS	Tankyrase-1; Poly-ADP-ribosyltransferase involved in various processes such as Wnt signaling pathway, telomere length and vesicle trafficking. Acts as an activator of the Wnt signaling pathway by mediating poly-ADP-ribosylation (PARsylation) of AXIN1 and AXIN2, 2 key components of the beta-catenin destruction complex: poly-ADP-ribosylated target proteins are recognized by RNF146, which mediates their ubiquitination and subsequent degradation. Also mediates PARsylation of BLZF1 and CASC3, followed by recruitment of RNF146 and subsequent ubiquitination. Mediates PARsylation of TERF1, the [...]
113	TNKS2	Tankyrase-2; Poly-ADP-ribosyltransferase involved in various processes such as Wnt signaling pathway, telomere length and vesicle trafficking. Acts as an activator of the Wnt signaling pathway by mediating poly-ADP-ribosylation of AXIN1 and AXIN2, 2 key components of the beta-catenin destruction complex: poly-ADP- ribosylated target proteins are recognized by RNF146, which mediates their ubiquitination and subsequent degradation. Also mediates poly-ADP-ribosylation of BLZF1 and CASC3, followed by recruitment of RNF146 and subsequent ubiquitination. Mediates poly-ADP-ribosylation of TER [...]
114	TOP1	DNA topoisomerase 1; Releases the supercoiling and torsional tension of DNA introduced during the DNA replication and transcription by transiently cleaving and rejoining one strand of the DNA duplex. Introduces a single-strand break via transesterification at a target site in duplex DNA. The scissile phosphodiester is attacked by the catalytic tyrosine of the enzyme, resulting in the formation of a DNA-(3'-phosphotyrosyl)-enzyme intermediate and the expulsion of a 5'-OH DNA strand. The free DNA strand then rotates around the intact phosphodiester bond on the opposing strand, thus remov [...]
115	TRPC5	Short transient receptor potential channel 5; Thought to form a receptor-activated non-selective calcium permeant cation channel. Probably is operated by a phosphatidylinositol second messenger system activated by receptor tyrosine kinases or G-protein coupled receptors. Has also been shown to be calcium-selective (By similarity). May also be activated by intracellular calcium store depletion; Protein phosphatase 1 regulatory subunits
116	TST	Thiosulfate sulfurtransferase; Formation of iron-sulfur complexes, cyanide detoxification or modification of sulfur-containing enzymes. Other thiol compounds, besides cyanide, can act as sulfur ion acceptors. Also has weak mercaptopyruvate sulfurtransferase (MST) activity (By similarity). Together with MRPL18, acts as a mitochondrial import factor for the cytosolic 5S rRNA. Only the nascent unfolded cytoplasmic form is able to bind to the 5S rRNA
117	TSTD1	Thiosulfate:glutathione sulfurtransferase; Thiosulfate:glutathione sulfurtransferase (TST) required to produce glutathione persulfide (GSS(-)), a central intermediate in hydrogen sulfide metabolism. Provides the link between the first step in mammalian H(2)S metabolism performed by the sulfide:quinone oxidoreductase (SQOR) which catalyzes the conversion of H(2)S to thiosulfate, and the sulfur dioxygenase (SDO) which uses GSS(-) as substrate. The thermodynamic coupling of the irreversible SDO and reversible TST reactions provides a model for the physiologically relevant reaction with th [...]
118	TTR	Transthyretin; Thyroid hormone-binding protein. Probably transports thyroxine from the bloodstream to the brain; Gla domain containing

119	TYR	Tyrosinase; This is a copper-containing oxidase that functions in the formation of pigments such as melanins and other polyphenolic compounds. Catalyzes the initial and rate limiting step in the cascade of reactions leading to melanin production from tyrosine. In addition to hydroxylating tyrosine to DOPA (3,4-dihydroxyphenylalanine), also catalyzes the oxidation of DOPA to DOPA-quinone, and possibly the oxidation of DHI (5,6- dihydroxyindole) to indole-5,6 quinone; Belongs to the tyrosinase family
120	UBE3A	Ubiquitin-protein ligase E3A; E3 ubiquitin-protein ligase which accepts ubiquitin from an E2 ubiquitin-conjugating enzyme in the form of a thioester and transfers it to its substrates. Several substrates have been identified including the RAD23A and RAD23B, MCM7 (which is involved in DNA replication), annexin A1, the PML tumor suppressor, and the cell cycle regulator CDKN1B. Catalyzes the high-risk human papilloma virus E6-mediated ubiquitination of p53/TP53, contributing to the neoplastic progression of cells infected by these viruses. Additionally, may function as a cellular quality [...]
121	VEGFA	Vascular endothelial growth factor A; Growth factor active in angiogenesis, vasculogenesis and endothelial cell growth. Induces endothelial cell proliferation, promotes cell migration, inhibits apoptosis and induces permeabilization of blood vessels. Binds to the FLT1/VEGFR1 and KDR/VEGFR2 receptors, heparan sulfate and heparin. NRP1/Neuropilin-1 binds isoforms VEGF-165 and VEGF-145. Isoform VEGF165B binds to KDR but does not activate downstream signaling pathways, does not activate angiogenesis and inhibits tumor growth. Binding to NRP1 receptor initiates a signaling pathway needed fo [...]
122	XDH	Xanthine dehydrogenase/oxidase; Key enzyme in purine degradation. Catalyzes the oxidation of hypoxanthine to xanthine. Catalyzes the oxidation of xanthine to uric acid. Contributes to the generation of reactive oxygen species. Has also low oxidase activity towards aldehydes (in vitro)