RT² Profiler PCR Array (96-Well Format and 384-Well [4 x 96] Format)

Human Mitochondrial Energy Metabolism

Cat. no. 330231 PAHS-008ZA

For pathway expression analysis

Format	**For use with the following real-time cyclers**
RT² Profiler PCR Array, Format A	Applied Biosystems® models 5700, 7000, 7300, 7500, 7700, 7900HT, ViiA™ 7 (96-well block); Bio-Rad® models iCycler®, iQ™5, MyiQ™, MyiQ2; Bio-Rad/MJ Research Chromo4™; Eppendorf® Mastercycler® ep realplex models 2, 2s, 4, 4s; Stratagene® models Mx3005P®, Mx3000P®; Takara TP-800
RT² Profiler PCR Array, Format C	Applied Biosystems models 7500 (Fast block), 7900HT (Fast block), StepOnePlus™, ViiA 7 (Fast block)
RT² Profiler PCR Array, Format D	Bio-Rad CFX96™; Bio-Rad/MJ Research models DNA Engine Opticon®, DNA Engine Opticon 2; Stratagene Mx4000®
RT² Profiler PCR Array, Format E	Applied Biosystems models 7900HT (384-well block), ViiA 7 (384-well block); Bio-Rad CFX384™
RT² Profiler PCR Array, Format F	Roche® LightCycler® 480 (96-well block)
RT² Profiler PCR Array, Format G	Roche LightCycler 480 (384-well block)
RT² Profiler PCR Array, Format H	Fluidigm® BioMark™

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Description

The Human Mitochondrial Energy Metabolism RT² Profiler PCR Array profiles the expression of 84 key genes involved in mitochondrial respiration, including genes encoding components of the electron transport chain and oxidative phosphorylation complexes. Oxidation of NADH and FADH2, the metabolites from glycolysis and the TCA cycle, occurs via a series of four protein complexes embedded in the inner mitochondrial membrane: NADH-coenzyme Q reductase, succinate-coenzyme Q reductase, coenzyme Q-cytochrome c reductase, and cytochrome c oxidase. The free energy generated from these processes drives oxidative phosphorylation and ATP synthesis via a fifth protein complex (ATP Synthase). Dysregulation of these processes is a major pathological consequence of cancer progression. Many tumors contain decreased amounts of mitochondrial respiratory chain components, although the exact mechanism for this repression is unclear. However, recent studies demonstrate that the important tumor suppressor p53 induces the expression of COX2, an essential component for cytochrome c oxidase function. Mitochondrial dysfunction also contributes to metabolic syndrome and obesity, where excess β-oxidation overloads oxidative phosphorylation by generating excessive amounts of NADH. Using real-time PCR, you can easily and reliably analyze the expression of a focused panel of genes involved in mitochondrial energy metabolism with this array.

For further details, consult the *RT² Profiler PCR Array Handbook*.

Shipping and storage

RT² Profiler PCR Arrays in formats A, C, D, E, F, and G are shipped at ambient temperature, on dry ice, or blue ice packs depending on destination and accompanying products. RT² Profiler PCR Arrays in format H are shipped on dry ice or blue ice packs.

For long term storage, keep plates at –20°C.

Note: Ensure that you have the correct RT² Profiler PCR Array format for your real-time cycler (see table above).

Note: Open the package and store the products appropriately immediately on receipt.

Array layout (96-well)

For 384-well 4 x 96 PCR arrays, genes are present in a staggered format. Refer to the *RT^2 Profiler PCR Array Handbook* for layout.

	1	2	3	4	5	6	7	8	9	10	11	12
A	ATP12A	ATP4A	ATP4B	ATP5A1	ATP5B	ATP5C1	ATP5F1	ATP5G1	ATP5G2	ATP5G3	ATP5H	ATP5I
B	ATP5J	ATP5J2	ATP5L	ATP5O	ATP6V0A2	ATP6V0D2	ATP6V1C2	ATP6V1E2	ATP6V1G3	BCS1L	COX4I1	COX4I2
C	COX5A	COX5B	COX6A1	COX6A2	COX6B1	COX6B2	COX6C	COX7A2	COX7A2L	COX7B	COX8A	COX8C
D	CYC1	LHPP	NDUFA1	NDUFA10	NDUFA11	NDUFA2	NDUFA3	NDUFA4	NDUFA5	NDUFA6	NDUFA7	NDUFA8
E	NDUFAB1	NDUFB10	NDUFB2	NDUFB3	NDUFB4	NDUFB5	NDUFB6	NDUFB7	NDUFB8	NDUFB9	NDUFC1	NDUFC2
F	NDUFS1	NDUFS2	NDUFS3	NDUFS4	NDUFS5	NDUFS6	NDUFS7	NDUFS8	NDUFV1	NDUFV2	NDUFV3	OXA1L
G	PPA1	PPA2	SDHA	SDHB	SDHC	SDHD	UQCR11	UQCRC1	UQCRC2	UQCRFS1	UQCRH	UQCRQ
H	ACTB	B2M	GAPDH	HPRT1	RPLP0	HGDC	RTC	RTC	RTC	PPC	PPC	PPC

Gene table: RT^2 Profiler PCR Array

Position	UniGene	GenBank	Symbol	Description
A01	Hs.147111	NM_001676	ATP12A	ATPase, H+/K+ transporting, nongastric, alpha polypeptide
A02	Hs.36992	NM_000704	ATP4A	ATPase, H+/K+ exchanging, alpha polypeptide
A03	Hs.434202	NM_000705	ATP4B	ATPase, H+/K+ exchanging, beta polypeptide
A04	Hs.298280	NM_004046	ATP5A1	ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit 1, cardiac muscle
A05	Hs.406510	NM_001686	ATP5B	ATP synthase, H+ transporting, mitochondrial F1 complex, beta polypeptide
A06	Hs.271135	NM_005174	ATP5C1	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1
A07	Hs.514870	NM_001688	ATP5F1	ATP synthase, H+ transporting, mitochondrial Fo complex, subunit B1
A08	Hs.80986	NM_005175	ATP5G1	ATP synthase, H+ transporting, mitochondrial Fo complex, subunit C1 (subunit 9)
A09	Hs.524464	NM_001002031	ATP5G2	ATP synthase, H+ transporting, mitochondrial Fo complex, subunit C2 (subunit 9)
A10	Hs.429	NM_001689	ATP5G3	ATP synthase, H+ transporting, mitochondrial Fo complex, subunit C3 (subunit 9)
A11	Hs.514465	NM_006356	ATP5H	ATP synthase, H+ transporting, mitochondrial Fo complex, subunit d
A12	Hs.85539	NM_007100	ATP5I	ATP synthase, H+ transporting, mitochondrial Fo complex, subunit E
B01	Hs.246310	NM_001685	ATP5J	ATP synthase, H+ transporting, mitochondrial Fo complex, subunit F6
B02	Hs.521056	NM_004889	ATP5J2	ATP synthase, H+ transporting, mitochondrial Fo complex, subunit F2
B03	Hs.486360	NM_006476	ATP5L	ATP synthase, H+ transporting, mitochondrial Fo complex, subunit G
B04	Hs.409140	NM_001697	ATP5O	ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit
B05	Hs.201939	NM_012463	ATP6V0A2	ATPase, H+ transporting, lysosomal V0 subunit a2
B06	Hs.436360	NM_152565	ATP6V0D2	ATPase, H+ transporting, lysosomal 38kDa, V0 subunit d2
B07	Hs.580464	NM_144583	ATP6V1C2	ATPase, H+ transporting, lysosomal 42kDa, V1 subunit C2
B08	Hs.437691	NM_080653	ATP6V1E2	ATPase, H+ transporting, lysosomal 31kDa, V1 subunit E2
B09	Hs.127743	NM_133262	ATP6V1G3	ATPase, H+ transporting, lysosomal 13kDa, V1 subunit G3
B10	Hs.471401	NM_004328	BCS1L	BCS1-like (S. cerevisiae)
B11	Hs.433419	NM_001861	COX4I1	Cytochrome c oxidase subunit IV isoform 1
B12	Hs.277101	NM_032609	COX4I2	Cytochrome c oxidase subunit IV isoform 2 (lung)
C01	Hs.401903	NM_004255	COX5A	Cytochrome c oxidase subunit Va
C02	Hs.1342	NM_001862	COX5B	Cytochrome c oxidase subunit Vb
C03	Hs.497118	NM_004373	COX6A1	Cytochrome c oxidase subunit VIa polypeptide 1
C04	Hs.250760	NM_005205	COX6A2	Cytochrome c oxidase subunit VIa polypeptide 2
C05	Hs.431668	NM_001863	COX6B1	Cytochrome c oxidase subunit Vib polypeptide 1 (ubiquitous)
C06	Hs.550544	NM_144613	COX6B2	Cytochrome c oxidase subunit VIb polypeptide 2 (testis)
C07	Hs.351875	NM_004374	COX6C	Cytochrome c oxidase subunit VIc
C08	Hs.70312	NM_001865	COX7A2	Cytochrome c oxidase subunit VIIa polypeptide 2 (liver)
C09	Hs.339639	NM_004718	COX7A2L	Cytochrome c oxidase subunit VIIa polypeptide 2 like
C10	Hs.522699	NM_001866	COX7B	Cytochrome c oxidase subunit VIIb
C11	Hs.433901	NM_004074	COX8A	Cytochrome c oxidase subunit VIIIA (ubiquitous)
C12	Hs.666459	NM_182971	COX8C	Cytochrome c oxidase subunit VIIIC
D01	Hs.289271	NM_001916	CYC1	Cytochrome c-1
D02	Hs.527748	NM_022126	LHPP	Phospholysine phosphohistidine inorganic pyrophosphate phosphatase
D03	Hs.534168	NM_004541	NDUFA1	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 1, 7.5kDa
D04	Hs.277677	NM_004544	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 10, 42kDa

Position	UniGene	GenBank	Symbol	Description
D05	Hs.406062	NM_175614	NDUFA11	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 11, 14.7kDa
D06	Hs.534333	NM_002488	NDUFA2	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2, 8kDa
D07	Hs.198269	NM_004542	NDUFA3	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 3, 9kDa
D08	Hs.50098	NM_002489	NDUFA4	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4, 9kDa
D09	Hs.651219	NM_005000	NDUFA5	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5, 13kDa
D10	Hs.274416	NM_002490	NDUFA6	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6, 14kDa
D11	Hs.333427	NM_005001	NDUFA7	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 7, 14.5kDa
D12	Hs.495039	NM_014222	NDUFA8	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 8, 19kDa
E01	Hs.189716	NM_005003	NDUFAB1	NADH dehydrogenase (ubiquinone) 1, alpha/beta subcomplex, 1, 8kDa
E02	Hs.513266	NM_004548	NDUFB10	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 10, 22kDa
E03	Hs.655788	NM_004546	NDUFB2	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 2, 8kDa
E04	Hs.109760	NM_002491	NDUFB3	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 3, 12kDa
E05	Hs.304613	NM_004547	NDUFB4	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 4, 15kDa
E06	Hs.718447	NM_002492	NDUFB5	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5, 16kDa
E07	Hs.493668	NM_182739	NDUFB6	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 6, 17kDa
E08	Hs.532853	NM_004146	NDUFB7	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 7, 18kDa
E09	Hs.523215	NM_005004	NDUFB8	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8, 19kDa
E10	Hs.15977	NM_005005	NDUFB9	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9, 22kDa
E11	Hs.84549	NM_002494	NDUFC1	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 1, 6kDa
E12	Hs.407860	NM_004549	NDUFC2	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2, 14.5kDa
F01	Hs.471207	NM_005006	NDUFS1	NADH dehydrogenase (ubiquinone) Fe-S protein 1, 75kDa (NADH-coenzyme Q reductase)
F02	Hs.173611	NM_004550	NDUFS2	NADH dehydrogenase (ubiquinone) Fe-S protein 2, 49kDa (NADH-coenzyme Q reductase)
F03	Hs.502528	NM_004551	NDUFS3	NADH dehydrogenase (ubiquinone) Fe-S protein 3, 30kDa (NADH-coenzyme Q reductase)
F04	Hs.528222	NM_002495	NDUFS4	NADH dehydrogenase (ubiquinone) Fe-S protein 4, 18kDa (NADH-coenzyme Q reductase)
F05	Hs.632385	NM_004552	NDUFS5	NADH dehydrogenase (ubiquinone) Fe-S protein 5, 15kDa (NADH-coenzyme Q reductase)
F06	Hs.408257	NM_004553	NDUFS6	NADH dehydrogenase (ubiquinone) Fe-S protein 6, 13kDa (NADH-coenzyme Q reductase)
F07	Hs.211914	NM_024407	NDUFS7	NADH dehydrogenase (ubiquinone) Fe-S protein 7, 20kDa (NADH-coenzyme Q reductase)
F08	Hs.90443	NM_002496	NDUFS8	NADH dehydrogenase (ubiquinone) Fe-S protein 8, 23kDa (NADH-coenzyme Q reductase)
F09	Hs.7744	NM_007103	NDUFV1	NADH dehydrogenase (ubiquinone) flavoprotein 1, 51kDa
F10	Hs.464572	NM_021074	NDUFV2	NADH dehydrogenase (ubiquinone) flavoprotein 2, 24kDa
F11	Hs.473937	NM_021075	NDUFV3	NADH dehydrogenase (ubiquinone) flavoprotein 3, 10kDa
F12	Hs.151134	NM_005015	OXA1L	Oxidase (cytochrome c) assembly 1-like
G01	Hs.437403	NM_021129	PPA1	Pyrophosphatase (inorganic) 1
G02	Hs.654957	NM_176869	PPA2	Pyrophosphatase (inorganic) 2
G03	Hs.440475	NM_004168	SDHA	Succinate dehydrogenase complex, subunit A, flavoprotein (Fp)
G04	Hs.465924	NM_003000	SDHB	Succinate dehydrogenase complex, subunit B, iron sulfur (Ip)
G05	Hs.444472	NM_003001	SDHC	Succinate dehydrogenase complex, subunit C, integral membrane protein, 15kDa
G06	Hs.356270	NM_003002	SDHD	Succinate dehydrogenase complex, subunit D, integral membrane protein
G07	Hs.8372	NM_006830	UQCR11	Ubiquinol-cytochrome c reductase, complex III subunit XI
G08	Hs.119251	NM_003365	UQCRC1	Ubiquinol-cytochrome c reductase core protein I
G09	Hs.528803	NM_003366	UQCRC2	Ubiquinol-cytochrome c reductase core protein II
G10	Hs.170107	NM_006003	UQCRFS1	Ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1
G11	Hs.481571	NM_006004	UQCRH	Ubiquinol-cytochrome c reductase hinge protein
G12	Hs.146602	NM_014402	UQCRQ	Ubiquinol-cytochrome c reductase, complex III subunit VII, 9.5kDa
H01	Hs.520640	NM_001101	ACTB	Actin, beta
H02	Hs.534255	NM_004048	B2M	Beta-2-microglobulin
H03	Hs.592355	NM_002046	GAPDH	Glyceraldehyde-3-phosphate dehydrogenase
H04	Hs.412707	NM_000194	HPRT1	Hypoxanthine phosphoribosyltransferase 1
H05	Hs.546285	NM_001002	RPLP0	Ribosomal protein, large, P0
H06	N/A	SA_00105	HGDC	Human Genomic DNA Contamination
H07	N/A	SA_00104	RTC	Reverse Transcription Control
H08	N/A	SA_00104	RTC	Reverse Transcription Control
H09	N/A	SA_00104	RTC	Reverse Transcription Control
H10	N/A	SA_00103	PPC	Positive PCR Control
H11	N/A	SA_00103	PPC	Positive PCR Control
H12	N/A	SA_00103	PPC	Positive PCR Control

Related products

For optimal performance, RT² Profiler PCR Arrays should be used together with the RT² First Strand Kit for cDNA synthesis and RT2 SYBR® Green qPCR Mastermixes for PCR.

Product	Contents	Cat. no.
RT² First Strand Kit (12)	Enzymes and reagents for cDNA synthesis	330401
RT² SYBR Green qPCR Mastermix (2)*	For 2 x 96 assays in 96-well plates; suitable for use with real-time cyclers that do not require a reference dye, including: Bio-Rad models CFX96, CFX384, DNA Engine Opticon 2; Bio-Rad/MJ Research Chromo4; Roche LightCycler 480 (96-well and 384-well); all other cyclers	330500
RT² SYBR Green ROX™ qPCR Mastermix (2)*	For 2 x 96 assays in 96-well plates; suitable for use with the following real-time cyclers: Applied Biosystems models 5700, 7000, 7300, 7500 [Standard and FAST], 7700, 7900HT 96-well block [Standard and FAST] and 384-well block, StepOnePlus; Eppendorf Mastercycler ep realplex models 2, 2S, 4, 4S; Stratagene models Mx3000P, Mx3005P, Mx4000; Takara TP-800	330520
RT² SYBR Green Fluor qPCR Mastermix (2)*	For 2 x 96 assays in 96-well plates; suitable for use with the following real-time cyclers: Bio-Rad models iCycler, iQ5, MyiQ, MyiQ2	330510

* Larger kit sizes available; please inquire.

RT^2 Profiler PCR Array products are intended for molecular biology applications. These products are not intended for the diagnosis, prevention, or treatment of a disease.

For up-to-date licensing information and product-specific disclaimers, see the respective QIAGEN kit handbook or user manual. QIAGEN kit handbooks and user manuals are available at www.qiagen.com or can be requested from QIAGEN Technical Services or your local distributor.

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