abcam

ab14746

Anti-UQCRFS1/RISP antibody [5A5]

Key facts

Isotype	IgG2b
Host species	Mouse
Storage buffer	pH: 7.5 Preservative: 0.02% Sodium azide Constituents: HEPES buffered saline
Form	Liquid
Clonality	Monoclonal
Immunogen	The exact immunogen used to generate this antibody is proprietary information.
Clone number	5A5
Purification technique	Affinity purification Immunogen
Light chain type	kappa
Concentration	1 mg/mL The concentration of this product may be batch-dependent Batch concentration finder →
Purification notes	Near homogeneity as judged by SDS-PAGE. The antibody was produced in vitro using hybridomas grown in serum-free medium, and then purified by biochemical fractionation.

Reactivity data

Flow Cyt

Tested

Species	Human
Dilution info	1 µg for 10^6 Cells

Notes	ab170192 - Mouse monoclonal IgG2b, is suitable for use as an isotype control with this antibody.

Expected

Species	Mouse
Dilution info	1 µg for 10^6 Cells
Notes	ab170192 - Mouse monoclonal IgG2b, is suitable for use as an isotype control with this antibody.

Species	Cow
Dilution info	1 µg for 10^6 Cells
Notes	ab170192 - Mouse monoclonal IgG2b, is suitable for use as an isotype control with this antibody.

Predicted

Species	Rat, Pig
Dilution info	-
Notes	-

WB

Tested

Species	Human
Dilution info	1 µg/mL
Notes	-

Species	Mouse
Dilution info	1 µg/mL
Notes	-

Expected

Species	Rat
Dilution info	1 µg/mL

Notes	-

Species	Cow
Dilution info	1 µg/mL
Notes	-

Predicted

Species	Pig
Dilution info	-
Notes	-

IHC-P

Tested

Species	Human
Dilution info	2 µg/mL
Notes	-

Expected

Species	Mouse
Dilution info	2 µg/mL
Notes	-

Species	Rat
Dilution info	2 µg/mL
Notes	-

Species	Cow
Dilution info	2 µg/mL
Notes	-

Predicted

Species	Pig
Dilution info	-
Notes	-

Target data

See full target information UQCRFS1

Function	Cytochrome b-c1 complex subunit Rieske, mitochondrial. Component of the ubiquinol-cytochrome c oxidoreductase, a multisubunit transmembrane complex that is part of the mitochondrial electron transport chain which drives oxidative phosphorylation. The respiratory chain contains 3 multisubunit complexes succinate dehydrogenase (complex II, CII), ubiquinol-cytochrome c oxidoreductase (cytochrome b-c1 complex, complex III, CIII) and cytochrome c oxidase (complex IV, CIV), that cooperate to transfer electrons derived from NADH and succinate to molecular oxygen, creating an electrochemical gradient over the inner membrane that drives transmembrane transport and the ATP synthase. The cytochrome b-c1 complex catalyzes electron transfer from ubiquinol to cytochrome c, linking this redox reaction to translocation of protons across the mitochondrial inner membrane, with protons being carried across the membrane as hydrogens on the quinol. In the process called Q cycle, 2 protons are consumed from the matrix, 4 protons are released into the intermembrane space and 2 electrons are passed to cytochrome c. The Rieske protein is a catalytic core subunit containing a [2Fe-2S] iron-sulfur cluster. It cycles between 2 conformational states during catalysis to transfer electrons from the quinol bound in the Q(0) site in cytochrome b to cytochrome c1 (By similarity). Incorporation of UQCRFS1 is the penultimate step in complex III assembly (By similarity). Cytochrome b-c1 complex subunit 9. Component of the ubiquinol-cytochrome c oxidoreductase (cytochrome b-c1 complex, complex III, CIII). UQCRFS1 undergoes proteolytic processing once it is incorporated in the complex III dimer. One of the fragments, called subunit 9, corresponds to its mitochondrial targeting sequence (MTS) (PubMed:2996928, PubMed:8386158). The proteolytic processing is necessary for the correct insertion of UQCRFS1 in the complex III dimer, but the persistence of UQCRFS1-derived fragments may prevent newly imported UQCRFS1 to be processed and assembled into complex III and is detrimental for the complex III structure and function (By similarity).

Storage

Shipped at conditions	Blue Ice
Appropriate short-term storage conditions	+4°C
Appropriate long-term storage conditions	+4°C

Notes

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Supplementary info

This supplementary information is collated from multiple sources and compiled automatically.

Activity summary	UQCRFS1 also known as RISP functions as an essential component of the mitochondrial electron transport chain. The protein weighs approximately 29 kDa and plays an important role in the transfer of electrons from ubiquinol to cytochrome c within complex III also named cytochrome bc1 complex. UQCRFS1 expresses primarily in tissues with high energy requirements such as heart and skeletal muscle due to their reliance on aerobic metabolism for ATP production.
Biological function summary	RISP belongs to the cytochrome bc1 complex a large multimeric structure involved in mitochondrial respiratory function. By facilitating electron transfer it contributes to the establishment of the proton gradient across the inner mitochondrial membrane. This gradient drives ATP synthesis through oxidative phosphorylation highlighting its importance for cellular energy homeostasis. The reduction and oxidation of ubiquinone and cytochrome c ensure effective electron flow within this system.
Pathways	RISP integrates into essential processes within the respiratory chain and oxidative phosphorylation pathways. It directly interacts with other proteins in complex III such as UQCRH and UQCRC1 to facilitate protein complex stability and function. Additionally RISP supports the interaction between complex III and complex IV by aiding in the electron transfer ensuring efficient ATP production. This association clarifies the interprotein dynamics needed for proper mitochondrial respiratory operation.
Associated diseases and disorders	RISP connects to mitochondrial dysfunction and related pathologies. Mitochondrial complex III deficiencies often link to neurodegenerative disorders like Leigh syndrome due to defective oxidative phosphorylation. Such deficiencies may result from perturbations in RISP function or expression affecting electron transport chain efficiency. Furthermore disruptions in RISP activity relate to ischemic conditions where hypoxic stress compromises ATP production implicating it together with cytochrome c in cellular energy crises.

Product promise

Tested

We have tested this species and application combination and it works. It is covered by our product promise.

Expected

We have not tested this specific species and application combination in-house, but expect it will work. It is covered by our product promise.

Predicted

This species and application combination has not been tested, but we predict it will work based on strong homology. However, this combination is not covered by our product promise.

Not recommended

We do not recommend this combination. It is not covered by our product promise.

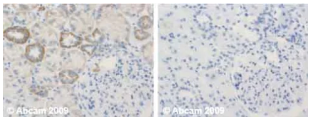
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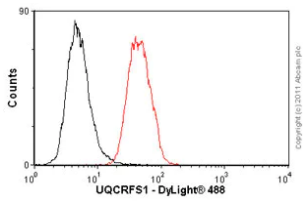
7 product images



Immunohistochemistry (Formalin/PFA-fixed paraffin-embedded sections) - Anti-UQCRFS1/RISP antibody [5A5] (ab14746)

UQCRFS1/RISP Immunohistochemistry (Formalin/PFA-fixed paraffin-embedded sections) staining using mouse Anti-UQCRFS1/RISP antibody

Human normal kidney (cortex). Staining is observed intracellular. Left panel: with primary antibody at 2 ug/ml. Right panel: isotype control. Sections were stained using an automated system DAKO Autostainer Plus , at room temperature: sections were rehydrated and antigen retrieved with the Dako 3 in 1 AR buffers citrate EDTA pH 9.0 in a DAKO PT Link. Slides were peroxidase blocked in 3% H2O2 in methanol for 10 mins. They were then blocked with Dako Protein block for 10 minutes (containing casein 0.25% in PBS) then incubated with primary antibody for 20 min and detected with Dako envision flex amplification kit for mouse for 30 minutes. Colorimetric detection was completed with Diaminobenzidine for 5 minutes. Slides were counterstained with Haematoxylin and coverslipped under DePeX. Please note that for manual staining we recommend to optimize the primary antibody concentration and incubation time (overnight incubation), and amplification may be required.

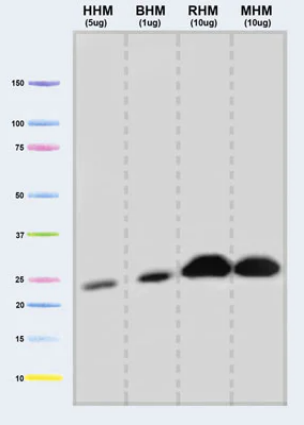


Flow Cytometry - Anti-UQCRFS1/RISP antibody [5A5] (ab14746)

UQCRFS1/RISP Flow Cytometry staining using mouse Anti-UQCRFS1/RISP antibody

Overlay histogram showing Raji cells stained with ab14746 (red line). The cells were fixed with 80% methanol (5 min) and then permeabilized with 0.1% PBS-Tween for 20 min. The cells were then incubated in 1x PBS / 10% normal goat serum / 0.3M glycine to block non-specific protein-protein interactions. The cells were then incubated with the antibody (ab14746, 1µg/1x10^6 cells) for 30 min at 22°C. The secondary antibody used was DyLight® 488 goat anti-mouse IgG (H+L) (ab96879) at 1/500 dilution for 30 min at 22°C. Isotype control antibody (black line) was mouse IgG2b [PLPV219] (ab91366, 2µg/1x10^6 cells) used under the same conditions. Acquisition of >5,000 events was performed. This antibody gave a positive signal in Raji cells fixed with 4%

paraformaldehyde (10 min)/permeabilized in 0.1% PBS-Tween used under the same conditions.



Western blot - Anti-UQCRFS1/RISP antibody [5A5] (ab14746)

All lanes:
Western blot - Anti-UQCRFS1/RISP antibody [5A5] (ab14746) at 1 µg/mL

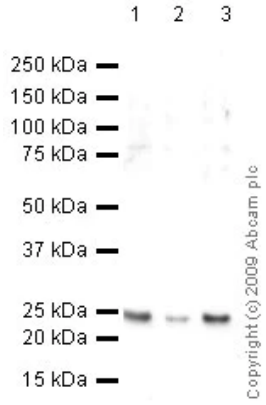
Lane 1:
Isolated mitochondria from human heart at 5 µg

Lane 2:
Isolated mitochondria from bovine heart at 1 µg

Lane 3:
Isolated mitochondria from rat heart at 10 µg

Lane 4:
Isolated mitochondria from mouse heart at 10 µg

Predicted band size: 30 kDa



Western blot - Anti-UQCRFS1/RISP antibody [5A5] (ab14746)

All lanes:
Western blot - Anti-UQCRFS1/RISP antibody [5A5] (ab14746) at 0.5 µg/mL

Lane 1:
Hela Whole Cell Lysate - Hydroxyurea Treated at 10 µg

Lane 2:
Hela Whole Cell Lysate - Bleomycin Treated at 10 µg

Lane 3:
Hela Whole Cell Lysate - Staurosporine Treated at 10 µg

Secondary

All lanes:
Mouse IgG - H&L - Pre-Adsorbed (HRP) at 1/3000 dilution

Predicted band size: 30 kDa

Observed band size: 25 kDa

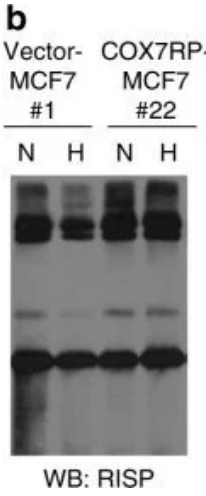


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Western blot - Anti-UQCRFS1/RISP antibody [5A5] (ab14746)

UQCRFS1/RISP Western blot staining using mouse Anti-UQCRFS1/RISP antibody

Western Blotting using Anti-UQCRFS1/RISP antibody [5A5], ab14746. Publication image from Ikeda, K. et al., 2019, Nat Commun, 31511525. Legend direct from paper.

COX7RP facilitates supercomplex assembly in hypoxia and modulates metabolic pathways. a–d Mitochondrial proteins of COX7RP-MCF7 cells exposed to normoxic (N) and hypoxic (H: 1% O2) conditions were solubilized with digitonin (4 g g−1) and subjected to BN-PAGE. Western blot analysis was performed with antibodies for NDUFA9 a, RISP b, COX1 c, COX7RP d, and Fp70 e. Positions corresponding to CI + CIII2 + CIVn, CIII2 + CIVn, CIII2 or CIVn, and CIV are indicated. e COX7RP-MCF7 cells were cultured in normoxic or hypoxic conditions (1% O2) for 24 h and cell extracts were subjected to metabolome analysis using capillary electrophoresis time-of-flight mass spectrometry (CE-TOFMS) for cation analysis and capillary electrophoresis-tandem mass spectrometry (CE-MS/MS) for anion analysis. Metabolites in the TCA cycle are schematically shown. The intracellular concentration (pmol/million cells) of key metabolites involved in the TCA cycle and glutathione synthesis pathway are shown as means ± SD (n = 3 biologically independent samples). Source data are provided as a Source Data file

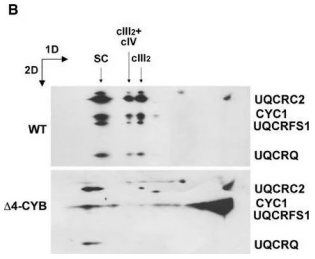


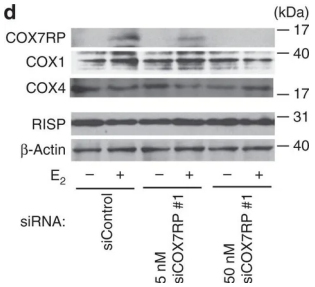
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Western blot - Anti-UQCRFS1/RISP antibody [5A5] (ab14746)

UQCRFS1/RISP Western blot staining using mouse Anti-UQCRFS1/RISP antibody

Western Blotting using Anti-UQCRFS1/RISP antibody [5A5], ab14746. Publication image from Protasoni, M. et al., 2020, EMBO J, 31912925. Legend direct from paper.

Blue‐native gel electrophoresis (BNGE) mass spectrometry and immunodetection analysis of cIII2‐related proteinsComplexome profiles of cIII2 structural subunits generated by analyzing the peptide content in each of the 64 slices in which the gel lanes were excised (see also Figs EV1 and EV2). The graphs plot the relative peptide peak intensities along the lane, setting the maximum to 1.0, versus the molecular mass calculated using the individual complexes and supercomplexes as the standards to generate a calibration curve. The relative amounts of the proteins between the two cell lines were determined by calculating the H/L ratios of peptides that were present in both WT (blue traces) and δ4‐CYB samples (red traces). The represented values are the mean ± SEM of the two reciprocal labeling experiments.Second‐dimension BNGE of digitonin‐solubilized samples from WT and δ4‐CYB cells, Western blot and immunodetection of the indicated cIII2 structural subunits with specific antibodies. The immunodetection patterns were equivalent to the complexome profiles.Quantification of the total peak area under the curves (AUC) defined by the peptide intensity peaks for the indicated cIII2 subunits. The x‐axis values were the slice number (1‐64), and the y‐axis values were the relative peptide intensity. The graph shows the mean ± SD (n = 2). Two‐way ANOVA with Sidak's multiple comparisons test **P = 0.0083 (UQCRC2); **P = 0.0033 (UQCRFS1); *P = 0.0224; n.s. = non‐significant.Complexome profiles of two cIII2 assembly factors (BCS1L and LYRM7 or MZM1L) generated in the same way as in (A). The represented values are the mean ± SEM of the two reciprocal labeling experiments.Source data are available online for this figure.



Western blot - Anti-UQCRFS1/RISP antibody [5A5] (ab14746)

UQCRFS1/RISP Western blot staining using mouse Anti-UQCRFS1/RISP antibody

Western Blotting using Anti-UQCRFS1/RISP antibody [5A5], ab14746. Publication image from Ikeda, K. et al., 2019, Nat Commun, 31511525. Legend direct from paper.

Inhibition of COX7RP expression suppresses estrogen-induced cell proliferation and ATP production in MCF7 cells. a siCOX7RP attenuates hormone-dependent growth of MCF7 cells. MCF7

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cells were transfected with siCOX7RP or siControl for the indicated times and cell growth was estimated by the DNA amount. b Silencing of COX7RP decreases COX activity. COX activity was assessed in MCF7 cells treated with siCOX7RP or siControl. c Silencing of COX7RP decreases ATP production. ATP production in mitochondria was assessed in MCF7 cells treated with siCOX7RP or siControl. Data are presented as means ± SD (n = 3 independent experiments). *P < 0.05, **P < 0.01, Student’ s t test. d siCOX7RP attenuates estrogen-induced COX7RP expression. Cell lysates were subjected to western blotting using antibodies for COX7RP, COX1, COX4, RISP, and β-actin. Source data are provided as a Source Data file

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