

Reactome Analysis Result

23 November, 2021

Introduction

This report summarizes the pathway analysis result created by the **Reactome Analysis Service**. For more information, visit <https://www.reactome.org>.

In this reports, pathways found differentially expressed at an adjusted p-value ≤ 0.05 are considered to be significantly regulated.

Analysis Overview

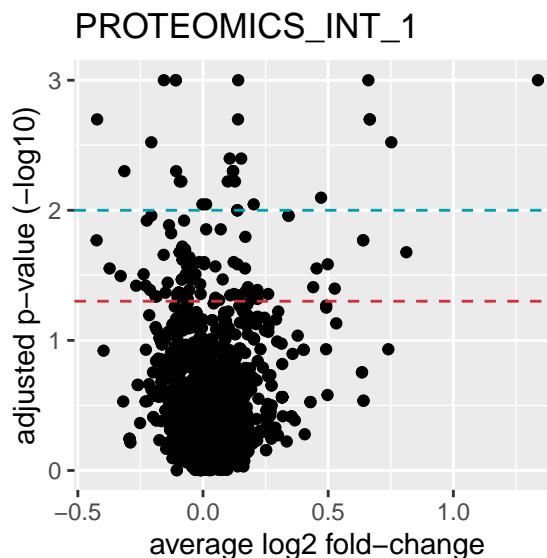
- Number of datasets analysed: 1
- Reactome version: 78
- Disease pathways were included

Dataset summaries

PROTEOMICS_INT_1:

- 2095 pathways
- 5438 fold changes for genes / proteins

Pathway analysis



These volcano plots summarize the pathway results for every dataset. Every point is one pathway. The x-axis represents the average fold-change of all genes / proteins within that pathway. The y-axis represents the p-value where “higher” values are more significant (-log10 transformation). The red line represents $p = 0.05$, and the blue line $p = 0.01$.

Note

Since this result only contains a single datasets, some analyses are not included in this report.

Top-regulated pathways

Dissolution of Fibrin Clot (R-HSA-75205)

	PROTEOMICS_INT_1
Regulation	Up
FDR	0.001
Av. FC	0.661
N Genes	6

Defective B3GALTL causes Peters-plus syndrome (PpS) (R-HSA-5083635)

	PROTEOMICS_INT_1
Regulation	Up
FDR	0.001
Av. FC	1.338
N Genes	1

Respiratory electron transport (R-HSA-611105)

	PROTEOMICS_INT_1
Regulation	Up
FDR	0.001
Av. FC	0.141
N Genes	93

Respiratory electron transport, ATP synthesis by chemiosmotic coupling, and heat production by uncoupling proteins. (R-HSA-163200)

	PROTEOMICS_INT_1
Regulation	Up
FDR	0.002
Av. FC	0.14
N Genes	107

Intestinal absorption (R-HSA-8963676)

	PROTEOMICS_INT_1
Regulation	Up
FDR	0.002
Av. FC	0.666
N Genes	1

Intestinal hexose absorption (R-HSA-8981373)

	PROTEOMICS_INT_1
Regulation	Up
FDR	0.002
Av. FC	0.666
N Genes	1

O-glycosylation of TSR domain-containing proteins (R-HSA-5173214)

	PROTEOMICS_INT_1
Regulation	Up
FDR	0.003
Av. FC	0.752
N Genes	2

Complex I biogenesis (R-HSA-6799198)

	PROTEOMICS_INT_1
Regulation	Up
FDR	0.004
Av. FC	0.153
N Genes	55

Activation of caspases through apoptosome-mediated cleavage (R-HSA-111459)

	PROTEOMICS_INT_1
Regulation	Up
FDR	0.004
Av. FC	0.107
N Genes	5

SMAC (DIABLO) binds to IAPs (R-HSA-111463)

	PROTEOMICS_INT_1
Regulation	Up
FDR	0.005
Av. FC	0.12
N Genes	6

SMAC(DIABLO)-mediated dissociation of IAP:caspase complexes (R-HSA-111464)

	PROTEOMICS_INT_1
Regulation	Up
FDR	0.005
Av. FC	0.12
N Genes	6

SMAC, XIAP-regulated apoptotic response (R-HSA-111469)

	PROTEOMICS_INT_1
Regulation	Up
FDR	0.005
Av. FC	0.12
N Genes	6

The citric acid (TCA) cycle and respiratory electron transport (R-HSA-1428517)

	PROTEOMICS_INT_1
Regulation	Up
FDR	0.006
Av. FC	0.128
N Genes	147

RAB geranylgeranylation (R-HSA-8873719)

	PROTEOMICS_INT_1
Regulation	Up
FDR	0.006
Av. FC	0.099
N Genes	41

Non-integrin membrane-ECM interactions (R-HSA-3000171)

	PROTEOMICS_INT_1
Regulation	Up
FDR	0.008
Av. FC	0.472
N Genes	14

Synthesis of PI (R-HSA-1483226)

	PROTEOMICS_INT_1
Regulation	Up
FDR	0.009
Av. FC	0.202
N Genes	2

Signaling by Retinoic Acid (R-HSA-5362517)

	PROTEOMICS_INT_1
Regulation	Up
FDR	0.009
Av. FC	0.012
N Genes	15

mRNA Editing: A to I Conversion (R-HSA-75064)

	PROTEOMICS_INT_1
Regulation	Up
FDR	0.01
Av. FC	0.137
N Genes	1

C6 deamination of adenosine (R-HSA-75102)

	PROTEOMICS_INT_1
Regulation	Up
FDR	0.01
Av. FC	0.137
N Genes	1

Formation of editosomes by ADAR proteins (R-HSA-77042)

	PROTEOMICS_INT_1
Regulation	Up
FDR	0.01
Av. FC	0.137
N Genes	1

Amplification of signal from the kinetochores (R-HSA-141424)

	PROTEOMICS_INT_1
Regulation	Down
FDR	0.001
Av. FC	-0.109
N Genes	78

Amplification of signal from unattached kinetochores via a MAD2 inhibitory signal (R-HSA-141444)

	PROTEOMICS_INT_1
Regulation	Down
FDR	0.001
Av. FC	-0.109
N Genes	78

TP53 Regulates Transcription of Genes Involved in G2 Cell Cycle Arrest (R-HSA-6804114)

	PROTEOMICS_INT_1
Regulation	Down
FDR	0.001
Av. FC	-0.156
N Genes	12

Phosphorylation of Emi1 (R-HSA-176417)

	PROTEOMICS_INT_1
Regulation	Down
FDR	0.002
Av. FC	-0.423
N Genes	5

vRNP Assembly (R-HSA-192905)

	PROTEOMICS_INT_1
Regulation	Down
FDR	0.003
Av. FC	-0.206
N Genes	2

Mitotic Spindle Checkpoint (R-HSA-69618)

	PROTEOMICS_INT_1
Regulation	Down
FDR	0.005
Av. FC	-0.107
N Genes	90

DNA replication initiation (R-HSA-68952)

	PROTEOMICS_INT_1
Regulation	Down
FDR	0.005
Av. FC	-0.314
N Genes	6

Resolution of Sister Chromatid Cohesion (R-HSA-2500257)

	PROTEOMICS_INT_1
Regulation	Down
FDR	0.006
Av. FC	-0.093
N Genes	103

EML4 and NUDC in mitotic spindle formation (R-HSA-9648025)

	PROTEOMICS_INT_1
Regulation	Down
FDR	0.006
Av. FC	-0.087
N Genes	94

Depolymerisation of the Nuclear Lamina (R-HSA-4419969)

	PROTEOMICS_INT_1
Regulation	Down
FDR	0.009
Av. FC	-0.002
N Genes	10

Activation of NIMA Kinases NEK9, NEK6, NEK7 (R-HSA-2980767)

	PROTEOMICS_INT_1
Regulation	Down
FDR	0.011
Av. FC	-0.206
N Genes	7

RHO GTPases Activate Formins (R-HSA-5663220)

	PROTEOMICS_INT_1
Regulation	Down
FDR	0.012
Av. FC	-0.076
N Genes	109

Inhibition of replication initiation of damaged DNA by RB1/E2F1 (R-HSA-113501)

	PROTEOMICS_INT_1
Regulation	Down
FDR	0.012
Av. FC	-0.225
N Genes	9

Condensation of Prophase Chromosomes (R-HSA-2299718)

	PROTEOMICS_INT_1
Regulation	Down
FDR	0.013
Av. FC	-0.136
N Genes	16

Telomere C-strand synthesis initiation (R-HSA-174430)

	PROTEOMICS_INT_1
Regulation	Down
FDR	0.015
Av. FC	-0.127
N Genes	8

Phosphorylation of proteins involved in the G2/M transition by Cyclin A:Cdc2 complexes (R-HSA-170145)

	PROTEOMICS_INT_1
Regulation	Down
FDR	0.017
Av. FC	-0.425
N Genes	2

Golgi Cisternae Pericentriolar Stack Reorganization (R-HSA-162658)

	PROTEOMICS_INT_1
Regulation	Down
FDR	0.019
Av. FC	-0.083
N Genes	12

HDR through Homologous Recombination (HRR) or Single Strand Annealing (SSA) (R-HSA-5693567)

	PROTEOMICS_INT_1
Regulation	Down
FDR	0.02
Av. FC	-0.072
N Genes	68

Cell Cycle Checkpoints (R-HSA-69620)

	PROTEOMICS_INT_1
Regulation	Down
FDR	0.02
Av. FC	-0.075
N Genes	208

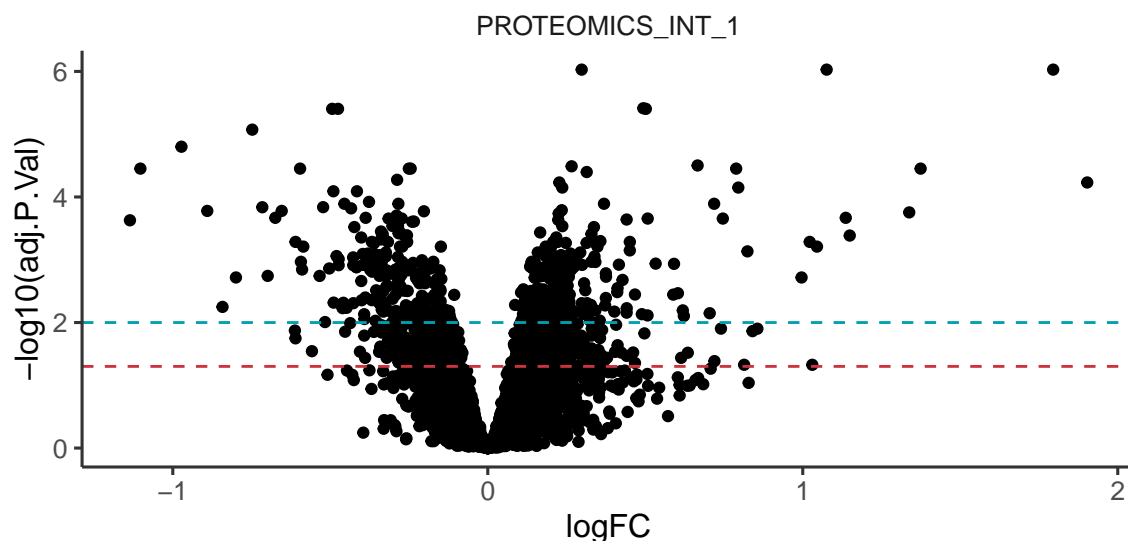
Defective pyroptosis (R-HSA-9710421)

	PROTEOMICS_INT_1
Regulation	Down
FDR	0.021
Av. FC	-0.094
N Genes	17

Protein / Gene level results

Classical differential expression analysis performed on the genes / proteins of every dataset.

Note: Depending on the gene set analysis method used, the approach used to assess differential expression at the gene / protein level may vary to the approach used for the pathway level.



Top up-regulated protein/genes

PROTEOMICS_INT_1

Identifier	logFC	AveExpr	t	P.Value	adj.P.Val	B
Q6VY07	0.2981411	-3.330347	11.256649	0e+00	9.00e-07	13.512228
P10124	1.0758634	-3.436961	10.958151	0e+00	9.00e-07	13.072510
P07093	1.7950301	-3.648968	10.886924	0e+00	9.00e-07	12.965976
Q14526	0.4937650	-3.346909	9.874967	0e+00	3.90e-06	11.382741
P55210	0.5018522	-3.347932	9.674250	0e+00	3.90e-06	11.052700
P22732	0.6661504	-3.371800	8.238839	1e-07	3.15e-05	8.528124
Q9NTJ5	0.2662144	-3.329345	8.174521	1e-07	3.25e-05	8.408046
Q53EL6	0.7885746	-3.393077	8.042928	1e-07	3.54e-05	8.160474
P24821	1.3742473	-3.552465	7.928183	1e-07	3.54e-05	7.942515
Q02880	0.3141782	-3.332768	7.819433	1e-07	4.01e-05	7.734149

Top down-regulated protein/genes

PROTEOMICS_INT_1

Identifier	logFC	AveExpr	t	P.Value	adj.P.Val	B
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Q3B7T1	-0.4939674	-3.347583	-9.591376	0e+00	3.90e-06	10.914831
O43683	-0.4754083	-3.345550	-9.544663	0e+00	3.90e-06	10.836706
P52292	-0.7477266	-3.382343	-9.050093	0e+00	8.50e-06	9.990956
Q15004	-0.9725313	-3.428959	-8.651745	0e+00	1.58e-05	9.284570
Q9Y5A9	-0.2504660	-3.328601	-8.015943	1e-07	3.54e-05	8.109390
P10276	-1.1027702	-3.453823	-8.004244	1e-07	3.54e-05	8.087211
Q12834	-0.5958105	-3.362719	-7.966410	1e-07	3.54e-05	8.015342
Q9UBU8	-0.2447627	-3.328334	-7.910868	1e-07	3.54e-05	7.909456
Q5JSZ5	-0.2878530	-3.331210	-7.651067	2e-07	5.33e-05	7.408110
Q96R06	-0.4900834	-3.350464	-7.326987	4e-07	8.11e-05	6.768764
