

APPENDICES

Appendix 1 | Chapter 3 | Systematic Review | Medline search strategy

- | | |
|--|---|
| 1. first period*.tw. | exp gonadal steroid hormones/ or exp inhibins! |
| 2. menarche/ | 29. exp progesterone/ |
| 3. menarch*.tw. | 30. progest*.tw. |
| 4. 1 or 2 or 3 | 31. menstrual diar*.tw. |
| 5. Menstruation/ | 32. menstrual cycle/ or fertile period/ or follicular phase/ or luteal phase/ |
| 6. Menstrua*.tw. | 33. exp estradiol/ |
| 7. exp Ovulation/ | 34. oestradiol.tw. |
| 8. ovulat* .tw. | 35. oestra*.tw. |
| 9. period "" .tw. | 36. or/12-35 |
| 10. menses.tw. | 37. 4 and 11 and 36 |
| 11. 5 or 6 or 7 or 8 or 9 or 10 | 38. exp adolescent/ |
| 12. exp menstruation disturbances/ | 39. exp schools/ |
| 13. anovulation/ | 40. exp students/ |
| 14. amenorrh*.tw. | 41. exp puberty/ |
| 15. oligomenorrh*.tw. | 42. (student* or school-student* or high-school student*).tw. |
| 16. polymenorrh* .tw. | 43. (school* or high-school*).tw. |
| 17. metromenorrhagia.tw. | 44. (adol* or teen* or juvenile* or youth).tw. |
| 18. metrorrhagia.tw. | 45. pubert*.tw. |
| 19. menorrhagia.tw. | 46. or/38-45 |
| 20. (length* adj4 (menstru* or period*)).tw. | 47. 37 and 46 |
| 21. menstrua length* .tw. | 48. female/ |
| 22. menstrual frequenc. .tw. | 49. girl*.tw. |
| 23. (frequenc* adj4 (menstru* or period*)).tw. | 50. wom?n.tw. |
| 24. periodicity/ or time factors/ | 51. 48 or 49 or 50 |
| 25. duration* .tw. | 52. 47 and 51 |
| 26. flow*.tw. | 53. limit 52 to humans |
| 27. volume*.tw. | |
| 28. hormones/ or gonadal hormones/ or exp corpus luteum hormones/ or | |

*Search strategy used to for MEDLINE. Similar strategies were used for other electronic databases, modified to comply with search rules of each database. * denotes use of truncation*

Appendix 2 | Chapter 3 | Systematic Review | Quality ratings

Question and comments on the quality item	Max Score	Bayer 1940	Dewhurst 1971	Widholm 1971 + 1973	Winter 1973	Widholm 1974	Apter 1978	Brown 1978
Are the study aims, objectives or hypotheses clearly described? (Yes=1; No=0)	1	0	1	1	1	1	1	1
Is the study design clearly stated (e.g. cross-sectional/longitudinal)? (Yes=1; No=0)	1	0	0	1	1	1	1	0
Are the primary outcomes to be measured clearly described in the introduction or methods section? (Yes=1; No/if any are first mentioned in results=0)	1	0	1	1	1	1	1	1
Has the aim or primary outcome been met or answered clearly? (Yes=1; No=0)	1	0	1	1	1	1	1	1
Were sampling procedures sufficiently described? (Yes=2; Partially=1; No/unable to determine=0) (Information on sampling frame (e.g., census, convenience sample and how the sample size was determined and adequacy of sample size)	2	1	1	2	0	2	0	0
Are inclusion/exclusion criteria clearly defined? (Yes=1; No=0)	1	0	0	0	1	0	0	0
Were response rate, compliance rate and/or proportion of dropouts/exclusions reported? (Yes=1; No=0)	1	0	1	1	1	0	0	0
Was the study population sufficiently described (Yes=2; Partially=1; No/unable to determine=0) (Information on participant age, gynaecological age, age at menarche etc.)	2	1	2	1	2	2	2	2
Was the study population representative of the normal/target population? (Yes=1; No/unable to determine=0) (Sample would be representative if they comprised the entire source population, an unselected sample of consecutive patients, or a random community-based sample.)	1	0	1	1	0	0	0	0
Were the techniques/procedures used to obtain the outcome variables valid? (Yes=2; Partially=1; No/unable to determine=0) (i.e. use of validated methods and assays to assess ovulation, ovulatory assessment appropriately timed with menstrual cycle, menstrual cycle recorded using contemporaneous diary)	2	2	2	1	2	1	1	0
Were appropriate and valid definitions used and provided for study outcomes? (Yes=2; Partially=1; No/unable to determine=0) (e.g. definitions of dysmenorrhoea, normal and irregular menstrual cycles, ovulation etc.)	2	0	1	1	2	0	0	1
Has the distribution of the data been described and presented appropriately? (Yes=1; No=0) (i.e. Standard deviations, standard error or confidence intervals presented for normally distributed data, range or inter quartile range presented for non-normally distributed data.)	1	0	1	1	1	1	1	1
Were actual probability values reported? (Yes or not applicable=1; No=0) (Rather than $p < 0.05$, unless $p < 0.001$)	1	0	1	0	1	0	0	1
Were appropriate statistical tests used to assess main outcomes? (Yes or not applicable=1; No=0) (Non-parametric methods should be used for small sample sizes and non-normally distributed data. Where little statistical analysis has been undertaken but there is no evidence of bias, the question should be answered yes.)	1	0	0	1	1	1	1	0
Was missing data accounted for? (Yes or not applicable=1; No=0)	1	1	1	0	1	1	1	0
Score	19	5	14	13	16	12	10	8

Lemarchand -Beraud 1982	MacMahon 1982	Apter & Vihko 1983 +	Metcalf 1983	Flug 1984 + 1985	Read 1984	Borsos 1986 + 1988	Uche 1986	Venturoli 1987	Mijanovic 1990	Wilson 1992	Zhang 2008	Codner 2011	De Sanctis 2014	Sandhya 2015	Max Total Score	Actual Total Score	% of Total score
1	1	1	1	1	0	1	1	1	0	1	1	1	1	1	22	19	86.4
0	0	1	0	1	0	0	0	1	0	0	1	0	1	1	22	10	45.5
1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	22	21	95.5
1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	22	20	90.9
1	2	1	1	2	2	1	1	2	2	1	1	2	2	2	44	29	65.9
0	1	0	1	1	0	0	1	1	1	1	1	1	1	1	22	12	54.5
1	1	0	0	1	0	0	1	1	1	1	1	1	1	1	22	14	63.6
2	2	2	2	2	2	1	1	1	2	2	2	2	2	2	44	39	88.6
0	1	1	0	1	1	1	1	0	1	1	1	1	1	1	22	14	63.6
1	1	1	1	2	1	1	2	1	1	1	2	1	1	1	44	27	61.4
1	1	1	1	1	1	0	2	0	1	1	1	1	1	1	44	19	43.2
1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	22	21	95.5
0	1	1	1	1	0	1	1	0	0	1	1	1	1	1	22	14	63.6
1	0	1	0	0	1	0	0	1	1	1	1	1	1	0	22	13	59.1
0	0	1	0	1	0	1	1	1	1	1	1	1	1	1	22	16	72.7
11	14	14	11	17	11	10	15	13	13	15	17	16	17	16	418	288	68.9

Appendix 3 | Chapter 3 | Systematic Review | Table of excluded studies

Author	Year	Justification
Engle et al.	1934	Unable to extract data for first menarcheal year (inappropriate)
Collett et al.	1954	Participants older than first menarcheal year (irrelevant focus)
Baandes et al.	1968	Unable to extract data for first menarcheal year (inappropriate)
Treloar et al.	1967	Contemporaneously recorded data combined with historically recalled data (inappropriate)
Perez et al.	1970	Unable to retrieve
Richter et al.	1972	Unable to extract data for first menarcheal year (inappropriate)
Winter et al.	1973	Inadequate methods/data
Adamopoulos et al.	1974	Unable to extract data for first menarcheal year (inappropriate)
Presl et al.	1974	Unable to extract data for first menarcheal year (inappropriate)
Sherman et al.	1975	Participants older than first menarcheal year (irrelevant focus)
Widholm et al.	1975	Review article
Kadanoff et al.	1976	Unable to extract data for first menarcheal year (inappropriate)
Lee et al.	1976	Unable to extract data for first menarcheal year (inappropriate)
Penny et al.	1977	Unable to extract data for first menarcheal year (inappropriate)
Widholm et al.	1977	Unable to retrieve
Carol et al.	1978	Unable to extract data for first menarcheal year (inappropriate)
Lemarchand-Beraud et al.	1978	Unable to extract data for first menarcheal year (inappropriate)
Andreoli et al.	1979	Review article
Apter et al.	1980	Duplicate data. Apter and Vihko 1983 and 1984 included.
Billewicz et al.	1980	Unable to extract data for first menarcheal year (inappropriate)
Pezzini et al.	1983	Inadequate methods/data
Apter et al.	1984	Unable to extract data for first menarcheal year (inappropriate)
Mansfield et al.	1984	Review article
World Health Organisation	1986	Unable to extract data for first menarcheal year (inappropriate)
Bernstein et al.	1987	Unable to extract data for first menarcheal year (inappropriate)
Lin et al.	1987	Unable to retrieve
Venturoli et al.	1987	Unable to extract data for first menarcheal year (inappropriate)
Mel'nikova et al.	1991	Unable to retrieve
Odujinrin et al.	1991	Unable to extract data for first menarcheal year (inappropriate)
Vuorento et al.	1992	Unable to extract data for first menarcheal year (inappropriate)
Venturoli et al.	1994	Unable to extract data for first menarcheal year (inappropriate)
Venturoli et al.	1995	Unable to extract data for first menarcheal year (inappropriate)
Apter et al.	1997	Review article
Harlow et al.	1997	Unable to extract data for first menarcheal year (inappropriate)
Spence et al.	1997	Review article
Ibanez et al.	1999	Unable to extract data for first menarcheal year (inappropriate)
Legro et al.	2000	Hormone data not timed with menstrual cycle (inappropriate)
Van Hooff et al.	2000	Unable to extract data for first menarcheal year (inappropriate) and estradiol not displayed in extractable way
Groschl et al.	2001	Unable to extract data for first menarcheal year (inappropriate)

Kurdzielewicz et al	2001	Hormone data not timed with menstrual cycle (inappropriate)
Clavel-Chapelon et al.	2002	Unable to extract data for first menarcheal year (inappropriate)
Crofton et al.	2002	Unable to extract data for first menarcheal year (inappropriate)
Browner-Elhanan et al.	2003	Unable to extract data for first menarcheal year (inappropriate)
Jacks et al.	2005	Unable to extract data for first menarcheal year (inappropriate)
Adams Hillard	2008	Review article
Bandini et al.	2008	Unable to extract data for first menarcheal year (inappropriate)
ACOG Committee on Adolescent Health Care	2009	Review article/guideline
Dorn et al.	2009	Unable to extract data for first menarcheal year (inappropriate)
Negriff et al.	2009	Unable to extract data for first menarcheal year (inappropriate)
Gray et al.	2010	Participants younger than first menarcheal year (irrelevant focus)
Dossus et al.	2012	Inadequate methods/data
Gumanga et al.	2012	Unable to extract data for first menarcheal year (inappropriate)
Hosokawa et al.	2012	Inadequate methods/data
Rigon et al.	2012	Unable to extract data for first menarcheal year (inappropriate)
Barcelos et al.	2013	Unable to extract data for first menarcheal year (inappropriate)
Clancy et al.	2013	Participants older than first menarcheal year (irrelevant focus)
Delara et al.	2013	Unable to extract data for first menarcheal year (inappropriate)
Kordi et al.	2013	Unable to extract data for first menarcheal year (inappropriate)
Lee et al.	2013	Unable to extract data for first menarcheal year (inappropriate)
Tucci et al.	2013	Unable to extract data for first menarcheal year (inappropriate)
Vani et al.	2013	Unable to extract data for first menarcheal year (inappropriate)
Biro et al.	2014	Unable to extract data for first menarcheal year (inappropriate)
Kosibova et al.	2014	Unable to extract data for first menarcheal year (inappropriate)
Abdelmoty et al.	2015	Unable to extract data for first menarcheal year (inappropriate)
Ajay et al.	2015	Unable to extract data for first menarcheal year (inappropriate)
Aribo et al.	2015	Unable to extract data for first menarcheal year (inappropriate)
Glueck et al.	2015	Unable to extract data for first menarcheal year (inappropriate)
Nooh et al.	2015	Participants older than first menarcheal year (irrelevant focus)
Nooh et al.	2016	Participants older than first menarcheal year (irrelevant focus)
Nwokocha et al.	2016	Unable to extract data for first menarcheal year (inappropriate)
Hoppenbrouwers et al.	2016	Unable to extract data for first menarcheal year (inappropriate)
Ravi et al.	2016	Unable to extract data for first menarcheal year (inappropriate)
Sharma et al.	2016	Unable to extract data for first menarcheal year (inappropriate)
Ryan	2017	Review article
Akbarzadeh et al.	2017	Unable to extract data for first menarcheal year (inappropriate)
Adams Hillard	2017	Unable to extract data for first menarcheal year (inappropriate)
Yücel et al.	2018	Unable to extract data for first menarcheal year (inappropriate)
Peña et al.	2018	Unable to extract data for first menarcheal year (inappropriate)
<i>Data were unable to be extracted from the first menarcheal year where data were presented by chronological or bone age as opposed to gynaecological age, or combined across many gynaecological years.</i>		

Appendix 4 | Chapter 5 | The PCOS proteome. PCOS and controls | Table of differential expressed proteins

Accession	Protein	Gene	Unique peptides	Confidence score	Anova (p)	Max fold change	PCOS		Control	
							Mean normalised abundance	SD	Mean normalised abundance	SD
Q9HBV1	Popeye domain-containing protein 3	POPDC3	1	4.2	0.015	∞	59	65	0	0
Q8N635	Meiosis-specific with OB domain-containing protein	MEIOB	1	4.8	0.000	1775.5	187	192	0	0
Q96KW9	Sperm acrosome-associated protein 7	SPACA7	1	10.8	0.046	872.0	1,520	2,756	2	4
Q75534	Cold shock domain-containing protein E1	CSDE1	1	11.0	0.005	36.4	1,341	1,539	37	24
Q9Y3C7	Mediator of RNA polymerase II transcription subunit 31	MED31	1	5.3	0.020	35.0	28,377	40,447	811	1,320
P78325	Disintegrin & metalloproteinase domain-containing protein 8	ADAM8	3	41.0	0.017	24.0	8,178	14,656	341	107
Q9Y657	Spindlin-1	SPIN1	2	14.4	0.034	16.4	11,789	22,663	719	260
Q9UDY6	Tripartite motif-containing protein 10	TRIM10	1	9.4	0.002	16.3	267	127	16	15
O95969	Secretoglobin family 1D member 2	SCGB1D2	2	23.3	0.010	14.9	1,967	2,138	132	144
Q9BXS1	Isopentenyl-diphosphate delta-isomerase 2	IDI2	1	7.4	0.035	14.7	17,240	16,620	1,173	888
Q96EY4	Translation machinery-associated protein 16	TMA16	2	10.6	0.023	10.9	7,185	6,812	656	279
A6NFR6	Uncharacterized protein C5orf60	C5orf60	2	21.0	0.030	9.1	520	889	57	99
Q9HAV7	GrpE protein homolog 1_ mitochondrial	GRPEL1	1	4.5	0.006	9.0	213	206	24	36
Q9P2E3	NFX1-type zinc finger-containing protein 1	ZNFX1	1	9.0	0.016	8.6	20,305	28,285	2,362	1,174
Q6P9G9	Zinc finger protein 449	ZNF449	1	10.7	0.013	8.6	18,260	18,227	2,132	1,230
PoDMQ5	Putative transmembrane protein INAFM2	INAFM2	2	33.7	0.005	8.2	2,223	1,792	270	147
P20020	Plasma membrane calcium-transporting ATPase 1	ATP2B1	2	11.0	0.035	8.2	1,959	1,963	240	149
Q14203*	Dynactin subunit 1	DCTN1	5	67.1	0.024	8.1	28,057	24,638	3,460	2,563
A1A4S6; Q9UNA1*	Rho GTPase-activating protein 10	ARHGAP10	1	19.1	0.000	8.1	4,234	2,210	524	170
P15814	Immunoglobulin lambda-like polypeptide 1	IGLL1	1	27.1	0.035	7.9	1,872	2,199	236	116
Q9UBF9	Myotilin	MYOT	3	25.0	0.011	7.6	1,807	1,351	236	213
Q9UBP4*	Dickkopf-related protein 3	DKK3	17	116.0	0.032	7.5	36,375	40,028	4,820	1,845
Q96L42	Potassium voltage-gated channel subfamily H member 8	KCNH8	1	16.6	0.045	7.4	205	226	28	15
Q9Y3B4	Splicing factor 3B subunit 6	SF3B6	1	10.6	0.035	7.4	17,901	24,066	2,421	756
Q6PEY0	Gap junction beta-7 protein	GJB7	2	14.1	0.001	7.4	686	547	93	39
Q9H4L7	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A containing DEAD/H box 1	SMARCAD1	2	35.2	0.002	6.8	6,218	5,233	915	314
Q9H6Y5	PDZ domain-containing protein MAGIX	MAGIX	1	10.8	0.043	6.6	1,293	1,940	196	60
Q68CR1	Protein sel-1 homolog 3	SEL1L3	2	22.4	0.029	6.5	1,452	1,572	223	103
Q9H741	UPF0454 protein C12orf49	C12orf49	1	5.1	0.045	6.4	1,514	2,761	238	397
O95947	T-box transcription factor TBX6	TBX6	1	4.6	0.004	6.2	73	54	12	27

Q9ULU4	Protein kinase C-binding protein 1	ZMYND8	4	21.7	0.031	6.2	7,170	8,154	1,161	640
Q8N6Ro	eEF1A lysine and N-terminal methyltransferase	EEF1AKNMT	1	13.7	0.025	5.7	1,482	1,257	261	177
P23246	Splicing factor_ proline- and glutamine-rich	SFPQ	3	29.2	0.011	5.2	8,108	6,452	1,557	444
O95490	Adhesion G protein-coupled receptor L2	ADGRL2	1	27.3	0.017	5.1	13,867	13,018	2,722	536
Q8N9L7	Putative uncharacterized protein FLJ36925	5 SV	1	3.9	0.019	5.0	410	396	81	48
Q7Z794*	Keratin_type II cytoskeletal 1b	KRT77	2	73.5	0.030	5.0	159	171	32	51
Q13217	DnaJ homolog subfamily C member 3	DNAJC3	2	9.3	0.009	4.9	9,921	10,473	2,010	649
Q96BQ1	Protein FAM3D	FAM3D	6	35.9	0.044	4.8	5,451	4,437	1,139	1,289
P01189	Pro-opiomelanocortin	POMC	2	10.6	0.032	4.8	36,489	41,088	7,645	3,847
Q5VWJ9	Sorting nexin-30	SNX30	2	32.8	0.044	4.6	792	960	172	176
P47224	Guanine nucleotide exchange factor MSS4	RABIF	1	4.9	0.011	4.6	1,566	1,423	342	386
Q92830	Histone acetyltransferase KAT2A	KAT2A	3	23.5	0.007	4.6	139	80	30	23
O95164	Ubiquitin-like protein 3	UBL3	2	22.8	0.021	4.5	1,058	860	233	170
Q86UN3	Reticulon-4 receptor-like 2	RTN4RL2	25	212.4	0.007	4.4	39,085	35,541	8,961	5,404
B1AJZ9	Forkhead-associated domain-containing protein 1	FHAD1	4	30.9	0.006	4.3	865	549	199	127
Q9HoW8	Protein SMG9	SMG9	2	23.6	0.003	4.2	503	337	119	65
Q969S9	Ribosome-releasing factor 2_mitochondrial	GFM2	1	10.9	0.024	4.2	878	917	208	175
Q15543*	Transcription initiation factor TFIID subunit 13	TAF13	4	18.7	0.038	3.9	4,336	5,195	1,098	441
Q9BRL6	Serine/arginine-rich splicing factor 8	SRSF8	1	11.4	0.047	3.9	730	624	187	199
Q9H4S2	GS homeobox 1	GSX1	2	9.7	0.005	3.9	1,180	607	304	311
P17858*	ATP-dependent 6-phosphofructokinase_liver type	PFKL	5	48.0	0.048	3.7	4,161	4,062	1,112	738
Q8NGJ7	Olfactory receptor 51A2	OR51A2	1	5.7	0.044	3.7	3,919	2,840	1,063	1,031
Q07699	Sodium channel subunit beta-1	SCN1B	1	6.9	0.016	3.4	415	304	121	88
Q16832	Discoidin domain-containing receptor 2	DDR2	8	77.8	0.048	3.4	9,169	8,055	2,687	2,259
Q01082*	Spectrin beta chain_non-erythrocytic 1	SPTBN1	12	86.7	0.005	3.4	2,557	1,369	751	143
Q9UGI8	Testin	TES	5	65.4	0.004	3.4	5,676	2,493	1,683	1,012
Q86SH2	Zygote arrest protein 1	ZAR1	5	42.5	0.031	3.3	5,412	3,308	1,620	1,425
Q04721*	Neurogenic locus notch homolog protein 2	NOTCH2	15	132.9	0.029	3.3	18,531	17,530	5,553	5,881
P01877	Immunoglobulin heavy constant alpha 2	IGHA2	16	223.1	0.022	3.3	30,497	25,878	9,300	7,031
Q8NB42	Zinc finger protein 527	ZNF527	2	20.1	0.018	3.3	5,529	3,630	1,693	1,687
P0CF74; AoM8Q6	Immunoglobulin lambda constant 6	IGLC6	1	123.8	0.010	3.2	1,108	557	349	195
Q16557; P11464	Pregnancy-specific beta-1-glycoprotein 3	PSG3	2	11.1	0.006	3.2	1,470	764	465	108
O14618*	Copper chaperone for superoxide dismutase	CCS	1	16.2	0.025	3.1	387	183	123	114
Q86YB8*	ERO1-like protein beta	ERO1B	3	46.2	0.016	3.1	3,494	2,174	1,137	414
O43291	Kunitz-type protease inhibitor 2	SPINT2	20	186.2	0.032	3.0	30,628	21,157	10,156	3,389
Q9Y623*	Myosin-4	MYH4	3	39.2	0.006	3.0	2,904	1,577	977	397
Q9NVJ2	ADP-ribosylation factor-like protein 8B	ARL8B	2	16.9	0.023	2.9	1,408	1,015	490	165

Q15751	Probable E3 ubiquitin-protein ligase HERC1	HERC1	6	29.2	0.045	2.9	1,069	935	375	105
P27105	Erythrocyte band 7 integral membrane protein	STOM	18	189.6	0.000	2.7	22,422	8,983	8,203	1,617
AoAoC4DH29	Immunoglobulin heavy variable 1-3	IGHV1-3	1	26.8	0.022	2.7	806	450	296	378
Q9H7Z3	Protein NRDE2 homolog	NRDE2	5	32.4	0.024	2.7	19,047	10,004	7,093	2,435
O43320	Fibroblast growth factor 16	FGF16	2	10.2	0.013	2.6	41,281	19,620	15,744	5,665
Q9GZP4	PITH domain-containing protein 1	PITHD1	6	50.8	0.009	2.6	1,030	513	400	110
P01906	HLA class II histocompatibility antigen_ DQ alpha 2 chain	HLA-DQA2	1	11.2	0.048	2.5	6,957	5,529	2,738	3,133
Q9NWS0	PIH1 domain-containing protein 1	PIH1D1	1	5.6	0.036	2.5	1,636	1,365	650	355
Q53GA4	Pleckstrin homology-like domain family A member 2	PHLDA2	1	16.4	0.000	2.4	206	40	87	26
Q9UQ53	Alpha-1_3-mannosyl-glycoprotein 4-beta-N-acetylglucosaminyltransferase B	MGAT4B	3	15.9	0.034	2.4	845	456	359	106
Q9Y5S8*	NADPH oxidase 1	NOX1	3	16.9	0.040	2.3	2,263	1,527	991	298
Q9Y608	Leucine-rich repeat flightless-interacting protein 2	LRRFIP2	5	55.5	0.004	2.2	7,006	2,582	3,140	1,047
P16402; Q02539	Histone H1.3	HIST1H1D	3	95.1	0.035	2.2	8,140	1,493	3,683	2,272
P04745	Alpha-amylase 1	AMY1A	60	981.0	0.038	2.2	121,676	46,107	55,232	31,901
Q9NS64	Protein reprimo	RPRM	1	4.3	0.036	2.2	1,444	950	671	315
P07339*	Cathepsin D	CTSD	51	411.2	0.023	2.2	36,932	19,643	17,171	6,931
P11021*	Endoplasmic reticulum chaperone BiP	HSPA5	70	677.0	0.014	2.1	48,570	22,777	23,051	6,432
Q02410	Amyloid-beta A4 precursor protein-binding family A member 1	APBA1	3	23.4	0.038	2.1	5,584	3,216	2,669	644
Q9HCJ0	Trinucleotide repeat-containing gene 6C protein	TNRC6C	2	35.6	0.019	2.1	763	427	365	114
Q02543	60S ribosomal protein L18a	RPL18A	1	5.1	0.049	2.0	1,806	890	892	462
Q8TD57	Dynein heavy chain 3_ axonemal	DNAH3	9	56.8	0.035	2.0	4,337	2,210	2,172	965
Q8IUY3	GRAM domain-containing protein 2A	GRAMD2A	1	3.6	0.029	2.0	1,393	452	701	396
AoAoB4J1Vo	Immunoglobulin heavy variable 3-15	IGHV3-15	6	56.6	0.009	2.0	19,038	5,785	9,626	3,661
O14578	Citron Rho-interacting kinase	CIT	3	21.6	0.015	2.0	4,265	1,573	2,175	1,071
A5LHX3	Proteasome subunit beta type-11	PSMB11	1	5.0	0.008	1.9	503	225	262	58
P48163	NADP-dependent malic enzyme	ME1	1	11.3	0.043	1.9	296	148	155	89
Q9BZS1	Forkhead box protein P3	FOXP3	1	4.6	0.031	1.9	763	337	406	399
A6NCM1	IQ and AAA domain-containing protein 1-like	IQCA1L	2	11.0	0.027	1.9	700	308	375	135
AoAoB4J1Yg	Immunoglobulin heavy variable 3-72	IGHV3-72	1	40.6	0.012	1.8	4,607	1,355	2,497	986
P43251	Biotinidase	BTD	25	195.3	0.009	1.8	22,702	4,805	12,347	4,900
Q8N1N4*	Keratin_type II cytoskeletal 78	KRT78	34	383.6	0.045	1.8	14,783	6,058	8,103	5,927
AoAVF1	Intraflagellar transport protein 56	TTC26	2	31.9	0.033	1.8	1,316	243	727	335
P00749*	Urokinase-type plasminogen activator	PLAU	46	391.5	0.035	1.8	36,615	14,189	20,329	8,078
P01766	Immunoglobulin heavy variable 3-13	IGHV3-13	1	46.9	0.023	1.8	2,345	477	1,314	538
Q7Z4G1	COMM domain-containing protein 6	COMM6	1	9.4	0.018	1.8	522	192	295	86
P16278*	Beta-galactosidase	GLB1	31	357.9	0.010	1.8	18,479	3,420	10,474	3,789

Q5VSP4	Putative lipocalin 1-like protein 1	LCN1P1	2	34.1	0.032	1.7	1,565	515	901	809
Q32M84	BTB/POZ domain-containing protein 16	BTBD16	5	29.8	0.041	1.7	6,606	2,410	3,821	2,449
Q9Y6N8	Cadherin-10	CDH10	1	26.4	0.025	1.7	986	273	575	285
Q86VY4	Testis-specific Y-encoded-like protein 5	TSPYL5	1	9.6	0.006	1.7	837	191	500	180
P07205*	Phosphoglycerate kinase 2	PGK2	10	151.2	0.040	1.7	4,684	1,456	2,826	1,371
Q8WWP7	GTPase IMAP family member 1	GIMAP1	2	9.4	0.005	1.6	985	168	605	175
Q43175*	D-3-phosphoglycerate dehydrogenase	PHGDH	8	56.7	0.021	1.6	2,961	768	1,825	691
P01602	Immunoglobulin kappa variable 1-5	IGKV1-5	5	41.5	0.046	1.6	21,174	8,554	13,233	3,337
P55957*	BH3-interacting domain death agonist	BID	3	38.6	0.025	1.6	3,587	1,207	2,289	338
P20073	Annexin A7	ANXA7	7	66.4	0.046	1.6	2,865	1,045	1,844	241
Q9BZR6	Reticulon-4 receptor	RTN4R	3	27.7	0.002	1.6	651	104	419	84
Q12913*	Receptor-type tyrosine-protein phosphatase eta	PTPRJ	39	388.3	0.039	1.4	27,375	7,272	18,953	4,880
P53634*	Dipeptidyl peptidase 1	CTSC	36	386.3	0.048	1.4	13,162	3,639	9,215	1,884
Q8WUU4	Zinc finger protein 296	ZNF296	4	18.7	0.020	-1.2	1,379	177	1,717	247
Q15746*	Myosin light chain kinase_ smooth muscle	MYLK	34	276.5	0.008	-1.3	32,088	3,370	41,979	7,131
P22105	Tenascin-X	TNXB	268	2563.6	0.018	-1.3	96,877	26,316	127,683	10,552
Q01974*	Tyrosine-protein kinase transmembrane receptor ROR2	ROR2	13	76.4	0.032	-1.4	7,525	1,979	10,281	1,890
O95971	CD160 antigen	CD160	7	67.2	0.040	-1.4	2,254	390	3,168	964
P62993*	Growth factor receptor-bound protein 2	GRB2	12	102.5	0.028	-1.4	3,325	1,025	4,740	1,041
P34931*	Heat shock 70 kDa protein 1-like	HSPA1L	2	169.8	0.023	-1.5	2,777	622	4,073	1,108
Q3KP22	Membrane-anchored junction protein	MAJIN	1	10.3	0.040	-1.5	2,136	471	3,150	975
Q53FA7	Quinone oxidoreductase PIG3	TP53I3	13	113.0	0.037	-1.5	2,155	610	3,229	924
Q7Z3B1	Neuronal growth regulator 1	NEGR1	41	335.5	0.038	-1.5	42,270	8,045	63,747	20,010
Q9UQN3*	Charged multivesicular body protein 2b	CHMP2B	8	69.6	0.010	-1.5	3,118	536	4,705	1,242
Q494V2	Cilia- and flagella-associated protein 100	CFAP100	5	38.6	0.024	-1.5	30,708	11,027	47,261	8,062
Q6UX73	UPF0764 protein C16orf89	C16orf89	9	84.4	0.031	-1.5	2,550	485	3,928	1,295
O14498	Ig superfamily containing leucine-rich repeat protein	ISLR	3	25.4	0.013	-1.5	364	83	564	160
Q9NQ31	A-kinase-interacting protein 1	AKIP1	2	34.3	0.043	-1.6	468	149	726	239
P22392*	Nucleoside diphosphate kinase B	NME2	3	95.8	0.032	-1.6	3,315	683	5,146	1,736
Q9H223	EH domain-containing protein 4	EHD4	12	90.5	0.002	-1.6	1,060	228	1,671	297
Q9H257	Caspase recruitment domain-containing protein 9	CARD9	2	10.4	0.028	-1.6	1,081	465	1,717	404
Q6P1K2	Polyamine-modulated factor 1	PMF1	6	30.3	0.028	-1.6	3,100	1,259	4,933	1,435
Q3ZCM7*	Tubulin beta-8 chain	TUBB8	2	57.4	0.029	-1.6	96	41	152	31
Q58FF6	Putative heat shock protein HSP 90-beta 4	HSP90AB4P	1	27.0	0.031	-1.6	635	319	1,011	186
P57087*	Junctional adhesion molecule B	JAM2	3	15.0	0.033	-1.6	1,994	344	3,188	1,237
Q15555; Q15691*	Microtubule-associated protein RP/EB family member 2	MAPRE2	3	37.9	0.041	-1.6	466	192	751	210
P10643*	Complement component C7	C7	41	348.1	0.040	-1.6	15,269	2,774	24,843	11,091
P68036	Ubiquitin-conjugating enzyme E2 L3	UBE2L3	1	11.3	0.039	-1.6	1,778	879	2,897	770

P02458*	Collagen alpha-1(II) chain	COL2A1	6	54.1	0.033	-1.6	30,887	6,519	50,431	22,241
O43719	HIV Tat-specific factor 1	HTATSF1	7	38.5	0.019	-1.7	2,831	602	4,695	1,446
Q5T1S8	Noncompact myelin-associated protein	NCMAP	2	21.7	0.030	-1.7	4,786	1,843	7,984	2,780
Q8NEJ9	Neuroguidin	NGDN	3	14.0	0.016	-1.7	232	103	387	46
P62834*	Ras-related protein Rap-1A	RAP1A	1	68.6	0.012	-1.7	1,567	459	2,647	935
O75369*	Filamin-B	FLNB	65	565.3	0.046	-1.7	21,703	8,870	37,410	17,060
Q14CN4*	Keratin_type II cytoskeletal 72	KRT72	6	117.1	0.026	-1.7	8,270	3,487	14,279	4,366
P36952	Serpin B5	SERPINB5	14	210.7	0.009	-1.7	1,152	346	2,002	651
Q8N339	Metallothionein-1M	MT1M	3	13.8	0.017	-1.8	185	40	326	145
P28072*	Proteasome subunit beta type-6	PSMB6	3	22.0	0.020	-1.8	363	68	642	243
P15531*	Nucleoside diphosphate kinase A	NME1	1	61.3	0.022	-1.8	287	69	509	206
O43790*	Keratin_type II cuticular Hb6	KRT86	2	160.3	0.050	-1.8	243	45	436	208
Q6DN03; Q6DRA6	Putative histone H2B type 2-C	HIST2H2BC	1	18.1	0.033	-1.8	122	53	222	75
Q5VT79	Annexin A8-like protein 1	ANXA8L1	14	134.0	0.033	-1.8	21,321	5,418	38,933	18,024
Q8NC51	Plasminogen activator inhibitor 1 RNA-binding protein	SERBP1	10	92.5	0.009	-1.8	1,346	518	2,461	612
Q9ULL5	Proline-rich protein 12	PRR12	4	27.4	0.014	-1.8	607	149	1,111	444
P41218	Myeloid cell nuclear differentiation antigen	MNDA	15	102.4	0.025	-1.9	2,020	581	3,773	2,181
P27487	Dipeptidyl peptidase 4	DPP4	54	597.9	0.010	-1.9	139,068	43,510	262,570	106,225
P29966*	Myristoylated alanine-rich C-kinase substrate	MARCKS	11	116.5	0.007	-1.9	3,578	967	6,802	2,465
P24522	Growth arrest & DNA damage-inducible protein GADD45alpha	GADD45A	1	5.0	0.040	-1.9	204	267	389	146
O95084	Serine protease 23	PRSS23	2	27.7	0.011	-1.9	1,032	257	1,979	890
O15231	Zinc finger protein 185	ZNF185	27	236.3	0.011	-1.9	9,355	3,285	17,979	6,113
O75264	Small integral membrane protein 24	SMIM24	4	35.3	0.028	-1.9	2,906	930	5,598	2,227
P13667	Protein disulfide-isomerase A4	PDIA4	11	77.1	0.006	-1.9	1,234	365	2,386	839
O15173	Membrane-associated progesterone receptor component 2	PGRMC2	3	21.1	0.015	-1.9	181	146	350	110
O75347	Tubulin-specific chaperone A	TBCA	6	43.3	0.011	-1.9	1,477	425	2,868	1,178
P54289*	Voltage-dependent calcium channel subunit alpha-2/delta-1	CACNA2D1	7	56.4	0.048	-1.9	1,059	163	2,058	1,090
P00751*	Complement factor B	CFB	59	556.2	0.038	-2.0	53,113	11,636	104,459	71,184
Q13332*	Receptor-type tyrosine-protein phosphatase S	PTPRS	50	553.6	0.045	-2.0	7,877	1,245	15,517	8,278
Q865G5	Protein S100-A7A	S100A7A	5	102.5	0.019	-2.0	1,369	364	2,702	1,241
Q5VTE0; P68104	Putative elongation factor 1-alpha-like 3	EEF1A1P5	32	251.3	0.039	-2.0	48,901	9,597	97,879	64,107
O75223	Gamma-glutamylcyclotransferase	GGCT	20	266.4	0.017	-2.0	22,822	9,498	46,079	20,718
Q14764	Major vault protein	MVP	14	106.8	0.019	-2.0	4,601	1,734	9,332	4,255
Q8TBY8	Polyamine-modulated factor 1-binding protein 1	PMFBP1	13	120.8	0.008	-2.1	4,904	1,487	10,070	3,816
P48048	ATP-sensitive inward rectifier potassium channel 1	KCNJ1	3	14.8	0.016	-2.1	814	315	1,696	906
O92764*	Keratin_type I cuticular Ha5	KRT35	6	71.2	0.031	-2.1	44,111	13,308	91,952	53,432
Q03403	Trefoil factor 2	TFF2	9	57.6	0.049	-2.1	34,540	6,196	72,179	42,197

Q92765*	Secreted frizzled-related protein 3	FRZB	3	18.8	0.049	-2.1	3,003	1,144	6,294	3,476
Q05209*	Tyrosine-protein phosphatase non-receptor type 12	PTPN12	4	23.5	0.003	-2.1	2,617	1,123	5,489	1,449
P12259*	Coagulation factor V	F5	19	146.6	0.017	-2.1	3,256	820	6,831	3,370
P12956	X-ray repair cross-complementing protein 6	XRCC6	4	35.8	0.003	-2.1	1,030	365	2,187	709
Q6E0U4	Dermokine	DMKN	6	45.2	0.035	-2.1	1,597	1,417	3,413	1,963
O43852	Calumenin	CALU	23	210.1	0.044	-2.1	8,067	5,619	17,271	8,303
O43405	Cochlin	COCH	4	37.1	0.015	-2.1	3,051	1,566	6,540	3,568
O15484*	Calpain-5	CAPN5	1	17.4	0.037	-2.1	351	172	754	439
P62328	Thymosin beta-4	TMSB4X	3	43.3	0.030	-2.1	5,317	2,582	11,432	5,041
Q03154	Aminoacylase-1	ACY1	31	323.0	0.017	-2.2	131,335	31,429	285,371	171,361
Q13200*	26S proteasome non-ATPase regulatory subunit 2	PSMD2	2	15.0	0.023	-2.2	247	148	538	219
O95497	Pantetheinase	VNN1	12	115.2	0.038	-2.2	36,897	10,849	80,651	52,523
P67809	Nuclease-sensitive element-binding protein 1	YBX1	6	63.3	0.011	-2.2	5,182	1,641	11,356	5,789
Q00973	Beta-1_4 N-acetylgalactosaminyltransferase 1	B4GALNT1	1	10.4	0.028	-2.2	384	136	849	507
P25325*	3-mercaptopyruvate sulfurtransferase	MPST	7	52.7	0.003	-2.2	1,385	430	3,099	1,471
P60981	Dextrin	DSTN	6	49.0	0.044	-2.2	1,710	253	3,840	2,386
P20396	Pro-thyrotropin-releasing hormone	TRH	3	18.6	0.010	-2.3	2,270	531	5,119	2,830
P14854	Cytochrome c oxidase subunit 6B1	COX6B1	6	57.0	0.011	-2.3	10,210	2,691	23,093	12,802
P07954	Fumarate hydratase_mitochondrial	FH	3	19.7	0.027	-2.3	226	132	515	242
Q8NEG2	Uncharacterized protein C7orf57	C7orf57	3	14.8	0.032	-2.3	333	162	761	477
P24298*	Alanine aminotransferase 1	GPT	3	23.2	0.039	-2.3	4,545	2,474	10,560	5,964
Q92820*	Gamma-glutamyl hydrolase	GGH	31	317.8	0.043	-2.3	38,415	17,706	89,675	63,934
P31151	Protein S100-A7	S100A7	7	141.2	0.008	-2.3	12,644	2,930	29,517	13,810
Q8N126	Cell adhesion molecule 3	CADM3	8	76.5	0.050	-2.3	5,779	1,531	13,500	9,581
Q9Y653	Adhesion G-protein coupled receptor G1	ADGRG1	13	90.1	0.020	-2.3	5,951	2,637	13,917	9,130
Q9NWD9	Protein BEX4	BEX4	1	4.9	0.028	-2.4	486	111	1,150	990
Q04759; A5PLN9*	Protein kinase C theta type	PRKCQ	8	71.1	0.044	-2.4	5,548	3,426	13,145	8,801
Q9NP79	Vacuolar protein sorting-associated protein VTA1 homolog	VTA1	15	135.1	0.046	-2.4	3,433	885	8,145	5,879
P08195	4F2 cell-surface antigen heavy chain	SLC3A2	33	260.4	0.042	-2.4	8,683	3,715	20,706	14,143
P49721*	Proteasome subunit beta type-2	PSMB2	2	21.3	0.019	-2.4	1,012	309	2,415	1,380
Q8TCT8	Signal peptide peptidase-like 2A	SPPL2A	3	34.0	0.015	-2.4	1,338	709	3,195	1,731
Q9Y3B9	RRP15-like protein	RRP15	3	15.2	0.017	-2.4	3,268	942	7,805	5,055
Q14204*	Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	5	44.4	0.028	-2.4	912	605	2,206	1,020
Q6ZTA4	Tripartite motif-containing protein 67	TRIM67	1	9.2	0.001	-2.4	2,261	440	5,509	2,295
Q86WBo	Nuclear-interacting partner of ALK	ZC3HC1	2	26.0	0.025	-2.4	473	224	1,155	613
Q96C23*	Aldose 1-epimerase	GALM	8	75.0	0.046	-2.5	40,683	22,907	99,863	73,405
P18065	Insulin-like growth factor-binding protein 2	IGFBP2	32	242.8	0.007	-2.5	9,944	6,311	24,587	9,905
Q6UY11	Protein delta homolog 2	DLK2	4	34.2	0.040	-2.5	3,771	628	9,330	7,987

P08670; P12036*	Vimentin	VIM	41	537.0	0.017	-2.5	21,436	5,251	53,110	28,574
P07910	Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC	3	62.5	0.047	-2.5	692	362	1,730	1,086
P54727	UV excision repair protein RAD23 homolog B	RAD23B	3	17.7	0.035	-2.5	804	525	2,018	1,082
P31942	Heterogeneous nuclear ribonucleoprotein H3	HNRNPH3	3	14.5	0.014	-2.5	321	97	808	581
P07108	Acyl-CoA-binding protein	DBI	6	67.3	0.049	-2.6	17,286	7,023	44,246	36,417
Q9HBB8	Cadherin-related family member 5	CDHR5	6	71.3	0.027	-2.6	2,332	1,352	6,014	3,733
Q9H6X2	Anthrax toxin receptor 1	ANTXR1	6	61.8	0.031	-2.6	21,961	7,662	56,884	42,602
P07711*	Cathepsin L1	CTSL	25	238.8	0.048	-2.6	39,399	13,720	102,433	84,197
P04196*	Histidine-rich glycoprotein	HRG	22	176.5	0.031	-2.6	8,477	3,534	22,115	15,060
Q02878	60S ribosomal protein L6	RPL6	1	11.9	0.018	-2.7	908	783	2,412	1,208
P07225*	Vitamin K-dependent protein S	PROS1	2	21.1	0.008	-2.7	3,184	884	8,468	5,889
Q15643	Thyroid receptor-interacting protein 11	TRIP11	7	50.9	0.010	-2.7	3,589	2,051	9,557	5,225
P30613*	Pyruvate kinase PKLR	PKLR	5	48.6	0.029	-2.7	2,300	1,795	6,181	3,333
O00526	Uroplakin-2	UPK2	1	13.1	0.045	-2.7	4,520	1,029	12,350	8,410
Q5T440	Putative transferase CAF17_mitochondrial	IBA57	2	15.0	0.046	-2.8	265	167	731	443
P40189*	Interleukin-6 receptor subunit beta	IL6ST	37	275.2	0.018	-2.8	34,881	18,584	96,838	70,022
Q8N944	APC membrane recruitment protein 3	AMER3	1	4.5	0.046	-2.8	1,296	756	3,632	2,498
P04792*	Heat shock protein beta-1	HSPB1	18	266.8	0.027	-2.8	20,617	11,964	58,009	32,134
Q5KU26	Collectin-12	COLEC12	54	464.4	0.003	-2.8	20,897	7,064	59,425	31,826
P48735*	Isocitrate dehydrogenase [NADP]_mitochondrial	IDH2	4	21.0	0.020	-2.9	3,293	1,612	9,393	6,678
O95185	Netrin receptor UNC5C	UNC5C	4	28.6	0.007	-2.9	7,925	5,065	22,610	9,346
Q9Y2G5	GDP-fucose protein O-fucosyltransferase 2	POFUT2	2	20.2	0.013	-2.9	12,345	4,403	35,315	21,423
P61244*	Protein max	MAX	9	41.1	0.029	-2.9	2,859	2,284	8,190	6,403
O75874*	Isocitrate dehydrogenase [NADP] cytoplasmic	IDH1	33	239.5	0.001	-2.9	8,439	2,022	24,436	11,104
Q9H2M3*	S-methylmethionine-homocysteine S-methyltransferase BHMT2	BHMT2	12	125.2	0.000	-2.9	8,224	1,800	23,835	6,630
P20810*	Calpastatin	CAST	49	488.9	0.035	-2.9	13,769	5,278	40,050	27,875
Q04828; P52895	Aldo-keto reductase family 1 member C1	AKR1C1	1	15.3	0.024	-2.9	301	409	878	527
O60259*	Kallikrein-8	KLK8	3	19.9	0.039	-2.9	1,210	877	3,539	1,908
Q9H9H4*	Vacuolar protein sorting-associated protein 37B	VPS37B	2	16.9	0.025	-3.0	584	286	1,738	1,564
O14907	Tax1-binding protein 3	TAX1BP3	1	7.0	0.030	-3.0	1,187	1,117	3,550	2,696
Q9BXL3	Cytosolic 5'-nucleotidase 1A	NT5C1A	4	19.6	0.016	-3.0	504	238	1,507	1,167
Q7Z692	Carcinoembryonic antigen-related cell adhesion molecule 19	CEACAM19	1	5.6	0.032	-3.0	726	270	2,196	2,239
Q9ULC0	Endomucin	EMCN	1	19.6	0.037	-3.0	1,271	263	3,858	3,978
Q96FW1	Ubiquitin thioesterase OTUB1	OTUB1	4	32.7	0.026	-3.1	2,620	1,255	8,060	6,641
P68363; Q9BQE3*	Tubulin alpha-1B chain	TUBA1B	7	181.2	0.005	-3.1	5,081	2,101	15,677	10,386
Q15007	Pre-mRNA-splicing regulator WTAP	WTAP	5	25.1	0.012	-3.1	1,485	682	4,637	3,453

Q9NZA1	Chloride intracellular channel protein 5	CLIC5	8	57.2	0.049	-3.1	4,281	1,677	13,443	11,396
P28482	Mitogen-activated protein kinase 1	MAPK1	1	4.1	0.026	-3.2	265	266	845	519
A7E2U8	UPF0602 protein C4orf47	C4orf47	1	7.9	0.036	-3.2	920	280	2,986	2,735
Q06323*	Proteasome activator complex subunit 1	PSME1	5	57.8	0.022	-3.3	1,721	661	5,598	3,447
P00709	Alpha-lactalbumin	LALBA	1	4.4	0.012	-3.3	53	30	173	136
Q8TAC1	Rieske domain-containing protein	RFESD	2	14.8	0.014	-3.3	810	218	2,671	1,824
P04275*	von Willebrand factor	VWF	6	40.9	0.008	-3.3	2,022	1,130	6,723	4,029
Q12889	Oviduct-specific glycoprotein	OVGP1	20	145.9	0.013	-3.3	3,902	1,911	12,980	9,856
Q969J2	Zinc finger protein with KRAB and SCAN domains 4	ZKSCAN4	3	19.8	0.035	-3.3	1,301	475	4,343	3,603
Q9UHV9	Prefoldin subunit 2	PFDN2	4	33.1	0.039	-3.4	11,019	5,645	36,918	33,744
Q8WUD1	Ras-related protein Rab-2B	RAB2B	1	41.8	0.010	-3.4	7,184	2,108	24,081	17,889
Q96FE7	Phosphoinositide-3-kinase-interacting protein 1	PIK3IP1	14	125.9	0.044	-3.4	127,946	84,632	434,516	411,873
P40261	Nicotinamide N-methyltransferase	NNMT	1	4.8	0.028	-3.4	1,592	1,227	5,469	5,136
P05387; P05386	60S acidic ribosomal protein P2	RPLP2	6	47.4	0.004	-3.5	996	651	3,451	1,815
P01860*	Immunoglobulin heavy constant gamma 3	IGHG3	27	514.0	0.005	-3.5	70,427	20,290	245,293	185,445
Q6UXB4	C-type lectin domain family 4 member G	CLEC4G	12	114.6	0.024	-3.5	11,634	6,094	41,126	38,365
Q9Y279	V-set and immunoglobulin domain-containing protein 4	VSIG4	7	57.4	0.003	-3.5	4,152	1,885	14,732	7,810
Q9NRX4	14 kDa phosphohistidine phosphatase	PHPT1	10	101.4	0.044	-3.7	15,032	5,925	55,376	52,493
Q8N488	RING1 and YY1-binding protein	RYBP	1	5.4	0.008	-3.7	57	50	209	139
P31939*	Bifunctional purine biosynthesis protein PURH	ATIC	5	42.5	0.039	-3.8	519	378	1,950	1,742
Q9Y247	Protein FAM50B	FAM50B	3	38.9	0.007	-3.8	3,071	1,455	11,650	10,842
P07196*	Neurofilament light polypeptide	NEFL	14	158.9	0.010	-3.8	1,590	466	6,049	5,189
P17275	Transcription factor jun-B	JUNB	1	14.9	0.044	-4.0	2,073	667	8,377	8,976
Q7Z419	E3 ubiquitin-protein ligase RNF144B	RNF144B	2	9.8	0.042	-4.1	936	744	3,870	4,160
P01599	Immunoglobulin kappa variable 1-17	IGKV1-17	4	63.5	0.048	-4.2	1,738	1,158	7,243	6,726
Q6PIZ9	T-cell receptor-associated transmembrane adapter 1	TRAT1	1	11.8	0.042	-4.2	1,479	1,572	6,186	6,350
Q8NI99	Angiopoietin-related protein 6	ANGPTL6	9	75.1	0.025	-4.3	6,892	1,669	29,493	28,441
Q43829	Zinc finger and BTB domain-containing protein 14	ZBTB14	1	5.0	0.020	-4.3	404	581	1,733	1,273
Q05655*	Protein kinase C delta type	PRKCD	2	15.2	0.002	-4.3	1,226	914	5,304	2,049
O15162	Phospholipid scramblase 1	PLSCR1	3	18.8	0.044	-4.4	590	430	2,584	2,639
Q96EU7	C1GALT1-specific chaperone 1	C1GALT1C1	4	33.8	0.011	-4.4	652	453	2,886	2,902
Q9Y6D5	Brefeldin A-inhibited guanine nucleotide-exchange protein 2	ARFGEF2	1	12.7	0.002	-4.5	662	296	2,991	1,900
Q96NH3; Q99665	Protein broad-minded	TBC1D32	3	37.6	0.015	-4.5	5,576	2,434	25,270	23,453
Q8IX03	Protein KIBRA	WWC1	3	21.6	0.037	-4.6	1,235	467	5,619	5,834
Q8NCI6*	Beta-galactosidase-1-like protein 3	GLB1L3	2	15.3	0.048	-4.6	3,569	2,097	16,265	14,312
O60894	Receptor activity-modifying protein 1	RAMP1	1	5.3	0.009	-4.8	1,273	898	6,103	5,503
Q16378	Proline-rich protein 4	PRR4	5	26.2	0.000	-4.8	3,161	748	15,324	8,044

Q8NHY5	Checkpoint protein HUS1B	HUS1B	1	8.2	0.029	-4.9	3,035	2,820	14,754	12,766
Q96JB1	Dynein heavy chain 8_ axonemal	DNAH8	1	14.2	0.009	-4.9	8,906	3,532	43,857	36,324
P22307*	Non-specific lipid-transfer protein	SCP2	6	58.0	0.036	-5.0	9,899	7,165	49,917	48,361
Q9Y2V2	Calcium-regulated heat-stable protein 1	CARHSP1	1	6.3	0.031	-5.1	108	205	551	474
Q9U1I2	ATPase inhibitor_ mitochondrial	ATP5IF1	1	4.0	0.020	-5.1	1,031	663	5,250	5,309
Q8WWU7	Intelectin-2	ITLN2	4	30.1	0.002	-5.2	628	337	3,260	2,229
Q15109	Advanced glycosylation end product-specific receptor	AGER	1	17.6	0.049	-5.3	331	212	1,761	2,707
Q32M92	Uncharacterized protein C15orf32	C15orf32	2	9.8	0.041	-5.6	41	31	232	230
Q08499	cAMP-specific 3'-5'-cyclic phosphodiesterase 4D	PDE4D	1	4.7	0.035	-6.0	311	277	1,854	2,147
Q9NPQ8	Synembryn-A	RIC8A	2	21.1	0.006	-6.3	16,202	10,902	102,624	88,355
O00161	Synaptosomal-associated protein 23	SNAP23	1	11.3	0.019	-6.7	47	45	314	316
P35346	Somatostatin receptor type 5	SSTR5	1	15.1	0.010	-7.0	4,049	1,630	28,365	30,406
Q16719	Kynureninase	KYNU	1	5.8	0.038	-7.2	276	62	1,992	2,317
Q8N8B7	Transcription elongation factor A N-terminal and central domain-containing protein	TCEANC	1	4.2	0.026	-7.3	371	325	2,712	3,006
Q96F83	Uncharacterized protein CLBA1	CLBA1	3	14.1	0.012	-7.4	262	245	1,930	1,809
Q9PoW2	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1-related	HMG20B	1	9.4	0.005	-7.9	438	449	3,477	3,315
P10588	Nuclear receptor subfamily 2 group F member 6	NR2F6	3	10.3	0.005	-7.9	196	144	1,557	1,436
P06681*	Complement C2	C2	1	25.2	0.009	-8.3	1,600	353	13,240	17,113
O75153	Clustered mitochondria protein homolog	CLUH	3	15.7	0.018	-10.1	265	189	2,677	2,642
Q9BRP8	Partner of Y14 and mago	PYM1	1	5.3	0.031	-10.2	7	13	70	54
Q96A26	Protein FAM162A	FAM162A	1	6.7	0.003	-11.3	145	140	1,648	1,270
Q5VZB9	Doublesex- and mab-3-related transcription factor A1	DMRTA1	1	10.3	0.030	-13.6	40	61	545	733
Q86TD4	Sarcalumenin	SRL	1	25.9	0.044	-16.6	41	101	686	1,110
Q6IQ22	Ras-related protein Rab-12	RAB12	1	23.7	0.005	-17.5	5	7	96	100
Q09328	Alpha-1_6-mannosylglycoprotein 6-beta-N-acetylglucosaminyltransferase A	MGAT5	1	26.8	0.008	-20.9	41	57	847	1,047

Differentially expressed proteins in PCOS vs. healthy control study. Differentially expressed proteins are ranked according to maximum fold change. The following data are displayed; protein and gene name; accession number; total and unique peptide count; Progenesis Q1 confidence score; Progenesis Q1 ANOVA p value; the maximum fold change expressed as a positive number if more abundant in the PCOS cohort and a negative number if more abundant in the control cohort; the fraction and total number of fractions in which the protein was identified; protein mass; and the normalised abundance of the protein in each sample. * = protein in significant IPA pathway

Appendix 5 | Chapter 6 | The PCOS proteome. PCOS and insulin resistance | Table of differential expressed proteins

Accession	Protein	Gene	Unique peptides	Confidence score	p value	Fold change	PCOS normalised abundance		IR normalised abundance	
							Mean	SD	Mean	SD
O43242	26S proteasome non-ATPase regulatory subunit 3	PSMD3	1	13.0	0.048	∞	807	974	0	0
P59190	Ras-related protein Rab-15	RAB15	1	37.8	0.031	∞	133	187	0	0
Q9NS61	Kv channel-interacting protein 2	KCNIP2	1	17.6	0.020	∞	132	132	0	0
P36406	E3 ubiquitin-protein ligase TRIM23	TRIM23	1	5.0	0.020	∞	473	491	0	0
Q13838	Spliceosome RNA helicase DDX39B	DDX39B	1	15.3	0.015	∞	132	144	0	0
AoA075B6Ro	T cell receptor gamma variable 2	TRGV2	1	4.9	0.004	∞	2,267	2,661	0	0
Q66K79	Carboxypeptidase Z	CPZ	1	10.8	0.001	∞	87	89	0	0
Q9UBW5	Bridging integrator 2	BIN2	1	16.2	0.000	-∞	0	0	112	136
Q9Y5X9	Endothelial lipase	LIPG	1	11.5	0.028	6108.9	41,496	79,178	7	11
Q8N635	Meiosis-specific with OB domain-containing protein	MEIOB	1	4.8	0.002	411.5	187	192	0	1
Q9Y4W2	Ribosomal biogenesis protein LAS1L	LAS1L	2	13.9	0.002	119.7	30,374	35,588	254	92
Q07812*	Apoptosis regulator BAX	BAX	2	15.1	0.032	69.5	167	207	2	4
Q9GZR5	Elongation of very long chain fatty acids protein 4	ELOVL4	2	13.8	0.019	54.9	892	1,074	16	18
P12004	Proliferating cell nuclear antigen	PCNA	2	16.4	0.006	51.3	209	265	4	7
P62424	60S ribosomal protein L7a	RPL7A	1	20.1	0.018	44.2	444	844	10	12
P61018	Ras-related protein Rab-4B	RAB4B	1	13.5	0.048	40.7	9,314	14,344	229	79
P19404	NADH dehydrogenase [ubiquinone] flavoprotein 2_ mitochondrial	NDUFV2	3	15.6	0.005	34.7	970	1,276	28	13
P48595	Serpin B10	SERPINB10	1	10.3	0.015	33.6	947	1,131	28	17
Q9UKY3	Putative inactive carboxylesterase 4	CES1P1	3	32.3	0.016	23.0	1,137	1,000	49	15
Q2TB90	Putative hexokinase HKDC1	HKDC1	2	26.0	0.014	20.5	3,635	3,506	177	162
Q9UFD9; PoDN81	RIMS-binding protein 3C	RIMBP3C	2	23.9	0.004	20.2	1,733	1,400	86	78
P41208	Centrin-2	CETN2	1	5.3	0.018	17.9	161	177	9	16
O95817	BAG family molecular chaperone regulator 3	BAG3	6	36.0	0.034	15.8	3,160	4,979	200	16
P30085	UMP-CMP kinase	CMPK1	8	64.9	0.012	15.2	2,481	2,179	163	83
Q96A33	Coiled-coil domain-containing protein 47	CCDC47	1	5.0	0.023	15.0	930	1,509	62	31
Q9HAV7	GrpE protein homolog 1_ mitochondrial	GRPEL1	1	4.5	0.012	14.8	213	206	14	13
Q9P256	Ankyrin repeat and MYND domain-containing protein 1	ANKMY1	3	28.8	0.016	13.9	2,150	1,861	154	156
Q7Z794*	Keratin_type II cytoskeletal 1b	KRT77	2	73.5	0.021	13.6	159	171	12	9
Q7oYC4	Talanin	ZNF365	1	10.4	0.014	13.2	221	221	17	26
Q9P2X8	Putative uncharacterized protein encoded by LINC00474	LINC00474	1	10.7	0.042	13.1	5,974	5,454	457	257
Q9Ho82	Ras-related protein Rab-33B	RAB33B	4	59.8	0.011	13.1	1,528	1,308	117	58
Q96MT4	Uncharacterized protein encoded by LINC01600	LINC01600	1	5.5	0.041	11.1	378	542	34	26

P61326; Q96A72	Protein mago nashi homolog	MAGOH	1	4.7	0.040	10.8	74	90	7	6
P51649	Succinate-semialdehyde dehydrogenase_ mitochondrial	ALDH5A1	2	9.5	0.028	10.8	230	232	21	18
P00367*	Glutamate dehydrogenase 1_ mitochondrial	GLUD1	6	37.5	0.007	10.3	1,978	1,670	191	106
Q9H2U2	Inorganic pyrophosphatase 2_ mitochondrial	PPA2	1	31.7	0.018	9.9	20	22	2	1
P49862	Kallikrein-7	KLK7	1	5.3	0.036	9.4	306	339	33	36
P14317	Hematopoietic lineage cell-specific protein	HCLS1	2	10.5	0.014	9.2	500	569	54	4
P61601	Neurocalcin-delta	NCALD	1	20.2	0.015	9.2	630	671	69	48
Q86Y39	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 11	NDUFA11	4	35.9	0.017	8.5	7,219	7,036	845	490
Q8NCD3	Holliday junction recognition protein	HJURP	2	17.5	0.017	8.4	2,818	2,422	337	223
Q8IU4	Putative protein SNX29P2	SNX29P2	3	17.9	0.041	8.1	181	251	22	10
O00151	PDZ and LIM domain protein 1	PDLIM1	1	18.7	0.034	7.6	3,284	4,536	431	30
P20132*	L-serine dehydratase/L-threonine deaminase	SDS	2	15.9	0.042	7.5	4,325	4,061	576	83
P08473*	Neprilysin	MME	30	308.9	0.034	7.1	32,767	31,448	4,607	1,213
O14579	Coatomer subunit epsilon	COPE	2	19.8	0.008	7.1	200	151	28	19
Q9COL4	Thrombospondin type-1 domain-containing protein 7B	THSD7B	2	38.2	0.031	6.1	2,476	1,954	405	152
P82930	28S ribosomal protein S34_ mitochondrial	MRPS34	1	5.5	0.003	5.3	271	132	51	4
P19793*	Retinoic acid receptor RXR-alpha	RXRA	1	21.5	0.026	5.3	1,505	1,351	286	142
Q8IZQ1	WD repeat and FYVE domain-containing protein 3	WDFY3	3	41.0	0.042	5.1	3,068	2,398	600	37
Q9HBA0	Transient receptor potential cation channel subfamily V member 4	TRPV4	1	10.6	0.009	5.0	1,207	830	241	63
A1L390	Pleckstrin homology domain-containing family G member 3	PLEKHG3	1	10.2	0.035	4.9	1,190	957	242	206
Q7RTS7*	Keratin_type II cytoskeletal 74	KRT74	5	80.4	0.050	4.7	615	533	131	42
P21333*	Filamin-A	FLNA	61	535.2	0.014	4.5	31,173	15,632	6,954	2,376
P29692	Elongation factor 1-delta	EEF1D	2	12.0	0.004	4.3	310	118	72	37
O43818	U3 small nucleolar RNA-interacting protein 2	RRP9	2	19.5	0.047	4.3	1,520	1,530	352	115
A1L4Q6	Putative uncharacterized protein FLJ41423	5 SV	2	9.4	0.025	4.3	1,960	866	457	366
P29218	Inositol monophosphatase 1	IMPA1	7	81.0	0.006	4.2	5,532	3,111	1,305	123
P12532	Creatine kinase U-type_ mitochondrial	CKMT1A	4	15.8	0.049	4.1	286	233	69	47
Q6ZS81	WD repeat- and FYVE domain-containing protein 4	WDFY4	5	31.9	0.045	4.0	2,416	1,898	600	39
Q9HAC8	Ubiquitin domain-containing protein 1	UBTD1	1	5.1	0.016	4.0	183	119	45	21
Q86YM7	Homer protein homolog 1	HOMER1	5	29.5	0.009	4.0	2,670	1,460	669	164
Q9HoW8	Protein SMG9	SMG9	2	23.6	0.028	4.0	503	337	126	90
P35998	26S proteasome regulatory subunit 7	PSMC2	4	31.7	0.023	4.0	370	215	94	16
P00709	Alpha-lactalbumin	LALBA	1	4.4	0.020	3.9	53	30	14	24
Q9UKR0	Kallikrein-12	KLK12	1	6.2	0.039	3.9	86	64	22	10
Q15327	Ankyrin repeat domain-containing protein 1	ANKRD1	1	5.4	0.032	3.7	874	503	239	75
B5MCY1	Tudor domain-containing protein 15	TDRD15	2	24.2	0.016	3.6	1,675	881	468	578
Q9UFNo	Protein NipSnap homolog 3A	NIPSNAP3A	2	17.9	0.028	3.6	490	334	137	34
Q75531	Barrier-to-autointegration factor	BANF1	4	29.2	0.028	3.6	209	96	59	72

O14618	Copper chaperone for superoxide dismutase	CCS	1	16.2	0.016	3.5	387	183	111	62
Q15375*	Ephrin type-A receptor 7	EPHA7	38	388.1	0.006	3.4	30,221	17,391	8,819	446
Q3MII6	TBC1 domain family member 25	TBC1D25	3	22.3	0.046	3.3	1,717	949	519	273
P41217	OX-2 membrane glycoprotein	CD200	3	27.9	0.013	3.3	2,550	847	775	774
Q8N807	Protein disulfide-isomerase-like protein of the testis	PDILT	1	6.2	0.012	3.3	2,623	1,679	802	133
Q9Y4A5	Transformation/transcription domain-associated protein	TRRAP	5	33.2	0.037	3.2	390	245	121	42
Q5VW00	DDB1- and CUL4-associated factor 12-like protein 2	DCAF12L2	1	10.5	0.033	3.2	10,186	5,612	3,201	2,141
P09544	Protein Wnt-2	WNT2	2	13.9	0.018	3.1	1,026	576	327	87
Q9UFE4	Coiled-coil domain-containing protein 39	CCDC39	6	41.3	0.049	3.1	9,859	6,870	3,185	1,724
O95980*	Reversion-inducing cysteine-rich protein with Kazal motifs	RECK	4	26.3	0.028	3.1	951	532	311	150
P61160*	Actin-related protein 2	ACTR2	10	78.6	0.046	3.0	3,051	1,522	1,004	405
A6NMZ2	Sentan	SNTN	2	21.1	0.004	2.9	1,593	535	546	284
Q96ER9	Coiled-coil domain-containing protein 51	CCDC51	1	11.2	0.040	2.9	10,484	6,053	3,596	1,126
P82980*	Retinol-binding protein 5	RBP5	7	48.1	0.019	2.9	3,243	1,724	1,125	121
P46940*	Ras GTPase-activating-like protein IQGAP1	IQGAP1	31	347.2	0.046	2.9	5,562	4,185	1,944	491
Q5T5A4	Uncharacterized protein C1orf194	C1orf194	1	15.2	0.033	2.9	3,760	1,763	1,317	610
O75351	Vacuolar protein sorting-associated protein 4B	VPS4B	19	221.9	0.021	2.8	21,817	10,623	7,680	2,616
O43175*	D-3-phosphoglycerate dehydrogenase	PHGDH	8	56.7	0.000	2.8	2,961	768	1,043	158
O75367	Core histone macro-H2A.1	H2AFY	6	44.2	0.008	2.8	940	371	331	70
Q9Y623*	Myosin-4	MYH4	3	39.2	0.044	2.8	2,904	1,577	1,049	661
Q9Y4H4	G-protein-signaling modulator 3	GPSM3	1	5.6	0.010	2.7	1,468	452	551	300
Q12788	Transducin beta-like protein 3	TBL3	1	16.8	0.028	2.6	4,271	2,124	1,634	178
P05186	Alkaline phosphatase_ tissue-nonspecific isozyme	ALPL	2	9.8	0.034	2.6	643	364	249	142
Q14116*	Interleukin-18	IL18	5	30.1	0.049	2.6	646	459	252	58
Q8NET6*	Carbohydrate sulfotransferase 13	CHST13	2	15.0	0.012	2.5	2,286	867	904	386
P19823*	Inter-alpha-trypsin inhibitor heavy chain H2	ITIH2	31	261.3	0.037	2.5	5,794	3,304	2,292	194
P33991	DNA replication licensing factor MCM4	MCM4	1	15.1	0.008	2.5	324	100	130	15
Q9NQV8	PR domain zinc finger protein 8	PRDM8	2	34.6	0.009	2.5	20,428	7,962	8,268	2,093
O95831*	Apoptosis-inducing factor 1_ mitochondrial	AIFM1	5	53.7	0.017	2.4	7,911	2,838	3,335	658
Q9H6B4	CXADR-like membrane protein	CLMP	6	45.1	0.026	2.4	2,205	920	938	280
Q9Y5K2	Kallikrein-4	KLK4	1	5.3	0.005	2.3	8,498	2,350	3,618	965
P29401	Transketolase	TKT	14	113.7	0.002	2.3	2,345	641	1,005	144
Q3ZCM7*	Tubulin beta-8 chain	TUBB8	2	57.4	0.046	2.3	96	41	41	18
Q0ZLH3	Pejvakin	PJKV	3	24.7	0.004	2.3	1,052	293	459	86
Q9HCJ0	Trinucleotide repeat-containing gene 6C protein	TNRC6C	2	35.6	0.045	2.3	763	427	334	38
Q86Y46*	Keratin_ type II cytoskeletal 73	KRT73	12	210.2	0.012	2.3	8,778	3,100	3,874	1,107
Q96C19	EF-hand domain-containing protein D2	EFHD2	10	119.1	0.015	2.2	2,404	889	1,071	70
Q8NCC3	Group XV phospholipase A2	PLA2G15	1	15.7	0.032	2.2	1,549	633	708	371
P20851*	C4b-binding protein beta chain	C4BPB	3	19.9	0.036	2.2	1,290	571	596	210

O15061	Synemin	SYNM	3	13.4	0.043	2.1	3,161	1,334	1,487	759
Q14964	Ras-related protein Rab-39A	RAB39A	5	34.0	0.030	2.1	8,065	3,315	3,928	930
Q8NHO9	ATP-dependent RNA helicase DDX55	DDX55	8	107.5	0.050	2.0	28,654	8,841	14,041	7,808
Q13263	Transcription intermediary factor 1-beta	TRIM28	1	15.0	0.031	2.0	754	240	372	138
Q13099	Intraflagellar transport protein 88 homolog	IFT88	2	13.8	0.003	2.0	616	119	305	79
P46060	Ran GTPase-activating protein 1	RANGAP1	5	35.3	0.025	2.0	4,737	1,885	2,361	423
P98160*	Basement membrane-specific heparan sulfate proteoglycan core protein	HSPG2	357	2739.0	0.019	2.0	167,645	46,387	84,035	24,071
O94772	Lymphocyte antigen 6H	LY6H	1	25.3	0.021	2.0	1,939	684	983	241
Q9UPS8	Ankyrin repeat domain-containing protein 26	ANKRD26	8	67.3	0.022	1.9	2,058	663	1,077	319
Q16719	Kynureninase	KYNU	1	5.8	0.007	1.9	276	62	148	34
Q5XKE5*	Keratin_type II cytoskeletal 79	KRT79	11	223.7	0.027	1.9	7,875	2,307	4,250	1,379
O75891	Cytosolic 10-formyltetrahydrofolate dehydrogenase	ALDH1L1	7	69.6	0.025	1.8	1,603	416	882	224
O43488	Aflatoxin B1 aldehyde reductase member 2	AKR7A2	1	11.3	0.018	1.8	1,142	288	630	219
P49789	Bis(5'-adenosyl)-triphosphatase	FHIT	3	19.3	0.048	1.8	372	124	206	81
Q96Q15; Q6P435	Serine/threonine-protein kinase SMG1	SMG1	8	54.0	0.039	1.7	3,679	1,341	2,116	103
P29508	Serpin B3	SERPINB3	41	812.3	0.010	1.7	59,634	13,916	35,044	3,618
Q96TA2	ATP-dependent zinc metalloprotease YME1L1	YME1L1	5	32.1	0.013	1.7	2,230	491	1,324	316
Q03252*	Lamin-B2	LMNB2	16	137.4	0.024	1.7	5,156	1,353	3,085	617
P11717*	Cation-independent mannose-6-phosphate receptor	IGF2R	6	40.3	0.005	1.6	1,691	318	1,036	67
Q96MR9	Zinc finger protein 560	ZNF560	3	23.1	0.020	1.6	1,215	324	753	45
O14745	Na(+)/H(+) exchange regulatory cofactor NHE-RF1	SLC9A3R1	21	200.5	0.019	1.6	32,493	6,304	20,332	3,061
O94760	N(G)_N(G)-dimethylarginine dimethylaminohydrolase 1	DDAH1	3	57.7	0.002	1.6	1,011	144	645	45
O43423; P39687	Acidic leucine-rich nuclear phosphoprotein 32 family member C	ANP32C	1	6.0	0.012	1.5	1,176	218	784	79
Q99456*	Keratin_type I cytoskeletal 12	KRT12	22	338.8	0.021	1.5	5,825	1,085	3,971	529
P08727*	Keratin_type I cytoskeletal 19	KRT19	52	907.4	0.041	1.5	10,875	2,507	7,497	1,025
P14314	Glucosidase 2 subunit beta	PRKCSH	23	260.6	0.039	1.4	9,386	2,072	6,625	527
Q10471	Polypeptide N-acetylgalactosaminyltransferase 2	GALNT2	3	22.0	0.004	1.4	1,727	164	1,220	190
O95755	Ras-related protein Rab-36	RAB36	2	22.9	0.035	-1.3	6,581	885	8,414	903
Q86TH1	ADAMTS-like protein 2	ADAMTSL2	5	64.7	0.041	-1.3	3,072	462	4,133	811
Q9UNN8	Endothelial protein C receptor	PROCR	21	123.7	0.049	-1.4	40,849	5,143	56,578	14,933
P11277*	Spectrin beta chain_erythrocytic	SPTB	14	128.4	0.044	-1.4	10,801	1,816	15,061	3,407
Q7Z3B1	Neuronal growth regulator 1	NEGR1	41	335.5	0.016	-1.4	42,270	8,045	58,948	3,574
O00584	Ribonuclease T2	RNASET2	10	113.4	0.027	-1.4	5,927	1,095	8,408	1,410
Q9HCU0	Endosialin	CD248	28	253.7	0.009	-1.4	46,575	7,172	66,631	4,887
Q9H8L6	Multimerin-2	MMRN2	31	271.2	0.031	-1.4	22,634	4,498	32,620	1,817
P78380	Oxidized low-density lipoprotein receptor 1	OLR1	20	175.6	0.015	-1.5	24,213	3,946	35,368	5,139
P00558	Phosphoglycerate kinase 1	PGK1	30	384.8	0.036	-1.5	191,801	39,874	280,869	69,537

O43692	Peptidase inhibitor 15	PI15	2	40.7	0.009	-1.5	15,981	2,735	23,824	3,109
Q5VTE0; P68104	Putative elongation factor 1-alpha-like 3	EEF1A1P5	32	251.3	0.018	-1.5	48,901	9,597	72,948	11,459
P82970	High mobility group nucleosome-binding domain-containing protein 5	HMGN5	39	276.8	0.009	-1.5	16,484	1,758	24,621	5,890
Q9BRT3	Migration and invasion enhancer 1	MIEN1	7	82.3	0.004	-1.5	12,875	1,220	19,261	3,739
P00751*	Complement factor B	CFB	59	556.2	0.024	-1.5	53,113	11,636	79,497	14,429
Q9UMR5	Lysosomal thioesterase PPT2	PPT2	5	22.2	0.005	-1.5	985	168	1,478	59
Q6UX73	UPFo764 protein C16orf89	C16orf89	9	84.4	0.048	-1.5	2,550	485	3,844	1,204
Q8NFZ8	Cell adhesion molecule 4	CADM4	47	416.9	0.024	-1.5	37,838	9,134	57,049	5,030
P57076	Cilia- and flagella-associated protein 298	CFAP298	3	31.2	0.021	-1.5	1,389	343	2,098	278
Q6UXD5	Seizure 6-like protein 2	SEZ6L2	13	135.6	0.017	-1.5	6,634	1,295	10,031	1,255
P81605	Dermcidin	DCD	3	30.8	0.047	-1.5	23,666	7,276	36,202	3,038
P22105	Tenascin-X	TNXB	268	2563.6	0.024	-1.5	96,877	26,316	148,403	18,416
P43115	Prostaglandin E2 receptor EP3 subtype	PTGER3	3	26.2	0.033	-1.5	2,893	683	4,444	537
P54753*	Ephrin type-B receptor 3	EPHB3	16	171.8	0.015	-1.5	30,655	6,175	47,436	8,474
Q9BY67*	Cell adhesion molecule 1	CADM1	29	316.2	0.010	-1.6	27,106	6,255	42,095	2,216
P10912*	Growth hormone receptor	GHR	4	26.8	0.017	-1.6	837	173	1,320	328
P16035*	Metalloproteinase inhibitor 2	TIMP2	7	65.3	0.021	-1.6	12,477	3,422	19,733	67
Q9NU53	Glycoprotein integral membrane protein 1	GINM1	23	225.9	0.001	-1.6	109,344	12,150	173,759	22,676
P36957*	Dihydropyridyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex_mitochondrial	DLST	22	202.1	0.026	-1.6	80,687	21,618	128,781	12,680
O60812; PoDMR1	Heterogeneous nuclear ribonucleoprotein C-like 1	HNRNPCL1	5	85.2	0.036	-1.6	4,876	931	7,811	2,774
P62633	Cellular nucleic acid-binding protein	CNBP	6	41.2	0.012	-1.6	8,899	1,634	14,374	3,395
Q9BWU0	Kanadaplin	SLC4A1AP	3	19.2	0.025	-1.6	13,223	3,216	21,523	4,097
P30086*	Phosphatidylethanolamine-binding protein 1	PEBP1	29	307.1	0.028	-1.6	39,338	10,730	64,133	13,608
Q04756*	Hepatocyte growth factor activator	HGFAC	29	235.9	0.020	-1.6	39,679	7,631	64,741	16,966
Q5TAB7	Protein ripply2	RIPPLY2	2	10.1	0.047	-1.6	2,608	951	4,260	685
Q3KP22	Membrane-anchored junction protein	MAJIN	1	10.3	0.034	-1.6	2,136	471	3,500	1,047
P07225*	Vitamin K-dependent protein S	PROS1	2	21.1	0.038	-1.7	3,184	884	5,296	1,683
Q9HAD4	WD repeat-containing protein 41	WDR41	2	14.0	0.034	-1.7	2,462	821	4,109	403
P61026	Ras-related protein Rab-10	RAB10	7	73.4	0.032	-1.7	7,907	1,197	13,289	5,499
Q9HAV0*	Guanine nucleotide-binding protein subunit beta-4	GNB4	4	57.5	0.006	-1.7	4,051	877	6,879	812
P16278*	Beta-galactosidase	GLB1	31	357.9	0.002	-1.7	18,479	3,420	31,438	1,679
P42785	Lysosomal Pro-X carboxypeptidase	PRCP	22	230.1	0.042	-1.7	9,419	3,407	16,056	1,303
Q5J537	NHL repeat-containing protein 3	NHLRC3	8	73.4	0.005	-1.7	1,813	325	3,093	656
Q8WVV5	Butyrophilin subfamily 2 member A2	BTN2A2	5	153.3	0.003	-1.7	40,205	7,002	68,786	10,616
Q7KYR7	Butyrophilin subfamily 2 member A1	BTN2A1	2	152.6	0.003	-1.7	4,526	788	7,743	1,195
O75487	Glypican-4	GPC4	20	177.0	0.035	-1.7	10,466	2,659	17,932	6,767

P14324*	Farnesyl pyrophosphate synthase	FDPS	8	61.7	0.043	-1.7	2,950	1,075	5,063	768
P01127*	Platelet-derived growth factor subunit B	PDGFB	8	53.9	0.047	-1.7	13,046	5,772	22,431	5,697
P12259*	Coagulation factor V	F5	19	146.6	0.009	-1.7	3,256	820	5,600	587
P34931*	Heat shock 70 kDa protein 1-like	HSPA1L	2	169.8	0.002	-1.7	2,777	622	4,779	257
P24821	Tenascin	TNC	117	934.2	0.011	-1.7	166,084	43,143	286,470	29,468
Q9Y6U3	Adseverin	SCIN	10	70.6	0.026	-1.7	2,384	354	4,124	1,645
Q8NBS9	Thioredoxin domain-containing protein 5	TXNDC5	14	102.0	0.027	-1.7	9,959	2,824	17,243	4,725
P99999*	Cytochrome c	CYCS	7	87.8	0.036	-1.7	5,286	1,859	9,189	1,759
O15145*	Actin-related protein 2/3 complex subunit 3	ARPC3	7	59.1	0.044	-1.7	2,387	895	4,170	1,284
P09668	Pro-cathepsin H	CTSH	27	179.2	0.026	-1.7	8,560	1,974	14,970	5,291
O00515	Ladinin-1	LAD1	15	131.3	0.038	-1.7	44,145	14,988	77,230	9,278
Q8NBJ4	Golgi membrane protein 1	GOLM1	85	812.7	0.027	-1.8	74,172	18,997	130,374	42,612
P24844*	Myosin regulatory light polypeptide 9	MYL9	3	35.4	0.043	-1.8	12,987	3,585	22,869	7,737
P01861*	Immunoglobulin heavy constant gamma 4	IGHG4	18	367.4	0.044	-1.8	27,221	11,154	48,132	13,964
Q9UN37*	Vacuolar protein sorting-associated protein 4A	VPS4A	16	159.2	0.011	-1.8	27,627	7,102	49,383	6,055
Q9UPY8*	Microtubule-associated protein RP/EB family member 3	MAPRE3	4	23.5	0.005	-1.8	3,445	680	6,166	1,336
P19256	Lymphocyte function-associated antigen 3	CD58	9	89.7	0.003	-1.8	11,915	2,268	21,420	4,491
Q8IZP7*	Heparan-sulfate 6-O-sulfotransferase 3	HS6ST3	2	22.8	0.037	-1.8	836	318	1,505	169
P78423	Fractalkine	CX3CL1	1	14.0	0.044	-1.8	2,671	1,151	4,812	1,008
P16070*	CD44 antigen	CD44	41	253.1	0.002	-1.8	62,600	13,587	113,135	11,316
P04083; Q9P2R7	Annexin A1	ANXA1	107	988.2	0.025	-1.8	597,075	160,687	###	319,296
Q8N126	Cell adhesion molecule 3	CADM3	8	76.5	0.044	-1.8	5,779	1,531	10,515	4,135
Q5H9L2	Transcription elongation factor A protein-like 5	TCEAL5	3	22.3	0.004	-1.8	939	197	1,715	328
Q03403	Trefoil factor 2	TFF2	9	57.6	0.040	-1.8	34,540	6,196	63,272	32,354
Q8N339	Metallothionein-1M	MT1M	3	13.8	0.010	-1.8	185	40	341	85
Q9HCN6*	Platelet glycoprotein VI	GP6	13	116.1	0.008	-1.8	14,669	3,311	26,980	7,833
O75144	ICOS ligand	ICOSLG	18	165.2	0.017	-1.8	24,906	7,882	45,843	5,954
P17050	Alpha-N-acetylgalactosaminidase	NAGA	4	38.8	0.032	-1.8	908	307	1,672	204
P08962	CD63 antigen	CD63	3	26.5	0.031	-1.8	1,849	667	3,418	812
Q96C57	Protein CUSTOS	CUSTOS	5	42.7	0.006	-1.9	3,084	318	5,714	2,069
P62834*	Ras-related protein Rap-1A	RAP1A	1	68.6	0.009	-1.9	1,567	459	2,905	464
Q6DK17	Transmembrane protein PVRIG	PVRIG	3	22.8	0.016	-1.9	1,713	472	3,187	822
P78552*	Interleukin-13 receptor subunit alpha-1	IL13RA1	7	47.2	0.014	-1.9	5,952	1,630	11,118	1,668
Q12864*	Cadherin-17	CDH17	10	103.1	0.012	-1.9	1,901	510	3,572	1,009
A8MZG2	Uncharacterized protein C16orf90	C16orf90	1	5.5	0.049	-1.9	570	188	1,075	327
P02788	Lactotransferrin	LTF	118	1081.0	0.043	-1.9	56,171	26,729	106,078	24,612
P30501; Q29960	HLA class I histocompatibility antigen_Cw-2 alpha chain	HLA-C	5	75.9	0.013	-1.9	25,346	7,086	47,930	10,712

Q6GTX8	Leukocyte-associated immunoglobulin-like receptor 1	LAIR1	18	153.2	0.020	-1.9	71,637	25,832	136,027	22,582
P14780*	Matrix metalloproteinase-9	MMP9	50	431.8	0.010	-1.9	22,686	7,308	43,100	4,366
Q496F6	CMRF35-like molecule 2	CD300E	8	86.9	0.047	-1.9	3,026	1,031	5,763	2,832
Q01974	Tyrosine-protein kinase transmembrane receptor ROR2	ROR2	13	76.4	0.004	-1.9	7,525	1,979	14,342	675
P08134*	Rho-related GTP-binding protein RhoC	RHOC	7	72.3	0.050	-1.9	3,524	1,444	6,729	1,959
Q7Z7D3	V-set domain-containing T-cell activation inhibitor 1	VTCN1	5	40.4	0.034	-1.9	28,554	13,135	54,532	12,391
Q99574	Neuroserpin	SERPINI1	17	187.3	0.016	-1.9	4,344	1,336	8,299	2,549
A6NI73	Leukocyte immunoglobulin-like receptor subfamily A member 5	LILRA5	5	71.6	0.016	-1.9	6,484	1,626	12,390	3,856
P18206*	Vinculin	VCL	55	538.3	0.009	-1.9	20,421	6,666	39,257	5,065
P38606	V-type proton ATPase catalytic subunit A	ATP6V1A	25	191.9	0.015	-1.9	14,256	4,656	27,485	5,934
Q8WUD1	Ras-related protein Rab-2B	RAB2B	1	41.8	0.035	-1.9	7,184	2,108	13,938	5,533
P29992*	Guanine nucleotide-binding protein subunit alpha-11	GNA11	9	80.0	0.045	-1.9	6,020	2,345	11,701	2,913
Q14134	Tripartite motif-containing protein 29	TRIM29	26	197.9	0.024	-1.9	13,241	4,478	25,753	7,929
Q6ZMN7	PDZ domain-containing RING finger protein 4	PDZRN4	3	30.0	0.044	-1.9	4,908	2,209	9,560	2,561
P20810*	Calpastatin	CAST	49	488.9	0.035	-1.9	13,769	5,278	26,820	8,755
P05155*	Plasma protease C1 inhibitor	SERPING1	66	657.1	0.021	-1.9	60,707	19,025	118,318	20,507
P23526	Adenosylhomocysteinase	AHCY	12	144.1	0.010	-2.0	5,501	1,269	10,735	2,956
P10619	Lysosomal protective protein	CTSA	26	220.8	0.003	-2.0	12,826	2,997	25,158	4,372
P35609*	Alpha-actinin-2	ACTN2	9	239.8	0.011	-2.0	8,884	2,199	17,466	5,815
Q13477*	Mucosal addressin cell adhesion molecule 1	MADCAM1	11	113.4	0.018	-2.0	11,521	4,379	22,756	318
Q8TDQ0	Hepatitis A virus cellular receptor 2	HAVCR2	20	223.4	0.009	-2.0	20,646	6,433	40,835	9,894
P07476*	Involucrin	IVL	71	661.2	0.045	-2.0	63,177	22,925	125,066	46,592
Q02930*	Cyclic AMP-responsive element-binding protein 5	CREB5	7	53.9	0.015	-2.0	46,601	13,304	92,342	32,227
Q9BYF1	Angiotensin-converting enzyme 2	ACE2	2	14.5	0.014	-2.0	309	79	614	172
Q8NEJ9	Neuroguidin	NGDN	3	14.0	0.048	-2.0	232	103	462	130
P10645	Chromogranin-A	CHGA	47	423.3	0.030	-2.0	64,345	25,982	128,310	47,951
Q86WX3	Active regulator of SIRT1	RPS19BP1	3	15.5	0.024	-2.0	968	311	1,936	656
P13797	Plastin-3	PLS3	24	297.6	0.024	-2.0	17,996	5,279	36,028	10,567
P04899*	Guanine nucleotide-binding protein G(i) subunit alpha-2	GNAI2	15	193.0	0.010	-2.0	14,203	4,628	28,582	5,630
P78362*	SRSF protein kinase 2	SRPK2	3	24.6	0.029	-2.0	3,170	1,525	6,427	2,065
P48735*	Isocitrate dehydrogenase [NADP]_ mitochondrial	IDH2	4	21.0	0.049	-2.0	3,293	1,612	6,678	1,802
P01042*	Kininogen-1	KNG1	178	1328.5	0.044	-2.0	217,625	78,280	443,958	174,112
Q9NQ84	G-protein coupled receptor family C group 5 member C	GPRC5C	21	188.4	0.019	-2.1	16,983	7,732	34,993	4,941
P49747*	Cartilage oligomeric matrix protein	COMP	59	517.9	0.017	-2.1	41,201	14,440	85,028	30,506
Q5IJ48	Protein crumbs homolog 2	CRB2	8	63.7	0.020	-2.1	984	326	2,036	643
P60981	Destrin	DSTN	6	49.0	0.007	-2.1	1,710	253	3,556	1,372
P17813	Endoglin	ENG	3	32.7	0.005	-2.1	2,705	788	5,633	1,207
Q01538	Myelin transcription factor 1	MYT1	2	22.9	0.021	-2.1	738	154	1,541	812
Q9BYE9	Cadherin-related family member 2	CDHR2	29	276.6	0.002	-2.1	119,944	26,873	251,777	9,089

O60494	Cubilin	CUBN	248	2116.5	0.012	-2.1	34,375	11,022	72,587	17,283
P29323*	Ephrin type-B receptor 2	EPHB2	42	434.0	0.002	-2.1	10,864	2,733	22,962	3,757
P62258*	14-3-3 protein epsilon	YWHAE	30	314.1	0.003	-2.1	9,468	1,666	20,018	6,899
P14136*	Glial fibrillary acidic protein	GFAP	9	145.8	0.002	-2.1	3,355	654	7,160	1,956
Q6NXT6	Transmembrane anterior posterior transformation protein 1 homolog	TAPT1	1	15.6	0.050	-2.1	3,539	2,976	7,606	1,284
Q96FE7	Phosphoinositide-3-kinase-interacting protein 1	PIK3IP1	14	125.9	0.042	-2.2	127,946	84,632	275,524	95,726
O94907	Dickkopf-related protein 1	DKK1	1	10.0	0.031	-2.2	39,696	14,164	85,578	32,104
A7E2U8	UPFo602 protein C4orf47	C4orf47	1	7.9	0.014	-2.2	920	280	1,989	761
P54289*	Voltage-dependent calcium channel subunit alpha-2/delta-1	CACNA2D1	7	56.4	0.012	-2.2	1,059	163	2,299	1,027
Q9Y247	Protein FAM50B	FAM50B	3	38.9	0.013	-2.2	3,071	1,455	6,700	1,752
Q9Y624*	Junctional adhesion molecule A	F11R	11	137.7	0.007	-2.2	10,780	3,600	23,518	7,882
P16112	Aggrecan core protein	ACAN	25	221.4	0.011	-2.2	4,898	1,611	10,712	2,894
Q9NP79	Vacuolar protein sorting-associated protein VTA1 homolog	VTA1	15	135.1	0.008	-2.2	3,433	885	7,526	2,719
Q2M215*	Keratin_type I cytoskeletal 24	KRT24	2	65.6	0.009	-2.2	252	69	552	174
P40227	T-complex protein 1 subunit zeta	CT6A	9	58.3	0.001	-2.2	23,458	3,870	51,526	12,731
Q86WV1	Src kinase-associated phosphoprotein 1	SKAP1	2	13.7	0.044	-2.2	776	250	1,707	918
P61981*	14-3-3 protein gamma	YWHAH	7	99.9	0.047	-2.2	2,576	1,193	5,676	2,364
O00468*	Agrin	AGRN	60	467.8	0.006	-2.2	15,691	4,362	34,582	11,909
Q15746*	Myosin light chain kinase_smooth muscle	MYLK	34	276.5	0.000	-2.2	32,088	3,370	70,849	7,154
P11117	Lysosomal acid phosphatase	ACP2	42	335.7	0.005	-2.2	21,867	5,999	48,326	8,775
Q66PJ3	ADP-ribosylation factor-like protein 6-interacting protein 4	ARL6IP4	4	38.7	0.023	-2.2	4,655	2,320	10,310	2,075
P67809	Nuclease-sensitive element-binding protein 1	YBX1	6	63.3	0.011	-2.2	5,182	1,641	11,593	3,957
Q92764*	Keratin_type I cuticular Ha5	KRT35	6	71.2	0.004	-2.2	44,111	13,308	99,074	16,463
O43451	Maltase-glucoamylase_intestinal	MGAM	77	768.8	0.043	-2.3	16,026	8,566	36,068	10,199
Q16698	2_4-dienoyl-CoA reductase_mitochondrial	DEC1	13	108.0	0.041	-2.3	6,442	3,723	14,513	5,216
AoAV02	Solute carrier family 12 member 8	SLC12A8	2	16.4	0.021	-2.3	839	376	1,898	673
P15311*	Ezrin	EZR	60	750.2	0.011	-2.3	35,174	8,075	79,565	34,381
A6NJL1	Zinc finger and SCAN domain-containing protein 5B	ZSCAN5B	6	33.8	0.032	-2.3	26,764	12,619	60,719	24,570
Q5KU26	Collectin-12	COLEC12	54	464.4	0.028	-2.3	20,897	7,064	47,474	23,961
AoAoB4J1U7	Immunoglobulin heavy variable 6-1	IGHV6-1	5	21.7	0.000	-2.3	15,072	2,465	34,355	6,630
Q14573	Inositol_1_4_5-trisphosphate receptor type 3	ITPR3	5	26.8	0.017	-2.3	443	211	1,012	255
Q9HB40	Retinoid-inducible serine carboxypeptidase	SCPEP1	12	132.1	0.033	-2.3	4,442	1,126	10,165	5,994
Q76510	Urotensin-2B	UTS2B	1	9.9	0.024	-2.3	819	296	1,892	697
Q9UKN7	Unconventional myosin-XV	MYO15A	11	96.3	0.003	-2.3	7,184	1,435	16,712	5,799
Q8NG11	Tetraspanin-14	TSPAN14	1	5.6	0.042	-2.3	51,220	25,189	119,309	43,936
Q95967	EGF-containing fibulin-like extracellular matrix protein 2	EFEMP2	14	161.3	0.038	-2.3	22,575	10,950	52,803	17,984
Q61FG1	Olfactory receptor 52E8	OR52E8	2	16.3	0.025	-2.3	3,336	1,653	7,805	2,457
Q9P1Z3	Potassium/sodium hyperpolarization-activated cyclic nucleotide-gated channel 3	HCN3	1	25.7	0.000	-2.3	228,367	19,724	535,593	47,301
P07954*	Fumarate hydratase_mitochondrial	FH	3	19.7	0.035	-2.4	226	132	533	111

Q14847*	LIM and SH3 domain protein 1	LASP1	13	138.3	0.014	-2.4	15,996	6,081	38,164	12,685
Q9HgB4	Sideroflexin-1	SFXN1	2	13.3	0.040	-2.4	5,277	2,359	12,631	5,250
Q9ULCo	Endomucin	EMCN	1	19.6	0.002	-2.4	1,271	263	3,068	821
Q96GDo	Pyridoxal phosphate phosphatase	PDXP	1	4.9	0.029	-2.4	1,046	468	2,528	1,164
Q14118*	Dystroglycan	DAG1	23	214.5	0.009	-2.4	10,368	2,859	25,190	11,309
Q14515	SPARC-like protein 1	SPARCL1	92	717.7	0.041	-2.4	29,382	12,824	71,617	29,645
Q05209*	Tyrosine-protein phosphatase non-receptor type 12	PTPN12	4	23.5	0.030	-2.4	2,617	1,123	6,388	3,338
Q86XR7	TIR domain-containing adapter molecule 2	TICAM2	2	9.3	0.004	-2.4	1,659	289	4,056	1,669
P61247	40S ribosomal protein S3a	RPS3A	4	32.5	0.019	-2.5	799	215	1,966	1,032
Q9UHG3*	Prenylcysteine oxidase 1	PCYOX1	4	24.9	0.003	-2.5	1,266	416	3,127	731
Q9UPX8*	SH3 and multiple ankyrin repeat domains protein 2	SHANK2	1	24.1	0.038	-2.5	1,032	493	2,590	1,348
Q68CJ6	Nuclear GTPase SLIP-GC	NUGGC	3	14.5	0.021	-2.5	6,809	2,430	17,092	6,303
P07196	Neurofilament light polypeptide	NEFL	14	158.9	0.005	-2.5	1,590	466	3,991	1,504
P25940*	Collagen alpha-3(V) chain	COL5A3	29	325.0	0.016	-2.5	9,910	2,225	24,966	14,605
O43719	HIV Tat-specific factor 1	HTATSF1	7	38.5	0.001	-2.5	2,831	602	7,174	1,440
P05106	Integrin beta-3	ITGB3	2	14.0	0.003	-2.5	1,225	294	3,113	1,270
P01624	Immunoglobulin kappa variable 3-15	IGKV3-15	2	34.7	0.031	-2.5	8,604	4,018	21,906	3,781
Q4VC44	FLYWCH-type zinc finger-containing protein 1	FLYWCH1	2	8.6	0.035	-2.6	720	270	1,836	925
P10153	Non-secretory ribonuclease	RNASE2	30	190.9	0.017	-2.6	76,395	40,821	195,118	19,453
A6NHA9	Olfactory receptor 4C46	OR4C46	1	5.1	0.008	-2.6	157	45	403	181
Q16378	Proline-rich protein 4	PRR4	5	26.2	0.024	-2.6	3,161	748	8,153	4,654
PoDJ93	Small integral membrane protein 13	SMIM13	2	10.1	0.034	-2.6	613	343	1,581	390
Q9HgH4	Vacuolar protein sorting-associated protein 37B	VPS37B	2	16.9	0.010	-2.6	584	286	1,508	417
Q9Col9	Leucine-rich repeat-containing protein 27	LRRC27	2	24.1	0.001	-2.6	3,126	723	8,090	1,308
P16870	Carboxypeptidase E	CPE	41	356.7	0.024	-2.6	13,278	5,116	34,428	18,929
P00734*	Prothrombin	F2	64	579.0	0.025	-2.6	53,191	26,443	138,453	27,335
P24855	Deoxyribonuclease-1	DNASE1	13	154.5	0.013	-2.6	26,063	12,095	67,866	20,384
Q96PQ1	Sialic acid-binding Ig-like lectin 12	SIGLEC12	3	15.5	0.041	-2.6	737	380	1,930	761
P34896*	Serine hydroxymethyltransferase_cytosolic	SHMT1	13	116.4	0.005	-2.6	19,771	7,383	51,839	13,682
Q99715*	Collagen alpha-1(XII) chain	COL12A1	118	977.1	0.000	-2.6	30,099	6,694	79,664	15,008
O00526	Uroplakin-2	UPK2	1	13.1	0.016	-2.6	4,520	1,029	11,975	6,622
AoAoC4DH72	Immunoglobulin kappa variable 1-6	IGKV1-6	2	55.9	0.007	-2.7	7,663	2,479	20,437	9,316
Q7Z419	E3 ubiquitin-protein ligase RNF144B	RNF144B	2	9.8	0.035	-2.7	936	744	2,521	785
Q95497	Pantetheinase	VNN1	12	115.2	0.014	-2.7	36,897	10,849	100,184	59,998
Q9P1V8	Sterile alpha motif domain-containing protein 15	SAMD15	3	32.8	0.035	-2.7	1,463	848	3,975	1,967
Q7L5L3	Lysophospholipase D GDPD3	GDPD3	1	16.7	0.034	-2.8	123	64	337	112
P51654	Glypican-3	GPC3	6	63.6	0.025	-2.8	3,334	2,050	9,232	3,771
Q13474	Dystrophin-related protein 2	DRP2	1	4.2	0.034	-2.8	665	333	1,845	1,020
Q9BVK6	Transmembrane emp24 domain-containing protein 9	TMED9	3	22.1	0.020	-2.8	8,234	4,172	22,875	9,003

Q15166*	Serum paraoxonase/lactonase 3	PON3	3	31.2	0.001	-2.8	514	115	1,430	423
Q9UP83	Conserved oligomeric Golgi complex subunit 5	COG5	2	15.6	0.038	-2.8	3,861	2,113	10,830	5,629
Q6P173	Leukocyte immunoglobulin-like receptor subfamily A member 6	LILRA6	1	34.6	0.012	-2.8	429	142	1,207	660
P15328	Folate receptor alpha	FOLR1	37	319.0	0.012	-2.8	29,897	15,018	84,446	12,648
Q01518; P40123	Adenylyl cyclase-associated protein 1	CAP1	22	229.3	0.016	-2.8	24,314	13,028	68,821	21,091
Q969J2	Zinc finger protein with KRAB and SCAN domains 4	ZKSCAN4	3	19.8	0.007	-2.8	1,301	475	3,691	1,713
Q8N2S1	Latent-transforming growth factor beta-binding protein 4	LTBP4	48	367.6	0.020	-2.8	82,231	44,458	233,364	48,603
P12724	Eosinophil cationic protein	RNASE3	4	30.5	0.026	-2.9	6,291	3,235	18,042	6,903
O95757	Heat shock 70 kDa protein 4L	HSPA4L	1	21.3	0.030	-2.9	2,731	2,042	7,855	3,272
Q14764	Major vault protein	MVP	14	106.8	0.004	-2.9	4,601	1,734	13,258	1,110
P55291*	Cadherin-15	CDH15	8	88.6	0.011	-2.9	46,601	20,013	134,918	20,219
O15273	Telethonin	TCAP	1	9.7	0.023	-2.9	947	468	2,752	1,182
Q8IZS5	Orofacial cleft 1 candidate gene 1 protein	OFCC1	2	21.8	0.044	-2.9	185	125	542	176
Q9H6X2	Anthrax toxin receptor 1	ANTXR1	6	61.8	0.024	-2.9	21,961	7,662	64,223	32,662
Q9NSI8	SAM domain-containing protein SAMSN-1	SAMSN1	2	20.0	0.018	-2.9	233	139	683	310
Q8NI99	Angiopoietin-related protein 6	ANGPTL6	9	75.1	0.048	-2.9	6,892	1,669	20,184	17,665
Q9BRC7	1-phosphatidylinositol 4_5-bisphosphate phosphodiesterase delta-4	PLCD4	3	10.0	0.009	-3.0	402	183	1,206	233
Q00973	Beta-1_4 N-acetylgalactosaminyltransferase 1	B4GALNT1	1	10.4	0.021	-3.0	384	136	1,160	623
Q93074*	Mediator of RNA polymerase II transcription subunit 12	MED12	3	23.8	0.031	-3.0	6,954	4,586	21,041	10,832
O43633*	Charged multivesicular body protein 2a	CHMP2A	4	50.2	0.034	-3.1	1,011	760	3,096	678
Q96JB1	Dynein heavy chain 8_ axonemal	DNAH8	1	14.2	0.015	-3.1	8,906	3,532	27,341	13,876
P58107	Epiplakin	EPPK1	13	113.2	0.028	-3.1	6,772	4,773	20,822	8,311
Q8WTX7	Cytosolic arginine sensor for mTORC1 subunit 1	CASTOR1	2	15.2	0.037	-3.1	262	123	810	538
Q8IZP2	Putative protein FAM10A4	ST13P4	6	56.1	0.019	-3.1	2,207	1,005	6,909	4,188
Q13873*	Bone morphogenetic protein receptor type-2	BMPR2	6	94.9	0.016	-3.2	10,281	8,130	32,517	11,373
P13671*	Complement component C6	C6	24	211.1	0.000	-3.3	4,201	1,181	13,691	3,440
P04275*	von Willebrand factor	VWF	6	40.9	0.026	-3.3	2,022	1,130	6,652	4,029
Q6ZTR6	Putative uncharacterized protein C18orf65	C18orf65	1	5.3	0.002	-3.3	3,451	1,040	11,464	4,244
Q9BRJ6	Uncharacterized protein C7orf50	C7orf50	1	10.2	0.004	-3.4	410	263	1,380	276
Q9NRX4	14 kDa phosphohistidine phosphatase	PHPT1	10	101.4	0.044	-3.4	15,032	5,925	51,222	30,568
Q96MC5	bMERB domain-containing protein 1	BMERB1	2	19.9	0.017	-3.4	1,147	721	3,932	922
P11047*	Laminin subunit gamma-1	LAMC1	39	317.5	0.013	-3.5	36,717	21,044	128,777	30,682
P02794	Ferritin heavy chain	FTH1	2	9.3	0.004	-3.5	4,505	1,898	15,839	6,225
Q9NQS3*	Nectin-3	NECTIN3	4	27.0	0.025	-3.5	2,254	1,207	7,936	3,836
P26641	Elongation factor 1-gamma	EEF1G	11	106.9	0.043	-3.6	5,513	1,361	19,706	17,716
O75874*	Isocitrate dehydrogenase [NADP] cytoplasmic	IDH1	33	239.5	0.006	-3.6	8,439	2,022	30,217	19,798
Q6ZMJ2	Scavenger receptor class A member 5	SCARA5	4	28.8	0.004	-3.6	775	370	2,782	1,099
Q9ULH7	Myocardin-related transcription factor B	MRTFB	1	13.7	0.004	-3.7	941	343	3,439	2,115

P17275	Transcription factor jun-B	JUNB	1	14.9	0.049	-3.7	2,073	667	7,613	5,282
P04114*	Apolipoprotein B-100	APOB	4	37.9	0.000	-3.8	5,628	1,648	21,566	6,511
P06681*	Complement C2	C2	1	25.2	0.001	-4.0	1,600	353	6,377	3,131
P78367	Homeobox protein Nkx-3.2	NKX3-2	1	29.7	0.030	-4.1	8,498	6,397	34,983	16,973
Q9NQ92	Coordinator of PRMT5 and differentiation stimulator	COPRS	1	5.0	0.012	-4.2	155	156	657	169
P56211	cAMP-regulated phosphoprotein 19	ARPP19	1	14.2	0.036	-4.3	80	45	346	277
O75897*	Sulfotransferase 1C4	SULT1C4	1	15.7	0.007	-4.3	6,511	4,095	28,240	6,077
Q05655*	Protein kinase C delta type	PRKCD	2	15.2	0.034	-4.5	1,226	914	5,509	4,354
Q5VY09	Immediate early response gene 5 protein	IER5	1	9.8	0.002	-4.8	196	79	946	598
Q9Y240	C-type lectin domain family 11 member A	CLEC11A	1	10.5	0.032	-4.9	1,603	1,067	7,889	3,353
Q8NC16*	Beta-galactosidase-1-like protein 3	GLB1L3	2	15.3	0.039	-5.1	3,569	2,097	18,238	14,756
Q9P2D1	Chromodomain-helicase-DNA-binding protein 7	CHD7	8	50.9	0.016	-5.3	1,351	1,113	7,103	5,378
O75153	Clustered mitochondria protein homolog	CLUH	3	15.7	0.015	-5.3	265	189	1,402	587
A8MTL3	RING finger protein 212B	RNF212B	2	22.9	0.040	-6.2	470	553	2,910	3,194
Q16644	MAP kinase-activated protein kinase 3	MAPKAPK3	1	10.0	0.042	-6.4	936	785	6,012	3,736
Q32M92	Uncharacterized protein C15orf32	C15orf32	2	9.8	0.032	-6.9	41	31	284	247
Q81X04	Ubiquitin-conjugating enzyme E2 variant 3	UEVLD	8	55.3	0.006	-7.0	1,697	1,008	11,815	9,692
Q96TC7	Regulator of microtubule dynamics protein 3	RMDN3	2	9.9	0.006	-8.2	431	481	3,523	2,420
Q86TD4	Sarcalumenin	SRL	1	25.9	0.018	-10.7	41	101	441	520
Q9UHD0	Interleukin-19	IL19	1	9.5	0.020	-20.7	26	31	530	291
Q8WTU2	Scavenger receptor cysteine-rich domain-containing group B protein	SSC4D	1	11.4	0.049	-23.5	72	72	1,687	2,249
Q96LB4	V-type proton ATPase subunit G 3	ATP6V1G3	1	15.6	0.012	-26.7	91	119	2,437	2,147
Q9UIG4	Psoriasis susceptibility 1 candidate gene 2 protein	PSORS1C2	1	7.3	0.038	-28.2	30	22	835	1,320

Differentially expressed proteins in PCOS vs. insulin resistance study. Differentially expressed proteins are ranked according to maximum fold change. The following data are displayed; protein and gene name; accession number; total and unique peptide count; Progenesis Q1 confidence score; Progenesis Q1 ANOVA p value; the maximum fold change expressed as a positive number if more abundant in the PCOS cohort and a negative number if more abundant in the IR cohort; the fraction and total number of fractions in which the protein was identified; protein mass; and the normalised abundance of the protein in each sample. * = protein in significant IPA pathway