

### Supplementary Tables

**Supplementary Table 1.** The list of hamster cholesterol synthesis proteins used to generate an inclusion list for targeted LC-MS/MS

Accession ID	Name	Name description
EGW05732	Thiolase 2	Acetyl-CoA acetyltransferase, cytosolic
EGW00729	HMGCS	Hydroxymethylglutaryl-CoA synthase, cytoplasmic
EGW03272	HMGCR	3-hydroxy-3-methylglutaryl-coenzyme A reductase
EGW10615	MK	Mevalonate kinase
EGV98107	PMK	Phosphomevalonate kinase
EGV94082	MVD	Diphosphomevalonate decarboxylase
EGV95102	IDI1	Isopentenyl-diphosphate Delta-isomerase 1
EGV95103	IDI2	Isopentenyl-diphosphate Delta-isomerase 2
XP_003501631	FPPS	Farnesyl pyrophosphate synthase
XP_003509928	GGPPS	Geranylgeranyl pyrophosphate synthase
ERE90221	SQS	Squalene synthase
EGV91499	SM	Squalene monooxygenase
ERE88051	LS	Lanosterol synthase
EGV95701	LDM	Lanosterol 14-alpha demethylase
EGW12250	DHCR14	Delta(14)-sterol reductase
ERE72972	LBR	Lamin-B receptor
ERE92332	SC4MOL	Methylsterol monooxygenase 1
EGW03873	NSDHL	Sterol-4-alpha-carboxylate 3-dehydrogenase, decarboxylating
ERE73196	HSD17B7	3-keto-steroid reductase-like protein
XP_003505155	Sterol isomerase	3-beta-hydroxysteroid-Delta(8),Delta(7)-isomerase
XP_003511419	SC5D	Lathosterol oxidase
ERE81054	DHCR7	7-dehydrocholesterol reductase
XP_003495787	DHCR24	24-dehydrocholesterol reductase

**Supplementary Table 2.** Cholesterol synthesis proteins identified by LC-MS/MS after DHCR24 immunoprecipitation

Accession ID	Name / Name description	Experiment	Found? (peptide sequence(s) identified)	Protein coverage (%)	Mascot score	Expect (p-value)	Modifications	Precursor charge (+)	Observed m/z	Appm	Missed cleavages		
XP_003495787.1	DHCR24 / 24-dehydrocholesterol reductase	IP1	Y	5.39	82.75								
			LTQGETLR		40	2.40E-02		2	459.25656	0.8	0		
			LTQGETLRK		37	2.70E-02		2	523.30328	-0.76	1		
					LNSIGNYYKPWFFK		56	4.60E-04		2	888.96008	1.15	0
		IP2	Y	8.14	196.93								
			EGLEYIPLR		65	3.90E-05		2	545.30035	-0.46	0		
			FTHESQR		37	1.30E-02		2	452.71722	-0.01	0		
			GLEFVLIHQQR		51	4.10E-04		2	606.34894	0.85	0		
			LTQGETLR		47	3.70E-03		2	459.25613	-0.13	0		
			LTQGETLRK		43	4.40E-03		2	523.30334	-0.64	1		
			VKHFEAR		37	1.50E-02		2	443.7482	-0.31	1		
		IP3	Y	3.10	51.96								
			FTHESQR		37	1.10E-02		2	452.7168	-0.96	0		
			LTQGETLRK		38	1.60E-02		2	523.30298	-1.34	1		
			LTQGETLR		40	1.70E-02		2	459.25638	0.4	0		
		IP3 (statin treated)	Y	3.10	63.57								
			FTHESQR		40	5.70E-03		2	452.71677	-1.02	0		
			LTQGETLRK		36	2.30E-02		2	523.30316	-0.99	1		
			LTQGETLR		39	2.00E-02		2	459.25604	-0.33	0		
		IP4 (statin treated)	Y	17.05	698.73								
			EGLEYIPLR		51	9.70E-04		2	545.30066	0.1	0		
FTHESQR			40	5.60E-03		2	452.71683	-0.89	0				
GLEFVLIHQQR			41	3.90E-03		2	606.34845	0.04	0				
HVENYLK			36	3.40E-02		2	451.74002	-0.33	0				
HYYHR			29	1.50E-02		2	388.18539	0.12	0				
LTQGETLR			50	1.70E-03		2	459.25598	-0.46	0				
LTQGETLRK			45	2.40E-03		2	523.30334	-0.64	1				
LYEQHHVVQDMLVPMK			41	8.80E-03	M11(Oxidation); M15(Oxidation)	3	666.99731	-0.14	0				
NIMINLMDILEVDTKK			75	4.00E-06	M3(Oxidation); M7(Oxidation)	2	961.50012	-2.32	1				
TNREGLEYIPLR			45	4.10E-03		2	730.89783	1.86	1				
ERE81054	DHCR7 / 7-dehydrocholesterol reductase	IP1	Y	2.32	39.25								
			LLVSGFWGVAR		39	1.30E-02		2	602.84589	0.6	0		
		IP2	Y**	7.01	93.06								
			FLPGYVGGVQEGAVTPAGVVNK		46	2.00E-03		2	1080.08374	4.89	0		
			LLVSGFWGVAR		39	8.80E-03		2	602.84589	0.6	0		
		IP3	Y	2.32	59.04								
			LLVSGFWGVAR		41	6.20E-03		2	602.8457	0.3	0		
		IP3 (statin treated)	Y*	2.32	25.40								
			LLVSGFWGVAR		25	2.20E-01		2	602.84583	0.5	0		
		IP4 (statin treated)	Y*	1.81	29.28								
YTATVPYR			24	2.10E-01		2	485.75381	1.11	0				

Accession ID	Name / Name description	Experiment	Found? (peptide sequence(s) identified)	Protein coverage (%)	Mascot score	Expect (p-value)	Modifications	Precursor charge (+)	Observed m/z	Appm	Missed cleavages
ERE90221	SQS / Squalene synthase	IP1	N	-	-						
		IP2	Y	2.99	48.40						
			SFAAVIQALDGEIR		40	1.00E-02		2	745.40411	-0.03	0
		IP3	N	-	-						
		IP3 (statin treated)	Y	2.99	34.29						
			QVLEDFPTISLEFR		34.00	4.00E-02		2	847.44324	-0.26	0
EGW05732	Thiolase 2 / Acetyl-CoA acetyltransferase, cytosolic	IP4 (statin treated)	Y	2.13	59.54						
			DYLEDQQEGR		40	3.60E-03		2	626.77698	2.07	0
		IP1	Y	6.80	105.71						
			DFSATDLTEFAAR		71	9.00E-06		2	722.34222	1.42	0
			LEDTLWAGLTDQHVK		35	5.30E-02		2	863.44415	0.19	0
		IP2	Y	14.11	133.91						
EGW03272	HMGCR / 3-hydroxy-3-methylglutaryl-coenzyme A reductase		AGIPKEEVK		31	4.80E-02		2	485.7818	-0.52	1
			EVYMGNVLQGGEGQAPTR		60	9.20E-05 M4(Oxidation)		2	961.4588	1.55	0
			LGSIAIQGAIEK		49	8.50E-04		2	600.35352	0.23	0
			TPIGSFMGSLASQPATK		64	4.60E-05 M7(Oxidation)		2	854.93225	-0.18	0
		IP3	N	-	-						
		IP3 (statin treated)	N	-	-						
		IP4 (statin treated)	N	-	-						
		IP1	N	-	-						
		IP2	N	-	-						
		IP3	N	-	-						
EGV91499	SQLE / Squalene monooxygenase	IP3 (statin treated)	N*	-	-						
		IP4 (statin treated)	Y**	6.59	417.98						
			ATFVLGASGTSPVAAR		50	1.10E-03		2	801.4364	0.53	0
			FLSDAEIHQLVNAK		58	1.30E-04		2	780.93439	-1.13	0
			LPEPSSLQYLPYR		38	1.60E-02		2	781.91498	0.84	0
			LSSVEEPEGVSQDR		70	6.90E-06		2	766.36652	1.45	0
ERE72972	LBR / Lamin-B receptor	IP1	N	-	-						
		IP2	N	-	-						
		IP3	N	-	-						
		IP3 (statin treated)	N	-	-						
		IP4 (statin treated)	Y**	14.44	116.61						
			EAFLEASQSAR		68	1.70E-05		2	604.80005	1.8	0
EGW05732	Thiolase 2 / Acetyl-CoA acetyltransferase, cytosolic		ELHAPLTVVADGLFSK		41	6.10E-03		2	848.96912	2.37	0
		IP1	N	-	-						
		IP2	Y	5.49	204.02						
			VPAPLETFQVTTTPQR		63	4.30E-05		2	842.45831	1.68	0
			DELSPASSGNAVYDFFIGR		74	4.10E-06		2	1022.98523	0.99	0
		IP3	N	-	-						
EGW05732	Thiolase 2 / Acetyl-CoA acetyltransferase, cytosolic	IP3 (statin treated)	N	-	-						
		IP4 (statin treated)	N	-	-						

Accession ID	Name / Name description	Experiment	Found? (peptide sequence(s) identified)	Protein coverage (%)	Mascot score	Expect ( <i>p</i> -value)	Modifications	Precursor charge (+)	Observed <i>m/z</i>	Δppm	Missed cleavages
ERE73196	HSD17B7 / 3-keto-steroid reductase-like protein	IP1	N	-	-						
		IP2	N	-	-						
		IP3	N	-	-						
		IP3 (statin treated)	N	-	-						
		IP4 (statin treated)	Y	YLSSTTGFGTNYVR	4.20	38.33	1.70E-02		2	783.38336	-0.02
EGW03873	NSDHL / Sterol-4-alpha-carboxylate-3-dehydrogenase, decarboxylating	IP1	N	-	-						
		IP2	N	-	-						
		IP3	N	-	-						
		IP3 (statin treated)	N	-	-						
		IP4 (statin treated)	Y	DPQLVPILIDAAR	6.25	41.75	3.20E-03		2	710.91064	-1.34

**Notes:** Data from IP1 and IP2 were generated from a limited number of gel bands. Y, protein found; Y\*, protein inferred from a peptide identified with a Mascot Expect value > 0.05, as MS/MS spectra derived from this peptide match those obtained in other experiments where the same peptide was identified with a higher Mascot Ion Score; Y\*\*, protein found in EV as well, but with fewer peptide hits in EV; N, protein not found; N\*, protein found with more peptide hits in EV (data omitted). The Mascot scores, protein coverage, and number of peptide matches are all derived from peptides identified with Mascot Expect values < 0.05, except for underlined scores.