Electronic Supplement for:

Studies of Cell Signaling, Reactive Oxygen Species and Cytotoxicities Allow Enhanced Molecular Level Understanding of Selenium Mediated Arsenic Toxicity

by

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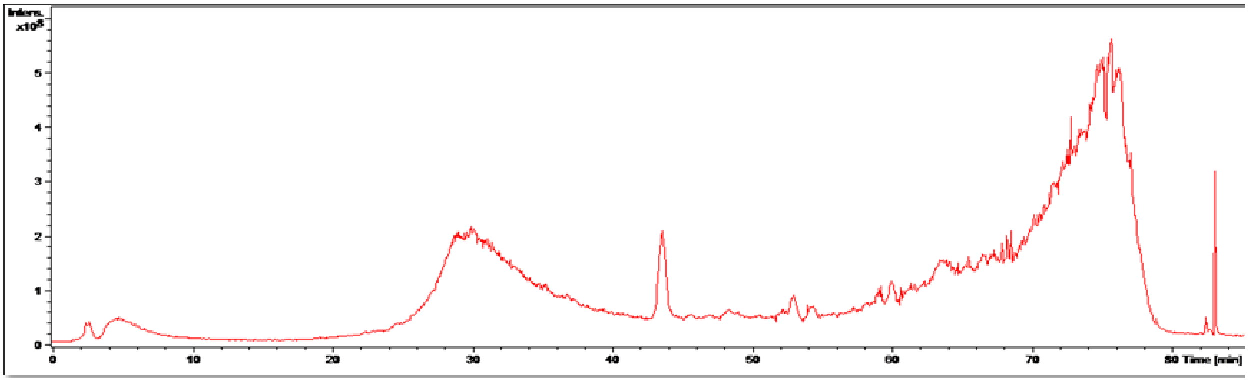

Figure S1a: A figure showing the total ion chromatogram (*β*-casein peptide) representing intensity (y-axis) vs time (x-axis). Loading and peptide trapping was performed at a flow rate of 4 *μ*L/min using 0.6% acetic acid (HOAc) and 2% formic acid (FA) in water. Solvents used for the nanoflow experiment were 0.6% HOAc/0.5% FA (solvent A) and 0.6% HOAc/0.5% FA/80% acetonitrile (ACN) (solvent B). Samples were loaded on-to the enrichment column at a flow rate of 3 μL min^{-1} with a 97:3 ratio of solvent A (0.1% FA (v/v) in water) and B (90% ACN, 0.1% FA (v/v) in water). After the enrichment column was loaded, the on-chip microfluidics switched to the analytical column at a flow rate of 0.3 μL min^{-1}. Gradient: 0–2 min, 2% B; 5–50 min, 40%B; 50–60 min, 70% B; 60–70 min, 90% B; 70–90 min, 0% B.

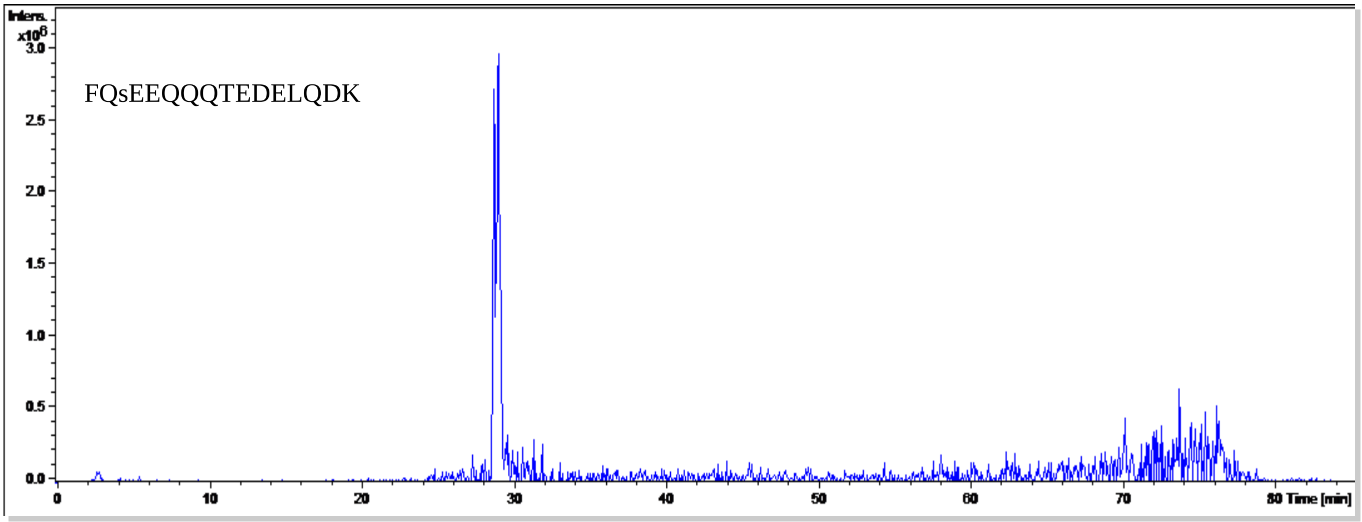

Figure S1b: A figure of an extracted ion chromatogram for the *β*-casein peptide containing intensity (y-axis) vs time (x-axis).

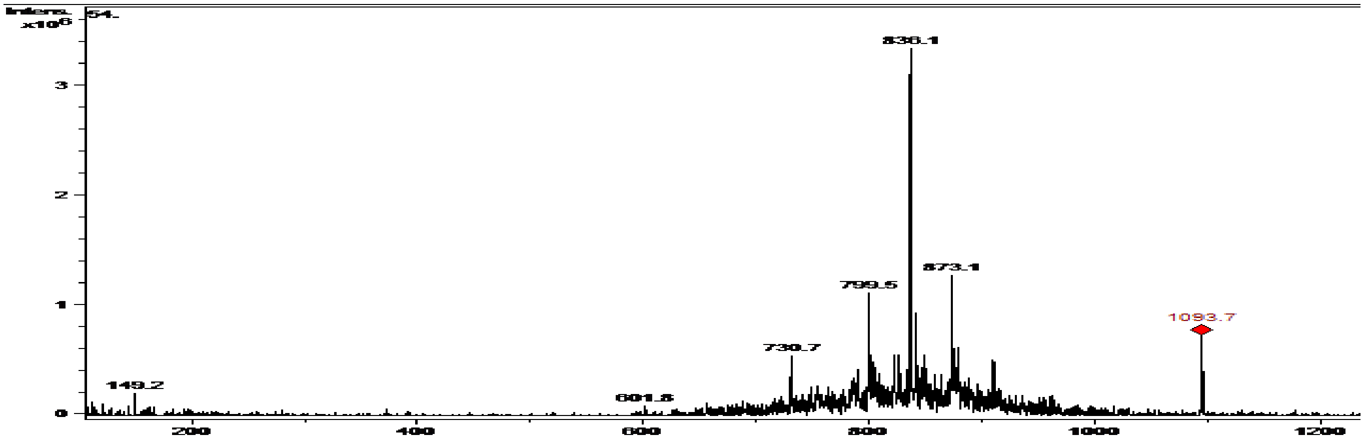

Figure S1c: A figure showing the mass spectra of *β*-casein peptide (m/z-1093.7) at the red diamond.

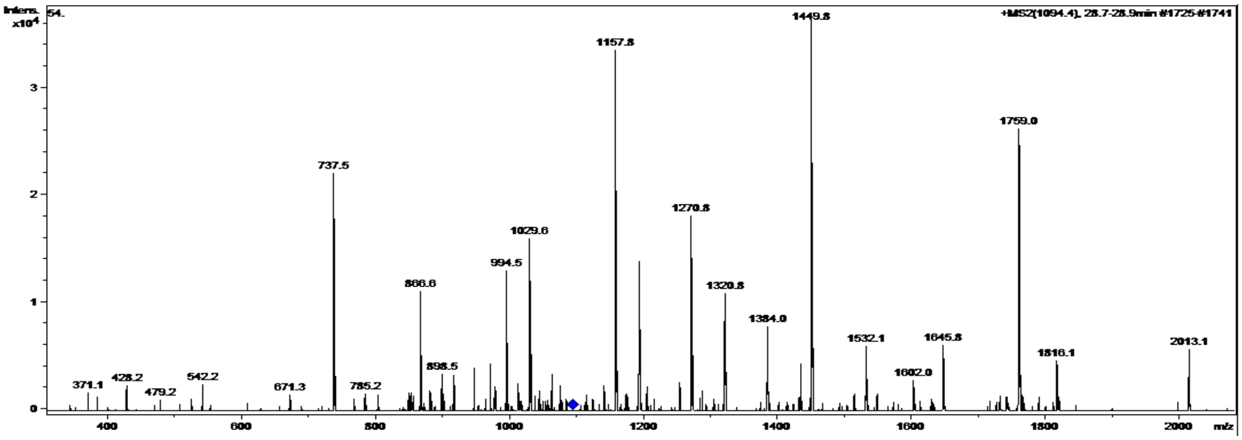

Figure S1d: A figure showing the MS/MS of the m/z-1093.7.

Data Base	**Parent charge**	**score**	**sequence**	**Matched parent mass**	**Accession number**	**Entry name**
Spectrum Mill	**2**	**19.74**	**(R)DMPIQAFLLYQEPVLGPVR(G)**	**2186.16**	**P02666**	**Beta-casein**
Mascot	**2**	**90.84**	**(R)DMPIQAFLLYQEPVLGPVR(G)**	**2186.86**	**P02666**	**Beta-casein**

Table S1: Shows the identification of Beta-casein using Spectrum Mill data base

No	Charge	Score	Peptide Intensity	Total Intensity	Sequence	Modifications	Matched parent mass	Accession number	Entry name	Variable Sites found in the study	UniprotKB Reported Variable Sites
1	2	16.67	86.8	4980063	(R)FQVWDYEEGEVEALLDR(Y)		2097.976	O43598	Deoxyribonucleoside 5'-monophosphate N-glycosidase	NR	S : 12, 28, 169
2	3	11.01	81.8	13196563	(K)DQFPEVYVPTVFENYVADIEVDGK(Q)		2773.324	P61586	Transforming protein RhoA	NR	S : 34, 37, 156
3	3	10.18	79.9	8300444	(K)TLRVLNLEYNQLttFPKALCFLPK(L)	C:Carbamidomethylation t:Phosphorylated T	2879.585	A4D1F6	Leucine-rich repeat and death domain-containing protein	T : 293, 294	NR
4	3	10.07	88.7	6941975	(R)YLLQYQEPIPCEQLVTALCDIK(Q)	C:Carbamidomethylation	2694.352	P25789	Proteasome subunit alpha type-4	NR	S : 13, 75
5	3	9.9	68.4	4812443	(R)ssNYEIITGHEEGYFTAIMLKK(S)	s:Phosphorylated S	2531.249	O95551	Tyrosyl-DNA phosphodiesterase 2	S : 195, 196	NR
6	3	9.1	78.5	3489902	(R)EQPAPNHRGsLPVtTIFSGPKHSR(S)	t:Phosphorylated T s:Phosphorylated S	2613.364	Q9P2P6	StAR-related lipid transfer protein 9	S : 3219 T : 3223	NR
7	3	8.81	64.9	5251199	(K)ALNTtDsSSSPSLADGIDTSGGGSIHVISR(D)	t:Phosphorylated T s:Phosphorylated S	2902.403	P49116	Nuclear receptor subfamily 2 group C member 2	T : 323 S: 325	S : 19, 46, 55, 68, 219 T : 224
8	3	7.87	64.1	8633731	(R)sPIPIRVETAQPAVEKPEIKPPRVR(K)	s:Phosphorylated S	2807.625	Q9H329	Band 4.1-like protein 4B	S : 650	NR
9	3	7.82	82.4	5297382	(K)MCLYFGsAFATPFLVVRHQLLKT(-)	C:Carbamidomethylation s:Phosphorylated S	2699.42	P15954	Cytochrome c oxidase subunit 7C, mitochondrial	S : 47	NR
10	3	7.67	88	3363724	(R)IAAQDLLLAVATDFQNESAAALAAAATR(H)		2786.468	Q96P70	Importin-9	NR	NR

11	3	7.4	60.4	6291673	(K)ASKEPVGCVNNIsFLASLAGStSRNR(L)	C:Carbamidomethylation t:Phosphorylated T s:Phosphorylated S	2735.389	Q86XD8	AN1-type zinc finger and ubiquitin domain-containing protein	S : 568 T : 577	NR
12	3	7.26	83.9	5962927	(R)LQAFFtsDTGLEYEAPKLYPAIPAAR(R)	t:Phosphorylated T s:Phosphorylated S	2869.477	Q9UBC3	DNA (cytosine-5)-methyltransferase	S : 552 T : 551	NR
13	3	7.25	100	2641592	(R)IDKAPSFTsQDFHGDVNLLK(E)	s:Phosphorylated S	2232.13	Q8NHP7	Exonuclease 3'-5' domain-containing protein 1	S : 370	NR
14	3	7.11	91.2	1798411	(K)RISDSEVsDYDCDDGIGVVSDYRHDGR(D)	C:Carbamidomethylation s:Phosphorylated S	3087.334	Q9UQ26	Regulating synaptic membrane exocytosis protein 2	S : 973	S : 366, 400, 427, 429, 1030, 1038 T : 973
15	3	7.01	85.8	5178341	(R)LLGAYLFIISRVQGQNLDSMLHGtGMK(S)	t:Phosphorylated T	2962.564	P36894	Bone morphogenetic protein receptor type-1A	T : 42	S : 215, 216, 218, 220
16	3	6.84	62	3161782	(R)GSYTEKDAsHLVGQVLGAVSYLHSLGIVHR(D)	s:Phosphorylated S	3193.675	Q6P2M8	Calcium/calmodulin-dependent protein kinase type 1B	S : 114	NR
17	3	6.75	93.3	1712349	(R)NLSFDSEEEELGELLQQFGELK(Y)		2554.22	Q9NW13	RNA-binding protein 28	NR	S : 122, 202
18	3	6.63	62.1	6217155	(K)RLVLTHFSQRYKPVALAR(E)		2155.261	Q9H777	Zinc phosphodiesterase ELAC protein 1	NR	NR
19	3	6.62	90.1	4703006	(R)TDERLNWIyYKDQTGNNR(V)	y:Phosphorylated Y	2286.09	O15537	Retinoschisin	Y : 165	NR
20	3	6.5	100	2165855	(K)LsQLKsQQVAAAAHEANKLFK(E)	s:Phosphorylated S	2282.262	Q12830	Nucleosome-remodeling factor subunit BPTF	S : 788, 792	S : 216, 572, 763, 817, 1231, 1300, 1827, 1833, 2098, 2465 T : 909, 1064 Y : 839

21	**3**	**6.41**	**81.4**	**1761384**	**(K)QTEFIItAEILRELsMECGLNNRIR(M)**	**C:Carbamidomethylation t:Phosphorylated T s:Phosphorylated S**	**3006.55**	**P49815**	**Tuberin**	**S : 41, 49**	**S : 939, 981, 1097, 1132, 1155, 1334, 1337, 1338, 1341, 1364, 1387, 1388, 1411, 1418, 1420, 1449, 1452, 1462, 1798 T : 927**
22	**3**	**6.27**	**91**	**2842742**	**(K)LPSSVFAsEFEEDVGLLNKAAPVSGPR(L)**	**s:Phosphorylated S**	**2816.447**	**Q96GA3**	**Protein LTV1 homolog**	**S : 116**	**S : 182, 188, 244, 331**
23	**3**	**6.19**	**87.6**	**5197425**	**(K)RVEIMAQCEEWIADIQQYsSDK(R)**	**C:Carbamidomethylation s:Phosphorylated S**	**2699.244**	**Q9NR09**	**Baculoviral IAP repeat-containing protein 6**	**S : 4781**	**S : 473, 480**
24	**3**	**6.06**	**64.5**	**2327496**	**(R)GGDVASMYTPNAQYCQMRCtFHPR(C)**	**C:Carbamidomethylation t:Phosphorylated T**	**2847.222**	**P03952**	**Plasma kallikrein**	**T : 52**	**NR**

Table S2: Proteins identified in fraction 1 of cells grown together with As(III) and SeMet, fraction isolated based on Size Exclusion Chromatography (SEC).

No	Charge	Score	Peptide Intensity	Total Intensity	Sequence	Modifications	Matched parent mass	Accession number	Protein name	Variable Sites found in the study	UniprotKB Reported Variable Sites
1	2	19.79	97.1	6288674	(R)IQEIIEQLDVTTSEYEK(E)		2038.02	P10809	60 kDa heat shock protein, mitochondrial	NR	S : 70
2	2	15.54	88.7	6790895	(K)ATAGDTHLGGEDFDNR(L)		1675.73	P34931	Heat shock 70 kDa protein	NR	NR
3	2	14.5	100	1E+07	(R)VEIIANDQGNR(I)		1228.62	P11021	78 kDa glucose-regulated protein	NR	T : 166, Y : 466, S : 571
4	2	11.62	79.7	1.5E+07	(K)DCGATWVVLGHSER(R)	C:Carbamidomethylation	1586.73	P60174	Triosephosphate isomerase	NR	S : 21, 80
5	2	11.5	100	9763194	(K)DSYVGDEAQSK(R)		1198.52	P62736	Actin, aortic smooth muscle	NR	S : 325
6	3	11.38	85.3	1.2E+07	(R)CTEPEDQLyyVKFLSLPEVR(Q)	C:Carbamidomethylation y:Phosphorylated Y	2486.22	Q9H3G5	Probable serine carboxypeptidase CPVL	Y : 328, 329	NR
7	2	10.8	80.1	9369689	(K)TAFQEALDAAGDK(L)		1336.63	P10599	Thioredoxin	NR	T : 100
8	2	9.98	81.4	2552994	(K)GHYTEGAELVDSVLDVVR(K)		1958.98	Q13885	Tubulin beta-2A chain	NR	S : 78, 95
9	3	9.84	95.4	3433608	(K)AEASSGDHPTDTEMKEEQK(S)		2089.89	Q02790	Peptidyl-prolyl cis-trans isomerase FKBP4	NR	T : 143, S : 451, 453
10	3	9.84	74.2	2.2E+07	(R)ASDTLSAEVRTRVGyVR(Q)	y:Phosphorylated Y	1879.99	Q9H254	Spectrin beta chain	Y : 2178	T : 2111, 2112 S: 2121
11	3	8.58	64.7	9424084	MSHLQsLLLDtLLGTKHVDSAALIK(I)	t:Phosphorylated T s:Phosphorylated S	2704.5	Q8NHR9	Profilin-4	S : 6, T : 11	NR
12	2	8.51	83	1.8E+07	(K)GDGPVQGIINFEQK(E)		1501.76	P00441	Superoxide dismutase	NR	S : 99

13	**3**	**8.31**	**90**	**1.4E+07**	**(R)DVVCEDEDAFCLsLENIATLQKLLR(Q)**	**C:Carbamidomethylation s:Phosphorylated S**	**2951.44**	**O43663**	**Protein regulator of cytokinesis**	**S : 211**	**S : 195, 265, 501, 513, 571, 592, 615 T: 470, 481, 616**
14	**3**	**8**	**100**	**2270809**	**(K)AGAAPYVQAFDSLLAGPVAEYLK(I)**		**2351.22**	**Q01518**	**Adenylyl cyclase-associated protein**	**NR**	**S : 290, 295, 301, 308, 310 T : 164, 307**
15	**2**	**7.91**	**84.1**	**6794591**	**(R)SVGDGETVEFDVVEGEK(G)**		**1795.82**	**P16989**	**DNA-binding protein A**	**NR**	**S : 2, 34, 38, 79, 134, 201, 203, 287, 369, 370 T : 287**
16	**3**	**7.8**	**75.7**	**8236621**	**(K)MAKSFTSEDDLVKLQILNLGAK(L)**		**2421.3**	**O00203**	**AP-3 complex subunit beta-1**	**NR**	**S : 276, 609, 661**
17	**2**	**7.69**	**91.8**	**3069351**	**(R)HPEIKVTAK(Y)**		**1022.59**	**Q96JM2**	**Zinc finger protein 462**	**NR**	**S : 1076, 1079, 1082, 2024 Y : 2083**
18	**2**	**7.52**	**83.3**	**6119478**	**(R)DADDAVYELNGK(D)**		**1309.59**	**Q08170**	**Serine/arginine-rich splicing factor 4**	**NR**	**S : 113, 222, 255, 300, 302, 304, 316, 322, 448, 458, 460, 462 Y : 53 T : 440**
19	**3**	**7.45**	**72.5**	**2476994**	**(R)DLLPSGSRDEPPPASQSTSQDCsQALKQSP(-)**	**C:Carbamidomethylation s:Phosphorylated S**	**3183.48**	**Q5JRA6**	**Melanoma inhibitory activity protein 3**	**S : 1900**	**S : 727, 1727, 1739, 1740, 1892, 1906 T : 382**
20	**3**	**7.4**	**68.2**	**2319204**	**(R)SLDAQSVyVATDSESYVPELQQLFK(G)**	**y:Phosphorylated Y**	**2817.38**	**Q9H488**	**GDP-fucose protein O-fucosyltransferase 1**	**Y : 307**	**NR**
21	**2**	**7.1**	**83.8**	**5427945**	**(R)DPENFPFVVLGNK(I)**		**1475.75**	**P51149**	**Ras-related protein Rab-7a**	**NR**	**S : 72 Y : 183**
22	**2**	**7.05**	**69.1**	**1.3E+09**	**(K)SSNVLLDQNLtPK(L)**	**t:Phosphorylated T**	**1428.76**	**O43187**	**Interleukin-1 receptor-associated kinase-like 2**	**T : 348**	**T : 368**
23	**2**	**7**	**67.3**	**6831116**	**(K)EKtIsVSSSKSGPVIAK(R)**	**t:Phosphorylated T s:Phosphorylated S**	**1717.96**	**Q8N3X1**	**Formin-binding protein 4**	**S : 285 T : 283**	**S : 18, 116, 172, 432, 435, 442, 499, 508, 963, 964, 965 T : 516, 517 Y : 113**

24	3	6.92	85	4142276	(K)FTEWAYGPVHSSLYDLsCIDtCEK(N)	C:Carbamidomethylation t:Phosphorylated T s:Phosphorylated S	2878.27	Q8NER1	Transient receptor potential cation channel subfamily V member	S : 386 T : 390	S : 117, 502, 775, 801, 821 T : 145, 371, 705
25	3	6.75	77.6	6825687	(K)STPSAPWITEMMNsVSEDtIK(E)	t:Phosphorylated T s:Phosphorylated S	2324.07	Q8WXI7	Mucin-16		NR
26	3	6.73	84.7	7615616	(K)SEFPIRTLKtLLHtLCK(L)	C:Carbamidomethylation t:Phosphorylated T	2057.15	Q14008	Cytoskeleton-associated protein	T : 1762, 1766	S : 816
27	2	6.73	93.6	9457260	(K)KVEEAEPEEFVVEK(V)		1661.82	Q13185	Chromobox protein homolog	NR	S : 93, 95, 97, 99, 176
28	2	6.72	75.2	1.1E+07	(R)yATALYsAASKQNK(L)	y:Phosphorylated Y s:Phosphorylated S	1515.78	P48047	ATP synthase subunit O, mitochondrial	S : 47 Y : 41	NR
29	3	6.67	67.4	3E+07	(K)LNTPSSLAVCADGELYVADLGNIRIR(F)	C:Carbamidomethylation	2817.45	Q6N022	Teneurin-4	NR	NR
30	3	6.6	88	7855747	(MGKAENyELYSVELGPGPGGDMAAK(M)	y:Phosphorylated Y	2584.2	P20648	Potassium-transporting ATPase alpha chain	Y : 7	S : 954
31	2	6.5	100	4018747	(K)EKsEFVDDITtR(R)	t:Phosphorylated T s:Phosphorylated S	1439.7	Q9Y6V0	Protein piccolo	S : 1428 T : 1436	S : 2895
32	2	6.45	97.4	2492273	(K)HGDPGDAAQQEAK(H)		1323.59	O14737	Programmed cell death protein	NR	S : 119
33	2	6.23	73.8	3691102	(K)TENNDHINLK(V)		1197.58	P61956	Small ubiquitin-related modifier	NR	NR
34	3	6.22	73	1.2E+07	(R)CQGsGDDNLTSLGtLNFPGR(T)	C:Carbamidomethylation t:Phosphorylated T s:Phosphorylated S	2108.96	P04150	Glucocorticoid receptor	S : 370 T : 380	S : 45, 134, 203, 211, 226, 234, 267 T : 8
35	3	6.22	74.4	2327828	(K)LFFHTEYEKtNPGMKPYGyKECGK(G)	C:Carbamidomethylation t:Phosphorylated T y:Phosphorylated Y	2924.37	P17025	Zinc finger protein 182	T : 199 Y : 208	NR
36	3	6.21	73	1.8E+07	(K)TTAPFKIPKtQASsNLLALVTR(H)	t:Phosphorylated T s:Phosphorylated S	2357.35	Q8IYT8	Serine/threonine-protein kinase ULK2	S : 617 T : 613	NR

37	**3**	**6.13**	**93.7**	**9979191**	**(K)AVGsLDPSADLSSQRGKVFK(L)**	**s:Phosphorylated S**	**2062.09**	**O14522**	**Receptor-type tyrosine-protein phosphatase**	**S : 529**	**NR**
38	**3**	**6.09**	**89.9**	**3329637**	**(R)DMQPLSPISVHERysSPTAGSAK(R)**	**y:Phosphorylated Y s:Phosphorylated S**	**2458.2**	**P28749**	**Retinoblastoma-like protein**	**S : 649 Y : 648**	**S : 640, 650, 749, 762, 964, 975, 988, 1009 T : 332, 369, 385, 997**

Table S3: Proteins identified in fraction 2 of cells grown together with As(III) and SeMet, fraction isolated based on Size Exclusion Chromatography (SEC).

No	Charge	Score	Peptide Intensity	Total Intensity	Sequence	Modifications	Matched parent mass	Accession number	Entry name	Variable Sites found in the study	UniprotKB Reported Variable Sites
1	2	11.29	95.1	8.79E+06	(K)DVNFEFPEFQL(-)		1384.642	P62081	40S ribosomal protein S7	NR	NR
2	3	10.25	67.7	1.29E+08	(R)QSQPPSIsFNKtINSR(I)	t:Phosphorylated T s:Phosphorylated S	1803.935	P82987	ADAMTS-like protein 3	S : 1189 T : 1193	NR
3	3	8.21	67.6	1.84E+08	(R)yANLGNVLILRSVSTAVYKR(F)	y:Phosphorylated Y	2237.276	O76090	Bestrophin-1	Y : 131	NR
4	3	7.85	68.5	4.58E+08	(K)WQVSREDQDKVAVLsQNR(T)	s:Phosphorylated S	2158.1	Q9BWD1	Acetyl-CoA acetyltransferase, cytosolic	S : 185	NR
5	3	7.21	84.6	5.67E+07	(R)HMSVALSWAVtSRQDPTSQK(V)	t:Phosphorylated T	2229.108	P55345	Protein arginine N-methyltransferase 2	T : 414	NR
6	3	7.15	75.2	1.38E+08	(K)RsSSMADGDNSyCLEAIIR(Q)	C:Carbamidomethylation y:Phosphorylated Y s:Phosphorylated S	2144.97	Q9ULV0	Myosin-Vb	S : 1642 Y : 1652	S : 1446 Y : 694
7	3	7.09	64.8	2.06E+07	(R)WVDPNSPVLLEDPVLCALAK(K)	C:Carbamidomethylation	2236.168	P42330	Aldo-keto reductase family 1 member C3	NR	NR
8	3	6.96	66.4	4.46E+07	(R)LTCEEEEEKMFGRGSR(H)	C:Carbamidomethylation	1957.874	P51532	Transcription activator BRG1	NR	S : 609, 610, 613, 655, 657, 660, 662, 695, 699, 721, 1382, 1452, 1570, 1575, 1586, 1627, 1631, 1640, 1642, 1644 T: 11, 609

9	**3**	**6.82**	**60.8**	**1.64E+07**	**(K)SsPGtQDLLGIQTGMMAPENK(V)**	**t:Phosphorylated T s:Phosphorylated S**	**2175.042**	**Q5SW79**	**Centrosomal protein of 170 kDa**	**S : 313 T : 316**	**T : 377, 501, 628, 937, 1533 S : 168, 354, 356, 359, 446, 502, 580, 630, 633, 636, 667, 838, 879, 930, 958, 1079, 1112, 1160, 1165, 1198, 1251, 1260, 1270, 1521, 1522, 1529, 1533**
10	**3**	**6.72**	**85.9**	**9.33E+07**	**(R)CGPRANGEEASSCAWVSRAPR(A)**	**C:Carbamidomethylation**	**2318.051**	**Q96N53**	**Putative uncharacterized protein encoded by NCRNA00167**	**NR**	**NR**
11	**3**	**6.64**	**67.5**	**1.27E+08**	**(R)STESVKSTVSETYLsKPSIAK(R)**	**s:Phosphorylated S**	**2242.181**	**Q7Z6B7**	**SLIT-ROBO Rho GTPase-activating protein 1**	**S : 421**	**S : 906, 917, 999, 1005, 1008, 1010, 1029, 1032 T : 1001, 1004**
12	**3**	**6.63**	**78.8**	**9.63E+06**	**(R)GGVSEGQMK(Q)**		**892.419**	**Q9HCK5**	**Protein argonaute-4**	**NR**	**S : 798**
13	**3**	**6.62**	**71.6**	**6.97E+06**	**(K)ETITKMLWStRtLLNITK(E)**	**t:Phosphorylated T**	**2149.205**	**Q5XG92**	**Carboxylesterase 4A**	**T : 383, 385**	**NR**
14	**3**	**6.59**	**65.9**	**1.83E+08**	**(K)AKPMCNtCGKVFSEASsLRR(H)**	**C:Carbamidomethylation t:Phosphorylated T s:Phosphorylated S**	**2299.11**	**Q9NPC7**	**Myoneurin**	**T : 306, S : 316**	**S : 289**
15	**3**	**6.58**	**67.9**	**1.67E+08**	**(R)DIHsGDFRDREGPPMDYR(G)**	**s:Phosphorylated S**	**2162.967**	**P78332**	**RNA-binding protein 6**	**S : 122**	**S : 360, 362, 891, 1022, 1025 T : 923 Y : 914**
16	**2**	**6.58**	**87.4**	**2.59E+06**	**(R)IGDQEFDSLPALLEFYK(I)**		**1984.99**	**P46108**	**Adapter molecule crk**	**NR**	**S : 41, 74 T : 42 Y : 136, 221, 239, 251**
17	**3**	**6.55**	**62.3**	**1.20E+08**	**(K)LRNRSSFStNVVYTTPGtR(V)**	**t:Phosphorylated T**	**2156.121**	**Q08828**	**Adenylate cyclase type 1**	**T : 554, 563**	**NR**

18	**3**	**6.43**	**60.2**	**1.29E+08**	**(R)GPPEGGLNEDERLLPKDK(K)**		**1964.008**	**P00519**	**Tyrosine-protein kinase ABL1**	**NR**	**S : 50, 446, 569, 618, 619, 620, 659, 683, 718, 805, 809, 855, 917, 919, 936, 949, 977 T : 392, 394, 613, 735, 781, 814, 844, 852 Y : 70, 185, 226, 253, 257, 264, 393, 469**
19	**3**	**6.24**	**73.2**	**1.69E+08**	**(R)AQNCNILLsRLKLSNDEIK(R)**	**C:Carbamidomethylation s:Phosphorylated S**	**2229.202**	**Q9Y4D1**	**Disheveled-associated activator of morphogenesis 1**	**S : 701**	**NR**
20	**3**	**6.2**	**73.7**	**1.56E+07**	**(K)VLySQGVKLFRFDAEVsQWK(E)**	**y:Phosphorylated Y s:Phosphorylated S**	**2400.271**	**A6NKT7**	**RanBP2-like and GRIP domain-containing protein 3**	**S : 1075 Y : 1061**	**NR**
21	**3**	**6.05**	**72.5**	**1.24E+08**	**(K)ELHVVYALsHVCGQDR(T)**	**C:Carbamidomethylation s:Phosphorylated S**	**1882.923**	**P20936**	**Ras GTPase-activating protein 1**	**S : 742**	**Y : 615**
22	**3**	**6.05**	**77.2**	**7.75E+07**	**(K)WDSEsNSERDVTKNSK(N)**	**s:Phosphorylated S**	**1881.857**	**P30414**	**NK-tumor recognition protein**	**S : 889**	**S: 347, 379, 406, 408, 410, 463, 572, 887, 889, 891, 1146 T : 343**
23	**3**	**6.04**	**70.4**	**1.84E+07**	**(K)HGLSYEVKPFLTALVDIVRsLK(K)**	**s:Phosphorylated S**	**2485.418**	**Q9Y5Q0**	**Fatty acid desaturase 3**	**S : 430**	**NR**
24	**3**	**6.03**	**61.2**	**2.74E+08**	**(R)SSGLSSRENSALTLTDSDNENK(S)**		**2325.08**	**Q9NT68**	**Teneurin-2**	**NR**	**S : 523 Y : 1150**

Table S4: Proteins identified in fraction 3 of cells grown together with As(III) and SeMet, fraction isolated based on Size Exclusion Chromatography (SEC).

No	Charge	Score	Peptide Intensity	Total Intensity	Sequence	Modifications	Matched parent mass	Accession number	Entry name	Variable Sites found in the study	UniprotKB Reported Variable Sites
1	3	8.61	63.2	1.07E+07	(R)GVKSSPIQTPNQTPQQAPVTPRK(E)		2459.336	Q8IZS6	Tctex1 domain-containing protein 3	NR	NR
2	3	8.47	69.2	1.76E+07	(K)tFLQREHQPFSLQCEAVYK(A)	C:Carbamidomethylation t:Phosphorylated T	2381.171	P08648	Integrin alpha-5	T : 944	NR
3	3	8.42	63.4	2.68E+06	(R)QFGALLQPGVNKFSLRMFGSQK(A)		2453.312	Q9UL51	Potassium/sodium hyperpolarization-activated cyclic nucleotide-gated channel 2	NR	S : 146, 779
4	3	8.22	63.6	2.47E+07	(K)stLKIPADKHLLQQLEMCVR(K)	C:Carbamidomethylation t:Phosphorylated T s:Phosphorylated S	2380.284	Q6NUP7	Serine/threonine-protein phosphatase 4 regulatory subunit 4	S : 634 T : 635	NR
5	3	8.04	66	1.34E+07	(K)FLYTVPNGNNPTGNSLTSERK(K)		2309.152	Q8N5Z0	Kynurenine/alpha-aminoadipate aminotransferase, mitochondrial	NR	NR
6	3	8.01	62.6	4.21E+06	(R)GPSLLQTPPRVPGQQALSRGDK(G)		2302.263	Q9UFV1	Putative TBC1 domain family member 29	NR	NR
7	3	7.73	69.8	8.87E+06	(R)FGLQGSAVASsFGNMMSKEKR(D)	s:Phosphorylated S	2232.09	Q8TE04	Pantothenate kinase 1	S: 496	NR
8	3	7.72	62.9	4.18E+07	(K)QNESRTTECKQNEstIVEPK(Q)	C:Carbamidomethylation t:Phosphorylated T s:Phosphorylated S	2378.125	Q6KC79	Nipped-B-like protein	S : 666 T : 667	S : 139, 150, 162, 274, 280, 284, 306, 318, 350, 353, 553, 849, 850, 912, 1089, 1090, 1096, 1150, 1152, 1154, 1160, 1459, 2509, 2511, 2513, 2658, 2672 T : 558, 646, 746, 914, 1458, 2667 Y : 1159
9	3	7.52	74.4	3.00E+06	(K)LSEETKVALTKLHNsLNEK(S)	s:Phosphorylated S	2154.177	O94874	E3 UFM1-protein ligase 1	S : 629	S : 458

10	3	7.26	63.4	9.31E+06	(R)VFEGPYKEYHEEAQKWDR(Y)		2311.078	Q9C0C4	Semaphorin-4C	NR	S : 832
11	3	7.05	69.6	4.59E+06	(K)yLGCKQDNsSSPKPSSVFR(N)	C:Carbamidomethylation y:Phosphorylated Y s:Phosphorylated S	2157.039	Q7Z4V0	Zinc finger protein 438	Y : 478 S : 486	NR
12	3	6.94	61.3	1.49E+07	(R)RIVFTITtGAGSAKQSPSSK(H)	t:Phosphorylated T	2036.113	Q8TEK3	Histone-lysine N-methyltransferase, H3 lysine-79 specific	T : 1051	S : 297, 374, 471, 596, 775, 882, 826, 834, 899, 902, 1001, 1009, 1104, 1246, 1349 T : 480, 900
13	3	6.9	60.9	3.27E+06	(K)ELHVVYALsHVCGQDR(T)	C:Carbamidomethylation s:Phosphorylated S	1882.923	P20936	Ras GTPase-activating protein1	S : 742	Y : 615
14	3	6.82	62	4.38E+06	(R)SENGSGsTMMQtKTFSSSSSSKK(M)	t:Phosphorylated T s:Phosphorylated S	2384.07	P53814	Smoothelin OS=Homo sapiens	S : 701 T: 706	S : 245, 301, 304, 341, 357, 503, 514, 576, 729 T : 351, 360
15	3	6.61	65.3	3.93E+07	(R)SVLDLVNYFLSPEKLTAENR(Y)		2308.218	Q9P2H5	Ubiquitin carboxyl-terminal hydrolase 35	NR	S : 613
16	3	6.51	81.1	1.86E+06	(K)MEGTGKKAVAGQQQAsVTAGK(V)	s:Phosphorylated S	2047.06	Q15025	TNFAIP3-interacting protein 1	S : 284	S : 99, 403 T : 438
17	3	6.38	62.1	5.02E+06	(R)DTNMIPGsPGSTELEGGFSRQRK(R)	s:Phosphorylated S	2464.189	Q12809	Potassium voltage-gated channel subfamily H member 2	S : 871	S : 320
18	3	6.38	61	1.44E+07	(R)NPAVLSAASFDGRISVYSIMGGStDGLR(Q)	t:Phosphorylated T	2841.42	O94979	Protein transport protein Sec31A	T : 338	S : 527, 532, 799, 1163 T : 1161
19	3	6.28	62.3	5.48E+06	(R)LMHKLSVEAPPKILVER(Y)		1960.141	P53990	IST1 homolog OS=Homo sapiens	NR	Y : 43
20	3	6.19	73.7	5.09E+06	(R)TREEWTSAQVPRGGEsQK(D)	s:Phosphorylated S	2046	Q6PRD1	Probable G-protein coupled receptor 179	S : 1616	NR
21	3	6.11	60.4	4.64E+06	(R)DPLMIFVLNEKVDEFSGVLR(V)		2321.221	Q9NZJ4	Sacsin	NR	S : 338, 4264 T : 4263 Y : 4333

Table S5: Proteins identified in fraction 4 of cells grown together with As(III) and SeMet, fraction isolated based on Size Exclusion Chromatography (SEC).

No	Charge	Score	Peptide Intensity	Total Intensity	Sequence	Modifications	Matched parent mass	Accession number	Entry name
1	3	18.76	90.2	6.61E+07	(K)LAYVAAGDLAPINAFIGGLAAQEVMK(A)		2603.39	P22314	Ubiquitin-like modifier-activating enzyme 1
2	2	18.39	97	1.47E+07	(R)LGFSEVELVQMVVDGVK(L)		1848.978	P12277	Creatine kinase B-type OS=Homo sapiens
3	3	16.45	88.6	7.81E+06	(R)NDFQLIGIQDGYLSLLQDSGEVR(E)		2580.294	P63241	Eukaryotic translation initiation factor 5A-1
4	3	15.21	84.1	4.67E+07	(R)YVEPIEDVPCGNIVGLVGVDQFLVK(T)	C:Carbamidomethylation	2759.432	P13639	Elongation factor 2 OS=Homo sapiens
5	3	13.47	88	2.80E+07	(K)DGPLNMILDDGGDLTNLIHTK(Y)		2252.123	P23526	Adenosylhomocysteinase
6	2	13.42	80.7	2.63E+07	(K)QIVWNGPVGVFEWEAFAR(G)		2105.06	P00558	Phosphoglycerate kinase 1
7	2	11.83	93.5	6.01E+06	(R)DLFEDELVPLFEK(A)		1593.805	O60506	Heterogeneous nuclear ribonucleoprotein Q
8	3	11.15	93.3	8.43E+06	(R)CLQILAAGLFLPGSVGITDPCESGNFR(V)	C:Carbamidomethylation	2892.438	Q12905	Interleukin enhancer-binding factor 2
9	3	10.83	86.3	1.08E+07	(K)ISFPAIQAAPSFSNSFPQIFR(D)		2325.203	P23381	Tryptophanyl-tRNA synthetase, cytoplasmic
10	2	10.32	83.5	2.39E+06	(K)ALINADELASDVAGAEALLDR(H)		2127.093	Q13813	Spectrin alpha chain
11	3	9.77	65.9	8.47E+06	(R)AVSTGVQAGIPMPCFTTALSFYDGYR(H)	C:Carbamidomethylation	2809.332	P52209	6-phosphogluconate dehydrogenase, decarboxylating
12	3	9.55	79.8	8.77E+06	(K)ASLVKNGAEFTDSLISNLLR(L)		2148.166	Q14562	ATP-dependent RNA helicase DHX8
13	2	9.2	90.3	4.77E+06	(K)LIIVSNPVDILTYVAWK(L)		1944.121	Q9BYZ2	L-lactate dehydrogenase A-like 6B
14	2	9	100	2.02E+06	(R)DQEGQDVLLFIDNIFR(F)		1921.965	P06576	ATP synthase subunit beta, mitochondrial
15	3	8.83	94.6	4.11E+06	(K)VMIPQDEYPEINFVGLLIGPR(G)		2400.263	Q15637	Splicing factor 1
16	3	8.8	92.4	7.73E+06	(R)YSLLPFWYTLLYQAHR(E)		2071.08	Q14697	Neutral alpha-glucosidase AB

17	3	8.64	89.4	5.42E+06	(R)NDFQLIGIQDGYLSLLQDSGEVR(E)		2580.294	P63241	Eukaryotic translation initiation factor 5A-1
18	2	8.5	100	3.61E+06	(K)FTASAGIQVVGDDLTVTNPK(R)		2033.055	P06733	Alpha-enolase
19	2	8.5	100	2.10E+06	(R)DQEGQDVLLFIDNIFR(F)		1921.965	P06576	ATP synthase subunit beta, mitochondrial
20	3	7.97	66.3	7.27E+06	(K)LISVFyAIVMPLLNPVIySLR(N)	y:Phosphorylated Y	2421.398	O95006	Olfactory receptor 2F2
21	3	7.91	84.6	4.55E+06	(R)ASTAAAPLAAWVKANIQYSHVLER(I)		2567.373	Q8NCM8	Cytoplasmic dynein 2 heavy chain 1
22	3	7.85	62.8	1.09E+07	(K)RTEDDPEVGGPCyTLYLEYLGGLVPILK(G)	C:Carbamidomethylation y:Phosphorylated Y	3167.597	Q9NRJ4	Tubby-related protein 4
23	3	7.74	92.2	1.30E+07	(R)sGHVKAFAHITGGGLLENIPR(V)	s:Phosphorylated S	2174.183	P22102	Trifunctional purine biosynthetic protein adenosine-3
24	3	7.54	66.7	7.02E+06	(R)GITQALNLVDsLSLKLETDTLLSAMLK(S)	s:Phosphorylated S	2887.606	P86452	Zinc finger BED domain-containing protein 6
25	2	7.5	100	7.23E+06	(K)DLVSSLTSGLLTIGDR(F)		1646.896	P53396	ATP-citrate synthase
26	3	7.41	85.2	6.66E+06	(R)AFADAMEVIPSTLAENAGLNPISTVTELR(N)		3030.545	P50991	T-complex protein 1 subunit delta
27	3	7.3	67.4	9.19E+06	(R)ALESLRQDWQAYQHRLSETR(T)		2487.249	Q8NF91	Nesprin-1 OS=Homo sapiens
28	3	7.16	64.9	1.83E+07	(K)HHFGINKPEKIIPsPDDsK(F)	s:Phosphorylated S	2159.124	Q9Y2H2	Phosphatidylinositide phosphatase SAC2
29	3	7.12	82.9	6.52E+06	(K)ItEELNLRSLETyERLEADK(K)	t:Phosphorylated T y:Phosphorylated Y	2422.246	Q15906	Vacuolar protein sorting-associated protein 72 homolog
30	3	7.12	75.6	1.41E+07	(R)ASSSGNQESSGQSCIILLFDVIKSAIR(Y)	C:Carbamidomethylation	2867.457	Q9BXW9	Fanconi anemia group D2 protein
31	3	6.85	80	6.42E+06	(R)RWGDSVLLVDLTHEEMPQSIVEATSR(L)		2968.483	Q9BYD3	39S ribosomal protein L4, mitochondrial
32	3	6.69	73.5	1.23E+07	(K)EEMLFEALVTRKTVtVGEK(L)	t:Phosphorylated T	2180.163	B2RTY4	Myosin-IXa
33	2	6.5	100	3.43E+06	(K)AAFDDAIAELDTLSEESYK(D)		2087.965	P62258	14-3-3 protein epsilon
34	3	6.5	100	4.70E+06	(R)AWNDVDALFtTKNWLGyTKK(R)	t:Phosphorylated T y:Phosphorylated Y	2371.208	Q9H9C1	VPS33B-interacting protein
35	3	6.5	100	5.30E+06	(K)HKPQAPVIVKTEEVINMHTFNDR(R)		2703.403	Q13002	Glutamate receptor, ionotropic kainate 2
36	3	6.41	81.6	1.98E+07	(K)LSSCIAAIAALSAKKAAsDSCK(E)	C:Carbamidomethylation s:Phosphorylated S	2223.147	Q9HCE3	Zinc finger protein 532
37	3	6.32	82.2	3.83E+06	(K)ESKSCtIGMVLRLWsDTK(I)	C:Carbamidomethylation t:Phosphorylated T s:Phosphorylated S	2111.062	Q8WYL5	Protein phosphatase Slingshot homolog 1

38	3	6.32	73.4	3.53E+06	(R)CLLAyFLDKGADELPYLRCPLHTIFK(L)	C:Carbamidomethylation y:Phosphorylated Y	3153.626	O60825	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2
39	3	6.3	94.3	4.75E+06	(R)YNEDLELEDAIHTAILTLK(E)		2201.134	P25787	Proteasome subunit alpha type-2
40	3	6.16	77.4	6.91E+06	(K)LyPGESIGQTSDISSPELMGVGSLLKK(Y)	y:Phosphorylated Y	2806.454	O95714	E3 ubiquitin-protein ligase HERC2
41	3	6.12	92.4	7.59E+06	(K)QFLEALLRNSAAPSKDDADHHFsR(S)	s:Phosphorylated S	2725.344	Q8NAP8	Zinc finger and BTB domain-containing protein 8B
42	3	6.1	73	7.24E+06	(R)AVSTGVQAGIPMPCFTTALSFYDGYR(H)	C:Carbamidomethylation	2809.332	P52209	6-phosphogluconate dehydrogenase, decarboxylating

Table S6: Proteins identified in fraction 1 of cells grown with only As(III), fraction isolated based on Size Exclusion Chromatography (SEC).

No	Charge	Score	Peptide Intensity	Total Intensity	Sequence	Modifications	Matched parent mass	Accession number	Entry name
1	2	19.31	92.7	2.11E+07	(K)VVIGMDVAASEFFR(S)		1540.78	P06733	Alpha-enolase
2	2	18.85	96.8	6.33E+06	(R)ETYEVLLSFIQAALGDQPR(D)		2150.11	O75643	U5 small nuclear ribonucleoprotein 200 kDa helicase
3	3	16.93	98.2	1.22E+07	(K)NMITGTSQADCAVLIVAAGVGEFEAGISK(N)	C:Carbamidomethylation	2909.44	P68104	Elongation factor 1-alpha 1
4	3	11.23	87.3	2.16E+08	(K)ITGMLLEIDNSELLHMLESPESLR(S)		2740.39	P11940	Polyadenylate-binding protein 1
5	3	10.61	77.5	5.42E+06	(K)QYDADLEQILIQWITTQCR(K)	C:Carbamidomethylation	2394.18	P37802	Transgelin-2
6	3	10.03	73.6	2.94E+07	(K)GyNPPYCQPKQGAFGSIDDGHLVPPTER(S)	C:Carbamidomethylation y:Phosphorylated Y	3100.46	Q6NVV9	Putative disintegrin and metalloproteinase domain-containing protein 5
7	2	9.16	92.4	9.41E+06	(K)KEESEESDDDMGFGLFD(-)		1949.76	P05386	60S acidic ribosomal protein P1
8	3	9	100	2.85E+06	(K)GIEGVQVIPLIPGAGEIIIADNIIK(F)		2542.49	P28288	ATP-binding cassette sub-family D member 3
9	3	8.65	72	7.00E+06	(K)LLVSNLDFGVSDADIQELFAEFGTLK(K)		2841.46	Q86V81	THO complex subunit 4
10	3	8.58	77.1	1.91E+07	(R)LYVGNIPFGITEEAMMDFFNAQMR(L)		2794.3	P26368	Splicing factor U2AF 65 kDa subunit
11	3	8.22	94	2.05E+08	(K)ITGMLLEIDNSELLHMLESPESLR(S)		2740.39	P11940	Polyadenylate-binding protein 1

12	3	8.16	81.7	1.67E+07	(R)AGTLTVEELGATLTSLLAQAQAQAR(A)		2513.36	P58107	Epiplakin
13	3	7.96	74.9	3.43E+06	(K)MssGGEKVVLKPNDVSVFTTLTINGR(L)	s:Phosphorylated S	2749.46	Q8WZA2	Rap guanine nucleotide exchange factor 4
14	2	7.89	95.5	2.80E+06	(R)GsYGDLGGPIITTQVTIPK(D)	s:Phosphorylated S	1917.03	P61978	Heterogeneous nuclear ribonucleoprotein K
15	3	7.43	84.3	7.20E+06	(K)MPSFGVSAPGKSMEASVDVSELK(A)		2353.14	Q8IVF2	Protein AHNAK2
16	3	7.42	72.9	1.41E+07	(R)HQEIWSILESVWITIyQNSTDVFQR(L)	y:Phosphorylated Y	3092.55	Q5T5J6	Transcriptional protein SWT1
17	3	7.34	89.6	2.77E+06	(K)FFLEEIQLGEELLAQGEYEK(G)		2385.19	Q15388	Mitochondrial import receptor subunit TOM20 homolog
18	3	7.16	91.5	5.55E+06	(R)ECGVGVIVTPEQIEEAVEAAINR(H)	C:Carbamidomethylation	2483.25	P47897	Glutaminyl-tRNA synthetase
19	3	7	100	2.60E+06	(R)LMEPIYLVEIQCPEQVVGGIYGVLNR(K)	C:Carbamidomethylation	2989.55	P13639	Elongation factor 2
20	3	6.53	74.7	3.99E+06	(R)GsGAGEKPYECADCAKAFGLFsHLVEHR(R)	C:Carbamidomethylation s:Phosphorylated S	3093.43	Q96EG3	Zinc finger protein 837
21	3	6.5	100	1.20E+07	(R)GLPFQANAQDIINFFAPLKPVR(I)		2456.35	Q12849	G-rich sequence factor 1
22	3	6.44	72.2	6.68E+06	(K)tVTSSAVCVSPDHDIyLAAQPR(K)	C:Carbamidomethylation t:Phosphorylated T y:Phosphorylated Y	2387.17	Q8WVZ9	Kelch repeat and BTB domain-containing protein 7
23	3	6.4	81	3.95E+06	(K)QSVQGAGTsyRNVLQAAIQK(S)	y:Phosphorylated Y s:Phosphorylated S	2119.13	O15519	CASP8 and FADD-like apoptosis regulator
24	3	6.36	80.3	3.54E+06	(K)LTLGLPTPKTDSYLQLHNKK(R)		2267.28	Q6NUN7	Uncharacterized protein C11orf63
25	3	6.34	80.9	3.89E+06	(R)GsQPPDMASALTDRTSRAPSTYTYTSRPR(A)	s:Phosphorylated S	3170.53	Q86UC2	Radial spoke head protein 3 homolog
26	3	6.17	84.3	1.46E+07	(K)EGPGHMGRsLDQTSPCPLVLVR(I)	C:Carbamidomethylation s:Phosphorylated S	2406.2	Q6XZF7	Dynamin-binding protein

Table S7: Proteins identified in Fraction 2 of of cells grown with only As(III), fraction isolated based on Size Exclusion Chromatography (SEC).

No	Charge	Score	Peptide Intensity	Total Intensity	Sequence	Modifications	Matched parent mass	Accession number	Entry name
1	2	17.78	91.9	1.06E+07	(K)SPYLYPLYGLGELPQGFAR(L)		2141.11	P31150	Rab GDP dissociation inhibitor alpha

2	2	16.51	90.7	1.91E+07	(R)YGINTTDIFQTVDLWEGK(N)		2100.03	P37802	Transgelin-2
3	2	11.5	100	3.41E+06	(K)VVIGMDVAASEFFR(S)		1540.78	P06733	Alpha-enolase OS=Homo sapiens GN=ENO1 PE=1 SV=2
4	3	11.01	76.9	7.18E+06	(R)NIQVDEANLLTWQGLIVPDNPPYDK(G)		2852.45	P68036	Ubiquitin-conjugating enzyme E2 L3
5	3	10.76	66.1	3.79E+08	(K)SsANAAGGANSGGGSSGGASGGGGGTDQDRVK(R)	s:Phosphorylated S	2651.16	P41225	Transcription factor SOX-3
6	3	10.3	80.1	8.80E+06	(K)TLVLSNLSYSATEETLQEVFEK(A)		2501.27	P19338	Nucleolin
7	3	9.19	60.9	1.11E+07	(R)KGAAPTPPGKtGPsAAQAGK(Q)	t:Phosphorylated T s:Phosphorylated S	1791.97	Q13428	Treacle protein
8	2	9.09	91.4	3.34E+06	(K)TEFLSFMNTELAAFTK(N)		1849.9	P31949	Protein S100-A11
9	3	9.07	69.5	2.18E+08	(R)sGSPSALRVLAEVQEGRAWINPK(E)	s:Phosphorylated S	2465.33	P49788	Retinoic acid receptor responder protein 1
10	3	8.83	65.9	1.25E+09	(K)AAGSTRQPIRGyVQPADTGHTAK(L)	y:Phosphorylated Y	2382.23	O95425	Supervillin
11	3	8.8	73	1.93E+08	(R)LtSLPPKGGTsNGYAKTASLGGGSR(L)	t:Phosphorylated T s:Phosphorylated S	2377.25	Q9UMD9	Collagen alpha-1(XVII) chain
12	3	8.65	76.1	2.44E+07	(R)RELDIGIsAtYCGAHSVPK(G)	C:Carbamidomethylation t:Phosphorylated T s:Phosphorylated S	2074.04	Q96NU7	Probable imidazolonepropionase
13	3	8.65	73	3.46E+08	(R)HPGLAVELELEPALPAEsVTR(V)	s:Phosphorylated S	2228.19	Q96CD0	F-box/LRR-repeat protein 8
14	3	8.62	65.9	1.34E+09	(R)SSVAAMHWMDGsVVTREHR(G)	s:Phosphorylated S	2156.01	P22891	Vitamin K-dependent protein Z
15	3	8.3	71.9	5.29E+07	(R)CRVVAQDsHFsIQTIK(E)	C:Carbamidomethylation s:Phosphorylated S	1888.97	Q8TDY2	RB1-inducible coiled-coil protein 1
16	3	8.26	65.5	1.40E+09	(R)DVYLSPRDDGYSTKDSYSSR(D)		2311.05	P38159	Heterogeneous nuclear ribonucleoprotein G
17	3	8	61.7	3.31E+08	(K)MTVCLETEKKSPLSWIEEK(G)	C:Carbamidomethylation	2308.16	P53004	Biliverdin reductase A
18	3	7.98	65.4	1.73E+08	(R)GPPGPQGPPGSPGRAGAVGtPGER(G)	t:Phosphorylated T	2153.09	Q96A84	EMI domain-containing protein 1
19	3	7.9	66	2.11E+07	(R)AGAsPGSRLLPGsPSLLLPAATWR(T)	s:Phosphorylated S	2375.32	Q495Z4	Uncharacterized protein C17orf65
20	3	7.87	66.4	7.32E+08	(R)RQssVLSQASTAGGDHEEYSNR(E)	s:Phosphorylated S	2379.09	A8K5M9	Uncharacterized protein C15orf62, mitochondrial
21	3	7.57	63.5	7.61E+07	(R)SLSKSDSDLLTCSPTEDATMGsR(S)	C:Carbamidomethylation s:Phosphorylated S	2458.11	Q92625	Ankyrin repeat and SAM domain-containing protein 1A

22	3	7.55	69.1	8.38E+06	(K)GSAALGGALALAERSsREGSSQR(M)	s:Phosphorylated S	2231.15	Q6NZ67	Mitotic-spindle organizing protein 2B
23	3	7.39	60.8	2.68E+08	(R)LPsDSAGIPQAGGEAEPHATAAGK(T)	s:Phosphorylated S	2232.09	Q99592	Zinc finger protein 238
24	3	7.39	68	4.77E+06	(R)AKGsVsLEQILPAEEEVR(A)	s:Phosphorylated S	1955.04	Q13115	Dual specificity protein phosphatase 4
25	3	7.37	63.1	5.93E+07	(K)ENsALAKGSPSSQSIPEKNSK(S)	s:Phosphorylated S	2159.09	Q9H1H9	Kinesin-like protein KIF13A
26	3	7.32	71.8	5.44E+06	(K)SSSEEVLERDLGMGDQKVSSR(G)		2309.1	Q96T83	Sodium/hydrogen exchanger 7
27	3	7.31	64.9	1.06E+08	(K)TRSSAGVTGTTGLSAKSGtsIPSAGK(T)	t:Phosphorylated T s:Phosphorylated S	2379.25	Q7Z5P9	Mucin-19
28	3	7.28	62.6	7.79E+07	(K)NtQsNEDLKQEKSELEEK(L)	t:Phosphorylated T s:Phosphorylated S	2149.03	Q08379	Golgin subfamily A member 2
29	2	7.25	93.9	4.46E+06	(R)DSLLQDGEFSMDLR(T)		1625.75	P07737	Profilin-1
30	3	7.25	66	1.28E+09	(K)tPEEDVKEVEVDRSETSTSLK(D)	t:Phosphorylated T	2378.16	Q99715	Collagen alpha-1(XII) chain
31	3	7.18	61.4	2.69E+08	(R)sPAPGLCPIyKPPETRPAK(W)	C:Carbamidomethylation y:Phosphorylated Y s:Phosphorylated S	2079.11	A2VEC9	SCO-spondin
32	3	7.09	62.8	4.14E+08	(K)sIFSKAQVEYLSISEDPK(K)	s:Phosphorylated S	2041.05	Q6ZRQ5	Protein MMS22-like
33	3	7.03	79.2	1.65E+09	(R)VsALNsVHCEHVEDEGESR(Y)	C:Carbamidomethylation s:Phosphorylated S	2153.95	Q13085	Acetyl-CoA carboxylase 1
34	3	7.02	65.8	9.56E+06	(K)sDLEtQISSLNEKLANLNR(K)	t:Phosphorylated T s:Phosphorylated S	2145.12	Q9BZF9	Uveal autoantigen with coiled-coil domains and ankyrin repeats
35	3	6.97	74.9	1.47E+08	(R)stDAPSQSTGDRKTGSVGSWGAAR(G)	t:Phosphorylated T s:Phosphorylated S	2379.13	Q9UPQ9	Trinucleotide repeat-containing gene 6B protein
36	3	6.94	73.7	1.20E+08	(R)LDVPPEGRCASAPARPALSAPAPR(L)	C:Carbamidomethylation	2456.28	Q9H3T2	Semaphorin-6C
37	3	6.94	61.1	1.29E+07	(R)TIPPELQEQLKTVKtLAK(E)	t:Phosphorylated T	2037.2	Q9H0J4	Glutamine-rich protein 2
38	3	6.8	68.8	1.72E+08	(K)SNIDIssGLEDEEPKRPLPRK(Q)	s:Phosphorylated S	2380.25	Q9BZ71	Membrane-associated phosphatidylinositol transfer protein 3
39	3	6.79	66.4	9.28E+06	(K)tRVTGDHVDLTTCPLAAGAQQEK(L)	C:Carbamidomethylation t:Phosphorylated T	2468.22	Q15828	Cystatin-M
40	3	6.76	65.4	7.89E+06	(R)CRRVsEAPsLPVVFIDGHYLGGAEK(I)	C:Carbamidomethylation s:Phosphorylated S	2757.41	A8MXD5	Glutaredoxin domain-containing cysteine-rich protein 1
41	3	6.67	90	4.28E+06	(K)GEDGEMVKLENLFEALNNK(N)		2150.04	P31944	Caspase-14
42	3	6.57	63.3	1.19E+08	(K)HVPGEIGLNYVLMADV		2311.25	Q13797	Integrin alpha-9

					AKKEK(G)				
43	3	6.56	66	7.13E+06	(K)FIGFGtDSWVyPNISIPEHGR(L)	t:Phosphorylated T y:Phosphorylated Y	2392.17	Q16281	Cyclic nucleotide-gated cation channel alpha-3
44	3	6.53	62	4.29E+07	(MGKGTVsGLVQVVDAETGK(V)	s:Phosphorylated S	1875.98	Q8IVU5	Putative uncharacterized protein C3orf46
45	3	6.53	69	1.15E+08	(R)APtFSYGPDGNGFSLGCsK(N)	C:Carbamidomethylation t:Phosphorylated T s:Phosphorylated S	1961.87	Q5W0Z9	Probable palmitoyltransferase ZDHHC20
46	3	6.28	64.4	1.50E+08	(R)KLLSAEERISQTVEILK(H)		1957.13	Q99719	Septin-5
47	3	6.27	65.3	4.54E+08	(K)sDLEtQISSLNEKLANLNR(K)	t:Phosphorylated T s:Phosphorylated S	2145.12	Q9BZF9	Uveal autoantigen with coiled-coil domains and ankyrin repeats
48	3	6.26	73.5	1.42E+08	(R)AHKGSTLSQWSLGNGTPVTsK(G)	s:Phosphorylated S	2156.11	Q7Z2K6	Endoplasmic reticulum metallopeptidase 1
49	3	6.21	75.1	3.76E+07	(R)VAVFGKDYGGyLsTYILPAK(G)	y:Phosphorylated Y s:Phosphorylated S	2162.15	P42658	Dipeptidyl aminopeptidase-like protein 6
50	3	6.21	63.4	9.28E+07	(K)LTVEEAVRMGIVGPEFKDK(L)		2118.13	Q15149	Plectin
51	3	6.16	66.1	9.65E+07	(R)KVHVsTVNPNyAGGEPKR(S)	y:Phosphorylated Y s:Phosphorylated S	1953.03	P17483	Homeobox protein Hox-B4
52	3	6.12	68.8	2.08E+07	(R)VYLEGtCVEWLRRYLENGK(E)	C:Carbamidomethylation t:Phosphorylated T	2385.2	P30455	HLA class I histocompatibility antigen, A-36 alpha chain
53	3	6.12	64.7	1.09E+07	(R)ADAtGATGVRLKEGGNINK(S)	t:Phosphorylated T	1871.99	Q96L93	Kinesin-like protein KIF16B
54	3	6.09	72.2	2.81E+07	(R)sLAGMKYHVMANHNSLPILK(A)	s:Phosphorylated S	2224.17	Q96ME7	Zinc finger protein 512
55	3	6.04	76.8	2.67E+08	(R)EtPsEEEQAQKQSGMEQGR(L)	t:Phosphorylated T s:Phosphorylated S	2148.95	Q6ZUT6	Uncharacterized protein C15orf52

Table S8: Proteins identified in fraction 3 of of cells grown with only As(III), fraction isolated based on Size Exclusion Chromatography (SEC).

No	Charge	Score	Peptide Intensity	Total Intensity	Sequence	Modifications	Accession number	Entry name
1	2	12.3	96.1	3.41E+06	(K)LPIDVTEGEVISLGLPFGK(V)		P26599	Polypyrimidine tract-binding protein 1
2	2	10	100	7.68E+06	(K)ILLANFLAQTEALMR(G)		P06744	Glucose-6-phosphate isomerase
3	2	9.73	94.4	1.21E+07	(R)DSLLQDGEFSMDLR(T)		P07737	Profilin-1

4	**2**	**8.81**	**70.6**	**2.13E+07**	**(K)EVSVRTGGLADKsSR(K)**	**s:Phosphorylated S**	**P52732**	**Kinesin-like protein KIF11**
5	**3**	**8.76**	**65.4**	**1.58E+06**	**(R)GKAyLRNAVVVItGATSGLGK(E)**	**t:Phosphorylated T<y:Phosphorylated Y**	**Q6IAN0**	**Dehydrogenase/reductase SDR family member 7B**
6	**2**	**8.63**	**94.1**	**4.49E+06**	**(K)ILLANFLAQTEALMR(G)**		**P06744**	**Glucose-6-phosphate isomerase**
7	**3**	**8.45**	**62.9**	**9.61E+07**	**(K)NtRNLDPLVYLLSKLTEDK(E)**	**t:Phosphorylated T**	**Q9BSJ2**	**Gamma-tubulin complex component 2**
8	**3**	**8.07**	**61**	**3.33E+06**	**(K)GKFLINLEGGDIREEsSYK(V)**	**s:Phosphorylated S**	**Q9NSE4**	**Isoleucyl-tRNA synthetase, mitochondrial**
9	**3**	**8.05**	**62.3**	**1.02E+07**	**(R)SKSPAstSSVNGTPGSQLSTPR(S)**	**t:Phosphorylated T s:Phosphorylated S**	**O15075**	**Serine/threonine-protein kinase DCLK1**
10	**3**	**7.87**	**65.8**	**8.18E+06**	**(K)RGITSKVLPLQLENIFYK(L)**		**Q03001**	**Dystonin**
11	**3**	**7.77**	**64.6**	**7.53E+06**	**(R)IQSLEATIEKLLSSEsK(L)**	**s:Phosphorylated S**	**Q86TI0**	**TBC1 domain family member 1**
12	**3**	**7.71**	**64.5**	**9.54E+06**	**(K)SLRFIDVEFSEPTIILFER(E)**		**Q9Y4K1**	**Absent in melanoma 1 protein**
13	**3**	**7.59**	**62.8**	**7.22E+07**	**(K)KMEEEGVSVSEMEATGAQGPSR(V)**		**Q96BT3**	**Centromere protein T**
14	**3**	**7.57**	**62.6**	**1.34E+07**	**(K)NGHANGHLNIGVDIPTPDGSFsIK(I)**	**s:Phosphorylated S**	**Q86VZ5**	**Phosphatidylcholine:ceramide cholinephosphotransferase 1**
15	**3**	**7.56**	**61.9**	**1.19E+07**	**(K)GKFLINLEGGDIREESsYK(V)**	**s:Phosphorylated S**	**Q9NSE4**	**Isoleucyl-tRNA synthetase, mitochondrial**
16	**2**	**7.5**	**100**	**1.18E+07**	**(R)DSLLQDGEFSMDLR(T)**		**P07737**	**Profilin-1**
17	**3**	**7.42**	**61.5**	**7.21E+07**	**(K)GYTGANQSRMAVSKtVLIPPELK(T)**	**t:Phosphorylated T**	**Q5VTH9**	**WD repeat-containing protein 78**
18	**3**	**7.4**	**67.2**	**6.88E+06**	**(R)YKASLFtEEEAEQYKQDLIR(E)**	**t:Phosphorylated T**	**O75132**	**Zinc finger BED domain-containing protein 4**
19	**3**	**7.3**	**71**	**4.07E+06**	**(R)ATNTDLLLAYANLMLLTLSTR(D)**		**P49792**	**E3 SUMO-protein ligase RanBP2**
20	**3**	**7.29**	**63.6**	**2.39E+07**	**(R)QLNVIDNQRTLSQMSHRLEPR(R)**		**Q8WZA2**	**Rap guanine nucleotide exchange factor 4**
21	**3**	**7.23**	**60.3**	**1.47E+07**	**(K)SQGSEWRyVLVSTVRTCAK(S)**	**C:Carbamidomethylation y:Phosphorylated Y**	**Q9BYK8**	**Peroxisomal proliferator-activated receptor A-interacting complex 285 kDa protein**
22	**3**	**7.15**	**64.6**	**3.22E+06**	**(K)sDLEtQISSLNEKLANLNR(K)**	**t:Phosphorylated T s:Phosphorylated S**	**Q9BZF9**	**Uveal autoantigen with coiled-coil domains and ankyrin repeats**
23	**3**	**7.05**	**65.6**	**4.40E+06**	**(R)SLSKSDSDLLTCSPTEDATMGsR(S)**	**C:Carbamidomethylation s:Phosphorylated S**	**Q92625**	**Ankyrin repeat and SAM domain-containing protein 1A**
24	**3**	**7.05**	**60.1**	**3.44E+06**	**(K)RREYQSPSEEESEPEAMEK(Q)**		**Q9Y468**	**Lethal(3)malignant brain tumor-like protein 1**
25	**3**	**7.04**	**67.7**	**6.12E+06**	**(K)MsALKQsTSEASVLGER(T)**	**s:Phosphorylated S**	**Q8NCK3**	**Zinc finger protein 485**

26	3	6.82	66.2	2.92E+06	(R)tPVNLSAASRPVCLPHPEHYFLPGSR(C)	C:Carbamidomethylation t:Phosphorylated T	Q5K4E3	Polyserase-2
27	3	6.81	74	4.43E+06	(R)KVRLEPVLPCVAALsSVGtLDR(K)	C:Carbamidomethylation t:Phosphorylated T s:Phosphorylated S	Q96P50	Arf-GAP with coiled-coil, ANK repeat and PH domain-containing protein 3
28	3	6.73	70.9	9.06E+06	(R)StDAPSQsTGDRKTGSVGSWGAAR(G)	t:Phosphorylated T s:Phosphorylated S	Q9UPQ9	Trinucleotide repeat-containing gene 6B protein
29	3	6.61	63	6.14E+07	(K)RGITSKVLPLQLENIFYK(L)		Q03001	Dystonin
30	3	6.5	64.6	2.79E+07	(R)LMVSRPFSVSQDGASQDHR(A)		Q9Y238	Deleted in lung and esophageal cancer protein 1
31	3	6.42	60.8	4.99E+06	(K)EVVESCRGKNLFFSTNIDDAIK(E)	C:Carbamidomethylation	O60701	UDP-glucose 6-dehydrogenase
32	3	6.28	64.2	2.25E+06	(K)MsQQVAELGREtEELRQMIK(I)	t:Phosphorylated T s:Phosphorylated S	Q8NF91	Nesprin-1
33	3	6.19	72	3.43E+07	(K)ANGVKPStVHIACTPQAAKAISNK(D)	C:Carbamidomethylation t:Phosphorylated T	Q96FA3	Protein pellino homolog 1
34	3	6.06	74	4.98E+06	(R)VSEPSGDSSAAGQPLGPAPPPPIRVR(V)		Q96HA7	Tonsoku-like protein
35	3	6.01	76	6.22E+06	(K)ENDFKGLTsLyGLILNNNK(L)	y:Phosphorylated Y s:Phosphorylated S	Q9BXN1	Asporin

Table S9: Proteins identified in fraction 4 of of cells grown with only As(III), fraction isolated based on Size Exclusion Chromatography (SEC).

No	Charge	Score	Peptide Intensity	Total Intensity	Sequence	Modifications	Matched parent mass	Accession number	Entry name
1	2	22.91	98.6	5.08E+06	(R)VTPVDYLLGVADLTGELMR(M)		2062.089	Q99598	Translin-associated protein X
2	2	20.39	98	6.58E+06	(R)DLVEAVAHILGIR(D)		1405.816	P49327	Fatty acid synthase
3	2	19.91	98	1.27E+07	(K)IEAELQDICNDVLELLDK(Y)	C:Carbamidomethylation	2130.064	P31946	14-3-3 protein beta/alpha
4	2	19.84	96.2	1.82E+07	(K)ITVVGVGQVGMACAISILGK(S)	C:Carbamidomethylation	1973.092	P07195	L-lactate dehydrogenase B chain
5	2	18.65	94.6	2.57E+07	(R)LISQIVSSITASLR(F)		1487.879	P68363	Tubulin alpha-1B chain
6	3	17.83	95.1	8.31E+06	(R)TLLEGSGLESIISIIHSSLAEPR(V)		2422.319	P49327	Fatty acid synthase

7	3	17.66	89.8	8.68E+06	(R)LGFSEVELVQMVVDGVK(L)		1848.978	P12277	Creatine kinase B-type
8	3	17.39	86.1	3.32E+07	(R)YVEPIEDVPCGNIVGLVGVDQFLVK(T)	C:Carbamidomethylation	2759.432	P13639	Elongation factor 2
9	2	16.95	98.8	4.18E+06	(K)DAQVVQVVLDGLSNILK(M)		1811.027	O00629	Importin subunit alpha-4
10	3	16.86	84.6	1.18E+07	(K)KPSETQELVQQVLSLATQDSDNPDLR(D)		2911.464	P63010	AP-2 complex subunit beta
11	3	16.64	73.4	7.91E+06	(K)LGCEVLGVSVDSQFTHLAWINTPR(K)	C:Carbamidomethylation	2699.361	P32119	Peroxiredoxin-2
12	3	16.55	84.6	6.35E+07	(R)IYDDDFFQNLDGVANALDNVDAR(M)		2600.19	P22314	Ubiquitin-like modifier-activating enzyme 1
13	2	16.37	96	2.76E+07	(R)AQLGVQAFADALLIIPK(V)		1768.037	P40227	T-complex protein 1 subunit zeta
14	2	15.69	86.8	7.60E+06	(R)ILSISADIETIGEILK(K)		1714.984	P61978	Heterogeneous nuclear ribonucleoprotein K
15	2	15	91.5	4.28E+06	(R)DQEGQDVLLFIDNIFR(F)		1921.965	P06576	ATP synthase subunit beta, mitochondrial
16	3	14.64	80.3	3.63E+07	(R)NDFQLIGIQDGYLSLLQDSGEVR(E)		2580.294	P63241	Eukaryotic translation initiation factor 5A-1
17	2	14.5	84.5	1.03E+07	(K)LIIVSNPVDILTYVAWK(L)		1944.121	Q9BYZ2	L-lactate dehydrogenase A-like 6B
18	3	14.43	97.5	1.60E+07	(R)TLLEGSGLESIISIIHSSLAEPR(V)		2422.319	P49327	Fatty acid synthase
19	3	14.35	83.1	1.33E+07	(R)ALDLFSDNAPPPELLEIINEDIAK(R)		2637.366	Q15084	Protein disulfide-isomerase A6
20	2	14.11	88.1	2.46E+07	(R)AQLGVQAFADALLIIPK(V)		1768.037	P40227	T-complex protein 1 subunit zeta
21	3	13.1	80.2	8.51E+07	(K)DGPLNMILDDGGDLTNLIHTK(Y)		2252.123	P23526	Adenosylhomocysteinase
22	2	12.58	93	8.62E+06	(K)ETPFELIEALLK(Y)		1402.783	Q08211	ATP-dependent RNA helicase A
23	3	12.53	92.1	2.94E+06	(K)FGVEQDVDMVFASFIR(K)		1859.9	P14618	Pyruvate kinase isozymes M1/M2
24	3	12.52	79	5.59E+06	(R)ECGVGVIVTPEQIEEAVEAAINR(H)	C:Carbamidomethylation	2483.245	P47897	Glutaminyl-tRNA synthetase
25	3	12.48	92.7	2.57E+07	(K)DAFDRNPELQNLLLDDFFK(S)		2310.14	P52209	6-phosphogluconate dehydrogenase, decarboxylating
26	3	12.36	96.9	1.07E+07	(K)DSLDPSFTHAMQLLTAEIEK(I)		2246.101	Q07666	KH domain-containing, RNA-binding, signal transduction-associated protein 1
27	2	11.64	77.6	6.19E+06	(R)LISQIVSSITASLR(F)		1487.879	P68363	Tubulin alpha-1B chain

28	3	11.47	81.3	1.16E+07	(K)SLQDIIAILGMDELSEEDKLTVSR(A)		2675.381	P06576	ATP synthase subunit beta, mitochondrial
29	2	11.26	83.9	1.38E+07	(K)ITVVGVGQVGMACAISILGK(S)	C:Carbamidomethylation	1973.092	P07195	L-lactate dehydrogenase B chain
30	3	11.05	83.7	3.05E+07	(R)NDFQLIGIQDGYLSLLQDSGEVR(E)		2580.294	P63241	Eukaryotic translation initiation factor 5A-1
31	2	10.96	97.9	3.91E+06	(K)SLELLPIILTALATK(K)		1595.998	Q9NVI1	Fanconi anemia group I protein
32	3	10.93	73.8	1.34E+07	(R)KFDVNTSAVQVLIEHIGNLDR(A)		2368.262	Q00610	Clathrin heavy chain 1
33	3	10.84	80.5	2.92E+07	(K)DGPLNMILDDGGDLTNLIHTK(Y)		2252.123	P23526	Adenosylhomocysteinase
34	3	10.68	62.6	7.23E+06	(K)QtPLSATAAPQTPDSDIFTFSVsLEIK(E)	t:Phosphorylated T s:Phosphorylated S	2864.456	Q9Y3P9	Rab GTPase-activating protein 1
35	3	10.51	78.1	6.49E+06	(K)sVDECKLHKGGyNGLNQCLPTMQSK(M)	C:Carbamidomethylation y:Phosphorylated Y s:Phosphorylated S	2864.349	Q8TD23	Zinc finger protein 675
36	3	10.47	70.3	7.67E+06	(K)FFEGPVTGIFSGYVNSMLQEYAK(N)		2584.243	P55060	Exportin-2
37	3	10.14	79.9	6.51E+06	(K)KPTETQELVQQVLSLATQDSDNPDLR(D)		2925.48	Q10567	AP-1 complex subunit beta-1
38	3	10.03	83.3	2.53E+07	(R)IVAFADAAVEPIDFPIAPVYAASMVLK(D)		2818.51	P24752	Acetyl-CoA acetyltransferase, mitochondrial
39	3	9.85	80.3	9.78E+06	(K)HFADLLPGFLQAVNDSCYQNDDSVLK(S)	C:Carbamidomethylation	2966.399	O00410	Importin-5
40	3	9.48	99.4	3.03E+07	(R)RLNGLSsSVEYNIMELEQELENVKTLK(T)	s:Phosphorylated S	3136.619	Q8WVP7	Limb region 1 protein homolog
41	3	9.47	69.4	1.17E+07	(K)YLEsKEDVADALLQTDQSLsEK(E)	s:Phosphorylated S	2482.22	P32456	Interferon-induced guanylate-binding protein 2
42	3	9.39	84.7	9.26E+06	(K)EQPLDEELKDAFQNAYLELGGLGER(V)		2834.384	P05023	Sodium/potassium-transporting ATPase subunit alpha-1
43	2	9.35	78.3	8.22E+06	(K)SLADELALVDVLEDK(L)		1629.858	P07195	L-lactate dehydrogenase B chain
44	3	9.11	80.8	1.16E+08	(K)GLDYEGGGCRFLRyDCVISSPR(K)	C:Carbamidomethylation y:Phosphorylated Y	2577.197	O60568	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 3

45	2	8.97	87.1	9.65E+06	(R)LGFSEVELVQMVVDGVK(L)		1848.978	P12277	Creatine kinase B-type
46	3	8.67	75.6	2.55E+07	(R)IVAFADAAVEPIDFPIAPVYAASMVLK(D)		2818.51	P24752	Acetyl-CoA acetyltransferase, mitochondrial
47	3	8.61	78.1	7.05E+06	(R)NDFQLIGIQDGYLSLLQDSGEVR(E)		2580.294	P63241	Eukaryotic translation initiation factor 5A-1
48	3	8.53	85.9	2.07E+06	(K)DAQVVQVVLDGLSNILK(M)		1811.027	O00629	Importin subunit alpha-4
49	2	8.33	83.7	2.74E+07	(K)MAVTFIGNSTAIQELFK(R)		1869.978	P07437	Tubulin beta chain
50	3	8.26	63.2	1.60E+07	(R)tCEGTEPWSRTTSLGDSLNAHSAAEK(A)	C:Carbamidomethylation t:Phosphorylated T	2805.274	Q13796	Protein Shroom2
51	3	8.23	94.1	3.25E+06	(K)LIIVSNPVDILTYVAWK(L)		1944.121	Q9BYZ2	L-lactate dehydrogenase A-like 6B
52	3	8.16	90.1	4.74E+06	(R)TLLEGSGLESIISIIHSSLAEPR(V)		2422.319	P49327	Fatty acid synthase
53	3	8.04	72.9	1.18E+07	(K)SLQDIIAILGMDELSEEDKLTVSR(A)		2675.381	P06576	ATP synthase subunit beta, mitochondrial
54	3	7.84	81.5	4.48E+06	(K)EMSPFSssSTTHLFSK(C)	s:Phosphorylated S	1772.816	Q8N8D9	Uncharacterized protein C5orf56
55	3	7.83	62.9	2.52E+07	(R)ANLTILFDKYLPTCLDTLR(T)	C:Carbamidomethylation	2267.21	Q9NYC9	Dynein heavy chain 9, axonemal
56	3	7.74	86.6	3.94E+06	(K)STAISLFYELSENDLNFIK(Q)		2204.112	P13639	Elongation factor 2
57	3	7.73	63.4	1.64E+07	(K)KISFNFSEIMAsTGWNSELK(L)	s:Phosphorylated S	2289.122	Q8TAL5	Uncharacterized protein C9orf43
58	2	7.73	89.2	1.08E+07	(R)HLVFPLLEFLSVK(E)		1541.909	P60228	Eukaryotic translation initiation factor 3 subunit E
59	3	7.68	63	9.66E+06	(K)ISSNEQPPAAWPPRQDMGsGLFGQR(W)	s:Phosphorylated S	2726.31	Q8N944	Protein FAM123C
60	3	7.67	64.4	1.94E+07	(R)LPLKLSHVQSQtNGGPSPTPK(A)	t:Phosphorylated T	2186.193	Q6PJG9	Leucine-rich repeat and fibronectin type-III domain-containing protein 4
61	3	7.61	79.1	3.95E+06	(R)FDPTQFQDCIIQGLTETGTDLEAVAK(F)	C:Carbamidomethylation	2897.387	Q7L1Q6	Basic leucine zipper and W2 domain-containing protein 1
62	3	7.53	63.9	8.08E+06	(K)VAyVQLAHGQtFTFPDLFPEK(D)	t:Phosphorylated T y:Phosphorylated Y	2408.229	Q16540	39S ribosomal protein L23, mitochondrial
63	2	7.5	100	6.81E+06	(R)AQLGVQAFADALLIIPK(V)		1768.037	P40227	T-complex protein 1 subunit zeta
64	2	7.48	88.3	3.04E+07	(K)MAVTFIGNSTAIQELFK(R)		1869.978	P07437	Tubulin beta chain

65	3	7.44	63.2	6.62E+06	(R)ITRSQPNHTPAGPPGPSSNPVsNGKEtR(R)	t:Phosphorylated T s:Phosphorylated S	2883.446	Q9BQ15	SOSS complex subunit B1
66	2	7.37	62.6	1.06E+07	(R)ANCINLPGWyHCECR(D)	C:Carbamidomethylation y:Phosphorylated Y	1949.82	Q99435	Protein kinase C-binding protein NELL2
67	2	7.3	80.2	6.36E+06	(R)AQLGVQAFADALLIIPK(V)		1768.037	P40227	T-complex protein 1 subunit zeta
68	3	7.26	82.9	6.64E+06	(R)TTFtLQQLEALEAVFAQtHYPDVFTR(E)	t:Phosphorylated T	3026.526	A6NNA5	Dorsal root ganglia homeobox protein
69	2	7.22	93.3	3.41E+07	(K)MAVTFIGNSTAIQELFK(R)		1869.978	P07437	Tubulin beta chain
70	3	7.12	77.7	2.50E+07	(R)INALTAASEAACLIVSVDETIK(N)	C:Carbamidomethylation	2289.201	Q99832	T-complex protein 1 subunit eta
71	3	7.06	91.1	2.19E+06	(R)TVPPAVTGITFLSGGQSEEEASINLNAINK(C)		3057.574	P04075	Fructose-bisphosphate aldolase A OS=Homo sapiens GN=ALDOA PE=1 SV=2
72	3	7.06	83.4	2.34E+07	(R)KLEGDSTDLSDQIAELQAQIAELK(M)		2615.341	P35579	Myosin-9
73	3	7.06	86.5	6.78E+06	(K)ICEEETGSTSIQAADSTAVNGSITPtDKK(I)	C:Carbamidomethylation t:Phosphorylated T	3010.416	Q49A26	Putative oxidoreductase GLYR1
74	2	7.01	64.2	4.26E+06	(R)LLEsMKAQyVAGNGFR(K)	y:Phosphorylated Y s:Phosphorylated S	1783.916	Q9UJX5	Anaphase-promoting complex subunit 4
75	3	6.96	61.9	2.67E+07	(K)tHGCPEWREECSFELPPGALDGLLR(A)	C:Carbamidomethylation t:Phosphorylated T	2926.361	Q9BXF6	Rab11 family-interacting protein 5
76	3	6.94	96	1.40E+07	(R)ILADLEDYLNELWEDKEGK(K)		2293.123	Q99613	Eukaryotic translation initiation factor 3 subunit C
77	3	6.93	78.7	2.54E+07	(R)TLQSGLALLYGFLPDFDWKK(I)		2312.233	Q8TE99	Acid phosphatase-like protein 2
78	3	6.85	76.7	2.77E+06	(R)AMERGGTVPADLEAAAASLPssKEVAELK(K)	s:Phosphorylated S	2898.488	Q9Y6D9	Mitotic spindle assembly checkpoint protein MAD1
79	3	6.81	92.6	4.33E+06	(K)LESEKLNVAEVtQSEIAQKQK(L)	t:Phosphorylated T	2372.267	Q9NVD7	Alpha-parvin
80	3	6.76	82.8	3.82E+06	(K)DFLTLCEKtSTGEKLSEFNQsEK(I)	C:Carbamidomethylation t:Phosphorylated T s:Phosphorylated S	2691.282	Q9BUY5	Zinc finger protein 426

81	3	6.66	79.4	5.35E+06	(R)LYKSNELFGSVIFKLPsNR(S)	s:Phosphorylated S	2212.213	Q86UK0	ATP-binding cassette sub-family A member 12
82	2	6.61	79.1	4.72E+06	(R)NTsLSETSRGGQPSVTtK(S)	t:Phosphorylated T s:Phosphorylated S	1849.925	Q12955	Ankyrin-3
83	2	6.57	88.3	8.98E+06	(K)ITVVGVGQVGMACAISILGK(S)	C:Carbamidomethylation	1973.092	P07195	L-lactate dehydrogenase B chain
84	3	6.56	74.7	4.90E+06	(R)VVNPKAFSTAGSSGSDEsHVAAAPPDICsR(T)	C:Carbamidomethylation s:Phosphorylated S	3014.427	Q9H3L0	Methylmalonic aciduria and homocystinuria type D protein, mitochondrial
85	3	6.55	70.4	3.28E+06	(K)TASMLWLLQQEMVtWRLLASLYRDR(I)	t:Phosphorylated T	3080.617	P57740	Nuclear pore complex protein Nup107
86	3	6.5	100	5.16E+06	(R)AVSIFNKEGCLEIVLKYLSR(F)	C:Carbamidomethylation	2339.279	Q7Z4Q2	HEAT repeat-containing protein 3
87	3	6.5	100	4.97E+06	(R)TLLEGSGLESIISIIHSSLAEPR(V)		2422.319	P49327	Fatty acid synthase
88	3	6.46	80.7	1.21E+07	(K)LLtVCKPFDLHASPHAsIK(R)	C:Carbamidomethylation t:Phosphorylated T s:Phosphorylated S	2134.148	Q3B820	Protein FAM161A
89	3	6.46	82.2	3.55E+06	(R)KCsELLYVFQtQLALKLLQCLK(V)	C:Carbamidomethylation t:Phosphorylated T s:Phosphorylated S	2696.488	Q86VV8	Rotatin
90	3	6.37	89.5	9.10E+06	(R)IETLEQKLtCLELIQNTHSQSCLK(S)	C:Carbamidomethylation t:Phosphorylated T	2886.47	Q9BYW2	Histone-lysine N-methyltransferase SETD2
91	3	6.3	70.5	3.47E+06	(R)DyLEANIDAIHRSTDHIEEsVR(E)	y:Phosphorylated Y s:Phosphorylated S	2583.243	Q9NQ75	Cas scaffolding protein family member 4
92	3	6.29	85.7	1.38E+07	(R)IWLKDKHLALQFIDWVLR(G)		2294.317	Q15849	Urea transporter 2
93	3	6.29	94	5.63E+06	(R)EVAAFAQFGSDLDAATQQLLSR(G)		2338.167	P25705	ATP synthase subunit alpha, mitochondrial
94	3	6.25	69.4	2.69E+07	(R)VLGYEVLYWTDDsKEsMIGKIR(V)	s:Phosphorylated S	2602.322	Q9UQ52	Contactin-6
95	3	6.24	67.2	1.49E+07	(R)KsQLIISPHSTTELPVLFYPSALGR(A)	s:Phosphorylated S	2754.519	A6PW82	Putative uncharacterized protein CXorf30

96	3	6.21	65.1	5.98E+06	(K)QCGsCWAFsATGALEGQMFRKTGK(L)	C:Carbamidomethylation s:Phosphorylated S	2678.227	O60911	Cathepsin L2
97	3	6.19	65.2	1.23E+07	(R)MEAMEKQIASLtGLVQSALLR(G)	t:Phosphorylated T	2289.231	Q9C0H9	SRC kinase signaling inhibitor 1
98	2	6.17	89.6	6.54E+06	(R)ASVRIRSsVEILR(V)	s:Phosphorylated S	1485.886	Q8N960	Centrosomal protein of 120 kDa
99	3	6.08	78.8	3.23E+06	(R)SGTGSGGSTPHISGPGPGRPSSKEGR(R)		2407.171	Q9H165	B-cell lymphoma/leukemia 11A
100	2	6.08	71.3	7.30E+06	(K)TQHGVLsQQFVELINK(C)	s:Phosphorylated S	1840.992	Q12846	Syntaxin-4

Table S10: Proteins identified in fraction 1 of cells grown with SeMet, fraction isolated based on Size Exclusion Chromatography (SEC).

No	Charge	Score	Peptide Intensity	Total Intensity	Sequence	Modifications	Matched parent mass	Accession number	Entry name
1	3	21.32	97.5	3.79E+08	(K)ITGMLLEIDNSELLHMLESPESLR(S)		2740.39	P11940	Polyadenylate-binding protein 1
2	2	21.25	97.5	8.82E+07	(K)VVIGMDVAASEFFR(S)		1540.783	P06733	Alpha-enolase
3	2	17.83	85.6	5.18E+06	(R)ETYEVLLSFIQAALGDQPR(D)		2150.113	O75643	U5 small nuclear ribonucleoprotein 200 kDa helicase
4	3	15.51	64.9	1.68E+07	(K)NMITGTSQADCAVLIVAAGVGEFEAGISK(N)	C:Carbamidomethylation	2909.438	P68104	Elongation factor 1-alpha 1
5	3	13.34	96.6	9.87E+06	(K)NLEVLNFFNNQIEELPTQISSLQK(L)		2818.462	Q15404	Ras suppressor protein 1
6	2	11.99	92.1	5.36E+06	(R)GPGTSFEFALAIVEALNGK(E)		1921.007	Q99497	Protein DJ-1
7	3	11	100	1.77E+07	(K)EALAQCVLAEIPQQVVGYFNTYK(L)	C:Carbamidomethylation	2641.333	O75131	Copine-3
8	3	10.67	75.1	1.62E+07	(R)QSGAFLSTSEGLILQLVGDAVHPQFK(E)		2742.446	Q96AB3	Isochorismatase domain-

									containing protein 2, mitochondrial
9	**2**	**9.96**	**89.2**	**1.51E+07**	**(K)KEESEESDDDMGFGLFD(-)**		**1949.759**	**P05386**	**60S acidic ribosomal protein P1**
10	**3**	**9.13**	**72.8**	**2.45E+07**	**(K)NSDPFAHSKDAsSTsSGQSGSKNEGDEER(G)**	**s:Phosphorylated S**	**3011.285**	**Q9Y2I7**	**1-phosphatidylinositol-3-phosphate 5-kinase**
11	**3**	**9**	**100**	**2.62E+06**	**(R)QVTITGSAASISLAQYLINVR(L)**		**2205.224**	**Q15366**	**Poly(rC)-binding protein 2**
12	**3**	**8.74**	**90.6**	**5.99E+06**	**(K)NMITGTSQADCAVLIVAAGVGEFEAGISK(N)**	**C:Carbamidomethylation**	**2909.438**	**P68104**	**Elongation factor 1-alpha 1**
13	**3**	**8.59**	**75.4**	**7.17E+06**	**(R)FDPTQFQDCIIQGLTETGTDLEAVAK(F)**	**C:Carbamidomethylation**	**2897.387**	**Q7L1Q6**	**Basic leucine zipper and W2 domain-containing protein 1**
14	**2**	**8.45**	**84.8**	**4.96E+06**	**(R)GPGTSFEFALAIVEALNGK(E)**		**1921.007**	**Q99497**	**Protein DJ-1**
15	**2**	**8.27**	**83**	**3.93E+06**	**(K)VADGKSVtGTDVDIVFsK(V)**	**t:Phosphorylated T s:Phosphorylated S**	**1837.954**	**Q9BW30**	**Tubulin polymerization-promoting protein family member 3**
16	**3**	**8.12**	**65.5**	**1.10E+07**	**(K)IYPLHELALWQPLHADsGFsKISK(T)**	**s:Phosphorylated S**	**2750.466**	**Q9NVR7**	**TBCC domain-containing protein 1**
17	**3**	**8.09**	**93.3**	**1.05E+07**	**(R)ALDLFSDNAPPPELLEIINEDIAK(R)**		**2637.366**	**Q15084**	**Protein disulfide-isomerase A6**
18	**3**	**7.6**	**67**	**3.17E+06**	**(-)MANLERtFIAIKPDGVQRGLVGEIIK(R)**	**t:Phosphorylated T**	**2868.613**	**P22392**	**Nucleoside diphosphate kinase B**
19	**2**	**7.5**	**100**	**2.29E+06**	**(K)SSsPAPADIAQTVQEDLR(T)**	**s:Phosphorylated S**	**1884.93**	**Q13283**	**Ras GTPase-activating protein-binding protein 1**
20	**2**	**7.44**	**86.5**	**3.70E+06**	**(R)ILSISADIETIGEILK(K)**		**1714.984**	**P61978**	**Heterogeneous nuclear ribonucleoprotein K**
21	**3**	**7.25**	**81.9**	**1.70E+07**	**(K)EALAQCVLAEIPQQVVGYFNTYK(L)**	**C:Carbamidomethylation**	**2641.333**	**O75131**	**Copine-3**

22	3	7.14	70.3	8.20E+06	(K)sIIQEKTSNFNAAIsLK(F)	s:Phosphorylated S	1864.017	P02748	Complement component C9
23	3	7	81.8	9.58E+06	(R)IFLLGLsIKLNGYLQRAILEEsR(Q)	s:Phosphorylated S	2646.534	O43825	Beta-1,3-galactosyltransferase 2
24	2	6.85	78.7	6.39E+06	(R)DSLLQDGEFSMDLR(T)		1625.748	P07737	Profilin-1
25	2	6.85	89.3	2.83E+06	(K)GYTSWAIGLSVADLAESIMK(N)		2112.068	P00338	L-lactate dehydrogenase A chain
26	3	6.79	91.9	1.00E+07	(R)TLLEGSGLESIISIIHSSLAEPR(V)		2422.319	P49327	Fatty acid synthase
27	3	6.77	79.6	7.14E+06	(K)MADALLFGNFGVQNITAAIQLYESLAK(E)		2898.507	Q5TEA6	Protein sel-1 homolog 2
28	3	6.5	100	3.17E+06	(R)FNIDLVSKLLysQGLLIDLLIK(S)	y:Phosphorylated Y s:Phosphorylated S	2518.49	P26374	Rab proteins geranylgeranyltransferase component A 2
29	3	6.41	80	5.05E+06	(K)LQNLLSELEAGLGIVLRRSDtNLtK(L)	t:Phosphorylated T	2753.552	Q8NCM8	Cytoplasmic dynein 2 heavy chain 1
30	3	6.39	93.2	8.09E+06	(R)GLPFQANAQDIINFFAPLKPVR(I)		2456.345	Q12849	G-rich sequence factor 1
31	3	6.39	94.4	8.96E+06	(R)FQKGRIEFENVHFsyADGR(E)	y:Phosphorylated Y s:Phosphorylated S	2300.121	Q9NP58	ATP-binding cassette sub-family B member 6, mitochondrial
32	3	6.38	86.8	3.64E+08	(K)ITGMLLEIDNSELLHMLESPESLR(S)		2740.39	P11940	Polyadenylate-binding protein 1
33	3	6.28	72.3	6.37E+07	(K)VLGSSIHMECKVSGSLPIsAQWFK(D)	C:Carbamidomethylation s:Phosphorylated S	2661.353	Q8WZ42	Titin
34	3	6.2	67.9	4.52E+06	(K)DQNYVEIMGRDVQESLKNGSAtGGGNK(V)	t:Phosphorylated T	2867.359	Q13416	Origin recognition complex subunit 2
35	3	6.2	83.8	6.18E+06	(K)QLNHFWEIVVQDGITLITK(E)		2254.223	P13010	X-ray repair cross-complementing protein 5

36	**2**	**6.15**	**76.8**	**3.37E+06**	**(R)SAtRGEIITPKTDtGR(S)**	**t:Phosphorylated T**	**1702.908**	**Q8TDW5**	**Synaptotagmin-like protein 5**
37	**3**	**6.11**	**72**	**6.64E+06**	**(R)RDGGVPADPDNIyLTTGASDGISTILK(I)**	**y:Phosphorylated Y**	**2746.389**	**Q8TD30**	**Alanine aminotransferase 2**
38	**3**	**6.04**	**79.1**	**6.67E+06**	**(R)EWTEQETLLLLEALEMYKDDWNK(V)**		**2897.391**	**Q92922**	**SWI/SNF complex subunit SMARCC1**

Table S11: Proteins identified in fraction 2 of cells grown with SeMet, fraction isolated based on Size Exclusion Chromatography (SEC).

No	**Charge**	**Score**	**Peptide Intensity**	**Total Intensity**	**Sequence**	**Modifications**	**Matched parent mass**	**Accession number**	**Entry name**
1	**2**	**17.34**	**97.9**	**8.15E+06**	**(K)DATNVGDEGGFAPNILENK(E)**		**1960.925**	**P06733**	**Alpha-enolase**
2	**3**	**16.59**	**89.3**	**9.96E+06**	**(K)AGAAPYVQAFDSLLAGPVAEYLK(I)**		**2351.228**	**Q01518**	**Adenylyl cyclase-associated protein 1**
3	**2**	**16.47**	**88.8**	**1.09E+07**	**(K)SPYLYPLYGLGELPQGFAR(L)**		**2141.107**	**P31150**	**Rab GDP dissociation inhibitor alpha**
4	**2**	**10**	**100**	**1.17E+07**	**(R)YGINTTDIFQTVDLWEGK(N)**		**2100.028**	**P37802**	**Transgelin-2**
5	**3**	**9.9**	**79.6**	**4.84E+06**	**(K)TLVLSNLSYSATEETLQEVFEK(A)**		**2501.266**	**P19338**	**Nucleolin**
6	**3**	**9.44**	**86.3**	**7.12E+06**	**(R)YVEPIEDVPCGNIVGLVGVDQFLVK(T)**	**C:Carbamidomethylation**	**2759.432**	**P13639**	**Elongation factor 2**
7	**3**	**8.82**	**61.1**	**4.94E+08**	**(K)GKGsTCAFTECILRSyGLK(T)**	**C:Carbamidomethylation y:Phosphorylated Y s:Phosphorylated S**	**2148.058**	**Q05932**	**Folylpolyglutamate synthase, mitochondrial**
8	**3**	**8.47**	**69.2**	**1.93E+07**	**(K)EDsCTASSKNYKNASGVVNSSPR(S)**	**C:Carbamidomethylation s:Phosphorylated S**	**2458.126**	**Q8N5G2**	**Macoilin**
9	**3**	**8.42**	**63**	**1.95E+09**	**(R)AHKGSTLSQWSLGNGtPVTSK(G)**	**t:Phosphorylated T**	**2156.11**	**Q7Z2K6**	**Endoplasmic reticulum metallopeptidase 1**
10	**3**	**8.41**	**61.1**	**5.72E+07**	**(R)GLEELHLEGLFPQELAR(A)**		**1951.028**	**Q6NSJ5**	**Leucine-rich repeat-containing protein 8E**
11	**3**	**8.26**	**70.4**	**6.29E+07**	**(K)DVGAKVTGFsEGVVDsVK(G)**	**s:Phosphorylated S**	**1793.928**	**O94876**	**Transmembrane and coiled-coil domains protein 1**

12	3	8.25	64.1	3.97E+08	(R)ELEKsQRSQIsSVNSDVEALR(R)	s:Phosphorylated S	2375.216	Q6WCQ1	Myosin phosphatase Rho-interacting protein
13	3	8.18	61.5	8.42E+06	(R)GLPGPPGPQGESRTGPPGsTGsR(G)	s:Phosphorylated S	2146.064	Q99715	Collagen alpha-1(XII) chain
14	3	7.95	66.3	4.45E+08	(R)VKVMtDLGSGPITLLtDRR(Y)	t:Phosphorylated T	2072.153	P25391	Laminin subunit alpha-1
15	3	7.89	62.9	1.15E+08	(R)GPQGSVHFAAIRtSDAGRyR(C)	t:Phosphorylated T y:Phosphorylated Y	2146.09	Q8NDA2	Hemicentin-2
16	3	7.62	62	4.99E+06	(K)HSGFSTSDNSIANtPQDYSGNMK(S)	t:Phosphorylated T	2458.058	Q9Y216	Myotubularin-related protein 7
17	3	7.58	66.5	1.66E+08	(K)ISAARFFQLLDRQPPISVyNtAGEK(W)	t:Phosphorylated T y:Phosphorylated Y	2821.499	O95342	Bile salt export pump
18	3	7.57	61.6	3.18E+07	(K)VNPDLQVEVKPSIRARK(I)		1949.129	Q96KR1	Zinc finger RNA-binding protein
19	3	7.45	63.4	5.10E+06	(R)sLLESVQKLDLEATIDKVVK(I)	s:Phosphorylated S	2228.275	Q13535	Serine/threonine-protein kinase ATR
20	3	7.41	69.6	1.02E+08	(K)ALyNCIHEDMKRLLPVVR(A)	C:Carbamidomethylation y:Phosphorylated Y	2227.184	Q9NZJ4	Sacsin
21	2	7.27	75.1	7.12E+06	(R)DSLLQDGEFSMDLR(T)		1625.748	P07737	Profilin-1
22	3	7.17	73.1	3.85E+06	(K)KAVKNFTEVHPDyGsHIQALLDK(Y)	y:Phosphorylated Y s:Phosphorylated S	2610.367	P04040	Catalase
23	3	7.14	60.2	1.23E+09	(K)LSTSAPKGLTKVNICMSR(I)	C:Carbamidomethylation	1963.046	Q9NP80	Calcium-independent phospholipase A2-gamma
24	3	6.94	63.5	4.88E+06	(K)SLIEGVIsGYNATVFAYGPTGCGK(T)	C:Carbamidomethylation s:Phosphorylated S	2461.207	Q2TAC6	Kinesin-like protein KIF19
25	3	6.89	67.9	2.79E+06	(-)MGKEQELLEAARTGHLPAVEK(L)		2307.213	Q92625	Ankyrin repeat and SAM domain-containing protein 1A
26	3	6.88	68.7	7.03E+08	(R)DGGIPADPNNVFLsTGASDAIVtVLK(L)	t:Phosphorylated T s:Phosphorylated S	2571.33	P24298	Alanine aminotransferase 1
27	3	6.85	60.7	8.30E+07	(R)tVCVPRTVGMPCsPCPQGR(Y)	C:Carbamidomethylation t:Phosphorylated T s:Phosphorylated S	2158.998	Q14532	Keratin, type I cuticular Ha2
28	3	6.79	65.5	9.39E+07	(R)FASRIIDSLFNtVtDKK(I)	t:Phosphorylated T	1955.06	O60701	UDP-glucose 6-dehydrogenase
29	3	6.79	89.8	3.97E+06	(R)GLPFQANAQDIINFFAPLKPVR(I)		2456.345	Q12849	G-rich sequence factor 1
30	3	6.78	75.9	6.62E+08	(R)DyPAGVTCVWHIVAPKNQLIELK(F)	C:Carbamidomethylation y:Phosphorylated Y	2651.401	Q9UKZ9	Procollagen C-endopeptidase enhancer 2
31	3	6.78	60.3	3.62E+06	(K)QMNIPGGDRstPAAVGAMEDK(S)	t:Phosphorylated T s:Phosphorylated S	2145.006	Q9UGI8	Testin
32	3	6.69	63	5.46E+07	(K)RLRsSSSsLSSSGAPSPK(G)	s:Phosphorylated S	1790.936	Q6RI45	Bromodomain and WD repeat-containing protein 3
33	3	6.64	65.9	6.44E+06	(R)SsHGIRSSGTSSGVLMVGPNFR(V)	s:Phosphorylated S	2233.114	P78368	Casein kinase I isoform gamma-2

34	3	6.62	71.6	3.26E+07	(R)SPSQGGsFSQVIFTNKSLGKR(D)	s:Phosphorylated S	2225.167	Q8NF99	Zinc finger protein 397
35	3	6.55	80.8	4.25E+08	(K)EFtNVyIKNFGEEVDDESLK(E)	t:Phosphorylated T y:Phosphorylated Y	2376.124	Q13310	Polyadenylate-binding protein 4
36	3	6.5	68.7	1.01E+08	(K)AAMYsVEITVEKDKVTGETR(V)	s:Phosphorylated S	2227.128	O75781	Paralemmin
37	3	6.49	81.5	1.34E+08	(R)HLWNHSIIEEEFVSLVtGCCYR(L)	C:Carbamidomethylation t:Phosphorylated T	2749.286	Q15021	Condensin complex subunit 1
38	3	6.49	71	7.77E+07	(R)GHAAFTSDPKPtIEVSGKK(Y)	t:Phosphorylated T	1970.034	P00390	Glutathione reductase, mitochondrial
39	3	6.48	62.7	3.76E+07	(K)AsDPGAASTKSGKAsTLSR(R)	s:Phosphorylated S	1791.92	Q86VM9	Zinc finger CCCH domain-containing protein 18
40	3	6.42	73.6	5.27E+06	(K)sDLEtQISSLNEKLANLNR(K)	t:Phosphorylated T s:Phosphorylated S	2145.115	Q9BZF9	Uveal autoantigen with coiled-coil domains and ankyrin repeats
41	3	6.34	63.7	7.60E+08	(K)sPyLGLGPGHSYVSLFLADR(C)	y:Phosphorylated Y s:Phosphorylated S	2149.108	O15091	Mitochondrial ribonuclease P protein 3
42	3	6.32	61.7	2.14E+08	(R)KtAIAsVSTLRNNEPNSQSK(F)	t:Phosphorylated T s:Phosphorylated S	2145.126	Q9H7T0	Cation channel sperm-associated protein subunit beta
43	3	6.29	66.1	2.77E+08	(R)KVHVsTVNPNyAGGEPKR(S)	y:Phosphorylated Y s:Phosphorylated S	1953.03	P17483	Homeobox protein Hox-B4
44	3	6.29	60.4	3.18E+06	(R)VsVFKCPSCPLLFAQKR(T)	C:Carbamidomethylation s:Phosphorylated S	2037.077	Q8N1G0	Zinc finger protein 687
45	3	6.17	68.1	5.40E+07	(K)LHCDsLETQIKSLHSENVK(L)	C:Carbamidomethylation s:Phosphorylated S	2238.118	Q5T0U0	Coiled-coil domain-containing protein 122
46	3	6.06	65.7	4.81E+06	(K)MTVCLETEKKSPLSWIEEK(G)	C:Carbamidomethylation	2308.156	P53004	Biliverdin reductase A
47	3	6.06	60.1	2.52E+06	(R)GTMyRRLQEFDGAVEDFLK(V)	y:Phosphorylated Y	2275.118	Q8NEE8	Tetratricopeptide repeat protein 16
48	3	6.05	71.6	1.72E+06	(R)KyVIIPTFWPTPKER(K)	y:Phosphorylated Y	1875.053	Q9H295	Transmembrane 7 superfamily member 4

Table S12: Proteins identified in fraction 3 of cells grown with SeMet, fraction isolated based on Size Exclusion Chromatography (SEC).

No	Charge	Score	Peptide Intensity	Total Intensity	Sequence	Modifications	Matched parent mass	Accession number	Entry name
1	2	16.58	85.7	5.58E+07	(K)ILLANFLAQTEALMR(G)		1703.951	P06744	Glucose-6-phosphate isomerase
2	2	12.54	89.9	4.68E+06	(R)YGINTTDIFQTVDLWEGK(N)		2100.028	P37802	Transgelin-2

3	3	9.98	68.5	1.04E+08	(R)RQREVtEITEIEEEYEISK(H)	t:Phosphorylated T	2381.183	Q8WZ42	Titin
4	3	9.03	66.2	8.07E+07	(K)LTVEEAVRMGIVGPEFKDK(L)		2118.126	Q15149	Plectin
5	3	8.76	68	9.26E+06	(K)QsDIMMRDNLFEIVTTSR(T)	s:Phosphorylated S	2156.048	Q9HB21	Pleckstrin homology domain-containing family A member 1
6	3	8.3	60.6	6.89E+07	(K)GYTSWSLLDKFEWEKGYsDR(Y)	s:Phosphorylated S	2467.157	Q6UWM7	Lactase-like protein
7	3	8.29	70.1	5.63E+07	(K)GKFLINLEGGDIREESsYK(V)	s:Phosphorylated S	2155.103	Q9NSE4	Isoleucyl-tRNA synthetase, mitochondrial
8	3	8.27	63.1	1.90E+07	(R)GPGPKGPVGtVSEAQLARR(L)	t:Phosphorylated T	1877.035	Q9NZM1	Myoferlin
9	3	8.21	68.6	4.49E+08	(R)LRRAADHDVGSELPPEGVLGALLR(V)		2541.39	Q9UHG2	ProSAAS
10	2	8.12	90.2	1.42E+07	(K)ILLANFLAQTEALMR(G)		1703.951	P06744	Glucose-6-phosphate isomerase
11	3	7.98	69.5	7.78E+06	(K)sDLEtQISSLNEKLANLNR(K)	t:Phosphorylated T s:Phosphorylated S	2145.115	Q9BZF9	Uveal autoantigen with coiled-coil domains and ankyrin repeats
12	2	7.97	86.9	2.29E+06	(R)VVPSDLYPLVLGFLR(D)		1687.978	Q14978	Nucleolar and coiled-body phosphoprotein 1
13	3	7.92	62.9	4.69E+06	(R)MNsNERVRIIsGSPLGSLAR(S)	s:Phosphorylated S	2157.156	Q9BXL7	Caspase recruitment domain-containing protein 11
14	3	7.89	67.8	5.99E+06	(R)LAKPVLCLGTLCTAFLTGLNR(V)	C:Carbamidomethylation	2318.272	Q8TBJ4	Lipid phosphate phosphatase-related protein type 1
15	3	7.86	73.7	1.56E+07	(K)HGAALQRSLTELDGLKIPSESGEK(L)		2536.337	Q969R2	Oxysterol-binding protein 2
16	3	7.72	65.7	1.06E+09	(K)AAsLPGKNGNPTFAAVTAGyDK(S)	y:Phosphorylated Y s:Phosphorylated S	2150.088	Q92545	
17	3	7.69	71.1	5.50E+06	(R)LAGDQGSEEAPQRPPASSAtLR(R)	t:Phosphorylated T	2238.111	Q9NPG4	Protocadherin-12
18	3	7.68	62.3	2.31E+07	(R)GALsKGSESLtLMFSHEDQKK(I)	t:Phosphorylated T s:Phosphorylated S	2293.149	Q8N3K9	Cardiomyopathy-associated protein 5
19	3	7.63	64.2	7.14E+06	(R)SELRLDLVLPsGQsFRWR(E)	s:Phosphorylated S	2159.172	O15527	N-glycosylase/DNA lyase

20	3	7.6	68.4	1.55E+06	(R)IsPGNQyIVSVSADGAILR(W)	y:Phosphorylated Y s:Phosphorylated S	1960.05	Q8N1V2	WD repeat-containing protein 16
21	3	7.53	63.8	3.15E+06	(K)IGTRSAEDPVSEVPAVsQHPR(T)	s:Phosphorylated S	2232.137	P25054	Adenomatous polyposis coli protein
22	3	7.53	67.7	2.68E+06	(K)tVQtAAANAASTAASSAAQNAFK(G)	t:Phosphorylated T	2152.063	O15126	Secretory carrier-associated membrane protein 1
24	3	7.43	63.8	8.72E+06	(K)HATENKVKNLTEEMAGLDETIAK(L)		2542.282	P12882	Myosin-1
25	3	7.29	71.5	3.20E+06	(R)DAGCRPYMAPERIDPsAsR(Q)	C:Carbamidomethylation s:Phosphorylated S	2148.991	P45985	Dual specificity mitogen-activated protein kinase kinase 4
26	2	7.14	73.1	3.24E+07	(K)DVNLEVTAKPVPLNsGVR(F)	s:Phosphorylated S	1908.055	Q13287	N-myc-interactor
27	3	7.03	82.2	1.01E+07	(R)AGPAPKGSsLQVTFPSETLNLSEK(C)	s:Phosphorylated S	2458.282	P35408	Prostaglandin E2 receptor EP4 subtype
28	3	6.97	61.5	1.11E+08	(R)GDINVCIVGDPstAKSQFLK(H)	C:Carbamidomethylation t:Phosphorylated T s:Phosphorylated S	2149.096	Q14566	DNA replication licensing factor MCM6
29	3	6.95	60.1	5.86E+07	(R)GLGMTLSYLFREPATINYPFEK(G)		2547.295	O00217	NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial
30	3	6.82	63.5	8.59E+06	(R)FGKyIDIyFNPSGVIEGAR(I)	y:Phosphorylated Y	2146.097	Q6PIF6	Myosin-VIIb
31	3	6.77	64.5	5.48E+07	(K)FDPNERYLHLAAKLLDAK(E)		2114.139	Q7Z478	ATP-dependent RNA helicase DHX29
32	3	6.71	68.3	5.58E+06	(R)EESTNLEDYEPNtVAsLLK(Q)	t:Phosphorylated T s:Phosphorylated S	2152.029	Q15311	RalA-binding protein 1
33	3	6.61	63.9	2.34E+07	(K)DSDDDsSDDEQEKKPEAPKLSK(K)	s:Phosphorylated S	2463.101	Q13435	Splicing factor 3B subunit 2
34	3	6.46	74	3.39E+07	(K)KKGSLDSDNDDSDCPysEK(V)	C:Carbamidomethylation y:Phosphorylated Y s:Phosphorylated S	2159.903	Q9Y6R1	Electrogenic sodium bicarbonate cotransporter 1
35	3	6.45	65.6	1.40E+07	(R)ADAPDAGAQSDSELPSYHQNDVSLDR(G)		2758.219	Q92538	Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1
36	3	6.35	62.3	5.15E+06	(K)RREYQSPSEEESEPEAMEK(Q)		2311.014	Q9Y468	Lethal(3)malignant brain tumor-like protein 1
37	2	6.33	62.5	1.53E+07	(R)DSLLQDGEFSMDLR(T)		1625.748	P07737	Profilin-1

38	**3**	**6.23**	**69.7**	**3.06E+07**	**(K)HSTyKYGRPDEIIEERIQTK(A)**	**y:Phosphorylated Y**	**2463.263**	**Q8NA23**	**WD repeat-containing protein 31**
39	**3**	**6.23**	**68.3**	**6.67E+06**	**(K)QEALQHLIRssGKLILLDK(L)**	**s:Phosphorylated S**	**2162.266**	**O14646**	**Chromodomain-helicase-DNA-binding protein 1**
40	**3**	**6.09**	**64.3**	**4.16E+06**	**(K)FWMTWKALGTLGLEERVNR(A)**		**2307.207**	**Q6ZQY3**	**Glutamate decarboxylase-like protein 1**
41	**3**	**6.05**	**69.4**	**1.04E+07**	**(K)SFLLNHLLQGLPGLEsGEGGRPR(G)**	**s:Phosphorylated S**	**2447.315**	**Q9ULX5**	**RING finger protein 112**
42	**3**	**6.01**	**70.1**	**1.25E+08**	**(K)MREGDELCGQEEAFRTWAK(K)**	**C:Carbamidomethylation**	**2313.039**	**P29475**	**Nitric oxide synthase, brain**

Table S13: Proteins identified in fraction 4 of cells grown with SeMet, fraction isolated based on Size Exclusion Chromatography (SEC).