

Additional file 3
Protein identification by Phenyx

spot #	Identified protein	Symbol	Swiss-Prot #	#pept.	Cov%	Score	sequence	charge	m/z	d m/z	z-score	P-value	Pos.	#MC	Modif							
spot 46	Programmed cell death 6-interacting protein	PDCD6IP	Q8WUM4	15	17	93.9	K/FLTLAALQDGVINEEALSVTLEDR/V	2	1253.304	-0.656	11.4	4.32E-27	584-606	0							
							K/LANQAADYFGDAFK/Q	2	767.464	-1.599	10.7	4.38E-23	216-229	0							
							K/LANQAADYFGDAFK/Q	2	765.844	0.021	10.1	3.07E-20	216-229	0							
							R/SVIEQGGIQTVDQLIK/E	2	864.594	-0.113	9.88	1.59E-19	423-438	0							
							K/FIQQTYPSGGEEQAQYCR/A	2	1081.974	-0.49	9.7	7.51E-19	24-41	0Cys_CAM::							
							K/LALASLGYEK/S	2	532.929	-0.126	9.57	5.11E-18	111-120	0							
							K/SCVLFNCAALASQIAAEQNLDNDEGLK/I	3	985.109	-0.642	9.21	9.09E-17	121-147	0Cys_CAM::Cys_CAM::							
							K/SLLSNLDEVK/K	2	559.359	-0.05	8.32	4.24E-13	554-563	0							
							K/LANQAADYFGDAFK/Q	2	764.319	1.546	7.84	1.65E-11	216-229	0							
							R/YDQICSEPK/F	2	708.384	-0.055	7.32	9.68E-10	71-81	0Cys_CAM::							
							K/FIQQTYPSGGEEQAQYCR/A	3	721.969	-0.644	6.9	2.12E-08	24-41	0Cys_CAM::							
							K/KTSEVDLAKPLVK/F	3	476.659	-0.039	6.26	1.93E-06	11-23	1							
							R/SVIEQGGIQTVDQLIK/E	3	576.789	-0.133	6.13	4.00E-06	423-438	0							
							K/ELPELLQR/N	2	499.179	0.109	5.65	7.87E-05	439-446	0							
							K/SLLSNLDEVK/K	2	623.609	-0.253	5.59	0.000107	554-564	1							
							spot146	Calreticulin	CALR	P27797	36	62	187	F/LITNDEAYAEFFGNETWGVTK/A	3	796.839	-0.466	11.5	5.37E-27	314-334	half
														T/NDEAYAEFFGNETWGVTK/A	2	1030.634	-0.186	10.6	1.10E-22	317-334	half
T/NDEAYAEFFGNETWGVTK/A	3	687.524	-0.223	9.96	9.42E-20	317-334								half							
K/SGTIFDNFLIT/N	2	614.369	-0.052	9.89	2.19E-19	306-316								half							
E/EFGNETWGVTK/A	2	634.379	-0.077	9.22	1.24E-16	324-334								half							
K/HEQNIDCGGGYVK/L	2	739.374	-0.543	9.22	1.16E-16	82-94								0Cys_CAM::							
K/FYQDEEKDKLQTSQDAR/F	3	696.534	-0.207	8.84	3.87E-15	39-56								2							
K/EQFLDGDGWTSR/W	2	706.194	-0.376	8.8	5.27E-15	8-19								0							
K/IDNSQVESGSLDDWDFLPPK/K	2	1196.864	-0.811	8.48	2.49E-14	169-189								0							
K/IKDPDASKPEDWDER/A	2	901.099	-0.175	7.63	7.37E-11	191-205								1							
K/HEQNIDCGGGYVK/L	3	492.644	0.245	7.5	3.21E-10	82-94								0Cys_CAM::							
T/NDEAYAEFFGNETWGVTK/A	2	1030.959	-0.511	7.49	1.87E-10	317-334								half							
R/CKDDEFTHLY/T	2	664.489	-0.204	7.19	2.70E-09	146-155								halfCys_CAM::							
L/SASFEPPSNK/G	2	557.444	-0.18	7.11	5.54E-09	61-70								half							
K/IDNSQVESGSLDDWDFLPPK/I	3	840.714	-0.311	7.05	6.00E-09	169-190								1							
K/IDNSQVESGSLDDWDFLPPK/K	2	1196.594	-0.541	7.05	2.03E-09	169-189								0							
K/IDNSQVESGSLDDWDFLPPK/K	3	798.054	-0.35	7.02	7.27E-09	169-189								0							
N/SLDQDTMHDGSEYNIMFGPDICGPGTK/K	3	1006.739	-0.314	7	7.13E-09	99-125								halfOxidation_M::Oxidation_M::Cys_CAM::							
F/GNETWGVTK/A	2	496.319	-0.073	6.81	5.03E-08	326-334								half							
M/FGPDICGPGTK/K	2	574.909	-0.135	6.77	5.97E-08	115-125								halfCys_CAM::							
K/IDNSQVESGSLDDWDFLPPK/K	2	1196.349	-0.296	6.7	2.45E-08	169-189								0							
R/QIDNPDYK/G	2	496.979	-0.241	6.68	1.23E-07	262-269								0							
K/GLQTSQDAR/F	2	488.529	-0.282	6.59	2.43E-07	48-56								0							
K/IKDPDASKPEDWDER/A	3	601.229	-0.278	6.55	2.76E-07	191-205								1							
Y/TLIVRPDNTYEVK/I	2	774.979	-0.554	6.38	6.55E-07	156-168								half							
K/IDNSQVESGSLDDWDFLPPK/K	2	1196.434	-0.381	6.27	4.05E-07	169-189								0							
K/IDNSQVESGSLDDWDFLPPK/K	3	798.054	-0.35	6.24	1.50E-06	169-189								0							
Y/TLIVRPDNTYEVK/I	3	517.019	-0.4	6.04	8.20E-06	156-168								half							
K/LFNPNSLDQDTMHDGSEYNIM/F	2	1172.904	-0.905	6.04	1.82E-06	95-114								halfOxidation_M::							
L/IVRPDNTYEVK/I	2	667.849	-0.49	5.99	9.25E-06	158-168								half							
K/HEQNIDCGGGYVK/L	3	493.044	-0.155	5.69	6.53E-05	82-94								0Cys_CAM::							
T/DSKPEDWDKPEHIPDPDAK/K	3	740.719	-0.372	5.68	5.02E-05	213-231								half							
-1/EPAVYFK/E	1	853.59	-0.145	5.52	3.39E-05	1-07								0							
Y/FKEQFLDGDGWTSR/W	3	562.824	-0.222	5.4	0.000304	6-19	half														
K/GTWIHPIDNPEYSPDPS/I	2	1027.984	-0.523	5.39	0.000191	270-287	half														
K/KPEDWDEEMDGEWPEPPVIQNPYK/G	3	993.384	-0.616	5.24	0.000457	232-255	0Oxidation_M::														
spot 206	Aldehyde dehydrogenase 1A3 a	ALDH1A3a	P47895	20	25	108.6	R/ANSTDYGLTAAVFTK/N	2	780.134	-0.243	10.5	2.76E-22	432-446	0							
							R/VFVEEQVSEFVR/R	3	544.594	-0.319	9.87	2.76E-19	320-332	0							
							K/TIPTDDNVVCFTR/H	2	769.524	-0.154	8.96	1.22E-15	155-167	0Cys_CAM::							
							K/FATCNPSTR/E	2	527.299	-0.056	8.26	6.61E-13	49-57	0Cys_CAM::							
							R/VFVEEQVSEFVR/R	2	816.254	-0.345	8.08	2.20E-12	320-332	0							
							R/ELGEYALAEYTEVK/T	3	539.039	-0.104	7.83	2.56E-11	488-501	0							
							K/IAFTGSTVEGK/L	2	555.174	0.122	7.75	4.20E-11	253-263	0							
							R/YFAGWADK/I	2	479.329	-0.102	7.58	1.88E-10	143-150	0							
							I/PTDDNVVCFTR/H	2	662.764	-0.46	7.37	7.29E-10	157-167	halfCys_CAM::							
							K/AVEAAQVAFQR/G	2	596.169	-0.849	7.27	1.72E-09	74-84	0							
							K/IAFTGSTVEGK/L	2	555.534	-0.238	7.17	3.35E-09	253-263	0							
							K/IFINNEWHESK/S	3	473.174	-0.272	7.15	4.78E-09	34-44	0							
							K/EEIFGPVQPILK/F	2	685.654	-0.264	7.08	5.63E-09	410-421	0							
							K/IFINNEWHESK/S	2	709.099	-0.25	7.06	6.63E-09	34-44	0							
							K/ILELIESGK/K	2	565.369	-0.024	6.71	9.36E-08	365-374	1							
							K/ILELIESGK/K	2	501.649	-0.351	6.22	2.73E-06	365-373	0							
							R/ELGEYALAEYTEVK/T	2	808.209	-0.31	6.21	1.81E-06	488-501	0							
K/AVEAAQVAFQR/G	2	596.064	-0.744	5.57	0.000123	74-84	0														
R/ANSTDYGLTAAVFTK/N	3	520.564	-0.301	5.52	0.000164	432-446	0														
R/AKKEIFGPVQPILK/F	3	561.854	-0.52	5.45	0.00024	407-421	1														
spot 207	Aldehyde dehydrogenase 1A3 b	ALDH1A3b	P47895	19	28	123	I/PTDDNVVCFTR/H	2	662.454	-0.15	10.6	1.34E-22	157-167	halfCys_CAM::							
							R/ANSTDYGLTAAVFTK/N	2	780.154	-0.263	10.5	4.26E-22	432-446	0							
							K/FATCNPSTR/E	2	527.354	-0.111	9.68	1.79E-18	49-57	0Cys_CAM::							

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							R/TDDEVVQREEEAIQLDGLNASQIR/E	3	910.659	-0.541	8.51	5.52E-14	23-46	1
							R/GLFDEYGSK/K	2	508.419	-0.179	8.43	1.90E-13	375-383	0
							R/LISLTDENALSGNEELTVK/I	2	1025.404	-1.87	8.08	1.74E-12	96-114	0
							K/NLLHVTDTGVGMTR/E	3	510.284	0.312	7.63	1.26E-10	122-135	0Oxidation_M::
							R/LSLNIDPAK/V	2	543.349	-0.053	6.97	1.65E-08	724-733	0
							K/FAFQAEVNR/M	2	541.434	-0.159	6.96	1.57E-08	55-63	0
							K/SGTSEFLN/K	2	491.804	-0.058	6.16	3.68E-06	148-156	0
spot 906	NADH-ubiquinone oxidoreductase 30 kDa subunit	NDUFS3	O75489	10	46	84.3	K/QLSAFGEYVAEILPK/Y	2	833.249	-0.3	12.4	1.06E-31	21-35	0
							K/DFPLSGYVELR/Y	2	648.904	-0.569	10.9	6.38E-24	165-175	0
							K/SLVDLTAVDVPTTR/Q	2	693.554	-0.168	10.5	3.50E-22	74-86	0
							R/VVAEPVELAQEFR/K	3	496.379	-0.111	9.55	6.72E-18	183-195	0
							K/TYTDELTPIEASVVFKA	2	950.739	-0.256	8.91	1.44E-15	109-125	0
							R/VVAEPVELAQEFR/K	2	744.154	-0.255	8.67	1.59E-14	183-195	0
							K/RVVAEPVELAQEFR/K	3	548.389	-0.087	8.58	4.51E-14	182-195	1
							R/KFDLNSPWAEFPVYR/Q	3	623.794	-0.145	8.4	2.12E-13	196-210	1
							R/LTDYGFEGHPPFR/K	3	518.129	-0.204	8.22	1.03E-12	151-163	0
							K/AANWYER/E	2	455.314	-0.099	6.83	4.27E-08	126-132	0
spot 912	Triosephosphate isomerase	TPI	P60174	12	42	77.1	K/SNVSDAVAQSTR/I	2	617.904	-0.099	12.6	6.71E-33	194-205	0
							R/HVFGESDELIGQK/V	2	730.189	-0.324	11.1	6.54E-25	100-112	0
							R/IYGGSVTGATCK/E	2	664.264	-0.424	9.76	7.33E-19	206-218	0Cys_CAM::
							K/DCGATWVVLGHSER/R	2	793.939	-0.066	8.76	6.91E-15	85-98	0Cys_CAM::
							K/DCGATWVVLGHSER/R	3	529.879	-0.295	8.71	1.63E-14	85-98	0Cys_CAM::
							R/HVFGESDELIGQK/V	3	487.044	-0.132	8.1	3.15E-12	100-112	0
							R/RHVFGESDELIGQK/V	3	539.084	-0.138	7.92	1.23E-11	99-112	1
							K/VTNGAFTGEISPGMIK/D	2	820.104	-0.69	7.86	1.33E-11	69-84	0Oxidation_M::
							K/VIADNVKDWISK/V	2	637.994	-0.153	6.85	3.30E-08	149-159	1
							K/IAVAAQNCYK/V	2	569.464	-0.174	6.43	6.19E-07	59-68	0Cys_CAM::
							K/TATPQQAQEVHEK/L	3	489.919	-0.34	5.65	8.29E-05	175-187	0
							K/VTNGAFTGEISPGMIK/D	2	812.299	-0.882	5.62	6.61E-05	69-84	0