



Suppl. Figure 1.

Supplemental Figure 2

- A. IPI00231678 (100%), 112,664.0 Da**
Poly [ADP-ribose] polymerase 1
13 unique peptides, 15 unique spectra, 15 total spectra, 197/1014 amino acids (19% coverage)

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MAEATERLYR V EYAKSGRAS CKKCSSEIPK DSLRMAIMVQ SPMFDGKVP
WYHFS CFWKV GHSIRQPDTE V DGFSEL RWD DQ QKVKKTAE AGGVAGKGQH
GGGGKA EKT L GDFAAEYAKS NRSTCKG CME KIEKGQMR L S KKMLDPEK PQ
LGMIDRWYHP TCFVKNRDEL GFRPEYSASQ LKGFSLLSAE DKEALKKQLP
AVKSEGRK KC DEVDGIDEVA KKKSKK GKDK ESSKLEKALK AQNELVWN I K
DELKKACSTN DLKELLIFNQ QQVPSGESAI LDRVADGMAF GALLPCKECS
GQLVFKSDAY YCTGDVTAWT KCMVKTQNP S RKEWVTPKEF REISY LKKL K
IKKQDR L FPP ESSAPAPPAP PVSITSAPTA VNSSAPADKP LSNMKILT LG
KLSQNKDEAK AMIEKLG GKL TGSANKASLC ISTKKEVEKM SKKMEEV KAA
NVRVVCEDFL QDVSASAKSL QELLSAHSLS SWGAEV KVEP GEVVVPK GKS
AAPS K KSKGA VKEEGV NKSE KRMK L TLKGG AAVDPDSGLE HSAHVLEKGG
K VFSATLGLV DIVKGTNSYY K LQLLESDKE SRYWIFRSWG RVGTVIGSNK
  
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B.

Sequence	Identification probability	SEAQUEST XCorr score	SEAQUEST deltaCn score	X! Tandem log(e) score	NTT	Modifications identified by spectrum	Observed m/z	Actual peptide mass	Charge	ΔAMU	ΔPPM	Start	Stop
(K)VVDRDSEAEVIRK(Y)	95%	3.65	0.27		2		549.21	1,644.60	3	0.75	450	803	816
(K)LQLLESDKESR(Y)	95%	2.85	0.25		2		659.58	1,317.15	2	0.45	340	572	582
(K)VFSATLGLVDIVK(G)	95%	3.43	0.30	2.60	2		681.50	1,360.98	2	0.19	140	552	564
(R)TTNFAGILSQGLR(I)	95%	4.44	0.44	4.64	2		689.49	1,376.96	2	0.22	160	866	878
(R)KCCDEVDGIDEVAK(K)	95%	3.32	0.31	1.68	2	Carbamidomethyl (+57)	739.60	1,477.18	2	0.50	340	209	221
(R)MAIMVQSPMFDGK(V)	95%	2.87	0.08	2.40	2	Oxidation (+16), Oxidation (+16), Oxidation (+16)	751.96	1,501.91	2	0.25	170	35	47
(K)KPLLNTDSVQAK(V)	95%	3.08	0.27	1.07	2		762.93	1,523.85	2	0.017	11	748	761
(R)VVCEDFLQDVSASAK(S)	95%	4.61	0.42	6.11	2	Carbamidomethyl (+57)	834.62	1,667.22	2	0.44	260	454	468
(R)GGSDDSSKDPIDVNYEK(L)	95%	3.33	0.28	3.01	2		913.60	1,825.18	2	0.38	210	780	796
(K)ALVEYIDLQKMP L GK(L)	95%	2.99	0.18	3.38	2	Oxidation (+16)	932.25	1,862.48	2	0.49	260	685	700
(K)GGAAVDPDSGLEHSAHVLEK(G)	95%	3.38	0.42	5.21	2		994.98	1,987.95	2	-0.0080	-4.0	529	548
(K)VEMLDNLDDIEVAYSLLR(G)	95%	3.22	0.35	3.16	2	Oxidation (+16)	1,061.54	2,121.06	2	-0.043	-20	762	779
(K)ELLIFNQQVPSGESAILDR(V)	95%	3.51	0.20	1.66	2		1,129.11	2,256.20	2	0.029	13	264	283
(K)VFSATLGLVDIVK(G)	90%	1.85	0.06	2.46	2		1,361.53	1,360.52	1	-0.27	-200	552	564
(R)VVCEDFLQDVSASAK(S)	92%			2.92	2	Carbamidomethyl (+57)	1,667.38	1,666.38	1	-0.41	-250	454	468

C.

IPI00210090 (100%), 87,749.4 Da

SP120

5 unique peptides, 5 unique spectra, 5 total spectra, 95/798 amino acids (12% coverage)

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MSSSPVNVKK LKVSELKEEL KKRRLSDKGL KADLMDR LQA ALDNEAGGRP
A M E P G N G S L D L G G D A A G R S G A G L E Q E A A A G A E D D E E E E G I S A L D G D Q M E L
G E E N G A A G A A D A G A M E E E E A A S E D E N G D D Q G F Q E G E D E L G D E E E G A G D E N
G H G E Q Q S Q P P A A A Q Q A S Q Q R G P G K E A A G K S S G P T S L F A V T V A P P G A R Q G Q
Q Q A G G D G K T E Q K A G D K K R G V K R P R E D H G R G Y F E Y I E E N K Y S R A K S P Q P P V
E E E D E H F D D T V V C L D T Y N C D L H F K I S R D R L S A S S L T M E S F A F L W A G G R A S
Y G V S K G K V C F E M K V T E K I P V R H L Y T K D I D I H E V R I G W S L T T S G M L L G E E E
F S Y G Y S L K G I K T C N C E T E D Y G E K F D E N D V I T C F A N F E T D E V E L S Y A K N G Q
D L G V A F K I S K E V L A D R P L F P H V L C H N C A V E F N F G Q K E K P Y F P I P E D C T F I
Q N V P L E D R V R G P K G P E E K K D C E V V M M I G L P G A G K T T W V T K H A A E N P G K Y N
I L G T N T I M D K M M V A G F K K Q M A D T G K L N T L L Q R A P Q C L G K F I E I A A R K K R N
F I L D Q T N V S A A A Q R R K M C L F A G F Q R K A V V V C P K D E D Y K Q R T Q K K A E V E G K

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D.

Sequence	Identification probability	SEAQUEST XCor score	SEAQUEST deltaCn score	X! Tandem log(e) score	NTT	Modifications identified by spectrum	Observed m/z	Actual peptide mass	Charge	ΔAMU	ΔPPM	Start	Stop
(K)KAEVEGKDLPEHAVLK(M)	95%	3.78	0.28		2		588.47	1,762.40	3	0.44	250	594	609
(K)Q ^M ADTGKLNLLQR(A)	95%	2.41	0.29	3.10	2	Oxidation (+16)	803.09	1,604.17	2	0.34	210	519	532
(K)SSGPTSLFAVTVAPPGAR(Q)	95%	2.57	0.27	2.89	2		858.15	1,714.29	2	0.38	220	180	197
(K)KDC ^E VVM ^M I ^M GLPGAGK(T)	95%	3.07	0.29	2.55	2	Carbamidomethyl (+57), Oxidation (+16), Oxidation (+16)	868.94	1,735.86	2	0.025	14	469	484
(R)LQAALDNEAGGRPAMEPGNGSLDL	95%	3.01	0.25	1.09	2	Oxidation (+16)	1,499.00	2,995.98	2	0.58	190	38	68