Supplementary Table 1s

Peptic peptides from NCap32L. Each peptide was identified by either ESI-MS/MS or MS^E with its m/z, charge state, sequence number, mass, and peptide sequence. The reporter peptide is in bold. The peptides in Figure 2 and Figure 5/6 are indicted with a star (*). Other selected peptides shown in Figures 1,2s are labeled with letters (a-o).

Ion observed m/z	Charge State(+)	HXMS Data	Sequence Number	Mass (Da)	Peptide Sequence
563.7	2		2-11	1125.4	GQQPGKVLGDQ
1126.7	1				
1090.4	2	*	2-60	2178.8	GQQPGKVLGDQRREPQG
727.0	3	*	2-63	2178.0	GQQPGKVLGDQRREPQGLSE
774.3	3		2-65	2319.9	GQQPGKVLGDQRREPQGLSEAA
523.7	2		66-73	1045.4	RWNSKENL
594.7	2	*	64-73	1187.4	AARWNSKENL
1188.6	1				
704.0	1		68-73	703.0	NSKENL
677.3	2		72-84	1352.6	NLLAGPSENDPNL
1126.5	1		74-84	1125.5	LAGPSENDPNL
637.3	2	a	74-85	1272.6	LAGPSENDPNLF
449.3	1	b	85-88	448.3	FVAL
580.4	1		86-90	579.4	VALYD
626.4	1		87-91	625.4	ALYDF
444.1	1		89-91	443.1	YDF
1029.6	2		89-106	2057.2	YDFVASGDNTLSITKGEK
776.4	1	c	92-99	775.4	VASGDNTL
811.5	1		91-98	810.5	FVASGDNT
923.5	1		91-99	922.5	FVASGDNTL
817.0	2		92-107	1632.0	VASGDNTLSITKGEKL
890.5	2		91-107	1779.0	FVASGDNTLSITKGEKL
986.9	3		92-118	2957.7	VASGDNTLSITKGEKLRVLGYNHNGEW
875.6	1		100-107	874.6	SITKGEKL
438.3	2	d			
1101.2	2		100-118	2200.4	SITKGEKLRVLGYNHNGEW
734.5	3	e			
570.8	2	f	107-116	1139.6	LRVLGYNHNG
672.8	2	g	108-118	1343.6	RVLGYNHNGEW
996.5	3		119-145	2986.5	CEAQTKNGQGWVPSNYITPVNSLEKHS
809.9	**2**	*	**119-133**	**1617.8**	**CEAQTKNGQGWVPSN**
933.6	1		120-128	932.6	EAQTKNGQG
693.9	2		121-133	1385.8	AQTKNGQGWVPSN
793.3	1		134-140	792.3	YITPVNS

906.5	1		134-141	905.5	YITPVNSL
934.5	2	h	142-157	1867.0	EKHSWYHGPVSRNAAE
623.4	3				
798.4	2		141-153	1594.8	LEKHSWYHGPVSR
1379.2	2		132-155	2756.4	SNYITPVNSLEKHSWYHGPVSRNA
919.8	3	i			
635.9	2		158-169	1269.8	YLLSSGINGSFL
881.5	1		160-168	880.5	LSSGINGSF
816.5	2		170-184	1631.0	VRESESSPGQRSISL
873.0	2	j	169-184	1744.0	LVRESESSPGQRSISL
582.4	3				
1006.9	4		169-203	4023.6	LVRESESSPGQRSISLRYEGRVYHYRINTASDGKL
1149.7	2	k	185-203	2297.4	RYEGRVYHYRINTASDGKL
836.0	2		193-207	1670.0	YRINTASDGKLYVSS
974.6	1		204-211	973.6	YVSSESRF
487.8	2	l			
651.9	2		204-214	1301.8	YVSSESRFNTL
923.9	2		204-228	1845.8	YVSSESRFNTLAELVHHHSTVADGL
1485.8	1		215-228	1484.8	AELVHHHSTVADGL
743.4	2	m			
643.4	2	n	217-228	1284.8	LVHHHSTVADGL
685.7	2		224-236	1369.4	VADGLITTLHYPA
629.4	3		230-245	1885.2	TTLHYPAPKRNKPTVY
1308.7	2		229-251	2615.4	ITTLHYPAPKRNKPTVYGVSPNY
1058.9	3	o	229-255	3173.7	ITTLHYPAPKRNKPTVYGVSPNYDKWE
663.3	2		246-255	1193.5	GVSPNYDKWE

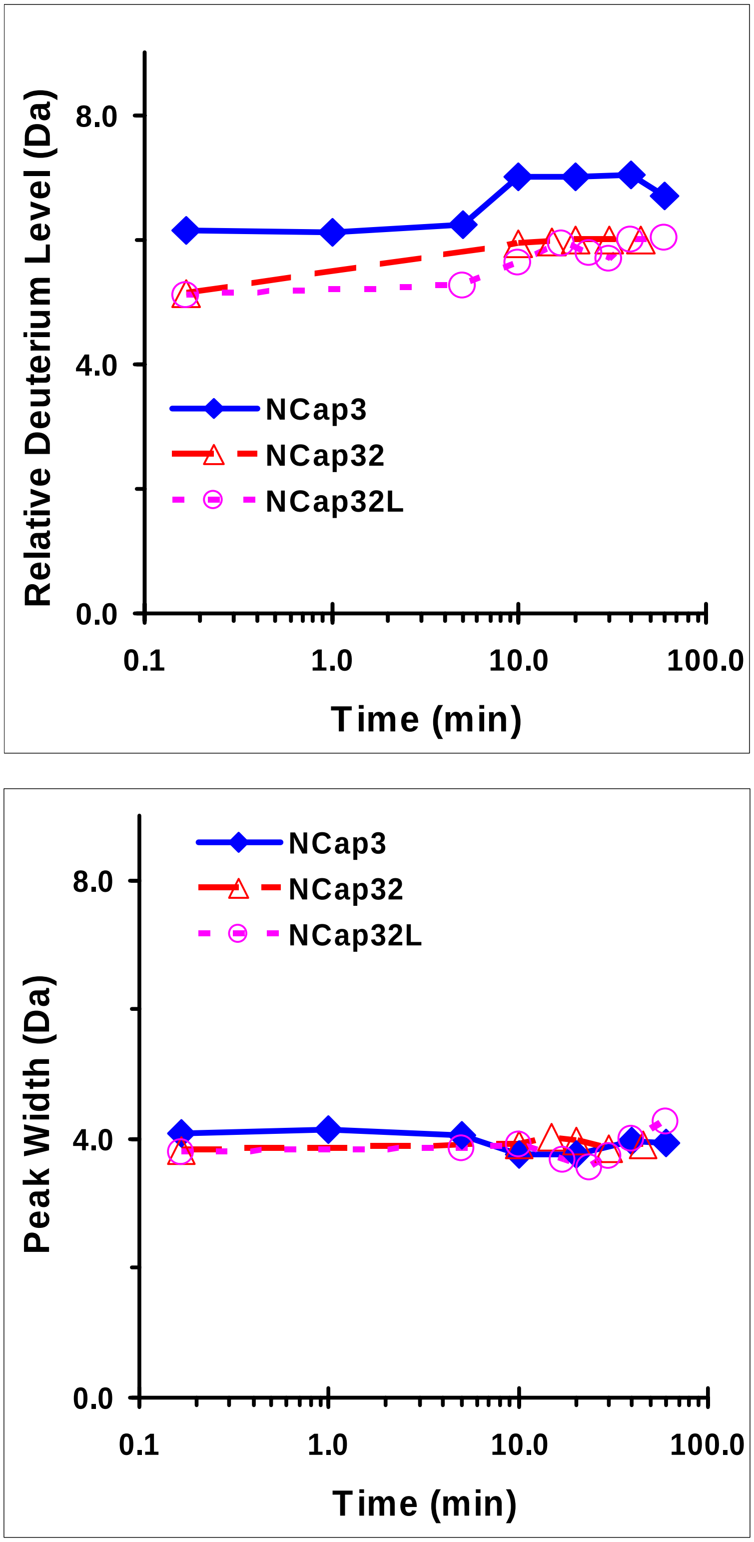
Supplementary Figure 1s

Peptic peptides of NCap32L. Each peptide that was identified by either ESI-MS/MS or MS^E is indicated by a line under the protein sequence (see also Supplementary Table 1s). The reporter peptide is labeled with dots under the sequence. The domains of each construct are indicated with arrows. The sequence is numbered for the Abl protein (top) which has deletions in the NCap [Ref 16] and for the Abl core construct (bottom) as prepared in Sf9 cells.

Supplementary Figure 2s

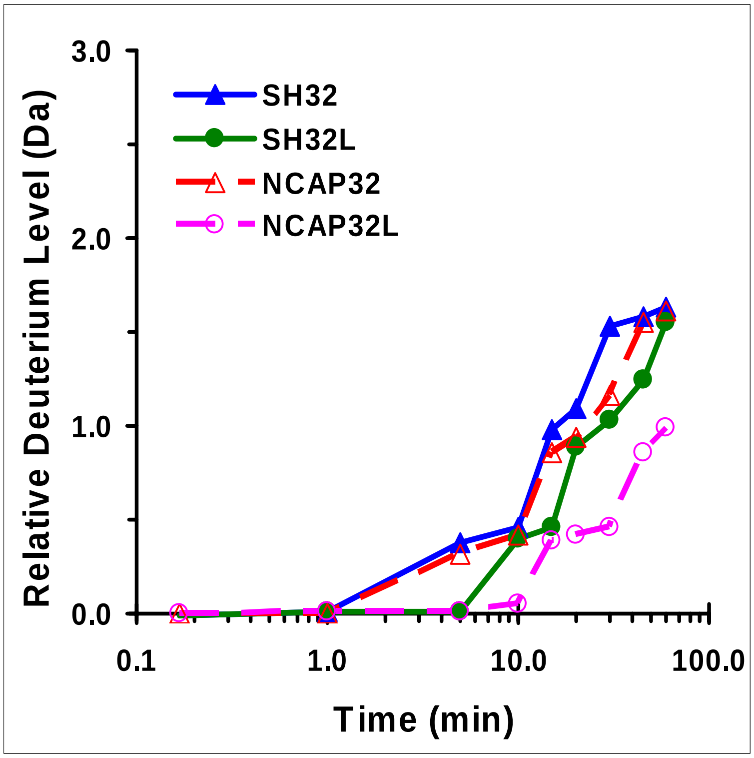
The relative deuterium uptake and peak width change of the selected peptides (panel a~o) of Abl SH32, SH32L, NCap32, NCap32L.

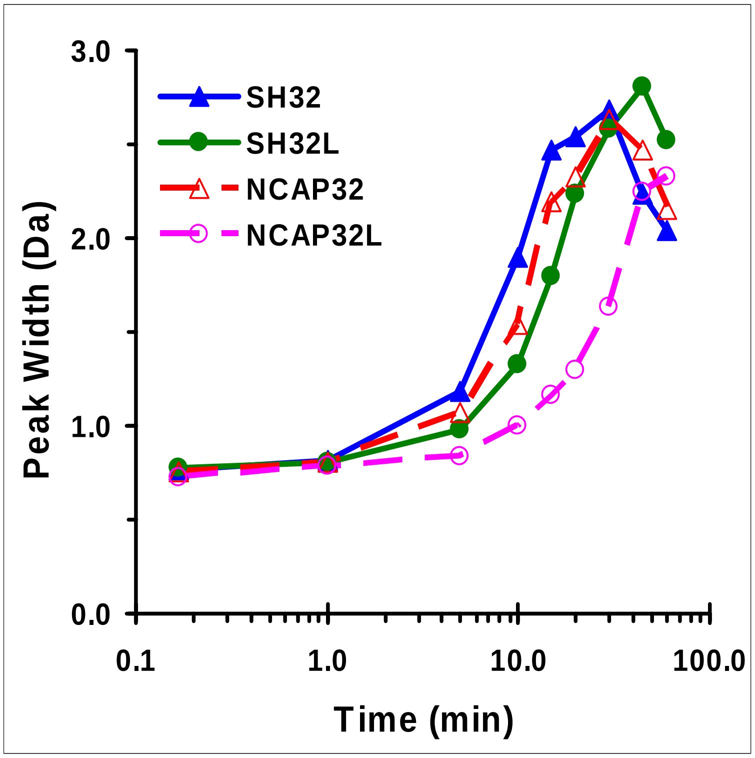
m/z= 637.3 (+2)
SH3: LAGPSENDPNLF Max=9



a

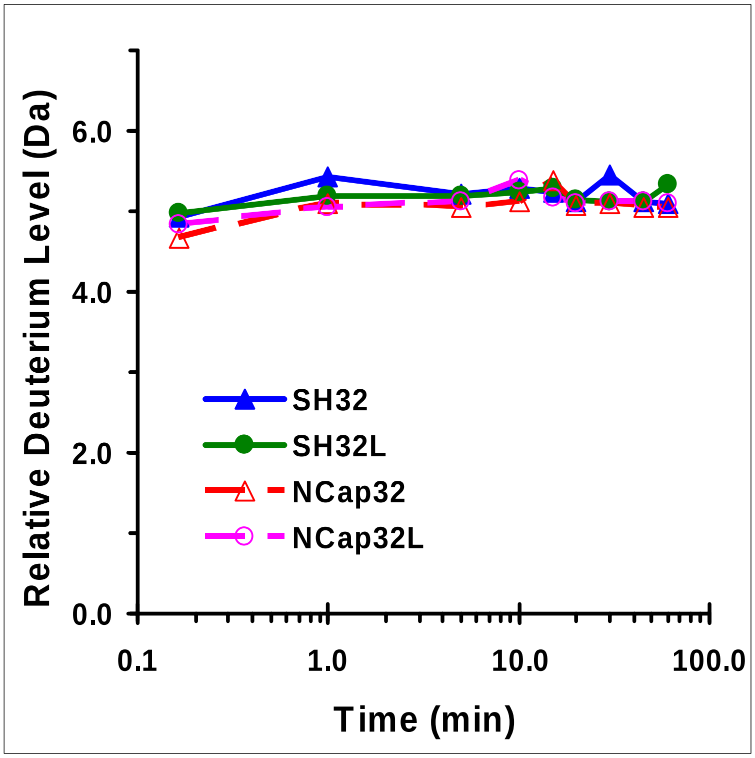
m/z= 449.3 (+1)
SH3: FVAL Max=3

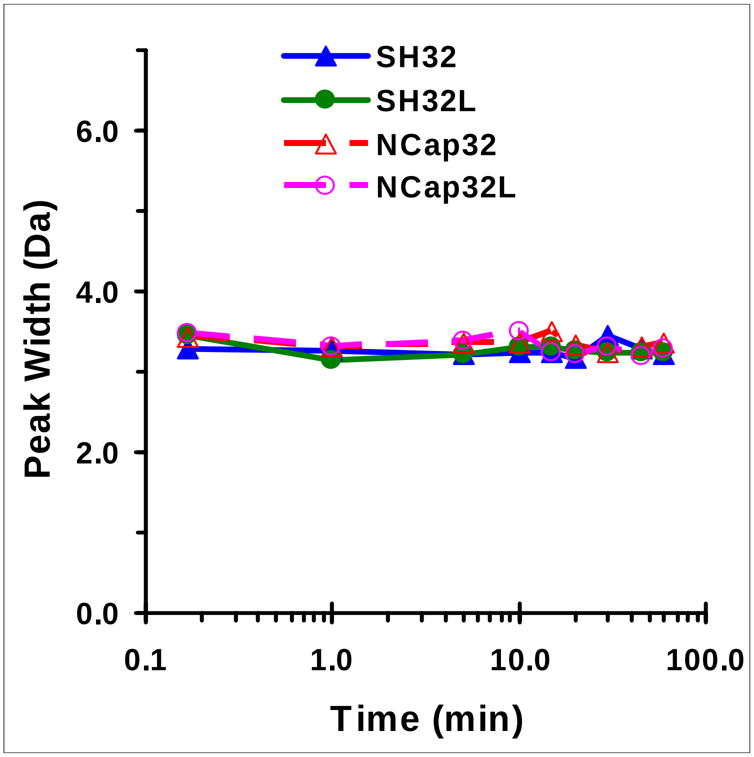




b

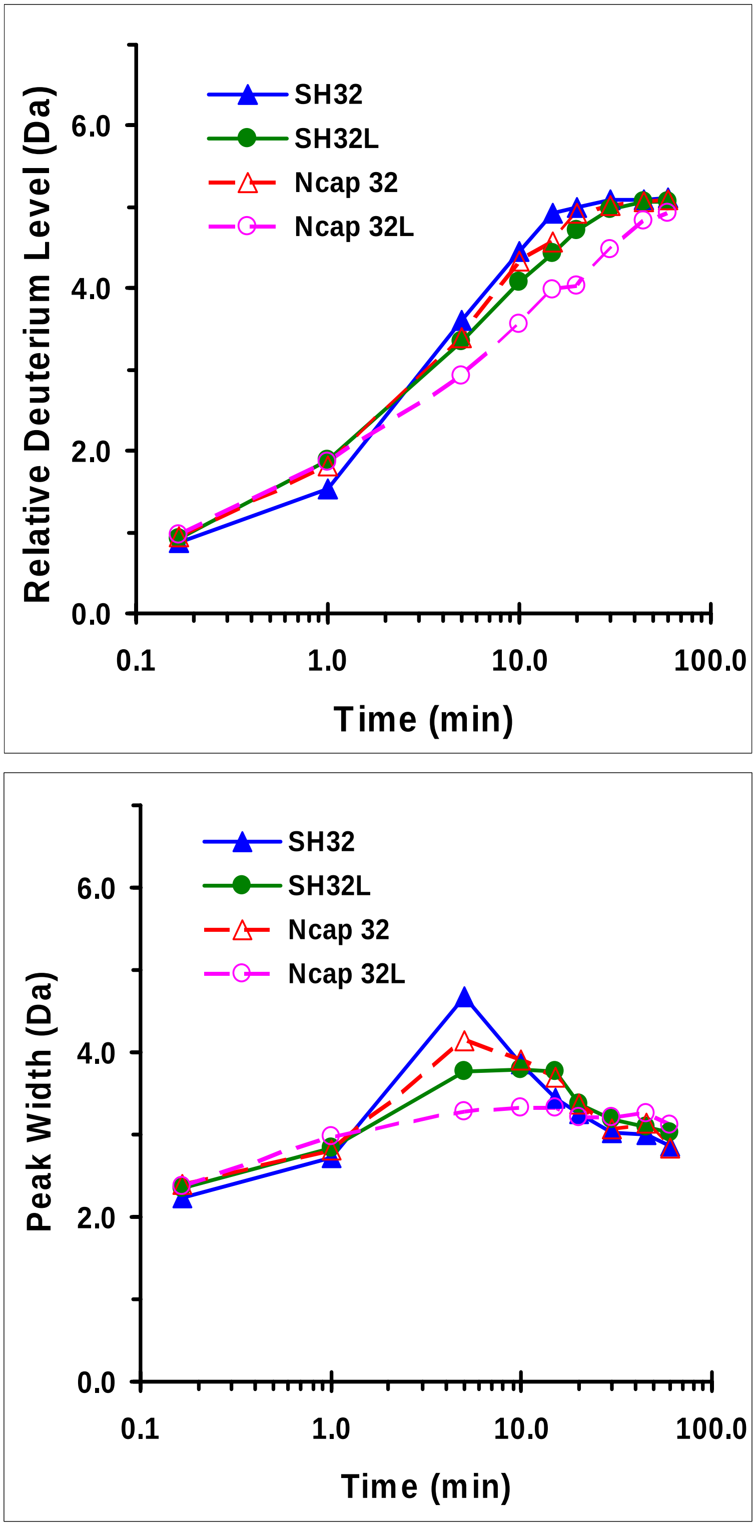
m/z= 776.4 (+1)
SH3: VASGDNTL Max=7





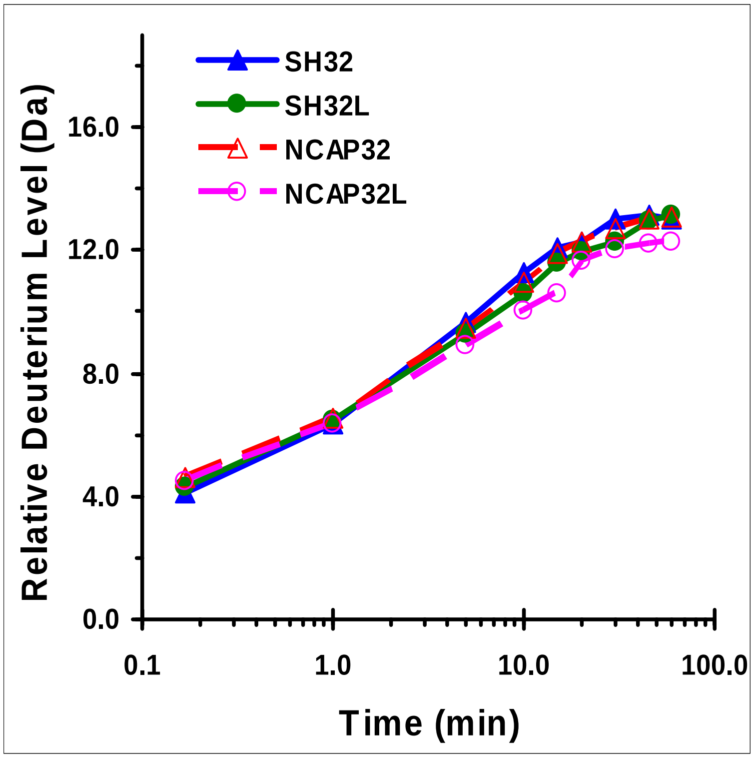
c

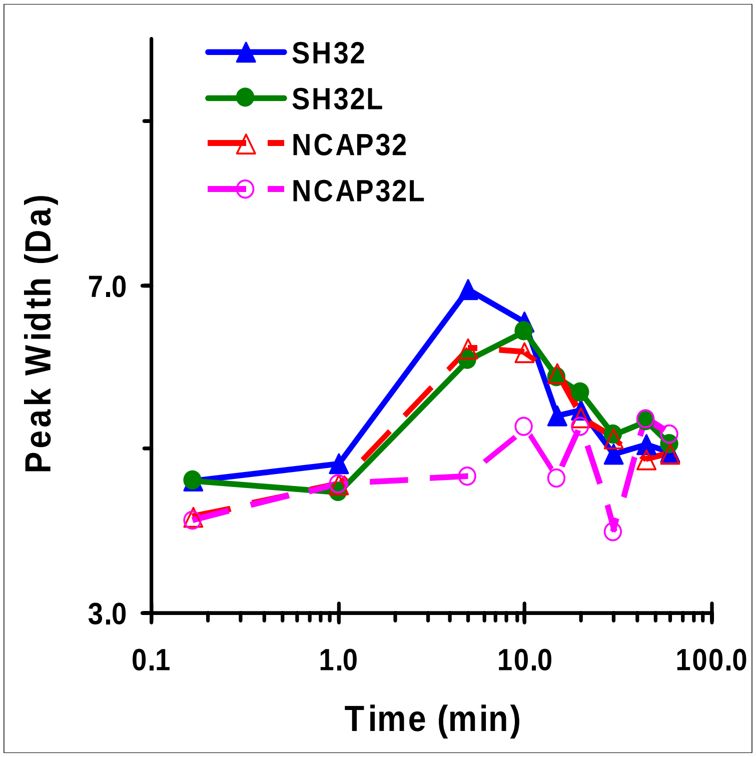
m/z= 438.3 (+2)
SH3: SITKGEKL Max=7



d

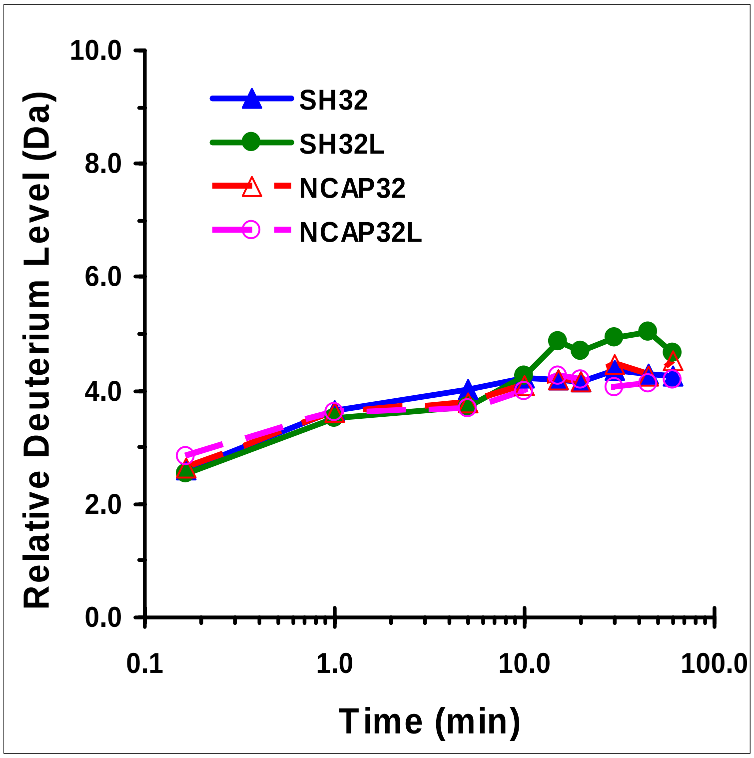
m/z= 734.5 (+3)
SH3: SITKGEKLRVLGYNHNGEW Max=19

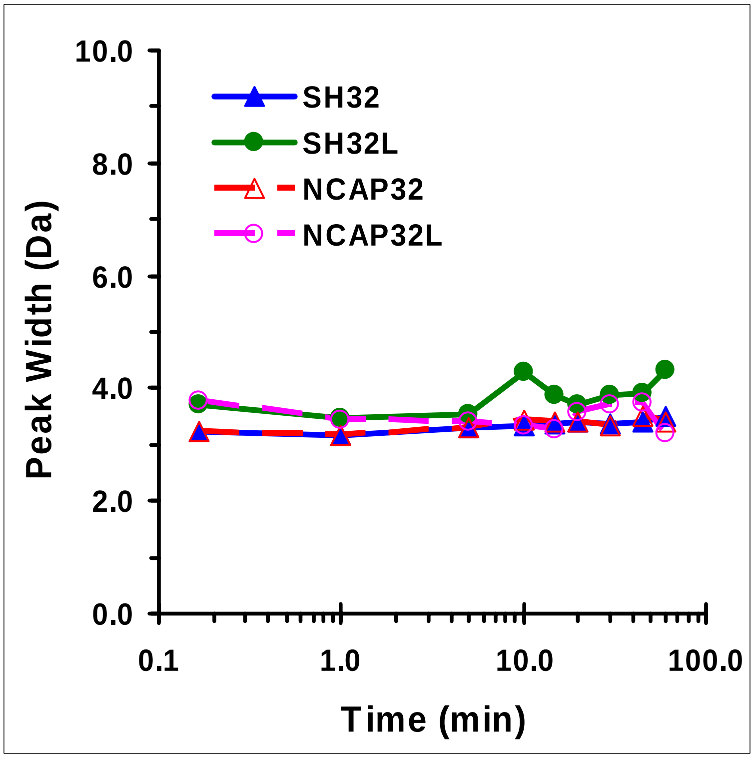




e

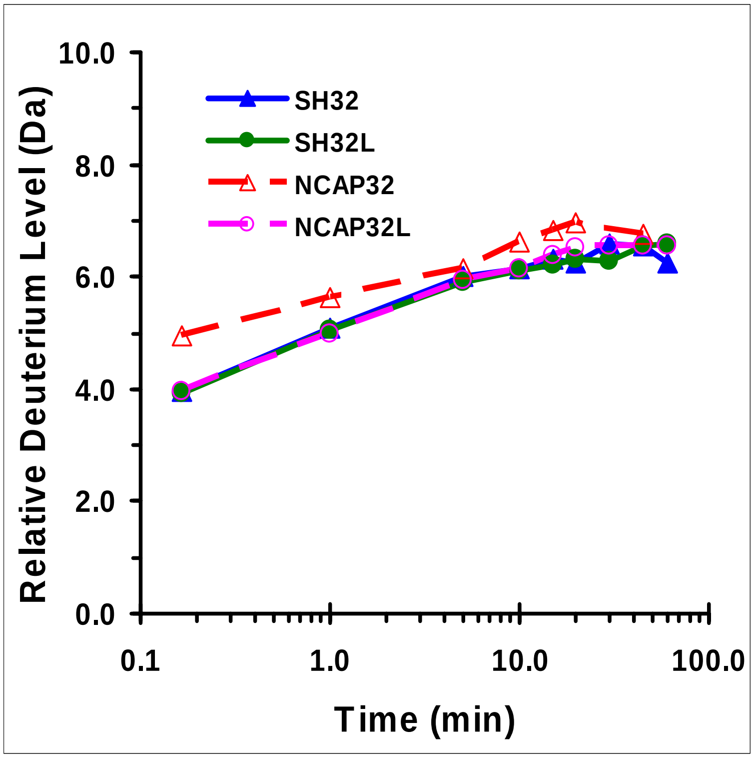
m/z= 570.8 (+2)
SH3: LRVLGYNHNG   Max=10

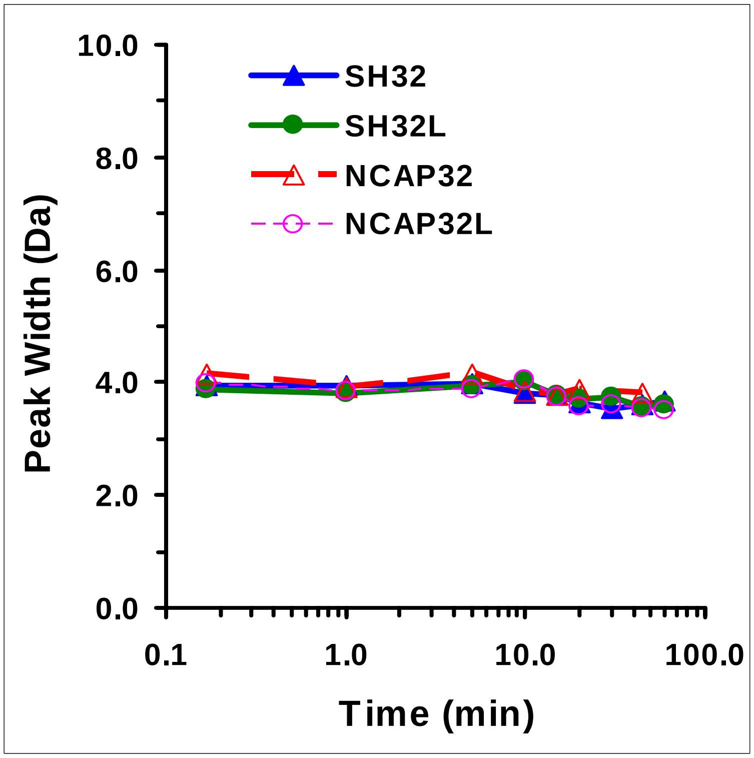




f

m/z= 672.8 (+2)
SH3: RVLGYNHNGEW Max=10

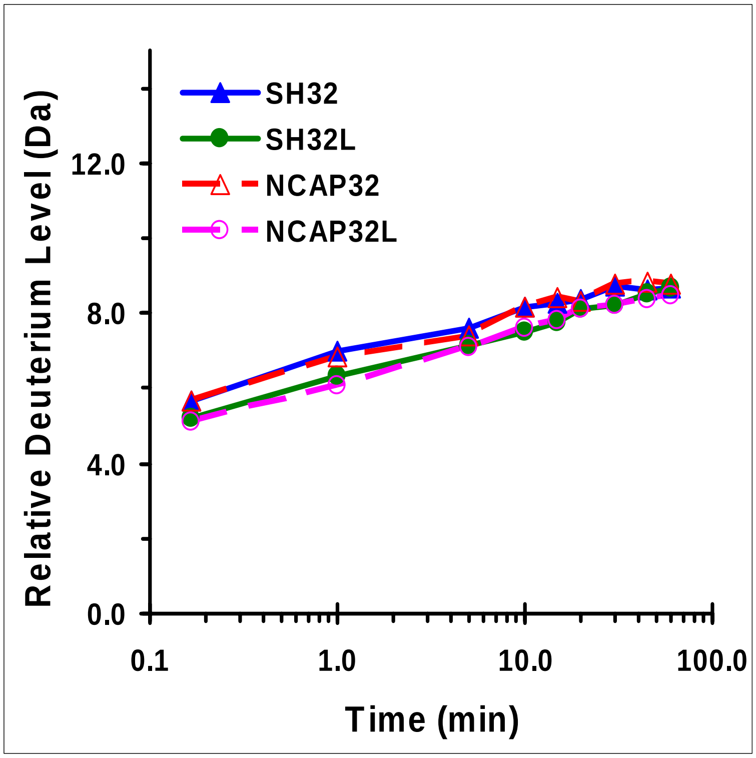


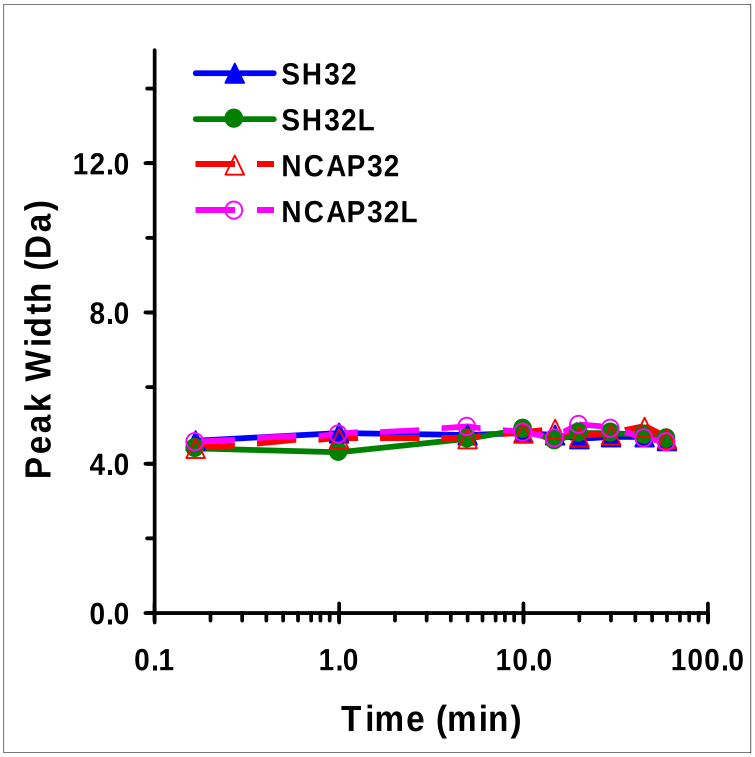


g

m/z= 934.5 (+2)

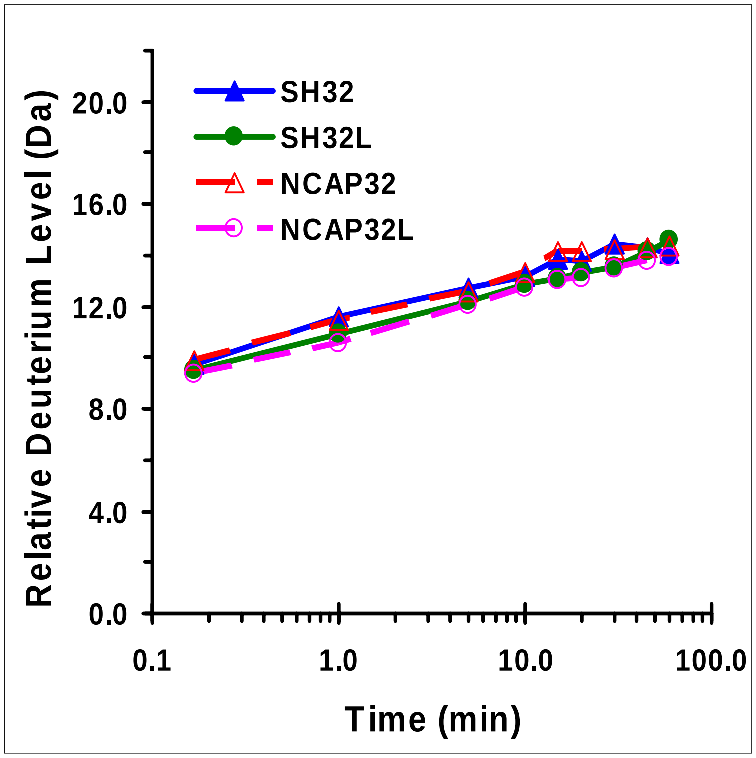
SH2: EKHSWYHGPVSRNAAE Max=15

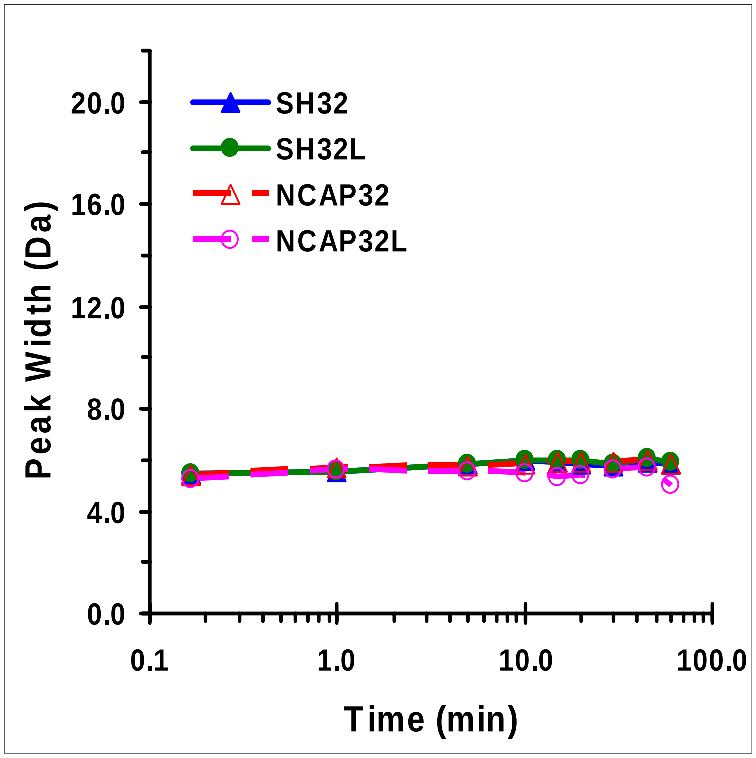




h

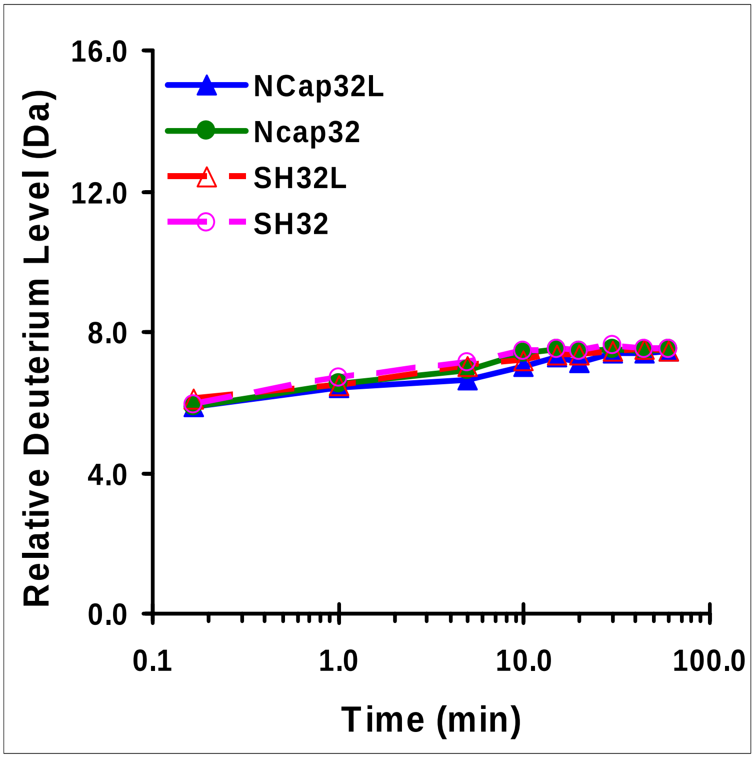
m/z= 919.8 (+3)
SH3-SH2: SNYITPVNSLEKHSWYHGPVSRNA   Max=22

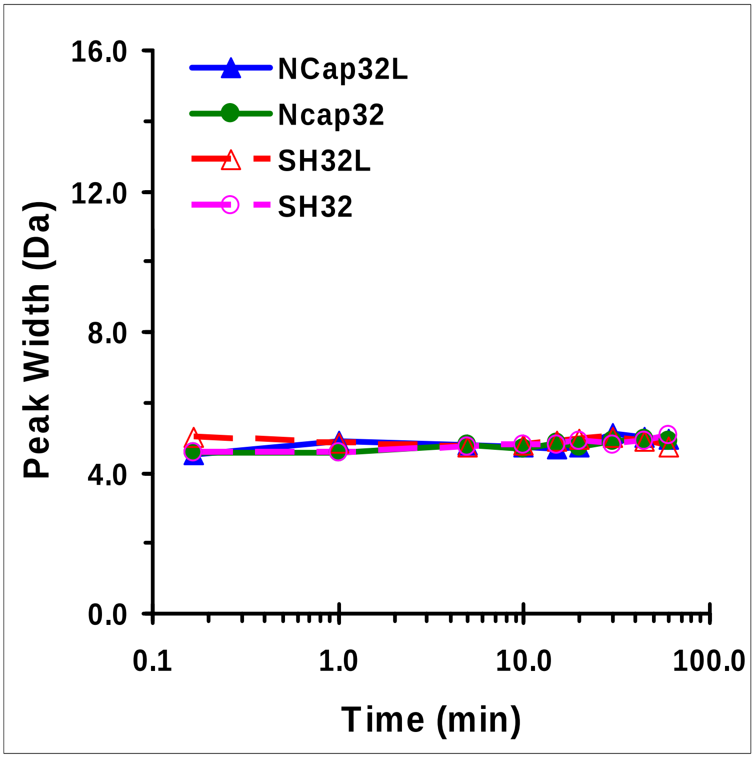




i

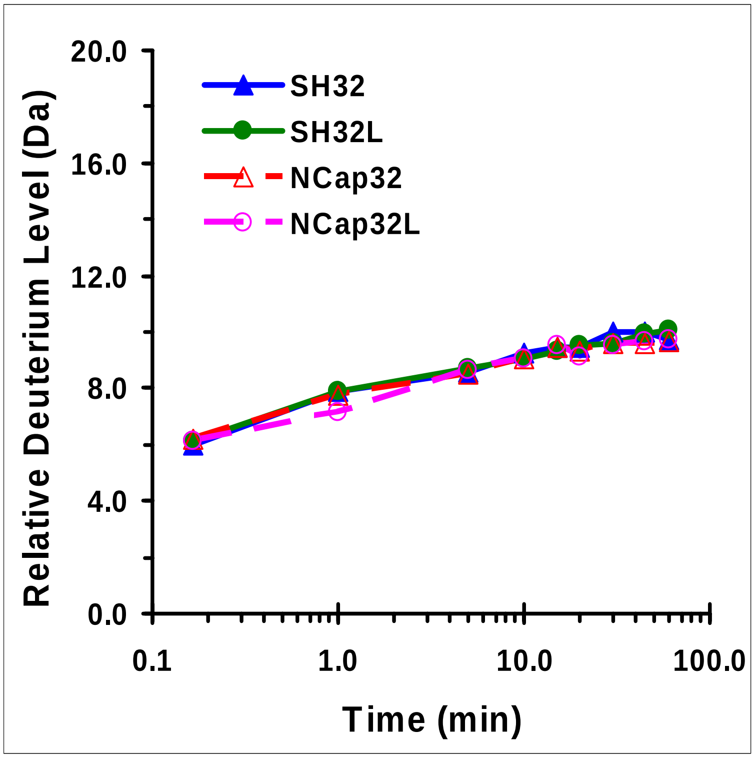
m/z= 873.0 (+2)
SH2: LVRESESSPGQRSISL Max=16

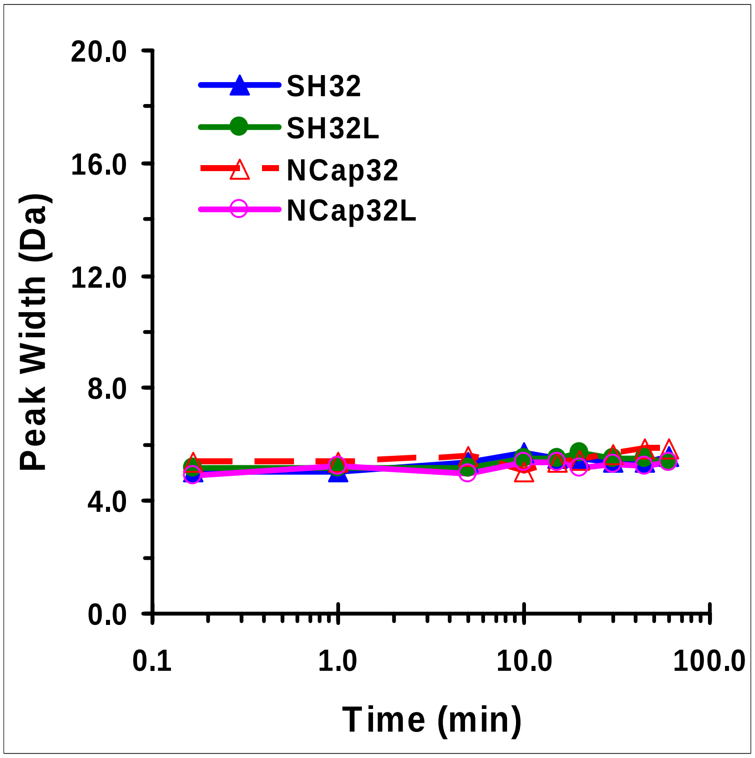




j

m/z= 1149.7 (+2)
SH2: RYEGRVYHYRINTASDGKL Max=20

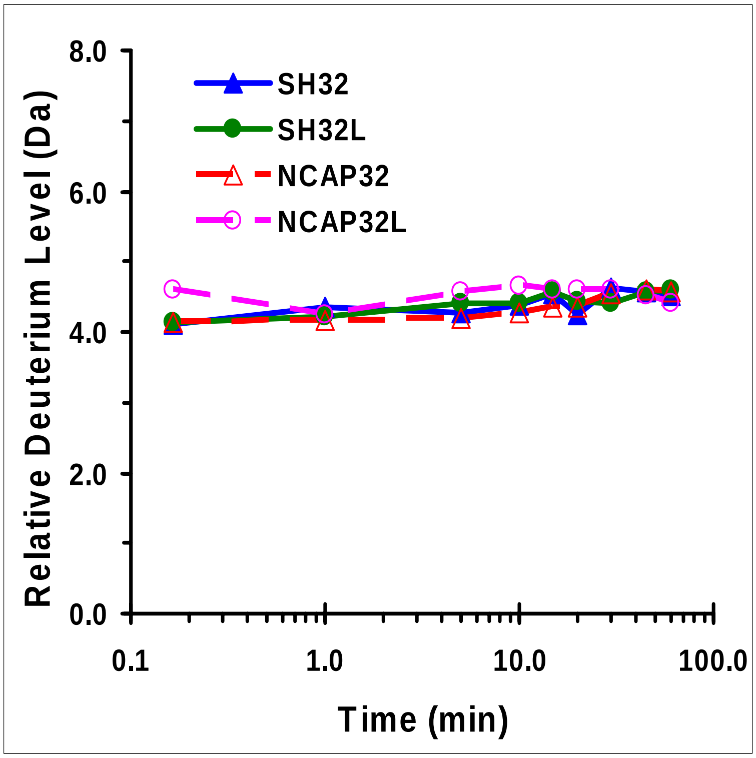


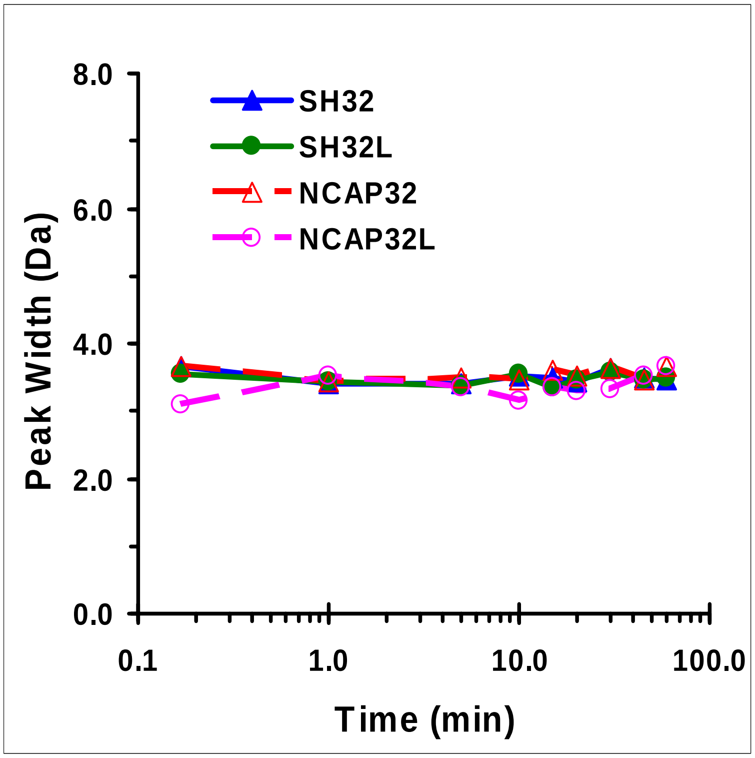


k

m/z= 487.8 (+2)

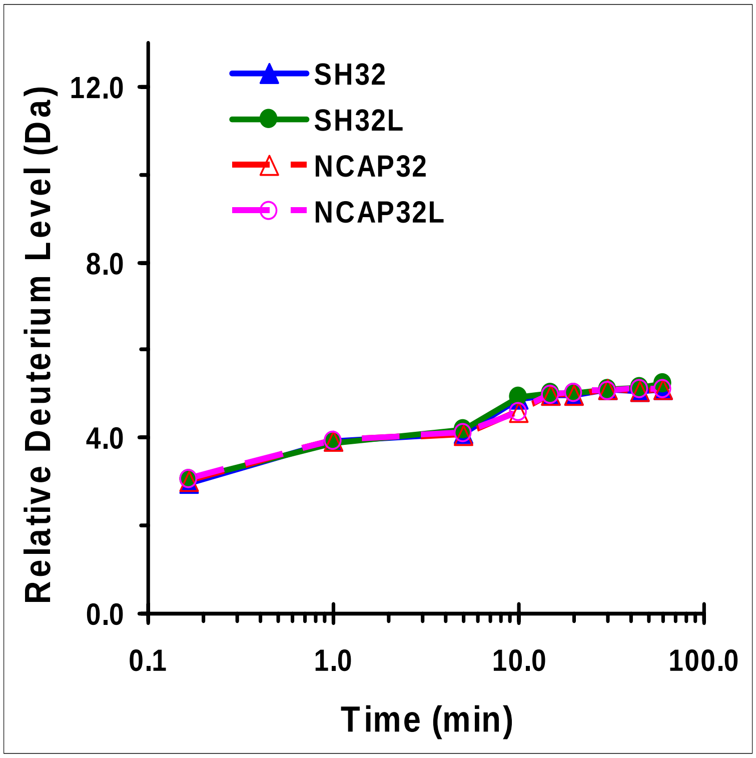
SH2: YVSSESRF Max=8

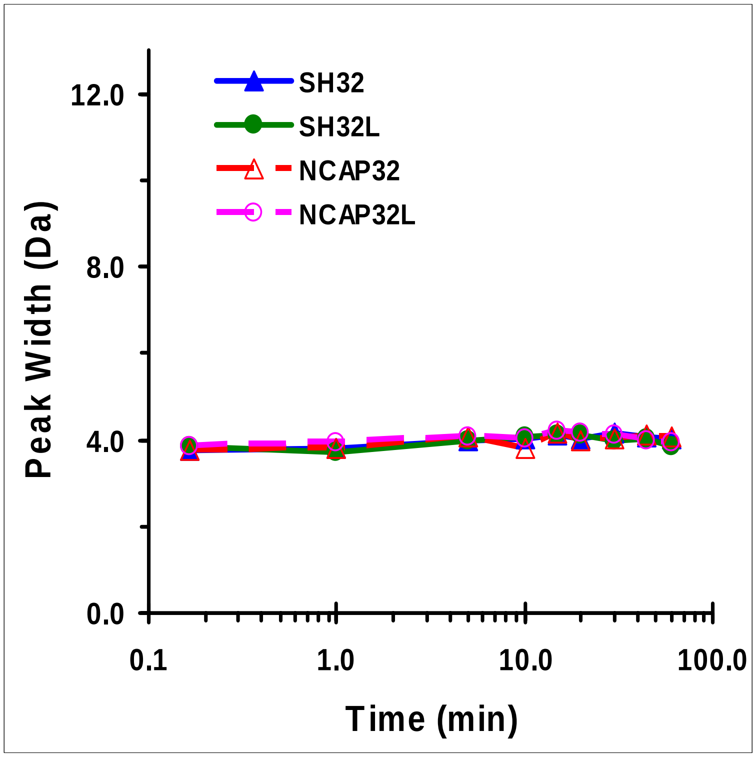




I

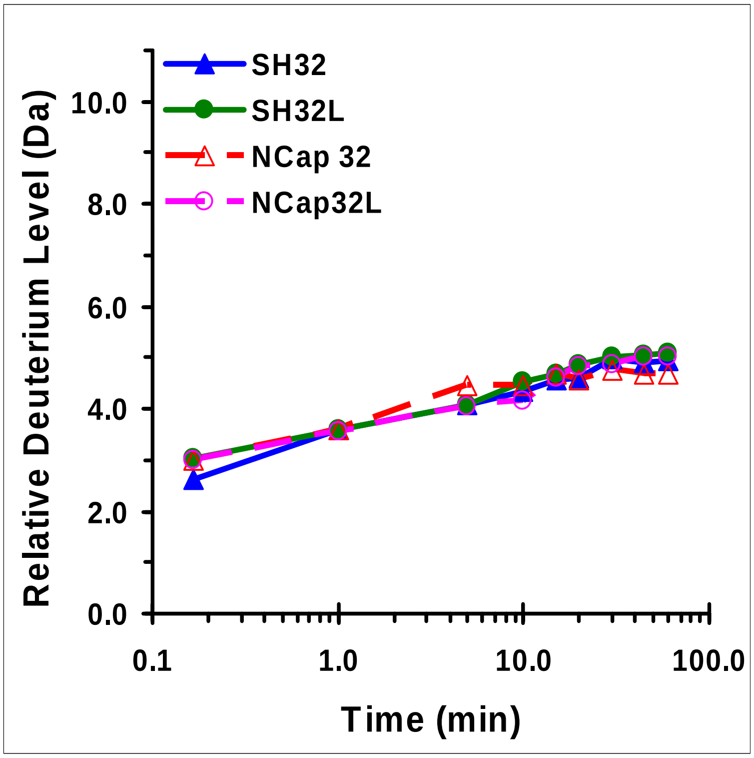
m/z= 743.4 (+2)
SH2: AELVHHHSTVADGL Max=13

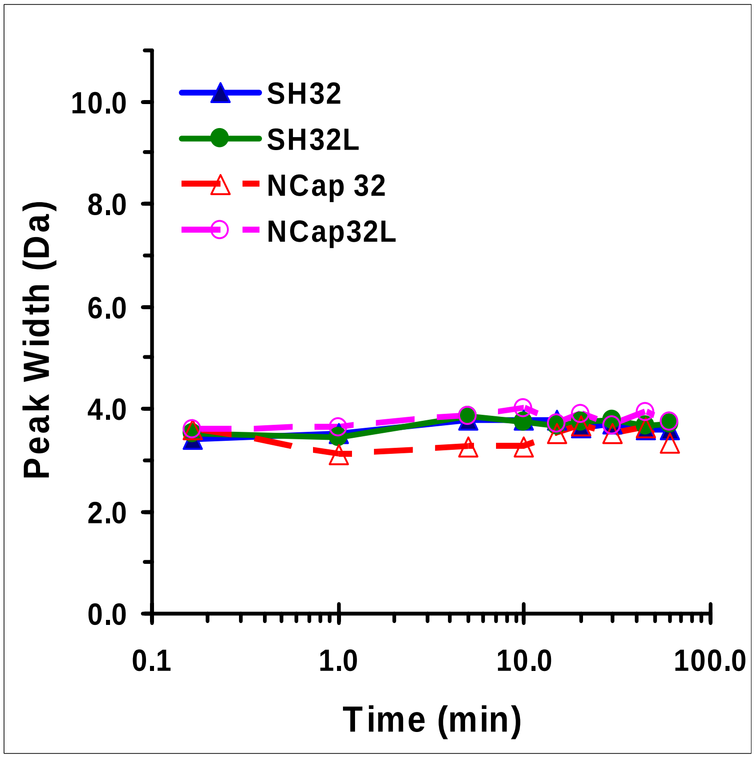




m

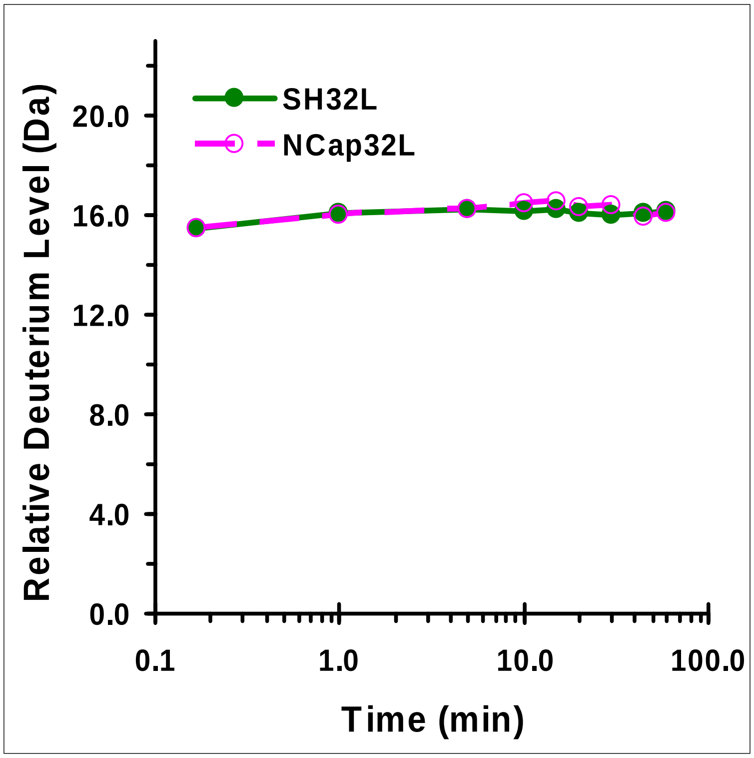
m/z= 643.4 (+2)
SH2: LVHHHSTVADGL Max=11

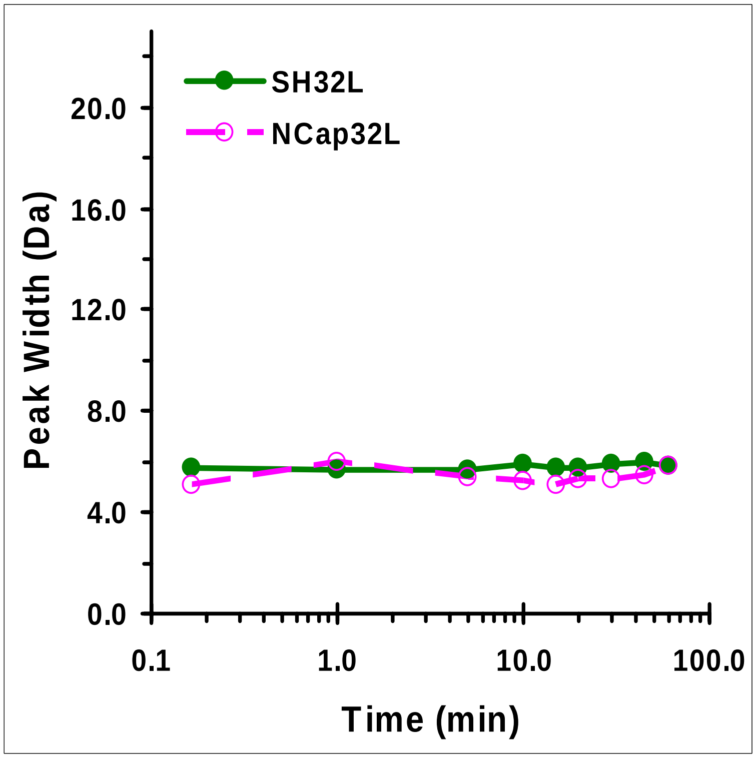




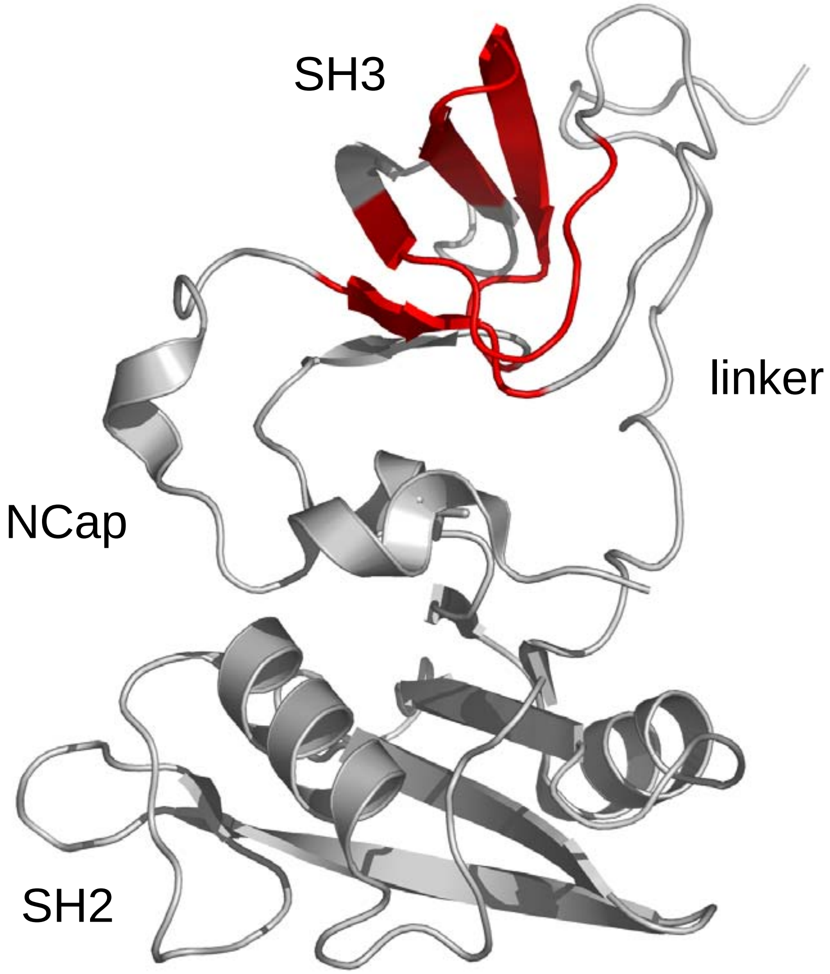
n

m/z= 1058.9 (+3)
SH2-kinase Linker: ITTLHYPAPKRNKPTVYGVSPNYDKWE
Max=23





O



Supplementary Figure 3s
Mapping changing of dynamics in NCap32L. PDB code:2FO0. NCap mainly affects the dynamics of the red regions in SH3 domain. These regions include the reporter peptide, peptide b, and peptide d as in the supplementary peptide map (Figure 1s). See also Figure 1b, right, which is in the same orientation.