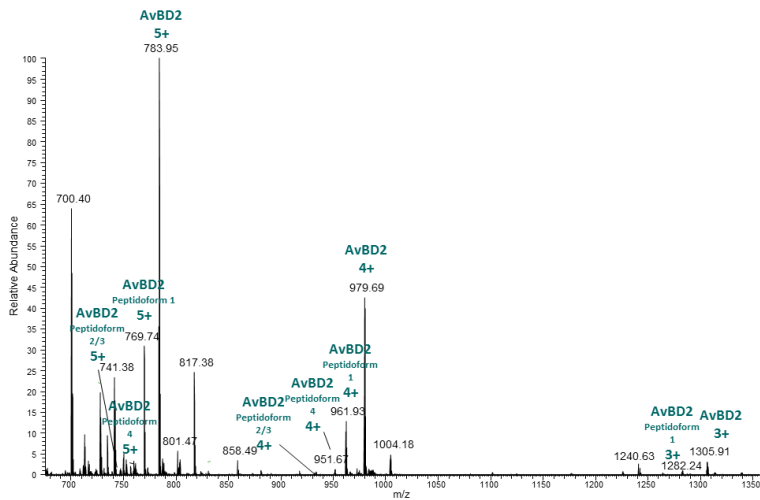


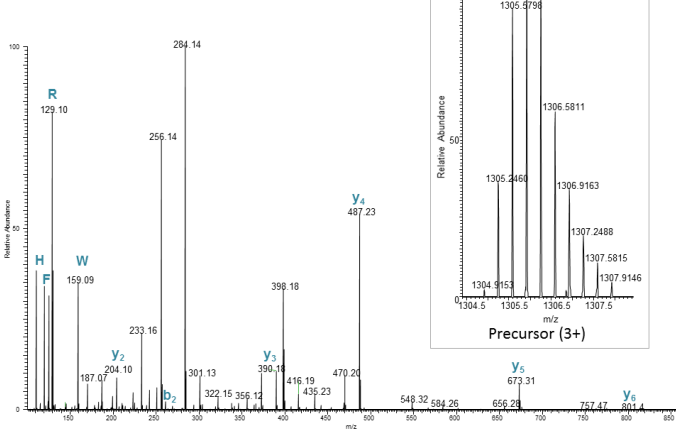
A



Protein description	m/z precursor (average)	z	Observed monoisotopic mass [M+H] ⁺	Theoretical monoisotopic mass [M+H] ⁺	Delta mass (Da)	Prosight probability E-value	b ions	y ions	Total ions
AvBD 2 full-length	1305.91	3	3913.7380	3913.7178	0.0202	1.14E-04	3	5	8
AvBD 2 peptidoform 1	961.92	4	3842.7092	3842.6807	0.0285	1.E-07	3	7	10
AvBD 2 peptidoform 2	933.41	4	3728.6644	3728.6378	0.0266	9.36E-06	6	4	10
AvBD 2 peptidoform 3	933.41	4	3729.6676	3729.5967	0.0709	9.36E-06	3	6	9
AvBD 2 peptidoform 4	951.16	4	3800.6676	3800.6338	0.0338	4.35E-06	6	4	10

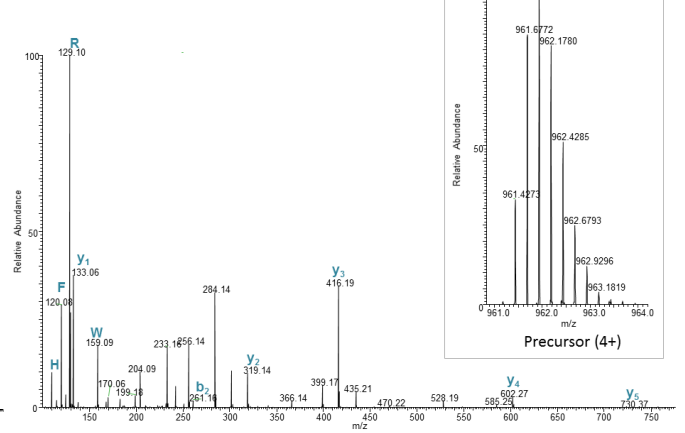
AvBD2 : full-length

LFCKGGSCHFGGCPSHLIKVGSCFGFRSCCKWPWNA



AvBD2 : peptidoform 1

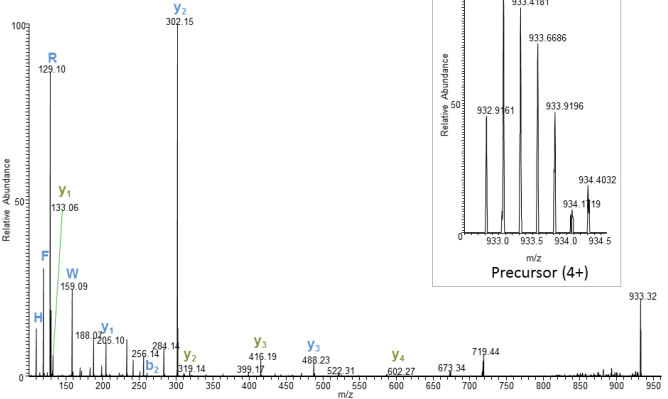
LFCKGGSCHFGGCPSHLIKVGSCFGFRSCCKWPWN



AvBD2 : peptidoform 2 and 3

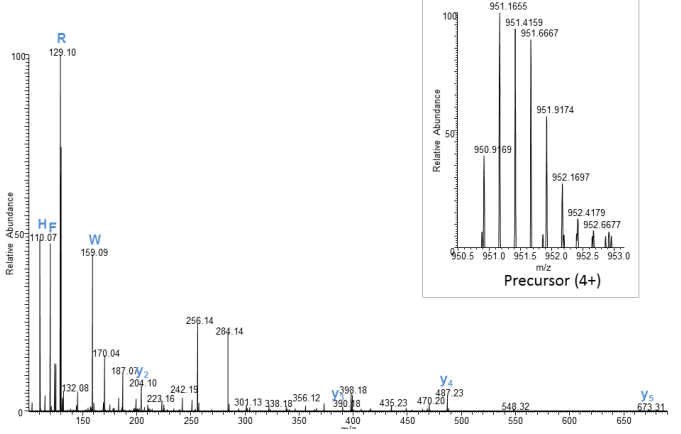
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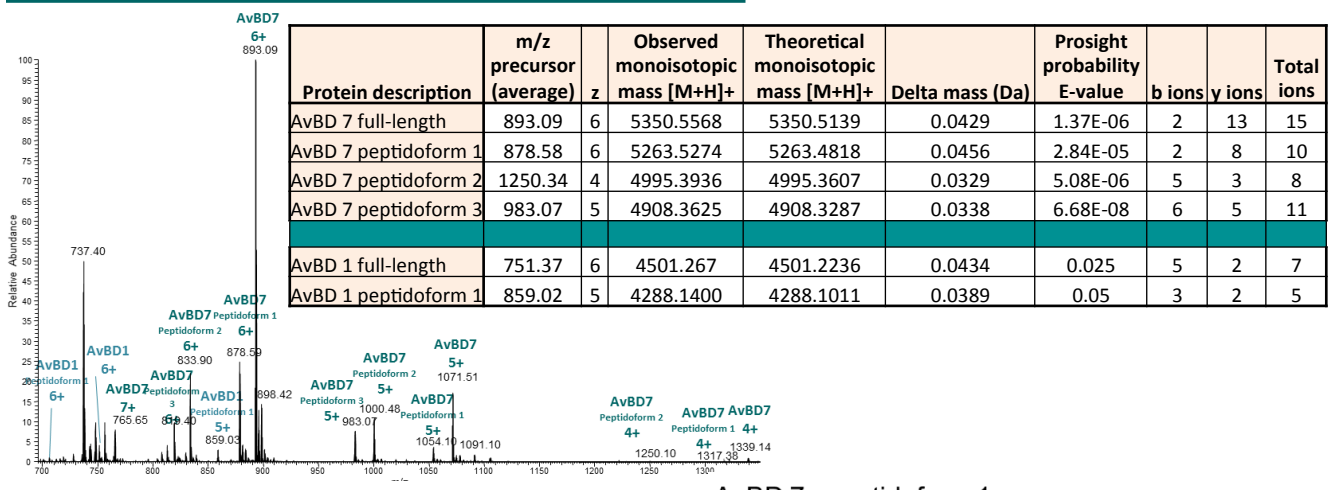


AvBD2 : peptidoform 4

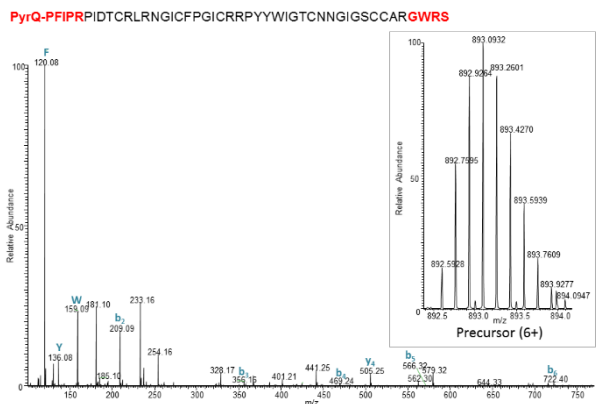
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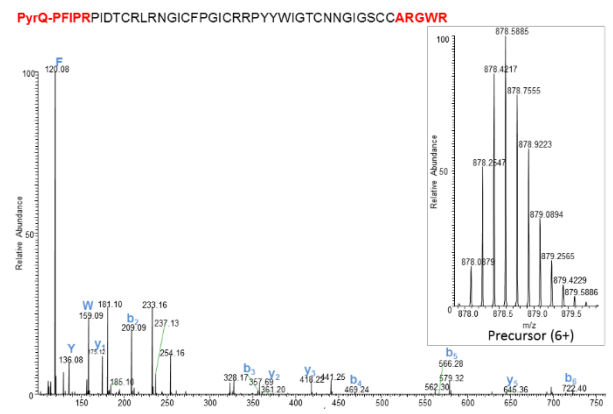
B NanoESI-MS spectra for structural characterization of AvBD1 and AvBD7 peptideforms



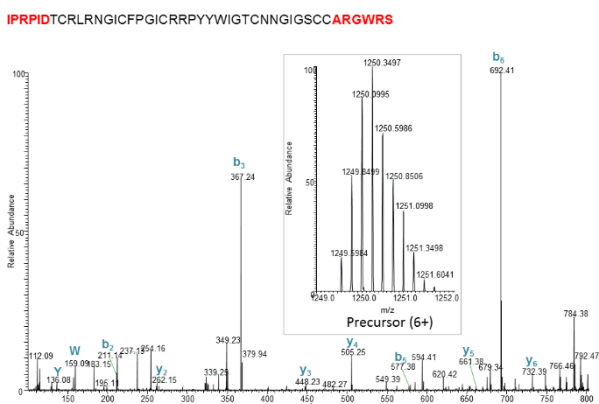
AvBD 7 : full-length



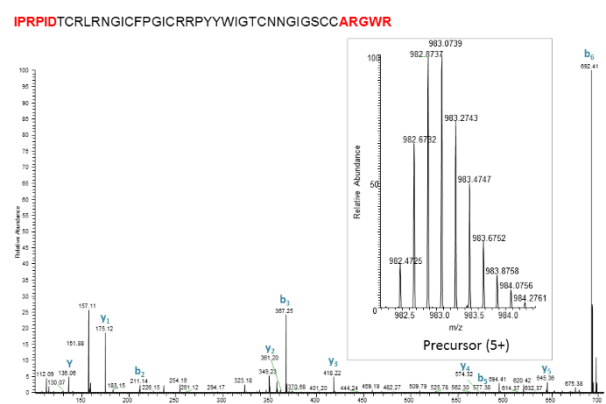
AvBD 7 : peptideform 1



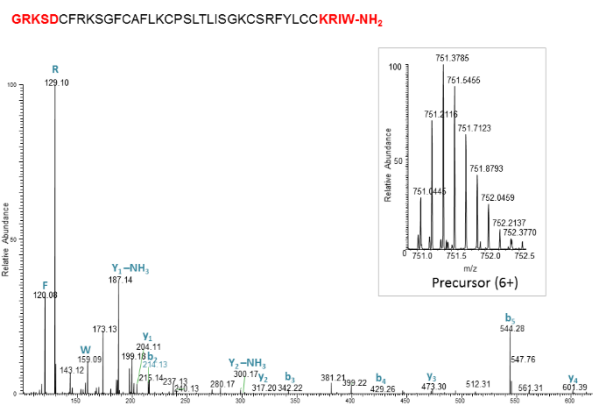
AvBD 7 : peptideform 2



AvBD 7 : peptideform 3



AvBD1 : full-length



AvBD1 : peptideform 1

