Correspondence of b- and y-fragments of the predicted peptide sequences to MS/MS spectra of selected m/z features.



Figure S1.1. Correspondence of b- and y-fragments of the predicted peptide SLVHQDWLN(-17)GK to MS/MS spectrum of m/z = 427.219^{3+} . Peptide sequence has been corrected to SVLHQDWLN(-17)GK after BLAST alignment and validation by Peptide fragmentation modeling utility.



Figure S1.2. Correspondence of b- and y-fragments of the predicted peptide TVVHQDWLN(+0.98)GKEYK or TVVHQN(+0.98)WLDGKEYK to MS/MS spectrum of m/z = 430.219^{4+} .



SVLHQDWLN(+0.98)GKEYK or SVLHQN(+0.98)WLDGKEYK to MS/MS spectrum of $m/z = 430.219^{4+}$.



Figure S1.4. Correspondence of b- and y-fragments of the predicted peptide LSC(+57)AASGLR to MS/MS spectrum of $m/z = 467.742^{2+}$.



Figure S1.5. Correspondence of b- and y-fragments of the predicted peptide HQDWLN(-17)GK to MS/MS spectrum of m/z = 490.733²⁺.





EVQLVESGGGLEQPGR to MS/MS spectrum of $m/z = 552.29^{3+}$.



Figure S1.8. Correspondence of b- and y-fragments of the predicted peptide TNYADSDLGR to MS/MS spectrum of $m/z = 556.254^{2+}$. Di-peptides DL and VE are equivalent in mass, and peptide sequence has been corrected to TNYADSVEGR after BLAST alignment.



Figure S1.5. Correspondence of 5- and y-magnetics of the predicted pepti FQ(+0.98)GWVTMTR to MS/MS spectrum of $m/z = 563.78^{2+}$.







