TABLE S1 Peptides identified by MS/MS analysis of IOE-II

Peptide sequence	Protein	Amino acid position
YGEPVFVR	IoxA	83-90
ETPIESETLK	IoxA	318-327
AKYGEPVFVR	IoxA	81-90
VQAGDVEDPSR	IoxA	380-390
DVVELGPGDEVK	IoxA	486-497
RQPAIDFSEVR	IoxA	397-407
LGMREDGAGQSGR	IoxA	355-367
IEQGSAEIWTWR	IoxA	437-448
QLDEGDMIMQFR	IoxA	368-379
ATNWIILSNDGNLR	IoxA	303-317
DSDNENDPNPDAFR	IoxA	190-203
VQAGDVEDPSRIPDFMR	IoxA	380-396
LDFTATNVYAGHAGFYLLFDEK	IoxA	168-189
MPVAQSVPQSDLLDPILGGMAPDPER	IoxA	1-26
GPEEDLAR	IoxC	128-135
FDEWTTR	IoxC	473-479
IQAIENALK	IoxC	344-352
HEVEVEFR	IoxC	612-619
TMEVVNDGTK	IoxC	41-50
VYSGMPLLNYK	IoxC	212-222
LAAIGMIGDLAPAK	IoxC	379-392
LAAIGMIGDLAPAKR	IoxC	379-393
SVDPETNSVTVHQVWGR	IoxC	229-245
SIPQWEIDVFGEAPSSSEAAK	IoxC	358-378
VDQEDIQFALDILEGNPINR	IoxC	192-211
RGHEDWAPFVMYFDDPNLR	IoxC	276-294
GWENTFHNTLPLNGQGPWFTFGR	IoxC	507-529
GGVGVPSVALDGSFFPMNEGERYEFDFK	IoxC	295-322
HFILSDTFSIDPSNVLDEEWTINYVVDVVK	IoxC	246-275
GVTPDLTADSTLFYVNNTIYGMLTGHDGTTGSQGR	IoxC	438-472