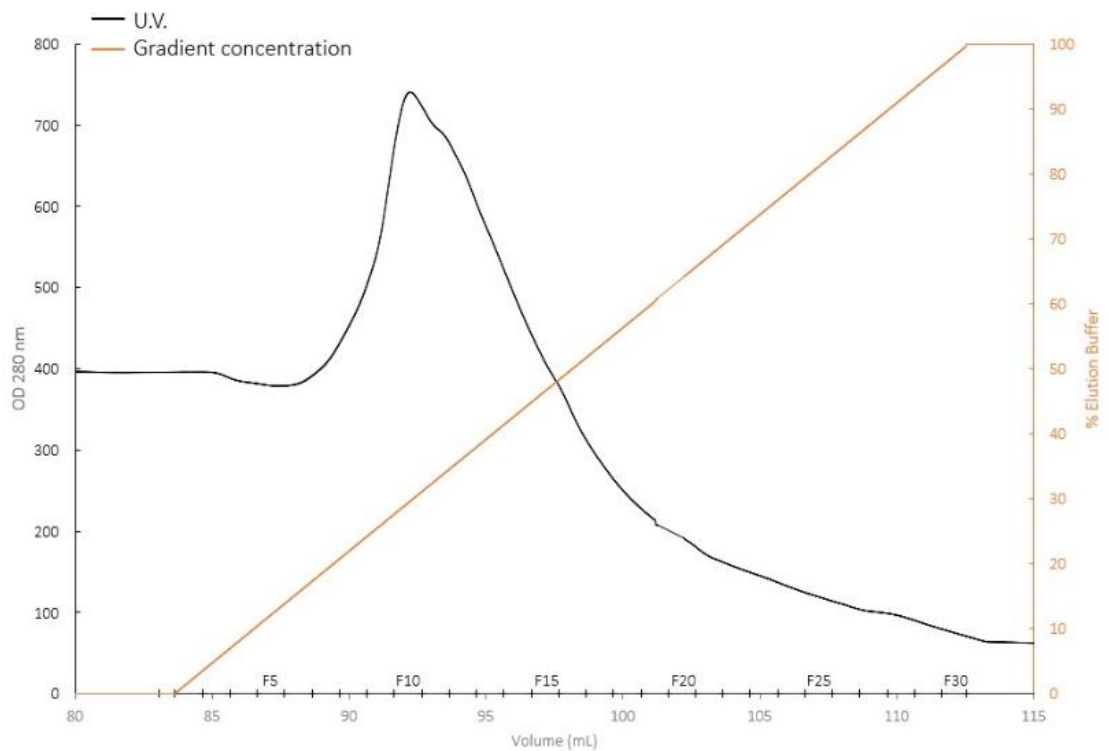
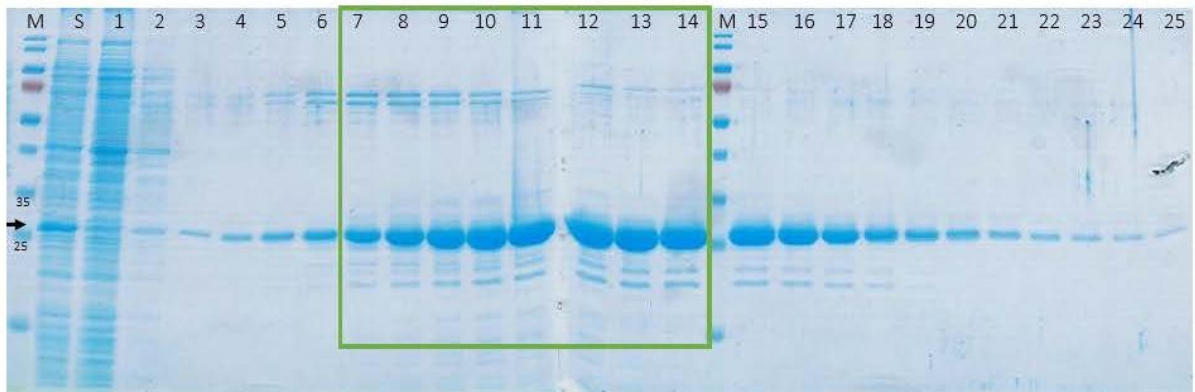


Supplementary Data

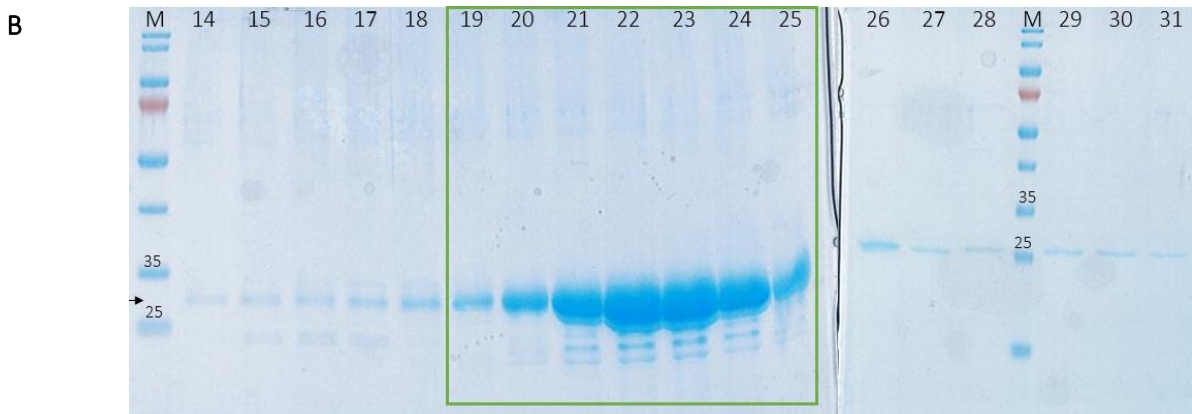
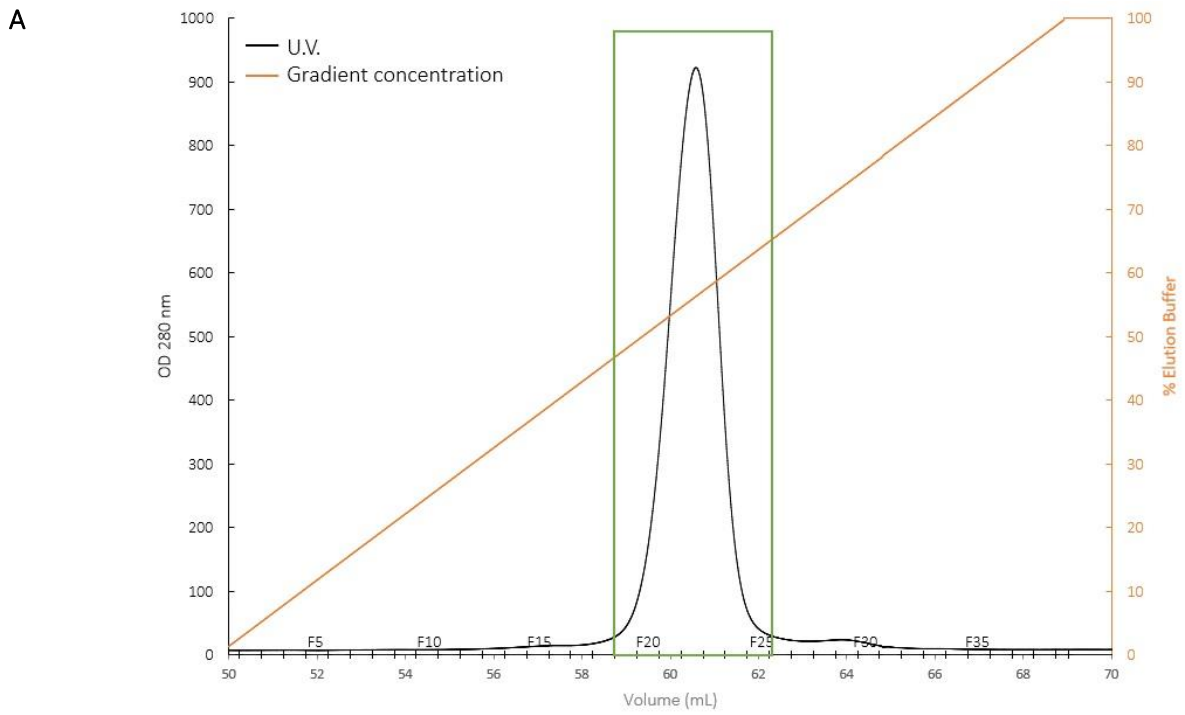
A



B



Supplementary Figure 1. 6His-Ulp1 purification on Ni-NTA column. A) Elution profile of Ni-NTA chromatography. UV curve and elution buffer gradient are in black and orange, respectively. B) Coomassie blue stained 12% SDS-PAGE gel from different sample fractions. Lane M: pre-stained protein marker. Lane S: Induced supernatant after lysis and centrifugation. Lanes 1 to 24: Fractions from elution gradient. The arrow indicates the 6His-Ulp1 protein (~28 kDa).



Supplementary Figure 2. 6His-Ulp1 purification on Heparin column. A) Elution profile of heparin chromatography. UV curve and elution buffer gradient are in black and orange, respectively. **B)** Coomassie blue stained 12% SDS-PAGE gel from different sample fractions. Lane M: pre-stained protein marker; Lanes 14 to 31: Fractions from elution gradient. The fractions containing 6His-Ulp1 proteins (F19 to F25) are indicated by a green rectangle.

Table 1. Detection by nanoLC-MS/MS of the peptides derived from Eat(A)v expressed in E. coli. Are indicated in columns: Prev. AA: Previous Amino-Acid in the protein sequence ; Peptide: sequence of the identified peptides; Next AA: Next Amino-Acid in the protein sequence ; Length: length of the identified peptides; PTMs: Post Translational Modifications detected; PSM Score : Peptide Spectrum Match Score; Start: start position of the identified peptides in the protein sequence; Stop: stop position of the identified peptides in the protein sequence; Calc. Mass: Calculated Mass of the theoretical peptide ; Exp. MoZ: Experimental Mass to Charge Ratio; Ppm: Difference between experimental and theoretical masses; Charge : charge of the peptide ions detected; Rank: Rank of the identified sequence; RT: Retention Time of the peptides; Protein Set Count: number of Protein Sets in which the peptides are assigned; ProteinSets : Name of the Protein Sets in which the peptides are assigned.

Prev. AA	Peptide	Next AA	Length	PTMs	PSM Score	Start	Stop	Calc. Mass	Exp. MoZ	Ppm	Charge	Missed Cl.	Rank	RT	Protein Set Count	Protein Sets
-	MSKIEK	N	7	Oxidation (M1)	25,92	1	7	863,478607	432,748	3,2825215	2	1	1	9,997784	1	1 (Eat(A)v_LSAP-resistance)
K	ITLLNLIQNK	L	10		55,02	45	54	1156,681549	579,34906	1,7424759	2	0	1	35,091667	1	1 (Eat(A)v_LSAP-resistance)
R	ELQLMQTDPPELLWR	E	14	Oxidation (M5)	83,97	99	112	1786,892349	894,45331	-0,15707916	2	0	1	35,46317	1	1 (Eat(A)v_LSAP-resistance)
R	EFSTLSGGEEK	T	10		66,19	113	122	1053,497849	527,75823	3,8455255	2	0	1	14,832667	1	1 (Eat(A)v_LSAP-resistance)
R	KQVAAYLK	K	8		44,65	153	160	919,549072	460,78411	4,987176	2	1	1	11,8336	1	1 (Eat(A)v_LSAP-resistance)
K	QVAAYLK	K	8		43,56	154	161	919,549072	460,78352	3,7067435	2	1	1	10,975467	1	1 (Eat(A)v_LSAP-resistance)
K	QVAAYLK	K	7		40,83	154	160	791,454117	396,73607	4,3744636	2	0	1	17,7425	1	1 (Eat(A)v_LSAP-resistance)
K	QGFVAVSHDR	G	10		70,64	164	173	1156,598923	579,30737	1,0918223	2	0	1	30,222834	1	1 (Eat(A)v_LSAP-resistance)
K	SQLELYGNSFVEEQK	K	17		54,37	189	205	2074,984711	1038,49915	-0,46364966	2	0	1	33,2435	1	1 (Eat(A)v_LSAP-resistance)
K	LRDFFEVAQNEK	L	12	Oxidation (M7)	67,32	207	218	1524,68782	763,35489	4,8522882	2	1	1	12,500883	1	1 (Eat(A)v_LSAP-resistance)
R	DEFEVAQNEK	L	10	Oxidation (M5)	51,14	209	218	1255,502655	628,76372	8,137464	2	0	1	10,779217	1	1 (Eat(A)v_LSAP-resistance)
K	TAAEKAWSR	S	10		26,12	229	238	1147,562149	574,78877	0,72983384	2	1	1	9,587466	1	1 (Eat(A)v_LSAP-resistance)
K	KQVGFIDTSR	R	11		88,76	247	257	1278,656815	640,33924	5,554118	2	1	1	17,094831	1	1 (Eat(A)v_LSAP-resistance)
K	QVGFIDTSR	R	10		78,09	248	257	1150,561859	576,29038	3,7732854	2	0	1	22,3645	1	1 (Eat(A)v_LSAP-resistance)
K	QVGFIDTSRR	V	11		42,14	248	258	1306,662964	436,56386	5,182926	3	1	1	17,897667	1	1 (Eat(A)v_LSAP-resistance)
K	GAVGADAAR	T	9		57,42	262	270	786,398407	394,20877	5,810407	2	0	1	6,2764163	1	1 (Eat(A)v_LSAP-resistance)
R	METQISEK	E	8	Oxidation (M1)	53,52	282	289	980,448441	491,22905	-4,98034	2	0	1	8,217183	1	1 (Eat(A)v_LSAP-resistance)
R	METQISEKEK	L	10	Oxidation (M1)	31,36	282	291	1237,585983	619,80233	3,3276849	2	1	1	7,3143835	1	1 (Eat(A)v_LSAP-resistance)
K	DIEYDLSLTVNSQASHHK	R	18	Oxidation (M10)	60,17	295	312	2103,95311	702,32849	4,998636	3	0	1	27,984667	1	1 (Eat(A)v_LSAP-resistance)
R	VAISGPNAGK	S	11		72,65	342	352	969,524338	485,77078	2,7482173	2	0	1	11,0539665	1	1 (Eat(A)v_LSAP-resistance)
K	HLISIASQNYEDNR	G	15		58,55	376	390	1795,8125	599,6138	3,931435	3	0	1	20,195333	1	1 (Eat(A)v_LSAP-resistance)
R	GTLAFAEK	N	9		58,02	391	399	964,486542	483,25212	3,2550402	2	0	1	22,049665	1	1 (Eat(A)v_LSAP-resistance)
K	NQVDYQAFNNLR	K	13		48,28	400	412	1593,789932	797,90736	6,4143195	2	0	1	35,205	1	1 (Eat(A)v_LSAP-resistance)
K	IEQVSVGGR	K	9	Oxidation (M4); Oxidation (M6)	54,91	425	433	1110,479767	556,24898	3,2728257	2	0	1	3,3258002	1	1 (Eat(A)v_LSAP-resistance)
K	VSTEISLER	I	10		71,44	490	499	1145,629181	573,82363	3,0732534	2	0	1	28,824	1	1 (Eat(A)v_LSAP-resistance)
K	VSTEISLERI	-	11		36,78	490	500	1258,713242	630,36233	-2,4858658	2	1	1	34,663166	1	1 (Eat(A)v_LSAP-resistance)