Chapter 6 Reference

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vpar vvul vcho vpar	TTGACCTACACCCTGCCCCTGCACAGTGATATGCTGTGCAACGAAAGTACCTACC	60
vvul vcho	CAGGCAAATTCTCTGCCACGACCCAGCTCTGGAGAGAGAG	120
vpar	GTGTCTGAATTCCATTCTGAAATCAGTACCTTGTCACCTGCTCCACTT	48
vvul	GTGTCTGAG <mark>TTCCA</mark> TTCTGAAATCAGTACCTTATCACCTGCTCCACTT	48
vcho	AAGGAGTCATCT <mark>GTGTCTGA</mark> G <mark>TTCCA</mark> AA <mark>CCGAAATCAGTA</mark> AG <mark>TT</mark> ATCGTCAAA <u>TCCA</u> ATT	180
vpar vvul vcho	TGGCAGTTTTTCGATAAGATTTGTTCCATCCCTCATCCATC	108 108 240
vpar	GCACAGTACATTATCAACTGGGCAACAGAGCAAGGCTTCGATGTTCGCCGAGACCCAACG	168
vvul	GCTCAGTACATCGTCAACTGGGCGACAGAGCAAGGTCTAGACGTCGTCGCGATCCAAC	168
vcho	GCTCAATACATTATCAACTGGGCTAAAGAACAAGGATTGGCCGTTCGTCGTGATGAGAC	300
vpar	GGCAACGTATTCATCAAAAAGCCAGCAACGCCTGGGATGGAAAACAAAAAGGGCGTGGT	228
vvul	GGCAATGTGTTTATTAAAAAGCCTGCGACACCAGGCATGGAAAACAAAAAGGGTGTTGT	228
vcho	GGTAACGTCTTTATTAAAAAAGCCAGCGACACCGGGCATGGAAAATCGTAAAGGTGTGGCTA	360
vpar	CTTCAAGCACAATTGACATGGTGCCACAGAAGAATGAAGACACTGACCACGACTTCACA	288
vvul	CTTCAAGCGCACATCGACATGGTGCCTCAGAAAAAACGAAGACACTCAACACGACTTCAC	288
vcho	CTTCAAGCGCACATTGATATGGTGCCGCAAAAAAAATGAAGACACAGTGCATGATTTCACC	420
vpar	AAAGATCCAATTCAACCGTACATCGATGGTGACTGGGTAACAGCGAAAGGCACGACGCT	348
vvul	ACC <mark>GATCC</mark> TATTCGTCCATACATTGACGGTGACTGGGTAACC <mark>GC</mark> AG <mark>AAGGTACGACGCT</mark> C	348
vcho	AAAGATCCG <mark>ATCC</mark> AGCCTTATATTGATGGTGAATGGGTTACTGCTAAAGGCACTACGCT	480
vpar	GGTGCAGACAACGGTATTGGTATGGCTTCTTGTCTTGCTGTATTAGCATCTAAAGATATC	408
vvul	GGTGCGGATAATGGGAATTGGCATGGCTTCCTGCCGTTGCGGTGTGGCCTCAACAGAGATATC	408
vcho	GGCGCGGATAATGGTATCGGCATGGCTTCTTGCCTAGCAGTACTGGCTTCTAAAGAGATAC	540
vpar	AAGCATGGGCCAATTGAAGTTCTACTAACAATTGATGAAGAAGCAGGCATGACTGGTGCA	468
vvul	AAGCATGGTCCAATTGAAGTACTGCTAACCATTGATGAAGAAGCGGGCATGACGGGTGCT	468
vcho	CAACATGGTCCAATTGAAGTTCTGCTGACTATTGATGAAGAAGCAGGCATGACCGGCGCT	600
vpar vvul vcho	TTCGGGCTTGAAGCAGGTTGGTTGGAAGGTGATATTCTTCTAAACACCGACTCCGAGCAA TTTGGTTTGG	528 528 660
vpar	GAAGGCGAAGTGTACATGGGCTGTGCTGGTGGTATCGATGGTGCGATGACTTTTGACATC	588
vvul	GACGGT <mark>GAAGTCTACATGGGCTGCGCAGGCGG</mark> TATCGACGCGCGCGATGACGTTTGATAT	588
vcho	GAAGGT <mark>GAAGTCTATATGGGCTGCGCGGGAGG</mark> CGTGA <mark>ACG</mark> CCGAGTTCACTTTCTCCATT	720
vpar	AAACCCCACCCATCCCTACTCCCTTTGTGACTCGTCAGCTAACCTTGAAGCGTTTAAAA	648
vvul	CAACCCCAAGCCGTTCCTGCGCGCTTTATTACTCCGTCAGTTAACGCTAAAAGCCTTAAAA	648
vcho	GAGCGTCAAGCCATCCCTGCTGCTGCTTATGTTGGCCCGCCAACTGATCTTAAAGGGTTTGAAA	780
vpar vvul vcho	GGCGGTCACTCTGGTTGTGATATCCACACTGGTCGTGGTAATGCCAACAAACTGCTTGGC GGCGGTCACTCAGGTTGTGACATCCACACTGGTCGTCGTAACGCAAACAAA	708 708 840

vpar	CGATTCCTAGCGGGCCATGCACAAGAGTTGGATCTTCGCTTGGTTGAATTCCGTGGT	768
vvul	CGTTTCCTTGCTGGCCACGCACAAGAATTGGATCTGCGTTTAGTAGAGTTCCGCGGTGGT	768
vcho	CGCTTTCTCGCAGGCCATGCGAAAGAATTAGATCTGCGCTTAGTCGAATTCCGTGGCGGT	900
vpar vvul vcho	AGTTTGCGTAATGCTATTCCTCGCGAAGCTTTCGTAACAGTTGCTGTTCCTGCTGAAAAC AGCCTGCGTAATGCGATTCCTCGTGAAGCATTCGTCAAAGTGGCGCTGCCTGC	828 828 960
vpar	CAAGAGAAACTTGCAGAGCTTTTCA <mark>AC</mark> TA <mark>CTACACTGA</mark> GCTATTAAAAAGCAGAGCTTGGC	888
vvul	CAAGATAAGCTTGCTCAACTGTTTGACTA <mark>CTACACTGA</mark> ACTTCTAAAAAGCGGAGCTGGG	888
vcho	GT <mark>AG</mark> CCG <mark>A</mark> ATTAGAAACCTTATTCC <mark>AC</mark> CG <mark>CTACACTGA</mark> GCTACTCAAAGCTGAACTGGGT	1020
vpar	AAAGTAGAAACGGGTATTGTGACGTTCAATGAAGAGATCGTAACCGAATCACAAGCTTTC	948
vvul	AAAGTGGAAACCAACATTGTCACGTTTAACCAAGCGGTTGATGTGGAAGCTGGTGTATTG	948
vcho	AAGGTTGAAACTCACTTGGTAACTTTCCTTGAAGCCAAAGAACTGCAAAGTGAAGTGCTG	1080
vpar	ACCGCGGCGGAC <mark>CAACAACG</mark> CTTTATTGCTGCTCTCAACGCATGTCCAAATGGCGTGATG	1008
vvul	ACTAACGCTGAT <mark>CAACAACG</mark> CTTTGTCGCTGCATTAAATGCT <u>TGTCCAAA</u> CGGTGTCATT	1008
vcho	ACCGCGCACACT <mark>CAACAACG</mark> TTTTGTTGCCGCTCTGAACACGTGTCCAAACGGTGTGATC	1140
vpar	CGCATGAGCGACGAAATTGAAGGTGTGGTTGAAACGTCACTGAACGTTGGCGTGATCACT	1068
vvul	CGCATGAGCGATGAGATTGAAGGTGTGGTTGAAACGTCGCTTAACGTGGGTGTAATCACC	1068
vcho	CGCATGAGCGATGATATTGCAGGTGTTGTAGAAACCTCACTCA	1200
vpar vvul vcho	ACTGAAGAAAATAAAGTGACTGTTCTGTGCCTAATTCGCTCTTTGATTGA	1128 1128 1260
vpar	AG <mark>CCAAGTAGA</mark> GA <mark>GCATG</mark> TTACGCTCTGTTGCTG <mark>AACTCGCAGGGGCACA</mark> AGTTGAGTTC	1188
vvul	AG <mark>CCAAGTCGA</mark> AA <mark>GCATG</mark> CTGACATCAGTAGCGG <mark>AACTGGCTGCTCCACACATCC</mark> TGTTC	1188
vcho	CA <mark>CCAAGTCGA</mark> GG <mark>GCATG</mark> TTGCAATCGCTGGCAC <mark>AACT</mark> TGCGGGGGCAGAGCTGGACCTT	1320
vpar	TCAGGCGCTTACCCTGGTTGGAAACCAGACGCTGATTCAGAAATTATGGCGATTTTCCGT	1248
vvul	TCTGCCGCTTACCCAGGTTGGAAACCGGATGCTGATTCTGAAATCATGGCGATCTTCCGT	1248
vcho	TCTGGTGCTTACCCTGGCTGGAAACCCGATGCTGATTCTGAAATCATGCATATTTTCCGT	1380
vpar	GATATGTACGAAGGCATTTACGGTCACAAACCAAACATCATGGTTATTCACGCAGGTCTT	1308
vvul	GATATGTAC <mark>GAAGGCATTTAC</mark> GGTCACAAACCGAACATCATGGTCATTCACGCGGGCCTA	1308
vcho	GATATGTA <mark>TGAAGGCATTTA</mark> TGG <mark>CCACAAACCGAATATCATGGT</mark> GATCCACGCGGGTCTT	1440
vpar vvul vcho	GAATCTGGTCTATTTAAAGAGCCTTACCCGAACATGGACATGGTTTCTTTC	1368 1368 1500
vpar	ATCAAGTTCCCTCACTCTCCTGATGAAAAAGTGAAGATTGATACCGTTCAACTGTTCTGG	1428
vvul	ATTAAATTCCCGCACTCTCCAGATGAGAAAGTGAAGATTGACACGGTACAACTCTACTGG	1428
vcho	ATCAAGTTCCCACATTCACCGGATGAAAAAGTGAAGATAGACACGGTTGATCTGTTCTGG	1560
vpar	GATCAAATGGTTGCGCTTCTAGAAGCAATTCCTGAGAAAGCGTAA	1473
vvul	GATCAAATGGTGGCGTTACTGGAAGCGATTCCTGAAAAGGCGTAA	1473
vcho	CAACAGATGGTGGCACTACTCGCCAATATCCCAGTGAAAGCCTAA	1605

Appendix 1. Nucleic acid sequence alignment of *Vibrio* **spp.** *pepD* **genes.** Abbreviations vpar, vvul, and vcho stand for *V. parahaemolyticus*, *V. vulnificus*, and *V. cholerae*, respectively. Conserved nucleic acids among the sequences are marked in black. Dashed lines indicate the gaps introduced for better alignment.

Appendix 2. Primers used in this thesis.

Sequencing and Expression			
F1 (sense)	5'-gtgtctgagttccattc-3'	$(1-17)^{a}$	
F2 (sense)	5'-TGGGCGACAGAGCAAGG-3'	(127-143)	
F3 (sense)	5'-TCTGGCGCTTACCCAGG-3'	(1189-1205)	
R1 (antisense)	3'-AAGGACTTTTCCGCATT-5'	(1457-1473)	
R2 (antisense)	3'-CGTAACTTGCGAACAGG-5'	(979-995)	
R3 (antisense)	3'-gtgactagtgctgaagt-5'	(270-286)	
N1 (sense)	5'-CGCGGATCC <u>CATATG</u> GTGTCTGAGTTCCATTC-3'	$(NdeI)^{b}$	

Mutagenesis

H80A-1	5'-gtgcttcaagcag <u>cgatcg</u> acatggtgccac-3'	$(PvuI)^{b}$
H80A-2	5'-gtggcaccatgt <u>cgatcg</u> ctgcttgaagcac-3'	(PvuI)
D82A-1	5'-gcacacatcg <u>ccatgg</u> tgccacaaaagaacg-3'	(NcoI)
D82A-2	5'-CGTTCTTTTGTGGCA <u>CCATGG</u> CGATGTGTGC-3'	(NcoI)
D119A-1	5'-CGCTCGGGGCAGCTAACGGCATCGGCATGGC-3'	(AvaI)
D119A-2	5'-GCCATGCCGATGCCGTTAGCTGCCCCGAGCG-3'	(AvaI)
E149A-1	5'-CTGACGATCGATGCAGAAGCAGGCATGACAGG-3'	(PvuI)
E149A-2	5'-CCTGTCATGCCTGCTTCTGCATCGATCGTCAG-3'	(PvuI)
E150A-1	5'-ACTATTGATGAAGCCGCGGGCATGACAGGTGC-3'	(SacII)
E150A-2	5'-gcacctgtcatgc <u>ccgcgg</u> cttcatcaatagt-3'	(SacII)
D173A-1	5'-CCTTCTAAATACA <u>GCTAGC</u> GAACAAGAAGGCG-3'	(NheI)
D173A-2	5'-CGCCTTCTTGTTC <u>GCTAGC</u> TGTATTTAGAAGG-3'	(NheI)
H461A-1	5'-CCAACCATCAAGTTCCCT <u>GCTAGC</u> CCAGATGAG-3'	(NheI)
H461A-2	5'-CTCATCTGG <u>GCTAGC</u> AGGGAACTTGATGGTTGG-3'	(NheI)

^a Corresponded sequence position. ^b Corresponded additional restriction site on primers (underlined).

Source	Name	Identity	Accession No.
V. parahaemolyticus	Aminoacylhistidine	94%	NP_797050
RIMD 2210633	dipeptidase		
Vibrio alginolyticus 12G01	Aminoacylhistidine	93%	ZP_01260299
	dipeptidase		
Vibrio vulnificus YJ016	Aminoacylhistidine	92%	NP_933645
	dipeptidase		
Vibrio vulnificus CMCP6	Aminoacylhistidine	91%	NP_759335
	dipeptidase		
Vibrio splendidus 12B01	Aminoacylhistidine	88%	ZP_00990223
	dipeptidase		
Vibrio fischeri ES114	Aminoacylhistidine	84%	YP_204119
	dipeptidase		
Vibrio cholerae O1 biovar	Aminoacylhistidine	82%	NP_231910
eltor str. N16961	dipeptidase		
Vibrio cholerae V51	Di- and tripeptidases	82%	ZP_00749022
Vibrio cholerae MO10	Di- and tripeptidases	81%	ZP_00759334
Vibrio cholerae O395	Di- and tripeptidases	81%	ZP_00757002
Vibrio cholerae V52	Di- and tripeptidases	81%	ZP_00746278
Vibrio cholerae RC385	Di- and tripeptidases	81%	ZP_00752195
Vibrio angustum S14	Putative aminoacylhistidine	76%	ZP_01235668
	dipeptidase		
Photobacterium profundum	Putative aminoacylhistidine	75%	ZP_01218945
ЗТСК	dipeptidase		
Photobacterium profundum	Putative aminoacylhistidine	75%	YP_129048
SS9	dipeptidase		
Shigella sonnei Ss046	Aminoacylhistidine	63%	YP_309297
	dipeptidase		
Yersinia mollaretii ATCC	Di- and tripeptidases	63%	ZP_00826723
43969			
Escherichia coli O157:H7	Aminoacylhistidine	63%	NP_285954
EDL933	dipeptidase (peptidase D)		

Appendix 3. Homology analysis of *V. alginolyticus pepD* amino acids.

Escherichia coli O157:H7	PepD	63%	NP_308291
str. Sakai			
Escherichia coli 53638	Di- and tripeptidases	63%	ZP_00735968
Shigella boydii BS512	Di- and tripeptidases	63%	ZP_00696913
Shigella dysenteriae 1012	Di- and tripeptidases	63%	ZP_00921840
Shigella boydii Sb227	Aminoacylhistidine	63%	YP_406787
	dipeptidase		
Escherichia coli E22	Di- and tripeptidases	63%	ZP_00730150
Escherichia coli B171	Di- and tripeptidases	63%	ZP_00711302
Escherichia coli E110019	Di- and tripeptidases	63%	ZP_00721352
Escherichia coli B7A	Di- and tripeptidases	63%	ZP_00717585
Escherichia coli HS	Di- and tripeptidases	63%	ZP_00704526
Escherichia coli E24377A	Di- and tripeptidases	63%	ZP_00702608
Yersinia pestis Nepa1516	Aminoacylhistidine	63%	YP_646797
	dipeptidase		



4.1 Production of PepD Monoclonal Antibody

4.1.1 Immunization of mice

The 4-week-old female BALB/c mice were immunized with an antigen that is prepared by emulsifying the purified PepD with Freund's adjuvant. PepD was mixed and homogenized with an equal amount of Freund's complete adjuvant by vortex. Each mouse was given a total $300 \ \mu$ L emulsion containing 125 μ g protein with an i.p. (intraperitoneal) injection and 3 s.c. (subcutaneous) injections onto the back. Mice were proceeded secondary and continuous immunization with protein and Freund's incomplete adjuvant mixture with the same volume and method as described above every 10-14 days.

After 3 times of immunization, blood samples of each mouse was collected by blood collecting tubes with 0.1% (wt/v) EDTA and centrifuged at 7,000 rpm for 7 min at 4 to obtain the supernatant containing polyclonal antibody (pAb) against PepD. The titer of pAb was determined by enzyme-linked immunosorbent assay (ELISA) method (see 2.10.4). Mice with a titer of pAb at a serum dilution of more than 1:1000 were chosen for the following cell fusion experiments. Each chosen mouse was carried out a final booster with the same dose of antigen resuspended only in sterilized phosphate buffered saline (PBS) by 1 i.p. and 1 i.v. (intravenous) injection.

4.1.2 Preparation of myeloma cells

The mouse myeloma cell line FO was used for cell fusion experiment. FO cell stocks in liquid nitrogen were quickly thawed out by 37 water bath following centrifugated at 1200 rpm for 5 min. The resultant supernatant was removed, and centrifuged cells were

resuspended by 6 mL pre-warmed Dulbecco's Modified Eagles Medium (DMEM) containing 10% bovine calf serum (BCS) and 1% 100X penicillin-streptomycin stock solution and cultured in 25 cm² flasks at 37 incubator supplemented with 5% carbon dioxide (CO_2).

The redundant cells were kept as frozen stocks for future usage. In brief, the cells in medium consist of DMEM, 20% fetal bovine serum (FBS) and 7% dimethyl sulfoxide (DMSO) were added to cryo tubes. The tubes were put in a cooler at -80 overnight and then stored in liquid nitrogen.

4.1.3 Fusion of myeloma cells with spleen cells

The cell fusion experiment was carried out by fusing previously prepared myeloma cells (FO) (see 2.10.2) with spleen cells from previously immunized mouse (see 2.10.1) to produce hydridoma cells. About 5 days later after final booster immunization, the mouse with highest titer was chosen to be sacrificed with ether. After the mouse sacrificed, the spleen was harvested in laminar flow and squeezed with pre-warmed DMEM (serum and antibiotics free) in a petri dish within a short time to obtain spleen cells. Then the FO cells were mixed with the filtered spleen cells at a ratio around 1:4 to 1:8 and the mixture was centrifuged at 1200 rpm for 5 min. The resultant supernatant was discarded and the pellet was resuspended again by pre-warmed DMEM (serum and antibiotics free) following centrifugation at 1200 rpm for 5 min. Repeat the step described above for one time.

After the last centrifugation, the suspernatant was discarded and the pellet was scattered. Cell fusion was carried out by adding 1 mL pre-warmed polyethylene glycol (PEG)/DMSO solution drop-by-drop to the mixed-cell pellet accompanied with stirring within 1 min and continuously stirring for another minute in water bath at 37 followed by adding 10 mL pre-warmed DMEM (serum and antibiotics free) within 2 min. The cell mixture was then centrifuged at 1000 rpm for 5 min and the resultant supernatant was removed. The pellet was resuspended again by pre-warmed DMEM (serum and antibiotics free) and centrifuged at 1000 rpm for 5 min. Repeat the step described above for one time.

After the last centrifugation, the suspernatant was discarded and the pellet resuspended by HT medium containing DMEM, 20% FBS, 1% 100X penicillin-streptomycin stock solution, 1% 100X L-glutamine stock solution, 1% 100X HT Supplement, and 1% 50X HAT Supplement. The final cell mixture was distributed as 100 μ L per well in five 96-well microtiter plates. The plates were cultured at 37 incubator supplemented with 5% CO₂. The hybridoma cells were cultured consequently with HY medium which is consist of HT medium without HAT Supplement.

4.1.4 Screening of hybridoma clone by ELISA method

The culture supernatant was collected and assayed by enzyme-linked immunosorbent assay (ELISA) method for screening the hybridoma cells which produce antibodies specific against PepD. Briefly, 100 μ L of 0.25 mg/mL purified PepD was initially coated on each well of 96-well microtiter ELISA plate at 4 overnight. Unbound proteins were washed out with 1X PBS buffer for 3 times, and the antigen-coated plate was blocked subsequently by adding 350 μ L blocking buffer consist of 5% non-fat milk in 1X PBS buffer on each well at RT for 1.5 hrs. Then the blocking buffer was washed out by 1X PBS buffer for 3 times followed by adding 100 μ L cell culture supernatant on each well at RT for 1.5 hrs. The plate was then washed with 1X PBS buffer for 5 times and the bound primary antibodies were detected using 100 μ L goat anti-mouse IgG conjugated horseradish peroxidase (HRP) at 1: 5,000 dilutions with 1X PBS buffer on each well for 1 hrs at RT. Finally, the plate was washed with 1X PBS

buffer for 5 times and developed by adding 50 μ L 3,3',5,5'-tetramethylbenzidine (TMB) solution on each well for 20 min in darkness followed by adding 50 μ L 2 M sulferic acid (H₂SO₄) to stop reaction. The absorbance was evaluated by Fluoroskan Ascent ELISA reader at 450 nm. The initial mouse serum-coated and non-fat milk blocked well were performed in the same way to serve as the positive and negative control, respectively.

4.1.5 Limiting dilution of hybridoma clones

The candidate hybridoma clones selected by ELISA method were diluted to obtain single cell line using "limiting dilution" method. In brief, each 10 μ L candidate hybridoma cell suspension was mixed with 10 mL pre-warmed HY medium in a petri dish and the mixture was transferred to a 96-well microtiter plate with 100 μ L on each well. The wells containing only a single cell clone was cultured, screened, and stocked as described above.

4.1.6 Ascites production in mice

Ascites is an intraperitoneal fluid extracted from mouse, which contains the desired antibodies at high concentrations. Each monoclonal hybridoma cell line with dosage of 10^6 cells in 0.5 mL sterile PBS was i.p. injected into a 6 to 8-week-old female BALB/c mouse which had i.p. injected 0.5 mL Pristane 2 days previously. The ascites was collected 7-10 days later and centrifuged at 7000 rpm for 7 min at 4 to obtain the resultant supernatant. The titer and specificity of each ascites were also assayed by ELISA method (see 2.10.4) and Western blot method (see 2.10.7), respectively. The desired ascites was stored with 0.05% sodium azide (NaN₃) added at 4 ready to use or at -20 with 50% glycerol as a frozen stock.

4.1.7 Western blot analysis

Western blot analysis was initially performed on 12.5% SDS-PAGE as described on 2.8.3. The resultant SDS-PAGE and a nitrocellulose (NC) membrane were soaked instantly in the transfer buffer for 30 sec. Then the gel was immediately transferred to a NC membrane at 30 Volt for 35 min with a semi-dry blotting apparatus. The NC membrane was blocked with blocking buffer for 1.5 hrs at RT. The membrane was then washed 3 times with 1X PBS buffer and incubated with the primary anti-PepD monoclonal antibody (mAb) at 1: 1,000 dilutions with 1X PBS buffer for 1.5 hrs at RT with gentle shaking, followed by washed 5 times with 1X PBS buffer to remove the unbound primary antibodies. The washed membrane was further incubated with the goat anti-mouse IgG conjugated HRP at 1: 5,000 dilutions with 1X PBS buffer for 1 hrs at RT with gentle shaking. Finally, the membrane was washed with 1X PBS buffer for 5 times. The immunoreactive bands were visualized with a chemiluminescence reagent and the autoradiography film.



Plasmid	R.E. ^a used	Excised frangment
pET-pepD-WT	AvaI	_b
pET-pepD-D119A	AvaI	1.2 kbp.
pET-pepD-D119AE150A	AvaI	1.2 kbp.
pET-pepD-WT	NcoI/NotI	1.6 kbp.
pET-pepD-D82A	NcoI/NotI	1.4, 0.2 kbp.
pET-pepD-WT	NdeI/NheI	-
pET-pepD-H461A	NdeI/NheI	1.4 kbp.
pET-pepD-WT	NheI/NotI	-
pET-pepD-D173A	NheI/NotI	1.0 kbp.
pET-pepD-WT	PvuI	-
pET-pepD-H80A	PvuI	2.4 kbp.
pET-pepD-E149A	PvuI	2.2 kbp.
pET-pepD-WT	SacII/NotI	-
pET-pepD-E150A	SacII/NotI	1.1 kbp.
pET-pepD-D119AE150A	SacII/NotI	1.1 kbp.

Appendix 4. The restriction enzyme used in expresson vectors check and the expected size of excised fragment.

^a R.E.= restriction enzymes. ^b No expected DNA fragment was excised.



Appendix 5. DNA agarose gel electrophoresis of site-directed mutated plasmid checked by restriction enzymes. *Lane M*, 10k-100 bp. DNA marker. *Lane 1*, pET-pepD-WT (*PvuI*). *Lane 2*, pET-pepD-H80A (*PvuI*). *Lane 3*, pET-pepD-E149A (*PvuI*). *Lane 4*, pET-pepD-WT (*AvaI*). *Lane 5*, pET-pepD-D119A (*AvaI*). *Lane 6*, pET-pepD-D119AE150A (*AvaI*). *Lane 7*, pET-pepD-WT (*NcoI/NotI*). *Lane 8*, pET-pepD-D82A (*NcoI/NotI*). *Lane 9*, pET-pepD-WT (*SacII/NotI*). *Lane 10*, pET-pepD-E150A (*SacII/NotI*). *Lane 11*, pET-pepD-D119AE150A (*SacII/NotI*). *Lane 12*, pET-pepD-WT (*NheI/NotI*). *Lane 13*, pET-pepD-D173A (*NheI/NotI*). *Lane 14*, pET-pepD-WT (*NdeI/NheI*). *Lane 15*, pET-pepD-H461 (*NdeI/NheI*).











Metal element analysis of PepD

Metal element content of purified PepD was determined using an inductively coupled plasma-mass spectrometry (ICP-MS) technique. Briefly, PepD was expressed and purified as described on 2.7, which ddH₂O was substituted for dH₂O through all the experimental steps. The purified and dialyzed fraction was digested by 10% nitric acid and sonicated for 60 min. The following ICP-MS analysis was performed at National Tsing Hua University.



Appendix 7. Metal contents of PepD protein. (A) Fe: Zn = 8.53: 1. (B) Fe: Zn = 3.87: 1. (C) Fe: Zn = 5.81: 1.