Supplemental Materials

Chitin heterodisaccharide, released from chitin by chitinase and chitin oligosaccharide deacetylase, enhances the chitin-metabolizing ability of *Vibrio parahaemolyticus*

Takako Hirano[#], Manabu Okubo, Hironobu Tsuda, Masahiro Yokoyama, Wataru Hakamata, and Toshiyuki Nishio

Department of Chemistry and Life Science, College of Bioresource Sciences, Nihon University, 1866 Kameino, Fujisawa, Kanagawa 252-0880, Japan

[#]Address correspondence to Takako Hirano, hirano.takako@nihon-u.ac.jp

Supplemental Figures

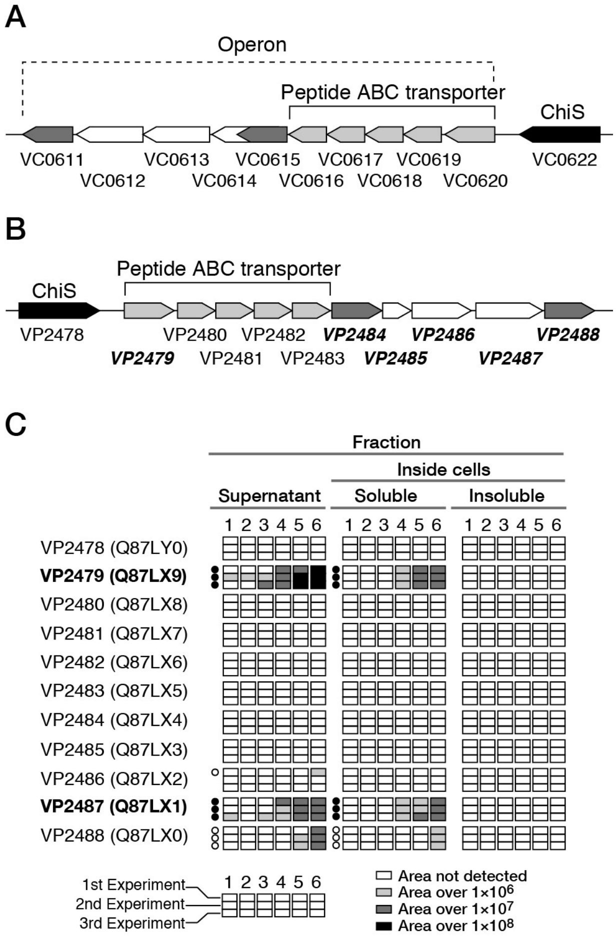

Fig. S1 Gene cluster of the ABC transporter for taking up $(GlcNAc)_2$ and ChiS.

(A) Gene cluster of ABC transporter in the *Vibrio cholerae* O1 EI Tor N16961 genome. **(B)** Gene cluster of the ABC transporter in the *Vibrio parahaemolyticus* RIMD2210633 genome. **(C)** Results of peptide mass fingerprinting analysis of the proteins encoded by the genes shown in **B**.

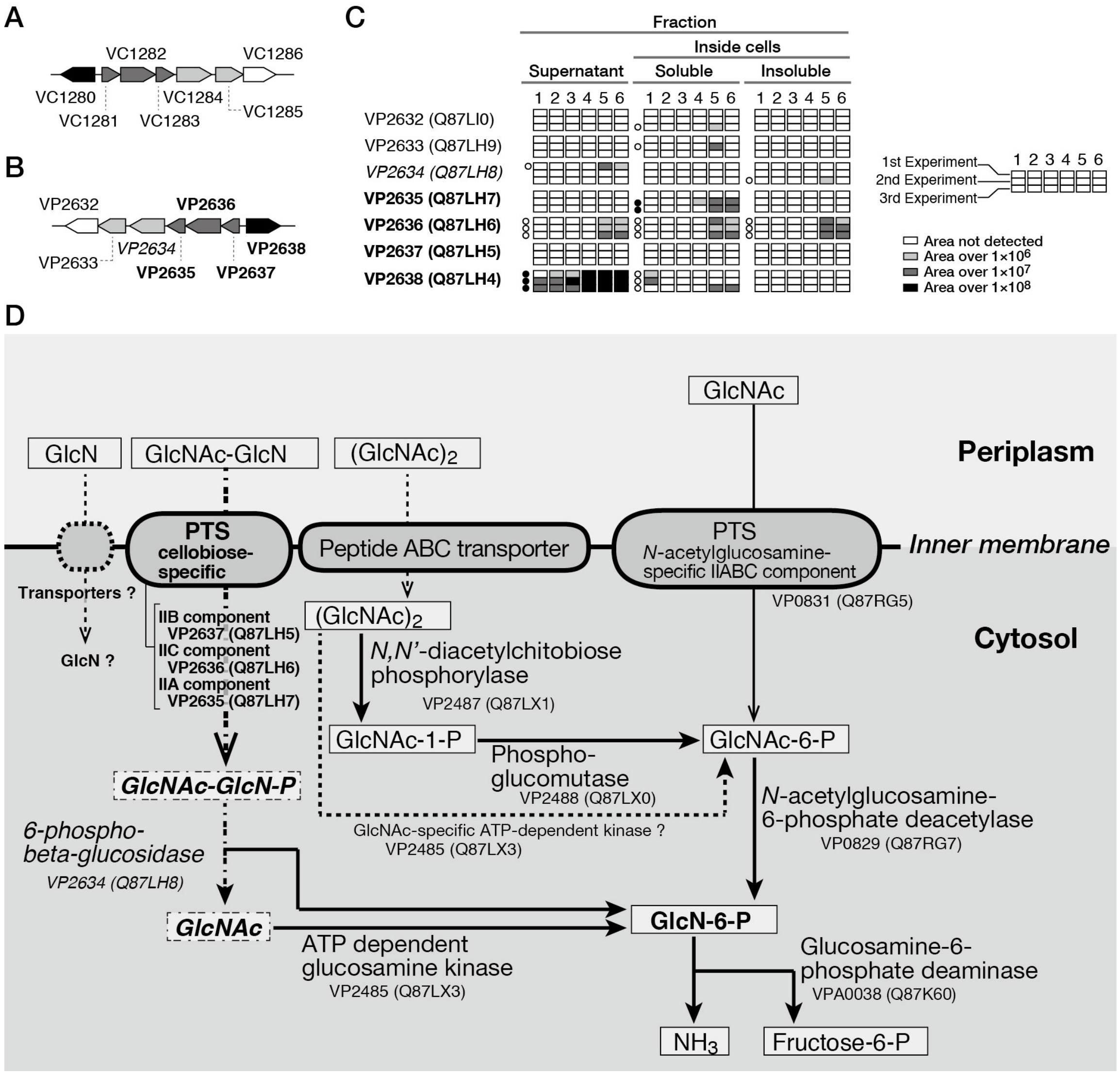

Fig. S2 Analysis of peptide mass fingerprinting (PMF) data and annotation of the gene cluster as a cellobiose-specific PTS and COD, and hypothetical pathway in the cytosol.

(A) Gene cluster of the cellobiose-specific PTS and COD in the *V. cholerae* O1 EI Tor N16961 genome. **(B)** Gene cluster of the cellobiose-specific PTS and COD in the *V. parahaemolyticus* RIMD2210633 genome. **(C)** Results of PMF analysis of the proteins encoded by the genes shown in **B**. **(D)** Hypothetical pathway in the cytosol of *V. parahaemolyticus* RIMD2210633. In **B**, **C**, and **D**, bold type and italics indicate proteins induced by GlcNAc-GlcN and the enzyme hypothetically functioning in this pathway, respectively. The reaction of endoglucanase-like protein (VP2484, Fig. 1 in main text) of *V. cholerae* does not hydrolyze $(GlcNAc)_2$ or $(GlcN)_2$ (20), and therefore, it does not act on phosphorylated $(GlcN)_2$. Thus, this enzyme cannot hydrolyze phosphorylated GlcNAc-GlcN, even if this heterodisaccharide could be transported via the PTS (VP2635-VP2637). Based on these data, we hypothesize that GlcNAc-GlcN is carried from the periplasm to the cytosol and phosphorylated by the PTS (VP2635-VP2637) (Fig. S2D). It is then hydrolyzed by another enzyme, such as 6-phospho-β-glucosidase (VP2634, EC 3.2.1.86) (Fig. S2D), which is a component of the PTS cluster that was detected twice at low coverage in our PMF analyses (Fig. S2C). With respect to the effect of GlcNAc-GlcN on gene expression, as we have already characterized the COD gene located adjacent to the PTS cluster (VP2635-VP2637), in a subsequent study we will investigate other genes within this cluster, including 6-phospho-β-glucosidase.

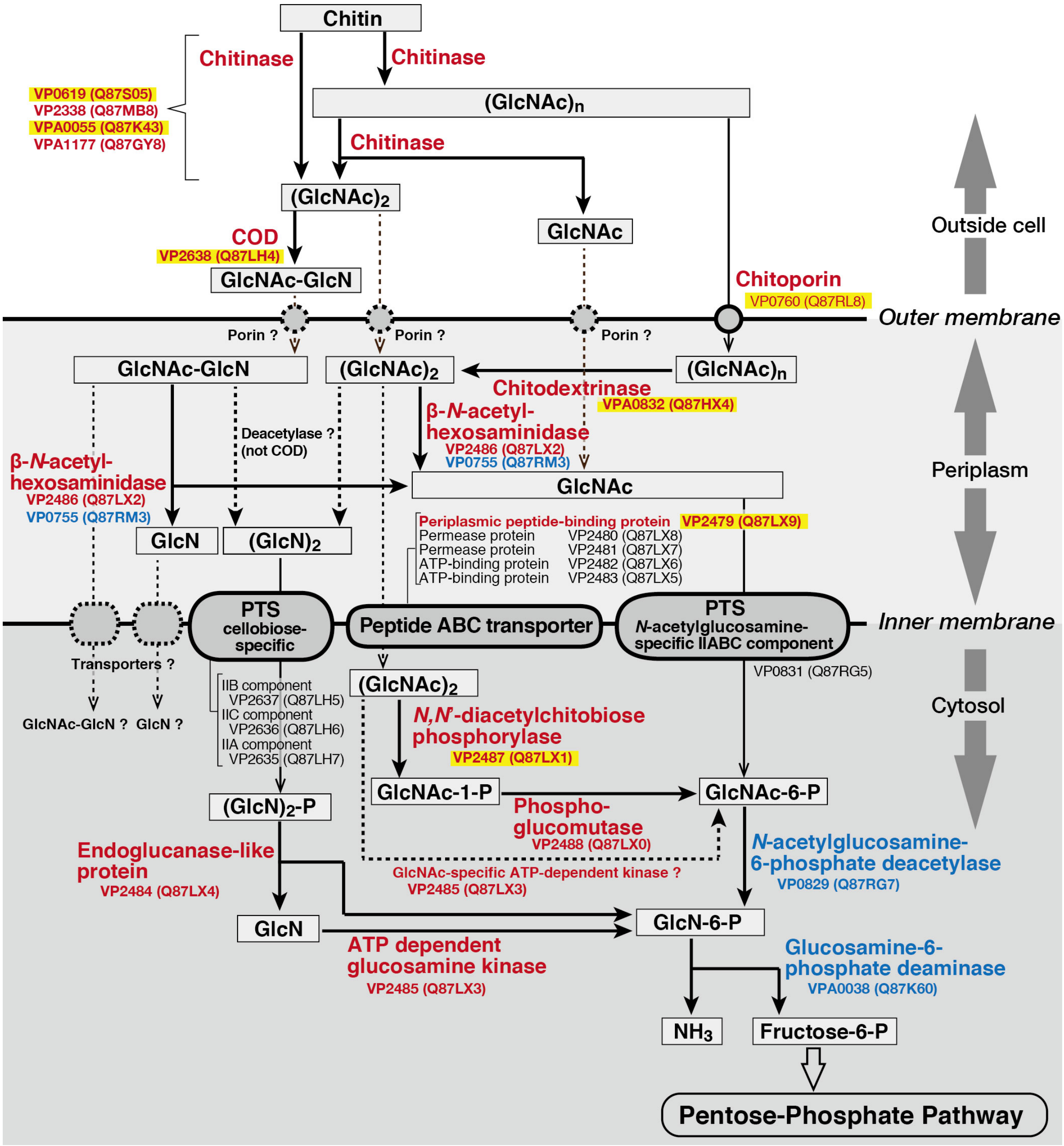

Fig. S3 Protein and gene expression patterns in the hypothetical chitin-degradation pathway in *Vibrio parahaemolyticus*.

The hypothetical pathway is the same as that shown in Figure 1. The numbers under the protein names and the corresponding numbers in parentheses are KEGG and UniProt IDs, respectively. Yellow-highlighted proteins exhibited higher expression levels in the presence of GlcNAc-GlcN than other sugars according to the results of PMF analyses. Font color corresponds to RT-qPCR analyses. Red and blue font indicate, respectively, genes that exhibited higher expression levels in the presence of GlcNAc-GlcN than (GlcNAc)$_2$, and those that exhibited no difference between sugars.

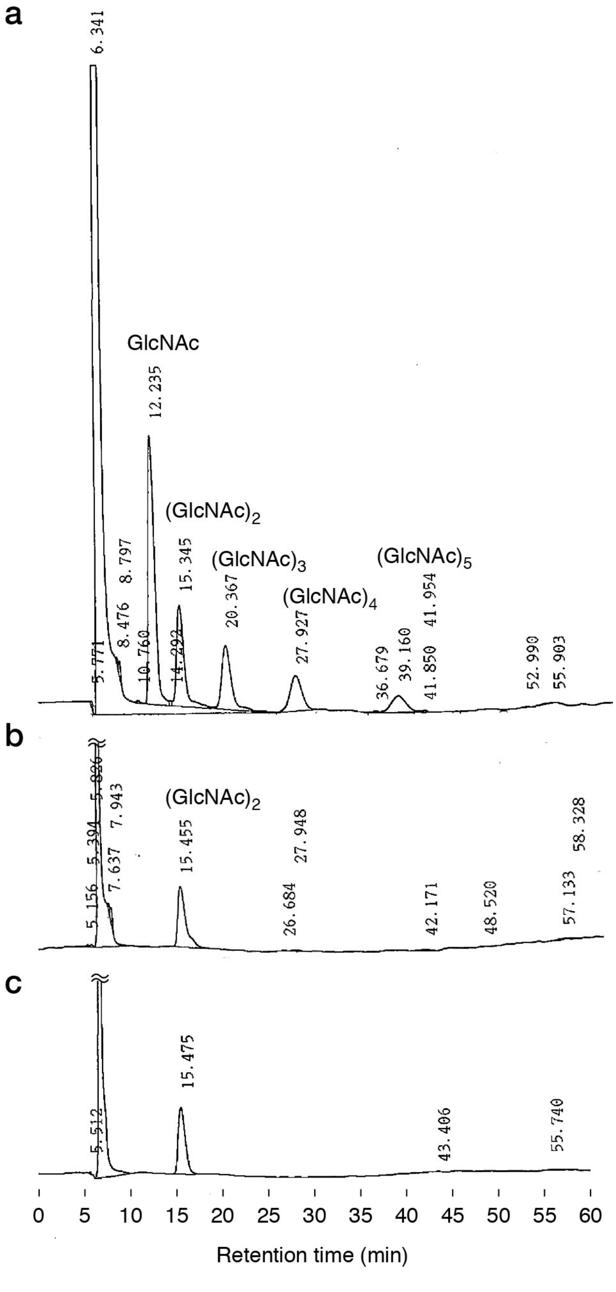

Fig. S4 HPLC analysis of purified (GlcNAc)$_2$.

HPLC analysis was performed using an LC-20 AD pump (Shimadzu, Kyoto, Japan) equipped with a Shodex RI-101 differential refractometer (Show Denko, Tokyo, Japan) and COSMOSIL Sugar-D column (ø4.5×250 mm, Nacalai Tesque, Kyoto, Japan). The analysis was conducted under the following conditions: mobile phase, acetonitrile/water 3:1 (v/v); flow rate, 0.5 mL/min; temperature, 30°C. **(a)** HPLC chromatograph of chitin oligosaccharides containing *N*-acetylglucosamine (Tokyo Chemical Industry, Tokyo, Japan). **(b)** HPLC chromatograph of (GlcNAc)$_2$ purchased from Seikagaku (Tokyo, Japan). **(c)** HPLC chromatograph of (GlcNAc)$_2$ produced from a mixture of GlcNAc and GlcNAc oligomers by Denazyme CBB-P1 (Nagase chemtaX, Osaka, Japan) and purified according to the method described in main text.

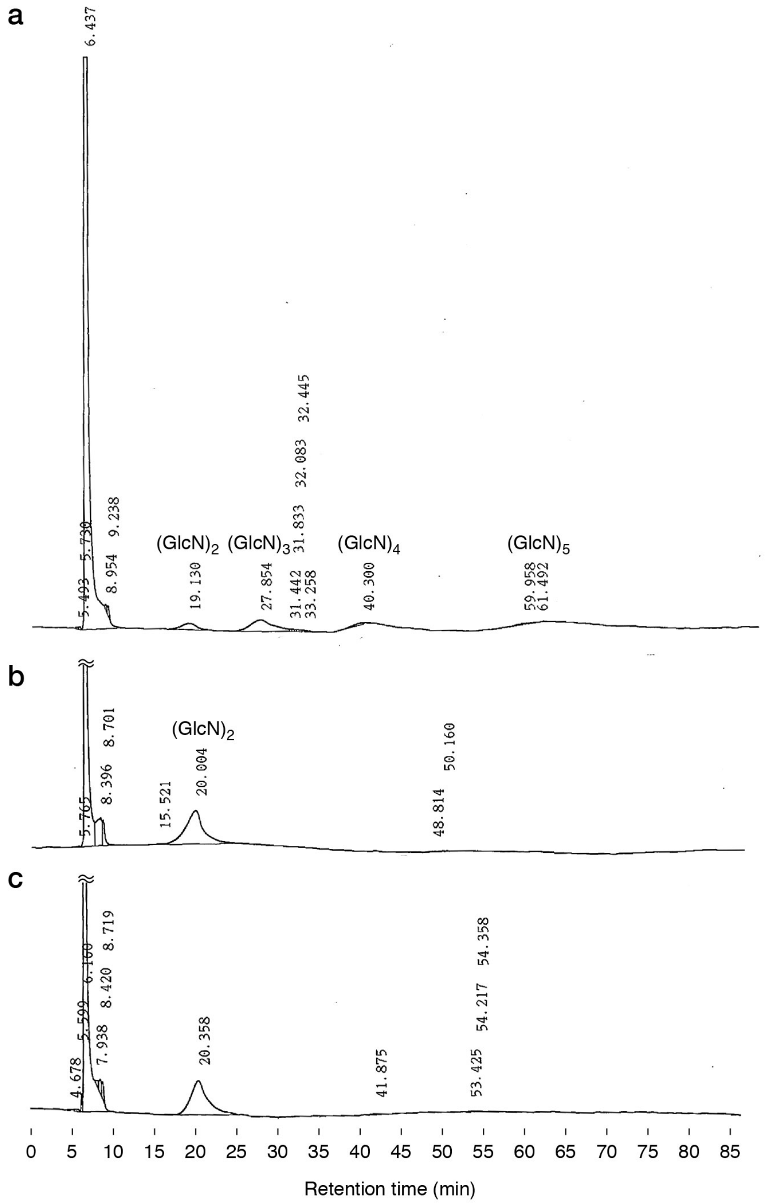

Fig. S5 HPLC analysis of purified $(GlcN)_2$.

HPLC analysis was performed using an LC-20 AD pump equipped with a Shodex RI-101 differential refractometer and COSMOSIL Sugar-D column (Ø4.5×250 mm). The analysis was conducted under the following conditions: mobile phase, acetonitrile/water 3:1 (v/v); flow rate, 0.5 mL/min; temperature, 30°C. **(a)** HPLC chromatograph of chitosan oligosaccharides (Tokyo Chemical Industry). **(b)** HPLC chromatograph of chitosan dimer [$(GlcN)_2 \cdot 2HCl$] purchased from Seikagaku Kogyo. **(c)** HPLC chromatograph of $(GlcN)_2$ produced from GlcN oligomers (chitosan oligosaccharides) treated with chitosanase L (HBI Enzymes, Hyogo, Japan) and purified according to the method described in main text and Supplemental Method 1.

<u>Supplemental Tables</u>

Table S1 Raw data from PMF analyses

Raw data from three PMF analyses are shown in the last pages of this document. The following information is shown in each column. Accession and Description correspond to UniProt ID and protein name, respectively. The specific coverage of each protein is shown in the blue-highlighted column. Peak area data are also shown in this Table, and colored dark-orange for high peak area. Proteins indicated by red font are shown in Figs. 1 and S3, and proteins indicated in blue font are also discussed in the main text.

Table S2　Primers used for RT-qPCR in this study

Protein name			Primer (5’→3’)		Annealing
NCBI Gene ID	KEGG ID	UniProt ID	(F: Forward prime, R: Reverse primer)		temperature (°C)
Target genes					
Chitinase			F:	GTGATGCATCTGTATTGCTG	55.1
1188094	VP0619	Q87S05	R:	CCAAGTCCGGTCAATTACATG	
Chitinase			F:	GATTGCGACAGACAATGAAG	55.1
1189851	VP2338	Q87MB8	R:	GTGAGAGTAATGCTAGGTGG	
Chitinase			F:	GATGCAGACAACGATACTCTTAC	55.1
1190734	VPA0055	Q87K43	R:	CCATTTGCCGAGATTTCACTG	
Chitinase			F:	CTCAGTTAACGTGCCATACAAAG	55.1
1191873	VPA1177	Q87GY8	R:	CATTGTCCAACCACCAAAAGAAG	
Chitin oligosaccharide deacetylase (COD)			F:	GGATCCAGCAACTAATTGGAC	55.1
1190182	VP2638	Q87LH4	R:	GTCCAGTCTGCTTGAGATAC	
Chitopolin			F:	GGCTCACTACAAGTTAGGTC	55.1
1188256	VP0760	Q87RL8	R:	CCAAGTTTGACCTTCAGATTC	
Chitodextrinase			F:	CATTTACGAACAACACAGGTC	55.1
1191521	VPA0832	Q87HX4	R:	GAAGCAATCACTTTCAAACCG	
β-*N*-acetyl-hexisosaminidase			F:	CTGAAGGTAGCAGAAGAGTC	55.1
1190001	VP2486	Q87LX2	R:	GTCGGTCTTTGATTGAACAG	
β-*N*-acetyl-hexisosaminidase			F:	CAGTGTACGAGTGGTCTAAG	55.1
1188251	VP0755	Q87RM3	R:	GTAGTAACCACGCTCTTTCG	
Periprasmic peptide-binding protein			F:	CGTTGAAGGTGCTAAGAAAC	60.8
1189994	VP2479	Q87LX9	R:	GTACTGTGTTGTTGAAGTCC	
N,N’-diacetyl- chitobiose phosphorylase			F:	GAAGTTCGTCATGGTTTGTC	55.1
1190002	VP2487	Q87LX1	R:	GGTTTGTCAGAGGTGTTCTTG	
Phosphoglucomutase			F:	GATTGCAAATTCAAACCAGC	60.8
1190003	VP2488	Q87LX0	R:	GTAGTAATGGCTCAGTACCAG	
N-acetylglucosamine-6-phosphate deacetylase			F:	CAGGCATTGTGGTATCAATC	55.1
1188326	VP0829	Q87RG7	R:	GCATTGAATAGGTGAGTTGC	
Endoglucanase-like protein			F:	CAATGGTGGTTTGGAACATC	55.1
1189999	VP2484	Q87LX4	R:	GCTCCACTTATCAAAGACCG	
ATP dependent glucosamine kinase			F:	CCTTAAAGGATTGGAGCAGC	58.2
(Putative GlcNAc-specific ATP-dependent kinase)			R:	CTAGAGGCGTTTTCTCTCTG	
1190000	VP2485	Q87LX3			
Glucosamine-6-phosphate deaminase			F:	CTCGCATCAAGACACTAACTG	55.1
1190717	VPA0038	Q87K60	R:	CTTCTAGTGCAAGTGCTTTG	
N-acetylglucosamine-binding protein A			F:	CAAGCTGGTCAATATTCGGAAG	55.1
1192294	VPA1598	Q87FT0	R:	CAATTTCAACACGCTCAAGG	
House-keeping gene					
RNA polymerase sigma factor RpoD (RpoD)			F:	CCAAGTTCAATCGTCTGTTG	55.1
1187872	VP0404	Q87SL8	R:	GTTCTTCTGCCTGAACCTTATC	

Primers were designed using Primer-BLAST (https://www.ncbi.nlm.nih.gov/tools/primer-blast/) with DNA sequences shown as Gene IDs enrolled in the NCBI database. Before using the designed primers, we checked the secondary structure of single-strand DNA using the DNA folding form of the mfold web server (http://unafold.rna.albany.edu/?q=mfold/DNA-Folding-Form). The two other IDs and the names of each protein on this table correspond to Fig. 1 in main manuscript. Before using these primer sets for RT-qPCR, we confirmed that each part of target gene amplified by PCR produced a single band on polyacrylamide gel electrophoresis, and the size of the DNA band on the gel corresponded with its theoretical value. Moreover, we confirmed that the part of the DNA sequence amplified in RT-qPCR corresponded to the appropriate target gene according to the following steps. After electrophoresis of the RT-qPCR products on polyacrylamide gels, the amplified DNAs were extracted and purified from the gels using an E.Z.N.A.® Poly-Gel DNA Extraction kit (OMEGA bio-tek, GA, USA), and the obtained DNAs were used for DNA sequencing carried out on an ABI 3130xl DNA sequencer using only one primer of each primer set and a Big Dye Terminator V3.1 Cycle Sequencing kit (Applied Biosystems, Carlsbad, CA, USA).

<u>Supplemental Methods</u>

Method 1 Preparation of $(GlcN)_2$.

We produced $(GlcN)_2$ from GlcN oligomers (chitosan oligosaccharides, Tokyo Chemical Industry, Japan) by hydrolysis using chitosanase L (HBI Enzymes, Hyogo, Japan), which was dialyzed in 0.5 M sodium acetate buffer (pH 5.2). A total of 0.9 g of GlcN oligomer was dissolved in 30 mL of 0.5 M sodium acetate buffer (pH 5.2), and approximately 1 mL of chitosanase L solution was added. Then, the mixture was incubated at 40°C for 16 h until GlcN oligomers were hydrolyzed into $(GlcN)_2$ and GlcN. The reaction mixture was chromatographed on a cation-exchange column (ø 1 cm × 10 cm) packed with Dowex 50W-X8, 200-400 mesh resin (FUJIFILM Wako Pure Chemical, Osaka, Japan) and extensively washed with H_2O. GlcN was eluted with 0.5 M HCl, and $(GlcN)_2$ was eluted using 1.0 M HCl. All of the solution containing $(GlcN)_2$ was chromatographed on an anion-exchange column (ø 3 cm × 15 cm) packed with IRA96SB resin (Organo, Tokyo, Japan), which had been activated as the OH^- form, in order to remove HCl. $(GlcN)_2$ was eluted from this column using approximately 350 mL of H_2O. The pH of the sample at this step was almost neutral. A few drops of 0.2 M HCl were then added in order to make the pH approximately 6.0, and the solution was evaporated with some ethanol using a rotary evaporator at room temperature until the volume was <50 mL. The solution was then filtered using a 0.45-µm cellulose acetate filter (DISMIC-13CP, Advantec MFS, CA, USA) and evaporated until the volume was approximately 2 mL. The solution was then dispensed into two centrifuge tubes (Nalgene™ Oak Ridge High-Speed Centrifuge Tubes, Thermo Fisher Scientific, MA, USA), cooled acetone was added to each tube, and the tubes were stored at 4°C to precipitate $(GlcN)_2$. The tubes were sealed with sealing cap assemblies (Thermo Fisher Scientific) in which the O-rings were replaced with chemical-resistant O-rings (Kalrez®, AS568 O-RING, Compound: 6375, Dow DuPont, MI, USA); $(GlcN)_2$ was collected by centrifugation at 4°C and 3,000 ×*g* for 5 min, and most of the acetone was removed from the tubes using a pipette. Cooled acetone was then added again, and the tubes were centrifuged to wash the $(GlcN)_2$. To remove the remaining acetone from the $(GlcN)_2$ precipitate, the tubes were placed on ice and stored in a fume hood. Finally, the precipitate was dissolved in a small amount of H_2O to obtain purified $(GlcN)_2$ in solution.

Method 2 Preparation of samples for LC-MS/MS analysis of proteins from SDS-PAGE gel fragments.

A 100-µL volume of a solution of 15 mM potassium ferricyanide and 50 mM sodium thiosulfate was added to each gel slice, and the sample was shaken for 10 min at room temperature. The solution was then removed, 500 µL of Milli-Q water was added, and the sample was shaken for 15 min. This step was repeated until the yellow solution was decolorized, after which 100 µL of acetonitrile was added, and the sample was shaken for 10 min. The acetonitrile was removed, and the gel slices were dried by evaporating. Next, 100 µL of solution containing 10 mM DTT and 25 mM ammonium hydrogen carbonate was added, and the sample was incubated at 56°C for 1 h with shaking in the dark. This solution was removed, and 100 µL of 25 mM ammonium hydrogen carbonate was added as a wash buffer and shaken for 10 min. The wash buffer was removed, and 100 µL of solution containing 55 mM iodoacetamide and 25 mM ammonium hydrogen carbonate was added to the sample tube and shaken for 45 min in the dark. The solution was removed, 100 µL of wash buffer was added, and the tube was shaken for 10 min. The solution was removed, 200 µL of 50% acetonitrile and 25 mM ammonium hydrogen carbonate was added for dehydration, and the tubes were shaken for 10 min. This dehydration process was carried out twice. The gel slices were dried by placing the tubes in a centrifugal evaporator. Next, 30 µL of trypsin solution containing 10 µg/mL of trypsin and 50 mM ammonium hydrogen carbonate was added, and the tubes were stored on ice for 30 min. The solution was removed, and the tubes were incubated at 37°C overnight (12 to 16 h), after which 50% acetonitrile and 5% trifluoroacetic acid was added to each tube and shaken for 30 min in order to extract proteins from the gel slices. After the protein-containing solution was removed, 25 µL of 50% acetonitrile and 5% trifluoroacetic acid was added to the gel slices, and proteins were extracted again using the same procedure. The protein solution was dried by evaporation using a centrifugal evaporator, and 13 µL of 0.1% formic acid was added. After shaking for 5 min, 10 µL of the sample was used for analysis. The samples were stored at 4°C until they were analyzed.

Table S1

1st Experiment (Supernatant Fraction)

Accession	Description	Coverage	MW [kDa]	Control	GlcNAc	GlcN	(GlcNAc)2	(GlcN)2	GlcNAc-GlcN
A7UEM1	Transhydrogenase alpha subunit (Fragment) OS=Vibrio parahaemolyticus GN=pntA PE=4 SV=1	19.6	15.5	4.70E+06	5.30E+06	2.20E+06	7.30E+06	5.00E+06	7.20E+06
A7UEQ6	Dihydro-orotase (Fragment) OS=Vibrio parahaemolyticus GN=pyrC PE=3 SV=1	9.8	17.8						2.60E+06
H6BAH9	Thermolabile hemolysin (Fragment) OS=Vibrio parahaemolyticus GN=tl PE=4 SV=1	10.8	13.6					4.00E+07	
O50286	Dihydrolipoyl dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=lpd PE=3 SV=2	48.0	51.0	1.40E+07	2.60E+07	1.60E+07	2.20E+07	3.90E+07	3.40E+07
O87081	Polar flagellin F OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=flaF PE=3 SV=2	5.6	40.5		1.30E+07		2.00E+07	2.00E+07	2.10E+07
P0A481	50S ribosomal protein L20 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplT PE=3 SV=1	8.5	13.4						5.10E+06
P19250	Thermostable direct hemolysin 2 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=tdh2 PE=1 SV=2	18.5	21.5	1.00E+07	1.80E+07	1.60E+07	1.50E+07	2.60E+07	2.20E+07
P22099	Anthranilate synthase component 1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=trpE PE=3 SV=2	3.9	59.7	1.90E+06	3.60E+06	2.00E+06	4.80E+06	2.70E+06	3.50E+06
P22848	5'-nucleotidase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=nutA PE=3 SV=2	2.1	62.1					4.10E+06	
P40611	Ribonuclease R OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rnr PE=3 SV=2	3.5	95.0		2.20E+06		3.80E+06	3.40E+06	
P59494	Maltoporin OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=lamB PE=3 SV=1	63.9	46.9	2.40E+08	3.00E+08	2.30E+08	2.80E+08	4.10E+08	3.70E+08
P59570	Outer membrane protein OmpK OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=ompK PE=3 SV=1	25.6	29.9	9.10E+06	1.40E+07	1.10E+07	1.70E+07	1.80E+07	1.70E+07
P59605	Argininosuccinate synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=argG PE=3 SV=1	40.6	44.5	2.20E+07	3.10E+07	2.30E+07	3.60E+07	6.00E+07	4.80E+07
P59620	Bifunctional protein ArgH OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=argH PE=3 SV=1	10.7	69.3	5.10E+06	4.80E+06	4.40E+06	7.40E+06	8.50E+06	9.50E+06
P66478	30S ribosomal protein S18 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpsR PE=3 SV=1	10.7	8.8					3.00E+06	2.50E+06
P74956	Lon protease OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=lon PE=3 SV=2	1.3	87.8					3.60E+06	
Q56702	Polar flagellin B/D OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=flaB PE=3 SV=2	54.0	40.1	8.20E+06	1.90E+07	1.10E+07	2.40E+07	2.30E+07	2.60E+07
Q56703	Polar flagellin A OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=flaA PE=3 SV=1	28.2	39.8		4.00E+06	6.00E+06	1.50E+07	1.40E+07	1.50E+07
Q56712	Polar flagellin C OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=flaC PE=3 SV=2	27.3	40.8	2.50E+06	1.10E+07	5.40E+06	1.60E+07	1.80E+07	1.70E+07
Q79YX4	Chemotaxis protein CheW OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2225 PE=4 SV=1	15.2	18.4		2.80E+06	2.30E+06		4.00E+06	4.20E+06
Q79YY8	Polar flagellar FlgE OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0778 PE=4 SV=1	14.9	47.3	1.40E+06	6.90E+06	5.20E+06	9.90E+06	7.40E+06	1.10E+07
Q877T5	Elongation factor Tu OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=tufA PE=3 SV=1	60.2	43.1	7.70E+07	1.70E+08	7.90E+07	1.50E+08	2.70E+08	2.40E+08
Q87FL7	Putative diaminopimelate decarboxylase protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1662 PE=3 SV=1	9.8	45.3	3.50E+06	3.70E+06	3.00E+06	2.30E+06	4.40E+06	3.60E+06
Q87FM0	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1659 PE=4 SV=1	57.9	68.7	4.70E+07	8.00E+07	6.20E+07	6.60E+07	1.30E+08	1.30E+08
Q87FM1	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1658 PE=4 SV=1	17.9	44.2	5.20E+06	8.90E+06	5.20E+06	9.30E+06	1.40E+07	1.10E+07
Q87FM2	Ferric siderophore receptor homolog OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1657 PE=3 SV=1	57.5	74.9	6.30E+07	1.10E+08	8.30E+07	1.00E+08	1.30E+08	1.10E+08
Q87FM3	Ferric vibrioferrin receptor OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1656 PE=3 SV=1	35.0	78.8	4.40E+07	7.20E+07	6.10E+07	7.50E+07	8.80E+07	8.90E+07
Q87FM9	Putative zinc protease, insulinase family OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1650 PE=3 SV=1	10.9	102.2	4.30E+06	4.80E+06	3.20E+06	5.10E+06	8.80E+06	7.10E+06
Q87FN1	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1648 PE=4 SV=1	3.3	62.7		2.50E+06	1.30E+06	2.30E+06	4.10E+06	
Q87FN4	Glycogen operon protein GlgX homolog OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1645 PE=4 SV=1	1.4	75.9	3.40E+06	4.20E+06	3.20E+06		7.50E+06	6.40E+06
Q87FN5	Putative maltose operon periplasmic protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1643 PE=4 SV=1	9.3	29.1	3.70E+06	6.00E+06	3.60E+06	3.90E+06	9.70E+06	7.90E+06
Q87FP0	Putative pullulanase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1638 PE=4 SV=1	35.8	144.5	1.90E+07	3.10E+07	1.40E+07	1.90E+07	1.80E+07	1.70E+07
Q87FQ8	Alpha-1,4 glucan phosphorylase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1620 PE=3 SV=1	34.4	92.3	2.10E+07	2.80E+07	2.10E+07	2.80E+07	5.00E+07	4.80E+07
Q87FQ9	4-alpha-glucanotransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1619 PE=3 SV=1	47.8	81.8	1.70E+07	2.30E+07	2.00E+07	2.40E+07	4.00E+07	3.40E+07
Q87FR0	1,4-alpha-glucan branching enzyme GlgB OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=glgB PE=3 SV=1	2.0	87.4	1.30E+06	1.30E+06		2.70E+06	2.10E+06	
Q87FR2	Alpha-amylase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1616 PE=4 SV=1	1.2	76.9					5.90E+06	3.60E+06
Q87FR7	Putative carboxypeptidase G2 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1611 PE=4 SV=1	5.1	40.4						
Q87FT0	GlcNAc-binding protein A OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=gbpA PE=3 SV=1	51.1	53.6	1.20E+07	3.60E+07	4.30E+07	3.50E+07	8.70E+07	1.00E+08
Q87FX6	Flagellar biosynthetic protein fliR OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1544 PE=3 SV=1	8.1	27.9		9.20E+06				
Q87G07	ScrA (Aminotransferase) OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1513 PE=3 SV=1	40.6	52.8	1.90E+07	3.00E+07	3.00E+07	4.70E+07	5.10E+07	6.80E+07
Q87G09	2-amino-3-ketobutyrate coenzyme A ligase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=kbl PE=3 SV=1	5.3	43.1	1.80E+06	3.20E+06	2.90E+06	3.10E+06		5.40E+06
Q87G18	L-lactate dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=lldD PE=3 SV=1	8.4	41.4	4.50E+06	3.30E+06		3.90E+06	6.90E+06	
Q87G21	Prolyl endopeptidase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1496 PE=4 SV=1	31.3	76.0	7.10E+06	1.10E+07	8.80E+06	1.30E+07	1.80E+07	1.40E+07
Q87G42	Purine nucleoside phosphorylase DeoD-type 2 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=deoD2 PE=3 SV=1	13.1	25.7		5.40E+06	3.80E+06	6.20E+06	9.60E+06	1.20E+07
Q87G48	Outer membrane lipoprotein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1469 PE=4 SV=1	57.1	8.7	6.00E+06	1.60E+07	5.30E+06	1.10E+07	1.30E+07	1.50E+07
Q87G50	Protease II OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1467 PE=4 SV=1	16.8	75.1		3.30E+06	4.80E+06	4.80E+06	8.00E+06	1.30E+07
Q87G52	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1465 PE=4 SV=1	17.2	84.5	3.30E+06	6.90E+06	6.80E+06	9.50E+06	1.00E+07	1.40E+07
Q87G82	Putative iron(III) compound receptor OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1435 PE=3 SV=1	2.9	77.0	1.90E+06	3.40E+06		3.30E+06		
Q87G89	Azurin OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1428 PE=4 SV=1	28.0	15.8	1.80E+07	2.40E+07	1.50E+07	2.40E+07	2.90E+07	3.10E+07
Q87GB6	Maltose ABC transporter, periplasmic maltose-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1401 PE=4 SV=1	71.4	42.1	4.70E+07	7.60E+07	5.40E+07	8.20E+07	1.50E+08	1.20E+08
Q87GK7	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1308 PE=4 SV=1	39.7	42.3	2.00E+07	4.00E+07	2.40E+07	3.60E+07	4.80E+07	5.10E+07
Q87GW1	Acetyl-CoA acetyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1204 PE=3 SV=1	3.2	41.5					9.00E+06	5.60E+06
Q87GW6	Periplasmic nitrate reductase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=napA PE=3 SV=1	1.7	92.9		2.60E+06	2.90E+06	4.40E+06	5.00E+06	3.50E+06
Q87GX9	Outer membrane protein OmpA OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1186 PE=3 SV=1	4.3	36.0						1.90E+06
Q87GY4	Transketolase 2 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=tkt2 PE=3 SV=1	5.7	72.0	5.30E+06	7.60E+06	3.10E+06	6.30E+06	9.50E+06	5.70E+06
Q87GY5	Transaldolase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=tal PE=3 SV=1	62.0	34.8	1.30E+07	1.90E+07	1.60E+07	2.50E+07	3.40E+07	3.80E+07
Q87GY8	Putative chitinase A OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1177 PE=3 SV=1	2.8	47.9						1.70E+06
Q87H02	Oxidoreductase, aldo/keto reductase 2 family OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1163 PE=4 SV=1	7.3	34.0		2.80E+06			4.10E+06	
Q87H16	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1149 PE=4 SV=1	4.6	45.3		4.10E+06				7.10E+06
Q87HF4	L-allo-threonine aldolase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1011 PE=4 SV=1	25.1	36.1	4.80E+06	1.40E+07	1.20E+07	1.50E+07	2.20E+07	1.80E+07
Q87HG0	D-lactate dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1005 PE=4 SV=1	8.5	64.3	5.20E+06	2.70E+06		5.80E+06	9.40E+06	5.90E+06
Q87HG6	Alpha-amylase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0999 PE=4 SV=1	14.6	58.4	1.20E+06	1.20E+07	1.40E+06	1.10E+07	3.00E+06	2.60E+06
Q87HI4	Ferric aerobactin receptor OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0979 PE=3 SV=1	39.4	79.2	2.50E+07	4.30E+07	3.30E+07	3.40E+07	4.60E+07	4.50E+07
Q87HL0	Putative biofilm-associated surface protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0953 PE=4 SV=1	0.4	247.1		2.30E+06			3.90E+06	
Q87HM7	Amino acid biosynthesis aminotransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0936 PE=4 SV=1	30.7	43.7	7.00E+06	9.50E+06	8.10E+06	1.30E+07	1.40E+07	1.70E+07
Q87HM8	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0935 PE=4 SV=1	4.8	25.7				1.00E+06	1.30E+06	1.90E+06
Q87HP1	NAD(P) transhydrogenase subunit alpha OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0922 PE=3 SV=1	24.3	54.8	6.30E+06	1.10E+07	2.20E+06	1.40E+07	1.60E+07	1.00E+07
Q87HP2	NAD(P) transhydrogenase subunit beta OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0921 PE=3 SV=1	4.6	48.6	5.30E+06	6.40E+06		6.20E+06	1.30E+07	2.10E+06
Q87HS4	Heme transport protein HutA OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0882 PE=3 SV=1	55.6	77.3	5.20E+07	8.90E+07	6.10E+07	7.40E+07	8.40E+07	7.60E+07
Q87HV6	UPF0312 protein VPA0850 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0850 PE=3 SV=1	25.9	20.3	6.90E+06	9.90E+06	8.00E+06	1.10E+07	1.10E+07	6.80E+06
Q87HX4	Chitodextrinase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0832 PE=4 SV=1	41.7	111.8			1.30E+07	9.40E+06	8.30E+07	1.70E+08
Q87I01	Aminomethyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0805 PE=3 SV=1	7.5	40.3		3.30E+06		3.10E+06	1.10E+07	7.90E+06
Q87I05	Glycine dehydrogenase (decarboxylating) OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=gcvP PE=3 SV=1	15.6	104.1	7.90E+06	1.20E+07	6.70E+06	1.10E+07	1.80E+07	1.70E+07
Q87I38	Catalase-peroxidase 2 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=katG2 PE=3 SV=1	1.9	80.7			4.20E+06			
Q87ID3	Methylglyoxal synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=mgsA PE=3 SV=1	10.6	17.0		2.90E+06			4.10E+06	
Q87IE2	Putaive Fe-regulated protein B OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0664 PE=3 SV=1	14.5	74.2	5.20E+06	7.80E+06	6.80E+06	8.30E+06	1.20E+07	1.20E+07
Q87IE9	Iron(III) ABC transporter, periplasmic iron-compound-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0657 PE=4 SV=1	17.9	33.5	1.80E+06	6.00E+06	8.50E+06	5.60E+06	1.20E+07	1.10E+07
Q87IG9	Arginine ABC transporter, periplasmic arginine-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0637 PE=3 SV=1	10.9	27.3	2.80E+06	5.20E+06	3.10E+06	6.50E+06	1.00E+07	9.40E+06
Q87IJ5	Acetate kinase 2 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=ackA2 PE=3 SV=1	24.4	42.6	1.10E+07	1.70E+07	1.40E+07	1.50E+07	3.50E+07	3.00E+07
Q87IS1	Putative phosphomannomutase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0535 PE=3 SV=1	44.0	61.6	1.40E+07	2.20E+07	1.70E+07	2.90E+07	3.90E+07	3.40E+07
Q87IY8	Prolyl endopeptidase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0468 PE=4 SV=1	4.2	84.2	1.00E+06		1.30E+06	2.30E+06		3.50E+06
Q87J24	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0429 PE=4 SV=1	6.8	20.2					4.90E+06	3.80E+06
Q87J25	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0428 PE=4 SV=1	6.4	19.1					4.30E+06	
Q87J46	Dihydroorotase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=pyrC PE=3 SV=1	4.7	37.8						2.60E+06
Q87J81	Phosphoenolpyruvate synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0372 PE=3 SV=1	52.2	88.1	4.60E+07	6.70E+07	3.70E+07	6.60E+07	1.00E+08	6.00E+07
Q87J86	Putrescine-binding periplasmic protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0367 PE=3 SV=1	32.3	38.7	9.90E+06	1.90E+07	1.80E+07	2.30E+07	3.70E+07	3.40E+07
Q87JD5	Putative outer membrane protein OmpV OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0318 PE=4 SV=1	23.3	28.1	1.90E+07	3.00E+07	2.40E+07	1.40E+07	2.00E+07	2.30E+07
Q87JG6	60 kDa chaperonin 2 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=groL2 PE=3 SV=1	2.3	56.3						
Q87JM2	Alkaline serine protease OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0227 PE=4 SV=1	14.0	71.0	6.70E+06	1.60E+07	5.30E+06	8.10E+06	1.10E+07	1.50E+07
Q87JR8	Phospho-beta-glucosidase B OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0180 PE=3 SV=1	9.5	53.0	3.00E+06	4.50E+06	3.70E+06	6.80E+06	6.30E+06	6.80E+06
Q87JS9	Agmatinase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0169 PE=3 SV=1	2.6	33.4	4.30E+06	5.40E+06	5.40E+06	5.90E+06	6.70E+06	8.10E+06
Q87JT1	Putative protease OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0167 PE=4 SV=1	3.9	82.1	2.90E+06		2.40E+06	3.40E+06	2.80E+06	2.20E+06
Q87JT2	Putative outer membrane protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0166 PE=4 SV=1	14.3	38.0	1.20E+08	1.60E+08	1.20E+08	1.40E+08	1.90E+08	2.00E+08
Q87JV9	Putative PmbA-related protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0139 PE=4 SV=1	2.9	47.7				2.70E+06	3.90E+06	4.30E+06
Q87JY6	Putative peptidase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0112 PE=3 SV=1	1.3	69.4						5.80E+05
Q87K02	Outer membrane protein OmpW OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0096 PE=4 SV=1	10.3	23.5	2.40E+07	2.70E+07	1.50E+07	1.20E+07	2.40E+07	2.00E+07
Q87K06	Spindolin-related protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0092 PE=4 SV=1	21.2	43.5					9.00E+06	2.40E+07
Q87K43	Chitinase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0055 PE=3 SV=1	58.4	90.0			1.80E+07	2.40E+07	2.40E+08	4.50E+08
Q87K60	Glucosamine-6-phosphate deaminase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=nagB PE=3 SV=1	36.8	29.6		7.90E+06		2.20E+07	5.50E+06	1.70E+07
Q87K67	Sodium/glutamate symporter OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0031 PE=4 SV=1	2.2	44.4						
Q87K87	Probable transcriptional regulatory protein VPA0011 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0011 PE=3 SV=1	4.2	26.1					2.00E+06	
Q87KA4	ATP synthase subunit b OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=atpF PE=3 SV=1	13.5	17.5				3.10E+06	4.90E+06	
Q87KA6	ATP synthase subunit alpha OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=atpA PE=3 SV=1	51.4	56.6	1.40E+07	2.20E+07	1.10E+07	2.40E+07	3.70E+07	2.80E+07
Q87KA7	ATP synthase gamma chain OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=atpG PE=3 SV=1	2.4	31.8					2.40E+06	
Q87KA8	ATP synthase subunit beta OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=atpD PE=3 SV=1	41.1	50.7	1.00E+07	1.60E+07	6.10E+06	1.60E+07	2.60E+07	1.70E+07
Q87KB6	Dihydroxy-acid dehydratase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=ilvD PE=3 SV=1	40.0	65.6	1.20E+07	1.70E+07	1.20E+07	2.00E+07	2.60E+07	2.50E+07

Q87KB7	Branched-chain amino acid amiotransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP3060 PE=3 SV=1	16.7	34.3	4.80E+06	9.20E+06	6.80E+06	1.10E+07	1.80E+07	2.00E+07
Q87KE1	N5-carboxyaminoimidazole ribonucleotide mutase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=purE PE=3 SV=1	8.1	16.6						
Q87KF0	Phosphomethylpyrimidine synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=thiC PE=3 SV=1	17.6	72.4	4.50E+06	5.60E+06	5.60E+06	5.50E+06	1.10E+07	7.30E+06
Q87KF6	Aminopeptidase P OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP3021 PE=4 SV=1	22.0	65.5	8.00E+06	7.10E+06	5.60E+06	8.50E+06	1.50E+07	1.50E+07
Q87KG4	DNA helicase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP3013 PE=4 SV=1	0.8	82.4	5.30E+05	9.20E+05				
Q87KI7	Putative uroporphyrin-III C-methyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2990 PE=4 SV=1	2.5	45.1				2.30E+06		
Q87KI9	Porphobilinogen deaminase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=hemC PE=3 SV=1	3.5	34.1		2.00E+06			5.60E+06	
Q87KJ3	Diaminopimelate decarboxylase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=lysA PE=3 SV=1	18.2	45.9	2.90E+06	5.90E+06	4.80E+06	6.80E+06	8.80E+06	8.20E+06
Q87KQ1	50S ribosomal protein L1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplA PE=3 SV=1	10.3	24.7		3.70E+06		5.30E+06	7.60E+06	6.50E+06
Q87KQ4	DNA-directed RNA polymerase subunit beta OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpoB PE=3 SV=1	27.3	149.5	1.20E+07	1.10E+07	7.20E+06	1.60E+07	1.80E+07	1.80E+07
Q87KQ5	DNA-directed RNA polymerase subunit beta' OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpoC PE=3 SV=1	29.6	154.8	1.20E+07	1.60E+07	6.90E+06	1.70E+07	2.00E+07	2.00E+07
Q87KR5	DNA-binding protein HU-2 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2911 PE=3 SV=1	63.7	9.6		3.80E+06		5.10E+06	1.10E+07	1.00E+07
Q87KT0	Bifunctional purine biosynthesis protein PurH OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=purH PE=3 SV=1	31.9	57.3	4.50E+06	8.50E+06	5.50E+06	9.70E+06	1.90E+07	1.30E+07
Q87KU4	Acetyl-CoA carboxylase, biotin carboxylase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2881 PE=4 SV=1	3.6	49.2	1.60E+06			4.00E+06	6.40E+06	3.10E+06
Q87KU7	Acetyl-coenzyme A synthetase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=acsA PE=3 SV=1	9.5	71.7	4.40E+06	4.40E+06	2.40E+06	3.30E+06	6.10E+06	5.80E+06
Q87KV2	Fumarate hydratase class II OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=fumC PE=3 SV=1	31.0	48.7	3.60E+07	5.50E+07	3.60E+07	5.80E+07	8.70E+07	8.30E+07
Q87KW2	Aspartate ammonia-lyase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2863 PE=3 SV=1	20.7	52.7	6.20E+06	1.00E+07	9.10E+06	1.20E+07	1.60E+07	1.90E+07
Q87KW5	Superoxide dismutase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2860 PE=3 SV=1	19.3	23.0	6.20E+06	7.00E+06	5.20E+06	1.10E+07	1.50E+07	1.30E+07
Q87KX0	ATP-dependent 6-phosphofructokinase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=pfkA PE=3 SV=1	3.4	34.6						
Q87KZ3	Protein-export protein SecB OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=secB PE=3 SV=1	7.8	17.2		1.70E+06			4.30E+06	
Q87KZ5	2,3-bisphosphoglycerate-independent phosphoglycerate mutase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=gpmI PE=3 SV=1	21.0	55.1	4.90E+06	6.50E+06	5.50E+06	1.20E+07	2.00E+07	1.40E+07
Q87L07	RNA-binding protein Hfq OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=hfq PE=3 SV=1	25.3	9.8		4.90E+06		6.90E+06	6.80E+06	8.00E+06
Q87L13	Tryptophan--tRNA ligase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=trpS PE=3 SV=1	6.8	37.6			1.80E+06	2.70E+06	3.00E+06	4.80E+06
Q87L18	Extracellular nuclease-related protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2799 PE=4 SV=1	3.8	105.9		5.30E+06	2.50E+06	3.80E+06	6.60E+06	4.10E+06
Q87L20	Acetylornithine aminotransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=argD PE=3 SV=1	33.7	43.3	3.90E+06	1.10E+07	1.00E+07	1.20E+07	1.70E+07	1.70E+07
Q87L23	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2794 PE=4 SV=1	12.5	29.2	1.60E+06	4.50E+06		5.40E+06		5.50E+06
Q87L38	Peptidyl-prolyl cis-trans isomerase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2778 PE=4 SV=1	11.9	28.3	1.30E+06	1.60E+06			3.80E+06	3.00E+06
Q87L44	30S ribosomal protein S7 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpsG PE=3 SV=1	12.2	17.7					4.70E+06	5.00E+06
Q87L45	Elongation factor G 1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=fusA1 PE=3 SV=1	20.3	77.5	4.20E+06	8.40E+06	7.50E+06	1.00E+07	1.90E+07	1.60E+07
Q87L48	Putative malate oxidoreductase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2767 PE=3 SV=1	11.3	46.1	3.90E+06	5.50E+06	5.40E+06	6.10E+06	9.70E+06	9.40E+06
Q87L50	Cystathionine gamma-synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2765 PE=3 SV=1	9.6	41.8	2.90E+06	6.10E+06	6.60E+06	1.20E+07	1.20E+07	1.60E+07
Q87L54	Phosphoenolpyruvate carboxylase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=ppc PE=3 SV=2	17.2	99.2	5.10E+06	3.80E+06	2.30E+06	9.90E+06	9.40E+06	4.30E+06
Q87L55	N-acetyl-gamma-glutamyl-phosphate reductase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=argC PE=3 SV=1	18.9	36.2	5.00E+06	5.90E+06	5.00E+06	6.40E+06	8.40E+06	1.60E+07
Q87L81	Glucose-6-phosphate isomerase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=pgi PE=3 SV=1	36.7	60.9	3.20E+07	4.90E+07	4.40E+07	5.00E+07	8.00E+07	8.40E+07
Q87L90	Sulfite reductase [NADPH] flavoprotein alpha-component OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=cysJ PE=3 SV=1	19.4	68.7	7.60E+06	9.00E+06	5.30E+06	7.90E+06	1.20E+07	1.60E+07
Q87L91	Sulfite reductase [NADPH] hemoprotein beta-component OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=cysI PE=3 SV=1	18.2	64.8	3.10E+06	2.00E+07	1.60E+07	2.20E+07	1.50E+07	3.80E+07
Q87L98	Aminotransferase, class V OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2714 PE=3 SV=1	2.4	40.8	3.20E+06					
Q87LB4	Putative V10 pilin OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2698 PE=4 SV=1	18.8	16.8	5.60E+06	6.00E+06	2.80E+06	7.50E+06	1.40E+07	9.20E+06
Q87LC0	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2692 PE=4 SV=1	3.4	159.5	1.80E+06	2.80E+06		7.60E+06		2.90E+06
Q87LF9	Ornithine carbamoyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=argF PE=3 SV=1	36.8	37.3	2.00E+07	2.60E+07	1.90E+07	3.10E+07	4.20E+07	5.30E+07
Q87LG6	Valine--tRNA ligase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=valS PE=3 SV=1	12.5	108.6	3.50E+06	9.60E+06	4.20E+06	1.00E+07	1.40E+07	1.20E+07
Q87LG8	Probable cytosol aminopeptidase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=pepA PE=3 SV=1	6.6	54.4		6.80E+06	2.50E+06		5.90E+06	5.60E+06
Q87LH4	Deacetylase DA1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2638 PE=4 SV=1	34.9	47.0		4.70E+06	7.10E+06	1.00E+08	1.00E+09	7.90E+08
Q87LH6	Permease IIC component OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2636 PE=4 SV=1	4.3	48.7					9.20E+06	7.20E+06
Q87LH8	6-phospho-beta-glucosidase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2634 PE=3 SV=1	6.1	48.3					1.20E+07	9.00E+06
Q87LK8	Transketolase 1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=tkt1 PE=3 SV=1	7.2	72.0	5.30E+06	6.60E+06	3.10E+06	6.00E+06	1.00E+07	5.70E+06
Q87LL1	Phosphoglycerate kinase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=pgk PE=3 SV=1	24.1	40.7	6.20E+06	1.10E+07	6.20E+06	1.30E+07	2.20E+07	2.00E+07
Q87LL2	Fructose-bisphosphate aldolase, class II OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2599 PE=4 SV=1	67.6	38.9	5.80E+07	1.00E+08	8.00E+07	1.10E+08	1.60E+08	1.60E+08
Q87LL8	D-3-phosphoglycerate dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2593 PE=3 SV=1	23.2	44.7	3.30E+06	7.10E+06	4.50E+06	1.10E+07	1.60E+07	9.80E+06
Q87LL9	Ribose-5-phosphate isomerase A OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpiA PE=3 SV=1	5.5	23.2		4.10E+06			5.40E+06	4.60E+06
Q87LM8	tRNA-modifying protein YgfZ OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2583 PE=3 SV=1	13.0	35.5	2.00E+06	2.60E+06	1.80E+06	2.50E+06	2.40E+06	3.50E+06
Q87LP2	Pyridoxine 5'-phosphate synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=pdxJ PE=3 SV=1	2.9	26.7		2.00E+06			3.20E+06	3.30E+06
Q87LQ0	Enolase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=eno PE=3 SV=1	45.7	45.5	2.50E+07	3.90E+07	2.50E+07	4.30E+07	7.00E+07	6.40E+07
Q87LR3	Alanine--tRNA ligase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=alaS PE=3 SV=1	3.4	93.9			2.60E+06			6.40E+06
Q87LR7	Oxaloacetate decarboxylase, alpha subunit OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2544 PE=4 SV=1	5.7	64.2	3.70E+06			4.60E+06	7.70E+06	6.00E+06
Q87LS1	Protease, insulinase family OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2540 PE=3 SV=1	7.7	105.7	3.00E+06	4.80E+06	2.00E+06	6.10E+06	8.30E+06	4.60E+06
Q87LS2	Glutamate--cysteine ligase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=gshA PE=3 SV=1	10.2	59.0		3.60E+06	2.50E+06	3.70E+06	4.70E+06	5.10E+06
Q87LT9	NadC OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2522 PE=3 SV=1	3.1	32.0						2.10E+06
Q87LU2	Pyruvate dehydrogenase E1 component OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2519 PE=4 SV=1	45.1	99.6	3.10E+07	4.00E+07	3.20E+07	5.60E+07	7.60E+07	6.70E+07
Q87LU3	Acetyltransferase component of pyruvate dehydrogenase complex OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2518 PE=3 SV=1	15.8	64.9	6.20E+06	8.10E+06	2.60E+06	7.10E+06	1.30E+07	1.10E+07
Q87LV1	Pantothenate synthetase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=panC PE=3 SV=1	3.0	33.4						
Q87LW3	Aconitate hydratase B OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2495 PE=3 SV=1	31.1	94.0	1.90E+07	2.00E+07	1.50E+07	2.20E+07	4.10E+07	2.90E+07
Q87LW7	Iron(III) ABC transporter, periplasmic iron-compound-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2491 PE=4 SV=1	55.8	37.7	4.50E+07	8.50E+07	7.30E+07	9.10E+07	1.60E+08	1.50E+08
Q87LX0	Putative phosphoglucomutase/phosphomannomutase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2488 PE=4 SV=1	15.3	52.3						1.40E+07
Q87LX1	N,N'-diacetylchitobiose phosphorylase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2487 PE=4 SV=1	32.2	90.0				1.40E+07	2.20E+07	6.30E+07
Q87LX2	Beta-N-hexosaminidase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2486 PE=4 SV=1	1.7	73.0						7.20E+06
Q87LX9	Peptide ABC transporter, periplasmic peptide-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2479 PE=4 SV=1	35.7	62.9				1.80E+07	7.00E+07	2.00E+08
Q87LZ1	Outer membrane protein U OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=ompU PE=3 SV=1	27.9	36.3	6.70E+07	1.10E+08	7.50E+07	9.60E+07	1.20E+08	8.90E+07
Q87LZ5	ATP-dependent zinc metalloprotease FtsH OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=ftsH PE=3 SV=1	2.7	72.9				2.60E+06	7.60E+05	
Q87M06	Polyribonucleotide nucleotidyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=pnp PE=3 SV=1	38.8	76.7	1.30E+07	1.90E+07	1.50E+07	2.10E+07	3.10E+07	3.20E+07
Q87M18	Peptide chain release factor 3 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=prfC PE=3 SV=1	1.9	59.2					4.20E+06	
Q87M22	Deoxyribose-phosphate aldolase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=deoC PE=3 SV=1	4.3	27.7	2.20E+06	4.60E+06	3.10E+06	5.30E+06	9.00E+06	8.00E+06
Q87M25	Purine nucleoside phosphorylase DeoD-type 1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=deoD1 PE=3 SV=1	14.2	25.9			5.00E+06		8.00E+06	
Q87M27	Phosphoserine phosphatase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2431 PE=4 SV=1	10.7	35.8		2.00E+06	1.30E+06	2.90E+06	3.90E+06	4.10E+06
Q87M30	Elongation factor G 2 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=fusA2 PE=3 SV=1	30.2	76.3	2.10E+07	3.70E+07	2.40E+07	4.10E+07	7.00E+07	6.50E+07
Q87MA3	Putative lipoprotein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2354 PE=4 SV=1	6.9	20.7						
Q87MB8	Chitinase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2338 PE=3 SV=1	9.8	89.1			4.80E+06	6.10E+06	2.70E+07	4.00E+07
Q87MD8	30S ribosomal protein S2 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpsB PE=3 SV=1	8.7	26.8	4.40E+06	6.50E+06		5.90E+06		
Q87MD9	Elongation factor Ts OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=tsf PE=3 SV=1	37.7	29.8	1.00E+07	1.40E+07	1.00E+07	1.70E+07	3.90E+07	2.30E+07
Q87ME0	Uridylate kinase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=pyrH PE=3 SV=1	4.5	26.1						
Q87ME6	Chaperone protein skp OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2309 PE=3 SV=1	11.4	18.5	2.10E+06	3.70E+06		1.70E+06	6.10E+06	6.10E+06
Q87ML9	Long-chain fatty acid transport protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2212 PE=4 SV=1	8.2	45.7	5.50E+06	6.50E+06	5.80E+06			7.40E+06
Q87MN7	3-oxoacyl-[acyl-carrier-protein] synthase I OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2194 PE=3 SV=1	2.2	42.6						2.00E+08
Q87MP2	Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta 1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=accD1 PE=3 SV=1	2.9	34.0				3.40E+06		3.40E+06
Q87MS0	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2161 PE=4 SV=1	10.2	35.2		3.30E+06		5.10E+06		
Q87MS4	Glyceraldehyde-3-phosphate dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2157 PE=3 SV=1	71.6	35.2	7.80E+07	1.50E+08	1.50E+08	2.00E+08	3.10E+08	3.50E+08
Q87MU7	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2134 PE=4 SV=1	2.0	45.4						2.90E+06
Q87MV7	Aspartate-semialdehyde dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=asd PE=3 SV=1	56.9	40.2	1.80E+07	3.10E+07	2.70E+07	3.50E+07	5.50E+07	5.80E+07
Q87MW0	Aldehyde-alcohol dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2121 PE=1 SV=1	13.9	97.1	4.30E+06	5.70E+06		7.20E+06	9.10E+06	7.30E+06
Q87MW3	Superoxide dismutase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2118 PE=3 SV=1	6.5	22.2					7.40E+06	6.40E+06
Q87MY5	Oligopeptide ABC transporter, periplasmic oligopeptide-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2091 PE=4 SV=1	24.1	62.3	5.20E+06	6.90E+06	2.90E+06	8.40E+06	1.10E+07	6.70E+06
Q87MZ3	Phosphate acetyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2083 PE=3 SV=1	5.7	76.6	3.50E+06	3.90E+06	4.10E+06	5.60E+06	6.00E+06	6.10E+06
Q87MZ6	ABC transporter substrate-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2080 PE=4 SV=1	17.4	33.2	2.30E+06	4.80E+06	4.10E+06	3.70E+06	6.50E+06	5.30E+06
Q87N07	Methionine--tRNA ligase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=metG PE=3 SV=2	6.0	77.9	4.50E+06	5.20E+06	4.60E+06	6.40E+06	1.10E+07	6.20E+06
Q87N29	PTS system, glucose-specific IIBC component OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2046 PE=4 SV=1	8.8	49.4	8.30E+06	1.00E+07	3.50E+06	9.60E+06	9.70E+06	1.10E+07
Q87N36	Pyruvate kinase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2039 PE=3 SV=1	4.8	51.7					3.40E+06	5.20E+06
Q87N45	30S ribosomal protein S1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2030 PE=3 SV=1	15.3	60.9	6.40E+06	8.30E+06	3.60E+06	1.00E+07	2.00E+07	1.00E+07
Q87N50	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2025 PE=4 SV=1	9.6	76.6	4.30E+06	6.90E+06	5.70E+06	1.00E+07	1.40E+07	1.40E+07
Q87N85	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1990 PE=4 SV=1	2.7	38.1						

Q87NA1	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=metE PE=3 SV=1	42.0	84.7	2.00E+07	2.30E+07	1.10E+07	3.20E+07	4.90E+07	2.90E+07
Q87NC6	Diaminobutyrate-pyruvate transaminase & L-2,4-diaminobutyrate decarboxylase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1942 PE=1 SV=1	4.2	104.3	1.50E+06			1.90E+06	2.70E+06	5.00E+06
Q87NC8	Carboxynorspermidine/carboxyspermidine decarboxylase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1940 PE=3 SV=1	2.1	42.0		1.90E+06	1.70E+06			3.80E+06
Q87ND3	Ribonucleoside-diphosphate reductase, beta subunit OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1935 PE=4 SV=1	6.6	43.7		5.60E+06				6.70E+05
Q87ND6	DNA gyrase subunit A OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=gyrA PE=3 SV=1	1.7	97.0		1.50E+06		1.90E+06	2.70E+06	2.60E+06
Q87NF7	Extracellular solute-binding protein, family 7 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1911 PE=3 SV=1	8.3	41.0		3.80E+06			3.50E+06	5.80E+06
Q87NG8	Aspartate aminotransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1900 PE=3 SV=1	62.6	45.4	7.20E+07	1.20E+08	9.60E+07	1.30E+08	1.90E+08	2.10E+08
Q87NH5	Asparagine--tRNA ligase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=asnS PE=3 SV=1	11.2	52.6	3.80E+06	5.10E+06	2.70E+06	5.10E+06	7.30E+06	8.10E+06
Q87P08	Glucose-6-phosphate 1-dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=zwf PE=3 SV=1	9.0	57.6	1.50E+06	2.60E+06		6.10E+06	7.80E+06	5.70E+06
Q87P10	6-phosphogluconate dehydrogenase, decarboxylating OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1708 PE=3 SV=1	33.8	52.5	1.20E+07	2.80E+07	2.00E+07	2.90E+07	4.00E+07	4.30E+07
Q87P32	Adenosine monophosphate-protein transferase VopS OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=vopS PE=1 SV=1	7.5	41.7		2.80E+06			4.70E+06	2.90E+06
Q87P59	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1659 PE=4 SV=1	4.3	67.0	2.10E+06		3.40E+06		4.30E+06	
Q87P63	Immunogenic protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1655 PE=4 SV=1	2.8	34.9	2.50E+07		3.00E+07	3.50E+07		6.00E+07
Q87PB3	Aminopeptidase N OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1604 PE=4 SV=1	18.2	98.4	3.00E+06	3.40E+06	4.50E+06	5.50E+06	6.90E+06	9.70E+06
Q87PB5	Putative NAD-glutamate dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1602 PE=4 SV=1	5.0	183.4	4.60E+06	8.40E+06		5.60E+06	3.90E+06	1.80E+06
Q87PC3	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1594 PE=4 SV=1	34.8	64.6	3.80E+06	1.10E+07	8.80E+06	1.30E+07	1.70E+07	1.90E+07
Q87PC5	3-hydroxydecanoyl-[acyl-carrier-protein] dehydratase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=fabA PE=3 SV=1	16.9	19.0	7.80E+06	1.70E+07	1.10E+07	1.30E+07	2.20E+07	2.80E+07
Q87PG1	Cbb3-type cytochrome c oxidase subunit OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1541 PE=3 SV=1	3.1	35.4					1.50E+06	
Q87PH6	Putrescine-binding periplasmic protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1526 PE=3 SV=1	15.5	39.7		4.10E+06	3.30E+06	7.70E+06	1.20E+07	1.40E+07
Q87PH7	Putrescine-binding periplasmic protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1525 PE=3 SV=1	4.1	39.0			3.50E+06			
Q87PK2	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1501 PE=1 SV=1	9.9	30.1	3.50E+06		2.30E+06		3.80E+06	5.00E+06
Q87PP6	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1455 PE=4 SV=1	5.3	18.0		8.30E+06	3.70E+06	6.20E+06		
Q87PV1	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1400 PE=4 SV=1	1.9	77.2				4.30E+06	5.70E+06	
Q87Q03	Oligopeptide ABC transporter, periplasmic oligopeptide-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1347 PE=4 SV=1	1.7	60.3	2.80E+06			6.20E+06	5.80E+06	
Q87Q24	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1326 PE=4 SV=1	7.0	57.7	3.30E+06	7.70E+06	5.30E+06	5.70E+06	7.00E+06	7.20E+06
Q87Q40	Succinylglutamate desuccinylase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=astE PE=1 SV=1	2.6	38.8		2.00E+06				4.00E+06
Q87Q42	Putative oligopeptidase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1308 PE=4 SV=1	5.5	68.0	1.90E+06	1.10E+06	2.00E+06	6.10E+05	2.60E+06	3.80E+06
Q87Q59	Phenylalanine--tRNA ligase beta subunit OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=pheT PE=3 SV=1	2.2	87.0	5.50E+06	5.40E+06	3.40E+06	5.50E+06	8.80E+06	7.20E+06
Q87Q70	Threonine--tRNA ligase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=thrS PE=3 SV=1	2.5	73.7				2.60E+06	2.60E+06	
Q87Q87	Phosphoribosylaminoimidazole-succinocarboxamide synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=purC PE=3 SV=1	24.5	41.0		3.90E+06	2.80E+06	5.40E+06	1.10E+07	1.10E+07
Q87Q99	Thioredoxin reductase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1251 PE=3 SV=1	24.5	34.5		9.00E+06	6.50E+06	5.90E+06	1.30E+07	1.40E+07
Q87QA3	Phosphoserine aminotransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=serC PE=3 SV=1	27.7	40.2	1.00E+07	1.70E+07	1.30E+07	1.80E+07	2.70E+07	2.10E+07
Q87QB9	Putative reductase VP1231 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1231 PE=3 SV=1	43.0	43.9	1.90E+07	2.90E+07	2.40E+07	3.10E+07	4.50E+07	4.60E+07
Q87QE2	UDP-sugar hydrolase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1207 PE=3 SV=1	2.1	61.3					4.10E+06	
Q87QE6	Heat shock protein HslJ OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1203 PE=4 SV=1	6.1	16.6			2.00E+06		4.60E+06	
Q87QF3	Putative ABC transporter, periplasmic substrate-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1196 PE=4 SV=1	2.6	42.6		2.00E+06	1.50E+06	2.20E+06		3.30E+06
Q87QG7	Cystathionine beta-lyase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1182 PE=3 SV=1	3.2	44.6	2.10E+06	4.80E+06		6.70E+06	8.90E+06	9.70E+06
Q87QJ9	Cysteine--tRNA ligase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=cysS PE=3 SV=1	4.8	52.0					2.80E+06	
Q87QK9	Histidine biosynthesis bifunctional protein HisB OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=hisB PE=3 SV=1	6.2	39.8		3.30E+06		3.10E+06	4.80E+06	
Q87QL0	Histidinol-phosphate aminotransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=hisC PE=3 SV=1	15.3	38.2	2.10E+06	3.00E+06	2.70E+06	4.60E+06	8.40E+06	6.20E+06
Q87QL1	Histidinol dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=hisD PE=3 SV=1	15.3	46.1	4.00E+06	5.50E+06	8.30E+06	4.50E+06	1.80E+07	1.10E+07
Q87QL2	ATP phosphoribosyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=hisG PE=3 SV=1	40.6	32.8	6.60E+06	7.00E+06	7.40E+06	9.80E+06	1.80E+07	2.10E+07
Q87QM1	Adenylosuccinate lyase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1128 PE=3 SV=1	28.7	51.4	7.10E+06	1.40E+07	1.30E+07	1.40E+07	1.90E+07	2.10E+07
Q87QP1	Serine--tRNA ligase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=serS PE=3 SV=1	16.3	48.8	3.70E+06	4.70E+06	5.10E+06	5.00E+06	1.10E+07	1.10E+07
Q87QP6	Alanine dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1103 PE=3 SV=1	37.7	39.9	1.20E+07	3.40E+07	1.50E+07	2.20E+07	2.80E+07	2.80E+07
Q87QS7	Putative helicase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1072 PE=4 SV=1	16.1	68.7	1.60E+06	2.60E+06	2.40E+06	4.40E+06	7.40E+06	6.20E+06
Q87QT8	Peptidoglycan-associated lipoprotein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1061 PE=3 SV=1	12.6	18.7	7.90E+06	1.00E+07	3.80E+06	1.00E+07	1.40E+07	1.10E+07
Q87QT9	Protein TolB OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=tolB PE=3 SV=1	17.8	49.8	2.50E+06	5.10E+06	4.60E+06	7.30E+06	4.40E+06	8.30E+06
Q87QX5	Glycogen synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=glgA PE=3 SV=1	2.1	54.0					3.60E+06	
Q87QX6	Glucose-1-phosphate adenylyltransferase 1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=glgC1 PE=3 SV=1	30.9	45.5	8.90E+06	1.50E+07	6.10E+06	1.10E+07	2.30E+07	1.70E+07
Q87QX7	DNA topoisomerase 1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=topA PE=3 SV=1	1.7	98.0						2.80E+06
Q87QX9	3-phosphoshikimate 1-carboxyvinyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=aroA PE=3 SV=1	2.6	46.1						
Q87QY7	Isocitrate dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1011 PE=4 SV=1	65.2	80.5	4.90E+07	6.80E+07	5.50E+07	6.00E+07	1.00E+08	8.70E+07
Q87QZ9	Amino acid ABC transporter, periplasmic amino acid-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0999 PE=3 SV=1	45.3	28.4	4.60E+06	9.80E+06	7.60E+06	1.00E+07	2.00E+07	2.10E+07
Q87R02	Putative 54 kDa polar flagellar sheath protein A OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0996 PE=4 SV=1	55.8	52.3	1.50E+07	3.20E+07	2.50E+07	3.20E+07	3.00E+07	4.40E+07
Q87R04	Formate acetyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0994 PE=4 SV=1	49.1	84.5	2.60E+07	4.80E+07	4.10E+07	7.30E+07	1.20E+08	9.60E+07
Q87R36	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0962 PE=4 SV=1	24.9	43.9	2.60E+06	5.60E+06	3.50E+06	7.40E+06	1.70E+07	1.00E+07
Q87R78	DNA-binding protein HU-beta OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0920 PE=3 SV=1	12.2	9.4						5.10E+06
Q87R80	ATP-dependent Clp protease proteolytic subunit OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=clpP PE=3 SV=1	12.5	22.0	3.10E+06	8.90E+06	4.70E+06		1.80E+07	1.80E+07
Q87R87	C4-dicarboxylate-binding periplasmic protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0910 PE=4 SV=1	32.2	37.1	7.20E+06	8.20E+06	8.50E+06	1.40E+07	2.10E+07	1.60E+07
Q87RD3	Formyltetrahydrofolate deformylase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=purU PE=3 SV=1	6.9	31.6		3.10E+06				
Q87RD6	Arginine--tRNA ligase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=argS PE=3 SV=1	32.1	63.8	5.80E+06	9.20E+06	9.70E+06	1.10E+07	1.80E+07	2.00E+07
Q87RE4	Zinc ABC transporter, periplasmic zinc-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0853 PE=3 SV=1	14.4	32.1	2.90E+06	5.70E+06	3.50E+06	8.20E+06	1.10E+07	6.90E+06
Q87RE7	Succinyl-CoA ligase [ADP-forming] subunit alpha OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0850 PE=3 SV=1	34.5	30.0	1.10E+07	2.40E+07	7.50E+06	1.50E+07	3.00E+07	2.60E+07
Q87RE8	Succinyl-CoA ligase [ADP-forming] subunit beta OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=sucC PE=3 SV=1	50.8	41.5	3.30E+07	5.60E+07	3.20E+07	3.60E+07	6.40E+07	5.50E+07
Q87RE9	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0848 PE=3 SV=1	11.7	43.7	3.90E+06	7.60E+06	2.70E+06	6.00E+06	1.40E+07	1.10E+07
Q87RF0	2-oxoglutarate dehydrogenase, E1 component OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0847 PE=4 SV=1	3.8	106.0	2.50E+06	2.00E+06			4.80E+06	
Q87RF5	Citrate synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0842 PE=3 SV=1	5.1	48.2		5.30E+06		5.90E+06	1.10E+07	
Q87RG4	Glutamine--tRNA ligase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=glnS PE=3 SV=1	19.2	63.9	1.10E+07	1.80E+07	1.20E+07	1.40E+07	2.20E+07	2.70E+07
Q87RG5	PTS system, N-acetylglucosamine-specific IIABC component OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0831 PE=4 SV=1	2.1	54.5				2.30E+06		
Q87RG7	N-acetylglucosamine-6-phosphate deacetylase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0829 PE=3 SV=1	6.1	40.7						
Q87RH5	Chaperone protein HtpG OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=htpG PE=3 SV=1	4.1	72.1					3.10E+06	
Q87RJ7	Cysteine synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0797 PE=3 SV=1	74.8	34.1	5.80E+07	9.40E+07	8.30E+07	1.00E+08	2.00E+08	2.00E+08
Q87RL6	Glutamate--tRNA ligase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=gltX PE=3 SV=1	37.3	53.4	9.30E+06	1.80E+07	1.40E+07	1.90E+07	3.00E+07	2.70E+07
Q87RL8	Putative chitoporin OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0760 PE=4 SV=1	29.0	40.8					1.80E+07	6.70E+07
Q87RM3	N,N'-diacetylchitobiase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0755 PE=4 SV=1	15.7	97.6				8.50E+06		1.50E+07
Q87RN8	Ribose-phosphate pyrophosphokinase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=prs PE=3 SV=1	8.0	33.9		2.70E+06		4.10E+06	7.00E+06	7.90E+06
Q87RQ0	Leucine--tRNA ligase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=leuS PE=3 SV=1	31.4	96.6	1.60E+07	2.40E+07	1.70E+07	2.30E+07	2.90E+07	2.60E+07
Q87RR2	Serine hydroxymethyltransferase 1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=glyA1 PE=3 SV=1	10.6	45.5	3.00E+06	6.80E+06		4.70E+06	5.10E+06	8.30E+06
Q87RS3	Lipoprotein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0704 PE=3 SV=1	23.4	29.1	1.80E+06	4.00E+06		5.40E+06	1.00E+07	7.60E+06
Q87RU4	6,7-dimethyl-8-ribityllumazine synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=ribH PE=3 SV=1	23.7	16.4		3.30E+06	1.10E+06	6.00E+06	2.60E+06	6.70E+06
Q87RU5	3,4-dihydroxy-2-butanone 4-phosphate synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=ribB PE=3 SV=1	5.4	40.1		7.50E+05			2.40E+06	
Q87RV5	Aminoacyl-histidine dipeptidase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0671 PE=4 SV=1	7.1	53.6	2.50E+06	3.80E+06		3.80E+06	5.60E+06	4.20E+06
Q87RV7	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0669 PE=4 SV=1	3.7	39.0						
Q87RW0	Phosphoribosylformylglycinamidine synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=purL PE=3 SV=1	4.4	141.6	1.10E+06	3.50E+06		3.00E+06	4.20E+06	
Q87RX3	Chaperone protein DnaK OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=dnaK PE=3 SV=1	47.6	69.0	1.20E+07	1.50E+07	8.20E+06	1.50E+07	4.10E+07	2.80E+07
Q87S05	Putative chitinase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0619 PE=4 SV=1	23.9	63.5	3.60E+06	6.60E+06	1.40E+07	1.50E+07	1.30E+08	2.00E+08
Q87S07	GMP synthase [glutamine-hydrolyzing] OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=guaA PE=3 SV=1	7.4	57.6		1.90E+06		2.20E+06	5.80E+06	7.00E+06
Q87S08	Inosine-5'-monophosphate dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=guaB PE=3 SV=1	2.9	51.9	1.30E+06		9.10E+05	2.80E+06	5.20E+06	2.50E+06
Q87S31	Inositol monophosphate family protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0593 PE=4 SV=1	9.4	29.1	1.30E+06		1.60E+06	2.40E+06	4.10E+06	5.60E+06
Q87S44	Antioxidant, AhpC/Tsa family OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0580 PE=4 SV=1	39.4	22.2	1.20E+07	2.60E+07	1.90E+07	2.70E+07	4.00E+07	4.50E+07
Q87S84	Putative carbon starvation protein A OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0540 PE=4 SV=1	2.4	53.3	1.30E+06	1.70E+06			2.70E+06	
Q87S99	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0525 PE=4 SV=1	7.5	43.9				4.00E+06	5.30E+06	5.20E+06

Q87SA8	Oxidoreductase Tas, aldo/keto reductase family OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0516 PE=4 SV=1	22.7	39.7	5.10E+06	7.90E+06	7.20E+06	7.40E+06	1.50E+07	1.70E+07
Q87SC7	Autonomous glycyl radical cofactor OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=grcA PE=3 SV=1	5.6	13.9			7.60E+06	1.60E+07	2.70E+07	
Q87SC8	Threonine synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0496 PE=4 SV=1	10.1	46.5	4.60E+06	5.40E+06		3.60E+06	6.70E+06	6.30E+06
Q87SC9	Homoserine kinase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=thrB PE=3 SV=1	2.8	34.4			2.60E+06		7.50E+06	
Q87SD0	Aspartokinase I/homoserine dehydrogenase, threonine-sensitive OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0494 PE=4 SV=1	1.5	88.4					4.30E+06	
Q87SE0	Glutamate synthase, large subunit OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0484 PE=4 SV=1	11.9	175.2	4.20E+06	6.60E+06	2.90E+06	1.40E+07	1.40E+07	1.00E+07
Q87SE2	Glutamate synthase, large subunit OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0482 PE=4 SV=1	22.0	162.9	9.80E+06	1.20E+07	7.40E+06	1.10E+07	1.80E+07	1.50E+07
Q87SE3	Glutamate synthase, small subunit OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0481 PE=4 SV=1	4.0	52.5					2.40E+06	
Q87SF3	Carbamoyl-phosphate synthase large chain OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=carB PE=3 SV=1	6.2	117.8	4.40E+06	6.00E+06	5.00E+06	8.00E+06	1.50E+07	9.20E+06
Q87SF4	Carbamoyl-phosphate synthase small chain OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=carA PE=3 SV=1	2.6	41.0					4.90E+06	3.60E+06
Q87SF5	4-hydroxy-tetrahydrodipicolinate reductase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=dapB PE=3 SV=1	18.2	28.6	3.60E+06	7.30E+06	4.50E+06	7.90E+06	1.20E+07	8.60E+06
Q87SH9	Stringent starvation protein A OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0444 PE=3 SV=1	12.3	24.3		1.80E+06		2.70E+06	5.70E+06	7.70E+06
Q87SI4	30S ribosomal protein S9 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpsI PE=3 SV=1	20.0	14.6	1.90E+06	2.80E+06		2.70E+06		5.30E+06
Q87SJ0	Protease DO OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0433 PE=4 SV=1	14.1	48.1		3.20E+06		5.50E+06	8.30E+06	5.00E+06
Q87SJ8	Outer membrane protein TolC OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0425 PE=4 SV=1	24.9	48.0	3.60E+06	5.90E+06	3.60E+06	5.60E+06	1.20E+07	7.90E+06
Q87SK3	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0420 PE=4 SV=1	10.2	59.2	2.10E+06	4.40E+06	2.90E+06	4.30E+06	4.90E+06	6.50E+06
Q87SR3	Glutamine--fructose-6-phosphate aminotransferase [isomerizing] OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=glmS PE=3 SV=2	3.1	66.8		1.30E+06		9.00E+05		
Q87SR6	Pyruvate kinase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0356 PE=3 SV=1	3.0	49.9	2.90E+06	5.50E+06		4.50E+06	1.10E+07	
Q87SS8	3-isopropylmalate dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=leuB PE=3 SV=1	35.8	39.3	8.00E+06	1.20E+07	1.10E+07	1.60E+07	2.70E+07	2.50E+07
Q87ST3	LPS-assembly protein LptD OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=lptD PE=3 SV=1	2.9	89.2	1.70E+06	2.80E+06			2.40E+06	3.20E+06
Q87ST4	Chaperone SurA OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=surA PE=3 SV=1	8.0	47.4	2.70E+06	4.50E+06	3.50E+06		5.10E+06	
Q87SU7	Malate dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=mdh PE=3 SV=1	58.2	32.2	1.30E+07	2.60E+07	1.30E+07	2.10E+07	3.90E+07	2.80E+07
Q87SV0	Immunogenic protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0323 PE=4 SV=1	58.7	34.5	2.90E+07	5.20E+07	4.40E+07	5.90E+07	9.90E+07	1.00E+08
Q87SW0	Fructose-1,6-bisphosphatase class 1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=fbp PE=3 SV=1	3.3	37.3		5.20E+06				
Q87SX0	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0302 PE=4 SV=1	3.8	23.3		5.30E+06	5.70E+06	7.00E+06	1.50E+07	1.20E+07
Q87SX9	Sulfate adenylyltransferase subunit 1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=cysN PE=3 SV=1	2.5	52.6				2.80E+06	4.80E+06	
Q87SY2	2',3'-cyclic-nucleotide 2'-phosphodiesterase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0290 PE=3 SV=1	13.1	72.1		5.30E+06	5.70E+06	5.30E+06	8.40E+06	7.40E+06
Q87SZ0	DNA-directed RNA polymerase subunit alpha OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpoA PE=3 SV=1	10.3	36.5	2.90E+06	3.50E+06	2.00E+06	4.80E+06	8.50E+06	6.40E+06
Q87SZ1	30S ribosomal protein S4 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpsD PE=3 SV=1	24.8	23.3	3.50E+06	5.20E+06		1.10E+06	5.40E+06	1.10E+07
Q87SZ2	30S ribosomal protein S13 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpsM PE=3 SV=1	11.0	13.3						5.10E+06
Q87T02	50S ribosomal protein L24 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplX PE=3 SV=1	9.5	11.2					2.70E+06	
Q87T13	50S ribosomal protein L3 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplC PE=3 SV=1	4.8	22.4		5.60E+06				
Q87T31	Triosephosphate isomerase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=tpiA PE=3 SV=1	23.0	26.9	4.60E+06	8.90E+06	7.40E+06	1.30E+07	2.00E+07	2.10E+07
Q87T36	Pilin glycosylation protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0234 PE=3 SV=1	33.2	43.4	1.30E+07	2.00E+07	1.70E+07	2.30E+07	3.40E+07	3.20E+07
Q87T41	dTDP-4-dehydrorhamnose 3,5-epimerase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0229 PE=4 SV=1	5.9	21.2					5.80E+06	6.30E+06
Q87T56	ADP-L-glycero-D-manno-heptose-6-epimerase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=hldD PE=3 SV=1	3.2	35.2						
Q87T66	Putative 3-chlorobenzoate-3,4-dioxygenase dyhydrogenase related protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0204 PE=4 SV=1	3.2	38.5		3.10E+06			6.80E+06	
Q87T98	Putative binding protein component of ABC transporter OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0172 PE=4 SV=1	9.4	69.6			2.30E+06	6.80E+06	7.80E+06	1.00E+07
Q87TA2	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0168 PE=3 SV=1	1.3	93.9				3.10E+06		3.60E+06
Q87TA4	Putative TolR OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0166 PE=3 SV=1	8.8	49.3		1.10E+06		3.90E+06	5.70E+06	
Q87TA8	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0162 PE=4 SV=1	2.7	45.5	2.20E+07	2.00E+07	3.00E+07	2.40E+07	4.60E+07	
Q87TB9	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0151 PE=4 SV=1	6.7	70.4		4.40E+06	3.50E+06	4.00E+06	5.60E+06	6.20E+06
Q87TE1	Phosphoenolpyruvate carboxykinase [ATP] OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=pckA PE=3 SV=1	71.0	60.0	6.20E+07	8.90E+07	4.90E+07	9.90E+07	9.00E+07	8.40E+07
Q87TE8	Glutamine synthetase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0121 PE=3 SV=1	58.4	51.5	1.00E+08	1.30E+08	1.10E+08	1.50E+08	2.00E+08	2.30E+08
Q87TG2	DNA polymerase I OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0107 PE=3 SV=1	8.8	103.1	3.80E+06	4.60E+06	3.00E+06	5.00E+06	8.40E+06	5.10E+06
Q87TG5	Delta-aminolevulinic acid dehydratase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0104 PE=3 SV=1	16.7	39.2	5.90E+06	8.90E+06	7.80E+06	9.20E+06	1.30E+07	1.40E+07
Q87TI3	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0086 PE=4 SV=1	13.6	15.3						
Q87TJ9	Oligopeptidase A OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0070 PE=3 SV=1	24.9	76.9	3.40E+07	5.20E+07	4.70E+07	7.00E+07	1.10E+08	1.10E+08
Q87TK1	Glutathione reductase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0068 PE=3 SV=1	24.6	49.2	1.10E+07	2.40E+07	2.00E+07	2.30E+07	3.50E+07	4.10E+07
Q87TM1	Peptide ABC transporter, periplasmic peptide-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0048 PE=4 SV=1	63.4	57.4	7.70E+07	1.30E+08	1.10E+08	1.20E+08	2.10E+08	2.00E+08
Q87TN4	Ketol-acid reductoisomerase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=ilvC PE=3 SV=1	57.5	54.7	3.20E+07	5.90E+07	4.70E+07	6.60E+07	1.10E+08	1.00E+08
Q87TR0	Amino acid ABC transporter, periplasmic amino acid-binding portion OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0008 PE=3 SV=1	22.2	27.5		2.90E+06		2.50E+06	5.70E+06	8.20E+06
Q99289	Thermolabile hemolysin OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0226 PE=1 SV=2	3.1	47.4					4.00E+07	
Q9ALY5	Cyclic AMP receptor protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2793 PE=4 SV=1	37.1	23.7	5.10E+06	9.30E+06	6.40E+06	9.20E+06	2.20E+07	1.50E+07
Q9L7P5	60 kDa chaperonin 1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=groL1 PE=3 SV=2	40.0	57.5	2.80E+07	3.90E+07	3.20E+07	3.80E+07	5.70E+07	3.70E+07
Q9ZBA2	Polar flagellin E OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=flaE PE=3 SV=2	1.6	40.7		3.50E+06		6.40E+06		5.80E+06

1st Experiment (Soulble Fraction)

Accession	Description	Coverage	MW [kDa]	Control	GlcNAc	GlcN	(GlcNAc)2	(GlcN)2	GlcNAc-GlcN
A7UEM1	Transhydrogenase alpha subunit (Fragment) OS=Vibrio parahaemolyticus GN=pntA PE=4 SV=1	7.0	15.5						4.20E+06
A7UET7	Protein RecA (Fragment) OS=Vibrio parahaemolyticus GN=recA PE=3 SV=1	42.4	26.0	8.60E+06	1.20E+07	1.10E+07	5.60E+06	1.50E+07	9.50E+06
A7UEX3	DNA gyrase beta-subunit (Fragment) OS=Vibrio parahaemolyticus GN=gyrB PE=4 SV=1	11.7	21.7			8.90E+06		4.90E+06	8.90E+06
A9Q6J2	Protein RecA (Fragment) OS=Vibrio parahaemolyticus GN=recA PE=3 SV=1	42.2	22.4	8.60E+06	1.20E+07	1.10E+07	5.60E+06	1.50E+07	1.40E+07
A9Q6M1	DNA gyrase B subunit (Fragment) OS=Vibrio parahaemolyticus GN=gyrB PE=4 SV=1	13.5	18.6			8.90E+06		4.90E+06	8.90E+06
A9Q6Q3	Phosphoglucomutase (Fragment) OS=Vibrio parahaemolyticus GN=pgm PE=3 SV=1	26.5	21.2	6.70E+06	1.10E+07	8.10E+06	1.20E+07	1.40E+07	1.30E+07
H6BAG3	Protein RecA (Fragment) OS=Vibrio parahaemolyticus GN=recA PE=3 SV=1	35.1	18.0	7.20E+06	1.30E+07	1.10E+07	2.80E+06	1.70E+07	
O50286	Dihydrolipoyl dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=lpd PE=3 SV=2	51.4	51.0	1.80E+07	3.10E+07	2.80E+07	3.20E+07	3.40E+07	3.20E+07
O51859	DNA gyrase subunit B OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=gyrB PE=3 SV=2	16.8	89.4	5.30E+06	7.70E+06	8.80E+06	1.00E+07	5.90E+06	9.50E+06
P0A2W2	Acyl carrier protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=acpP PE=3 SV=2	18.2	8.5					4.10E+06	4.70E+06
P0A481	50S ribosomal protein L20 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplT PE=3 SV=1	16.2	13.4		4.60E+06	9.60E+06	1.00E+07	1.20E+07	9.70E+06
P22097	Tryptophan synthase beta chain 1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=trpB1 PE=3 SV=2	8.3	43.0	3.00E+06	4.20E+06	5.60E+06	9.10E+06	2.60E+06	4.90E+06
P22099	Anthranilate synthase component 1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=trpE PE=3 SV=2	3.9	59.7		1.90E+06		5.30E+06	2.50E+06	2.60E+06
P40607	Adenylosuccinate synthetase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=purA PE=3 SV=3	26.0	47.7	1.10E+07	2.00E+07	1.70E+07	2.00E+07	3.00E+07	2.30E+07
P40611	Ribonuclease R OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rnr PE=3 SV=2	2.8	95.0	1.10E+06					
P59494	Maltoporin OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=lamB PE=3 SV=1	41.2	46.9	3.00E+07	2.70E+07	2.60E+07	2.60E+07	5.70E+07	5.10E+07
P59605	Argininosuccinate synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=argG PE=3 SV=1	56.2	44.5	4.30E+07	5.40E+07	5.50E+07	7.30E+07	9.10E+07	7.20E+07
P59620	Bifunctional protein ArgH OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=argH PE=3 SV=1	23.7	69.3	5.80E+06	7.80E+06	9.20E+06	1.70E+07	1.40E+07	1.00E+07
P66346	30S ribosomal protein S10 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpsJ PE=3 SV=1	34.0	11.7	7.30E+06	1.20E+07	1.80E+07	1.50E+07		2.10E+07
P66368	30S ribosomal protein S11 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpsK PE=3 SV=1	27.9	13.9	4.00E+06	7.80E+06	8.50E+06	1.20E+07	1.00E+07	1.00E+07
P66478	30S ribosomal protein S18 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpsR PE=3 SV=1	40.0	8.8	3.40E+06	1.20E+07	2.50E+07	2.10E+07	1.60E+07	2.10E+07
P66533	30S ribosomal protein S21 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpsU PE=3 SV=1	14.1	8.5						9.60E+05
P74956	Lon protease OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=lon PE=3 SV=2	28.4	87.8	7.20E+06	1.20E+07	1.30E+07	1.70E+07	1.60E+07	1.80E+07
Q79YV4	OpaR OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2516 PE=4 SV=1	5.9	23.6					3.90E+06	
Q79YX4	Chemotaxis protein CheW OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2225 PE=4 SV=1	30.5	18.4	2.10E+06		5.30E+06	2.70E+07	7.10E+06	2.60E+07
Q79YY3	BfdA OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1393 PE=4 SV=1	10.5	19.4			7.60E+06		3.30E+06	
Q877T5	Elongation factor Tu OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=tufA PE=3 SV=1	61.7	43.1	1.40E+08	2.60E+08	2.40E+08	3.20E+08	3.60E+08	3.00E+08
Q87FC8	ParB family protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1751 PE=4 SV=1	3.7	35.7		1.80E+06	1.90E+06	2.80E+06		2.40E+06
Q87FF3	Putative proline dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1726 PE=3 SV=1	7.8	114.9	2.80E+06	9.60E+06	2.50E+06			
Q87FL2	PTS system, glucose-specific IIBC component OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1667 PE=4 SV=1	1.7	51.1			3.40E+06			
Q87FL7	Putative diaminopimelate decarboxylase protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1662 PE=3 SV=1	29.3	45.3	1.20E+07	2.80E+07	2.70E+07	3.20E+07	4.60E+07	3.30E+07
Q87FL8	Putative AcsD OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1661 PE=4 SV=1	36.3	69.4	1.30E+07	2.10E+07	2.10E+07	2.20E+07	3.40E+07	2.30E+07
Q87FM0	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1659 PE=4 SV=1	59.3	68.7	6.10E+07	1.10E+08	1.00E+08	1.10E+08	1.30E+08	1.20E+08
Q87FM1	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1658 PE=4 SV=1	36.2	44.2	3.40E+07	6.00E+07	5.10E+07	5.40E+07	7.70E+07	6.50E+07
Q87FM2	Ferric siderophore receptor homolog OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1657 PE=3 SV=1	15.9	74.9	5.00E+06	6.50E+06	8.10E+06	1.10E+07	1.20E+07	1.90E+07
Q87FM3	Ferric vibrioferrin receptor OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1656 PE=3 SV=1	18.1	78.8	4.30E+06	5.40E+06	6.30E+06	7.00E+06	1.10E+07	1.40E+07
Q87FN1	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1648 PE=4 SV=1	6.3	62.7		3.60E+06		5.90E+06	8.70E+06	3.70E+06
Q87FQ8	Alpha-1,4 glucan phosphorylase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1620 PE=3 SV=1	36.4	92.3	2.00E+07	2.70E+07	2.40E+07	2.60E+07	4.30E+07	2.50E+07
Q87FQ9	4-alpha-glucanotransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1619 PE=3 SV=1	28.1	81.8	1.20E+07	1.50E+07	1.40E+07	1.60E+07	1.90E+07	1.30E+07
Q87FR0	1,4-alpha-glucan branching enzyme GlgB OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=glgB PE=3 SV=1	2.1	87.4		5.70E+06	6.50E+06		1.10E+07	8.40E+06
Q87FV6	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1572 PE=4 SV=1	23.9	41.8	2.80E+06	6.60E+06	4.70E+06	7.30E+06	9.70E+06	9.70E+06
Q87G18	L-lactate dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=lldD PE=3 SV=1	2.9	41.4	1.20E+06			3.00E+06		
Q87G21	Prolyl endopeptidase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1496 PE=4 SV=1	21.7	76.0	5.20E+06	9.00E+06	9.50E+06	1.30E+07	1.00E+07	1.50E+07
Q87G22	ABC transporter, ATP-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1495 PE=3 SV=1	2.0	60.6						2.30E+06
Q87G42	Purine nucleoside phosphorylase DeoD-type 2 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=deoD2 PE=3 SV=1	10.2	25.7			6.30E+06	1.10E+07	9.10E+06	
Q87G89	Azurin OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1428 PE=4 SV=1	28.0	15.8	1.00E+07	1.90E+07	1.70E+07	2.80E+07	2.70E+07	2.10E+07
Q87GA0	Putative glutathione S-transferase family protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1417 PE=3 SV=1	11.7	23.6		2.20E+06	3.70E+06	6.00E+06	6.80E+06	5.40E+06

Q87GB6	Maltose ABC transporter, periplasmic maltose-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1401 PE=4 SV=1	58.4	42.1	3.70E+07	6.20E+07	6.00E+07	5.80E+07	6.40E+07	6.00E+07
Q87GC0	Acyl-CoA thioester hydrolase-related protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1397 PE=4 SV=1	21.7	17.7	3.70E+06	9.40E+06	1.20E+07	1.10E+07	1.60E+07	1.20E+07
Q87GC8	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1389 PE=4 SV=1	5.8	39.4						
Q87GK7	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1308 PE=4 SV=1	16.6	42.3	3.80E+06		5.20E+06	2.90E+06	8.40E+06	1.20E+07
Q87GL1	Putative 3-oxoacyl-(Acyl carrier protein) reductase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1304 PE=3 SV=1	4.2	25.2	2.00E+06	4.90E+06	5.10E+06			5.10E+06
Q87GT5	Glyceraldehyde-3-phosphate dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1230 PE=3 SV=1	23.7	52.3	8.60E+06	1.80E+07	7.10E+06	1.40E+07	1.10E+07	9.20E+06
Q87GW0	Acetoacetyl-CoA reductase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1205 PE=3 SV=1	6.9	26.2					3.90E+06	4.00E+06
Q87GW1	Acetyl-CoA acetyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1204 PE=3 SV=1	10.0	41.5						3.30E+06
Q87GY0	Phospho-2-dehydro-3-deoxyheptonate aldolase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1185 PE=3 SV=1	24.9	38.3		3.00E+07	3.70E+07	5.50E+07	2.40E+07	8.60E+06
Q87GY4	Transketolase 2 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=tkt2 PE=3 SV=1	31.7	72.0	8.90E+06	1.10E+07	7.60E+06	1.50E+07	1.10E+07	1.30E+07
Q87GY5	Transaldolase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=tal PE=3 SV=1	53.8	34.8	1.10E+07	2.00E+07	2.10E+07	3.10E+07	2.60E+07	2.60E+07
Q87H02	Oxidoreductase, aldo/keto reductase 2 family OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1163 PE=4 SV=1	2.6	34.0				2.60E+06		
Q87H16	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1149 PE=4 SV=1	12.3	45.3	4.70E+06	1.00E+07	8.90E+06	1.30E+07	9.40E+06	6.30E+06
Q87HD1	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1034 PE=4 SV=1	7.2	55.3					1.10E+07	5.40E+06
Q87HD7	Putative ClpA/B-type chaperone OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1028 PE=4 SV=1	0.8	93.9					1.20E+07	1.40E+07
Q87HD8	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1027 PE=4 SV=1	18.2	17.7					9.90E+06	6.80E+06
Q87HF4	L-allo-threonine aldolase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1011 PE=4 SV=1	18.3	36.1	4.50E+06	6.60E+06	8.80E+06	1.10E+07	1.50E+07	1.30E+07
Q87HG0	D-lactate dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1005 PE=4 SV=1	6.2	64.3	4.00E+06	4.90E+06	5.80E+06	6.30E+06	6.50E+06	7.00E+06
Q87HI4	Ferric aerobactin receptor OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0979 PE=3 SV=1	4.8	79.2	2.70E+06			3.50E+06		3.50E+06
Q87HM7	Amino acid biosynthesis aminotransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0936 PE=4 SV=1	26.4	43.7	3.70E+06	9.70E+06	8.80E+06	1.10E+07	1.50E+07	1.30E+07
Q87HP1	NAD(P) transhydrogenase subunit alpha OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0922 PE=3 SV=1	6.0	54.8				4.70E+06		6.30E+06
Q87HS4	Heme transport protein HutA OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0882 PE=3 SV=1	19.8	77.3	6.60E+06	3.50E+06	8.10E+06	5.20E+06	7.50E+06	1.00E+07
Q87HV6	UPF0312 protein VPA0850 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0850 PE=3 SV=1	20.6	20.3			6.30E+06	5.50E+06	7.10E+06	4.90E+06
Q87I01	Aminomethyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0805 PE=3 SV=1	4.3	40.3		2.70E+06		3.30E+06	4.40E+06	3.90E+06
Q87I05	Glycine dehydrogenase (decarboxylating) OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=gcvP PE=3 SV=1	5.2	104.1	4.10E+06	5.40E+06	5.00E+06	5.20E+06	7.50E+06	
Q87IE9	Iron(III) ABC transporter, periplasmic iron-compound-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0657 PE=4 SV=1	20.5	33.5	1.80E+07	1.10E+07	1.10E+07	2.30E+07	1.80E+07	1.40E+07
Q87IG4	Putative glutathione S-transferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0642 PE=4 SV=1	5.1	24.3				4.80E+06		
Q87IJ5	Acetate kinase 2 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=ackA2 PE=3 SV=1	28.5	42.6	8.50E+06	1.30E+07	1.50E+07	1.70E+07	2.80E+07	1.90E+07
Q87IL1	ATP-binding component of molybdate transport system OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0595 PE=4 SV=1	1.7	55.4					4.50E+06	
Q87IM1	Tryptophan synthase beta chain 2 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=trpB2 PE=3 SV=1	4.2	44.2	2.20E+06	4.40E+06				
Q87IP0	Alcohol dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0566 PE=4 SV=1	24.9	40.2	1.10E+07	1.90E+07	6.00E+06	6.30E+06	1.20E+07	7.20E+06
Q87IQ4	Cold shock DNA-binding domain protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0552 PE=4 SV=1	36.2	7.5		1.10E+07	1.00E+07	1.30E+07	1.40E+07	8.80E+06
Q87IS1	Putative phosphomannomutase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0535 PE=3 SV=1	35.3	61.6	1.30E+07	2.00E+07	1.50E+07	2.50E+07	2.10E+07	2.10E+07
Q87IY8	Prolyl endopeptidase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0468 PE=4 SV=1	2.7	84.2		5.20E+06	2.60E+06	4.90E+06	1.00E+07	8.80E+06
Q87J24	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0429 PE=4 SV=1	6.8	20.2	2.90E+06	6.50E+06		8.40E+06	9.80E+06	6.90E+06
Q87J26	Coproporphyrinogen oxidase homolog PhuW OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0427 PE=4 SV=1	9.2	50.4	2.00E+06			6.20E+06	6.30E+06	5.20E+06
Q87J30	Hemin ABC transporter, periplasmic hemin-binding protein HutB OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0423 PE=4 SV=1	5.5	30.3						2.20E+06
Q87J33	LuxT OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0420 PE=1 SV=1	7.2	17.5		2.20E+06				
Q87J81	Phosphoenolpyruvate synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0372 PE=3 SV=1	53.2	88.1	9.70E+07	1.40E+08	1.00E+08	1.30E+08	1.30E+08	9.20E+07
Q87J86	Putrescine-binding periplasmic protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0367 PE=3 SV=1	22.4	38.7	3.50E+06	5.00E+06	7.70E+06	8.70E+06	1.20E+07	1.00E+07
Q87J88	Putative transcriptional regulator protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0365 PE=4 SV=1	3.4	33.2	3.10E+06					
Q87JD5	Putative outer membrane protein OmpV OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0318 PE=4 SV=1	4.7	28.1	2.10E+06	3.20E+06				7.60E+06
Q87JF1	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0302 PE=4 SV=1	10.9	14.7					6.40E+06	
Q87JN3	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0215 PE=4 SV=1	17.3	11.9						
Q87JR8	Phospho-beta-glucosidase B OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0180 PE=3 SV=1	4.1	53.0	2.10E+06	4.00E+06	2.50E+06	7.90E+06	4.80E+06	4.10E+06
Q87JS8	Biosynthetic arginine decarboxylase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=speA PE=3 SV=1	6.4	72.0	1.40E+06	6.20E+06	5.20E+06	5.60E+06	5.30E+06	4.20E+06
Q87JT2	Putative outer membrane protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0166 PE=4 SV=1	14.0	38.0	1.10E+07	8.70E+06	1.20E+07	1.60E+07	2.00E+07	1.70E+07
Q87JV9	Putative PmbA-related protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0139 PE=4 SV=1	2.9	47.7			3.20E+06			4.10E+06
Q87JW5	Putative ABC transporter substrate-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0133 PE=4 SV=1	4.4	34.7						2.60E+06
Q87K02	Outer membrane protein OmpW OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0096 PE=4 SV=1	6.5	23.5	3.80E+06	3.30E+06	4.00E+06	2.80E+06	7.00E+06	4.10E+06
Q87K50	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0047 PE=4 SV=1	4.4	31.1						
Q87K60	Glucosamine-6-phosphate deaminase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=nagB PE=3 SV=1	13.5	29.6		8.50E+06		1.60E+07		1.40E+07
Q87K95	Peptide ABC transporter, ATP-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0003 PE=3 SV=1	7.4	34.9						6.40E+06
Q87KA6	ATP synthase subunit alpha OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=atpA PE=3 SV=1	58.7	56.6	5.40E+07	8.20E+07	8.00E+07	9.30E+07	1.20E+08	9.60E+07
Q87KA7	ATP synthase gamma chain OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=atpG PE=3 SV=1	32.6	31.8	5.90E+06	1.40E+07	1.10E+07	1.80E+07	1.70E+07	1.60E+07
Q87KA8	ATP synthase subunit beta OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=atpD PE=3 SV=1	56.5	50.7	4.80E+07	7.70E+07	6.70E+07	8.30E+07	1.00E+08	7.50E+07
Q87KB5	L-threonine dehydratase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=ilvA PE=3 SV=1	11.8	56.6	4.60E+06	8.60E+06	4.30E+06		7.80E+06	6.00E+06
Q87KB6	Dihydroxy-acid dehydratase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=ilvD PE=3 SV=1	47.8	65.6	1.80E+07	2.50E+07	2.20E+07	3.20E+07	3.00E+07	3.10E+07
Q87KB7	Branched-chain amino acid amiotransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP3060 PE=3 SV=1	9.0	34.3	5.60E+06	1.00E+07	8.90E+06	1.40E+07	1.50E+07	1.40E+07
Q87KB9	Acetolactate synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP3058 PE=3 SV=1	4.9	59.2				2.30E+06	1.40E+06	
Q87KF6	Aminopeptidase P OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP3021 PE=4 SV=1	10.9	65.5	3.00E+06	9.20E+06	8.00E+06	1.10E+07	5.40E+06	7.50E+06
Q87KH7	Transcription termination factor Rho OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rho PE=3 SV=1	13.8	46.8		3.10E+06	3.50E+06	1.40E+06	6.80E+06	4.10E+06
Q87KJ3	Diaminopimelate decarboxylase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=lysA PE=3 SV=1	18.2	45.9	2.60E+06	4.50E+06	6.40E+06	6.80E+06	8.10E+06	7.80E+06
Q87KP9	Transcription termination/antitermination protein NusG OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=nusG PE=3 SV=2	5.5	20.7						5.50E+06
Q87KQ0	50S ribosomal protein L11 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplK PE=3 SV=1	27.5	14.7	1.10E+07	2.60E+07	3.20E+07	3.90E+07	2.50E+07	3.80E+07
Q87KQ1	50S ribosomal protein L1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplA PE=3 SV=1	48.9	24.7	1.30E+07	2.20E+07	2.70E+07	3.50E+07	3.20E+07	3.90E+07
Q87KQ2	50S ribosomal protein L10 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplJ PE=3 SV=1	13.6	17.3				7.50E+06	3.50E+06	
Q87KQ3	50S ribosomal protein L7/L12 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplL PE=3 SV=1	19.7	12.2	4.10E+06	1.10E+07	1.30E+07	1.80E+07	1.70E+07	1.60E+07
Q87KQ4	DNA-directed RNA polymerase subunit beta OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpoB PE=3 SV=1	41.6	149.5	1.60E+07	2.40E+07	2.70E+07	3.10E+07	2.90E+07	2.80E+07
Q87KQ5	DNA-directed RNA polymerase subunit beta' OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpoC PE=3 SV=1	36.8	154.8	1.70E+07	2.30E+07	2.90E+07	3.30E+07	3.00E+07	3.20E+07
Q87KQ6	Regulator of sigma D OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2920 PE=3 SV=1	9.8	18.6	1.80E+06					
Q87KR5	DNA-binding protein HU-2 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2911 PE=3 SV=1	63.7	9.6	8.40E+06	2.40E+07	2.70E+07	2.50E+07	1.80E+07	2.30E+07
Q87KS6	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2900 PE=4 SV=1	2.0	57.1		2.40E+06		4.20E+06		
Q87KT0	Bifunctional purine biosynthesis protein PurH OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=purH PE=3 SV=1	28.5	57.3	4.70E+06	8.00E+06	8.20E+06	1.30E+07	1.70E+07	1.20E+07
Q87KU4	Acetyl-CoA carboxylase, biotin carboxylase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2881 PE=4 SV=1	28.9	49.2	5.90E+06	1.00E+07	1.50E+07	1.30E+07	9.00E+07	1.30E+07
Q87KU7	Acetyl-coenzyme A synthetase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=acsA PE=3 SV=1	40.0	71.7	3.00E+07	3.40E+07	2.70E+07	2.50E+07	2.50E+07	3.30E+07
Q87KV2	Fumarate hydratase class II OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=fumC PE=3 SV=1	37.1	48.7	4.40E+07	7.70E+07	7.50E+07	9.50E+07	1.00E+08	8.80E+07
Q87KW2	Aspartate ammonia-lyase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2863 PE=3 SV=1	7.2	52.7	3.30E+06	4.50E+06	3.00E+06	6.00E+06	4.10E+06	4.30E+06
Q87KW5	Superoxide dismutase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2860 PE=3 SV=1	37.1	23.0	8.90E+06	1.70E+07	2.40E+07	1.50E+07	1.80E+07	2.30E+07
Q87KX0	ATP-dependent 6-phosphofructokinase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=pfkA PE=3 SV=1	18.8	34.6	3.10E+06	7.00E+06	7.70E+06	1.00E+07	9.60E+06	8.50E+06
Q87KX9	Elongation factor P OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=efp PE=3 SV=1	6.4	20.6				4.60E+06	6.40E+06	
Q87KY4	Fumarate reductase flavoprotein subunit OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2840 PE=3 SV=1	1.8	66.1	1.80E+06					
Q87KZ3	Protein-export protein SecB OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=secB PE=3 SV=1	9.7	17.2						6.40E+06
Q87KZ5	2,3-bisphosphoglycerate-independent phosphoglycerate mutase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=gpmI PE=3 SV=1	18.6	55.1	1.00E+07	1.50E+07	1.50E+07	1.90E+07	2.40E+07	2.20E+07
Q87L07	RNA-binding protein Hfq OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=hfq PE=3 SV=1	25.3	9.8		7.80E+06	1.20E+07	9.20E+06	8.20E+06	7.60E+06
Q87L13	Tryptophan--tRNA ligase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=trpS PE=3 SV=1	6.5	37.6				2.90E+06	1.80E+06	3.60E+06
Q87L20	Acetylornithine aminotransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=argD PE=3 SV=1	29.0	43.3	2.10E+06	8.80E+06	3.10E+06	1.30E+07	1.40E+07	8.50E+06
Q87L21	Arginine N-succinyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2796 PE=4 SV=1	4.4	37.7						
Q87L22	N-succinylglutamate 5-semialdehyde dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=astD PE=3 SV=1	3.9	52.0		4.20E+06	3.40E+06	4.90E+06	4.20E+06	
Q87L23	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2794 PE=4 SV=1	12.5	29.2		7.40E+06	6.00E+06	8.40E+06	6.10E+06	7.10E+06
Q87L38	Peptidyl-prolyl cis-trans isomerase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2778 PE=4 SV=1	7.7	28.3				1.90E+06		
Q87L39	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2777 PE=4 SV=1	3.8	26.6	2.80E+06		2.90E+06			
Q87L43	30S ribosomal protein S12 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpsL PE=3 SV=1	29.8	13.7	3.80E+06	6.40E+06	9.70E+06	1.00E+07	9.40E+06	1.40E+07
Q87L44	30S ribosomal protein S7 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpsG PE=3 SV=1	49.4	17.7	7.60E+06	2.00E+07	2.70E+07	2.70E+07	3.00E+07	3.20E+07
Q87L45	Elongation factor G 1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=fusA1 PE=3 SV=1	27.5	77.5	9.00E+06	1.20E+07	1.00E+07	1.40E+07	1.40E+07	1.40E+07
Q87L48	Putative malate oxidoreductase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2767 PE=3 SV=1	8.5	46.1	2.80E+06	3.30E+06	4.10E+06	4.80E+06	6.40E+06	4.80E+06
Q87L50	Cystathionine gamma-synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2765 PE=3 SV=1	9.6	41.8			5.60E+06	6.50E+06	9.40E+06	6.80E+06

Q87L51	Aspartokinase II/homoserine dehydrogenase, methionine-sensitive OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2764 PE=4 SV=1	12.0	87.8	3.20E+06	2.90E+06	4.40E+06	6.70E+06	6.20E+06	5.90E+06
Q87L52	Methylenetetrahydrofolate reductase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2763 PE=3 SV=1	20.3	33.3	7.10E+06	1.10E+07	1.40E+07	1.50E+07	1.20E+07	2.00E+07
Q87L54	Phosphoenolpyruvate carboxylase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=ppc PE=3 SV=2	32.6	99.2	1.00E+07	1.50E+07	1.30E+07	1.90E+07	2.00E+07	1.90E+07
Q87L55	N-acetyl-gamma-glutamyl-phosphate reductase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=argC PE=3 SV=1	10.2	36.2	4.20E+06	5.40E+06	5.70E+06	7.80E+06	4.70E+06	3.80E+06
Q87L56	Acetylglutamate kinase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=argB PE=3 SV=1	7.6	27.1					4.30E+06	
Q87L68	3-dehydroquinate synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=aroB PE=3 SV=1	12.3	40.0				5.70E+06	5.30E+06	5.10E+06
Q87L72	30S ribosomal protein S6 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpsF PE=3 SV=1	23.3	15.0		7.20E+06	8.00E+06	8.70E+06	7.50E+06	9.40E+06
Q87L75	50S ribosomal protein L9 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplI PE=3 SV=1	40.7	15.7	2.80E+06	9.60E+06	1.00E+07	1.30E+07	1.50E+07	1.50E+07
Q87L81	Glucose-6-phosphate isomerase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=pgi PE=3 SV=1	36.5	60.9	2.80E+07	3.80E+07	4.00E+07	3.40E+07	6.70E+07	5.10E+07
Q87L90	Sulfite reductase [NADPH] flavoprotein alpha-component OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=cysJ PE=3 SV=1	9.3	68.7	2.30E+06	4.00E+06	4.50E+06	7.60E+06	5.10E+06	4.80E+06
Q87L91	Sulfite reductase [NADPH] hemoprotein beta-component OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=cysI PE=3 SV=1	16.4	64.8	2.90E+06	4.90E+06	4.30E+06	7.60E+06	7.10E+06	8.00E+06
Q87L96	Aspartokinase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2715 PE=3 SV=1	26.0	48.8	6.80E+06	1.40E+07	1.00E+07	1.80E+07	1.70E+07	1.50E+07
Q87LA1	UTP--glucose-1-phosphate uridylyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2711 PE=3 SV=1	4.1	32.3				3.70E+06		3.60E+06
Q87LA3	Single-stranded DNA-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=ssb PE=3 SV=1	5.7	19.6	6.20E+06				1.20E+07	
Q87LB4	Putative V10 pilin OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2698 PE=4 SV=1	26.1	16.8			6.50E+06	6.70E+06	8.50E+06	7.40E+06
Q87LD6	PmbA protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2676 PE=4 SV=1	2.5	48.2						
Q87LF8	Aspartate carbamoyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=pyrB PE=3 SV=1	6.8	34.5			2.10E+06		3.00E+06	2.30E+06
Q87LF9	Ornithine carbamoyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=argF PE=3 SV=1	26.9	37.3	1.30E+07	1.80E+07	1.80E+07	2.40E+07	3.20E+07	2.20E+07
Q87LG6	Valine--tRNA ligase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=valS PE=3 SV=1	8.9	108.6	5.20E+06	7.20E+06	3.70E+06	6.90E+06	4.60E+06	4.20E+06
Q87LG8	Probable cytosol aminopeptidase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=pepA PE=3 SV=1	21.7	54.4	4.80E+06	1.00E+07	7.30E+06	1.10E+07	8.70E+06	1.10E+07
Q87LH4	Deacetylase DA1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2638 PE=4 SV=1	5.4	47.0	6.90E+06					
Q87LH6	Permease IIC component OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2636 PE=4 SV=1	5.6	48.7					1.10E+07	4.90E+06
Q87LH8	6-phospho-beta-glucosidase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2634 PE=3 SV=1	55.7	48.3				6.00E+06	1.10E+08	5.50E+07
Q87LH9	Carbohydrate deacetylase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2633 PE=3 SV=1	10.4	28.0					8.40E+06	
Q87LI0	Transcriptional regulator, LacI family OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2632 PE=4 SV=1	3.3	37.7					4.90E+06	
Q87LK1	Glutathione synthetase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=gshB PE=3 SV=1	12.7	35.2	4.10E+06		5.70E+06	6.70E+06	1.00E+07	9.00E+06
Q87LK6	S-adenosylmethionine synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=metK PE=3 SV=1	33.1	42.0	4.20E+06	1.00E+07	1.30E+07	1.10E+07	1.40E+07	1.30E+07
Q87LK8	Transketolase 1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=tkt1 PE=3 SV=1	31.8	72.0	1.30E+07	1.50E+07	1.40E+07	2.00E+07	2.50E+07	2.10E+07
Q87LL1	Phosphoglycerate kinase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=pgk PE=3 SV=1	53.9	40.7	2.20E+07	3.40E+07	4.00E+07	5.60E+07	6.90E+07	5.10E+07
Q87LL2	Fructose-bisphosphate aldolase, class II OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2599 PE=4 SV=1	67.9	38.9	5.10E+07	8.60E+07	8.30E+07	1.00E+08	1.20E+08	1.00E+08
Q87LL8	D-3-phosphoglycerate dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2593 PE=3 SV=1	46.1	44.7	1.60E+07	2.90E+07	2.80E+07	4.30E+07	4.80E+07	3.80E+07
Q87LL9	Ribose-5-phosphate isomerase A OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpiA PE=3 SV=1	5.5	23.2						3.00E+06
Q87LM8	tRNA-modifying protein YgfZ OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2583 PE=3 SV=1	7.1	35.5		2.60E+06		4.20E+06		1.30E+06
Q87LN1	L-aspartate oxidase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2580 PE=3 SV=1	11.9	60.9	2.10E+06	1.40E+06	2.00E+06	3.00E+06	8.80E+06	5.60E+06
Q87LN7	Elongation factor 4 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=lepA PE=3 SV=1	5.7	65.9	1.80E+06			1.70E+06		
Q87LP9	CTP synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=pyrG PE=3 SV=1	16.5	60.1	4.50E+06	3.70E+06	4.00E+06	8.70E+06	8.80E+06	1.10E+07
Q87LQ0	Enolase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=eno PE=3 SV=1	58.2	45.5	3.70E+07	6.40E+07	6.10E+07	8.40E+07	1.00E+08	8.80E+07
Q87LQ8	RNA polymerase sigma factor RpoS OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpoS PE=3 SV=1	27.0	36.5		6.70E+06	7.80E+06	1.10E+07	1.40E+07	1.60E+07
Q87LR1	Protein RecA OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=recA PE=3 SV=1	37.2	37.4	9.10E+06	1.30E+07	1.10E+07	1.00E+07	1.80E+07	1.20E+07
Q87LR3	Alanine--tRNA ligase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=alaS PE=3 SV=1	15.8	93.9	4.70E+06	6.80E+06	7.10E+06	9.50E+06	8.30E+06	9.30E+06
Q87LR5	Carbon storage regulator homolog OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=csrA PE=3 SV=1	18.5	7.1		5.00E+06	7.90E+06			
Q87LR7	Oxaloacetate decarboxylase, alpha subunit OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2544 PE=4 SV=1	3.5	64.2				4.50E+06		6.10E+06
Q87LS2	Glutamate--cysteine ligase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=gshA PE=3 SV=1	3.4	59.0				1.90E+06		2.00E+06
Q87LS7	Signal recognition particle protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=ffh PE=3 SV=1	3.0	50.2			2.80E+06	4.20E+06		
Q87LS8	30S ribosomal protein S16 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpsP PE=3 SV=1	28.0	9.1		7.70E+06	1.30E+07	1.50E+07		1.30E+07
Q87LT0	tRNA (guanine-N(1)-)-methyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=trmD PE=3 SV=1	8.5	27.8						2.20E+07
Q87LT1	50S ribosomal protein L19 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplS PE=3 SV=2	47.9	13.2	1.30E+07	1.30E+07	2.00E+07	1.70E+07	1.60E+07	1.70E+07
Q87LU2	Pyruvate dehydrogenase E1 component OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2519 PE=4 SV=1	47.5	99.6	4.30E+07	5.70E+07	6.50E+07	7.00E+07	1.10E+08	6.70E+07
Q87LU3	Acetyltransferase component of pyruvate dehydrogenase complex OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2518 PE=3 SV=1	33.8	64.9	2.20E+07	2.90E+07	3.40E+07	3.10E+07	3.30E+07	3.50E+07
Q87LW3	Aconitate hydratase B OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2495 PE=3 SV=1	39.2	94.0	2.40E+07	5.00E+07	2.30E+07	3.00E+07	3.20E+07	2.60E+07
Q87LW7	Iron(III) ABC transporter, periplasmic iron-compound-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2491 PE=4 SV=1	41.8	37.7	2.80E+07	5.00E+07	4.80E+07	5.50E+07	5.20E+07	5.40E+07
Q87LX0	Putative phosphoglucomutase/phosphomannomutase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2488 PE=4 SV=1	14.3	52.3						8.60E+06
Q87LX1	N,N'-diacetylchitobiose phosphorylase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2487 PE=4 SV=1	29.8	90.0				6.20E+06	9.40E+06	3.00E+07
Q87LX9	Peptide ABC transporter, periplasmic peptide-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2479 PE=4 SV=1	26.8	62.9				5.70E+06	3.50E+07	6.90E+07
Q87LZ1	Outer membrane protein U OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=ompU PE=3 SV=1	18.1	36.3	4.20E+06	6.90E+06	1.10E+07	1.30E+07	1.60E+07	1.30E+07
Q87LZ7	Phosphoglucosamine mutase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=glmM PE=3 SV=1	2.9	47.6				2.60E+06		
Q87M01	Transcription termination/antitermination protein NusA OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=nusA PE=3 SV=1	14.5	54.9	5.70E+06	9.10E+06	6.70E+06	9.10E+06	9.50E+06	8.50E+06
Q87M02	Translation initiation factor IF-2 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=infB PE=3 SV=1	20.8	99.3	1.20E+07	1.50E+07	1.60E+07	1.80E+07	1.60E+07	1.80E+07
Q87M06	Polyribonucleotide nucleotidyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=pnp PE=3 SV=1	39.9	76.7	1.40E+07	1.80E+07	1.90E+07	2.20E+07	2.20E+07	2.20E+07
Q87M22	Deoxyribose-phosphate aldolase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=deoC PE=3 SV=1	4.3	27.7	2.40E+06	5.70E+06	4.10E+06	5.60E+06		3.90E+06
Q87M25	Purine nucleoside phosphorylase DeoD-type 1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=deoD1 PE=3 SV=1	5.0	25.9					4.70E+06	2.00E+06
Q87M27	Phosphoserine phosphatase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2431 PE=4 SV=1	15.0	35.8	1.50E+06	2.90E+06	4.10E+06	4.30E+06	5.00E+06	5.10E+06
Q87M30	Elongation factor G 2 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=fusA2 PE=3 SV=1	51.7	76.3	5.20E+07	9.40E+07	8.50E+07	1.20E+08	1.20E+08	1.20E+08
Q87M78	2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-succinyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=dapD PE=3 SV=1	21.0	35.6	4.20E+06	7.80E+06	9.00E+06	1.00E+07	1.90E+07	1.50E+07
Q87MB7	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2339 PE=4 SV=1	8.1	27.5					1.30E+07	
Q87MC3	Proline--tRNA ligase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=proS PE=3 SV=1	23.3	63.2	5.10E+06	7.90E+06	5.90E+06	8.20E+06	1.10E+07	9.10E+06
Q87MD7	Methionine aminopeptidase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=map PE=3 SV=1	5.8	32.3				8.40E+06		
Q87MD8	30S ribosomal protein S2 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpsB PE=3 SV=1	43.4	26.8	8.80E+06	1.80E+07	2.00E+07	2.70E+07	1.60E+07	2.30E+07
Q87MD9	Elongation factor Ts OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=tsf PE=3 SV=1	63.7	29.8	2.60E+07	4.60E+07	4.60E+07	5.60E+07	6.80E+07	5.70E+07
Q87ME0	Uridylate kinase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=pyrH PE=3 SV=1	4.5	26.1						
Q87MH0	Phosphoribosylformylglycinamidine cyclo-ligase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=purM PE=3 SV=1	8.4	36.8				1.50E+06	7.90E+06	
Q87MI2	4-hydroxy-tetrahydrodipicolinate synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=dapA PE=3 SV=1	36.3	31.2	5.60E+06	1.40E+07	1.40E+07	1.40E+07	1.60E+07	1.50E+07
Q87MM9	Chorismate synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=aroC PE=3 SV=1	6.6	39.0		3.40E+06	2.80E+06	3.00E+06		4.50E+06
Q87MN7	3-oxoacyl-[acyl-carrier-protein] synthase I OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2194 PE=3 SV=1	25.3	42.6	6.10E+06	1.50E+08	8.80E+06	1.20E+08	1.40E+07	1.30E+07
Q87MN9	Aspartate-semialdehyde dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=asd PE=3 SV=1	8.0	37.2			5.60E+06			4.00E+06
Q87MP2	Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta 1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=accD1 PE=3 SV=1	5.2	34.0		4.30E+06	3.70E+06	5.10E+06	6.40E+06	6.70E+06
Q87MP6	Amidophosphoribosyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=purF PE=3 SV=1	11.5	56.0		6.40E+06	3.40E+06	6.00E+06	8.60E+06	4.10E+06
Q87MS4	Glyceraldehyde-3-phosphate dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2157 PE=3 SV=1	60.7	35.2	4.50E+07	8.40E+07	1.00E+08	1.30E+08	2.00E+08	1.60E+08
Q87MU6	Putative phage-related protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2135 PE=4 SV=1	1.9	81.4						
Q87MV7	Aspartate-semialdehyde dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=asd PE=3 SV=1	53.4	40.2	1.30E+07	2.60E+07	2.80E+07	3.10E+07	3.80E+07	3.50E+07
Q87MW0	Aldehyde-alcohol dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2121 PE=1 SV=1	39.8	97.1	2.80E+07	4.30E+07	4.30E+07	5.50E+07	4.50E+07	5.20E+07
Q87MY5	Oligopeptide ABC transporter, periplasmic oligopeptide-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2091 PE=4 SV=1	9.3	62.3	2.00E+06	6.60E+05	3.30E+06	1.30E+06	4.80E+06	5.60E+06
Q87MY9	Oligopeptide ABC transporter, ATP-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2087 PE=3 SV=1	6.5	36.9						
Q87MZ3	Phosphate acetyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2083 PE=3 SV=1	39.2	76.6	1.10E+07	1.50E+07	1.50E+07	1.60E+07	2.20E+07	1.90E+07
Q87MZ4	Acetate kinase 1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=ackA1 PE=3 SV=1	36.7	43.0	8.10E+06	1.40E+07	1.30E+07	1.70E+07	2.10E+07	1.70E+07
Q87MZ6	ABC transporter substrate-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2080 PE=4 SV=1	8.1	33.2	1.90E+06	4.50E+06	4.00E+06	3.00E+06		3.70E+06
Q87N07	Methionine--tRNA ligase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=metG PE=3 SV=2	8.9	77.9	5.30E+06	9.30E+06	7.40E+06	1.00E+07	1.00E+07	7.60E+06
Q87N21	Malonyl CoA-acyl carrier protein transacylase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2055 PE=3 SV=1	5.5	32.3	3.10E+06	6.20E+06	7.20E+06			1.20E+07
Q87N23	3-oxoacyl-[acyl-carrier-protein] synthase 2 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2052 PE=3 SV=1	7.0	43.4				5.30E+06	7.60E+05	5.80E+06
Q87N29	PTS system, glucose-specific IIBC component OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2046 PE=4 SV=1	5.3	49.4	3.40E+06	6.00E+06	9.00E+06	1.60E+07	4.20E+06	9.80E+06
Q87N36	Pyruvate kinase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2039 PE=3 SV=1	6.9	51.7		2.50E+06	3.30E+06		5.70E+06	4.60E+06
Q87N45	30S ribosomal protein S1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2030 PE=3 SV=1	53.6	60.9	5.30E+07	8.10E+07	9.80E+07	1.30E+08	1.10E+08	9.00E+07
Q87N50	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2025 PE=4 SV=1	8.0	76.6	3.30E+06	6.90E+06	4.80E+06	5.70E+06	7.00E+06	7.00E+06
Q87N83	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1992 PE=4 SV=1	19.1	37.6	3.20E+06	6.60E+06	5.70E+06	5.20E+06	1.50E+07	9.30E+06
Q87NA1	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=metE PE=3 SV=1	61.4	84.7	1.30E+08	1.60E+08	1.80E+08	2.20E+08	2.70E+08	2.50E+08
Q87NC0	Elongation factor P-like protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1948 PE=3 SV=1	4.3	20.7		4.70E+06				
Q87NC6	Diaminobutyrate-pyruvate transaminase & L-2,4-diaminobutyrate decarboxylase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1942 PE=1 SV=1	4.9	104.3	4.00E+06		5.40E+06	6.50E+06	4.50E+06	

Q87NC7	Putative carboxynorspermidine dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1941 PE=4 SV=1	2.2	46.5		5.20E+06				6.50E+06
Q87NC8	Carboxynorspermidine/carboxyspermidine decarboxylase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1940 PE=3 SV=1	1.9	42.0						8.60E+06
Q87ND1	CinA-like protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1937 PE=3 SV=1	2.7	45.3				4.40E+06		3.90E+06
Q87ND4	Ribonucleoside-diphosphate reductase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1934 PE=3 SV=1	8.3	85.6	4.10E+06	4.50E+06		4.30E+06	7.50E+06	
Q87ND6	DNA gyrase subunit A OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=gyrA PE=3 SV=1	17.4	97.0	1.10E+07	1.50E+07	1.10E+07	1.20E+07	9.70E+06	1.30E+07
Q87NE7	GTP cyclohydrolase-2 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=ribA PE=3 SV=1	5.6	22.3						
Q87NG8	Aspartate aminotransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1900 PE=3 SV=1	62.8	45.4	5.00E+07	8.30E+07	8.50E+07	1.10E+08	1.50E+08	1.10E+08
Q87NH5	Asparagine--tRNA ligase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=asnS PE=3 SV=1	45.1	52.6	3.00E+07	4.40E+07	3.80E+07	4.80E+07	5.90E+07	4.90E+07
Q87NU6	Succinate-semialdehyde dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1772 PE=3 SV=1	2.3	51.8						4.50E+05
Q87NW7	Homoserine O-succinyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=metA PE=3 SV=1	3.5	36.2						
Q87NZ4	Putative DNA polymerase III, epsilon subunit OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1724 PE=4 SV=1	6.0	28.0						
Q87P08	Glucose-6-phosphate 1-dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=zwf PE=3 SV=1	4.2	57.6		4.50E+06		5.40E+06	6.40E+06	4.70E+06
Q87P10	6-phosphogluconate dehydrogenase, decarboxylating OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1708 PE=3 SV=1	27.6	52.5	7.80E+06	1.50E+07	1.50E+07	1.70E+07	2.00E+07	1.60E+07
Q87P15	Aldehyde dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1703 PE=3 SV=1	8.1	55.7		6.50E+06		1.00E+07		4.30E+06
Q87P20	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1698 PE=4 SV=1	9.3	38.5		3.80E+06	5.20E+06	4.30E+06	6.30E+06	3.80E+06
Q87P32	Adenosine monophosphate-protein transferase VopS OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=vopS PE=1 SV=1	10.6	41.7			3.60E+06		5.00E+06	
Q87P42	Putative transcriptional regulator OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1676 PE=4 SV=1	7.2	34.5						
Q87P59	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1659 PE=4 SV=1	16.8	67.0	8.10E+06	1.10E+07	1.10E+07	7.00E+06	1.00E+07	7.30E+06
Q87P60	Low calcium response locus protein H OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1658 PE=4 SV=1	16.7	18.1		3.90E+06		2.10E+06	4.30E+06	
Q87P62	Putative translocator protein PopD OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1656 PE=4 SV=1	19.8	35.3	4.50E+06	6.70E+06	7.10E+06	4.20E+06		4.70E+06
Q87P63	Immunogenic protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1655 PE=4 SV=1	2.8	34.9	1.70E+07	3.90E+07		2.90E+07		3.90E+07
Q87PB0	RNA chaperone ProQ OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=proQ PE=3 SV=1	10.0	23.2			2.90E+06	2.80E+06		6.70E+06
Q87PB1	Tail-specific protease OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1606 PE=4 SV=1	1.2	75.6						2.70E+06
Q87PB3	Aminopeptidase N OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1604 PE=4 SV=1	4.1	98.4	5.00E+05	9.90E+05			2.70E+06	2.20E+06
Q87PB5	Putative NAD-glutamate dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1602 PE=4 SV=1	3.3	183.4	3.70E+06	7.70E+06	4.30E+06		4.50E+06	
Q87PC5	3-hydroxydecanoyl-[acyl-carrier-protein] dehydratase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=fabA PE=3 SV=1	15.1	19.0	7.40E+06	1.00E+07	8.50E+06	9.20E+06	1.20E+07	1.10E+07
Q87PE6	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1564 PE=4 SV=1	24.4	56.4	5.70E+06	9.50E+06	5.40E+06	1.10E+07	1.30E+07	1.10E+07
Q87PG6	Fumarate and nitrate reduction regulatory protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1536 PE=4 SV=1	4.4	27.8						
Q87PH6	Putrescine-binding periplasmic protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1526 PE=3 SV=1	12.4	39.7	3.20E+05		9.20E+06	1.70E+07		
Q87PK8	N-acetyl-D-glucosamine kinase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=nagK PE=3 SV=1	2.3	32.8					2.80E+06	
Q87PU8	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1403 PE=4 SV=1	11.4	55.5	6.90E+06		9.80E+06		1.10E+07	4.10E+06
Q87PV8	Putative ClpA/B-type protease OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1392 PE=3 SV=1	1.0	97.9			1.40E+06			
Q87PZ8	Putative glutathione S-transferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1352 PE=3 SV=1	9.5	25.2		5.90E+06				
Q87Q42	Putative oligopeptidase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1308 PE=4 SV=1	3.2	68.0			3.40E+05	1.60E+06		
Q87Q53	Phosphoribosylglycinamide formyltransferase 2 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=purT PE=3 SV=1	13.8	42.9					3.70E+06	2.60E+06
Q87Q59	Phenylalanine--tRNA ligase beta subunit OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=pheT PE=3 SV=1	11.1	87.0	5.70E+06	1.20E+09	9.30E+06	1.00E+09	1.10E+07	9.70E+06
Q87Q70	Threonine--tRNA ligase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=thrS PE=3 SV=1	13.9	73.7	4.80E+06	8.50E+06	8.20E+06	1.20E+07	1.20E+07	1.20E+07
Q87Q81	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1269 PE=4 SV=1	4.4	25.3					3.80E+06	
Q87Q87	Phosphoribosylaminoimidazole-succinocarboxamide synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=purC PE=3 SV=1	18.5	41.0	1.80E+06	4.20E+06	4.80E+06	4.70E+06	7.30E+06	5.60E+06
Q87Q92	NAD-dependent malic enzyme OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=maeA PE=3 SV=1	1.6	62.3					6.30E+06	
Q87Q99	Thioredoxin reductase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1251 PE=3 SV=1	7.8	34.5					2.10E+07	3.80E+06
Q87QA3	Phosphoserine aminotransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=serC PE=3 SV=1	33.5	40.2	8.60E+06	1.50E+07	1.40E+07	1.90E+07	2.30E+07	2.00E+07
Q87QB9	Putative reductase VP1231 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1231 PE=3 SV=1	34.3	43.9	1.30E+07	2.00E+07	1.60E+07	2.30E+07	3.00E+07	2.50E+07
Q87QG7	Cystathionine beta-lyase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1182 PE=3 SV=1	8.0	44.6	3.30E+06	6.00E+06	5.10E+06	5.60E+06	7.10E+06	6.80E+06
Q87QJ9	Cysteine--tRNA ligase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=cysS PE=3 SV=1	11.1	52.0	1.70E+06		2.70E+06	6.00E+06	6.40E+06	5.20E+06
Q87QK5	Histidine biosynthesis bifunctional protein HisIE OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=hisI PE=3 SV=1	7.1	23.2						2.20E+06
Q87QL0	Histidinol-phosphate aminotransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=hisC PE=3 SV=1	15.3	38.2	3.40E+06	6.00E+06	4.70E+06	9.30E+06	8.60E+06	5.70E+06
Q87QL1	Histidinol dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=hisD PE=3 SV=1	7.7	46.1	2.00E+06	4.20E+06	5.00E+06	6.00E+06	6.30E+06	7.60E+06
Q87QL2	ATP phosphoribosyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=hisG PE=3 SV=1	27.9	32.8	6.90E+05	4.70E+06	6.10E+06	8.20E+06	9.30E+06	8.50E+06
Q87QM1	Adenylosuccinate lyase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1128 PE=3 SV=1	29.8	51.4	3.90E+06	8.90E+06	1.30E+07	1.40E+07	2.10E+07	1.40E+07
Q87QP1	Serine--tRNA ligase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=serS PE=3 SV=1	38.4	48.8	8.90E+06	1.20E+07	1.30E+07	1.90E+07	2.10E+07	1.90E+07
Q87QP5	Leucine-responsive regulatory protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1104 PE=4 SV=1	31.1	18.8		7.10E+06	6.10E+06	8.70E+06	8.80E+06	
Q87QP6	Alanine dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1103 PE=3 SV=1	43.9	39.9	1.60E+07	3.70E+07	2.40E+07	3.70E+07	2.40E+07	2.30E+07
Q87QP8	Cys regulon transcriptional activator OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1101 PE=4 SV=1	3.7	36.1					2.50E+06	2.00E+06
Q87QS7	Putative helicase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1072 PE=4 SV=1	24.4	68.7	3.90E+06	6.80E+06	6.60E+06	7.60E+06	1.00E+07	9.70E+06
Q87QT9	Protein TolB OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=tolB PE=3 SV=1	9.3	49.8			4.60E+06	5.70E+06	7.10E+06	9.90E+06
Q87QV2	Aspartate--tRNA ligase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=aspS PE=3 SV=1	35.0	65.7	1.20E+07	2.00E+07	1.90E+07	2.50E+07	2.90E+07	2.50E+07
Q87QX6	Glucose-1-phosphate adenylyltransferase 1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=glgC1 PE=3 SV=1	52.6	45.5	1.70E+07	2.30E+07	2.50E+07	3.00E+07	3.10E+07	3.30E+07
Q87QX7	DNA topoisomerase 1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=topA PE=3 SV=1	1.7	98.0						2.20E+06
Q87QX9	3-phosphoshikimate 1-carboxyvinyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=aroA PE=3 SV=1	5.2	46.1		3.70E+06	3.40E+06	3.70E+06		4.00E+06
Q87QY4	ATP-dependent Clp protease, ATP-binding subunit ClpA OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1014 PE=3 SV=1	11.1	83.3	2.10E+06	4.10E+06	2.60E+06	3.50E+06	8.10E+06	4.50E+06
Q87QY7	Isocitrate dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1011 PE=4 SV=1	53.0	80.5	3.00E+07	4.60E+07	3.40E+07	3.90E+07	4.30E+07	3.90E+07
Q87QZ9	Amino acid ABC transporter, periplasmic amino acid-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0999 PE=3 SV=1	30.6	28.4	2.70E+06	8.30E+06	7.20E+06	7.10E+06	8.80E+06	1.00E+07
Q87R04	Formate acetyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0994 PE=4 SV=1	60.4	84.5	4.90E+07	5.30E+07	6.10E+07	8.10E+07	1.10E+08	9.70E+07
Q87R36	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0962 PE=4 SV=1	17.9	43.9	2.10E+06	4.40E+06	1.20E+07	8.00E+06	1.20E+07	9.90E+06
Q87R38	Uridine phosphorylase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0960 PE=3 SV=1	2.8	26.9						
Q87R78	DNA-binding protein HU-beta OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0920 PE=3 SV=1	28.9	9.4	1.10E+07	3.50E+07	3.90E+07	4.30E+07	2.50E+07	4.10E+07
Q87R80	ATP-dependent Clp protease proteolytic subunit OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=clpP PE=3 SV=1	9.0	22.0		1.40E+07	1.50E+07	1.10E+07	1.90E+07	1.80E+07
Q87R81	Trigger factor OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=tig PE=3 SV=1	47.2	48.2	1.40E+07	2.50E+07	2.70E+07	2.90E+07	2.60E+07	3.30E+07
Q87R87	C4-dicarboxylate-binding periplasmic protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0910 PE=4 SV=1	17.5	37.1	7.60E+06	4.40E+06	4.40E+06	1.20E+07	1.10E+07	1.10E+07
Q87RD3	Formyltetrahydrofolate deformylase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=purU PE=3 SV=1	3.2	31.6			6.80E+06			
Q87RD6	Arginine--tRNA ligase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=argS PE=3 SV=1	16.5	63.8	2.40E+06	7.10E+06	3.80E+06	7.90E+06	8.20E+06	7.40E+06
Q87RE4	Zinc ABC transporter, periplasmic zinc-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0853 PE=3 SV=1	19.5	32.1	2.40E+06	7.80E+06	5.10E+06	6.80E+06	8.00E+06	1.00E+07
Q87RE7	Succinyl-CoA ligase [ADP-forming] subunit alpha OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0850 PE=3 SV=1	34.5	30.0	1.20E+07	2.70E+07	1.60E+07	2.50E+07	2.70E+07	2.10E+07
Q87RE8	Succinyl-CoA ligase [ADP-forming] subunit beta OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=sucC PE=3 SV=1	50.8	41.5	3.20E+07	6.40E+07	4.40E+07	5.00E+07	5.80E+07	4.50E+07
Q87RE9	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0848 PE=3 SV=1	33.2	43.7	2.10E+07	3.70E+07	2.60E+07	3.60E+07	3.70E+07	3.20E+07
Q87RF0	2-oxoglutarate dehydrogenase, E1 component OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0847 PE=4 SV=1	19.0	106.0	1.20E+07	1.50E+07	1.30E+07	1.70E+07	1.30E+07	1.30E+07
Q87RF2	Succinate dehydrogenase flavoprotein subunit OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0845 PE=3 SV=1	13.6	64.2	4.90E+06	1.30E+07	7.20E+06	8.90E+06	1.10E+07	1.10E+07
Q87RF5	Citrate synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0842 PE=3 SV=1	41.5	48.2	3.40E+07	5.10E+07	4.70E+07	5.10E+07	6.50E+07	5.00E+07
Q87RF8	Phosphoglucomutase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0839 PE=3 SV=1	26.6	59.2	8.10E+06	1.30E+07	1.30E+07	1.60E+07	2.10E+07	1.80E+07
Q87RG4	Glutamine--tRNA ligase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=glnS PE=3 SV=1	11.2	63.9	4.40E+06	6.20E+06	8.10E+06	1.20E+07	1.20E+07	1.10E+07
Q87RG8	N-acetylglucosamine repressor OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0828 PE=4 SV=1	5.2	43.8		1.50E+06		2.00E+06	3.00E+06	1.70E+06
Q87RH0	Asparagine synthetase B, glutamine-hydrolyzing OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0826 PE=4 SV=1	22.9	62.3	5.10E+06	9.30E+06	7.60E+06	9.60E+06	1.20E+07	1.50E+07
Q87RH5	Chaperone protein HtpG OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=htpG PE=3 SV=1	21.1	72.1	4.50E+06	6.40E+06	8.00E+06	8.00E+06	1.20E+07	1.00E+07
Q87RJ7	Cysteine synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0797 PE=3 SV=1	72.7	34.1	4.40E+07	6.90E+07	7.60E+07	7.70E+07	9.10E+07	9.60E+07
Q87RK0	Phosphoenolpyruvate-protein phosphotransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0794 PE=3 SV=1	22.6	63.2	2.50E+06	9.50E+06	9.40E+06	1.10E+07	2.00E+06	1.60E+07
Q87RK1	PTS system, glucose-specific IIA component OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0793 PE=4 SV=1	22.5	17.9	2.20E+06	9.40E+06	8.20E+06	1.10E+07	1.30E+07	1.30E+07
Q87RL6	Glutamate--tRNA ligase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=gltX PE=3 SV=1	36.5	53.4	7.50E+06	1.10E+07	1.10E+07	1.10E+07	1.50E+07	1.30E+07
Q87RL8	Putative chitoporin OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0760 PE=4 SV=1	16.1	40.8						1.30E+07
Q87RM3	N,N'-diacetylchitobiase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0755 PE=4 SV=1	2.6	97.6						2.50E+06
Q87RN8	Ribose-phosphate pyrophosphokinase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=prs PE=3 SV=1	37.3	33.9	5.40E+06	9.30E+06	8.50E+06	1.30E+07	1.60E+07	1.20E+07
Q87RQ0	Leucine--tRNA ligase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=leuS PE=3 SV=1	20.7	96.6	1.00E+07	1.30E+07	1.20E+07	1.60E+07	1.20E+07	1.30E+07
Q87RR2	Serine hydroxymethyltransferase 1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=glyA1 PE=3 SV=1	50.0	45.5	3.10E+07	5.70E+07	5.20E+07	7.40E+07	1.00E+08	7.30E+07
Q87RS3	Lipoprotein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0704 PE=3 SV=1	3.7	29.1						3.50E+06
Q87RT8	Exodeoxyribonuclease 7 small subunit OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=xseB PE=3 SV=1	8.8	8.9		3.40E+06				
Q87RU4	6,7-dimethyl-8-ribityllumazine synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=ribH PE=3 SV=1	16.0	16.4			3.40E+06	3.10E+06	3.10E+06	2.60E+06

Q87RU5	3,4-dihydroxy-2-butanone 4-phosphate synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=ribB PE=3 SV=1	11.4	40.1	1.00E+06	3.10E+06	2.40E+06	3.30E+06	7.30E+06	3.80E+06
Q87RU9	Gamma-glutamyl phosphate reductase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=proA PE=3 SV=1	14.2	44.7	1.70E+06	5.10E+06	2.80E+06	5.60E+06	6.00E+06	5.70E+06
Q87RV5	Aminoacyl-histidine dipeptidase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0671 PE=4 SV=1	4.7	53.6			4.90E+06	5.30E+06	5.70E+06	4.10E+06
Q87RV7	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0669 PE=4 SV=1	26.4	39.0	3.60E+06	7.30E+06	9.00E+06	8.80E+06	1.30E+07	1.30E+07
Q87RW0	Phosphoribosylformylglycinamidine synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=purL PE=3 SV=1	20.0	141.6	6.30E+06	1.00E+07	1.30E+07	1.30E+07	1.70E+07	1.30E+07
Q87RX2	Chaperone protein DnaJ OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=dnaJ PE=3 SV=1	3.1	41.0		2.30E+06				
Q87RX3	Chaperone protein DnaK OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=dnaK PE=3 SV=1	57.0	69.0	1.30E+07	2.50E+07	2.30E+07	2.80E+07	3.20E+07	3.30E+07
Q87RZ5	Homocysteine synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0629 PE=3 SV=1	2.8	45.7				1.40E+06		3.10E+06
Q87S07	GMP synthase [glutamine-hydrolyzing] OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=guaA PE=3 SV=1	10.4	57.6	4.40E+06	8.60E+06	5.80E+06	1.30E+07	1.50E+07	1.10E+07
Q87S08	Inosine-5'-monophosphate dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=guaB PE=3 SV=1	32.2	51.9	6.60E+06	9.70E+06	8.60E+06	1.30E+07	1.60E+07	8.90E+06
Q87S12	GTPase Der OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=der PE=3 SV=1	1.6	55.8					2.60E+06	
Q87S15	Histidine--tRNA ligase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=hisS PE=3 SV=1	2.6	47.1						
Q87S21	Peptidase B OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=pepB PE=3 SV=1	10.2	46.6	2.40E+06	8.40E+06	3.60E+06	6.80E+06	9.30E+06	7.20E+06
Q87S28	Cysteine desulfurase IscS OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=iscS PE=3 SV=1	1.5	45.0						2.40E+06
Q87S44	Antioxidant, AhpC/Tsa family OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0580 PE=4 SV=1	43.3	22.2	1.40E+07	4.00E+07	3.70E+07	4.20E+07	4.90E+07	4.10E+07
Q87S63	Chaperone protein ClpB OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=clpB PE=3 SV=1	28.8	95.8	6.90E+06	8.60E+06	8.90E+06	1.40E+07	1.80E+07	1.30E+07
Q87S68	Putative sigma-54 modulation protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0556 PE=4 SV=1	8.3	12.4						5.90E+06
Q87S69	Chorismate mutase/prephenate dehydratase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0555 PE=4 SV=1	3.1	44.2						1.70E+06
Q87S73	ABC transporter, ATP-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0551 PE=3 SV=1	14.6	62.2	3.30E+06	5.80E+06	3.70E+06	5.10E+06	5.20E+06	5.80E+06
Q87S78	Phospho-2-dehydro-3-deoxyheptonate aldolase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0546 PE=3 SV=1	6.7	39.7		3.60E+06		9.10E+06		4.70E+06
Q87S90	Isoleucine--tRNA ligase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=ileS PE=3 SV=1	5.8	105.2	4.70E+06	4.30E+06	4.70E+06	8.20E+06	6.60E+06	5.30E+06
Q87SA8	Oxidoreductase Tas, aldo/keto reductase family OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0516 PE=4 SV=1	12.2	39.7		6.60E+06	4.10E+06	8.50E+06	9.10E+06	6.60E+06
Q87SB1	Lysine--tRNA ligase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=lysS PE=3 SV=1	34.9	57.5	2.70E+07	1.80E+07	3.70E+07	5.10E+07	5.70E+07	4.50E+07
Q87SC7	Autonomous glycyl radical cofactor OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=grcA PE=3 SV=1	38.4	13.9	5.90E+06	8.50E+06		1.40E+07	1.80E+07	1.10E+07
Q87SC8	Threonine synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0496 PE=4 SV=1	43.4	46.5	7.60E+06	9.40E+06	1.10E+07	1.50E+07	1.90E+07	1.60E+07
Q87SC9	Homoserine kinase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=thrB PE=3 SV=1	5.3	34.4					4.20E+06	
Q87SD0	Aspartokinase I/homoserine dehydrogenase, threonine-sensitive OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0494 PE=4 SV=1	32.2	88.4	1.60E+07	1.90E+07	1.70E+07	2.10E+07	2.50E+07	2.10E+07
Q87SD5	Aerobic respiration control protein FexA OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0489 PE=4 SV=1	4.6	26.9		5.70E+06	5.00E+06	5.30E+06		7.70E+06
Q87SE0	Glutamate synthase, large subunit OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0484 PE=4 SV=1	16.3	175.2	5.80E+06	7.40E+06	8.70E+06	1.40E+07	1.10E+07	1.20E+07
Q87SE1	Glutamate synthase, small subunit OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0483 PE=4 SV=1	10.4	53.3			1.10E+06	6.20E+06	4.40E+06	2.70E+06
Q87SE2	Glutamate synthase, large subunit OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0482 PE=4 SV=1	10.4	162.9	7.90E+06	6.00E+06	7.50E+06	8.50E+06	4.80E+06	4.80E+06
Q87SF3	Carbamoyl-phosphate synthase large chain OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=carB PE=3 SV=1	32.2	117.8	1.00E+07	1.40E+07	1.50E+07	1.90E+07	1.90E+07	1.80E+07
Q87SF4	Carbamoyl-phosphate synthase small chain OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=carA PE=3 SV=1	16.6	41.0	2.90E+06	6.30E+06	6.60E+06	7.60E+06	8.50E+06	6.70E+06
Q87SF5	4-hydroxy-tetrahydrodipicolinate reductase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=dapB PE=3 SV=1	8.6	28.6	4.90E+06	7.30E+06	6.20E+06	7.20E+06	1.10E+07	9.20E+06
Q87SF7	Protein translocase subunit SecA OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=secA PE=3 SV=1	8.7	103.1	2.50E+06	6.00E+06	4.50E+06	5.70E+06	2.00E+06	4.30E+06
Q87SG0	Cell division protein FtsZ OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=ftsZ PE=3 SV=1	22.5	42.5	7.90E+06	1.20E+07	1.10E+07	1.50E+07	1.80E+07	1.50E+07
Q87SH9	Stringent starvation protein A OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0444 PE=3 SV=1	30.8	24.3	5.80E+06	1.30E+07	1.40E+07	1.30E+07	5.50E+07	1.70E+07
Q87SI4	30S ribosomal protein S9 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpsI PE=3 SV=1	49.2	14.6	9.80E+06	2.10E+07	2.80E+07	3.20E+07	3.20E+07	3.10E+07
Q87SI5	50S ribosomal protein L13 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplM PE=3 SV=1	54.2	16.0	7.40E+06	7.30E+06	1.60E+07	2.40E+07	1.20E+07	2.90E+07
Q87SJ0	Protease DO OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0433 PE=4 SV=1	17.6	48.1	2.80E+06	9.00E+06	6.10E+06	1.20E+07	9.60E+06	1.20E+07
Q87SJ3	DNA topoisomerase 4 subunit B OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=parE PE=3 SV=1	1.9	69.5						6.50E+06
Q87SK0	Glutamate-ammonia-ligase adenylyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=glnE PE=3 SV=1	1.3	109.1	2.20E+06					
Q87SL8	RNA polymerase sigma factor RpoD OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpoD PE=3 SV=1	11.0	70.7	8.20E+06	1.00E+07	9.60E+06	1.30E+07	1.30E+07	1.40E+07
Q87SR3	Glutamine--fructose-6-phosphate aminotransferase [isomerizing] OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=glmS PE=3 SV=2	31.6	66.8	2.50E+06	1.00E+07	1.10E+07	1.80E+07	1.10E+07	2.00E+07
Q87SR6	Pyruvate kinase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0356 PE=3 SV=1	34.5	49.9	9.70E+06	1.20E+07	1.00E+07	2.20E+07	2.50E+07	2.50E+07
Q87SS0	Acetolactate synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0352 PE=3 SV=1	3.5	63.0	3.90E+06			5.90E+06		
Q87SS7	2-isopropylmalate synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=leuA PE=3 SV=1	22.3	56.1	3.40E+06	8.00E+06	3.00E+06	9.90E+06	9.00E+06	7.70E+06
Q87SS8	3-isopropylmalate dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=leuB PE=3 SV=1	39.1	39.3	5.30E+06	1.50E+07	1.30E+07	1.50E+07	1.80E+07	1.50E+07
Q87SS9	3-isopropylmalate dehydratase large subunit OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=leuC PE=3 SV=1	6.8	50.6				1.20E+07		2.00E+06
Q87SU3	50S ribosomal protein L27 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpmA PE=3 SV=1	42.4	9.2		5.80E+06	9.90E+06	1.00E+07	4.60E+06	1.30E+07
Q87SU4	50S ribosomal protein L21 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplU PE=3 SV=1	60.2	11.5	4.30E+06	1.20E+07	1.60E+07	1.90E+07	1.30E+07	1.80E+07
Q87SU7	Malate dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=mdh PE=3 SV=1	75.2	32.2	2.80E+07	5.80E+07	4.60E+07	5.80E+07	5.70E+07	4.80E+07
Q87SV0	Immunogenic protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0323 PE=4 SV=1	46.3	34.5	2.80E+07	5.00E+07	4.90E+07	4.70E+07	5.60E+07	5.60E+07
Q87SW0	Fructose-1,6-bisphosphatase class 1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=fbp PE=3 SV=1	29.0	37.3	6.50E+06	1.90E+07	1.20E+07	1.20E+07	1.40E+07	7.90E+06
Q87SX0	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0302 PE=4 SV=1	3.8	23.3	6.40E+06	1.20E+07		1.30E+07	1.80E+07	1.30E+07
Q87SX9	Sulfate adenylyltransferase subunit 1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=cysN PE=3 SV=1	27.1	52.6	6.50E+06	9.80E+06	9.30E+06	1.50E+07	1.70E+07	1.20E+07
Q87SY0	Sulfate adenylyltransferase subunit 2 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=cysD PE=3 SV=1	8.9	35.0				6.50E+06	7.10E+06	8.00E+06
Q87SY2	2',3'-cyclic-nucleotide 2'-phosphodiesterase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0290 PE=3 SV=1	4.9	72.1		3.10E+06		4.30E+06	1.20E+07	3.90E+06
Q87SY9	50S ribosomal protein L17 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplQ PE=3 SV=1	44.4	14.2		1.30E+07	1.60E+07	1.70E+07	2.00E+07	1.30E+07
Q87SZ0	DNA-directed RNA polymerase subunit alpha OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpoA PE=3 SV=1	33.6	36.5	1.00E+07	2.20E+07	2.20E+07	2.00E+07	2.90E+07	2.50E+07
Q87SZ1	30S ribosomal protein S4 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpsD PE=3 SV=1	50.0	23.3	1.80E+07	3.00E+07	3.50E+07	4.40E+07	4.20E+07	4.80E+07
Q87SZ2	30S ribosomal protein S13 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpsM PE=3 SV=1	56.8	13.3	7.30E+06	1.70E+07	2.60E+07	2.70E+07	2.30E+07	2.90E+07
Q87SZ4	50S ribosomal protein L15 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplO PE=3 SV=1	34.0	14.9	6.90E+06	8.30E+06	1.00E+07	2.00E+07	1.70E+07	1.50E+07
Q87SZ5	50S ribosomal protein L30 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpmD PE=3 SV=1	24.1	6.6						6.40E+06
Q87SZ6	30S ribosomal protein S5 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpsE PE=3 SV=1	69.5	17.6	9.30E+06	2.40E+07	3.40E+07	3.70E+07	3.60E+07	3.90E+07
Q87SZ7	50S ribosomal protein L18 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplR PE=3 SV=1	56.4	12.6	6.20E+06	1.20E+07	1.50E+07	1.30E+07	2.00E+07	2.30E+07
Q87SZ8	50S ribosomal protein L6 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplF PE=3 SV=1	72.3	18.8	6.70E+06	1.70E+07	2.20E+07	2.70E+07	1.90E+07	3.00E+07
Q87SZ9	30S ribosomal protein S8 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpsH PE=3 SV=1	23.8	14.0	7.20E+06	1.90E+07	2.70E+07	1.90E+07	2.40E+07	2.50E+07
Q87T00	30S ribosomal protein S14 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpsN PE=3 SV=1	6.9	11.4			6.10E+06	6.30E+06		9.00E+06
Q87T01	50S ribosomal protein L5 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplE PE=3 SV=1	76.0	20.1	1.20E+07	2.30E+07	3.10E+07	3.90E+07	4.10E+07	3.60E+07
Q87T02	50S ribosomal protein L24 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplX PE=3 SV=1	20.0	11.2	7.40E+06	5.00E+06	7.10E+06	1.90E+07		1.00E+07
Q87T03	50S ribosomal protein L14 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplN PE=3 SV=1	33.3	13.6	5.50E+06	1.10E+07	1.30E+07	1.60E+07	1.40E+07	1.80E+07
Q87T04	30S ribosomal protein S17 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpsQ PE=3 SV=1	16.7	9.6			3.30E+06	7.70E+06		4.40E+06
Q87T06	50S ribosomal protein L16 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplP PE=3 SV=1	40.4	15.5	6.70E+06	1.30E+07	1.60E+07	1.80E+07	1.50E+07	1.70E+07
Q87T07	30S ribosomal protein S3 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpsC PE=3 SV=1	47.8	25.6	1.10E+07	2.40E+07	3.30E+07	4.10E+07	4.70E+07	4.30E+07
Q87T08	50S ribosomal protein L22 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplV PE=3 SV=1	31.8	12.1		4.50E+06	6.70E+06	8.40E+06	6.50E+06	1.20E+07
Q87T09	30S ribosomal protein S19 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpsS PE=3 SV=1	8.7	10.4	5.10E+06	8.70E+06	1.20E+07	1.10E+07		1.70E+07
Q87T10	50S ribosomal protein L2 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplB PE=3 SV=1	24.8	29.9				9.20E+06	8.30E+06	4.80E+06
Q87T11	50S ribosomal protein L23 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplW PE=3 SV=1	22.0	11.1			1.10E+07			2.00E+07
Q87T12	50S ribosomal protein L4 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplD PE=3 SV=1	39.0	21.9	1.00E+07	2.20E+07	3.50E+07	4.00E+07	3.30E+07	4.00E+07
Q87T13	50S ribosomal protein L3 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplC PE=3 SV=1	53.1	22.4	9.40E+06	3.00E+07	3.50E+07	4.50E+07	4.50E+07	4.50E+07
Q87T21	ATP-dependent protease ATPase subunit HslU OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=hslU PE=3 SV=1	13.1	49.8		2.50E+06	4.60E+06	4.30E+06		8.80E+06
Q87T31	Triosephosphate isomerase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=tpiA PE=3 SV=1	16.4	26.9	7.30E+06	1.00E+07	1.30E+07	5.20E+06	1.60E+07	6.60E+06
Q87T34	Nucleotide sugar dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0236 PE=3 SV=1	30.2	43.1	4.60E+06	9.50E+06	8.90E+06	1.40E+07	1.60E+07	1.40E+07
Q87T36	Pilin glycosylation protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0234 PE=3 SV=1	40.2	43.4	1.30E+07	2.00E+07	1.90E+07	2.60E+07	3.30E+07	2.80E+07
Q87T38	Putative carbamoylphosphate synthase large subunit, short form OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0232 PE=4 SV=1	2.2	36.4						5.20E+06
Q87T41	dTDP-4-dehydrorhamnose 3,5-epimerase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0229 PE=4 SV=1	5.9	21.2		3.30E+06	3.10E+06		6.60E+06	3.90E+06
Q87T46	Putative dTDP-4-dehydrorhamnose reductase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0224 PE=4 SV=1	7.6	32.4			2.90E+06	4.10E+06	6.80E+06	6.20E+06
Q87T47	Glucose-1-phosphate thymidylyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0223 PE=3 SV=1	11.3	32.3		2.70E+06	3.50E+06		6.20E+06	3.60E+06
Q87T48	dTDP-glucose 4,6-dehydratase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0222 PE=3 SV=1	16.9	40.9		5.40E+06	9.80E+06	1.10E+07	1.20E+07	1.60E+07
Q87T56	ADP-L-glycero-D-manno-heptose-6-epimerase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=hldD PE=3 SV=1	7.3	35.2		3.40E+06		3.70E+06		
Q87T63	Putative oxidoreductase (Flagellin modification) OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0207 PE=4 SV=1	6.3	27.4					6.00E+06	
Q87T65	Putative glutamate-1-semialdehyde 2,1-aminomutase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0205 PE=3 SV=1	16.4	48.9	2.90E+06	4.40E+06	4.50E+06	6.40E+06	8.20E+06	7.00E+06
Q87T66	Putative 3-chlorobenzoate-3,4-dioxygenase dyhydrogenase related protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0204 PE=4 SV=1	8.7	38.5				7.00E+06	6.70E+06	9.60E+06
Q87T85	50S ribosomal protein L28 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpmB PE=3 SV=1	33.3	9.0	3.40E+06	1.20E+07	1.30E+07	1.30E+07	1.90E+07	1.30E+07
Q87T98	Putative binding protein component of ABC transporter OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0172 PE=4 SV=1	1.8	69.6		5.60E+06	4.20E+06	5.70E+06	7.30E+06	7.10E+06
Q87TA8	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0162 PE=4 SV=1	2.7	45.5						5.60E+06
Q87TA9	Guanylate kinase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=gmk PE=3 SV=1	6.8	23.4						
Q87TC0	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0150 PE=4 SV=1	1.3	85.1						6.60E+05
Q87TE1	Phosphoenolpyruvate carboxykinase [ATP] OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=pckA PE=3 SV=1	61.4	60.0	6.60E+07	8.80E+07	6.00E+07	1.30E+08	8.30E+07	9.70E+07

Q87TE8	Glutamine synthetase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0121 PE=3 SV=1	54.4	51.5	6.40E+07	9.20E+07	8.80E+07	1.30E+08	1.20E+08	1.20E+08
Q87TG2	DNA polymerase I OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0107 PE=3 SV=1	3.0	103.1	3.20E+06	2.10E+06	2.20E+06			
Q87TG5	Delta-aminolevulinic acid dehydratase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0104 PE=3 SV=1	12.2	39.2	3.40E+06	7.30E+06	7.40E+06	1.00E+07	1.00E+07	9.10E+06
Q87TJ9	Oligopeptidase A OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0070 PE=3 SV=1	20.3	76.9	9.60E+06	3.70E+07	3.90E+07	5.00E+07	6.70E+07	5.40E+07
Q87TK0	Ribosomal RNA large subunit methyltransferase J OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rlmJ PE=3 SV=1	7.2	32.2						
Q87TK1	Glutathione reductase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0068 PE=3 SV=1	13.2	49.2	6.30E+06	1.80E+07	9.60E+06	1.10E+07	3.00E+07	2.10E+07
Q87TM1	Peptide ABC transporter, periplasmic peptide-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0048 PE=4 SV=1	49.9	57.4	4.10E+07	7.40E+07	6.40E+07	7.80E+07	7.70E+07	7.30E+07
Q87TN4	Ketol-acid reductoisomerase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=ilvC PE=3 SV=1	51.0	54.7	3.20E+07	5.30E+07	4.60E+07	5.80E+07	9.00E+07	6.50E+07
Q87TP7	Glycine--tRNA ligase alpha subunit OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=glyQ PE=3 SV=1	8.5	34.9		5.10E+06	5.00E+06			5.20E+06
Q87TP8	Glycine--tRNA ligase beta subunit OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=glyS PE=3 SV=1	28.3	76.2	6.00E+06	9.20E+06	8.90E+06	1.10E+07	1.50E+07	1.10E+07
Q9ALY5	Cyclic AMP receptor protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2793 PE=4 SV=1	51.0	23.7	1.30E+07	2.60E+07	3.20E+07	3.60E+07	4.30E+07	3.20E+07
Q9L5X8	BipA OS=Vibrio parahaemolyticus GN=bipA PE=1 SV=1	21.2	66.9	5.80E+06	8.10E+06	4.80E+06	1.30E+07	1.10E+07	7.50E+06
Q9L7P5	60 kDa chaperonin 1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=groL1 PE=3 SV=2	44.6	57.5	1.80E+07	4.10E+07	4.20E+07	5.00E+07	6.70E+07	5.50E+07
1st Experiment (Insoluble Fraction)									
Accession	**Description**	**Coverage**	**MW [kDa]**	**Control**	**GlcNAc**	**GlcN**	**(GlcNAc)2**	**(GlcN)2**	**GlcNAc-GlcN**
O50286	Dihydrolipoyl dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=lpd PE=3 SV=2	4.84210526	50.956	1.00E+06	3.40E+06			2.40E+06	8.30E+05
P59494	Maltoporin OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=lamB PE=3 SV=1	30.5555556	46.933	5.00E+07	5.90E+07	3.90E+07		4.30E+07	3.50E+07
Q877T5	Elongation factor Tu OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=tufA PE=3 SV=1	4.06091371	43.125						3.70E+06
Q87FM2	Ferric siderophore receptor homolog OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1657 PE=3 SV=1	10.1769912	74.942	5.00E+06	8.10E+06	7.90E+06		4.40E+06	1.00E+07
Q87FM3	Ferric vibrioferrin receptor OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1656 PE=3 SV=1	5.05617978	78.834	2.50E+06	5.30E+06	3.40E+06		4.50E+06	4.80E+06
Q87G18	L-lactate dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=lldD PE=3 SV=1	9.2348285	41.373	5.60E+06		3.90E+06		2.20E+06	3.70E+06
Q87GK7	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1308 PE=4 SV=1	17.3684211	42.312	7.60E+06	1.40E+07	1.20E+07		7.60E+06	1.30E+07
Q87GW2	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1203 PE=4 SV=1	12.173913	13.13						2.60E+06
Q87HI4	Ferric aerobactin receptor OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0979 PE=3 SV=1	1.65517241	79.175		2.60E+06				
Q87HP1	NAD(P) transhydrogenase subunit alpha OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0922 PE=3 SV=1	4.44015444	54.772		2.70E+06				3.30E+06
Q87HS4	Heme transport protein HutA OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0882 PE=3 SV=1	2.88600289	77.294	5.20E+06	6.30E+06	4.40E+06		6.90E+06	5.20E+06
Q87JD5	Putative outer membrane protein OmpV OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0318 PE=4 SV=1	4.65116279	28.131	3.70E+06	3.80E+06	2.10E+06			4.70E+06
Q87JT2	Putative outer membrane protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0166 PE=4 SV=1	11.4613181	37.95	1.80E+07	1.50E+07	1.20E+07		1.70E+07	1.50E+07
Q87K02	Outer membrane protein OmpW OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0096 PE=4 SV=1	6.54205607	23.453		3.40E+06	1.90E+06		2.50E+06	3.10E+06
Q87K33	Putative LysR-family transcriptional regulatory protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0065 PE=4 SV=1	3.38983051	33.123						
Q87KA6	ATP synthase subunit alpha OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=atpA PE=3 SV=1	6.50095602	56.601	1.80E+06					2.90E+06
Q87KA8	ATP synthase subunit beta OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=atpD PE=3 SV=1	3.21199143	50.664		1.70E+06				
Q87KQ1	50S ribosomal protein L1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplA PE=3 SV=1	10.7296137	24.676	1.80E+06	2.60E+06				
Q87L75	50S ribosomal protein L9 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplI PE=3 SV=1	7.33333333	15.699	1.40E+06					2.80E+06
Q87LB4	Putative V10 pilin OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2698 PE=4 SV=1	25.4545455	16.796	1.10E+07	1.20E+07			3.80E+06	1.10E+07
Q87LH6	Permease IIC component OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2636 PE=4 SV=1	4.25055928	48.725					1.20E+07	8.90E+06
Q87LR7	Oxaloacetate decarboxylase, alpha subunit OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2544 PE=4 SV=1	5.37815126	64.235					3.70E+06	
Q87LU2	Pyruvate dehydrogenase E1 component OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2519 PE=4 SV=1	1.24013529	99.601		2.60E+06	1.70E+06		2.90E+06	1.90E+06
Q87LU3	Acetyltransferase component of pyruvate dehydrogenase complex OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2518 PE=3 SV=1	1.75438596	64.93		3.50E+06			3.10E+06	
Q87LZ1	Outer membrane protein U OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=ompU PE=3 SV=1	13.0563798	36.263	1.50E+07	1.30E+07	1.40E+07		1.00E+07	1.20E+07
Q87LZ5	ATP-dependent zinc metalloprotease FtsH OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=ftsH PE=3 SV=1	1.66163142	72.936		3.00E+06				
Q87MY5	Oligopeptide ABC transporter, periplasmic oligopeptide-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2091 PE=4 SV=1	8.07899461	62.342	2.00E+06	3.80E+06	2.90E+06		6.20E+06	4.00E+06
Q87N29	PTS system, glucose-specific IIBC component OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2046 PE=4 SV=1	5.25210084	49.407	1.00E+07	1.10E+07	6.80E+06		5.00E+06	7.90E+06
Q87N45	30S ribosomal protein S1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2030 PE=3 SV=1	5.57553957	60.905		2.60E+06				
Q87QT8	Peptidoglycan-associated lipoprotein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1061 PE=3 SV=1	6.89655172	18.701					3.30E+06	5.70E+06
Q87R04	Formate acetyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0994 PE=4 SV=1	1.71503958	84.466		5.80E+05				
Q87R36	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0962 PE=4 SV=1	3.10880829	43.935	1.40E+07				2.70E+07	1.20E+07
Q87RE9	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0848 PE=3 SV=1	9.72568579	43.675	2.60E+06	2.40E+06	1.70E+06		2.10E+06	2.90E+06
Q87RG5	PTS system, N-acetylglucosamine-specific IIABC component OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0831 PE=4 SV=1	3.25047801	54.543		3.00E+06	3.40E+06		5.30E+06	
Q87RL8	Putative chitoporin OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0760 PE=4 SV=1	9.91957105	40.764						1.50E+07
Q87RS3	Lipoprotein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0704 PE=3 SV=1	14.4981413	29.052	5.20E+06	4.00E+06	4.20E+06		4.30E+06	8.90E+06
Q87S84	Putative carbon starvation protein A OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0540 PE=4 SV=1	4.8582996	53.283	3.30E+06					3.00E+06
Q87SZ1	30S ribosomal protein S4 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpsD PE=3 SV=1	4.36893204	23.319						2.40E+06
Q87SZ8	50S ribosomal protein L6 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplF PE=3 SV=1	12.9943503	18.767	1.70E+06	2.20E+06			1.90E+06	1.60E+06
Q87T01	50S ribosomal protein L5 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplE PE=3 SV=1	4.46927374	20.118						1.80E+06
Q87T07	30S ribosomal protein S3 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpsC PE=3 SV=1	6.03448276	25.565						1.50E+06
Q87T13	50S ribosomal protein L3 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplC PE=3 SV=1	4.784689	22.36		3.70E+06			2.50E+06	
Q87TA4	Putative TolR OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0166 PE=3 SV=1	2.20750552	49.324		1.60E+06				
Q87TE8	Glutamine synthetase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0121 PE=3 SV=1	3.41151386	51.451		4.50E+06			2.10E+06	3.00E+06
Q87TM2	Peptide ABC transporter, ATP-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0047 PE=3 SV=1	2.45183888	63.65		6.60E+05			7.10E+05	
Q9L7P5	60 kDa chaperonin 1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=groL1 PE=3 SV=2	3.10786106	57.537					7.80E+05	
2nd Experiment (Supernatant Fraction)									
Accession	**Description**	**Coverage**	**MW [kDa]**	**Control**	**GlcNAc**	**GlcN**	**(GlcNAc)2**	**(GlcN)2**	**GlcNAc-GlcN**
A7UEM1	Transhydrogenase alpha subunit (Fragment) OS=Vibrio parahaemolyticus GN=pntA PE=4 SV=1	32.2	15.5	5.90E+06	1.10E+07	9.90E+06	6.40E+06	9.60E+06	1.10E+07
A7UEQ6	Dihydro-orotase (Fragment) OS=Vibrio parahaemolyticus GN=pyrC PE=3 SV=1	9.8	17.8	3.80E+06	6.40E+06			7.90E+06	8.70E+06
A7UET7	Protein RecA (Fragment) OS=Vibrio parahaemolyticus GN=recA PE=3 SV=1	4.5	26.0		1.70E+06	2.30E+06	9.60E+05		
A9Q6J2	Protein RecA (Fragment) OS=Vibrio parahaemolyticus GN=recA PE=3 SV=1	5.2	22.4		1.70E+06	2.30E+06	9.60E+05		
H6BAH9	Thermolabile hemolysin (Fragment) OS=Vibrio parahaemolyticus GN=tl PE=4 SV=1	10.8	13.6	4.80E+07					
O50286	Dihydrolipoyl dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=lpd PE=3 SV=2	57.5	51.0	4.10E+07	4.40E+07	3.60E+07	2.20E+07	4.90E+07	4.90E+07
O87081	Polar flagellin F OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=flaF PE=3 SV=2	5.6	40.5	4.70E+07	8.40E+07	7.70E+07	7.60E+07	7.20E+07	1.10E+08
P0A2W2	Acyl carrier protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=acpP PE=3 SV=2	18.2	8.5	2.40E+07	2.40E+07	2.40E+07			
P0A308	ATP synthase subunit c OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=atpE PE=3 SV=1	21.4	8.6	7.30E+07	3.60E+07	3.60E+07	4.60E+07	5.60E+07	5.40E+07
P0A481	50S ribosomal protein L20 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplT PE=3 SV=1	23.1	13.4	1.70E+07	1.20E+07	1.60E+07	8.70E+06	1.40E+07	2.10E+07
P19249	Thermostable direct hemolysin 1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=tdh1 PE=1 SV=2	24.3	21.3	8.70E+06	1.30E+07	1.80E+07	1.40E+07	1.50E+07	2.60E+07
P19250	Thermostable direct hemolysin 2 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=tdh2 PE=1 SV=2	41.3	21.5	6.40E+07	6.10E+07	8.10E+07	3.90E+07	7.40E+07	9.90E+07
P22099	Anthranilate synthase component 1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=trpE PE=3 SV=2	3.9	59.7	2.80E+06		4.20E+06		3.60E+06	3.50E+06
P22848	5'-nucleotidase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=nutA PE=3 SV=2	2.1	62.1	1.50E+07	1.50E+07	1.20E+07	1.10E+07	1.30E+07	2.00E+07
P40605	Protein HflK OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=hflK PE=3 SV=1	4.0	44.2	2.70E+06					
P59494	Maltoporin OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=lamB PE=3 SV=1	70.6	46.9	9.50E+08	8.40E+08	7.50E+08	5.60E+08	7.90E+08	6.70E+08
P59562	UPF0234 protein VP1617 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1617 PE=3 SV=1	5.6	18.1		2.60E+06	4.30E+06		5.60E+06	5.20E+06
P59570	Outer membrane protein OmpK OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=ompK PE=3 SV=1	25.6	29.9	6.70E+07	7.60E+07	5.90E+07	5.70E+07	6.10E+07	5.80E+07
P59605	Argininosuccinate synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=argG PE=3 SV=1	32.9	44.5	3.50E+07	2.50E+07	3.70E+07	2.00E+07	3.70E+07	4.40E+07
P66346	30S ribosomal protein S10 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpsJ PE=3 SV=1	23.3	11.7		9.90E+06	1.10E+07			
P66478	30S ribosomal protein S18 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpsR PE=3 SV=1	26.7	8.8	1.30E+07	1.50E+07	1.40E+07	7.30E+06	1.20E+07	1.00E+07
Q56702	Polar flagellin B/D OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=flaB PE=3 SV=2	81.2	40.1	4.00E+07	9.00E+07	7.60E+07	8.50E+07	6.90E+07	1.10E+08
Q56703	Polar flagellin A OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=flaA PE=3 SV=1	56.9	39.8	3.00E+07	8.00E+07	6.20E+07	8.00E+07	6.10E+07	6.40E+07
Q56712	Polar flagellin C OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=flaC PE=3 SV=2	54.4	40.8	4.40E+07	7.70E+07	6.70E+07	6.80E+07	7.00E+07	9.80E+07
Q79YX1	Chemotaxis protein CheY OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2231 PE=4 SV=1	8.7	14.3			5.30E+06			7.60E+06
Q79YX4	Chemotaxis protein CheW OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2225 PE=4 SV=1	20.7	18.4	5.70E+06	6.70E+06	1.20E+07	1.00E+07	9.00E+06	9.10E+06
Q79YY5	Hook-associated protein type 3 FlgL OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0786 PE=4 SV=1	11.6	45.0	8.90E+06	6.60E+06	1.50E+07	6.60E+06	1.70E+07	1.40E+07
Q79YY8	Polar flagellar FlgE OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0778 PE=4 SV=1	35.5	47.3	4.20E+07	6.50E+07	4.60E+07	4.40E+07	4.60E+07	6.20E+07
Q877T5	Elongation factor Tu OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=tufA PE=3 SV=1	53.3	43.1	1.10E+08	1.10E+08	1.30E+08	6.90E+07	1.30E+08	1.30E+08
Q87FL2	PTS system, glucose-specific IIBC component OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1667 PE=4 SV=1	5.2	51.1			1.00E+07			
Q87FL7	Putative diaminopimelate decarboxylase protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1662 PE=3 SV=1	12.8	45.3	8.70E+06	5.50E+06	1.10E+07	3.10E+06	2.50E+06	8.30E+06
Q87FM0	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1659 PE=4 SV=1	53.0	68.7	6.60E+07	5.50E+07	9.40E+07	4.80E+07	1.00E+08	1.00E+08
Q87FM1	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1658 PE=4 SV=1	15.6	44.2	1.60E+07	1.50E+07	1.70E+07	5.60E+06	1.30E+07	1.40E+07
Q87FM2	Ferric siderophore receptor homolog OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1657 PE=3 SV=1	58.4	74.9	1.90E+08	2.10E+08	1.90E+08	1.40E+08	1.80E+08	1.70E+08
Q87FM3	Ferric vibrioferrin receptor OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1656 PE=3 SV=1	44.4	78.8	1.40E+08	1.70E+08	1.50E+08	1.10E+08	1.60E+08	1.30E+08
Q87FM9	Putative zinc protease, insulinase family OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1650 PE=3 SV=1	5.2	102.2	1.20E+07		4.60E+06	4.20E+06	3.40E+06	
Q87FN1	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1648 PE=4 SV=1	2.8	62.7		5.10E+06		3.40E+06	5.00E+06	3.50E+06
Q87FN5	Putative maltose operon periplasmic protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1643 PE=4 SV=1	45.7	29.1	3.00E+07	2.80E+07	2.30E+07	1.80E+07	2.90E+07	2.50E+07
Q87FN6	Putative CymC protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1642 PE=4 SV=1	19.0	18.6	1.60E+07	9.80E+06	9.10E+06	7.00E+06	1.80E+07	1.10E+07
Q87FN7	Putative maltogenic amylase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1641 PE=4 SV=1	5.8	58.6	4.20E+06		5.40E+06			
Q87FP0	Putative pullulanase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1638 PE=4 SV=1	43.5	144.5	5.90E+07	5.20E+07	3.20E+07	4.00E+07	4.30E+07	3.40E+07
Q87FQ8	Alpha-1,4 glucan phosphorylase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1620 PE=3 SV=1	25.7	92.3	1.60E+07	1.40E+07	2.60E+07	1.20E+07	3.90E+07	2.90E+07

Q87FQ9	4-alpha-glucanotransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1619 PE=3 SV=1	28.2	81.8	2.10E+07	1.70E+07	2.30E+07	1.00E+07	2.90E+07	2.50E+07
Q87FT0	GlcNAc-binding protein A OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=gbpA PE=3 SV=1	61.0	53.6	1.50E+08	1.70E+08	2.30E+08	1.50E+08	2.50E+08	3.00E+08
Q87G07	ScrA (Aminotransferase) OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1513 PE=3 SV=1	45.3	52.8	1.30E+08	1.70E+08	1.10E+08	1.30E+08	1.80E+08	1.90E+08
Q87G09	2-amino-3-ketobutyrate coenzyme A ligase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=kbl PE=3 SV=1	2.8	43.1		3.90E+06	4.30E+06			
Q87G18	L-lactate dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=lldD PE=3 SV=1	19.8	41.4	1.70E+07	1.40E+07	1.30E+07	4.20E+06	9.20E+06	7.50E+06
Q87G21	Prolyl endopeptidase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1496 PE=4 SV=1	23.0	76.0	1.20E+07	1.50E+07	1.10E+07	9.20E+06	1.10E+07	1.70E+07
Q87G30	Putative acetyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1487 PE=4 SV=1	7.2	18.5		1.80E+06				
Q87G42	Purine nucleoside phosphorylase DeoD-type 2 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=deoD2 PE=3 SV=1	21.6	25.7	2.60E+07	2.50E+07	2.10E+07	1.60E+07	2.20E+07	2.70E+07
Q87G48	Outer membrane lipoprotein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1469 PE=4 SV=1	57.1	8.7	3.40E+07	4.80E+07	3.20E+07	2.30E+07	3.60E+07	3.10E+07
Q87G50	Protease II OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1467 PE=4 SV=1	22.2	75.1	8.30E+06	6.60E+06	1.50E+07	9.90E+06	1.50E+07	4.10E+07
Q87G52	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1465 PE=4 SV=1	25.9	84.5	1.30E+07	1.50E+07	1.80E+07	1.80E+07	2.20E+07	2.50E+07
Q87G53	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1464 PE=4 SV=1	5.0	52.2						2.70E+06
Q87G54	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1463 PE=4 SV=1	18.6	20.8					1.30E+07	1.10E+07
Q87G82	Putative iron(III) compound receptor OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1435 PE=3 SV=1	2.3	77.0	2.90E+06	4.50E+06				
Q87G89	Azurin OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1428 PE=4 SV=1	66.7	15.8	1.40E+08	1.60E+08	1.20E+08	1.10E+08	9.60E+07	1.20E+08
Q87GB6	Maltose ABC transporter, periplasmic maltose-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1401 PE=4 SV=1	76.0	42.1	3.70E+08	3.00E+08	3.00E+08	2.20E+08	3.40E+08	3.50E+08
Q87GC0	Acyl-CoA thioester hydrolase-related protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1397 PE=4 SV=1	8.1	17.7	7.00E+06		1.10E+07			
Q87GE0	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1376 PE=4 SV=1	1.8	165.8	5.20E+06	2.50E+06			4.10E+06	5.70E+06
Q87GK7	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1308 PE=4 SV=1	29.5	42.3	6.60E+07	6.00E+07	5.20E+07	3.70E+07	5.80E+07	5.00E+07
Q87GL7	Putative glutathione S-transferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1298 PE=4 SV=1	2.5	32.2						
Q87GN7	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1278 PE=4 SV=1	5.4	13.0	1.30E+07	1.30E+07	8.20E+06	8.30E+06		
Q87GS2	Putative cytosine deaminase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1243 PE=4 SV=1	2.6	48.0		2.90E+06		1.80E+06		
Q87GW1	Acetyl-CoA acetyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1204 PE=3 SV=1	21.4	41.5	1.10E+07	8.00E+06	1.10E+07	5.10E+06	8.80E+06	7.40E+06
Q87GW2	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1203 PE=4 SV=1	25.2	13.1	8.20E+06	3.70E+06	3.20E+06			
Q87GW6	Periplasmic nitrate reductase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=napA PE=3 SV=1	1.7	92.9			3.50E+06			
Q87GX9	Outer membrane protein OmpA OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1186 PE=3 SV=1	23.7	36.0	4.70E+07	4.40E+07	4.50E+07	3.00E+07	7.30E+06	8.00E+06
Q87GY0	Phospho-2-dehydro-3-deoxyheptonate aldolase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1185 PE=3 SV=1	2.0	38.3	9.30E+07	5.50E+07				
Q87GY4	Transketolase 2 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=tkt2 PE=3 SV=1	5.7	72.0	1.70E+07	1.30E+07	1.10E+07		7.60E+06	1.30E+07
Q87GY5	Transaldolase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=tal PE=3 SV=1	69.3	34.8	4.80E+07	4.40E+07	5.70E+07	4.10E+07	6.80E+07	7.20E+07
Q87GY8	Putative chitinase A OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1177 PE=3 SV=1	4.7	47.9					5.30E+06	7.00E+06
Q87H02	Oxidoreductase, aldo/keto reductase 2 family OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1163 PE=4 SV=1	9.9	34.0	8.40E+06	8.10E+06	7.50E+06	4.80E+06	1.00E+07	8.90E+06
Q87H16	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1149 PE=4 SV=1	2.7	45.3		3.50E+06	2.20E+06			
Q87HF0	Putative succinate dehydrogenase subunit Sdh OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1015 PE=4 SV=1	3.6	36.2	4.30E+06	3.20E+06				
Q87HF4	L-allo-threonine aldolase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1011 PE=4 SV=1	29.6	36.1	2.10E+07	2.00E+07	2.00E+07	2.00E+07	3.40E+07	3.30E+07
Q87HG0	D-lactate dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1005 PE=4 SV=1	9.9	64.3	9.90E+06	6.20E+06	6.40E+06	3.90E+06	6.30E+06	
Q87HG6	Alpha-amylase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0999 PE=4 SV=1	36.1	58.4	5.20E+07	5.40E+07	2.90E+07	7.20E+07	4.30E+07	6.50E+07
Q87HI4	Ferric aerobactin receptor OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0979 PE=3 SV=1	40.1	79.2	6.80E+07	6.80E+07	6.80E+07	4.60E+07	7.20E+07	6.00E+07
Q87HL0	Putative biofilm-associated surface protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0953 PE=4 SV=1	0.4	247.1	1.40E+07	1.40E+07	1.30E+07	1.00E+07	1.10E+07	1.10E+07
Q87HM1	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0942 PE=4 SV=1	4.8	33.0		3.90E+06			5.00E+06	5.10E+06
Q87HM7	Amino acid biosynthesis aminotransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0936 PE=4 SV=1	32.9	43.7	2.10E+07	1.60E+07	1.70E+07	1.20E+07	2.20E+07	2.30E+07
Q87HM8	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0935 PE=4 SV=1	18.1	25.7	3.10E+06	4.60E+06	2.60E+06	2.70E+06	3.10E+06	3.30E+06
Q87HM9	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0934 PE=4 SV=1	3.9	22.6	6.10E+06	7.80E+06				5.50E+06
Q87HP1	NAD(P) transhydrogenase subunit alpha OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0922 PE=3 SV=1	30.7	54.8	1.80E+07	2.50E+07	2.10E+07	1.50E+07	1.10E+07	1.90E+07
Q87HP2	NAD(P) transhydrogenase subunit beta OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0921 PE=3 SV=1	12.7	48.6	1.80E+07	1.90E+07	1.30E+07	1.10E+07	1.20E+07	2.00E+07
Q87HS4	Heme transport protein HutA OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0882 PE=3 SV=1	72.0	77.3	1.50E+08	1.60E+08	1.50E+08	1.10E+08	1.40E+08	1.20E+08
Q87HV6	UPF0312 protein VPA0850 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0850 PE=3 SV=1	34.9	20.3	5.30E+07	4.90E+07	4.40E+07	3.30E+07	3.30E+07	4.70E+07
Q87HX4	Chitodextrinase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0832 PE=4 SV=1	51.6	111.8	3.70E+06	6.80E+06	6.80E+07	2.60E+07	3.50E+08	5.10E+08
Q87HY6	Amino acid ABC transporter, periplasmic amino acid-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0820 PE=4 SV=1	6.2	30.6			5.70E+06	8.60E+06	1.60E+07	1.30E+07
Q87HZ6	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0810 PE=4 SV=1	24.6	21.1	6.80E+06	1.10E+07		8.00E+06	8.20E+06	3.30E+06
Q87I01	Aminomethyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0805 PE=3 SV=1	11.6	40.3	1.10E+07	8.40E+06	1.10E+07	6.20E+06	1.20E+07	7.30E+06
Q87I05	Glycine dehydrogenase (decarboxylating) OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=gcvP PE=3 SV=1	6.2	104.1	9.30E+06	1.20E+07			1.30E+07	1.10E+07
Q87I11	Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta 2 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=accD2 PE=3 SV=1	2.4	32.1		8.60E+06	6.60E+06	4.40E+06	5.80E+06	6.50E+06
Q87ID3	Methylglyoxal synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=mgsA PE=3 SV=1	15.2	17.0	8.50E+06	7.30E+06	1.40E+07		9.70E+06	
Q87IE2	Putaive Fe-regulated protein B OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0664 PE=3 SV=1	30.1	74.2	2.10E+07	2.40E+07	2.10E+07	1.80E+07	2.20E+07	2.20E+07
Q87IE9	Iron(III) ABC transporter, periplasmic iron-compound-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0657 PE=4 SV=1	53.6	33.5	3.60E+07	3.80E+07	4.80E+07	3.40E+07	3.90E+07	5.60E+07
Q87IG9	Arginine ABC transporter, periplasmic arginine-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0637 PE=3 SV=1	44.9	27.3	4.00E+07	4.00E+07	4.40E+07	2.70E+07	3.00E+07	4.30E+07
Q87IJ5	Acetate kinase 2 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=ackA2 PE=3 SV=1	31.2	42.6	3.40E+07	3.50E+07	3.60E+07	2.20E+07	4.30E+07	4.50E+07
Q87IP0	Alcohol dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0566 PE=4 SV=1	5.5	40.2	4.80E+06	2.80E+06				
Q87IP4	Putative chemotaxis transducer OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0562 PE=4 SV=1	3.4	73.9				7.60E+05		
Q87IQ4	Cold shock DNA-binding domain protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0552 PE=4 SV=1	26.1	7.5	7.40E+06	8.60E+06				
Q87IS1	Putative phosphomannomutase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0535 PE=3 SV=1	47.2	61.6	3.30E+07	3.50E+07	4.10E+07	2.80E+07	4.70E+07	4.70E+07
Q87IS9	Outer membrane protein N, non-specific porin OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0527 PE=4 SV=1	4.3	37.8		4.50E+06				
Q87IX8	Putative oxidoreductase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0478 PE=4 SV=1	4.7	51.0						
Q87IY2	Spermidine n1-acetyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0474 PE=4 SV=1	6.8	21.1						3.00E+06
Q87IY8	Prolyl endopeptidase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0468 PE=4 SV=1	6.1	84.2	2.60E+06	1.50E+06	3.90E+06		4.70E+06	3.90E+06
Q87J24	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0429 PE=4 SV=1	6.8	20.2	4.90E+06	6.20E+06	7.30E+06	3.30E+06	7.00E+06	1.00E+07
Q87J25	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0428 PE=4 SV=1	6.4	19.1						9.60E+06
Q87J30	Hemin ABC transporter, periplasmic hemin-binding protein HutB OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0423 PE=4 SV=1	10.0	30.3					2.40E+06	3.60E+06
Q87J46	Dihydroorotase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=pyrC PE=3 SV=1	4.7	37.8	3.80E+06	6.40E+06			7.90E+06	8.70E+06
Q87J78	Adenylosuccinate synthetase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=purA PE=3 SV=1	1.9	45.6				5.10E+06		1.00E+07
Q87J81	Phosphoenolpyruvate synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0372 PE=3 SV=1	48.3	88.1	6.50E+07	5.70E+07	5.40E+07	2.80E+07	6.40E+07	4.40E+07
Q87J86	Putrescine-binding periplasmic protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0367 PE=3 SV=1	50.3	38.7	8.00E+07	7.70E+07	9.00E+07	6.30E+07	9.50E+07	1.00E+08
Q87JD5	Putative outer membrane protein OmpV OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0318 PE=4 SV=1	40.3	28.1	4.50E+07	4.90E+07	3.40E+07	3.80E+07	6.30E+07	4.90E+07
Q87JG6	60 kDa chaperonin 2 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=groL2 PE=3 SV=1	2.3	56.3						
Q87JK1	Putative outer membrane protein OmpA OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0248 PE=3 SV=1	11.4	35.5		7.70E+06			2.80E+06	
Q87JK3	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0246 PE=4 SV=1	3.0	45.6		2.20E+06	5.80E+06			3.70E+06
Q87JM2	Alkaline serine protease OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0227 PE=4 SV=1	23.8	71.0	5.10E+07	7.30E+07	5.90E+07	5.30E+07	5.30E+07	6.10E+07
Q87JR8	Phospho-beta-glucosidase B OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0180 PE=3 SV=1	16.2	53.0	1.20E+07	1.20E+07	1.00E+07	2.60E+06	1.00E+07	9.30E+06
Q87JS9	Agmatinase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0169 PE=3 SV=1	4.9	33.4	1.30E+07	1.40E+07	1.80E+07		7.30E+06	
Q87JT1	Putative protease OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0167 PE=4 SV=1	1.4	82.1		7.20E+06				
Q87JT2	Putative outer membrane protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0166 PE=4 SV=1	34.4	38.0	9.20E+08	8.60E+08	7.10E+08	6.30E+08	7.50E+08	6.60E+08
Q87JU6	Biopolymer transport protein ExbB-related protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0152 PE=3 SV=1	3.1	49.2	6.40E+06					
Q87JV9	Putative PmbA-related protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0139 PE=4 SV=1	2.9	47.7	2.50E+06				4.50E+06	3.30E+06
Q87JW6	Putative transcriptional activator OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0132 PE=4 SV=1	6.8	24.9	8.20E+06	9.20E+06	1.70E+07	6.40E+06	1.40E+07	9.60E+06
Q87K02	Outer membrane protein OmpW OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0096 PE=4 SV=1	36.4	23.5	2.00E+08	7.60E+07	9.00E+07	3.80E+07	1.20E+08	7.80E+07
Q87K06	Spindolin-related protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0092 PE=4 SV=1	37.2	43.5	9.40E+06	2.00E+07	1.60E+07	1.80E+07	6.90E+07	1.30E+08
Q87K09	Putative siderophore utilization protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0089 PE=4 SV=1	5.1	29.0					1.10E+07	1.20E+07
Q87K43	Chitinase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0055 PE=3 SV=1	67.3	90.0	8.20E+06	7.90E+06	8.20E+07	7.90E+07	9.40E+08	1.30E+09
Q87K60	Glucosamine-6-phosphate deaminase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=nagB PE=3 SV=1	49.6	29.6		4.80E+07		5.50E+07	2.20E+07	4.50E+07
Q87K87	Probable transcriptional regulatory protein VPA0011 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0011 PE=3 SV=1	4.2	26.1						1.80E+06
Q87KA3	ATP synthase subunit a OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=atpB PE=3 SV=1	3.0	30.1	4.30E+06					
Q87KA4	ATP synthase subunit b OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=atpF PE=3 SV=1	49.4	17.5	2.10E+07	2.20E+07	1.70E+07	9.60E+06	1.50E+07	1.40E+07
Q87KA5	ATP synthase subunit delta OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=atpH PE=3 SV=1	8.5	19.4		2.10E+06				
Q87KA6	ATP synthase subunit alpha OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=atpA PE=3 SV=1	55.6	56.6	5.20E+07	5.20E+07	4.40E+07	3.30E+07	3.80E+07	4.10E+07
Q87KA7	ATP synthase gamma chain OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=atpG PE=3 SV=1	13.9	31.8	9.30E+06	6.00E+06	1.20E+07	6.30E+06	1.70E+07	4.00E+06
Q87KA8	ATP synthase subunit beta OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=atpD PE=3 SV=1	50.7	50.7	3.70E+07	4.00E+07	3.40E+07	2.40E+07	2.20E+07	2.80E+07
Q87KB2	Putative cyclohexadienyl dehydratase signal peptide protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP3065 PE=3 SV=1	4.3	29.0	2.00E+06		2.70E+06			3.30E+06
Q87KB6	Dihydroxy-acid dehydratase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=ilvD PE=3 SV=1	39.6	65.6	2.10E+07	2.10E+07	2.00E+07	1.70E+07	2.50E+07	2.40E+07
Q87KB7	Branched-chain amino acid amiotransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP3060 PE=3 SV=1	26.9	34.3	3.60E+07	3.50E+07	3.50E+07	2.60E+07	4.20E+07	4.30E+07
Q87KC1	Putative periplasmic protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP3056 PE=4 SV=1	3.5	35.5	3.30E+06	3.20E+06			3.00E+06	

Q87KC3	Thiol:disulfide interchange protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP3054 PE=3 SV=1	23.5	22.8	1.30E+07	1.30E+07	1.80E+07	6.40E+06	1.40E+07	1.50E+07
Q87KD4	Methionyl-tRNA formyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=fmt PE=3 SV=1	3.8	34.1						
Q87KE1	N5-carboxyaminoimidazole ribonucleotide mutase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=purE PE=3 SV=1	8.1	16.6		2.00E+07	2.20E+07		2.30E+07	2.20E+07
Q87KE3	Oxygen-dependent coproporphyrinogen-III oxidase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=hemF PE=3 SV=1	3.6	35.4		3.60E+06				
Q87KF0	Phosphomethylpyrimidine synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=thiC PE=3 SV=1	4.5	72.4	1.70E+06		2.40E+06		4.10E+06	3.60E+06
Q87KF6	Aminopeptidase P OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP3021 PE=4 SV=1	13.9	65.5	1.20E+07	8.60E+06	9.60E+06	6.20E+06	9.70E+06	1.20E+07
Q87KG4	DNA helicase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP3013 PE=4 SV=1	0.8	82.4	2.00E+06		2.40E+06			
Q87KI7	Putative uroporphyrin-III C-methyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2990 PE=4 SV=1	5.5	45.1	4.60E+06	6.00E+06	4.60E+06	4.40E+06		1.60E+06
Q87KI9	Porphobilinogen deaminase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=hemC PE=3 SV=1	3.5	34.1						4.00E+06
Q87KJ3	Diaminopimelate decarboxylase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=lysA PE=3 SV=1	21.1	45.9	1.10E+07	1.20E+07	9.50E+06	9.50E+06	9.60E+06	1.40E+07
Q87KK7	Glyceraldehyde-3-phosphate dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2970 PE=3 SV=1	2.4	36.4						
Q87KN9	Vitamin B12 transporter BtuB OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=btuB PE=3 SV=1	1.4	69.3	1.90E+06					
Q87KQ0	50S ribosomal protein L11 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplK PE=3 SV=1	36.6	14.7	1.80E+07	1.70E+07	2.00E+07	1.10E+07		8.30E+06
Q87KQ1	50S ribosomal protein L1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplA PE=3 SV=1	26.2	24.7	1.60E+07	1.80E+07	1.90E+07	1.10E+07	1.60E+07	1.50E+07
Q87KQ2	50S ribosomal protein L10 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplJ PE=3 SV=1	13.6	17.3		5.60E+06	3.40E+06			
Q87KQ4	DNA-directed RNA polymerase subunit beta OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpoB PE=3 SV=1	17.4	149.5	7.80E+06	9.40E+06	8.80E+06	3.90E+06	1.20E+07	1.20E+07
Q87KQ5	DNA-directed RNA polymerase subunit beta' OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpoC PE=3 SV=1	13.8	154.8	9.30E+06	8.80E+06	1.30E+07	5.50E+06	1.60E+07	1.20E+07
Q87KR5	DNA-binding protein HU-2 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2911 PE=3 SV=1	63.7	9.6	2.80E+07	3.10E+07	3.10E+07	2.10E+07	4.40E+07	5.10E+07
Q87KS8	Phosphoribosylamine--glycine ligase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=purD PE=3 SV=1	6.8	45.8			7.80E+06			8.40E+06
Q87KT0	Bifunctional purine biosynthesis protein PurH OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=purH PE=3 SV=1	25.3	57.3	7.40E+06	6.80E+06	9.90E+06	4.80E+06	1.50E+07	1.50E+07
Q87KU7	Acetyl-coenzyme A synthetase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=acsA PE=3 SV=1	7.2	71.7	1.60E+07	9.50E+06	1.10E+07	6.60E+06	1.20E+07	1.30E+07
Q87KV2	Fumarate hydratase class II OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=fumC PE=3 SV=1	38.4	48.7	5.40E+07	5.00E+07	6.80E+07	2.80E+07	6.60E+07	6.80E+07
Q87KW2	Aspartate ammonia-lyase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2863 PE=3 SV=1	27.3	52.7	2.00E+07	1.50E+07	2.00E+07	8.50E+06	2.60E+07	1.60E+07
Q87KW5	Superoxide dismutase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2860 PE=3 SV=1	37.1	23.0	4.40E+07	3.30E+07	4.30E+07	2.60E+07	4.80E+07	5.20E+07
Q87KX0	ATP-dependent 6-phosphofructokinase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=pfkA PE=3 SV=1	17.2	34.6	8.30E+06	8.10E+06	8.80E+06	1.20E+07	1.70E+07	8.30E+06
Q87KX4	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2850 PE=4 SV=1	11.0	20.2	8.40E+06	9.40E+06	8.00E+06	5.60E+06	8.90E+06	6.00E+06
Q87KX9	Elongation factor P OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=efp PE=3 SV=1	6.4	20.6	3.60E+06				6.90E+06	1.40E+07
Q87KZ3	Protein-export protein SecB OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=secB PE=3 SV=1	15.6	17.2					1.20E+07	9.00E+06
Q87KZ5	2,3-bisphosphoglycerate-independent phosphoglycerate mutase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=gpmI PE=3 SV=1	16.1	55.1	8.10E+06	1.00E+07	9.30E+06	9.50E+06	1.70E+07	1.40E+07
Q87L07	RNA-binding protein Hfq OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=hfq PE=3 SV=1	39.1	9.8	1.50E+07	2.20E+07	2.00E+07	1.20E+07	3.00E+07	2.70E+07
Q87L13	Tryptophan--tRNA ligase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=trpS PE=3 SV=1	6.5	37.6	4.30E+06	5.70E+06	5.90E+06	3.00E+06	7.30E+06	6.80E+06
Q87L18	Extracellular nuclease-related protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2799 PE=4 SV=1	9.2	105.9	7.60E+06	1.40E+07	1.10E+07	1.10E+07	8.30E+06	9.90E+06
Q87L20	Acetylornithine aminotransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=argD PE=3 SV=1	33.7	43.3	2.10E+07	2.40E+07	2.10E+07	1.80E+07	2.40E+07	2.50E+07
Q87L23	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2794 PE=4 SV=1	37.6	29.2	2.10E+07	2.80E+07	1.50E+07	1.70E+07	1.10E+07	2.00E+07
Q87L24	Phosphoribulokinase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2792 PE=4 SV=1	4.5	32.7		5.00E+06				
Q87L38	Peptidyl-prolyl cis-trans isomerase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2778 PE=4 SV=1	25.0	28.3	1.00E+07	7.90E+06	1.20E+07	5.40E+06	5.00E+06	3.40E+06
Q87L43	30S ribosomal protein S12 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpsL PE=3 SV=1	8.9	13.7	5.10E+06	3.70E+06				
Q87L44	30S ribosomal protein S7 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpsG PE=3 SV=1	51.3	17.7	2.80E+07	2.40E+07	3.00E+07	1.80E+07	4.00E+07	4.00E+07
Q87L45	Elongation factor G 1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=fusA1 PE=3 SV=1	8.9	77.5	3.40E+06	6.80E+06	1.10E+07	9.10E+06	1.20E+07	1.40E+07
Q87L48	Putative malate oxidoreductase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2767 PE=3 SV=1	15.1	46.1	1.60E+07	1.20E+07	1.10E+07	5.60E+06	9.00E+06	1.10E+07
Q87L50	Cystathionine gamma-synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2765 PE=3 SV=1	14.2	41.8	1.90E+07	1.10E+07	1.70E+07	1.20E+07	2.40E+07	2.10E+07
Q87L55	N-acetyl-gamma-glutamyl-phosphate reductase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=argC PE=3 SV=1	30.5	36.2	1.50E+07	1.40E+07	1.60E+07	7.80E+06	1.20E+07	1.60E+07
Q87L72	30S ribosomal protein S6 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpsF PE=3 SV=1	17.1	15.0	6.90E+06	7.70E+06	1.00E+07			4.60E+06
Q87L75	50S ribosomal protein L9 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplI PE=3 SV=1	15.3	15.7	8.50E+06	6.50E+06	1.10E+07			1.90E+06
Q87L81	Glucose-6-phosphate isomerase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=pgi PE=3 SV=1	40.7	60.9	7.00E+07	6.30E+07	6.70E+07	4.40E+07	8.30E+07	8.80E+07
Q87L90	Sulfite reductase [NADPH] flavoprotein alpha-component OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=cysJ PE=3 SV=1	7.7	68.7	9.30E+06	5.40E+06	9.10E+06	3.80E+06	1.00E+07	9.90E+06
Q87L91	Sulfite reductase [NADPH] hemoprotein beta-component OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=cysI PE=3 SV=1	6.2	64.8			7.10E+06	3.00E+06	9.10E+06	5.10E+06
Q87L98	Aminotransferase, class V OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2714 PE=3 SV=1	2.4	40.8	7.50E+06					
Q87LA3	Single-stranded DNA-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=ssb PE=3 SV=1	8.0	19.6	9.10E+06	1.00E+07	8.00E+06			
Q87LB4	Putative V10 pilin OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2698 PE=4 SV=1	31.5	16.8	3.50E+07	2.60E+07	2.70E+07	2.00E+07	2.00E+07	2.10E+07
Q87LC0	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2692 PE=4 SV=1	0.7	159.5						
Q87LF6	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2656 PE=4 SV=1	12.4	13.8	9.70E+06	9.10E+06	8.70E+06	5.70E+06		9.00E+06
Q87LF8	Aspartate carbamoyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=pyrB PE=3 SV=1	10.0	34.5	4.80E+06					
Q87LF9	Ornithine carbamoyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=argF PE=3 SV=1	45.5	37.3	4.70E+07	4.00E+07	3.70E+07	3.50E+07	5.10E+07	4.90E+07
Q87LG8	Probable cytosol aminopeptidase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=pepA PE=3 SV=1	10.4	54.4						4.80E+06
Q87LH4	Deacetylase DA1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2638 PE=4 SV=1	36.8	47.0	5.50E+07	5.10E+07	1.00E+08	4.70E+08	4.10E+09	3.10E+09
Q87LH6	Permease IIC component OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2636 PE=4 SV=1	9.2	48.7					1.70E+07	1.10E+07
Q87LK6	S-adenosylmethionine synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=metK PE=3 SV=1	2.9	42.0				2.80E+06		
Q87LK8	Transketolase 1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=tkt1 PE=3 SV=1	7.2	72.0	1.70E+07	1.20E+07	1.20E+07		7.60E+06	8.40E+06
Q87LL1	Phosphoglycerate kinase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=pgk PE=3 SV=1	45.1	40.7	3.10E+07	3.10E+07	3.60E+07	2.40E+07	3.30E+07	3.50E+07
Q87LL2	Fructose-bisphosphate aldolase, class II OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2599 PE=4 SV=1	68.4	38.9	1.60E+08	1.70E+08	1.80E+08	1.40E+08	2.00E+08	2.30E+08
Q87LL3	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2598 PE=4 SV=1	2.8	31.0	2.20E+06	2.20E+06				
Q87LL8	D-3-phosphoglycerate dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2593 PE=3 SV=1	28.0	44.7	1.40E+07	1.50E+07	1.80E+07	1.40E+07	2.70E+07	2.70E+07
Q87LL9	Ribose-5-phosphate isomerase A OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpiA PE=3 SV=1	28.0	23.2	1.10E+07	1.10E+07	1.20E+07	5.80E+06	8.70E+06	7.30E+06
Q87LM8	tRNA-modifying protein YgfZ OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2583 PE=3 SV=1	3.7	35.5						
Q87LP2	Pyridoxine 5'-phosphate synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=pdxJ PE=3 SV=1	14.4	26.7	7.70E+06	7.30E+06	8.10E+06	1.00E+07	9.90E+06	1.10E+07
Q87LQ0	Enolase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=eno PE=3 SV=1	56.6	45.5	7.30E+07	6.70E+07	7.60E+07	5.70E+07	7.00E+07	9.30E+07
Q87LR1	Protein RecA OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=recA PE=3 SV=1	3.2	37.4		1.70E+06	2.30E+06	9.60E+05		
Q87LR3	Alanine--tRNA ligase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=alaS PE=3 SV=1	2.1	93.9					3.60E+06	7.00E+06
Q87LR5	Carbon storage regulator homolog OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=csrA PE=3 SV=1	18.5	7.1	1.70E+07	2.40E+07	1.70E+07	4.80E+06	1.30E+07	2.50E+07
Q87LR7	Oxaloacetate decarboxylase, alpha subunit OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2544 PE=4 SV=1	6.7	64.2	8.90E+06	7.00E+06	6.60E+06	4.20E+06	5.40E+06	4.10E+06
Q87LS1	Protease, insulinase family OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2540 PE=3 SV=1	7.3	105.7	5.70E+06	8.10E+06	5.80E+06	6.10E+06	1.50E+07	1.20E+07
Q87LS2	Glutamate--cysteine ligase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=gshA PE=3 SV=1	8.4	59.0		2.70E+06	2.20E+06			7.80E+06
Q87LS3	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2538 PE=4 SV=1	4.9	23.3					6.20E+06	2.30E+06
Q87LS8	30S ribosomal protein S16 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpsP PE=3 SV=1	8.5	9.1						
Q87LT1	50S ribosomal protein L19 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplS PE=3 SV=2	10.3	13.2	6.60E+06	6.10E+06	7.90E+06	3.30E+06	4.00E+06	5.30E+06
Q87LT9	NadC OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2522 PE=3 SV=1	6.4	32.0		4.10E+06	5.20E+06		6.20E+06	8.20E+06
Q87LU2	Pyruvate dehydrogenase E1 component OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2519 PE=4 SV=1	33.9	99.6	4.30E+07	4.00E+07	4.80E+07	3.10E+07	4.40E+07	4.10E+07
Q87LU3	Acetyltransferase component of pyruvate dehydrogenase complex OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2518 PE=3 SV=1	26.3	64.9	1.50E+07	1.50E+07	1.80E+07	7.60E+06	1.30E+07	1.60E+07
Q87LU4	Carbonic anhydrase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2514 PE=3 SV=1	10.8	25.2	9.00E+06				7.50E+06	1.80E+07
Q87LV1	Pantothenate synthetase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=panC PE=3 SV=1	3.0	33.4		3.90E+06				
Q87LW3	Aconitate hydratase B OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2495 PE=3 SV=1	23.8	94.0	2.80E+07	1.70E+07	2.50E+07	5.60E+06	2.40E+07	2.30E+07
Q87LW7	Iron(III) ABC transporter, periplasmic iron-compound-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2491 PE=4 SV=1	57.9	37.7	2.30E+08	2.50E+08	2.70E+08	2.00E+08	3.20E+08	3.20E+08
Q87LX0	Putative phosphoglucomutase/phosphomannomutase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2488 PE=4 SV=1	14.0	52.3					6.50E+06	1.80E+07
Q87LX1	N,N'-diacetylchitobiose phosphorylase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2487 PE=4 SV=1	27.6	90.0				7.30E+06	2.80E+07	5.70E+07
Q87LX9	Peptide ABC transporter, periplasmic peptide-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2479 PE=4 SV=1	40.4	62.9	3.30E+06	3.00E+06	6.50E+06	2.70E+07	1.50E+08	3.20E+08
Q87LZ1	Outer membrane protein U OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=ompU PE=3 SV=1	31.8	36.3	3.20E+08	4.10E+08	2.80E+08	2.30E+08	2.10E+08	2.10E+08
Q87LZ5	ATP-dependent zinc metalloprotease FtsH OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=ftsH PE=3 SV=1	1.2	72.9	4.60E+06					
Q87M05	30S ribosomal protein S15 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpsO PE=3 SV=1	13.5	10.1		2.50E+07				
Q87M06	Polyribonucleotide nucleotidyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=pnp PE=3 SV=1	27.1	76.7	1.40E+07	1.40E+07	1.50E+07	7.90E+06	1.80E+07	1.90E+07
Q87M22	Deoxyribose-phosphate aldolase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=deoC PE=3 SV=1	12.8	27.7	1.30E+07	1.00E+07	1.30E+07	9.50E+06	1.00E+07	3.60E+06
Q87M25	Purine nucleoside phosphorylase DeoD-type 1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=deoD1 PE=3 SV=1	18.8	25.9	1.60E+07	1.20E+07	1.90E+07	1.30E+07		1.80E+07
Q87M27	Phosphoserine phosphatase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2431 PE=4 SV=1	10.7	35.8	4.80E+06	4.00E+06	4.20E+06	3.40E+06		6.00E+06
Q87M30	Elongation factor G 2 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=fusA2 PE=3 SV=1	26.4	76.3	3.90E+07	3.90E+07	7.30E+07	4.10E+07	7.40E+07	8.90E+07
Q87MA3	Putative lipoprotein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2354 PE=4 SV=1	6.3	20.7	3.50E+06	5.90E+06				4.40E+06
Q87MB8	Chitinase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2338 PE=3 SV=1	12.6	89.1	1.20E+07	1.40E+07	2.70E+07	1.60E+07	8.70E+07	9.70E+07
Q87MD8	30S ribosomal protein S2 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpsB PE=3 SV=1	35.1	26.8	2.60E+06	1.60E+07	1.70E+07	1.50E+07	2.00E+07	
Q87MD9	Elongation factor Ts OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=tsf PE=3 SV=1	26.3	29.8	1.60E+07	1.60E+07	2.10E+07	7.70E+06	2.00E+07	2.00E+07
Q87ME0	Uridylate kinase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=pyrH PE=3 SV=1	4.5	26.1	4.20E+06	5.30E+06	6.50E+06	5.70E+06	7.60E+06	
Q87ME6	Chaperone protein skp OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2309 PE=3 SV=1	25.3	18.5		7.50E+06	8.50E+06	5.80E+06	1.40E+07	1.00E+07
Q87ME8	3-hydroxyacyl-[acyl-carrier-protein] dehydratase FabZ OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=fabZ PE=3 SV=1	13.3	16.8	8.50E+06	7.20E+06		3.70E+06	1.20E+07	1.60E+07
Q87MG7	Phosphoheptose isomerase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=gmhA PE=3 SV=1	40.8	20.8	1.40E+07	1.40E+07	1.30E+07	9.00E+06	1.20E+07	9.80E+06
Q87MH3	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2282 PE=4 SV=1	2.5	43.4	4.20E+06		5.10E+06			

Q87MI2	4-hydroxy-tetrahydrodipicolinate synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=dapA PE=3 SV=1	24.3	31.2	5.70E+06	7.80E+06	7.90E+06		4.90E+06	9.50E+06
Q87MI3	Outer membrane protein assembly factor BamC OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=bamC PE=3 SV=1	11.2	38.1	5.90E+06	4.50E+06	5.20E+06		5.00E+06	
Q87ML9	Long-chain fatty acid transport protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2212 PE=4 SV=1	24.0	45.7	2.40E+07	2.00E+07	2.10E+07	1.40E+07	1.60E+07	1.70E+07
Q87MN7	3-oxoacyl-[acyl-carrier-protein] synthase I OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2194 PE=3 SV=1	2.2	42.6	2.80E+08	2.00E+08	1.80E+06	2.60E+08		
Q87MP2	Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta 1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=accD1 PE=3 SV=1	9.7	34.0	6.40E+06	8.60E+06	6.30E+06	4.90E+06	5.90E+06	7.10E+06
Q87MS0	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2161 PE=4 SV=1	30.8	35.2	1.70E+07	2.00E+07	1.40E+07	1.30E+07	1.50E+07	1.60E+07
Q87MS4	Glyceraldehyde-3-phosphate dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2157 PE=3 SV=1	73.4	35.2	3.50E+08	3.80E+08	4.20E+08	3.10E+08	5.00E+08	5.60E+08
Q87MV7	Aspartate-semialdehyde dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=asd PE=3 SV=1	64.7	40.2	6.60E+07	7.20E+07	7.90E+07	6.00E+07	1.10E+08	1.00E+08
Q87MW0	Aldehyde-alcohol dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2121 PE=1 SV=1	3.3	97.1	5.90E+06	5.90E+06	5.50E+06	3.90E+06	4.00E+06	3.40E+06
Q87MW3	Superoxide dismutase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2118 PE=3 SV=1	10.1	22.2	1.30E+07	1.20E+07	1.20E+07	1.90E+07	1.20E+07	1.50E+07
Q87MY5	Oligopeptide ABC transporter, periplasmic oligopeptide-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2091 PE=4 SV=1	24.1	62.3	1.50E+07	1.70E+07	1.30E+07	7.80E+06	8.50E+06	8.90E+06
Q87MZ3	Phosphate acetyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2083 PE=3 SV=1	2.2	76.6			4.20E+06		3.10E+06	
Q87MZ6	ABC transporter substrate-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2080 PE=4 SV=1	41.1	33.2	1.60E+07	1.70E+07	2.50E+07	1.60E+07	2.30E+07	3.00E+07
Q87N07	Methionine--tRNA ligase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=metG PE=3 SV=2	3.9	77.9	3.80E+06	4.30E+06	5.40E+06	2.70E+06	4.80E+06	6.40E+06
Q87N21	Malonyl CoA-acyl carrier protein transacylase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2055 PE=3 SV=1	12.4	32.3	6.50E+06	1.20E+07	2.10E+07		2.10E+07	2.40E+07
Q87N29	PTS system, glucose-specific IIBC component OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2046 PE=4 SV=1	14.9	49.4	2.30E+07	2.10E+07	1.60E+07	1.20E+07	9.70E+06	7.90E+06
Q87N36	Pyruvate kinase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2039 PE=3 SV=1	2.5	51.7			2.90E+06			
Q87N45	30S ribosomal protein S1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2030 PE=3 SV=1	14.2	60.9	1.50E+07	1.30E+07	1.60E+07	9.80E+06	8.60E+06	7.60E+06
Q87N50	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2025 PE=4 SV=1	7.8	76.6	9.10E+06	1.30E+07		3.30E+06	1.20E+07	1.10E+07
Q87N84	5-methyltetrahydropteroyltriglutamate-homocysteine methyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1991 PE=4 SV=1	5.8	38.5	4.30E+06				4.70E+06	7.10E+06
Q87NA1	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=metE PE=3 SV=1	29.6	84.7	3.10E+07	2.40E+07	2.80E+07	1.70E+07	2.50E+07	2.40E+07
Q87NC7	Putative carboxynorspermidine dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1941 PE=4 SV=1	3.8	46.5			7.20E+06			
Q87NC8	Carboxynorspermidine/carboxyspermidine decarboxylase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1940 PE=3 SV=1	6.6	42.0	4.80E+06	3.80E+06	6.00E+06	3.40E+06	5.60E+06	5.70E+06
Q87ND3	Ribonucleoside-diphosphate reductase, beta subunit OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1935 PE=4 SV=1	6.6	43.7			9.20E+06		1.00E+07	
Q87NF0	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1918 PE=4 SV=1	3.8	38.5		7.40E+06	3.60E+06	2.90E+06	5.10E+06	5.40E+06
Q87NF7	Extracellular solute-binding protein, family 7 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1911 PE=3 SV=1	26.0	41.0	1.70E+07	2.10E+07	7.80E+06	1.70E+07	1.50E+07	1.70E+07
Q87NG8	Aspartate aminotransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1900 PE=3 SV=1	63.0	45.4	2.70E+08	2.90E+08	2.40E+08	2.10E+08	3.60E+08	3.60E+08
Q87NH5	Asparagine--tRNA ligase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=asnS PE=3 SV=1	22.5	52.6	1.20E+07	8.10E+06	9.50E+07	9.60E+06	1.10E+08	1.20E+08
Q87NM9	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1839 PE=4 SV=1	3.4	20.0						
Q87NU7	4-aminobutyrate aminotransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1771 PE=3 SV=1	2.8	45.1		3.10E+06				
Q87P08	Glucose-6-phosphate 1-dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=zwf PE=3 SV=1	6.6	57.6	6.60E+06	6.40E+06	4.40E+06	3.50E+06	6.50E+06	5.30E+06
Q87P09	DevB protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1709 PE=4 SV=1	13.0	26.0	1.60E+07	1.40E+07	1.60E+07	8.60E+06	1.60E+07	2.00E+07
Q87P10	6-phosphogluconate dehydrogenase, decarboxylating OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1708 PE=3 SV=1	29.7	52.5	3.80E+07	4.50E+07	4.60E+07	3.50E+07	5.10E+07	5.10E+07
Q87P62	Putative translocator protein PopD OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1656 PE=4 SV=1	9.3	35.3	2.40E+06				1.20E+07	
Q87P63	Immunogenic protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1655 PE=4 SV=1	2.8	34.9	9.20E+07	9.80E+07	1.00E+08	7.30E+07	1.40E+08	1.40E+08
Q87P76	Putative trypsin OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1642 PE=4 SV=1	1.7	54.0					6.40E+06	5.50E+06
Q87P98	Amino acid ABC transporter, periplasmic amino acid-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1620 PE=4 SV=1	6.4	36.7	5.10E+06		4.60E+06			
Q87PB1	Tail-specific protease OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1606 PE=4 SV=1	2.7	75.6	2.20E+06	2.70E+06				
Q87PB3	Aminopeptidase N OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1604 PE=4 SV=1	5.1	98.4	4.90E+06	3.80E+06	4.60E+06	2.60E+06	7.30E+06	5.90E+06
Q87PB5	Putative NAD-glutamate dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1602 PE=4 SV=1	1.2	183.4						
Q87PB7	Dihydroorotate dehydrogenase (quinone) OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=pyrD PE=3 SV=1	3.3	36.9		6.50E+06				
Q87PC3	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1594 PE=4 SV=1	48.2	64.6	2.60E+07	3.60E+07	3.00E+07	2.60E+07	3.30E+07	4.10E+07
Q87PC5	3-hydroxydecanoyl-[acyl-carrier-protein] dehydratase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=fabA PE=3 SV=1	22.7	19.0	4.90E+07	5.60E+07	5.60E+07	4.30E+07	6.40E+07	6.40E+07
Q87PF9	Cytochrome c oxidase, subunit CcoO OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1543 PE=4 SV=1	4.9	23.6	2.70E+06	3.30E+06				
Q87PG1	Cbb3-type cytochrome c oxidase subunit OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1541 PE=3 SV=1	3.1	35.4		2.20E+06				
Q87PH6	Putrescine-binding periplasmic protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1526 PE=3 SV=1	29.0	39.7	4.70E+07	4.10E+07	5.00E+07	2.90E+07	4.80E+07	5.20E+07
Q87PH7	Putrescine-binding periplasmic protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1525 PE=3 SV=1	15.4	39.0	1.10E+07	1.20E+07	1.40E+07	9.70E+06	5.10E+06	1.10E+07
Q87PK2	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1501 PE=1 SV=1	32.0	30.1	1.30E+07	1.20E+07	9.90E+06	1.00E+07	1.50E+07	2.20E+07
Q87PP6	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1455 PE=4 SV=1	16.4	18.0	2.90E+07	3.90E+07	1.90E+07	1.90E+07	1.70E+07	2.00E+07
Q87Q03	Oligopeptide ABC transporter, periplasmic oligopeptide-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1347 PE=4 SV=1	1.7	60.3	1.00E+07	1.20E+07		9.00E+06	6.60E+06	9.00E+06
Q87Q24	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1326 PE=4 SV=1	18.8	57.7	2.00E+07	2.30E+07	1.80E+07	9.60E+06	1.90E+07	1.70E+07
Q87Q40	Succinylglutamate desuccinylase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=astE PE=1 SV=1	9.6	38.8		2.70E+06		4.10E+06	7.30E+06	7.50E+06
Q87Q42	Putative oligopeptidase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1308 PE=4 SV=1	5.3	68.0	7.30E+05	1.90E+06			2.70E+06	3.20E+06
Q87Q56	Integration host factor subunit alpha OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=ihfA PE=3 SV=1	9.2	11.2			2.60E+07			
Q87Q59	Phenylalanine--tRNA ligase beta subunit OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=pheT PE=3 SV=1	1.2	87.0			5.20E+06			5.90E+06
Q87Q80	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1270 PE=4 SV=1	2.1	112.8			2.10E+07		1.80E+07	2.80E+07
Q87Q83	Putative lipoprotein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1267 PE=3 SV=1	5.4	23.7		1.80E+06				
Q87Q87	Phosphoribosylaminoimidazole-succinocarboxamide synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=purC PE=3 SV=1	36.8	41.0	1.30E+07	1.60E+07	2.50E+07	1.20E+07	2.30E+07	2.00E+07
Q87Q99	Thioredoxin reductase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1251 PE=3 SV=1	27.3	34.5	1.70E+07	1.80E+07	1.40E+07	1.20E+07	1.90E+07	1.90E+07
Q87QA3	Phosphoserine aminotransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=serC PE=3 SV=1	25.5	40.2	3.60E+07	3.30E+07	3.40E+07	2.10E+07	3.50E+07	4.00E+07
Q87QA7	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1243 PE=4 SV=1	29.3	19.8	1.60E+07	1.80E+07	6.10E+06	1.50E+07	1.70E+07	1.10E+07
Q87QB7	Glutaredoxin 1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1233 PE=4 SV=1	12.5	10.0			4.90E+06			
Q87QB9	Putative reductase VP1231 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1231 PE=3 SV=1	46.5	43.9	4.40E+07	4.10E+07	4.30E+07	3.30E+07	5.30E+07	5.20E+07
Q87QE2	UDP-sugar hydrolase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1207 PE=3 SV=1	9.0	61.3	1.70E+07	1.80E+07	1.80E+07	1.30E+07	1.00E+07	2.50E+07
Q87QE6	Heat shock protein HslJ OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1203 PE=4 SV=1	26.4	16.6	4.20E+07	2.50E+07	3.80E+07	2.40E+07	3.40E+07	3.50E+07
Q87QF3	Putative ABC transporter, periplasmic substrate-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1196 PE=4 SV=1	2.6	42.6	6.20E+06	5.50E+06	6.80E+06		7.90E+06	7.70E+06
Q87QG7	Cystathionine beta-lyase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1182 PE=3 SV=1	3.2	44.6		5.00E+06	8.30E+06		1.20E+07	1.10E+07
Q87QJ9	Cysteine--tRNA ligase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=cysS PE=3 SV=1	3.7	52.0						
Q87QK7	1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino] imidazole-4-carboxamide isomerase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=hisA PE=3 SV=1	20.8	26.4	1.00E+07	7.50E+06	9.30E+06	4.30E+06	7.50E+06	8.20E+06
Q87QK9	Histidine biosynthesis bifunctional protein HisB OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=hisB PE=3 SV=1	6.2	39.8	4.30E+06	5.30E+06	4.90E+06	3.40E+06	3.90E+06	6.00E+06
Q87QL0	Histidinol-phosphate aminotransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=hisC PE=3 SV=1	10.1	38.2	3.30E+06		4.40E+06		6.50E+06	5.10E+06
Q87QL1	Histidinol dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=hisD PE=3 SV=1	13.5	46.1	7.80E+06	6.50E+06	1.70E+07	9.70E+06	1.80E+07	1.30E+07
Q87QL2	ATP phosphoribosyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=hisG PE=3 SV=1	29.2	32.8	1.30E+07	1.30E+07	1.80E+07	1.20E+07	2.10E+07	2.70E+07
Q87QM1	Adenylosuccinate lyase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1128 PE=3 SV=1	30.9	51.4	1.70E+07	2.20E+07	2.60E+07	1.50E+07	2.40E+07	2.20E+07
Q87QP1	Serine--tRNA ligase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=serS PE=3 SV=1	13.6	48.8	6.20E+06	1.80E+07	1.20E+07		2.00E+07	1.40E+07
Q87QP6	Alanine dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1103 PE=3 SV=1	47.6	39.9	4.60E+07	6.10E+07	3.20E+07	3.60E+07	3.20E+07	4.00E+07
Q87QS7	Putative helicase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1072 PE=4 SV=1	6.1	68.7					6.10E+06	5.20E+06
Q87QT7	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1062 PE=4 SV=1	5.6	28.3		9.00E+06	5.10E+06			7.00E+06
Q87QT8	Peptidoglycan-associated lipoprotein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1061 PE=3 SV=1	12.6	18.7	3.30E+07	4.20E+07	3.50E+07	2.90E+07	2.70E+07	2.70E+07
Q87QT9	Protein TolB OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=tolB PE=3 SV=1	28.4	49.8	1.60E+07	1.60E+07	1.30E+07	1.20E+07	1.00E+07	1.00E+07
Q87QV2	Aspartate--tRNA ligase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=aspS PE=3 SV=1	2.0	65.7	1.00E+06					
Q87QV7	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1043 PE=4 SV=1	7.3	28.1	4.90E+06	5.80E+06	4.90E+06	3.70E+06	5.50E+06	
Q87QW2	Chromosome partition protein MukB OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=mukB PE=3 SV=1	0.6	169.6					5.50E+06	3.10E+06
Q87QX6	Glucose-1-phosphate adenylyltransferase 1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=glgC1 PE=3 SV=1	32.8	45.5	1.10E+07	9.50E+06	1.40E+07	4.20E+06	1.70E+07	1.60E+07
Q87QY7	Isocitrate dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1011 PE=4 SV=1	60.7	80.5	7.20E+07	6.50E+07	7.00E+07	3.80E+07	8.20E+07	7.70E+07
Q87QZ9	Amino acid ABC transporter, periplasmic amino acid-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0999 PE=3 SV=1	72.5	28.4	3.60E+07	6.30E+07	6.80E+07	5.20E+07	7.40E+07	8.30E+07
Q87R02	Putative 54 kDa polar flagellar sheath protein A OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0996 PE=4 SV=1	61.3	52.3	6.60E+07	9.50E+07	7.80E+07	7.60E+07	8.00E+07	8.10E+07
Q87R04	Formate acetyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0994 PE=4 SV=1	38.4	84.5	3.30E+07	3.80E+07	4.50E+07	3.10E+07	6.50E+07	7.00E+07
Q87R31	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0967 PE=4 SV=1	8.7	21.8	2.10E+07	2.10E+07	1.80E+07	1.40E+07		1.60E+07
Q87R32	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0966 PE=4 SV=1	7.7	14.7	5.50E+06	5.60E+06	4.60E+06	2.60E+06		
Q87R36	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0962 PE=4 SV=1	22.5	43.9	2.10E+07	1.10E+07	1.30E+07	1.20E+07	1.20E+07	1.30E+07
Q87R38	Uridine phosphorylase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0960 PE=3 SV=1	27.0	26.9	1.30E+07	9.60E+06	9.80E+06	5.40E+06	8.30E+06	8.30E+06
Q87R48	Lipoprotein-related protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0950 PE=4 SV=1	28.5	15.8	8.60E+06	8.80E+06	1.20E+07	9.50E+06	1.10E+07	
Q87R77	Peptidylprolyl isomerase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0921 PE=4 SV=1	1.3	68.8			3.50E+06			
Q87R78	DNA-binding protein HU-beta OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0920 PE=3 SV=1	28.9	9.4	2.60E+07	3.20E+07	3.60E+07	1.60E+07	3.20E+07	4.30E+07

Q87R80	ATP-dependent Clp protease proteolytic subunit OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=clpP PE=3 SV=1	16.0	22.0	2.40E+07	2.70E+07	2.70E+07	1.80E+07	3.10E+07	4.40E+07
Q87R87	C4-dicarboxylate-binding periplasmic protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0910 PE=4 SV=1	47.9	37.1	4.80E+07	4.40E+07	4.80E+07	5.20E+07	6.60E+07	6.90E+07
Q87RC1	Putative lytic murein transglycosylase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0876 PE=4 SV=1	3.1	36.7						3.90E+06
Q87RD3	Formyltetrahydrofolate deformylase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=purU PE=3 SV=1	27.8	31.6	4.90E+06	8.70E+06	3.90E+06	7.60E+06	1.70E+07	7.30E+06
Q87RD6	Arginine--tRNA ligase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=argS PE=3 SV=1	20.1	63.8	9.30E+06	7.90E+06	1.10E+07	7.20E+06	1.40E+07	1.40E+07
Q87RE4	Zinc ABC transporter, periplasmic zinc-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0853 PE=3 SV=1	18.2	32.1	9.80E+06	6.70E+06	5.70E+06		6.90E+06	6.20E+06
Q87RE7	Succinyl-CoA ligase [ADP-forming] subunit alpha OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0850 PE=3 SV=1	52.1	30.0	6.10E+07	5.60E+07	5.40E+07	3.20E+07	5.00E+07	5.20E+07
Q87RE8	Succinyl-CoA ligase [ADP-forming] subunit beta OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=sucC PE=3 SV=1	52.8	41.5	8.80E+07	8.10E+07	7.40E+07	4.90E+07	7.80E+07	8.00E+07
Q87RE9	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0848 PE=3 SV=1	31.4	43.7	2.40E+07	2.40E+07	2.10E+07	3.60E+06	1.40E+07	1.80E+07
Q87RF0	2-oxoglutarate dehydrogenase, E1 component OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0847 PE=4 SV=1	2.0	106.0		2.90E+06	3.30E+06			
Q87RF5	Citrate synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0842 PE=3 SV=1	5.4	48.2	1.20E+07	1.20E+07	1.10E+07			
Q87RG2	Flavodoxin OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0835 PE=3 SV=1	10.7	19.8					3.30E+06	
Q87RG4	Glutamine--tRNA ligase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=glnS PE=3 SV=1	12.9	63.9	1.40E+07	1.70E+07	1.50E+07	1.10E+07	1.90E+07	2.20E+07
Q87RH4	Adenylate kinase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=adk PE=3 SV=1	25.2	23.3	1.90E+07	1.20E+07	1.40E+07	6.10E+06	1.20E+07	1.30E+07
Q87RI9	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0805 PE=4 SV=1	13.8	33.4	1.10E+07	1.60E+07	6.90E+06	1.10E+07	2.10E+07	2.10E+07
Q87RJ2	Putative exported protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0802 PE=4 SV=1	2.1	51.7					4.20E+06	7.00E+06
Q87RJ7	Cysteine synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0797 PE=3 SV=1	84.8	34.1	2.70E+08	2.50E+08	2.70E+08	1.70E+08	3.30E+08	3.00E+08
Q87RK1	PTS system, glucose-specific IIA component OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0793 PE=4 SV=1	8.3	17.9	7.20E+06	7.90E+06				
Q87RK5	Polar flagellar hook associated protein type 1 FlgK OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0785 PE=4 SV=1	15.3	71.2	1.30E+07	1.50E+07	1.20E+07	1.20E+07	1.50E+07	1.70E+07
Q87RL4	Outer membrane protein OmpA OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0764 PE=3 SV=1	8.5	34.1	3.70E+06	5.10E+06	2.90E+06			
Q87RL6	Glutamate--tRNA ligase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=gltX PE=3 SV=1	34.4	53.4	3.00E+07	2.90E+07	3.00E+07	1.70E+07	3.40E+07	3.20E+07
Q87RL8	Putative chitoporin OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0760 PE=4 SV=1	33.8	40.8				2.00E+07	6.20E+07	1.80E+08
Q87RM2	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0756 PE=4 SV=1	6.5	25.1		2.00E+06				
Q87RM3	N,N'-diacetylchitobiase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0755 PE=4 SV=1	13.7	97.6				9.60E+06		2.20E+07
Q87RN0	2-dehydro-3-deoxyphosphooctonate aldolase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=kdsA PE=3 SV=1	18.7	30.8	7.10E+06	6.20E+06	9.20E+06		6.80E+06	1.40E+07
Q87RN8	Ribose-phosphate pyrophosphokinase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=prs PE=3 SV=1	21.7	33.9	5.90E+06	7.80E+06	9.90E+06	6.90E+06	5.20E+06	1.00E+07
Q87RP4	tRNA-2-methylthio-N(6)-dimethylallyladenosine synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=miaB PE=3 SV=1	4.6	53.7					4.40E+06	
Q87RQ0	Leucine--tRNA ligase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=leuS PE=3 SV=1	17.0	96.6	8.30E+06	7.30E+06	1.20E+07	8.10E+06	1.50E+07	1.60E+07
Q87RQ1	LPS-assembly lipoprotein LptE OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=lptE PE=3 SV=1	11.7	20.5	4.70E+06	6.50E+06		3.10E+06	5.70E+06	3.60E+06
Q87RR2	Serine hydroxymethyltransferase 1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=glyA1 PE=3 SV=1	11.1	45.5	1.20E+07	1.60E+07	1.50E+07	5.60E+06	1.10E+07	
Q87RS3	Lipoprotein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0704 PE=3 SV=1	48.0	29.1	2.50E+07	2.50E+07	2.00E+07	1.60E+07	1.50E+07	2.00E+07
Q87RU4	6,7-dimethyl-8-ribityllumazine synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=ribH PE=3 SV=1	37.8	16.4	7.90E+06	7.50E+06	7.50E+06	6.10E+06	9.70E+06	8.10E+06
Q87RU5	3,4-dihydroxy-2-butanone 4-phosphate synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=ribB PE=3 SV=1	8.4	40.1	2.80E+06	2.40E+06	3.20E+06	2.10E+06	3.80E+06	3.50E+06
Q87RV5	Aminoacyl-histidine dipeptidase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0671 PE=4 SV=1	7.1	53.6	7.30E+06	6.00E+06	4.90E+06	4.20E+06	6.40E+06	5.30E+06
Q87RV7	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0669 PE=4 SV=1	11.0	39.0			4.70E+06	2.60E+06	8.10E+06	5.50E+06
Q87RW0	Phosphoribosylformylglycinamidine synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=purL PE=3 SV=1	1.0	141.6		4.80E+06	6.10E+06	3.70E+06		
Q87RW7	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0659 PE=4 SV=1	2.5	47.4					7.90E+06	9.60E+06
Q87RX3	Chaperone protein DnaK OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=dnaK PE=3 SV=1	48.7	69.0	3.10E+07	3.10E+07	2.90E+07	1.70E+07	2.60E+07	3.30E+07
Q87RX8	DNA repair protein RecN OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0648 PE=3 SV=1	5.1	61.4						
Q87S05	Putative chitinase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0619 PE=4 SV=1	43.9	63.5	2.10E+07	2.20E+07	4.60E+07	2.80E+07	2.60E+08	2.90E+08
Q87S07	GMP synthase [glutamine-hydrolyzing] OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=guaA PE=3 SV=1	9.1	57.6	7.80E+06	8.10E+06	9.90E+06	5.80E+06	1.10E+07	1.40E+07
Q87S08	Inosine-5'-monophosphate dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=guaB PE=3 SV=1	2.9	51.9						2.00E+06
Q87S13	Outer membrane protein assembly factor BamB OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=bamB PE=3 SV=1	2.1	41.5		6.00E+06	6.40E+06			6.20E+06
Q87S31	Inositol monophosphate family protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0593 PE=4 SV=1	9.4	29.1	2.50E+06	2.50E+06	5.40E+06		6.00E+06	5.70E+06
Q87S35	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0589 PE=4 SV=1	11.9	11.8	1.20E+07	1.20E+07		7.90E+06		1.10E+07
Q87S40	Isocitrate lyase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0584 PE=4 SV=1	13.8	48.0	1.50E+07	9.50E+06		4.30E+06	5.00E+06	1.40E+07
Q87S44	Antioxidant, AhpC/Tsa family OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0580 PE=4 SV=1	51.7	22.2	1.00E+08	1.20E+08	1.40E+08	7.80E+07	1.10E+08	1.20E+08
Q87S63	Chaperone protein ClpB OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=clpB PE=3 SV=1	0.9	95.8						3.10E+06
Q87S84	Putative carbon starvation protein A OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0540 PE=4 SV=1	2.4	53.3	6.70E+06	7.40E+06	6.00E+06	3.30E+06	3.80E+06	4.10E+06
Q87S99	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0525 PE=4 SV=1	13.2	43.9	7.90E+06		9.40E+06	5.60E+06	1.10E+07	8.00E+06
Q87SA8	Oxidoreductase Tas, aldo/keto reductase family OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0516 PE=4 SV=1	22.7	39.7	1.40E+07	1.60E+07	1.90E+07	1.20E+07	2.60E+07	2.60E+07
Q87SB4	Thiol:disulfide interchange protein DsbC OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0510 PE=4 SV=1	4.2	28.6			5.50E+06			4.90E+06
Q87SC7	Autonomous glycyl radical cofactor OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=grcA PE=3 SV=1	7.2	13.9	4.80E+06		7.00E+06	2.00E+06		
Q87SC8	Threonine synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0496 PE=4 SV=1	6.1	46.5	8.80E+06	7.70E+06	1.00E+07	4.90E+06	8.60E+06	7.80E+06
Q87SC9	Homoserine kinase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=thrB PE=3 SV=1	2.8	34.4	8.00E+06	7.70E+06	1.60E+07	9.80E+06	2.10E+07	1.90E+07
Q87SD2	Putative 4-hydroxy-4-methyl-2-oxoglutarate aldolase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0492 PE=3 SV=1	6.3	17.7	5.00E+06					
Q87SD6	Putative DNA polymerase III, beta chain OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0488 PE=4 SV=1	8.4	17.3	6.30E+07	8.40E+07			3.10E+07	
Q87SE0	Glutamate synthase, large subunit OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0484 PE=4 SV=1	5.2	175.2		8.50E+06	6.70E+06	7.60E+06	9.70E+06	1.20E+07
Q87SE2	Glutamate synthase, large subunit OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0482 PE=4 SV=1	9.3	162.9	1.10E+07	8.50E+06	9.90E+06	5.70E+06	9.00E+06	9.80E+06
Q87SE3	Glutamate synthase, small subunit OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0481 PE=4 SV=1	7.2	52.5	5.10E+06	2.80E+06				5.70E+06
Q87SF3	Carbamoyl-phosphate synthase large chain OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=carB PE=3 SV=1	2.1	117.8	4.30E+06	5.40E+06	5.80E+06	2.80E+06	4.40E+06	1.10E+07
Q87SF5	4-hydroxy-tetrahydrodipicolinate reductase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=dapB PE=3 SV=1	26.4	28.6	2.40E+07	2.00E+07	1.70E+07	1.60E+07	1.70E+07	2.20E+07
Q87SG0	Cell division protein FtsZ OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=ftsZ PE=3 SV=1	2.9	42.5		4.90E+06				
Q87SH4	Penicillin-binding protein activator LpoA OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=lpoA PE=3 SV=1	2.5	67.5		6.00E+06				
Q87SH9	Stringent starvation protein A OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0444 PE=3 SV=1	12.3	24.3	7.70E+06	8.50E+06	6.30E+06	4.10E+06	6.90E+06	7.80E+06
Q87SI4	30S ribosomal protein S9 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpsI PE=3 SV=1	40.0	14.6	1.40E+07	1.30E+07	1.40E+07	8.40E+06	1.20E+07	1.10E+07
Q87SI5	50S ribosomal protein L13 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplM PE=3 SV=1	12.7	16.0	8.10E+06	9.10E+06	1.00E+07	6.80E+06	7.60E+06	6.90E+06
Q87SI9	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0434 PE=4 SV=1	13.6	16.5		8.50E+06		4.90E+06		
Q87SJ0	Protease DO OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0433 PE=4 SV=1	14.5	48.1	7.80E+06	1.30E+07	1.20E+07	8.30E+06	5.10E+06	1.10E+07
Q87SJ8	Outer membrane protein TolC OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0425 PE=4 SV=1	36.2	48.0	1.90E+07	1.80E+07	1.50E+07	9.70E+06	1.40E+07	1.20E+07
Q87SK3	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0420 PE=4 SV=1	7.0	59.2	2.50E+06		2.90E+06		3.90E+06	2.60E+06
Q87SL6	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0406 PE=4 SV=1	7.5	16.1						
Q87SR6	Pyruvate kinase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0356 PE=3 SV=1	10.2	49.9	9.20E+06	1.10E+07	9.80E+06	8.40E+06	1.10E+07	1.10E+07
Q87SS8	3-isopropylmalate dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=leuB PE=3 SV=1	44.9	39.3	4.30E+07	3.90E+07	3.70E+07	2.70E+07	4.70E+07	4.90E+07
Q87ST3	LPS-assembly protein LptD OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=lptD PE=3 SV=1	1.8	89.2	3.10E+06	4.00E+06	3.70E+06		3.10E+06	
Q87ST4	Chaperone SurA OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=surA PE=3 SV=1	4.4	47.4		7.70E+06				
Q87SU4	50S ribosomal protein L21 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplU PE=3 SV=1	47.6	11.5	9.40E+06	1.20E+07	1.50E+07	7.50E+06	1.00E+07	1.10E+07
Q87SU7	Malate dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=mdh PE=3 SV=1	61.7	32.2	3.70E+07	3.80E+07	3.90E+07	2.50E+07	3.40E+07	4.20E+07
Q87SV0	Immunogenic protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0323 PE=4 SV=1	70.8	34.5	1.60E+08	1.60E+08	1.70E+08	1.20E+08	2.30E+08	2.50E+08
Q87SV6	Thiamin ABC transporter, periplasmic thiamin-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0316 PE=4 SV=1	15.2	36.5	3.70E+06	7.80E+06	1.30E+07	1.30E+07	2.00E+07	2.60E+06
Q87SW0	Fructose-1,6-bisphosphatase class 1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=fbp PE=3 SV=1	3.3	37.3	5.80E+06	6.50E+06				
Q87SX0	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0302 PE=4 SV=1	3.8	23.3	5.60E+07	5.80E+07	6.30E+07	3.90E+07	4.80E+07	6.00E+07
Q87SX9	Sulfate adenylyltransferase subunit 1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=cysN PE=3 SV=1	2.5	52.6		2.50E+06	3.90E+06			
Q87SY2	2',3'-cyclic-nucleotide 2'-phosphodiesterase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0290 PE=3 SV=1	14.1	72.1	7.10E+06	1.00E+07	1.20E+07	8.80E+06	1.20E+07	1.20E+07
Q87SY9	50S ribosomal protein L17 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplQ PE=3 SV=1	14.3	14.2	1.10E+07	1.40E+07	1.40E+07	6.10E+06	1.40E+07	
Q87SZ0	DNA-directed RNA polymerase subunit alpha OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpoA PE=3 SV=1	26.4	36.5	1.70E+07	8.40E+06	1.60E+07	7.10E+06	1.20E+07	1.50E+07
Q87SZ1	30S ribosomal protein S4 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpsD PE=3 SV=1	35.9	23.3	2.30E+07	2.40E+07	2.40E+07	9.90E+06	3.60E+07	3.90E+07
Q87SZ2	30S ribosomal protein S13 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpsM PE=3 SV=1	50.8	13.3	2.10E+07	1.90E+07	2.00E+07	1.60E+07	1.80E+07	2.00E+07
Q87SZ4	50S ribosomal protein L15 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplO PE=3 SV=1	6.3	14.9	6.80E+06	8.20E+06	7.80E+06			
Q87SZ6	30S ribosomal protein S5 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpsE PE=3 SV=1	15.6	17.6	7.90E+06	1.20E+07	1.30E+07			8.80E+06
Q87SZ7	50S ribosomal protein L18 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplR PE=3 SV=1	29.9	12.6	7.20E+06	6.30E+06	7.50E+06	6.20E+06	6.30E+06	5.60E+06
Q87SZ8	50S ribosomal protein L6 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplF PE=3 SV=1	22.0	18.8	1.10E+07	1.10E+07	1.00E+07	4.60E+06	6.20E+06	7.20E+06
Q87SZ9	30S ribosomal protein S8 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpsH PE=3 SV=1	6.2	14.0	1.10E+07	1.10E+07	7.50E+06	7.10E+06	9.70E+06	1.10E+07
Q87T01	50S ribosomal protein L5 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplE PE=3 SV=1	26.8	20.1	1.60E+07	1.40E+07	1.40E+07	1.30E+07	1.50E+07	2.40E+07
Q87T02	50S ribosomal protein L24 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplX PE=3 SV=1	9.5	11.2	1.60E+07		1.80E+07	1.10E+07	1.00E+07	
Q87T03	50S ribosomal protein L14 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplN PE=3 SV=1	12.2	13.6	1.00E+07	8.90E+06	1.20E+07			
Q87T04	30S ribosomal protein S17 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpsQ PE=3 SV=1	9.5	9.6						
Q87T07	30S ribosomal protein S3 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpsC PE=3 SV=1	17.7	25.6	1.20E+07	1.10E+07	1.40E+07	7.90E+06		
Q87T08	50S ribosomal protein L22 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplV PE=3 SV=1	21.8	12.1	5.90E+06	6.50E+06	8.50E+06			
Q87T09	30S ribosomal protein S19 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpsS PE=3 SV=1	28.3	10.4	1.00E+07		2.00E+07	8.70E+06	1.80E+07	1.50E+07
Q87T11	50S ribosomal protein L23 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplW PE=3 SV=1	7.0	11.1		7.60E+06	7.50E+06			
Q87T12	50S ribosomal protein L4 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplD PE=3 SV=1	13.5	21.9	1.30E+07	1.10E+07	1.30E+07	7.40E+06	8.20E+06	8.30E+06

Q87T13	50S ribosomal protein L3 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplC PE=3 SV=1	13.4	22.4	1.80E+07	1.50E+07	1.80E+07	8.60E+06	8.30E+06	
Q87T23	Regulator of ribonuclease activity A OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rraA PE=3 SV=1	6.5	18.4	8.30E+06					
Q87T31	Triosephosphate isomerase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=tpiA PE=3 SV=1	23.0	26.9	3.20E+07	3.50E+07	3.00E+07	2.10E+07	1.30E+07	3.90E+07
Q87T36	Pilin glycosylation protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0234 PE=3 SV=1	43.2	43.4	4.40E+07	4.60E+07	4.40E+07	3.20E+07	5.40E+07	5.30E+07
Q87T41	dTDP-4-dehydrorhamnose 3,5-epimerase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0229 PE=4 SV=1	38.5	21.2	7.60E+06	1.10E+07	9.60E+06	8.40E+06	9.60E+06	7.30E+06
Q87T51	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0219 PE=4 SV=1	8.0	20.6	7.60E+06	8.10E+06	6.20E+06			
Q87T56	ADP-L-glycero-D-manno-heptose-6-epimerase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=hldD PE=3 SV=1	4.2	35.2			6.90E+06			
Q87T64	Putative amidohydrolase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0206 PE=4 SV=1	7.4	30.7	6.20E+06	4.60E+06	8.50E+06		4.30E+06	
Q87T66	Putative 3-chlorobenzoate-3,4-dioxygenase dyhydrogenase related protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0204 PE=4 SV=1	11.1	38.5	6.90E+06				8.20E+06	9.30E+06
Q87T85	50S ribosomal protein L28 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpmB PE=3 SV=1	12.8	9.0	1.00E+07	1.20E+07	1.70E+07		1.40E+07	1.10E+07
Q87T94	Putative alpha helix protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0176 PE=4 SV=1	2.1	33.2						
Q87T98	Putative binding protein component of ABC transporter OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0172 PE=4 SV=1	4.8	69.6	3.30E+06			1.40E+07		1.50E+07
Q87TA4	Putative TolR OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0166 PE=3 SV=1	5.5	49.3	8.90E+06	8.10E+06	5.30E+06	4.10E+06		
Q87TB9	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0151 PE=4 SV=1	3.4	70.4	3.90E+06	6.10E+06			6.30E+06	6.30E+06
Q87TE1	Phosphoenolpyruvate carboxykinase [ATP] OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=pckA PE=3 SV=1	72.1	60.0	1.30E+08	1.40E+08	1.00E+08	9.60E+07	1.20E+08	1.30E+08
Q87TE8	Glutamine synthetase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0121 PE=3 SV=1	54.4	51.5	1.60E+08	1.70E+08	1.70E+08	1.30E+08	2.10E+08	2.20E+08
Q87TG5	Delta-aminolevulinic acid dehydratase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0104 PE=3 SV=1	17.0	39.2	1.30E+07	1.40E+07	1.50E+07	8.70E+06	1.60E+07	1.40E+07
Q87TJ9	Oligopeptidase A OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0070 PE=3 SV=1	17.1	76.9	2.40E+07	1.20E+08	3.60E+07	9.40E+07	1.30E+08	1.40E+08
Q87TK1	Glutathione reductase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0068 PE=3 SV=1	28.6	49.2	5.00E+07	4.80E+07	4.50E+07	3.40E+07	5.70E+07	5.80E+07
Q87TM1	Peptide ABC transporter, periplasmic peptide-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0048 PE=4 SV=1	70.8	57.4	2.60E+08	3.00E+08	3.10E+08	2.30E+08	3.80E+08	3.80E+08
Q87TM2	Peptide ABC transporter, ATP-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0047 PE=3 SV=1	1.8	63.7						
Q87TN4	Ketol-acid reductoisomerase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=ilvC PE=3 SV=1	57.5	54.7	9.10E+07	1.00E+08	9.30E+07	7.00E+07	1.20E+08	1.40E+08
Q87TR0	Amino acid ABC transporter, periplasmic amino acid-binding portion OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0008 PE=3 SV=1	46.4	27.5	1.50E+07	1.40E+07	2.00E+07	1.00E+07	1.80E+07	2.60E+07
Q99289	Thermolabile hemolysin OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0226 PE=1 SV=2	10.3	47.4	4.80E+07				1.10E+07	
Q9ALY5	Cyclic AMP receptor protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2793 PE=4 SV=1	36.2	23.7	1.50E+07	2.00E+07	2.40E+07	7.90E+06	2.50E+07	2.00E+07
Q9L7P5	60 kDa chaperonin 1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=groL1 PE=3 SV=2	46.4	57.5	5.50E+07	5.10E+07	5.40E+07	3.80E+07	6.20E+07	7.30E+07
Q9ZBA2	Polar flagellin E OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=flaE PE=3 SV=2	1.6	40.7	6.80E+06	1.50E+07	1.40E+07		1.40E+07	1.70E+07

2nd Experiment (Soulble Fraction)

Accession	Description	Coverage	MW [kDa]	Control	GlcNAc	GlcN	(GlcNAc)2	(GlcN)2	GlcNAc-GlcN
A7UEM1	Transhydrogenase alpha subunit (Fragment) OS=Vibrio parahaemolyticus GN=pntA PE=4 SV=1	7.0	15.5						
A7UET7	Protein RecA (Fragment) OS=Vibrio parahaemolyticus GN=recA PE=3 SV=1	39.1	26.0	9.30E+06	3.80E+06	1.30E+07	1.20E+07	1.70E+07	1.30E+07
A7UEX3	DNA gyrase beta-subunit (Fragment) OS=Vibrio parahaemolyticus GN=gyrB PE=4 SV=1	5.1	21.7	5.70E+06					
A9Q6J2	Protein RecA (Fragment) OS=Vibrio parahaemolyticus GN=recA PE=3 SV=1	33.6	22.4	9.30E+06	4.30E+06	1.30E+07	1.20E+07	1.70E+07	1.30E+07
A9Q6M1	DNA gyrase B subunit (Fragment) OS=Vibrio parahaemolyticus GN=gyrB PE=4 SV=1	5.9	18.6	5.70E+06					
A9Q6Q3	Phosphoglucomutase (Fragment) OS=Vibrio parahaemolyticus GN=pgm PE=3 SV=1	18.9	21.2		8.20E+06	1.00E+07	8.20E+06	1.20E+07	1.10E+07
H6BAG3	Protein RecA (Fragment) OS=Vibrio parahaemolyticus GN=recA PE=3 SV=1	35.1	18.0	7.90E+06	4.30E+06	1.10E+07	1.30E+07	1.40E+07	1.10E+07
O50286	Dihydrolipoyl dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=lpd PE=3 SV=2	48.2	51.0	1.60E+07	2.40E+07	2.20E+07	2.20E+07	3.10E+07	2.50E+07
O51859	DNA gyrase subunit B OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=gyrB PE=3 SV=2	4.0	89.4	5.70E+06	5.70E+06			5.10E+06	3.70E+06
P0A2W2	Acyl carrier protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=acpP PE=3 SV=2	18.2	8.5	3.70E+06	4.90E+06	5.60E+06	2.80E+07	3.10E+07	2.20E+07
P22095	Tryptophan synthase alpha chain OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=trpA PE=3 SV=2	7.1	28.6				6.50E+06	6.80E+06	
P22097	Tryptophan synthase beta chain 1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=trpB1 PE=3 SV=2	2.3	43.0				6.40E+06	6.10E+06	
P22099	Anthranilate synthase component 1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=trpE PE=3 SV=2	1.8	59.7				2.70E+06		
P40607	Adenylosuccinate synthetase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=purA PE=3 SV=3	31.3	47.7	8.90E+06	1.60E+07	1.30E+07	1.20E+07	1.80E+07	1.60E+07
P46235	Probable lactoylglutathione lyase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=gloA PE=3 SV=2	19.6	15.0		9.10E+05				
P59494	Maltoporin OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=lamB PE=3 SV=1	32.2	46.9	2.90E+07	2.20E+07	2.90E+07	2.40E+07	4.50E+07	3.60E+07
P59570	Outer membrane protein OmpK OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=ompK PE=3 SV=1	8.6	29.9	3.10E+06				4.60E+06	4.60E+06
P59605	Argininosuccinate synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=argG PE=3 SV=1	48.3	44.5	3.10E+07	3.60E+07	3.70E+07	4.70E+07	6.10E+07	4.80E+07
P59620	Bifunctional protein ArgH OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=argH PE=3 SV=1	22.9	69.3	4.20E+06	6.70E+06	6.40E+06	8.60E+06	8.50E+06	8.50E+06
P66478	30S ribosomal protein S18 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpsR PE=3 SV=1	40.0	8.8	1.10E+07	1.10E+07	1.70E+07	2.10E+07	2.10E+07	1.70E+07
P74956	Lon protease OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=lon PE=3 SV=2	11.2	87.8	3.80E+06	5.50E+06	7.00E+06	5.20E+06	8.70E+06	7.10E+06
Q79YV4	OpaR OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2516 PE=4 SV=1	5.9	23.6					4.80E+06	
Q79YX4	Chemotaxis protein CheW OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2225 PE=4 SV=1	29.3	18.4	4.40E+06	6.00E+06	4.70E+07	2.70E+07	8.10E+06	7.80E+06
Q79YY3	BfdA OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1393 PE=4 SV=1	17.4	19.4			5.80E+06		5.80E+06	
Q79YZ2	Chemotaxis CheV OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0773 PE=4 SV=1	2.6	34.1				2.80E+06		2.80E+06
Q877T5	Elongation factor Tu OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=tufA PE=3 SV=1	64.2	43.1	1.20E+08	1.80E+08	1.70E+08	3.00E+08	3.40E+08	2.50E+08
Q87FC8	ParB family protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1751 PE=4 SV=1	3.7	35.7		1.30E+06	1.80E+06	1.70E+06	1.30E+06	
Q87FF2	Transcriptional regulator, AraC/XylS family OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1727 PE=4 SV=1	3.3	30.3						6.70E+06
Q87FF4	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1725 PE=4 SV=1	5.1	25.5		2.80E+06				
Q87FL7	Putative diaminopimelate decarboxylase protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1662 PE=3 SV=1	31.8	45.3	1.70E+07	2.50E+07	2.60E+07	2.20E+07	3.20E+07	2.70E+07
Q87FL8	Putative AcsD OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1661 PE=4 SV=1	11.8	69.4	8.20E+06	1.20E+07	1.20E+07	9.10E+06	1.40E+07	1.10E+07
Q87FM0	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1659 PE=4 SV=1	48.5	68.7	5.20E+07	7.90E+07	7.50E+07	6.70E+07	9.20E+07	7.60E+07
Q87FM1	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1658 PE=4 SV=1	36.2	44.2	3.70E+07	5.70E+07	5.50E+07	5.70E+07	7.20E+07	6.40E+07
Q87FM2	Ferric siderophore receptor homolog OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1657 PE=3 SV=1	10.6	74.9		5.40E+06	6.70E+06	5.90E+06	7.40E+06	8.90E+06
Q87FM3	Ferric vibrioferrin receptor OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1656 PE=3 SV=1	9.6	78.8		4.50E+06	5.30E+06	5.30E+06	7.20E+06	9.20E+06
Q87FN1	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1648 PE=4 SV=1	6.3	62.7		2.00E+06	2.80E+06	3.10E+06	3.60E+06	3.00E+06
Q87FQ8	Alpha-1,4 glucan phosphorylase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1620 PE=3 SV=1	23.0	92.3	1.50E+07	1.70E+07	2.00E+07	1.20E+07	2.80E+07	1.30E+07
Q87FQ9	4-alpha-glucanotransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1619 PE=3 SV=1	20.7	81.8	7.60E+06	8.90E+06	8.40E+06	7.50E+06	1.00E+07	6.00E+06
Q87FR0	1,4-alpha-glucan branching enzyme GlgB OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=glgB PE=3 SV=1	1.3	87.4					5.80E+06	
Q87FV6	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1572 PE=4 SV=1	19.8	41.8	3.20E+06	2.40E+06	3.80E+06	6.40E+06	7.40E+06	7.50E+06
Q87G18	L-lactate dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=lldD PE=3 SV=1	2.9	41.4					3.40E+06	1.90E+06
Q87G21	Prolyl endopeptidase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1496 PE=4 SV=1	14.5	76.0	2.10E+06	4.20E+06	5.90E+06	4.50E+06	9.80E+06	7.10E+06
Q87G42	Purine nucleoside phosphorylase DeoD-type 2 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=deoD2 PE=3 SV=1	15.7	25.7			5.20E+06	1.00E+07		8.10E+06
Q87G48	Outer membrane lipoprotein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1469 PE=4 SV=1	16.7	8.7			2.20E+06	2.70E+06	3.40E+06	4.20E+06
Q87G89	Azurin OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1428 PE=4 SV=1	24.0	15.8	1.80E+07	3.00E+07	2.20E+07	6.00E+07	3.20E+07	3.30E+07
Q87GA0	Putative glutathione S-transferase family protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1417 PE=3 SV=1	7.8	23.6		5.00E+06	5.90E+06	6.60E+06	6.60E+06	7.80E+06
Q87GB6	Maltose ABC transporter, periplasmic maltose-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1401 PE=4 SV=1	67.3	42.1	5.40E+07	6.50E+07	5.50E+07	8.60E+07	9.70E+07	6.90E+07
Q87GC0	Acyl-CoA thioester hydrolase-related protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1397 PE=4 SV=1	47.8	17.7	1.20E+07	1.70E+07	1.70E+07	1.60E+07	2.40E+07	2.10E+07
Q87GK7	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1308 PE=4 SV=1	10.5	42.3		3.60E+06	5.80E+06		1.00E+07	1.20E+07
Q87GL1	Putative 3-oxoacyl-(Acyl carrier protein) reductase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1304 PE=3 SV=1	7.5	25.2	4.30E+06	5.70E+06	6.10E+06	5.30E+06	1.00E+07	9.50E+06
Q87GL7	Putative glutathione S-transferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1298 PE=4 SV=1	9.8	32.2		4.60E+06	4.30E+06	5.80E+06		3.80E+06
Q87GT5	Glyceraldehyde-3-phosphate dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1230 PE=3 SV=1	22.4	52.3	9.00E+06	1.40E+07	5.20E+06	2.50E+07	6.40E+06	5.80E+06
Q87GU2	UPF0502 protein VPA1223 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1223 PE=3 SV=1	4.2	23.9						1.80E+06
Q87GW0	Acetoacetyl-CoA reductase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1205 PE=3 SV=1	16.3	26.2					9.60E+06	6.50E+06
Q87GW1	Acetyl-CoA acetyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1204 PE=3 SV=1	19.4	41.5				2.40E+06	9.20E+06	9.60E+06
Q87GX9	Outer membrane protein OmpA OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1186 PE=3 SV=1	4.3	36.0						2.50E+06
Q87GY0	Phospho-2-dehydro-3-deoxyheptonate aldolase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1185 PE=3 SV=1	27.1	38.3	1.30E+07	1.40E+07	3.10E+07	1.70E+07	1.90E+07	1.50E+07
Q87GY4	Transketolase 2 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=tkt2 PE=3 SV=1	24.7	72.0	7.20E+06	8.60E+06	8.00E+06	1.20E+07	1.30E+07	1.10E+07
Q87GY5	Transaldolase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=tal PE=3 SV=1	61.7	34.8	2.10E+07	2.50E+07	2.40E+07	3.30E+07	3.20E+07	2.90E+07
Q87H02	Oxidoreductase, aldo/keto reductase 2 family OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1163 PE=4 SV=1	4.6	34.0					3.50E+06	
Q87H16	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1149 PE=4 SV=1	10.4	45.3	5.30E+06	1.10E+07	8.30E+06	9.10E+06	6.80E+06	9.00E+06
Q87HD1	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1034 PE=4 SV=1	5.8	55.3					7.90E+06	4.50E+06
Q87HD8	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1027 PE=4 SV=1	19.5	17.7					1.00E+07	5.60E+06
Q87HF4	L-allo-threonine aldolase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1011 PE=4 SV=1	22.2	36.1	4.60E+06	7.10E+06	6.60E+06	7.40E+06	1.10E+07	5.60E+06
Q87HG0	D-lactate dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1005 PE=4 SV=1	2.5	64.3		4.30E+06	5.60E+06			4.30E+06
Q87HI4	Ferric aerobactin receptor OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0979 PE=3 SV=1	1.8	79.2						2.90E+06
Q87HM7	Amino acid biosynthesis aminotransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0936 PE=4 SV=1	25.1	43.7	5.00E+06	7.60E+06	6.40E+06	8.10E+06	9.00E+06	7.50E+06
Q87HP1	NAD(P) transhydrogenase subunit alpha OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0922 PE=3 SV=1	5.4	54.8		1.60E+06				
Q87HP4	Transcriptional regulator OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0919 PE=4 SV=1	12.7	24.9				5.60E+06	6.00E+06	5.70E+06
Q87HS4	Heme transport protein HutA OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0882 PE=3 SV=1	8.8	77.3		4.90E+06	5.70E+06	3.50E+06	5.40E+06	5.10E+06
Q87HV6	UPF0312 protein VPA0850 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0850 PE=3 SV=1	27.0	20.3	8.00E+06	8.70E+06	9.90E+06	1.10E+07	1.20E+07	9.80E+06
Q87HY6	Amino acid ABC transporter, periplasmic amino acid-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0820 PE=4 SV=1	3.3	30.6						2.10E+06

Table S1

Q87I01	Aminomethyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0805 PE=3 SV=1	7.5	40.3	1.70E+06	3.20E+06	3.40E+06	4.50E+06	5.00E+06	3.70E+06
Q87I11	Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta 2 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=accD2 PE=3 SV=1	4.8	32.1	2.30E+06	3.60E+06		3.80E+06	5.00E+06	
Q87I98	Putative acetyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0708 PE=4 SV=1	5.5	20.9			3.00E+06	3.00E+06	5.50E+06	
Q87IE9	Iron(III) ABC transporter, periplasmic iron-compound-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0657 PE=4 SV=1	25.5	33.5	2.90E+06	1.10E+07	1.30E+07	1.40E+07	2.00E+07	1.60E+07
Q87IG4	Putative glutathione S-transferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0642 PE=4 SV=1	10.2	24.3						3.60E+06
Q87IG5	Putative transcriptional regulator, LysR family OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0641 PE=4 SV=1	2.9	30.7					4.00E+06	
Q87IG9	Arginine ABC transporter, periplasmic arginine-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0637 PE=3 SV=1	15.0	27.3	2.10E+06		3.60E+06	8.60E+06	6.90E+06	5.00E+06
Q87IJ5	Acetate kinase 2 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=ackA2 PE=3 SV=1	32.7	42.6	1.10E+07	1.60E+07	1.60E+07	1.30E+07	2.70E+07	2.00E+07
Q87IL1	ATP-binding component of molybdate transport system OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0595 PE=4 SV=1	3.9	55.4	2.30E+06	2.40E+06				
Q87IP0	Alcohol dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0566 PE=4 SV=1	24.9	40.2	1.40E+07	1.70E+07	7.00E+06	8.50E+06	1.30E+07	9.50E+06
Q87IQ4	Cold shock DNA-binding domain protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0552 PE=4 SV=1	36.2	7.5	5.20E+06	1.20E+07	1.10E+07	2.80E+07	1.90E+07	1.70E+07
Q87IS1	Putative phosphomannomutase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0535 PE=3 SV=1	29.6	61.6	1.40E+07	1.70E+07	1.50E+07	2.20E+07	2.10E+07	1.70E+07
Q87IW3	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0493 PE=4 SV=1	3.8	29.0					2.00E+06	
Q87IY8	Prolyl endopeptidase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0468 PE=4 SV=1	2.7	84.2		4.10E+06	4.90E+06		9.70E+06	6.30E+06
Q87IZ0	Universal stress protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0466 PE=3 SV=1	8.5	16.3		2.90E+06		8.60E+06		
Q87J24	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0429 PE=4 SV=1	6.8	20.2			8.20E+06	1.40E+07	1.90E+07	1.20E+07
Q87J25	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0428 PE=4 SV=1	6.4	19.1					7.70E+06	5.60E+06
Q87J26	Coproporphyrinogen oxidase homolog PhuW OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0427 PE=4 SV=1	7.9	50.4		3.10E+06			4.80E+06	
Q87J30	Hemin ABC transporter, periplasmic hemin-binding protein HutB OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0423 PE=4 SV=1	4.5	30.3				2.40E+06		
Q87J33	LuxT OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0420 PE=1 SV=1	15.0	17.5				2.20E+06	4.90E+06	
Q87J34	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0419 PE=1 SV=1	15.2	10.9		3.90E+06		6.00E+06		3.60E+06
Q87J41	NH(3)-dependent NAD(+) synthetase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=nadE PE=3 SV=1	6.2	30.2			1.90E+06			
Q87J81	Phosphoenolpyruvate synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0372 PE=3 SV=1	51.1	88.1	6.40E+07	9.00E+07	6.40E+07	7.20E+07	8.30E+07	5.30E+07
Q87J86	Putrescine-binding periplasmic protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0367 PE=3 SV=1	20.6	38.7	5.70E+06	8.10E+06	7.90E+06	1.10E+07	1.00E+07	1.30E+07
Q87JD5	Putative outer membrane protein OmpV OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0318 PE=4 SV=1	4.7	28.1		4.60E+06	6.20E+06	3.40E+06	1.20E+07	7.50E+06
Q87JF1	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0302 PE=4 SV=1	7.0	14.7					2.30E+06	
Q87JK3	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0246 PE=4 SV=1	3.0	45.6						1.70E+06
Q87JR8	Phospho-beta-glucosidase B OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0180 PE=3 SV=1	3.7	53.0		2.50E+06	1.50E+06		5.40E+06	2.40E+06
Q87JS8	Biosynthetic arginine decarboxylase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=speA PE=3 SV=1	3.0	72.0			1.90E+06	1.40E+06		
Q87JT2	Putative outer membrane protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0166 PE=4 SV=1	11.5	38.0	1.10E+07	1.20E+07	1.50E+07	1.20E+07	2.00E+07	1.50E+07
Q87JV9	Putative PmbA-related protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0139 PE=4 SV=1	2.9	47.7					2.30E+06	2.30E+06
Q87JW5	Putative ABC transporter substrate-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0133 PE=4 SV=1	4.4	34.7		2.60E+06				
Q87JW7	Hydroxyethylthiazole kinase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=thiM PE=3 SV=1	7.6	27.7				2.20E+06		3.00E+06
Q87JZ1	Putative transcriptional regulator OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0107 PE=4 SV=1	3.8	35.6						
Q87K02	Outer membrane protein OmpW OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0096 PE=4 SV=1	6.5	23.5	7.20E+06	3.40E+06	4.60E+06			5.10E+06
Q87K43	Chitinase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0055 PE=3 SV=1	3.1	90.0	3.50E+06					
Q87K60	Glucosamine-6-phosphate deaminase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=nagB PE=3 SV=1	23.7	29.6		8.60E+06		1.40E+07	6.70E+06	1.10E+07
Q87KA4	ATP synthase subunit b OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=atpF PE=3 SV=1	9.0	17.5		2.00E+06		1.30E+06		2.70E+06
Q87KA5	ATP synthase subunit delta OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=atpH PE=3 SV=1	8.5	19.4					5.50E+06	
Q87KA6	ATP synthase subunit alpha OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=atpA PE=3 SV=1	61.4	56.6	5.20E+07	7.20E+07	6.70E+07	7.00E+07	9.60E+07	7.10E+07
Q87KA7	ATP synthase gamma chain OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=atpG PE=3 SV=1	22.9	31.8	8.20E+06	1.00E+07	1.10E+07	1.20E+07	1.60E+07	1.00E+07
Q87KA8	ATP synthase subunit beta OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=atpD PE=3 SV=1	56.5	50.7	4.20E+07	5.90E+07	5.10E+07	5.80E+07	8.50E+07	6.20E+07
Q87KB5	L-threonine dehydratase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=ilvA PE=3 SV=1	5.4	56.6	4.20E+06	5.10E+06	5.00E+06	7.10E+06	7.40E+06	8.00E+06
Q87KB6	Dihydroxy-acid dehydratase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=ilvD PE=3 SV=1	38.5	65.6	1.40E+07	1.90E+07	1.60E+07	2.20E+07	2.30E+07	1.90E+07
Q87KB7	Branched-chain amino acid amiotransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP3060 PE=3 SV=1	13.8	34.3	1.10E+07	1.00E+07	1.30E+07	2.00E+07	2.20E+07	2.00E+07
Q87KC3	Thiol:disulfide interchange protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP3054 PE=3 SV=1	4.5	22.8		2.60E+06	3.00E+06	4.50E+06		4.90E+06
Q87KF0	Phosphomethylpyrimidine synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=thiC PE=3 SV=1	2.0	72.4		1.90E+06				
Q87KF6	Aminopeptidase P OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP3021 PE=4 SV=1	9.9	65.5	3.20E+06	7.10E+06	5.00E+06	6.40E+06	6.30E+06	5.70E+06
Q87KH7	Transcription termination factor Rho OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rho PE=3 SV=1	2.6	46.8				2.10E+06		
Q87KJ3	Diaminopimelate decarboxylase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=lysA PE=3 SV=1	24.7	45.9	3.60E+06	4.50E+06	4.50E+06	4.60E+06	6.40E+06	7.10E+06
Q87KP9	Transcription termination/antitermination protein NusG OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=nusG PE=3 SV=2	5.5	20.7			5.80E+06	7.30E+06	9.80E+06	
Q87KQ0	50S ribosomal protein L11 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplK PE=3 SV=1	40.8	14.7	2.50E+06	5.30E+06	6.90E+06	2.30E+07	1.60E+07	1.20E+07
Q87KQ1	50S ribosomal protein L1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplA PE=3 SV=1	43.8	24.7	1.50E+07	2.10E+07	2.50E+07	3.90E+07	4.30E+07	3.50E+07
Q87KQ3	50S ribosomal protein L7/L12 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplL PE=3 SV=1	29.5	12.2	9.40E+06	1.80E+07	1.40E+07	4.70E+07	3.90E+07	2.90E+07
Q87KQ4	DNA-directed RNA polymerase subunit beta OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpoB PE=3 SV=1	38.1	149.5	1.20E+07	1.40E+07	1.60E+07	1.50E+07	2.00E+07	1.40E+07
Q87KQ5	DNA-directed RNA polymerase subunit beta' OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpoC PE=3 SV=1	30.7	154.8	1.10E+07	1.40E+07	1.40E+07	1.60E+07	2.70E+07	1.50E+07
Q87KQ6	Regulator of sigma D OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2920 PE=3 SV=1	9.8	18.6		4.40E+06			1.00E+07	7.30E+06
Q87KR5	DNA-binding protein HU-2 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2911 PE=3 SV=1	63.7	9.6	2.90E+07	2.90E+07	3.50E+07	6.80E+07	6.50E+07	5.80E+07
Q87KT0	Bifunctional purine biosynthesis protein PurH OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=purH PE=3 SV=1	20.9	57.3	4.40E+06	6.70E+06	5.70E+06	8.60E+06	1.40E+07	7.40E+06
Q87KU4	Acetyl-CoA carboxylase, biotin carboxylase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2881 PE=4 SV=1	30.0	49.2	7.60E+06	1.00E+07	1.90E+07	1.00E+07	1.40E+07	1.20E+07
Q87KU7	Acetyl-coenzyme A synthetase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=acsA PE=3 SV=1	28.0	71.7	1.80E+07	2.30E+07	2.10E+07	1.30E+07	1.60E+07	2.00E+07
Q87KV2	Fumarate hydratase class II OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=fumC PE=3 SV=1	32.8	48.7	4.20E+07	5.90E+07	6.20E+07	6.30E+07	8.40E+07	6.60E+07
Q87KW2	Aspartate ammonia-lyase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2863 PE=3 SV=1	3.9	52.7	1.70E+06	3.80E+06	3.30E+06	3.90E+06	4.10E+06	
Q87KW5	Superoxide dismutase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2860 PE=3 SV=1	34.2	23.0	1.40E+07	1.90E+07	2.20E+07	2.70E+07	4.60E+07	2.80E+07
Q87KX0	ATP-dependent 6-phosphofructokinase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=pfkA PE=3 SV=1	17.2	34.6	8.20E+06	1.10E+07	1.10E+07	9.30E+06	1.70E+07	9.10E+06
Q87KX9	Elongation factor P OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=efp PE=3 SV=1	6.4	20.6				1.40E+07	1.70E+07	1.20E+07
Q87KZ3	Protein-export protein SecB OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=secB PE=3 SV=1	23.4	17.2		3.50E+06		5.70E+06	1.20E+07	9.60E+06
Q87KZ5	2,3-bisphosphoglycerate-independent phosphoglycerate mutase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=gpmI PE=3 SV=1	24.5	55.1	7.40E+06	1.10E+07	1.30E+07	1.50E+07	1.90E+07	1.60E+07
Q87L07	RNA-binding protein Hfq OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=hfq PE=3 SV=1	25.3	9.8	6.00E+06	8.10E+06	9.60E+06	1.60E+07	1.60E+07	1.50E+07
Q87L13	Tryptophan--tRNA ligase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=trpS PE=3 SV=1	3.6	37.6			1.90E+06	2.40E+06	2.70E+06	2.60E+06
Q87L20	Acetylornithine aminotransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=argD PE=3 SV=1	26.8	43.3	6.30E+06	1.20E+07	8.40E+06	1.10E+07	1.00E+07	9.70E+06
Q87L22	N-succinylglutamate 5-semialdehyde dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=astD PE=3 SV=1	3.9	52.0		4.00E+06	2.00E+06	3.40E+06		
Q87L23	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2794 PE=4 SV=1	32.7	29.2	2.60E+06	9.60E+06	6.00E+06	2.10E+07	1.20E+07	1.20E+07
Q87L33	Peptidyl-prolyl cis-trans isomerase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2783 PE=4 SV=1	19.7	20.4				1.30E+07	1.30E+07	8.60E+06
Q87L44	30S ribosomal protein S7 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpsG PE=3 SV=1	44.9	17.7	9.60E+06	4.40E+06	1.40E+07	1.60E+07	1.30E+07	1.10E+07
Q87L45	Elongation factor G 1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=fusA1 PE=3 SV=1	14.4	77.5	4.30E+06	4.10E+06	4.40E+06	6.00E+06	8.60E+06	3.90E+06
Q87L48	Putative malate oxidoreductase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2767 PE=3 SV=1	8.5	46.1	2.70E+06	3.70E+06	3.70E+06	4.20E+06	6.70E+06	5.40E+06
Q87L50	Cystathionine gamma-synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2765 PE=3 SV=1	9.6	41.8		6.10E+06	6.30E+06	6.90E+06	8.90E+06	5.40E+06
Q87L51	Aspartokinase II/homoserine dehydrogenase, methionine-sensitive OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2764 PE=4 SV=1	7.7	87.8	1.60E+06	1.70E+06		2.80E+06	2.90E+06	2.60E+06
Q87L52	Methylenetetrahydrofolate reductase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2763 PE=3 SV=1	24.7	33.3	6.30E+06	7.90E+06	8.80E+06	8.30E+06	1.60E+07	1.30E+07
Q87L54	Phosphoenolpyruvate carboxylase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=ppc PE=3 SV=2	22.3	99.2	6.20E+06	9.80E+06	1.00E+07	9.10E+06	1.30E+07	1.00E+07
Q87L55	N-acetyl-gamma-glutamyl-phosphate reductase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=argC PE=3 SV=1	5.1	36.2	3.90E+06	6.30E+06	5.20E+06	5.60E+06	7.40E+06	6.50E+06
Q87L68	3-dehydroquinate synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=aroB PE=3 SV=1	12.3	40.0			3.40E+06	3.20E+06	6.90E+06	3.50E+06
Q87L72	30S ribosomal protein S6 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpsF PE=3 SV=1	23.3	15.0	6.30E+06	6.80E+06	1.30E+07	2.10E+07	2.00E+07	1.70E+07
Q87L75	50S ribosomal protein L9 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplI PE=3 SV=1	46.0	15.7	5.70E+06	1.20E+07	1.40E+07	2.40E+07	2.30E+07	2.00E+07
Q87L81	Glucose-6-phosphate isomerase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=pgi PE=3 SV=1	34.9	60.9	1.80E+07	2.30E+07	2.50E+07	2.30E+07	3.00E+07	2.90E+07
Q87L90	Sulfite reductase [NADPH] flavoprotein alpha-component OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=cysJ PE=3 SV=1	3.0	68.7				3.90E+06		
Q87L91	Sulfite reductase [NADPH] hemoprotein beta-component OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=cysI PE=3 SV=1	4.2	64.8		3.50E+06	2.70E+06		4.60E+06	3.70E+06
Q87L96	Aspartokinase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2715 PE=3 SV=1	24.7	48.8	4.70E+06	1.00E+07	8.80E+06	1.20E+07	1.20E+07	1.10E+07
Q87LA1	UTP--glucose-1-phosphate uridylyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2711 PE=3 SV=1	4.1	32.3		2.90E+06		4.00E+06	3.50E+06	3.00E+06
Q87LA3	Single-stranded DNA-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=ssb PE=3 SV=1	13.6	19.6			1.00E+07	8.60E+06	1.20E+07	1.20E+07
Q87LB4	Putative V10 pilin OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2698 PE=4 SV=1	31.5	16.8	5.80E+06	6.60E+06	9.20E+06	1.00E+07	1.10E+07	9.10E+06
Q87LF6	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2656 PE=4 SV=1	12.4	13.8				3.70E+06		
Q87LF8	Aspartate carbamoyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=pyrB PE=3 SV=1	4.2	34.5			4.10E+06		5.50E+06	
Q87LF9	Ornithine carbamoyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=argF PE=3 SV=1	35.9	37.3	2.20E+07	2.30E+07	1.80E+07	2.60E+07	3.40E+07	2.70E+07
Q87LG8	Probable cytosol aminopeptidase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=pepA PE=3 SV=1	8.0	54.4		1.40E+06	3.50E+06		5.30E+06	
Q87LH4	Deacetylase DA1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2638 PE=4 SV=1	8.9	47.0	1.80E+07					
Q87LH6	Permease IIC component OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2636 PE=4 SV=1	4.3	48.7					9.40E+06	4.60E+06

Q87LH7	PTS system, cellobiose-specific IIA component OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2635 PE=4 SV=1	31.1	11.6				1.30E+06	2.10E+07	1.00E+07
Q87LH8	6-phospho-beta-glucosidase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2634 PE=3 SV=1	55.7	48.3				6.70E+06	7.60E+07	3.40E+07
Q87LH9	Carbohydrate deacetylase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2633 PE=3 SV=1	5.2	28.0					1.10E+07	
Q87LK1	Glutathione synthetase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=gshB PE=3 SV=1	8.2	35.2	3.20E+06	3.50E+06	4.40E+06	7.30E+06	9.10E+06	7.40E+06
Q87LK2	Ribosomal RNA small subunit methyltransferase E OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2610 PE=3 SV=1	4.9	27.2						1.70E+06
Q87LK6	S-adenosylmethionine synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=metK PE=3 SV=1	11.7	42.0	5.20E+06	6.00E+06	7.50E+06	6.00E+06	8.50E+06	7.40E+06
Q87LK8	Transketolase 1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=tkt1 PE=3 SV=1	23.9	72.0	1.20E+07	1.50E+07	1.50E+07	1.50E+07	1.80E+07	1.60E+07
Q87LL1	Phosphoglycerate kinase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=pgk PE=3 SV=1	43.8	40.7	1.50E+07	2.40E+07	3.10E+07	3.90E+07	5.40E+07	4.20E+07
Q87LL2	Fructose-bisphosphate aldolase, class II OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2599 PE=4 SV=1	67.0	38.9	4.70E+07	6.90E+07	7.50E+07	7.80E+07	1.10E+08	9.40E+07
Q87LL8	D-3-phosphoglycerate dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2593 PE=3 SV=1	42.4	44.7	1.50E+07	2.10E+07	1.80E+07	2.30E+07	3.00E+07	2.10E+07
Q87LM8	tRNA-modifying protein YgfZ OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2583 PE=3 SV=1	3.4	35.5		2.80E+06	2.20E+06	3.30E+06		3.70E+06
Q87LN1	L-aspartate oxidase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2580 PE=3 SV=1	8.7	60.9	4.70E+06	3.10E+06	2.00E+06	3.90E+06	5.10E+06	
Q87LN5	Sigma-E factor regulatory protein RseB OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2576 PE=4 SV=1	2.8	36.0				1.30E+06		
Q87LP2	Pyridoxine 5'-phosphate synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=pdxJ PE=3 SV=1	6.2	26.7		3.10E+07			3.30E+06	
Q87LP9	CTP synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=pyrG PE=3 SV=1	10.8	60.1	3.60E+06	5.50E+06	2.80E+06	5.70E+06	7.60E+06	6.50E+06
Q87LQ0	Enolase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=eno PE=3 SV=1	54.5	45.5	2.80E+07	3.80E+07	4.10E+07	6.60E+07	8.70E+07	7.10E+07
Q87LQ8	RNA polymerase sigma factor RpoS OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpoS PE=3 SV=1	24.8	36.5	1.30E+06	3.60E+06	3.60E+06	6.20E+06	7.70E+06	1.20E+07
Q87LR1	Protein RecA OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=recA PE=3 SV=1	34.9	37.4	9.30E+06	5.70E+06	1.30E+07	1.30E+07	1.70E+07	1.30E+07
Q87LR3	Alanine--tRNA ligase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=alaS PE=3 SV=1	6.2	93.9		4.10E+06	3.60E+06	4.30E+06	4.00E+06	4.40E+06
Q87LR5	Carbon storage regulator homolog OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=csrA PE=3 SV=1	18.5	7.1	3.00E+06		4.00E+06	9.60E+06	8.90E+06	1.40E+07
Q87LS4	S-ribosylhomocysteine lyase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=luxS PE=3 SV=1	12.2	19.0				4.70E+06	4.30E+06	3.30E+06
Q87LT1	50S ribosomal protein L19 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplS PE=3 SV=2	40.2	13.2	3.70E+06	4.40E+06	1.80E+07	2.00E+07	1.60E+07	1.10E+07
Q87LU2	Pyruvate dehydrogenase E1 component OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2519 PE=4 SV=1	36.4	99.6	4.60E+07	3.60E+07	4.20E+07	3.30E+07	4.40E+07	3.50E+07
Q87LU3	Acetyltransferase component of pyruvate dehydrogenase complex OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2518 PE=3 SV=1	26.3	64.9	1.30E+07	1.40E+07	2.10E+07	1.70E+07	2.10E+07	1.80E+07
Q87LW2	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2496 PE=4 SV=1	1.7	86.2						
Q87LW3	Aconitate hydratase B OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2495 PE=3 SV=1	29.0	94.0	2.50E+07	1.90E+07	1.70E+07	1.30E+07	2.00E+07	1.20E+07
Q87LW7	Iron(III) ABC transporter, periplasmic iron-compound-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2491 PE=4 SV=1	40.1	37.7	2.70E+07	3.80E+07	2.90E+07	4.90E+07	5.20E+07	4.40E+07
Q87LX0	Putative phosphoglucomutase/phosphomannomutase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2488 PE=4 SV=1	5.3	52.3						4.90E+06
Q87LX1	N,N'-diacetylchitobiose phosphorylase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2487 PE=4 SV=1	20.0	90.0				3.70E+06	8.10E+06	1.70E+07
Q87LX9	Peptide ABC transporter, periplasmic peptide-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2479 PE=4 SV=1	21.3	62.9				3.80E+06	2.40E+07	4.60E+07
Q87LZ1	Outer membrane protein U OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=ompU PE=3 SV=1	19.3	36.3	3.00E+06	5.50E+06	8.70E+06	9.20E+06	1.20E+07	9.10E+06
Q87LZ2	Transcription elongation factor GreA OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=greA PE=3 SV=1	7.0	17.5				3.00E+06		
Q87LZ5	ATP-dependent zinc metalloprotease FtsH OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=ftsH PE=3 SV=1	2.7	72.9		3.10E+06				
Q87M01	Transcription termination/antitermination protein NusA OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=nusA PE=3 SV=1	14.3	54.9	6.00E+06	9.00E+06	8.40E+06	6.50E+06	6.50E+06	7.20E+06
Q87M02	Translation initiation factor IF-2 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=infB PE=3 SV=1	10.5	99.3	3.50E+06	6.10E+06	5.40E+06	7.20E+06	9.00E+06	7.00E+06
Q87M05	30S ribosomal protein S15 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpsO PE=3 SV=1	6.7	10.1	9.20E+06	8.80E+06	1.30E+07	1.40E+07		
Q87M06	Polyribonucleotide nucleotidyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=pnp PE=3 SV=1	35.9	76.7	6.10E+06	1.00E+07	1.30E+07	1.10E+07	1.40E+07	1.20E+07
Q87M22	Deoxyribose-phosphate aldolase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=deoC PE=3 SV=1	4.3	27.7	3.40E+06	5.80E+06	3.20E+06	9.50E+06	6.60E+06	5.70E+06
Q87M25	Purine nucleoside phosphorylase DeoD-type 1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=deoD1 PE=3 SV=1	10.0	25.9		3.70E+06		6.70E+06	9.00E+06	5.80E+06
Q87M27	Phosphoserine phosphatase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2431 PE=4 SV=1	4.6	35.8		2.20E+06				
Q87M30	Elongation factor G 2 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=fusA2 PE=3 SV=1	48.3	76.3	3.50E+07	5.40E+07	5.50E+07	6.30E+07	7.80E+07	6.10E+07
Q87M55	Beta-galactosidase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2403 PE=3 SV=1	1.6	118.9	3.20E+06					
Q87M78	2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-succinyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=dapD PE=3 SV=1	21.0	35.6	5.30E+06	1.10E+07	7.70E+06	1.10E+07	1.80E+07	1.50E+07
Q87MC3	Proline--tRNA ligase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=proS PE=3 SV=1	16.5	63.2	3.20E+06	4.70E+06	4.50E+06	5.90E+06	6.50E+06	4.10E+06
Q87MD8	30S ribosomal protein S2 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpsB PE=3 SV=1	7.0	26.8				6.20E+06		
Q87MD9	Elongation factor Ts OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=tsf PE=3 SV=1	66.5	29.8	3.30E+07	4.50E+07	4.80E+07	5.60E+07	7.50E+07	6.50E+07
Q87ME6	Chaperone protein skp OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2309 PE=3 SV=1	21.1	18.5	3.30E+06	3.50E+06	6.10E+06	6.40E+06	6.00E+06	5.30E+06
Q87ME8	3-hydroxyacyl-[acyl-carrier-protein] dehydratase FabZ OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=fabZ PE=3 SV=1	8.0	16.8			2.70E+06	2.60E+06		2.80E+06
Q87MG7	Phosphoheptose isomerase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=gmhA PE=3 SV=1	11.5	20.8		1.20E+06	3.30E+06	4.30E+06	4.30E+06	
Q87MH0	Phosphoribosylformylglycinamidine cyclo-ligase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=purM PE=3 SV=1	5.5	36.8					4.70E+06	
Q87MI2	4-hydroxy-tetrahydrodipicolinate synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=dapA PE=3 SV=1	40.4	31.2	9.60E+06	1.50E+07	1.40E+07	1.80E+07	2.80E+07	2.10E+07
Q87MI6	Succinyl-diaminopimelate desuccinylase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=dapE PE=3 SV=1	3.4	41.0						2.80E+06
Q87MM8	50S ribosomal protein L3 glutamine methyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=prmB PE=3 SV=1	3.5	35.2						
Q87MM9	Chorismate synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=aroC PE=3 SV=1	7.5	39.0		2.70E+06	2.70E+06	4.80E+06	4.80E+06	
Q87MN7	3-oxoacyl-[acyl-carrier-protein] synthase I OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2194 PE=3 SV=1	19.6	42.6	6.00E+06	3.10E+07	5.50E+06	8.30E+06	1.10E+07	9.00E+06
Q87MN9	Aspartate-semialdehyde dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=asd PE=3 SV=1	4.5	37.2				4.70E+06		
Q87MP2	Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta 1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=accD1 PE=3 SV=1	7.5	34.0	2.50E+06	3.60E+06		4.10E+06	5.90E+06	5.00E+06
Q87MP6	Amidophosphoribosyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=purF PE=3 SV=1	6.9	56.0	2.30E+06			2.50E+06	2.40E+06	
Q87MR4	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2167 PE=4 SV=1	11.7	11.1				3.50E+06		
Q87MS4	Glyceraldehyde-3-phosphate dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2157 PE=3 SV=1	58.6	35.2	6.20E+07	8.40E+07	1.00E+08	1.20E+08	1.60E+08	1.20E+08
Q87MV7	Aspartate-semialdehyde dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=asd PE=3 SV=1	56.1	40.2	2.10E+07	3.00E+07	2.70E+07	3.10E+07	3.70E+07	3.40E+07
Q87MW0	Aldehyde-alcohol dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2121 PE=1 SV=1	26.3	97.1	1.40E+07	1.90E+07	1.90E+07	1.90E+07	2.70E+07	2.20E+07
Q87MW3	Superoxide dismutase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2118 PE=3 SV=1	6.5	22.2					3.30E+06	
Q87MY5	Oligopeptide ABC transporter, periplasmic oligopeptide-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2091 PE=4 SV=1	2.5	62.3					4.70E+06	
Q87MZ3	Phosphate acetyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2083 PE=3 SV=1	34.3	76.6	6.80E+06	9.30E+06	1.00E+07	9.80E+06	1.30E+07	1.20E+07
Q87MZ4	Acetate kinase 1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=ackA1 PE=3 SV=1	26.4	43.0	7.60E+06	1.20E+07	1.20E+07	1.40E+07	1.90E+07	1.60E+07
Q87MZ6	ABC transporter substrate-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2080 PE=4 SV=1	17.4	33.2	3.00E+06	5.90E+06	4.80E+06	6.80E+06	8.50E+06	7.90E+06
Q87N07	Methionine--tRNA ligase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=metG PE=3 SV=2	8.0	77.9	3.40E+06	5.10E+06	4.60E+06	5.20E+06	6.00E+06	4.90E+06
Q87N14	Ribonuclease E OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rne PE=3 SV=1	2.1	114.1		3.00E+06				
Q87N15	Ribosomal large subunit pseudouridine synthase C OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rluC PE=3 SV=1	2.2	36.1	2.60E+06					
Q87N21	Malonyl CoA-acyl carrier protein transacylase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2055 PE=3 SV=1	5.5	32.3		7.70E+06		1.00E+07	1.30E+07	1.00E+07
Q87N29	PTS system, glucose-specific IIBC component OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2046 PE=4 SV=1	5.3	49.4		4.90E+06	4.40E+06	7.30E+06		7.20E+06
Q87N42	Oxidoreductase, short-chain dehydrogenase/reductase family OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2033 PE=3 SV=1	4.0	27.0					3.30E+06	2.10E+06
Q87N45	30S ribosomal protein S1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2030 PE=3 SV=1	46.2	60.9	3.80E+07	5.30E+07	7.90E+07	7.30E+07	9.30E+07	6.90E+07
Q87N50	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2025 PE=4 SV=1	6.2	76.6	1.80E+06	5.30E+06	4.00E+06	4.50E+06	5.90E+06	5.60E+06
Q87N83	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1992 PE=4 SV=1	14.5	37.6		5.20E+06	6.50E+06	3.10E+06	9.40E+06	6.20E+06
Q87N88	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1987 PE=4 SV=1	6.0	20.0				2.40E+06	3.70E+06	3.80E+06
Q87NA1	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=metE PE=3 SV=1	61.4	84.7	9.00E+07	1.00E+08	1.20E+08	1.20E+08	1.80E+08	1.50E+08
Q87NB4	Putative metal-dependent phosphoesterase YciV OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1954 PE=4 SV=1	7.7	31.9						
Q87NB5	Putative translation factor OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1953 PE=4 SV=1	4.9	22.9		1.90E+07				
Q87NC0	Elongation factor P-like protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1948 PE=3 SV=1	13.8	20.7		4.30E+06		5.80E+06	9.70E+06	8.50E+06
Q87NC6	Diaminobutyrate-pyruvate transaminase & L-2,4-diaminobutyrate decarboxylase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1942 PE=1 SV=1	1.4	104.3						
Q87NC7	Putative carboxynorspermidine dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1941 PE=4 SV=1	8.2	46.5		2.60E+06		4.50E+06	5.10E+06	
Q87ND6	DNA gyrase subunit A OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=gyrA PE=3 SV=1	9.0	97.0	2.00E+06	3.60E+06	3.40E+06	2.70E+06	6.30E+06	3.30E+06
Q87NE7	GTP cyclohydrolase-2 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=ribA PE=3 SV=1	5.6	22.3				3.10E+06		2.80E+06
Q87NG8	Aspartate aminotransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1900 PE=3 SV=1	62.8	45.4	7.00E+07	1.00E+08	1.10E+08	9.60E+07	1.40E+08	1.20E+08
Q87NH5	Asparagine--tRNA ligase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=asnS PE=3 SV=1	43.6	52.6	2.60E+07	3.00E+07	3.00E+07	3.30E+07	4.00E+07	3.60E+07
Q87NU8	Putative exopolyphosphatase Ppx1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1770 PE=4 SV=1	2.5	34.5						8.20E+06
Q87P08	Glucose-6-phosphate 1-dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=zwf PE=3 SV=1	2.0	57.6						
Q87P09	DevB protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1709 PE=4 SV=1	4.2	26.0				6.90E+06	8.60E+06	
Q87P10	6-phosphogluconate dehydrogenase, decarboxylating OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1708 PE=3 SV=1	18.7	52.5	7.10E+06	8.70E+06	8.80E+06	9.90E+06	1.20E+07	1.10E+07
Q87P15	Aldehyde dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1703 PE=3 SV=1	9.5	55.7		4.30E+06		7.70E+06		
Q87P20	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1698 PE=4 SV=1	2.1	38.5		3.90E+06			4.40E+06	
Q87P32	Adenosine monophosphate-protein transferase VopS OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=vopS PE=1 SV=1	13.7	41.7	2.60E+06	3.60E+06	3.20E+06		3.10E+06	2.00E+06

Q87P47	Putative translocation protein in type III secretion OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1671 PE=4 SV=1	3.4	36.4		2.40E+06				
Q87P59	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1659 PE=4 SV=1	17.0	67.0	4.00E+06	1.00E+07	9.20E+06	3.30E+06	9.20E+06	5.30E+06
Q87P60	Low calcium response locus protein H OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1658 PE=4 SV=1	25.9	18.1		4.30E+06		3.10E+06	6.00E+06	4.10E+06
Q87P61	Putative translocator protein PopB OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1657 PE=4 SV=1	3.8	41.3		2.10E+06	2.90E+06			1.70E+06
Q87P62	Putative translocator protein PopD OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1656 PE=4 SV=1	5.1	35.3	4.60E+06	5.30E+06	7.30E+06	4.60E+06	6.60E+06	4.90E+06
Q87P63	Immunogenic protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1655 PE=4 SV=1	2.8	34.9		3.10E+07		2.90E+07	4.00E+07	3.00E+07
Q87PB0	RNA chaperone ProQ OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=proQ PE=3 SV=1	4.8	23.2			6.70E+06	9.40E+06	7.60E+06	7.20E+06
Q87PB3	Aminopeptidase N OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1604 PE=4 SV=1	1.3	98.4		1.50E+06				
Q87PB5	Putative NAD-glutamate dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1602 PE=4 SV=1	0.4	183.4		1.00E+06				
Q87PB8	Cell division protein ZapC OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=zapC PE=3 SV=1	4.4	20.8	2.20E+06					3.10E+06
Q87PC5	3-hydroxydecanoyl-[acyl-carrier-protein] dehydratase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=fabA PE=3 SV=1	22.1	19.0	1.60E+07	1.20E+07	1.60E+07	1.40E+07	2.00E+07	1.60E+07
Q87PE6	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1564 PE=4 SV=1	13.9	56.4	3.60E+06	7.60E+06	5.10E+06	5.10E+06	7.40E+06	5.60E+06
Q87PG6	Fumarate and nitrate reduction regulatory protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1536 PE=4 SV=1	4.4	27.8			2.00E+06	1.30E+06	3.00E+06	
Q87PG7	Putative stress protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1535 PE=4 SV=1	13.7	35.3		2.50E+06		3.60E+06	4.60E+06	2.10E+06
Q87PH6	Putrescine-binding periplasmic protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1526 PE=3 SV=1	3.9	39.7			8.10E+06	8.40E+06	1.10E+07	8.60E+06
Q87PK8	N-acetyl-D-glucosamine kinase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=nagK PE=3 SV=1	8.9	32.8			9.20E+05		4.40E+06	3.50E+06
Q87PU8	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1403 PE=4 SV=1	9.0	55.5	4.90E+06	2.80E+06	3.30E+06		2.90E+06	
Q87Q40	Succinylglutamate desuccinylase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=astE PE=1 SV=1	4.4	38.8		2.70E+06				
Q87Q45	Adenosylcobinamide-GDP ribazoletransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=cobS PE=3 SV=1	2.6	29.2				5.60E+06		5.40E+06
Q87Q53	Phosphoribosylglycinamide formyltransferase 2 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=purT PE=3 SV=1	3.6	42.9						2.80E+06
Q87Q56	Integration host factor subunit alpha OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=ihfA PE=3 SV=1	19.4	11.2	6.20E+06		7.90E+06	3.00E+07	2.20E+07	
Q87Q59	Phenylalanine--tRNA ligase beta subunit OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=pheT PE=3 SV=1	4.7	87.0	3.00E+06	5.70E+06	6.20E+06	7.90E+06	9.80E+06	5.20E+06
Q87Q60	Phenylalanine--tRNA ligase alpha subunit OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=pheS PE=3 SV=1	6.4	36.9		2.90E+06	3.50E+06	4.40E+06	5.40E+06	4.10E+06
Q87Q70	Threonine--tRNA ligase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=thrS PE=3 SV=1	8.9	73.7	4.40E+06	9.50E+06	5.00E+06	1.10E+07	7.60E+06	7.60E+06
Q87Q80	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1270 PE=4 SV=1	2.1	112.8		1.90E+07		2.70E+07		2.50E+07
Q87Q87	Phosphoribosylaminoimidazole-succinocarboxamide synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=purC PE=3 SV=1	11.4	41.0	2.40E+06	5.40E+06	5.70E+06	7.50E+06	1.00E+07	6.50E+06
Q87Q92	NAD-dependent malic enzyme OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=maeA PE=3 SV=1	1.6	62.3			4.10E+06	5.00E+06		
Q87Q99	Thioredoxin reductase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1251 PE=3 SV=1	10.3	34.5	2.90E+06	5.10E+06	2.10E+06	5.30E+06	1.00E+07	5.80E+06
Q87QA3	Phosphoserine aminotransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=serC PE=3 SV=1	28.0	40.2	9.30E+06	1.20E+07	1.10E+07	1.50E+07	1.60E+07	1.40E+07
Q87QB0	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1240 PE=4 SV=1	4.9	34.4	6.40E+06	8.90E+06	5.50E+06	6.10E+06		6.20E+06
Q87QB9	Putative reductase VP1231 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1231 PE=3 SV=1	38.3	43.9	1.40E+07	1.80E+07	2.10E+07	2.00E+07	2.70E+07	2.10E+07
Q87QG7	Cystathionine beta-lyase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1182 PE=3 SV=1	3.2	44.6	3.60E+06		5.00E+06	5.50E+06	6.90E+06	7.00E+06
Q87QJ9	Cysteine--tRNA ligase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=cysS PE=3 SV=1	11.3	52.0	1.80E+06	4.30E+06	2.60E+06	3.50E+06	3.00E+06	3.10E+06
Q87QK5	Histidine biosynthesis bifunctional protein HisIE OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=hisI PE=3 SV=1	15.2	23.2				2.30E+06		
Q87QK6	Imidazole glycerol phosphate synthase subunit HisF OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=hisF PE=3 SV=1	6.2	28.4				1.20E+06		
Q87QK7	1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino] imidazole-4-carboxamide isomerase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=hisA PE=3 SV=1	14.7	26.4				4.60E+06	5.50E+06	4.40E+06
Q87QK8	Imidazole glycerol phosphate synthase subunit HisH OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=hisH PE=3 SV=1	6.9	22.3					9.70E+06	
Q87QK9	Histidine biosynthesis bifunctional protein HisB OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=hisB PE=3 SV=1	6.2	39.8		2.50E+06		1.80E+06	3.50E+06	
Q87QL0	Histidinol-phosphate aminotransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=hisC PE=3 SV=1	10.1	38.2	5.70E+06	6.30E+06	5.60E+06	7.70E+06	8.70E+06	9.00E+06
Q87QL1	Histidinol dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=hisD PE=3 SV=1	5.8	46.1			3.20E+06	4.00E+06	5.80E+06	4.50E+06
Q87QL2	ATP phosphoribosyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=hisG PE=3 SV=1	25.8	32.8	4.10E+06	6.90E+06	4.80E+06	8.80E+06	1.20E+07	9.00E+06
Q87QL6	DNA-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1133 PE=3 SV=1	9.6	15.1						
Q87QM1	Adenylosuccinate lyase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1128 PE=3 SV=1	26.1	51.4	5.20E+06	8.70E+06	9.20E+06	9.30E+06	1.30E+07	8.40E+06
Q87QP1	Serine--tRNA ligase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=serS PE=3 SV=1	33.1	48.8	7.80E+06	1.10E+07	1.10E+07	9.80E+06	1.50E+07	1.40E+07
Q87QP5	Leucine-responsive regulatory protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1104 PE=4 SV=1	31.1	18.8	5.70E+06	7.00E+06	4.70E+06	7.40E+06	1.00E+07	4.80E+06
Q87QP6	Alanine dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1103 PE=3 SV=1	42.2	39.9	1.70E+07	3.30E+07	2.10E+07	3.10E+07	2.20E+07	2.00E+07
Q87QP8	Cys regulon transcriptional activator OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1101 PE=4 SV=1	3.7	36.1						
Q87QS7	Putative helicase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1072 PE=4 SV=1	16.0	68.7	4.30E+06	5.80E+06	4.60E+06	4.60E+06	7.80E+06	5.80E+06
Q87QT9	Protein TolB OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=tolB PE=3 SV=1	7.3	49.8	9.60E+05	5.10E+06	5.00E+06	5.50E+06	6.40E+06	3.50E+06
Q87QV2	Aspartate--tRNA ligase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=aspS PE=3 SV=1	35.6	65.7	1.10E+07	1.70E+07	1.60E+07	1.50E+07	2.20E+07	1.60E+07
Q87QW9	HTH-type transcriptional repressor PurR OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=purR PE=3 SV=1	4.2	37.7			1.90E+06			
Q87QX6	Glucose-1-phosphate adenylyltransferase 1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=glgC1 PE=3 SV=1	26.2	45.5	1.60E+07	1.90E+07	1.90E+07	1.70E+07	2.50E+07	1.90E+07
Q87QX9	3-phosphoshikimate 1-carboxyvinyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=aroA PE=3 SV=1	4.7	46.1	2.20E+06		4.60E+06		5.00E+06	5.20E+06
Q87QY4	ATP-dependent Clp protease, ATP-binding subunit ClpA OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1014 PE=3 SV=1	4.2	83.3		2.20E+06			5.30E+06	2.90E+06
Q87QY7	Isocitrate dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1011 PE=4 SV=1	48.9	80.5	2.10E+07	2.70E+07	2.60E+07	2.50E+07	3.50E+07	2.80E+07
Q87QZ9	Amino acid ABC transporter, periplasmic amino acid-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0999 PE=3 SV=1	57.4	28.4	7.00E+06	1.20E+07	1.10E+07	1.50E+07	2.20E+07	1.60E+07
Q87R02	Putative 54 kDa polar flagellar sheath protein A OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0996 PE=4 SV=1	2.1	52.3						
Q87R04	Formate acetyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0994 PE=4 SV=1	47.4	84.5	3.50E+07	3.90E+07	4.20E+07	5.10E+07	7.30E+07	6.20E+07
Q87R36	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0962 PE=4 SV=1	21.2	43.9		4.90E+06	1.20E+07	6.50E+06	8.40E+06	8.80E+06
Q87R38	Uridine phosphorylase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0960 PE=3 SV=1	11.5	26.9	1.50E+06	7.40E+06	7.70E+06	7.00E+06	7.50E+06	6.50E+06
Q87R78	DNA-binding protein HU-beta OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0920 PE=3 SV=1	28.9	9.4	4.70E+07	4.30E+07	5.10E+07	9.10E+07	7.70E+07	6.60E+07
Q87R80	ATP-dependent Clp protease proteolytic subunit OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=clpP PE=3 SV=1	16.0	22.0	1.30E+07	2.20E+07	1.50E+07	2.00E+07	3.20E+07	2.50E+07
Q87R81	Trigger factor OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=tig PE=3 SV=1	53.5	48.2	1.50E+07	1.90E+07	2.30E+07	3.60E+07	4.80E+07	3.40E+07
Q87R87	C4-dicarboxylate-binding periplasmic protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0910 PE=4 SV=1	24.7	37.1	1.20E+07	4.80E+06	7.30E+06	2.00E+07	1.80E+07	1.50E+07
Q87RD3	Formyltetrahydrofolate deformylase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=purU PE=3 SV=1	3.2	31.6	5.30E+06	6.90E+06	7.30E+06	4.40E+06	7.60E+06	
Q87RD6	Arginine--tRNA ligase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=argS PE=3 SV=1	10.6	63.8		4.60E+06	3.30E+06	5.20E+06	6.60E+06	5.80E+06
Q87RE4	Zinc ABC transporter, periplasmic zinc-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0853 PE=3 SV=1	11.3	32.1	3.40E+06	4.00E+06	4.70E+06	6.00E+06	5.70E+06	3.90E+06
Q87RE7	Succinyl-CoA ligase [ADP-forming] subunit alpha OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0850 PE=3 SV=1	16.6	30.0	6.10E+06	1.50E+07	1.00E+07	1.40E+07	1.60E+07	1.20E+07
Q87RE8	Succinyl-CoA ligase [ADP-forming] subunit beta OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=sucC PE=3 SV=1	50.5	41.5	2.80E+07	4.30E+07	3.30E+07	3.90E+07	5.10E+07	3.50E+07
Q87RE9	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0848 PE=3 SV=1	33.2	43.7	1.90E+07	2.80E+07	2.60E+07	3.00E+07	3.10E+07	2.60E+07
Q87RF0	2-oxoglutarate dehydrogenase, E1 component OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0847 PE=4 SV=1	13.0	106.0	6.90E+06	8.90E+06	7.20E+06	7.70E+06	6.20E+06	5.40E+06
Q87RF2	Succinate dehydrogenase flavoprotein subunit OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0845 PE=3 SV=1	8.2	64.2	4.80E+06	1.10E+07	4.80E+06	8.40E+06	1.20E+07	9.40E+06
Q87RF5	Citrate synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0842 PE=3 SV=1	41.5	48.2	3.60E+07	4.50E+07	4.30E+07	3.70E+07	5.30E+07	4.00E+07
Q87RF8	Phosphoglucomutase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0839 PE=3 SV=1	22.1	59.2	6.60E+06	9.90E+06	1.10E+07	1.00E+07	1.50E+07	1.30E+07
Q87RG4	Glutamine--tRNA ligase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=glnS PE=3 SV=1	8.3	63.9	4.20E+06	6.10E+06	4.80E+06	5.70E+06	9.00E+06	5.20E+06
Q87RG8	N-acetylglucosamine repressor OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0828 PE=4 SV=1	2.5	43.8					2.60E+06	
Q87RH0	Asparagine synthetase B, glutamine-hydrolyzing OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0826 PE=4 SV=1	19.5	62.3	3.80E+06	3.90E+06	5.40E+06	6.90E+06	8.30E+06	7.30E+06
Q87RH4	Adenylate kinase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=adk PE=3 SV=1	20.6	23.3	3.10E+06	5.50E+06	4.90E+06	6.00E+06	6.50E+06	5.80E+06
Q87RH5	Chaperone protein HtpG OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=htpG PE=3 SV=1	6.0	72.1	2.50E+06	2.40E+06	6.20E+06	4.20E+06	5.40E+06	8.00E+06
Q87RJ7	Cysteine synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0797 PE=3 SV=1	72.4	34.1	5.90E+07	6.40E+07	7.80E+07	7.30E+07	1.10E+08	9.20E+07
Q87RJ9	Phosphocarrier protein HPr OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0795 PE=4 SV=1	9.4	9.1				1.20E+07		
Q87RK0	Phosphoenolpyruvate-protein phosphotransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0794 PE=3 SV=1	20.9	63.2		5.30E+06	6.40E+06	1.00E+07	1.10E+07	1.10E+07
Q87RK1	PTS system, glucose-specific IIA component OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0793 PE=4 SV=1	30.8	17.9	7.00E+06	8.00E+06	8.60E+06	2.80E+07	2.60E+07	1.80E+07
Q87RL6	Glutamate--tRNA ligase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=gltX PE=3 SV=1	27.0	53.4	6.60E+06	9.20E+06	9.20E+06	9.90E+06	1.20E+07	8.00E+06
Q87RL8	Putative chitoporin OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0760 PE=4 SV=1	11.8	40.8						1.40E+07
Q87RN8	Ribose-phosphate pyrophosphokinase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=prs PE=3 SV=1	38.5	33.9	6.50E+06	1.00E+07	1.00E+07	1.20E+07	1.60E+07	1.10E+07
Q87RP0	Ribosome-binding ATPase YchF OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=ychF PE=3 SV=1	3.1	41.8					4.10E+06	3.30E+06
Q87RQ0	Leucine--tRNA ligase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=leuS PE=3 SV=1	10.2	96.6	4.30E+06	5.60E+06	5.60E+06	6.60E+06	7.60E+06	6.40E+06
Q87RR2	Serine hydroxymethyltransferase 1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=glyA1 PE=3 SV=1	46.2	45.5	3.50E+07	5.20E+07	5.60E+07	6.50E+07	8.80E+07	6.30E+07
Q87RS3	Lipoprotein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0704 PE=3 SV=1	19.7	29.1			3.50E+06		5.60E+06	5.70E+06
Q87RU4	6,7-dimethyl-8-ribityllumazine synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=ribH PE=3 SV=1	36.5	16.4	2.70E+06	3.90E+06	4.10E+06	8.40E+06	7.70E+06	5.60E+06
Q87RU5	3,4-dihydroxy-2-butanone 4-phosphate synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=ribB PE=3 SV=1	11.4	40.1	1.70E+06	2.30E+06	1.70E+06	4.90E+06	6.10E+06	3.00E+06
Q87RU9	Gamma-glutamyl phosphate reductase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=proA PE=3 SV=1	17.1	44.7	2.30E+06	4.80E+06	3.70E+06	4.10E+06	6.20E+06	5.10E+06
Q87RV5	Aminoacyl-histidine dipeptidase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0671 PE=4 SV=1	3.1	53.6		2.60E+06	2.00E+06			

Q87RV7	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0669 PE=4 SV=1	20.5	39.0	2.70E+06	7.80E+06	7.70E+06	6.90E+06	5.70E+06	9.30E+06
Q87RW0	Phosphoribosylformylglycinamidine synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=purL PE=3 SV=1	13.4	141.6	3.60E+06	5.80E+06	6.40E+06	6.80E+06	1.10E+07	6.10E+06
Q87RX2	Chaperone protein DnaJ OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=dnaJ PE=3 SV=1	3.1	41.0					3.00E+06	2.60E+06
Q87RX3	Chaperone protein DnaK OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=dnaK PE=3 SV=1	52.3	69.0	8.70E+06	1.50E+07	1.70E+07	2.40E+07	3.40E+07	2.70E+07
Q87RZ5	Homocysteine synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0629 PE=3 SV=1	2.8	45.7	4.50E+05				1.60E+06	
Q87S07	GMP synthase [glutamine-hydrolyzing] OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=guaA PE=3 SV=1	6.6	57.6	5.10E+06	6.30E+06	3.80E+06	8.10E+06	9.00E+06	5.30E+06
Q87S08	Inosine-5'-monophosphate dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=guaB PE=3 SV=1	26.5	51.9	4.50E+06	8.00E+06	7.50E+06	8.60E+06	1.20E+07	8.10E+06
Q87S15	Histidine--tRNA ligase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=hisS PE=3 SV=1	5.5	47.1			2.00E+06	7.00E+06		2.30E+06
Q87S20	Nucleoside diphosphate kinase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=ndk PE=3 SV=1	6.4	15.9						1.50E+06
Q87S21	Peptidase B OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=pepB PE=3 SV=1	8.3	46.6		6.00E+06	4.40E+06	7.50E+06	7.70E+06	
Q87S40	Isocitrate lyase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0584 PE=4 SV=1	2.5	48.0				4.00E+06		
Q87S44	Antioxidant, AhpC/Tsa family OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0580 PE=4 SV=1	58.1	22.2	3.40E+07	5.00E+07	5.20E+07	9.30E+07	9.40E+07	8.10E+07
Q87S63	Chaperone protein ClpB OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=clpB PE=3 SV=1	14.5	95.8	2.80E+06	4.80E+06	5.50E+06	6.40E+06	7.10E+06	6.90E+06
Q87S69	Chorismate mutase/prephenate dehydratase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0555 PE=4 SV=1	3.1	44.2		1.40E+06			1.50E+06	1.30E+06
Q87S73	ABC transporter, ATP-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0551 PE=3 SV=1	5.2	62.2		7.20E+05				3.20E+06
Q87S77	T-protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0547 PE=4 SV=1	2.1	42.0						2.10E+06
Q87S78	Phospho-2-dehydro-3-deoxyheptonate aldolase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0546 PE=3 SV=1	2.0	39.7			4.00E+06		5.70E+06	5.40E+06
Q87S84	Putative carbon starvation protein A OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0540 PE=4 SV=1	2.4	53.3			1.70E+06			1.70E+06
Q87S90	Isoleucine--tRNA ligase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=ileS PE=3 SV=1	2.0	105.2	2.90E+06	2.70E+06	2.10E+06	3.30E+06		3.50E+06
Q87S93	30S ribosomal protein S20 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpsT PE=3 SV=1	11.6	9.5					7.20E+06	
Q87S99	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0525 PE=4 SV=1	3.1	43.9		2.80E+06				
Q87SA8	Oxidoreductase Tas, aldo/keto reductase family OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0516 PE=4 SV=1	14.2	39.7	4.20E+06	6.70E+06	5.80E+06	6.60E+06	6.50E+06	7.50E+06
Q87SB0	Sigma-54 dependent transcriptional regulator OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0514 PE=4 SV=1	2.0	49.6					3.00E+06	
Q87SB1	Lysine--tRNA ligase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=lysS PE=3 SV=1	30.1	57.5	1.20E+07	3.80E+07	1.40E+07	1.60E+07	1.30E+07	1.50E+07
Q87SC7	Autonomous glycyl radical cofactor OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=grcA PE=3 SV=1	73.6	13.9	7.90E+06	1.10E+07	9.20E+06	3.30E+07	3.80E+07	3.10E+07
Q87SC8	Threonine synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0496 PE=4 SV=1	38.5	46.5	9.00E+06	1.20E+07	1.10E+07	1.30E+07	1.70E+07	1.60E+07
Q87SC9	Homoserine kinase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=thrB PE=3 SV=1	2.8	34.4	3.40E+06	3.60E+06		4.80E+06	6.20E+06	4.90E+06
Q87SD0	Aspartokinase I/homoserine dehydrogenase, threonine-sensitive OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0494 PE=4 SV=1	18.9	88.4	9.70E+06	1.20E+07	9.60E+06	1.10E+07	1.40E+07	1.10E+07
Q87SD2	Putative 4-hydroxy-4-methyl-2-oxoglutarate aldolase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0492 PE=3 SV=1	6.3	17.7						4.90E+06
Q87SD5	Aerobic respiration control protein FexA OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0489 PE=4 SV=1	9.2	26.9		7.10E+06	6.90E+06	9.70E+06	6.80E+06	1.00E+07
Q87SE0	Glutamate synthase, large subunit OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0484 PE=4 SV=1	6.1	175.2	3.20E+06	3.10E+06	3.30E+06	6.00E+06	7.80E+06	5.20E+06
Q87SE1	Glutamate synthase, small subunit OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0483 PE=4 SV=1	9.0	53.3				5.00E+06	6.60E+06	
Q87SE2	Glutamate synthase, large subunit OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0482 PE=4 SV=1	3.5	162.9	3.00E+06	4.30E+06	5.10E+06	4.40E+06		4.50E+06
Q87SE3	Glutamate synthase, small subunit OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0481 PE=4 SV=1	4.0	52.5						1.80E+06
Q87SF3	Carbamoyl-phosphate synthase large chain OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=carB PE=3 SV=1	11.4	117.8	1.20E+07	6.00E+06	6.70E+06	8.50E+06	1.20E+07	8.00E+06
Q87SF4	Carbamoyl-phosphate synthase small chain OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=carA PE=3 SV=1	15.8	41.0	2.60E+06	5.90E+06	5.50E+06	7.70E+06	1.20E+07	8.80E+06
Q87SF5	4-hydroxy-tetrahydrodipicolinate reductase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=dapB PE=3 SV=1	18.2	28.6	4.70E+06	7.30E+06	8.20E+06	1.20E+07	1.20E+07	1.00E+07
Q87SF7	Protein translocase subunit SecA OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=secA PE=3 SV=1	4.8	103.1		2.30E+06	2.30E+06	6.90E+06		3.90E+06
Q87SH9	Stringent starvation protein A OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0444 PE=3 SV=1	43.1	24.3	1.20E+07	1.80E+07	1.80E+07	1.80E+07	2.40E+07	1.90E+07
Q87SI4	30S ribosomal protein S9 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpsI PE=3 SV=1	9.2	14.6				2.50E+06		
Q87SI5	50S ribosomal protein L13 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplM PE=3 SV=1	33.1	16.0		1.60E+06	7.40E+06	9.30E+06	1.50E+07	
Q87SJ0	Protease DO OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0433 PE=4 SV=1	26.4	48.1	5.10E+06	7.20E+06	6.70E+06	8.70E+06	1.50E+07	8.60E+06
Q87SL8	RNA polymerase sigma factor RpoD OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpoD PE=3 SV=1	8.2	70.7	4.50E+06	4.30E+06	6.40E+06	8.90E+06	9.00E+06	6.60E+06
Q87SR3	Glutamine--fructose-6-phosphate aminotransferase [isomerizing] OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=glmS PE=3 SV=2	24.6	66.8	3.90E+06	8.80E+06	6.70E+06	1.10E+07	4.90E+06	1.50E+07
Q87SR6	Pyruvate kinase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0356 PE=3 SV=1	15.7	49.9	4.00E+06	3.80E+06	4.90E+06	5.90E+06	1.30E+07	9.40E+06
Q87SS7	2-isopropylmalate synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=leuA PE=3 SV=1	8.7	56.1	3.40E+06	4.20E+06	3.50E+06	5.40E+06	4.80E+06	5.90E+06
Q87SS8	3-isopropylmalate dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=leuB PE=3 SV=1	40.8	39.3	1.00E+07	1.40E+07	1.30E+07	1.80E+07	2.10E+07	1.70E+07
Q87SS9	3-isopropylmalate dehydratase large subunit OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=leuC PE=3 SV=1	2.1	50.6		2.30E+06		6.40E+05	1.40E+06	
Q87ST4	Chaperone SurA OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=surA PE=3 SV=1	2.3	47.4						4.70E+06
Q87SU4	50S ribosomal protein L21 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplU PE=3 SV=1	60.2	11.5	1.10E+07	1.20E+07	1.80E+07	2.30E+07	2.60E+07	2.10E+07
Q87SU5	Octaprenyl-diphosphate synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0327 PE=3 SV=1	3.3	36.4			1.20E+06			
Q87SU7	Malate dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=mdh PE=3 SV=1	61.7	32.2	2.80E+07	3.60E+07	2.50E+07	3.70E+07	5.10E+07	2.70E+07
Q87SV0	Immunogenic protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0323 PE=4 SV=1	53.7	34.5	4.30E+07	5.10E+07	5.30E+07	5.20E+07	7.00E+07	6.10E+07
Q87SW0	Fructose-1,6-bisphosphatase class 1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=fbp PE=3 SV=1	29.9	37.3	8.00E+06	2.00E+07	9.90E+06	1.30E+07	7.30E+06	7.20E+06
Q87SW1	Inorganic pyrophosphatase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=ppa PE=3 SV=1	19.3	19.6			2.70E+06	1.10E+07	8.60E+06	7.00E+06
Q87SW6	Peptide methionine sulfoxide reductase MsrA OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=msrA PE=3 SV=1	9.9	23.6					3.00E+06	3.30E+06
Q87SX0	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0302 PE=4 SV=1	3.8	23.3	3.50E+06	4.50E+06	6.50E+06		1.50E+07	8.40E+06
Q87SX9	Sulfate adenylyltransferase subunit 1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=cysN PE=3 SV=1	22.5	52.6	5.70E+06	7.10E+06	7.20E+06	1.00E+07	1.40E+07	1.60E+07
Q87SY0	Sulfate adenylyltransferase subunit 2 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=cysD PE=3 SV=1	3.6	35.0		4.90E+06	5.10E+06	4.60E+06	7.10E+06	6.40E+06
Q87SY1	Uroporphyrin-III C-methyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0291 PE=3 SV=1	3.6	33.0					5.30E+06	
Q87SY2	2',3'-cyclic-nucleotide 2'-phosphodiesterase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0290 PE=3 SV=1	1.8	72.1				1.20E+06		
Q87SY7	Peptidyl-prolyl cis-trans isomerase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0285 PE=4 SV=1	6.3	21.8				5.20E+06	7.30E+06	4.20E+06
Q87SY9	50S ribosomal protein L17 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplQ PE=3 SV=1	38.9	14.2	1.00E+07	1.30E+07	1.90E+07	1.70E+07	2.30E+07	1.60E+07
Q87SZ0	DNA-directed RNA polymerase subunit alpha OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpoA PE=3 SV=1	43.0	36.5	1.30E+07	1.70E+07	1.70E+07	2.80E+07	3.60E+07	2.60E+07
Q87SZ1	30S ribosomal protein S4 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpsD PE=3 SV=1	39.3	23.3	2.30E+07	2.10E+07	3.50E+07	4.10E+07	4.20E+07	3.40E+07
Q87SZ2	30S ribosomal protein S13 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpsM PE=3 SV=1	56.8	13.3	1.00E+07	6.10E+06	1.70E+07	2.20E+07	2.00E+07	1.50E+07
Q87SZ4	50S ribosomal protein L15 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplO PE=3 SV=1	31.3	14.9	6.20E+06	9.60E+06	9.30E+06	1.50E+07	1.70E+07	1.40E+07
Q87SZ6	30S ribosomal protein S5 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpsE PE=3 SV=1	51.5	17.6	1.70E+07	1.70E+07	2.70E+07	2.80E+07	3.30E+07	2.40E+07
Q87SZ7	50S ribosomal protein L18 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplR PE=3 SV=1	15.4	12.6			3.20E+06	9.40E+06	6.50E+06	6.80E+06
Q87SZ8	50S ribosomal protein L6 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplF PE=3 SV=1	72.3	18.8	1.20E+07	1.00E+07	1.70E+07	2.80E+07	2.30E+07	1.40E+07
Q87SZ9	30S ribosomal protein S8 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpsH PE=3 SV=1	23.8	14.0	1.90E+07	2.00E+07	2.60E+07	3.40E+07	3.80E+07	2.60E+07
Q87T01	50S ribosomal protein L5 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplE PE=3 SV=1	52.0	20.1	1.60E+07	2.20E+07	2.80E+07	3.60E+07	3.90E+07	3.20E+07
Q87T02	50S ribosomal protein L24 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplX PE=3 SV=1	20.0	11.2	1.00E+07	1.10E+07	1.10E+07	2.60E+07	1.10E+07	7.20E+06
Q87T07	30S ribosomal protein S3 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpsC PE=3 SV=1	36.2	25.6	1.20E+07	1.50E+07	2.10E+07	2.40E+07	2.60E+07	2.20E+07
Q87T08	50S ribosomal protein L22 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplV PE=3 SV=1	38.2	12.1	1.10E+07	1.20E+07	1.10E+07	2.00E+07	1.70E+07	1.40E+07
Q87T09	30S ribosomal protein S19 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpsS PE=3 SV=1	8.7	10.4	4.00E+06		1.10E+07	1.20E+07	1.50E+07	7.60E+06
Q87T11	50S ribosomal protein L23 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplW PE=3 SV=1	15.0	11.1				1.20E+07		
Q87T12	50S ribosomal protein L4 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplD PE=3 SV=1	25.5	21.9				9.50E+06	6.50E+06	5.60E+06
Q87T13	50S ribosomal protein L3 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplC PE=3 SV=1	13.9	22.4			2.00E+06	6.80E+06		6.20E+06
Q87T21	ATP-dependent protease ATPase subunit HslU OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=hslU PE=3 SV=1	6.8	49.8	2.70E+06					4.40E+06
Q87T23	Regulator of ribonuclease activity A OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rraA PE=3 SV=1	11.2	18.4				3.20E+06		
Q87T31	Triosephosphate isomerase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=tpiA PE=3 SV=1	23.0	26.9	6.00E+06	7.40E+06	8.60E+06	1.30E+07	1.40E+07	1.50E+07
Q87T34	Nucleotide sugar dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0236 PE=3 SV=1	21.6	43.1	5.10E+06	7.40E+06	5.80E+06	8.40E+06	1.20E+07	6.50E+06
Q87T36	Pilin glycosylation protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0234 PE=3 SV=1	36.8	43.4	1.70E+07	2.30E+07	2.30E+07	2.30E+07	3.00E+07	2.40E+07
Q87T38	Putative carbamoylphosphate synthase large subunit, short form OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0232 PE=4 SV=1	12.1	36.4	6.60E+06	1.10E+07			4.10E+06	1.20E+07
Q87T41	dTDP-4-dehydrorhamnose 3,5-epimerase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0229 PE=4 SV=1	16.0	21.2	4.10E+06	6.80E+06	5.20E+06	1.00E+07	7.90E+06	6.50E+06
Q87T46	Putative dTDP-4-dehydrorhamnose reductase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0224 PE=4 SV=1	11.0	32.4			4.20E+06	3.70E+06	6.50E+06	5.00E+06
Q87T47	Glucose-1-phosphate thymidylyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0223 PE=3 SV=1	16.5	32.3	4.00E+06	6.90E+06	5.00E+06	4.30E+06	7.90E+06	7.60E+06
Q87T48	dTDP-glucose 4,6-dehydratase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0222 PE=3 SV=1	12.2	40.9	5.90E+06	1.00E+07	1.10E+07	1.40E+07	1.90E+07	1.50E+07
Q87T63	Putative oxidoreductase (Flagellin modification) OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0207 PE=4 SV=1	14.2	27.4		4.10E+06	4.30E+06		5.60E+06	3.00E+06
Q87T64	Putative amidohydrolase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0206 PE=4 SV=1	3.3	30.7		2.20E+06				
Q87T65	Putative glutamate-1-semialdehyde 2,1-aminomutase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0205 PE=3 SV=1	8.2	48.9	2.40E+06	4.70E+06	2.50E+06	4.40E+06	7.20E+06	3.30E+06
Q87T66	Putative 3-chlorobenzoate-3,4-dioxygenase dyhydrogenase related protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0204 PE=4 SV=1	10.8	38.5		3.80E+06		4.90E+06	6.00E+06	
Q87T85	50S ribosomal protein L28 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpmB PE=3 SV=1	12.8	9.0				7.70E+06		
Q87T98	Putative binding protein component of ABC transporter OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0172 PE=4 SV=1	1.8	69.6		4.80E+06	4.00E+06	4.70E+06	5.90E+06	4.80E+06
Q87TA8	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0162 PE=4 SV=1	2.7	45.5	1.90E+07	1.80E+07		2.30E+07		6.60E+06
Q87TE0	33 kDa chaperonin OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=hslO PE=3 SV=1	3.1	32.3					2.90E+06	
Q87TE1	Phosphoenolpyruvate carboxykinase [ATP] OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=pckA PE=3 SV=1	62.9	60.0	5.50E+07	7.10E+07	5.00E+07	8.20E+07	6.30E+07	6.80E+07
Q87TE8	Glutamine synthetase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0121 PE=3 SV=1	45.0	51.5	5.00E+07	6.10E+07	6.70E+07	7.90E+07	8.40E+07	7.40E+07
Q87TG5	Delta-aminolevulinic acid dehydratase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0104 PE=3 SV=1	14.2	39.2	4.60E+06	7.20E+06	7.10E+06	6.60E+06	7.40E+06	5.40E+06

Q87TJ9	Oligopeptidase A OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0070 PE=3 SV=1	11.9	76.9	2.10E+07	3.30E+07	9.30E+06	4.20E+07	6.20E+07	1.70E+07
Q87TK1	Glutathione reductase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0068 PE=3 SV=1	22.4	49.2	1.10E+07	1.40E+07	1.50E+07	1.60E+07	2.10E+07	1.90E+07
Q87TM1	Peptide ABC transporter, periplasmic peptide-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0048 PE=4 SV=1	63.2	57.4	4.50E+07	5.60E+07	6.40E+07	6.50E+07	8.50E+07	6.80E+07
Q87TN4	Ketol-acid reductoisomerase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=ilvC PE=3 SV=1	57.3	54.7	2.90E+07	4.00E+07	3.70E+07	4.30E+07	6.90E+07	5.10E+07
Q87TP7	Glycine--tRNA ligase alpha subunit OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=glyQ PE=3 SV=1	8.5	34.9	2.70E+06	4.20E+06	2.40E+06	3.90E+06	4.90E+06	5.50E+06
Q87TP8	Glycine--tRNA ligase beta subunit OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=glyS PE=3 SV=1	20.1	76.2	2.90E+06	4.30E+06	3.80E+06	4.60E+06	6.00E+06	3.90E+06
Q87TR0	Amino acid ABC transporter, periplasmic amino acid-binding portion OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0008 PE=3 SV=1	6.0	27.5			2.60E+06			
Q8GRF5	Ribosome-recycling factor OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=frr PE=1 SV=1	5.4	20.6	6.40E+06	7.90E+06	1.10E+07	1.50E+07	2.10E+07	1.70E+07
Q9ALY5	Cyclic AMP receptor protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2793 PE=4 SV=1	54.8	23.7	2.30E+07	3.20E+07	3.20E+07	2.70E+07	4.40E+07	3.20E+07
Q9L5X8	BipA OS=Vibrio parahaemolyticus GN=bipA PE=1 SV=1	8.9	66.9	2.60E+06	4.40E+06	4.70E+06	6.00E+06	5.80E+06	4.70E+06
Q9L7P5	60 kDa chaperonin 1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=groL1 PE=3 SV=2	45.9	57.5	2.20E+07	2.70E+07	3.60E+07	4.10E+07	6.00E+07	4.70E+07

2nd Experiment (Insoluble Fraction)

Accession	Description	Coverage	MW [kDa]	Control	GlcNAc	GlcN	(GlcNAc)2	(GlcN)2	GlcNAc-GlcN
A7UEM1	Transhydrogenase alpha subunit (Fragment) OS=Vibrio parahaemolyticus GN=pntA PE=4 SV=1	7.0	15.5	1.80E+06	5.00E+06	2.80E+06	4.00E+06	2.90E+06	4.30E+06
O50286	Dihydrolipoyl dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=lpd PE=3 SV=2	15.4	51.0	2.10E+06	6.00E+06	2.60E+06	3.30E+06	4.20E+06	2.90E+06
P0A308	ATP synthase subunit c OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=atpE PE=3 SV=1	21.4	8.6			4.70E+06		2.80E+07	2.50E+07
P59494	Maltoporin OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=lamB PE=3 SV=1	41.2	46.9	7.80E+07	1.10E+08	7.00E+07	8.00E+07	8.50E+07	6.80E+07
P59570	Outer membrane protein OmpK OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=ompK PE=3 SV=1	20.7	29.9	6.20E+06	1.40E+07	6.40E+06	9.60E+06	8.10E+06	7.00E+06
P66346	30S ribosomal protein S10 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpsJ PE=3 SV=1	9.7	11.7						
P66478	30S ribosomal protein S18 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpsR PE=3 SV=1	10.7	8.8		2.30E+06				1.50E+06
Q877T5	Elongation factor Tu OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=tufA PE=3 SV=1	18.0	43.1	5.10E+06	8.60E+06		7.10E+06	7.90E+06	4.30E+06
Q87FL2	PTS system, glucose-specific IIBC component OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1667 PE=4 SV=1	5.8	51.1			5.60E+06		4.10E+06	5.60E+06
Q87FM2	Ferric siderophore receptor homolog OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1657 PE=3 SV=1	18.6	74.9	9.20E+06	2.10E+07	1.20E+07	1.60E+07	1.40E+07	1.50E+07
Q87FM3	Ferric vibrioferrin receptor OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1656 PE=3 SV=1	16.7	78.8	1.00E+07	2.00E+07	1.00E+07	1.10E+07	1.50E+07	1.60E+07
Q87FN5	Putative maltose operon periplasmic protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1643 PE=4 SV=1	4.5	29.1		3.80E+06				1.70E+06
Q87FP0	Putative pullulanase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1638 PE=4 SV=1	1.1	144.5	8.50E+05					
Q87G18	L-lactate dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=lldD PE=3 SV=1	32.7	41.4	1.10E+07	1.90E+07	8.80E+06	1.20E+07	1.00E+07	8.30E+06
Q87G48	Outer membrane lipoprotein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1469 PE=4 SV=1	16.7	8.7	3.90E+06	1.40E+07	8.00E+06	9.40E+06	8.80E+06	
Q87G82	Putative iron(III) compound receptor OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1435 PE=3 SV=1	1.6	77.0		8.10E+05				
Q87GB6	Maltose ABC transporter, periplasmic maltose-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1401 PE=4 SV=1	2.6	42.1	1.50E+06			2.10E+06		
Q87GK7	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1308 PE=4 SV=1	29.5	42.3	1.80E+07	2.70E+07	1.30E+07	2.30E+07	2.00E+07	2.00E+07
Q87GW2	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1203 PE=4 SV=1	32.2	13.1	7.40E+06	1.30E+07	4.70E+06	7.10E+06	8.30E+06	1.10E+07
Q87GW3	Polyhydroxyalkanoic acid synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1202 PE=4 SV=1	1.5	67.2		5.50E+06		2.90E+06	5.20E+06	
Q87GX9	Outer membrane protein OmpA OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1186 PE=3 SV=1	5.2	36.0	3.40E+06	5.20E+06	2.50E+06	4.30E+06	3.70E+06	2.90E+06
Q87HG0	D-lactate dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1005 PE=4 SV=1	2.5	64.3			4.00E+06			
Q87HI4	Ferric aerobactin receptor OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0979 PE=3 SV=1	5.9	79.2	2.10E+06	4.70E+06	3.40E+06	3.90E+06	3.00E+06	4.30E+06
Q87HP1	NAD(P) transhydrogenase subunit alpha OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0922 PE=3 SV=1	20.1	54.8	2.80E+06	1.00E+07	2.80E+06	4.90E+06	7.80E+06	6.20E+06
Q87HP2	NAD(P) transhydrogenase subunit beta OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0921 PE=3 SV=1	2.6	48.6	3.50E+06					
Q87HS4	Heme transport protein HutA OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0882 PE=3 SV=1	20.1	77.3	6.30E+06	1.70E+07	1.10E+07	1.30E+07	1.20E+07	1.00E+07
Q87J81	Phosphoenolpyruvate synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0372 PE=3 SV=1	2.3	88.1		2.50E+06		1.80E+06		
Q87JD5	Putative outer membrane protein OmpV OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0318 PE=4 SV=1	4.7	28.1	6.90E+06	1.20E+07	8.50E+06	9.20E+06	8.50E+06	9.00E+06
Q87JT2	Putative outer membrane protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0166 PE=4 SV=1	14.0	38.0	3.30E+07	4.00E+07	2.90E+07	4.00E+07	3.00E+07	2.70E+07
Q87JU6	Biopolymer transport protein ExbB-related protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0152 PE=3 SV=1	9.2	49.2	2.30E+06	3.80E+06		3.20E+06	3.40E+06	3.50E+06
Q87K02	Outer membrane protein OmpW OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0096 PE=4 SV=1	6.5	23.5	1.90E+07	1.40E+07	7.60E+06	9.90E+06	1.10E+07	7.20E+06
Q87KA3	ATP synthase subunit a OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=atpB PE=3 SV=1	3.0	30.1				2.10E+06		1.90E+06
Q87KA4	ATP synthase subunit b OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=atpF PE=3 SV=1	43.6	17.5	9.30E+06	1.70E+07	7.60E+06	7.70E+06	7.10E+06	7.30E+06
Q87KA6	ATP synthase subunit alpha OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=atpA PE=3 SV=1	17.0	56.6	5.70E+06	7.30E+06	3.80E+06	5.80E+06	6.30E+06	7.00E+06
Q87KA8	ATP synthase subunit beta OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=atpD PE=3 SV=1	23.6	50.7	2.70E+06	6.50E+06	2.40E+06	2.60E+06	4.60E+06	3.70E+06
Q87KI7	Putative uroporphyrin-III C-methyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2990 PE=4 SV=1	2.5	45.1				1.50E+06		
Q87KN9	Vitamin B12 transporter BtuB OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=btuB PE=3 SV=1	1.8	69.3				2.60E+06	1.70E+06	
Q87KQ0	50S ribosomal protein L11 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplK PE=3 SV=1	21.1	14.7		8.40E+06		6.00E+06	6.80E+06	6.00E+06
Q87KQ1	50S ribosomal protein L1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplA PE=3 SV=1	21.5	24.7	4.90E+06	1.30E+07	6.40E+06	7.50E+06	9.90E+06	9.50E+06
Q87KQ2	50S ribosomal protein L10 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplJ PE=3 SV=1	13.6	17.3		4.00E+06			3.00E+06	2.30E+06
Q87KV2	Fumarate hydratase class II OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=fumC PE=3 SV=1	3.9	48.7		1.30E+06		1.20E+06		9.40E+05
Q87KX4	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2850 PE=4 SV=1	13.6	20.2	1.30E+06			2.70E+06		
Q87L38	Peptidyl-prolyl cis-trans isomerase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2778 PE=4 SV=1	32.7	28.3	5.30E+06	7.20E+06	5.20E+06	7.90E+06	8.40E+06	5.30E+06
Q87L72	30S ribosomal protein S6 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpsF PE=3 SV=1	8.5	15.0	3.20E+06	5.90E+06				
Q87L75	50S ribosomal protein L9 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplI PE=3 SV=1	30.7	15.7	3.30E+06	4.30E+06	3.80E+06	5.10E+06	3.80E+06	2.50E+06
Q87LB4	Putative V10 pilin OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2698 PE=4 SV=1	32.1	16.8	2.20E+07	3.90E+07	2.20E+07	2.90E+07	2.40E+07	2.10E+07
Q87LH6	Permease IIC component OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2636 PE=4 SV=1	7.4	48.7					2.00E+07	1.50E+07
Q87LL3	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2598 PE=4 SV=1	6.6	31.0		3.00E+06				
Q87LQ0	Enolase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=eno PE=3 SV=1	8.3	45.5		2.60E+06			2.20E+06	
Q87LR7	Oxaloacetate decarboxylase, alpha subunit OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2544 PE=4 SV=1	5.5	64.2	5.50E+06	6.10E+06		6.30E+06	7.40E+06	4.80E+06
Q87LT1	50S ribosomal protein L19 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplS PE=3 SV=2	20.5	13.2		1.00E+07			8.20E+06	3.90E+06
Q87LU2	Pyruvate dehydrogenase E1 component OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2519 PE=4 SV=1	2.4	99.6	3.20E+06	4.80E+06	3.30E+06	2.70E+06	5.00E+06	4.50E+06
Q87LU3	Acetyltransferase component of pyruvate dehydrogenase complex OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2518 PE=3 SV=1	5.3	64.9	3.30E+06	7.00E+06	4.80E+06	4.60E+06	5.60E+06	4.20E+06
Q87LZ1	Outer membrane protein U OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=ompU PE=3 SV=1	20.5	36.3	2.30E+07	4.40E+07	1.90E+07	3.30E+07	2.40E+07	2.30E+07
Q87LZ5	ATP-dependent zinc metalloprotease FtsH OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=ftsH PE=3 SV=1	4.8	72.9		4.60E+06			4.80E+06	5.30E+06
Q87M06	Polyribonucleotide nucleotidyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=pnp PE=3 SV=1	6.8	76.7	1.10E+06	1.90E+06		1.30E+06	2.00E+06	1.60E+06
Q87MA6	Na(+)-translocating NADH-quinone reductase subunit A OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=nqrA PE=3 SV=1	5.4	48.6	2.90E+06	4.40E+06	2.60E+06	3.10E+06	3.70E+06	3.40E+06
Q87MS0	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2161 PE=4 SV=1	5.1	35.2		1.50E+06				
Q87MS4	Glyceraldehyde-3-phosphate dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2157 PE=3 SV=1	8.5	35.2					4.40E+06	7.20E+06
Q87MW0	Aldehyde-alcohol dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2121 PE=1 SV=1	1.4	97.1			1.40E+06			
Q87MY5	Oligopeptide ABC transporter, periplasmic oligopeptide-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2091 PE=4 SV=1	17.1	62.3	5.70E+06	1.60E+07	9.50E+06	1.10E+07	1.20E+07	1.10E+07
Q87N29	PTS system, glucose-specific IIBC component OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2046 PE=4 SV=1	13.0	49.4	1.20E+07	1.80E+07	1.40E+07	1.20E+07	1.30E+07	1.30E+07
Q87N45	30S ribosomal protein S1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2030 PE=3 SV=1	9.4	60.9	3.10E+06	5.30E+06	1.60E+06	3.50E+06	4.30E+06	3.50E+06
Q87NA1	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=metE PE=3 SV=1	3.8	84.7			2.30E+06	4.30E+06	3.40E+06	2.90E+06
Q87NG8	Aspartate aminotransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1900 PE=3 SV=1	2.9	45.4	8.60E+05	1.30E+06	1.20E+06	2.60E+06		
Q87PH3	Spermidine/putrescine import ATP-binding protein PotA OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=potA PE=3 SV=1	2.4	42.7		1.90E+06				
Q87Q03	Oligopeptide ABC transporter, periplasmic oligopeptide-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1347 PE=4 SV=1	1.7	60.3		9.80E+06			8.10E+06	7.10E+06
Q87QA7	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1243 PE=4 SV=1	7.7	19.8		2.90E+06	1.40E+06			
Q87QP6	Alanine dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1103 PE=3 SV=1	4.0	39.9		2.00E+06		8.40E+05		8.50E+05
Q87QT8	Peptidoglycan-associated lipoprotein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1061 PE=3 SV=1	12.6	18.7	8.00E+06	1.20E+07	9.00E+06		1.20E+07	1.00E+07
Q87QU6	Cytochrome d ubiquinol oxidase, subunit I OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1053 PE=4 SV=1	1.9	60.3	2.00E+06			3.20E+06	2.70E+06	
Q87R04	Formate acetyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0994 PE=4 SV=1	1.7	84.5		1.10E+06			1.90E+06	
Q87R31	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0967 PE=4 SV=1	8.7	21.8	3.00E+06	5.30E+06				
Q87R36	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0962 PE=4 SV=1	3.1	43.9		9.30E+06				
Q87R77	Peptidylprolyl isomerase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0921 PE=4 SV=1	2.3	68.8		1.40E+06				
Q87R78	DNA-binding protein HU-beta OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0920 PE=3 SV=1	28.9	9.4		3.20E+06				3.10E+06
Q87R81	Trigger factor OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=tig PE=3 SV=1	3.0	48.2						1.30E+06
Q87RE8	Succinyl-CoA ligase [ADP-forming] subunit beta OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=sucC PE=3 SV=1	2.8	41.5		2.10E+06		9.30E+05		
Q87RE9	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0848 PE=3 SV=1	19.7	43.7	4.50E+06	8.60E+06	3.60E+06	5.20E+06	6.90E+06	5.40E+06
Q87RF0	2-oxoglutarate dehydrogenase, E1 component OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0847 PE=4 SV=1	2.6	106.0		2.50E+06				
Q87RF5	Citrate synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0842 PE=3 SV=1	2.6	48.2		4.20E+06				
Q87RG5	PTS system, N-acetylglucosamine-specific IIABC component OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0831 PE=4 SV=1	7.1	54.5			8.20E+06	9.70E+06	9.20E+06	1.30E+07
Q87RI9	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0805 PE=4 SV=1	14.8	33.4	5.00E+06	5.90E+06		3.10E+06	3.80E+06	7.40E+06
Q87RJ7	Cysteine synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0797 PE=3 SV=1	7.1	34.1					1.70E+06	1.00E+06
Q87RL4	Outer membrane protein OmpA OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0764 PE=3 SV=1	4.1	34.1		1.60E+06	8.50E+05			
Q87RL8	Putative chitoporin OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0760 PE=4 SV=1	19.0	40.8					5.00E+06	2.40E+07

Q87RS1	Methionine import ATP-binding protein MetN OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=metN PE=1 SV=1	4.1	37.5					1.00E+06	
Q87RS3	Lipoprotein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0704 PE=3 SV=1	34.9	29.1	1.30E+07	2.30E+07	1.60E+07	1.80E+07	1.80E+07	1.80E+07
Q87RV4	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0672 PE=4 SV=1	2.8	44.8		1.40E+06				
Q87S08	Inosine-5'-monophosphate dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=guaB PE=3 SV=1	2.2	51.9		9.90E+05				
Q87S35	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0589 PE=4 SV=1	11.9	11.8	5.40E+06	9.10E+06	4.80E+06	6.00E+06		5.40E+06
Q87S84	Putative carbon starvation protein A OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0540 PE=4 SV=1	4.9	53.3	3.10E+06	7.00E+06	3.00E+06	4.80E+06	3.40E+06	3.80E+06
Q87SI4	30S ribosomal protein S9 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpsI PE=3 SV=1	9.2	14.6	2.40E+06	4.40E+06	1.70E+06	2.70E+06	4.20E+06	2.80E+06
Q87SI5	50S ribosomal protein L13 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplM PE=3 SV=1	5.6	16.0		8.60E+06			8.50E+06	
Q87SJ8	Outer membrane protein TolC OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0425 PE=4 SV=1	6.8	48.0	2.30E+06	4.20E+06		2.90E+06	2.00E+06	2.50E+06
Q87SU4	50S ribosomal protein L21 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplU PE=3 SV=1	19.4	11.5	5.30E+06	8.00E+06	3.30E+06	4.10E+06	5.50E+06	3.40E+06
Q87SU7	Malate dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=mdh PE=3 SV=1	3.9	32.2				2.00E+06		
Q87SV0	Immunogenic protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0323 PE=4 SV=1	3.4	34.5		2.10E+06			1.70E+06	2.30E+06
Q87SZ1	30S ribosomal protein S4 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpsD PE=3 SV=1	20.4	23.3	3.00E+06	4.90E+06	1.20E+06	2.30E+06	3.10E+06	3.30E+06
Q87SZ6	30S ribosomal protein S5 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpsE PE=3 SV=1	10.8	17.6		4.00E+06				4.10E+06
Q87SZ7	50S ribosomal protein L18 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplR PE=3 SV=1	14.5	12.6	1.60E+06	4.00E+06		1.60E+06	3.60E+06	
Q87SZ8	50S ribosomal protein L6 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplF PE=3 SV=1	26.0	18.8	3.90E+06	5.80E+06	5.40E+06	4.50E+06	7.60E+06	4.60E+06
Q87T01	50S ribosomal protein L5 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplE PE=3 SV=1	25.1	20.1	1.90E+06	5.40E+06	2.40E+06	7.00E+06	7.50E+06	3.60E+06
Q87T12	50S ribosomal protein L4 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplD PE=3 SV=1	11.0	21.9	5.50E+06		3.50E+06		8.20E+06	
Q87T13	50S ribosomal protein L3 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplC PE=3 SV=1	13.4	22.4	5.30E+06	1.20E+07			7.50E+06	3.50E+06
Q87T87	Methyl-accepting chemotaxis protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0183 PE=1 SV=1	2.2	60.5				1.00E+06		
Q87TA4	Putative TolR OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0166 PE=3 SV=1	17.4	49.3		6.40E+06	2.00E+06	3.40E+06	3.60E+06	4.80E+06
Q87TE8	Glutamine synthetase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0121 PE=3 SV=1	10.2	51.5	5.70E+06	9.80E+06	5.00E+06	4.20E+06	6.50E+06	6.90E+06
Q87TH1	Sec-independent protein translocase protein TatA OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=tatA PE=3 SV=1	13.6	8.8			4.90E+06			
Q87TM0	Peptide ABC transporter, permease protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0049 PE=3 SV=1	3.5	37.9	4.80E+05	3.00E+06		1.90E+06		
Q87TM1	Peptide ABC transporter, periplasmic peptide-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0048 PE=4 SV=1	2.1	57.4		3.10E+06	1.30E+06		1.30E+06	1.40E+06
Q87TM2	Peptide ABC transporter, ATP-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0047 PE=3 SV=1	3.9	63.7	1.00E+07	1.80E+06	9.30E+05	1.20E+06	5.60E+06	1.00E+06
Q87TN4	Ketol-acid reductoisomerase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=ilvC PE=3 SV=1	11.5	54.7	1.70E+06	3.50E+06		1.80E+06	2.90E+06	2.70E+06
Q9ALY5	Cyclic AMP receptor protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2793 PE=4 SV=1	10.5	23.7	2.10E+06	3.50E+06			2.70E+06	4.70E+06
Q9L7P5	60 kDa chaperonin 1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=groL1 PE=3 SV=2	3.7	57.5	2.20E+06	4.10E+06		3.10E+06	3.40E+06	3.80E+06
Q9LCJ0	Na(+)-translocating NADH-quinone reductase subunit F OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=nqrF PE=3 SV=2	2.9	45.1		4.00E+06			3.60E+06	

3rd Experiment (Supernatant Fraction)

Accession	Description	Coverage	MW [kDa]	Control	GlcNAc	GlcN	(GlcNAc)2	(GlcN)2	GlcNAc-GlcN
A7UEM1	Transhydrogenase alpha subunit (Fragment) OS=Vibrio parahaemolyticus GN=pntA PE=4 SV=1	6.99300699	1.55E+01	7.90E+06	7.80E+06		9.40E+06	1.00E+07	8.20E+06
A7UEQ6	Dihydro-orotase (Fragment) OS=Vibrio parahaemolyticus GN=pyrC PE=3 SV=1	9.75609756	17.809		6.50E+06			6.10E+06	
H6BAH9	Thermolabile hemolysin (Fragment) OS=Vibrio parahaemolyticus GN=tl PE=4 SV=1	15	1.36E+01	4.70E+06	4.30E+06	1.50E+07		1.40E+07	4.50E+06
O50286	Dihydrolipoyl dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=lpd PE=3 SV=2	55.3684211	5.10E+01	4.00E+07	5.00E+07	5.00E+07	4.30E+07	6.10E+07	4.90E+07
O87081	Polar flagellin F OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=flaF PE=3 SV=2	5.57029178	4.05E+01	4.60E+07	6.80E+07	5.40E+07	5.80E+07	4.20E+07	5.90E+07
P0A2W2	Acyl carrier protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=acpP PE=3 SV=2	18.1818182	8.526	1.30E+07	1.60E+07				7.30E+06
P0A308	ATP synthase subunit c OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=atpE PE=3 SV=1	8.33333333	8.63E+00	5.90E+07			3.50E+07	7.10E+07	5.80E+07
P0A481	50S ribosomal protein L20 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplT PE=3 SV=1	15.3846154	1.34E+01	1.80E+07	1.70E+07	3.30E+07	1.30E+07	2.20E+07	3.40E+07
P19249	Thermostable direct hemolysin 1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=tdh1 PE=1 SV=2	29.6296296	2.13E+01	1.40E+07	2.10E+07	1.20E+07	1.30E+07	2.30E+07	2.10E+07
P19250	Thermostable direct hemolysin 2 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=tdh2 PE=1 SV=2	41.2698413	2.15E+01	1.00E+08	1.20E+08	9.90E+07	8.30E+07	7.30E+07	6.70E+07
P22099	Anthranilate synthase component 1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=trpE PE=3 SV=2	2.03327172	59.733	5.50E+06		4.00E+06	2.90E+06	3.10E+06	3.90E+06
P22848	5'-nucleotidase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=nutA PE=3 SV=2	2.14285714	6.21E+01	1.20E+07	1.40E+07	1.20E+07	9.60E+06	1.20E+07	1.30E+07
P40611	Ribonuclease R OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rnr PE=3 SV=2	2.39520958	9.50E+01		4.70E+07				5.60E+07
P59494	Maltoporin OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=lamB PE=3 SV=1	77.7777778	4.69E+01	1.10E+09	1.00E+09	9.00E+08	8.00E+08	8.30E+08	6.50E+08
P59562	UPF0234 protein VP1617 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1617 PE=3 SV=1	16.25	1.81E+01		1.30E+06	7.00E+06		5.00E+06	6.10E+06
P59570	Outer membrane protein OmpK OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=ompK PE=3 SV=1	25.5639098	29.857	5.70E+07	7.80E+07	6.30E+07	6.40E+07	6.50E+07	4.60E+07
P59605	Argininosuccinate synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=argG PE=3 SV=1	37.3762376	4.45E+01	3.30E+07	4.30E+07	3.80E+07	2.30E+07	4.60E+07	3.80E+07
P59620	Bifunctional protein ArgH OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=argH PE=3 SV=1	2.72435897	6.93E+01	5.60E+06	6.00E+06	5.60E+06	4.50E+06	7.30E+06	8.30E+06
P66478	30S ribosomal protein S18 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpsR PE=3 SV=1	26.6666667	8.84E+00	9.50E+06	1.00E+07	8.60E+06	1.10E+07	2.10E+07	1.40E+07
Q56702	Polar flagellin B/D OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=flaB PE=3 SV=2	75.9259259	4.01E+01	5.90E+07	1.10E+08	6.60E+07	9.40E+07	6.30E+07	6.70E+07
Q56703	Polar flagellin A OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=flaA PE=3 SV=1	59.3085106	3.98E+01	6.50E+07	1.20E+08	7.50E+07	9.80E+07	6.60E+07	7.00E+07
Q56712	Polar flagellin C OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=flaC PE=3 SV=2	50.78125	4.08E+01	3.80E+07	6.60E+07	4.90E+07	5.90E+07	3.90E+07	5.20E+07
Q79YX4	Chemotaxis protein CheW OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2225 PE=4 SV=1	47.5609756	1.84E+01	1.60E+07	5.00E+07	1.10E+07	6.40E+06	1.40E+07	1.00E+07
Q79YY5	Hook-associated protein type 3 FlgL OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0786 PE=4 SV=1	8.31234257	4.50E+01		2.80E+06	1.10E+07			
Q79YY8	Polar flagellar FlgE OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0778 PE=4 SV=1	33.6384439	4.73E+01	2.70E+07	5.20E+07	2.70E+07	3.70E+07	1.70E+07	2.80E+07
Q877T5	Elongation factor Tu OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=tufA PE=3 SV=1	43.1472081	4.31E+01	7.50E+07	1.00E+08	6.10E+07	4.30E+07	8.70E+07	6.70E+07
Q87FL7	Putative diaminopimelate decarboxylase protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1662 PE=3 SV=1	20.5	4.53E+01	1.30E+07	7.20E+06	1.10E+07	6.00E+06	1.50E+07	8.60E+06
Q87FM0	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1659 PE=4 SV=1	34.9180328	68.729	4.40E+07	4.00E+07	3.50E+07	1.70E+07	4.80E+07	3.80E+07
Q87FM1	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1658 PE=4 SV=1	22.5806452	44.22	1.60E+07	1.40E+07	1.60E+07	7.30E+06	2.50E+07	1.80E+07
Q87FM2	Ferric siderophore receptor homolog OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1657 PE=3 SV=1	61.79941	74.942	2.60E+08	3.00E+08	2.60E+08	2.30E+08	2.10E+08	1.60E+08
Q87FM3	Ferric vibrioferrin receptor OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1656 PE=3 SV=1	55.8988764	78.834	1.70E+08	2.30E+08	1.90E+08	1.60E+08	1.60E+08	1.20E+08
Q87FM9	Putative zinc protease, insulinase family OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1650 PE=3 SV=1	5.24590164	102.163	3.40E+06	5.00E+06	3.60E+06	5.50E+06		4.10E+06
Q87FN1	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1648 PE=4 SV=1	5.91304348	62.733	6.60E+06		4.50E+06		3.90E+06	3.50E+06
Q87FN5	Putative maltose operon periplasmic protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1643 PE=4 SV=1	42.3791822	2.91E+01	3.30E+07	3.90E+07	3.40E+07	2.60E+07	3.00E+07	2.50E+07
Q87FN6	Putative CymC protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1642 PE=4 SV=1	19.047619	18.564	1.40E+07	9.90E+06	8.50E+06	7.10E+06	1.20E+07	1.10E+07
Q87FN7	Putative maltogenic amylase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1641 PE=4 SV=1	5.59701493	5.86E+01			5.20E+06			
Q87FP0	Putative pullulanase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1638 PE=4 SV=1	34.4620015	1.44E+02	5.10E+07	4.80E+07	2.80E+07	3.30E+07	2.70E+07	1.80E+07
Q87FQ8	Alpha-1,4 glucan phosphorylase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1620 PE=3 SV=1	35.9853121	9.23E+01	4.00E+07	2.90E+07	4.00E+07	2.20E+07	4.80E+07	3.10E+07
Q87FQ9	4-alpha-glucanotransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1619 PE=3 SV=1	32.6446281	8.18E+01	2.80E+07	2.10E+07	3.20E+07	1.50E+07	3.10E+07	2.30E+07
Q87FR0	1,4-alpha-glucan branching enzyme GlgB OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=glgB PE=3 SV=1	1.32450331	8.74E+01		6.00E+06			9.50E+06	
Q87FT0	GlcNAc-binding protein A OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=gbpA PE=3 SV=1	56.0574949	5.36E+01	1.40E+08	1.90E+08	2.10E+08	1.60E+08	1.80E+08	2.00E+08
Q87FU4	UPF0319 protein VPA1584 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1584 PE=3 SV=1	8.52017937	2.43E+01		1.40E+07				
Q87FX3	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1547 PE=4 SV=1	7.16981132	30.964						
Q87G07	ScrA (Aminotransferase) OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1513 PE=3 SV=1	45.2991453	52.781	1.20E+08	1.70E+08	1.70E+08	1.80E+08	1.40E+08	1.40E+08
Q87G18	L-lactate dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=lldD PE=3 SV=1	19.7889182	4.14E+01	5.70E+06			2.50E+06	1.20E+07	5.80E+06
Q87G19	Putative L-lactate permease OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1498 PE=4 SV=1	1.59857904	5.89E+01	8.10E+06				9.50E+06	
Q87G21	Prolyl endopeptidase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1496 PE=4 SV=1	27.7695716	7.60E+01	1.60E+07	1.90E+07	1.60E+07	1.50E+07	2.00E+07	1.80E+07
Q87G42	Purine nucleoside phosphorylase DeoD-type 2 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=deoD2 PE=3 SV=1	32.6271186	2.57E+01	3.20E+07	3.80E+07	3.80E+07	2.50E+07	3.00E+07	3.10E+07
Q87G48	Outer membrane lipoprotein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1469 PE=4 SV=1	57.1428571	8.67E+00	2.20E+07	2.50E+07	1.80E+07	1.50E+07	2.30E+07	2.70E+07
Q87G50	Protease II OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1467 PE=4 SV=1	19.5195195	7.51E+01	1.00E+07	4.80E+07	5.90E+07	4.90E+07	4.50E+07	6.00E+07
Q87G52	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1465 PE=4 SV=1	17.578125	8.45E+01	1.00E+07	1.70E+07	2.10E+07	2.10E+07	1.00E+07	1.10E+07
Q87G54	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1463 PE=4 SV=1	4.25531915	2.08E+01		1.30E+07		8.80E+06		1.00E+07
Q87G82	Putative iron(III) compound receptor OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1435 PE=3 SV=1	3.01724138	7.70E+01			1.60E+06	1.70E+06	5.10E+06	1.80E+06
Q87G89	Azurin OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1428 PE=4 SV=1	43.3333333	1.58E+01	1.80E+08	2.40E+08	1.70E+08	1.10E+08	1.20E+08	1.30E+08
Q87GB6	Maltose ABC transporter, periplasmic maltose-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1401 PE=4 SV=1	76.0204082	42.1	4.50E+08	4.80E+08	4.10E+08	3.00E+08	3.90E+08	3.60E+08
Q87GC0	Acyl-CoA thioester hydrolase-related protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1397 PE=4 SV=1	9.9378882	1.77E+01						5.20E+06
Q87GE0	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1376 PE=4 SV=1	0.80160321	1.66E+02		3.20E+06				
Q87GK7	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1308 PE=4 SV=1	34.4736842	4.23E+01	9.40E+07	1.10E+08	9.50E+07	8.20E+07	8.20E+07	7.00E+07
Q87GM2	Putative antioxidant OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1293 PE=4 SV=1	9.55414013	16.468	7.60E+06					
Q87GN7	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1278 PE=4 SV=1	5.42635659	12.992	1.30E+07	2.00E+07	1.40E+07	1.00E+07		
Q87GS2	Putative cytosine deaminase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1243 PE=4 SV=1	2.58823529	4.80E+01		3.20E+06		2.50E+06		4.00E+06
Q87GT9	UPF0265 protein VPA1226 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1226 PE=3 SV=1	11.5384615	1.24E+01						4.20E+06
Q87GW1	Acetyl-CoA acetyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1204 PE=3 SV=1	12.9353234	4.15E+01	1.10E+07	8.20E+06	7.40E+06	7.10E+06		4.90E+06
Q87GW6	Periplasmic nitrate reductase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=napA PE=3 SV=1	1.68878166	9.29E+01	2.60E+06	3.60E+06	2.60E+06			
Q87GX9	Outer membrane protein OmpA OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1186 PE=3 SV=1	10.6382979	3.60E+01	1.00E+07	1.10E+07	6.00E+06	5.10E+06	6.60E+06	8.70E+06
Q87GY4	Transketolase 2 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=tkt2 PE=3 SV=1	5.73152338	71.978	1.10E+07			6.60E+06	1.40E+07	1.40E+07
Q87GY5	Transaldolase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=tal PE=3 SV=1	61.3924051	3.48E+01	7.10E+07	7.00E+07	7.80E+07	5.70E+07	7.30E+07	7.40E+07
Q87GY8	Putative chitinase A OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1177 PE=3 SV=1	5.34883721	4.79E+01					6.70E+06	7.20E+06
Q87H02	Oxidoreductase, aldo/keto reductase 2 family OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1163 PE=4 SV=1	7.28476821	3.40E+01	9.10E+06	7.80E+06	1.10E+07	6.30E+06	9.40E+06	8.60E+06
Q87H16	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1149 PE=4 SV=1	1.69082126	45.331	8.30E+06	6.70E+06	6.10E+06	4.80E+06		
Q87H82	Ribokinase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1083 PE=3 SV=1	6.8852459	3.22E+01						
Q87HF4	L-allo-threonine aldolase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1011 PE=4 SV=1	36.2275449	36.086	4.40E+07	4.80E+07	5.40E+07	3.90E+07	4.40E+07	3.90E+07
Q87HG0	D-lactate dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1005 PE=4 SV=1	1.58450704	64.257	7.00E+06				7.40E+06	7.00E+06
Q87HG6	Alpha-amylase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0999 PE=4 SV=1	36.6863905	5.84E+01	2.90E+07	5.60E+07	3.20E+07	9.40E+07	2.90E+07	4.70E+07
Q87HI4	Ferric aerobactin receptor OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0979 PE=3 SV=1	44.4137931	79.175	8.10E+07	9.20E+07	9.10E+07	6.80E+07	7.00E+07	5.30E+07

Q87HL0	Putative biofilm-associated surface protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0953 PE=4 SV=1	0.42789902	2.47E+02	1.50E+07	1.60E+07	1.50E+07	1.60E+07	1.50E+07	1.20E+07
Q87HM1	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0942 PE=4 SV=1	4.778157	3.30E+01	3.30E+06		5.60E+06	5.40E+06	6.60E+06	5.80E+06
Q87HM7	Amino acid biosynthesis aminotransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0936 PE=4 SV=1	25.1256281	43.653	1.60E+07	1.50E+07	1.80E+07	6.90E+06	2.50E+07	1.80E+07
Q87HM8	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0935 PE=4 SV=1	9.25110132	2.57E+01	2.80E+06	3.30E+06	3.40E+06	4.00E+06	3.10E+06	1.20E+06
Q87HM9	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0934 PE=4 SV=1	3.92156863	22.577	7.20E+06	6.40E+06		4.50E+06		
Q87HN2	Molybdenum ABC transporter, periplasmic molybdenum-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0931 PE=4 SV=1	9.96015936	2.70E+01			1.20E+07		3.70E+06	
Q87HP1	NAD(P) transhydrogenase subunit alpha OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0922 PE=3 SV=1	14.6718147	5.48E+01	1.20E+07	7.20E+06		1.40E+07	1.80E+07	1.30E+07
Q87HP2	NAD(P) transhydrogenase subunit beta OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0921 PE=3 SV=1	10.4803493	4.86E+01	1.00E+07	1.30E+07	1.10E+07	1.00E+07	2.00E+07	1.50E+07
Q87HP4	Transcriptional regulator OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0919 PE=4 SV=1	4.54545455	2.49E+01					4.50E+06	
Q87HP6	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0917 PE=4 SV=1	2.41286863	4.11E+01				5.20E+06		
Q87HS4	Heme transport protein HutA OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0882 PE=3 SV=1	71.1399711	7.73E+01	2.00E+08	2.30E+08	2.00E+08	1.70E+08	1.60E+08	1.30E+08
Q87HV6	UPF0312 protein VPA0850 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0850 PE=3 SV=1	38.6243386	20.283	6.80E+07	8.90E+07	7.00E+07	4.70E+07	3.50E+07	5.50E+07
Q87HX4	Chitodextrinase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0832 PE=4 SV=1	51.6129032	1.12E+02	2.30E+06	1.10E+07	7.60E+07	4.20E+07	2.50E+08	3.50E+08
Q87HY6	Amino acid ABC transporter, periplasmic amino acid-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0820 PE=4 SV=1	5.86080586	3.06E+01	1.50E+07	1.40E+07	1.50E+07	1.10E+07	1.30E+07	1.60E+07
Q87HZ6	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0810 PE=4 SV=1	24.6073298	21.082	1.30E+07	2.20E+07	1.70E+07	1.50E+07	1.20E+07	1.00E+07
Q87I03	Serine hydroxymethyltransferase 2 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=glyA2 PE=3 SV=1	5.10440835	46.478	5.80E+06				2.50E+06	
Q87I05	Glycine dehydrogenase (decarboxylating) OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=gcvP PE=3 SV=1	4.82180294	1.04E+02	6.00E+06		1.10E+07		9.00E+06	4.00E+06
Q87I10	Putative L-allo-threonine aldolase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0796 PE=4 SV=1	2.79329609	4.09E+01				4.50E+06		
Q87I38	Catalase-peroxidase 2 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=katG2 PE=3 SV=1	1.65745856	80.653	2.10E+07	2.20E+07		2.00E+07		
Q87ID3	Methylglyoxal synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=mgsA PE=3 SV=1	29.1390728	1.70E+01	2.70E+07	8.50E+06	7.70E+06	6.40E+06		
Q87IE2	Putaive Fe-regulated protein B OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0664 PE=3 SV=1	26.3473054	7.42E+01	3.00E+07	3.50E+07	3.10E+07	2.90E+07	2.50E+07	2.20E+07
Q87IE9	Iron(III) ABC transporter, periplasmic iron-compound-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0657 PE=4 SV=1	39.0728477	3.35E+01	4.80E+07	3.00E+07	4.70E+07	3.10E+07	4.70E+07	3.30E+07
Q87IG5	Putative transcriptional regulator, LysR family OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0641 PE=4 SV=1	2.88808664	3.07E+01						
Q87IG9	Arginine ABC transporter, periplasmic arginine-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0637 PE=3 SV=1	52.2267206	2.73E+01	4.50E+07	5.80E+07	3.40E+07	2.70E+07	3.20E+07	3.60E+07
Q87IJ5	Acetate kinase 2 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=ackA2 PE=3 SV=1	32.4937028	4.26E+01	4.30E+07	4.30E+07	5.60E+07	3.10E+07	5.00E+07	4.30E+07
Q87IP0	Alcohol dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0566 PE=4 SV=1	2.35602094	4.02E+01	3.80E+07					
Q87IP4	Putative chemotaxis transducer OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0562 PE=4 SV=1	0.88235294	7.39E+01	2.50E+07		3.20E+07	2.50E+07	4.80E+07	3.60E+07
Q87IQ0	GGDEF family protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0556 PE=4 SV=1	1.25	5.42E+01						
Q87IS1	Putative phosphomannomutase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0535 PE=3 SV=1	49.1134752	6.16E+01	4.70E+07	5.10E+07	5.30E+07	4.00E+07	5.40E+07	4.30E+07
Q87IS9	Outer membrane protein N, non-specific porin OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0527 PE=4 SV=1	4.29799427	3.78E+01		5.00E+06	4.90E+06			
Q87IY2	Spermidine n1-acetyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0474 PE=4 SV=1	15.3409091	2.11E+01					3.80E+06	1.90E+06
Q87IY8	Prolyl endopeptidase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0468 PE=4 SV=1	4.24403183	8.42E+01	3.70E+06	4.70E+06	6.10E+06	3.20E+06	3.60E+06	
Q87J02	Catalase-peroxidase 1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=katG1 PE=3 SV=1	1.66435506	80.435	2.10E+07	2.20E+07		2.00E+07		
Q87J24	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0429 PE=4 SV=1	6.81818182	2.02E+01	4.40E+06	7.70E+06	8.70E+06	3.50E+06	9.70E+06	9.60E+06
Q87J25	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0428 PE=4 SV=1	9.94152047	1.91E+01						
Q87J30	Hemin ABC transporter, periplasmic hemin-binding protein HutB OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0423 PE=4 SV=1	10.0346021	3.03E+01	5.50E+06		4.50E+06	3.30E+06	4.80E+06	4.20E+06
Q87J46	Dihydroorotase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=pyrC PE=3 SV=1	4.67836257	37.805		6.50E+06			6.10E+06	
Q87J78	Adenylosuccinate synthetase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=purA PE=3 SV=1	5.26315789	4.56E+01		2.40E+07	3.00E+07	7.40E+06	4.10E+07	2.30E+07
Q87J81	Phosphoenolpyruvate synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0372 PE=3 SV=1	46.163522	8.81E+01	6.70E+07	6.40E+07	6.00E+07	3.90E+07	7.00E+07	5.10E+07
Q87J86	Putrescine-binding periplasmic protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0367 PE=3 SV=1	50.2906977	38.671	1.10E+08	1.30E+08	1.20E+08	9.30E+07	1.10E+08	9.90E+07
Q87JD5	Putative outer membrane protein OmpV OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0318 PE=4 SV=1	40.3100775	2.81E+01	4.90E+07	6.10E+07	5.70E+07	4.90E+07	4.80E+07	3.70E+07
Q87JF1	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0302 PE=4 SV=1	6.97674419	14.722					3.90E+06	
Q87JG6	60 kDa chaperonin 2 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=groL2 PE=3 SV=1	9.58646617	5.63E+01	1.40E+07	8.60E+06	1.50E+07	8.10E+06	4.40E+06	9.80E+06
Q87JK3	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0246 PE=4 SV=1	2.5	4.56E+01			5.70E+06		5.70E+06	
Q87JM2	Alkaline serine protease OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0227 PE=4 SV=1	23.7813885	7.10E+01	7.50E+07	1.10E+08	8.00E+07	7.30E+07	4.60E+07	3.40E+07
Q87JM9	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0219 PE=4 SV=1	6.94444444	15.574						
Q87JR8	Phospho-beta-glucosidase B OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0180 PE=3 SV=1	14.9028078	52.96	1.60E+07	1.90E+07	1.20E+07	1.20E+07	7.70E+06	1.10E+07
Q87JS9	Agmatinase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0169 PE=3 SV=1	12.745098	3.34E+01	1.10E+07	1.30E+07	1.20E+07	1.20E+07	1.50E+07	
Q87JT1	Putative protease OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0167 PE=4 SV=1	1.52565881	8.21E+01			5.90E+06		6.50E+06	
Q87JT2	Putative outer membrane protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0166 PE=4 SV=1	23.2091691	37.95	8.80E+08	9.60E+08	7.20E+08	6.90E+08	5.80E+08	4.80E+08
Q87JU6	Biopolymer transport protein ExbB-related protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0152 PE=3 SV=1	3.07692308	4.92E+01					4.20E+06	
Q87JV4	D-lactate dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0144 PE=3 SV=1	12.3867069	3.67E+01	8.10E+06	8.20E+06	9.50E+06			1.70E+07
Q87JV9	Putative PmbA-related protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0139 PE=4 SV=1	5.14541387	4.77E+01	6.00E+06	7.70E+06	6.00E+06	6.00E+06	7.50E+06	5.40E+06
Q87JW6	Putative transcriptional activator OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0132 PE=4 SV=1	13.1818182	2.49E+01	2.10E+07	2.00E+07	2.20E+07	1.10E+07	1.60E+07	1.20E+07
Q87JW7	Hydroxyethylthiazole kinase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=thiM PE=3 SV=1	7.60456274	2.77E+01	3.90E+06					
Q87JY6	Putative peptidase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0112 PE=3 SV=1	2.27642276	6.94E+01						
Q87JZ2	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0106 PE=1 SV=1	4.36781609	49.13			5.20E+06			
Q87K02	Outer membrane protein OmpW OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0096 PE=4 SV=1	26.1682243	2.35E+01	1.40E+08	1.00E+08	1.30E+08	2.80E+07	1.10E+08	4.60E+07
Q87K06	Spindolin-related protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0092 PE=4 SV=1	37.244898	4.35E+01	2.00E+07	2.00E+07	1.40E+07	2.10E+07	5.40E+07	1.10E+08
Q87K09	Putative siderophore utilization protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0089 PE=4 SV=1	10.1167315	2.90E+01			6.90E+06			
Q87K41	UPF0345 protein VPA0057 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0057 PE=1 SV=1	10.6382979	10.206						
Q87K43	Chitinase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0055 PE=3 SV=1	59.4339623	9.00E+01	1.30E+07	2.20E+07	1.50E+08	1.40E+08	7.70E+08	1.00E+09
Q87K58	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0040 PE=4 SV=1	10.2564103	13.483	1.40E+07	1.10E+07			1.90E+07	1.50E+07
Q87K60	Glucosamine-6-phosphate deaminase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=nagB PE=3 SV=1	49.6240602	29.639	9.60E+06	6.80E+07	2.60E+07	8.00E+07	2.30E+07	4.40E+07
Q87KA3	ATP synthase subunit a OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=atpB PE=3 SV=1	5.18518519	3.01E+01	4.60E+06	3.60E+06		3.30E+06	2.90E+06	3.40E+06
Q87KA4	ATP synthase subunit b OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=atpF PE=3 SV=1	41.025641	17.549	1.10E+07	1.40E+07			1.40E+07	1.20E+07
Q87KA6	ATP synthase subunit alpha OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=atpA PE=3 SV=1	49.1395793	5.66E+01	3.10E+07	3.70E+07	2.50E+07	3.00E+07	3.90E+07	3.50E+07
Q87KA7	ATP synthase gamma chain OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=atpG PE=3 SV=1	10.7638889	3.18E+01				1.10E+07	1.20E+07	3.60E+06
Q87KA8	ATP synthase subunit beta OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=atpD PE=3 SV=1	31.9057816	5.07E+01	2.50E+07	2.60E+07	1.80E+07	2.20E+07	2.30E+07	2.50E+07
Q87KB6	Dihydroxy-acid dehydratase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=ilvD PE=3 SV=1	31.9738989	6.56E+01	2.30E+07	3.10E+07	2.10E+07	1.20E+07	2.00E+07	1.80E+07
Q87KB7	Branched-chain amino acid amiotransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP3060 PE=3 SV=1	27.2435897	3.43E+01	4.30E+07	4.70E+07	4.80E+07	3.50E+07	4.40E+07	4.40E+07
Q87KC1	Putative periplasmic protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP3056 PE=4 SV=1	10.0628931	3.55E+01			4.10E+06	3.10E+06		
Q87KC3	Thiol:disulfide interchange protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP3054 PE=3 SV=1	33.5	2.28E+01	2.50E+07	2.40E+07	2.70E+07	1.80E+07	1.10E+07	1.50E+07
Q87KD4	Methionyl-tRNA formyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=fmt PE=3 SV=1	3.80952381	3.41E+01	4.10E+06					
Q87KE1	N5-carboxyaminoimidazole ribonucleotide mutase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=purE PE=3 SV=1	8.07453416	16.588	1.50E+07	2.40E+07	2.60E+07	1.70E+07	2.30E+07	2.00E+07
Q87KE3	Oxygen-dependent coproporphyrinogen-III oxidase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=hemF PE=3 SV=1	3.60655738	3.54E+01	3.90E+06		5.90E+06			
Q87KE4	Shikimate dehydrogenase (NADP(+)) OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=aroE PE=3 SV=1	3.97111913	2.97E+01	6.80E+06		6.10E+06	3.10E+06	6.30E+06	4.90E+06
Q87KF0	Phosphomethylpyrimidine synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=thiC PE=3 SV=1	11.9195046	72.431	1.10E+07	3.70E+06	7.90E+06	1.30E+06	9.20E+06	6.80E+06
Q87KF6	Aminopeptidase P OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP3021 PE=4 SV=1	12.0805369	6.55E+01	1.80E+07	1.60E+07	1.10E+07	1.60E+07	1.10E+07	9.10E+06
Q87KG4	DNA helicase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP3013 PE=4 SV=1	0.82872928	82.398	1.90E+06				2.00E+06	1.90E+06
Q87KH6	Thioredoxin OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP3001 PE=3 SV=1	8.33333333	1.17E+01	9.30E+06	1.10E+07				
Q87KI2	NAD(P)H-flavin reductase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2995 PE=4 SV=1	3.79746835	2.64E+01		3.90E+06				
Q87KI7	Putative uroporphyrin-III C-methyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2990 PE=4 SV=1	2.97766749	4.51E+01						
Q87KI9	Porphobilinogen deaminase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=hemC PE=3 SV=1	7.69230769	3.41E+01	3.60E+06					4.80E+06
Q87KJ3	Diaminopimelate decarboxylase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=lysA PE=3 SV=1	28.7769784	4.59E+01	1.40E+07	1.90E+07	1.90E+07	1.30E+07	1.40E+07	1.60E+07
Q87KN9	Vitamin B12 transporter BtuB OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=btuB PE=3 SV=1	4.48717949	6.93E+01					1.80E+06	
Q87KQ0	50S ribosomal protein L11 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplK PE=3 SV=1	21.1267606	1.47E+01						1.10E+07
Q87KQ1	50S ribosomal protein L1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplA PE=3 SV=1	13.304721	2.47E+01	7.70E+06	1.00E+07	5.30E+06		9.50E+06	9.80E+06
Q87KQ4	DNA-directed RNA polymerase subunit beta OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpoB PE=3 SV=1	18.1818182	149.46	7.60E+06	9.00E+06	1.60E+07	8.80E+06	1.70E+07	1.30E+07
Q87KQ5	DNA-directed RNA polymerase subunit beta' OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpoC PE=3 SV=1	18.2142857	1.55E+02	1.00E+07	1.20E+07	1.60E+07	9.50E+06	1.90E+07	1.40E+07
Q87KR5	DNA-binding protein HU-2 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2911 PE=3 SV=1	63.7362637	9.56E+00	3.80E+07	5.00E+07	4.90E+07	3.90E+07	6.70E+07	7.40E+07
Q87KT0	Bifunctional purine biosynthesis protein PurH OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=purH PE=3 SV=1	17.1698113	5.73E+01	9.70E+06	1.00E+07	1.20E+07	8.00E+06	1.10E+07	8.30E+06
Q87KU7	Acetyl-coenzyme A synthetase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=acsA PE=3 SV=1	4.61538462	7.17E+01	6.80E+06				8.20E+06	7.40E+06
Q87KV2	Fumarate hydratase class II OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=fumC PE=3 SV=1	37.9609544	48.703	7.30E+07	5.80E+07	6.20E+07	3.80E+07	7.40E+07	6.50E+07
Q87KW2	Aspartate ammonia-lyase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2863 PE=3 SV=1	26.2939959	5.27E+01	1.60E+07	1.40E+07	2.00E+07	1.40E+07	1.80E+07	1.40E+07
Q87KW5	Superoxide dismutase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2860 PE=3 SV=1	44.5544554	2.30E+01	5.10E+07	6.50E+07	3.70E+07	3.40E+07	7.00E+07	3.80E+07
Q87KX0	ATP-dependent 6-phosphofructokinase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=pfkA PE=3 SV=1	11.5625	3.46E+01	1.10E+07	5.60E+06	1.10E+07	1.10E+07	6.20E+06	
Q87KX4	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2850 PE=4 SV=1	10.9947644	2.02E+01	8.30E+06	1.00E+07	7.70E+06	8.90E+06	1.20E+07	1.00E+07
Q87KZ3	Protein-export protein SecB OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=secB PE=3 SV=1	9.74025974	1.72E+01					8.90E+06	
Q87KZ5	2,3-bisphosphoglycerate-independent phosphoglycerate mutase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=gpmI PE=3 SV=1	22.1568627	5.51E+01	2.10E+07	1.80E+07	1.30E+07	1.50E+07	8.90E+06	2.80E+07
Q87L07	RNA-binding protein Hfq OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=hfq PE=3 SV=1	39.0804598	9.83E+00	2.20E+07	3.10E+07	2.50E+07	2.10E+07	4.40E+07	3.00E+07
Q87L13	Tryptophan--tRNA ligase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=trpS PE=3 SV=1	6.50887574	3.76E+01	8.10E+06	8.60E+06	1.10E+07	6.40E+06	9.70E+06	1.00E+07

Table S1

Q87L18	Extracellular nuclease-related protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2799 PE=4 SV=1	9.04471545	1.06E+02	1.40E+07	1.40E+07	1.20E+07	1.10E+07		6.00E+06
Q87L20	Acetylornithine aminotransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=argD PE=3 SV=1	34.7394541	4.33E+01	2.30E+07	2.40E+07	2.30E+07	1.90E+07	2.10E+07	2.10E+07
Q87L23	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2794 PE=4 SV=1	37.6425856	2.92E+01	3.10E+07	4.00E+07	1.90E+07	1.90E+07	1.90E+07	2.10E+07
Q87L24	Phosphoribulokinase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2792 PE=4 SV=1	4.4982699	32.737	8.70E+06	8.00E+06		5.60E+06	1.10E+07	5.00E+06
Q87L37	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2779 PE=4 SV=1	6.40243902	3.65E+01						1.10E+06
Q87L38	Peptidyl-prolyl cis-trans isomerase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2778 PE=4 SV=1	23.0769231	2.83E+01	8.10E+06	6.40E+06	3.50E+06	5.30E+06	8.70E+06	1.10E+07
Q87L44	30S ribosomal protein S7 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpsG PE=3 SV=1	40.3846154	1.77E+01	2.70E+07	2.80E+07	3.40E+07	2.10E+07	5.20E+07	4.10E+07
Q87L45	Elongation factor G 1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=fusA1 PE=3 SV=1	21.0300429	7.75E+01	1.60E+07	1.70E+07	2.10E+07	1.10E+07	2.00E+07	1.60E+07
Q87L48	Putative malate oxidoreductase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2767 PE=3 SV=1	21.6470588	46.135	1.90E+07	1.90E+07	1.60E+07	1.10E+07	1.50E+07	1.20E+07
Q87L50	Cystathionine gamma-synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2765 PE=3 SV=1	18.9119171	4.18E+01	2.30E+07	2.50E+07	2.80E+07	2.00E+07	2.60E+07	2.50E+07
Q87L55	N-acetyl-gamma-glutamyl-phosphate reductase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=argC PE=3 SV=1	31.7365269	36.154	1.40E+07	1.30E+07	1.70E+07	9.50E+06	1.20E+07	1.50E+07
Q87L71	Ribulose-phosphate 3-epimerase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2741 PE=3 SV=1	3.13901345	2.44E+01	6.10E+06	7.20E+06				
Q87L72	30S ribosomal protein S6 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpsF PE=3 SV=1	8.52713178	14.974	4.10E+06	5.20E+06		4.60E+06	8.10E+06	9.40E+06
Q87L75	50S ribosomal protein L9 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplI PE=3 SV=1	7.33333333	1.57E+01						5.20E+06
Q87L81	Glucose-6-phosphate isomerase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=pgi PE=3 SV=1	50.1818182	6.09E+01	9.40E+07	8.30E+07	1.20E+08	6.80E+07	1.20E+08	1.00E+08
Q87L90	Sulfite reductase [NADPH] flavoprotein alpha-component OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=cysJ PE=3 SV=1	11.5569823	6.87E+01	8.10E+06	1.40E+07	9.80E+06	9.10E+06	1.20E+07	1.10E+07
Q87L91	Sulfite reductase [NADPH] hemoprotein beta-component OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=cysI PE=3 SV=1	6.05536332	6.48E+01	6.70E+06	7.30E+06	7.80E+06	5.10E+06	9.60E+06	6.60E+06
Q87L98	Aminotransferase, class V OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2714 PE=3 SV=1	6.97050938	4.08E+01	7.20E+06		1.20E+07			
Q87LA3	Single-stranded DNA-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=ssb PE=3 SV=1	7.95454545	19.551	1.10E+07	1.30E+07		7.70E+06		1.40E+07
Q87LB4	Putative V10 pilin OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2698 PE=4 SV=1	36.3636364	1.68E+01	1.70E+07	2.30E+07	2.00E+07	1.80E+07	2.40E+07	2.60E+07
Q87LC0	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2692 PE=4 SV=1	0.89470062	1.59E+02	2.60E+06					
Q87LE1	Putative sigma-54 modulation protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2671 PE=4 SV=1	13.6842105	1.10E+01		1.80E+07				
Q87LF1	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2661 PE=4 SV=1	8.96226415	2.41E+01			1.30E+07			8.10E+06
Q87LF6	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2656 PE=4 SV=1	12.4031008	13.792	8.60E+06	1.10E+07				6.80E+06
Q87LF7	Aspartate carbamoyltransferase regulatory chain OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=pyrI PE=3 SV=1	5.22875817	1.74E+01			5.80E+06			
Q87LF8	Aspartate carbamoyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=pyrB PE=3 SV=1	13.592233	34.474		5.50E+06		2.40E+06		
Q87LF9	Ornithine carbamoyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=argF PE=3 SV=1	47.9041916	3.73E+01	6.20E+07	5.60E+07	6.50E+07	5.60E+07	7.50E+07	6.20E+07
Q87LG6	Valine--tRNA ligase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=valS PE=3 SV=1	0.94537815	1.09E+02						
Q87LG8	Probable cytosol aminopeptidase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=pepA PE=3 SV=1	6.57370518	5.44E+01	5.30E+06	3.20E+06		3.60E+06	9.20E+06	5.50E+06
Q87LH4	Deacetylase DA1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2638 PE=4 SV=1	36.7681499	4.70E+01	4.20E+07	6.20E+07	8.70E+07	6.20E+08	3.40E+09	2.10E+09
Q87LH6	Permease IIC component OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2636 PE=4 SV=1	9.84340045	4.87E+01					1.90E+07	1.10E+07
Q87LK8	Transketolase 1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=tkt1 PE=3 SV=1	7.22891566	7.20E+01	1.10E+07		1.50E+07	6.60E+06	1.40E+07	1.40E+07
Q87LL1	Phosphoglycerate kinase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=pgk PE=3 SV=1	22.0207254	40.707	1.80E+07	1.30E+07	1.30E+07	1.20E+07	1.10E+07	9.10E+06
Q87LL2	Fructose-bisphosphate aldolase, class II OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2599 PE=4 SV=1	68.4357542	3.89E+01	2.30E+08	2.70E+08	3.00E+08	2.30E+08	2.50E+08	2.60E+08
Q87LL8	D-3-phosphoglycerate dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2593 PE=3 SV=1	29.7560976	4.47E+01	1.20E+07	1.60E+07	1.90E+07	1.80E+07	2.40E+07	2.40E+07
Q87LL9	Ribose-5-phosphate isomerase A OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpiA PE=3 SV=1	16.9724771	2.32E+01	1.40E+07	1.20E+07	1.20E+07	6.90E+06	3.10E+07	2.80E+07
Q87LM8	tRNA-modifying protein YgfZ OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2583 PE=3 SV=1	3.72670807	3.55E+01		2.60E+06	2.90E+06	1.90E+06	4.10E+06	3.60E+06
Q87LP2	Pyridoxine 5'-phosphate synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=pdxJ PE=3 SV=1	19.3415638	2.67E+01	1.60E+07	2.50E+07	2.10E+07	1.90E+07	1.30E+07	1.10E+07
Q87LQ0	Enolase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=eno PE=3 SV=1	52.886836	4.55E+01	8.80E+07	9.50E+07	8.30E+07	6.70E+07	8.80E+07	8.10E+07
Q87LR3	Alanine--tRNA ligase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=alaS PE=3 SV=1	2.09302326	9.39E+01					4.80E+06	
Q87LR5	Carbon storage regulator homolog OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=csrA PE=3 SV=1	18.4615385	7.108	2.80E+07	3.00E+07	1.90E+07	1.30E+07	2.50E+07	2.50E+07
Q87LR7	Oxaloacetate decarboxylase, alpha subunit OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2544 PE=4 SV=1	3.52941176	6.42E+01	3.90E+06			3.50E+06	6.80E+06	7.70E+06
Q87LS1	Protease, insulinase family OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2540 PE=3 SV=1	10.4540655	1.06E+02	8.10E+06	7.50E+06	6.50E+06	6.30E+06	6.00E+06	4.80E+06
Q87LS2	Glutamate--cysteine ligase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=gshA PE=3 SV=1	8.42911877	5.90E+01	3.90E+06	4.50E+06	5.00E+06	3.40E+06	4.20E+06	
Q87LT1	50S ribosomal protein L19 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplS PE=3 SV=2	10.2564103	1.32E+01						
Q87LT9	NadC OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2522 PE=3 SV=1	15.9322034	3.20E+01	7.30E+06	5.30E+06	6.10E+06	6.80E+06	6.70E+06	6.70E+06
Q87LU2	Pyruvate dehydrogenase E1 component OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2519 PE=4 SV=1	35.9639233	9.96E+01	4.10E+07	4.30E+07	5.00E+07	3.80E+07	5.70E+07	5.40E+07
Q87LU3	Acetyltransferase component of pyruvate dehydrogenase complex OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2518 PE=3 SV=1	23.1259968	6.49E+01	1.30E+07	1.40E+07	1.90E+07	1.70E+07	2.90E+07	2.60E+07
Q87LV1	Pantothenate synthetase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=panC PE=3 SV=1	8.97009967	3.34E+01	6.20E+06	7.30E+06	5.40E+06			
Q87LW3	Aconitate hydratase B OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2495 PE=3 SV=1	19.3063584	94.013	2.20E+07	1.90E+07	2.20E+07	6.00E+06	3.20E+07	1.70E+07
Q87LW7	Iron(III) ABC transporter, periplasmic iron-compound-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2491 PE=4 SV=1	64.3916914	3.77E+01	3.70E+08	4.10E+08	4.60E+08	3.30E+08	4.00E+08	3.80E+08
Q87LX0	Putative phosphoglucomutase/phosphomannomutase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2488 PE=4 SV=1	17.8723404	5.23E+01					7.70E+06	1.60E+07
Q87LX1	N,N'-diacetylchitobiose phosphorylase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2487 PE=4 SV=1	25.1870324	9.00E+01	2.10E+06		3.80E+06	9.90E+06	2.50E+07	5.50E+07
Q87LX9	Peptide ABC transporter, periplasmic peptide-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2479 PE=4 SV=1	35.7142857	6.29E+01			1.10E+07	3.80E+07	1.50E+08	2.80E+08
Q87LZ1	Outer membrane protein U OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=ompU PE=3 SV=1	31.7507418	3.63E+01	3.20E+08	5.20E+08	3.60E+08	3.30E+08	2.60E+08	2.10E+08
Q87M02	Translation initiation factor IF-2 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=infB PE=3 SV=1	0.77348066	9.93E+01	6.10E+06				5.60E+06	
Q87M05	30S ribosomal protein S15 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpsO PE=3 SV=1	6.74157303	1.01E+01	2.50E+07		3.20E+07	2.50E+07	4.80E+07	3.60E+07
Q87M06	Polyribonucleotide nucleotidyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=pnp PE=3 SV=1	31.0829817	7.67E+01	2.00E+07	2.00E+07	2.60E+07	1.50E+07	2.70E+07	2.40E+07
Q87M18	Peptide chain release factor 3 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=prfC PE=3 SV=1	2.45746692	59.208			3.60E+06			
Q87M22	Deoxyribose-phosphate aldolase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=deoC PE=3 SV=1	10.0775194	2.77E+01	1.80E+07	1.70E+07	1.40E+07	1.30E+07	1.40E+07	1.70E+07
Q87M25	Purine nucleoside phosphorylase DeoD-type 1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=deoD1 PE=3 SV=1	24.2677824	2.59E+01	1.90E+07	1.50E+07	1.60E+07	1.30E+07	1.80E+07	2.00E+07
Q87M27	Phosphoserine phosphatase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2431 PE=4 SV=1	6.13496933	3.58E+01			4.50E+06	4.20E+06	4.10E+06	5.10E+06
Q87M30	Elongation factor G 2 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=fusA2 PE=3 SV=1	18.5344828	7.63E+01	8.30E+07	8.60E+07	9.80E+07	5.00E+07	9.50E+07	8.70E+07
Q87MA3	Putative lipoprotein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2354 PE=4 SV=1	17.989418	2.07E+01	3.50E+06	4.20E+06		2.40E+06	8.10E+06	4.00E+06
Q87MB7	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2339 PE=4 SV=1	8.09716599	27.536		1.50E+07	1.80E+07	2.50E+07	2.30E+07	
Q87MB8	Chitinase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2338 PE=3 SV=1	12.6179245	8.91E+01	1.20E+07	2.00E+07	3.40E+07	2.50E+07	6.30E+07	7.50E+07
Q87MD7	Methionine aminopeptidase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=map PE=3 SV=1	2.39726027	3.23E+01						2.20E+06
Q87MD8	30S ribosomal protein S2 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpsB PE=3 SV=1	16.1157025	2.68E+01	1.30E+07	6.60E+06	1.40E+07	1.70E+07	2.40E+07	9.50E+06
Q87MD9	Elongation factor Ts OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=tsf PE=3 SV=1	30.9608541	2.98E+01	1.70E+07	1.40E+07	1.80E+07	1.00E+07	3.30E+07	2.70E+07
Q87ME0	Uridylate kinase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=pyrH PE=3 SV=1	4.52674897	2.61E+01	4.10E+06					
Q87ME6	Chaperone protein skp OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2309 PE=3 SV=1	28.9156627	1.85E+01	2.20E+07	2.10E+07	2.20E+07	1.50E+07	3.00E+07	2.40E+07
Q87ME8	3-hydroxyacyl-[acyl-carrier-protein] dehydratase FabZ OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=fabZ PE=3 SV=1	18.6666667	1.68E+01	6.90E+06	9.90E+06	8.70E+06	4.80E+06	1.40E+07	1.20E+07
Q87MF3	Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=accA PE=3 SV=1	2.50783699	3.57E+01				5.50E+06		
Q87MG7	Phosphoheptose isomerase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=gmhA PE=3 SV=1	37.1727749	20.795	1.80E+07	1.80E+07	2.00E+07	1.10E+07	1.50E+07	1.40E+07
Q87MH3	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2282 PE=4 SV=1	6.25	4.34E+01	7.30E+06	8.70E+06	6.20E+06	5.40E+06		
Q87MI2	4-hydroxy-tetrahydrodipicolinate synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=dapA PE=3 SV=1	3.42465753	3.12E+01	5.30E+06					
Q87MI3	Outer membrane protein assembly factor BamC OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=bamC PE=3 SV=1	3.24483776	3.81E+01	6.50E+06	6.40E+06	4.00E+06			5.10E+06
Q87ML9	Long-chain fatty acid transport protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2212 PE=4 SV=1	19.9519231	4.57E+01	2.20E+07	2.40E+07	2.30E+07	1.70E+07	1.90E+07	1.30E+07
Q87MN8	Erythronate-4-phosphate dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=pdxB PE=3 SV=1	3.18302387	4.16E+01	7.70E+06		1.40E+07			
Q87MP2	Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta 1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=accD1 PE=3 SV=1	7.46753247	3.40E+01	5.20E+06	5.30E+06	1.90E+06	6.90E+06		4.80E+06
Q87MR4	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2167 PE=4 SV=1	11.7021277	1.11E+01	4.00E+06	7.30E+06	4.90E+06		5.90E+06	
Q87MS0	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2161 PE=4 SV=1	35.5555556	35.168	2.30E+07	2.80E+07	2.30E+07	1.90E+07	1.50E+07	1.60E+07
Q87MS4	Glyceraldehyde-3-phosphate dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2157 PE=3 SV=1	70.9969789	3.52E+01	4.00E+08	4.90E+08	5.90E+08	4.20E+08	5.60E+08	5.20E+08
Q87MV7	Aspartate-semialdehyde dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=asd PE=3 SV=1	71.6981132	4.02E+01	8.80E+07	9.50E+07	1.20E+08	8.10E+07	1.00E+08	9.80E+07
Q87MW0	Aldehyde-alcohol dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2121 PE=1 SV=1	3.44444444	9.71E+01				3.40E+06	5.60E+06	6.60E+06
Q87MW3	Superoxide dismutase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2118 PE=3 SV=1	6.53266332	2.22E+01	2.20E+07	1.90E+07	1.40E+07	1.00E+07	1.20E+07	1.20E+07
Q87MY5	Oligopeptide ABC transporter, periplasmic oligopeptide-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2091 PE=4 SV=1	16.5170557	6.23E+01	6.00E+06	8.20E+06	7.70E+06	8.90E+06	1.50E+07	1.40E+07
Q87MZ3	Phosphate acetyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2083 PE=3 SV=1	1.12044818	76.631		7.40E+06			9.30E+06	
Q87MZ6	ABC transporter substrate-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2080 PE=4 SV=1	37.0716511	3.32E+01	3.00E+07	3.90E+07	2.80E+07	1.90E+07	2.40E+07	2.40E+07
Q87N07	Methionine--tRNA ligase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=metG PE=3 SV=2	3.9244186	7.79E+01	6.30E+06	6.30E+06	7.40E+06	4.00E+06	7.00E+06	6.10E+06
Q87N21	Malonyl CoA-acyl carrier protein transacylase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2055 PE=3 SV=1	12.3778502	3.23E+01	2.00E+06	6.50E+06	1.60E+07			5.40E+06
Q87N29	PTS system, glucose-specific IIBC component OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2046 PE=4 SV=1	9.66386555	4.94E+01	1.80E+07	1.50E+07		1.40E+07	1.70E+07	1.60E+07
Q87N45	30S ribosomal protein S1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2030 PE=3 SV=1	15.1079137	6.09E+01	2.70E+06	3.00E+06	1.80E+06	3.90E+06	2.40E+07	7.80E+06
Q87N50	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2025 PE=4 SV=1	9.15915916	7.66E+01	7.20E+06	1.10E+07	9.20E+06	9.60E+06	1.20E+07	1.20E+07
Q87N76	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1999 PE=4 SV=1	2.65251989	4.02E+01		1.70E+06				
Q87NA1	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=metE PE=3 SV=1	26.9736842	8.47E+01	2.30E+07	2.10E+07	2.40E+07	2.40E+07	4.10E+07	4.20E+07
Q87NC6	Diaminobutyrate-pyruvate transaminase & L-2,4-diaminobutyrate decarboxylase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1942 PE=1 SV=1	1.35699374	1.04E+02					4.90E+06	
Q87NC7	Putative carboxynorspermidine dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1941 PE=4 SV=1	3.83693046	4.65E+01	7.50E+06					
Q87NC8	Carboxynorspermidine/carboxyspermidine decarboxylase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1940 PE=3 SV=1	2.12201592	4.20E+01	8.20E+06			4.10E+06	5.70E+06	5.90E+06

Q87ND3	Ribonucleoside-diphosphate reductase, beta subunit OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1935 PE=4 SV=1	5.0397878	4.37E+01	1.10E+07		8.40E+06	7.60E+06	1.00E+07	7.60E+06
Q87ND6	DNA gyrase subunit A OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=gyrA PE=3 SV=1	1.02505695	9.70E+01		1.40E+06				2.30E+06
Q87NF0	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1918 PE=4 SV=1	3.76811594	38.455	4.40E+06	6.10E+06	3.80E+06	3.60E+06	3.50E+06	
Q87NF7	Extracellular solute-binding protein, family 7 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1911 PE=3 SV=1	27.0718232	40.992	2.10E+07	2.50E+07	1.70E+07	2.00E+07	1.60E+07	1.70E+07
Q87NG8	Aspartate aminotransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1900 PE=3 SV=1	63.0434783	4.54E+01	2.90E+08	3.30E+08	3.90E+08	3.00E+08	3.70E+08	3.30E+08
Q87NH3	Transcriptional regulator, GntR family OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1896 PE=4 SV=1	4.53563715	5.23E+01						5.50E+07
Q87NH5	Asparagine--tRNA ligase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=asnS PE=3 SV=1	11.5879828	5.26E+01	1.00E+08	1.40E+07	9.00E+06	3.50E+06	1.30E+07	8.70E+06
Q87NM9	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1839 PE=4 SV=1	8.57142857	20.035	4.00E+06		3.20E+06		4.80E+06	
Q87NU7	4-aminobutyrate aminotransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1771 PE=3 SV=1	2.83687943	4.51E+01						
Q87NX4	Thermostable carboxypeptidase 1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1744 PE=4 SV=1	2.16535433	5.73E+01			6.10E+06			
Q87P08	Glucose-6-phosphate 1-dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=zwf PE=3 SV=1	13.1736527	57.604	9.70E+06	8.20E+06	1.30E+08	6.30E+06	1.10E+07	9.30E+06
Q87P09	DevB protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1709 PE=4 SV=1	4.20168067	2.60E+01	2.10E+07	2.60E+07	2.20E+07	1.40E+07	2.30E+07	2.00E+07
Q87P10	6-phosphogluconate dehydrogenase, decarboxylating OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1708 PE=3 SV=1	7.26141079	5.25E+01	2.30E+07	2.10E+07	2.50E+07	2.30E+07	2.60E+07	1.70E+07
Q87P32	Adenosine monophosphate-protein transferase VopS OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=vopS PE=1 SV=1	21.7054264	4.17E+01	9.70E+06	6.70E+06	9.00E+06		7.40E+06	7.70E+06
Q87P59	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1659 PE=4 SV=1	5.10708402	67.03	4.30E+06		6.00E+06		8.70E+06	8.10E+06
Q87P60	Low calcium response locus protein H OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1658 PE=4 SV=1	5.55555556	1.81E+01		7.30E+06	4.80E+06			4.70E+06
Q87P63	Immunogenic protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1655 PE=4 SV=1	2.78637771	34.901	1.50E+08	1.70E+08	1.70E+08	1.40E+08	1.90E+08	1.60E+08
Q87P76	Putative trypsin OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1642 PE=4 SV=1	5.42635659	5.40E+01					7.80E+06	4.70E+06
Q87PB3	Aminopeptidase N OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1604 PE=4 SV=1	7.24137931	9.84E+01	7.10E+06	3.90E+06	7.00E+06	3.90E+06	5.90E+06	4.90E+06
Q87PC3	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1594 PE=4 SV=1	45.9866221	64.624	2.40E+07	3.40E+07	2.70E+07	2.70E+07	2.10E+07	2.10E+07
Q87PC5	3-hydroxydecanoyl-[acyl-carrier-protein] dehydratase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=fabA PE=3 SV=1	22.6744186	1.90E+01	5.90E+07	7.60E+07	7.30E+07	5.90E+07	6.70E+07	6.00E+07
Q87PG1	Cbb3-type cytochrome c oxidase subunit OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1541 PE=3 SV=1	3.08641975	3.54E+01				1.40E+06	3.00E+06	
Q87PH6	Putrescine-binding periplasmic protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1526 PE=3 SV=1	31.5492958	3.97E+01	5.70E+07	6.10E+07	4.90E+07	3.70E+07	4.50E+07	4.10E+07
Q87PH7	Putrescine-binding periplasmic protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1525 PE=3 SV=1	12.7536232	3.90E+01	1.50E+07	2.00E+07	1.40E+07	1.30E+07	6.80E+06	1.30E+07
Q87PJ7	ABC transporter, ATP-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1504 PE=4 SV=1	2.0754717	5.98E+01			3.10E+06			
Q87PK2	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1501 PE=1 SV=1	52.9411765	3.01E+01	3.80E+07	3.50E+07	4.30E+07	2.50E+07	4.10E+07	3.70E+07
Q87PP6	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1455 PE=4 SV=1	16.374269	1.80E+01	3.30E+07	4.10E+07	2.30E+07	1.60E+07	1.70E+07	1.70E+07
Q87PV1	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1400 PE=4 SV=1	1.89504373	7.72E+01		1.40E+07		1.20E+07		
Q87Q03	Oligopeptide ABC transporter, periplasmic oligopeptide-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1347 PE=4 SV=1	1.67910448	6.03E+01				8.80E+06	1.60E+07	
Q87Q24	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1326 PE=4 SV=1	16.2878788	57.739	3.10E+07	2.30E+07	1.80E+07	1.50E+07	1.10E+07	1.10E+07
Q87Q40	Succinylglutamate desuccinylase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=astE PE=1 SV=1	17.5438596	38.813		5.50E+06	8.40E+06	3.30E+06	9.00E+06	1.50E+07
Q87Q42	Putative oligopeptidase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1308 PE=4 SV=1	5.50918197	6.80E+01	3.70E+06	4.00E+06	3.60E+06	2.90E+06	4.40E+06	3.40E+06
Q87Q53	Phosphoribosylglycinamide formyltransferase 2 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=purT PE=3 SV=1	5.62659847	42.864						
Q87Q56	Integration host factor subunit alpha OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=ihfA PE=3 SV=1	10.2040816	1.12E+01	1.10E+07	6.40E+06				
Q87Q83	Putative lipoprotein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1267 PE=3 SV=1	5.40540541	2.37E+01	2.70E+06			2.60E+06		3.00E+06
Q87Q87	Phosphoribosylaminoimidazole-succinocarboxamide synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=purC PE=3 SV=1	40.8719346	41.031	1.80E+07	2.70E+07	3.00E+07	1.80E+07	2.30E+07	2.10E+07
Q87Q92	NAD-dependent malic enzyme OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=maeA PE=3 SV=1	2.66903915	6.23E+01			6.30E+06			
Q87Q99	Thioredoxin reductase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1251 PE=3 SV=1	29.153605	3.45E+01	2.10E+07	2.20E+07	2.40E+07	1.40E+07	2.20E+07	2.00E+07
Q87QA3	Phosphoserine aminotransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=serC PE=3 SV=1	25.5494505	4.02E+01	3.60E+07	4.00E+07	4.00E+07	2.80E+07	3.80E+07	3.50E+07
Q87QA7	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1243 PE=4 SV=1	23.2044199	1.98E+01	1.50E+07	3.10E+07	1.70E+07	1.40E+07		
Q87QB7	Glutaredoxin 1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1233 PE=4 SV=1	12.5	1.00E+01		4.20E+06				
Q87QB9	Putative reductase VP1231 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1231 PE=3 SV=1	45.75	43.941	4.10E+07	3.70E+07	4.40E+07	2.70E+07	4.50E+07	3.90E+07
Q87QE2	UDP-sugar hydrolase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1207 PE=3 SV=1	7.62411348	61.263	1.10E+07	1.40E+07	8.60E+06	1.20E+07	8.20E+06	9.30E+06
Q87QE6	Heat shock protein HslJ OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1203 PE=4 SV=1	26.3513514	16.586	3.10E+07	5.60E+07	4.10E+07	3.50E+07	3.60E+07	3.60E+07
Q87QF3	Putative ABC transporter, periplasmic substrate-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1196 PE=4 SV=1	2.59067358	4.26E+01	8.60E+06	8.90E+06	9.70E+06	7.80E+06	7.60E+06	7.20E+06
Q87QG7	Cystathionine beta-lyase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1182 PE=3 SV=1	3.23383085	4.46E+01			6.60E+06	5.00E+06	8.20E+06	6.70E+06
Q87QK7	1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino] imidazole-4-carboxamide isomerase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=hisA PE=3 SV=1	19.5918367	2.64E+01	1.00E+07	1.10E+07		6.10E+06	7.10E+06	8.10E+06
Q87QK9	Histidine biosynthesis bifunctional protein HisB OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=hisB PE=3 SV=1	2.80112045	3.98E+01		4.50E+06	4.50E+06		4.80E+06	4.50E+06
Q87QL0	Histidinol-phosphate aminotransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=hisC PE=3 SV=1	10.1156069	3.82E+01	1.00E+07	8.70E+06	8.10E+06		1.50E+07	9.30E+06
Q87QL1	Histidinol dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=hisD PE=3 SV=1	25.2900232	46.07	2.60E+07	1.40E+07	2.70E+07	1.00E+07	2.60E+07	2.20E+07
Q87QL2	ATP phosphoribosyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=hisG PE=3 SV=1	33.557047	3.28E+01	3.20E+07	3.00E+07	3.20E+07	1.90E+07	3.00E+07	3.00E+07
Q87QL6	DNA-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1133 PE=3 SV=1	9.62962963	1.51E+01	5.80E+06					
Q87QM1	Adenylosuccinate lyase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1128 PE=3 SV=1	24.7807018	5.14E+01	2.10E+07	2.00E+07	2.50E+07	1.70E+07	1.80E+07	1.80E+07
Q87QP1	Serine--tRNA ligase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=serS PE=3 SV=1	17.7011494	4.88E+01	1.30E+07	1.20E+07	1.20E+07	7.00E+06	1.60E+07	1.40E+07
Q87QP6	Alanine dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1103 PE=3 SV=1	52.1390374	3.99E+01	4.80E+07	7.40E+07	4.80E+07	4.20E+07	3.50E+07	3.90E+07
Q87QT7	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1062 PE=4 SV=1	8.76494024	2.83E+01				7.60E+06		9.70E+06
Q87QT8	Peptidoglycan-associated lipoprotein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1061 PE=3 SV=1	12.6436782	1.87E+01	3.20E+07	3.50E+07	2.40E+07	2.90E+07	3.30E+07	3.30E+07
Q87QT9	Protein TolB OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=tolB PE=3 SV=1	37.5555556	4.98E+01	2.40E+07	2.80E+07	2.10E+07	2.30E+07	1.90E+07	1.70E+07
Q87QV2	Aspartate--tRNA ligase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=aspS PE=3 SV=1	1.52027027	6.57E+01					1.80E+06	
Q87QV7	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1043 PE=4 SV=1	3.62903226	2.81E+01	5.60E+06	6.10E+06	5.40E+06	3.60E+06		4.00E+06
Q87QX6	Glucose-1-phosphate adenylyltransferase 1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=glgC1 PE=3 SV=1	5.92592593	4.55E+01	8.60E+06					
Q87QX9	3-phosphoshikimate 1-carboxyvinyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=aroA PE=3 SV=1	4.69483568	4.61E+01	8.70E+06					
Q87QY7	Isocitrate dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1011 PE=4 SV=1	61.9433198	80.465	9.50E+07	9.60E+07	1.10E+08	6.30E+07	1.10E+08	8.20E+07
Q87QZ9	Amino acid ABC transporter, periplasmic amino acid-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0999 PE=3 SV=1	64.7286822	2.84E+01	8.40E+07	1.00E+08	1.00E+08	7.40E+07	8.50E+07	8.90E+07
Q87R02	Putative 54 kDa polar flagellar sheath protein A OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0996 PE=4 SV=1	55.3497942	52.283	5.80E+07	8.80E+07	8.10E+07	7.40E+07	5.70E+07	5.60E+07
Q87R04	Formate acetyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0994 PE=4 SV=1	50.3957784	8.45E+01	5.90E+07	7.70E+07	1.10E+08	8.00E+07	1.10E+08	1.10E+08
Q87R31	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0967 PE=4 SV=1	25	2.18E+01	2.40E+07		2.20E+07	2.00E+07		
Q87R32	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0966 PE=4 SV=1	33.8461538	14.666	4.30E+06	8.80E+06	5.50E+06	4.00E+06	4.30E+06	3.30E+06
Q87R36	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0962 PE=4 SV=1	27.2020725	43.935	1.30E+07	1.70E+07	1.80E+07	1.40E+07	1.70E+07	1.70E+07
Q87R38	Uridine phosphorylase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0960 PE=3 SV=1	28.968254	26.919	1.70E+07	1.30E+07	1.60E+07	9.40E+06	1.50E+07	1.00E+07
Q87R48	Lipoprotein-related protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0950 PE=4 SV=1	11.8055556	1.58E+01			9.50E+06			
Q87R78	DNA-binding protein HU-beta OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0920 PE=3 SV=1	28.8888889	9.402	1.80E+07	2.80E+07	2.80E+07	1.80E+07	5.40E+07	5.30E+07
Q87R80	ATP-dependent Clp protease proteolytic subunit OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=clpP PE=3 SV=1	16	21.961	3.40E+07	3.50E+07	3.30E+07	1.70E+07	3.00E+07	3.60E+07
Q87R87	C4-dicarboxylate-binding periplasmic protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0910 PE=4 SV=1	50.6024096	3.71E+01	4.70E+07	7.60E+07	8.90E+07	8.40E+07	8.60E+07	8.30E+07
Q87R99	Hypothetical lipoprotein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0898 PE=4 SV=1	7.57575758	1.49E+01	1.40E+06					
Q87RB8	Bifunctional protein FolD OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=folD PE=3 SV=1	3.14685315	3.08E+01			6.30E+06		7.10E+06	3.70E+06
Q87RC9	Putative outer membrane lipoprotein Slp OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0868 PE=4 SV=1	7.56756757	2.08E+01		3.20E+06				
Q87RD3	Formyltetrahydrofolate deformylase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=purU PE=3 SV=1	27.7978339	31.6	7.60E+06	9.70E+06	1.80E+07	1.10E+07	1.90E+07	1.60E+07
Q87RD6	Arginine--tRNA ligase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=argS PE=3 SV=1	23.3968804	6.38E+01	1.50E+07	1.50E+07	1.90E+07	1.10E+07	1.80E+07	1.50E+07
Q87RE4	Zinc ABC transporter, periplasmic zinc-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0853 PE=3 SV=1	22.260274	3.21E+01	1.30E+07	1.50E+07	1.80E+07	9.90E+06	2.20E+07	2.00E+07
Q87RE7	Succinyl-CoA ligase [ADP-forming] subunit alpha OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0850 PE=3 SV=1	35.1724138	3.00E+01	5.40E+07	5.30E+07	3.90E+07	2.40E+07	3.80E+07	2.70E+07
Q87RE8	Succinyl-CoA ligase [ADP-forming] subunit beta OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=sucC PE=3 SV=1	47.4226804	4.15E+01	8.70E+07	7.80E+07	6.80E+07	4.70E+07	7.60E+07	4.50E+07
Q87RE9	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0848 PE=3 SV=1	24.6882793	4.37E+01	2.00E+07	2.70E+07	2.50E+07	9.80E+06	4.00E+07	3.10E+07
Q87RF0	2-oxoglutarate dehydrogenase, E1 component OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0847 PE=4 SV=1	1.06269926	1.06E+02					1.50E+07	
Q87RF5	Citrate synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0842 PE=3 SV=1	7.92540793	48.188	4.60E+06	2.60E+06			2.20E+06	
Q87RG2	Flavodoxin OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0835 PE=3 SV=1	10.7344633	1.98E+01	7.80E+06					
Q87RG4	Glutamine--tRNA ligase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=glnS PE=3 SV=1	20.323741	6.39E+01	1.40E+07	1.60E+07	2.20E+07	1.50E+07	2.90E+07	2.20E+07
Q87RG7	N-acetylglucosamine-6-phosphate deacetylase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0829 PE=3 SV=1	3.96825397	4.07E+01		1.50E+07		1.10E+07		1.70E+07
Q87RH4	Adenylate kinase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=adk PE=3 SV=1	29.4392523	2.33E+01	1.90E+07	1.70E+07	1.40E+07	8.40E+06	1.10E+07	1.50E+07
Q87RI9	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0805 PE=4 SV=1	7.21311475	3.34E+01		1.60E+07	9.80E+06	1.40E+07	2.00E+07	1.80E+07
Q87RJ7	Cysteine synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0797 PE=3 SV=1	76.0869565	3.41E+01	2.90E+08	2.90E+08	3.40E+08	2.10E+08	3.40E+08	2.80E+08
Q87RK0	Phosphoenolpyruvate-protein phosphotransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0794 PE=3 SV=1	2.43902439	6.32E+01						3.80E+06
Q87RK5	Polar flagellar hook associated protein type 1 FlgK OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0785 PE=4 SV=1	10.371517	7.12E+01		2.10E+07	2.90E+06	1.40E+07		1.30E+07
Q87RL4	Outer membrane protein OmpA OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0764 PE=3 SV=1	4.38871473	34.052		2.70E+06				
Q87RL6	Glutamate--tRNA ligase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=gltX PE=3 SV=1	34.1772152	5.34E+01	3.90E+07	4.10E+07	4.10E+07	3.30E+07	3.20E+07	3.30E+07
Q87RL8	Putative chitoporin OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0760 PE=4 SV=1	27.3458445	4.08E+01				1.70E+07	6.90E+07	1.60E+08

Table S1

Q87RM3	N,N'-diacetylchitobiase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0755 PE=4 SV=1	12.797282	9.76E+01				8.50E+06		1.70E+07
Q87RN0	2-dehydro-3-deoxyphosphooctonate aldolase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=kdsA PE=3 SV=1	18.7279152	30.79	1.10E+07	1.20E+07	1.30E+07	7.60E+06	3.00E+06	9.30E+06
Q87RN8	Ribose-phosphate pyrophosphokinase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=prs PE=3 SV=1	21.0191083	3.39E+01	6.90E+06	8.80E+06	1.10E+07	8.00E+06	1.00E+07	9.50E+06
Q87RQ0	Leucine--tRNA ligase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=leuS PE=3 SV=1	17.9696616	96.593	1.70E+07	1.80E+07	2.00E+07	1.50E+07	1.90E+07	2.20E+07
Q87RQ1	LPS-assembly lipoprotein LptE OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=lptE PE=3 SV=1	11.6666667	20.459	5.40E+06	7.50E+06	6.40E+06	4.30E+06		4.10E+06
Q87RR2	Serine hydroxymethyltransferase 1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=glyA1 PE=3 SV=1	6.97115385	45.476			1.90E+06	3.40E+06	5.40E+06	3.70E+06
Q87RS3	Lipoprotein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0704 PE=3 SV=1	40.8921933	2.91E+01	1.60E+07	2.10E+07	1.20E+07	1.70E+07	2.60E+07	2.30E+07
Q87RU4	6,7-dimethyl-8-ribityllumazine synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=ribH PE=3 SV=1	44.8717949	1.64E+01	1.90E+07	1.40E+07	2.30E+07	1.70E+07	2.10E+07	1.40E+07
Q87RU5	3,4-dihydroxy-2-butanone 4-phosphate synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=ribB PE=3 SV=1	8.40108401	4.01E+01	3.40E+06	2.60E+06	3.10E+06		3.30E+06	3.70E+06
Q87RV5	Aminoacyl-histidine dipeptidase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0671 PE=4 SV=1	5.51020408	5.36E+01	5.40E+06	5.60E+06	5.40E+06	3.70E+06	8.80E+06	4.20E+06
Q87RV7	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0669 PE=4 SV=1	6.46067416	3.90E+01			7.60E+06			5.70E+06
Q87RX3	Chaperone protein DnaK OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=dnaK PE=3 SV=1	35.6357928	6.90E+01	2.60E+07	3.60E+07	3.30E+07	2.00E+07	2.70E+07	1.50E+07
Q87S05	Putative chitinase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0619 PE=4 SV=1	37.630662	6.35E+01	3.00E+07	3.60E+07	8.10E+07	5.70E+07	3.00E+08	2.90E+08
Q87S07	GMP synthase [glutamine-hydrolyzing] OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=guaA PE=3 SV=1	6.38297872	57.635	9.50E+06	8.10E+06	1.20E+07	4.10E+06	1.20E+07	9.20E+06
Q87S08	Inosine-5'-monophosphate dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=guaB PE=3 SV=1	7.55102041	5.19E+01	5.60E+06	4.10E+06	5.10E+06	2.80E+06	1.50E+07	
Q87S13	Outer membrane protein assembly factor BamB OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=bamB PE=3 SV=1	3.62694301	4.15E+01				2.70E+06		
Q87S15	Histidine--tRNA ligase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=hisS PE=3 SV=1	2.8436019	4.71E+01				7.40E+06		
Q87S21	Peptidase B OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=pepB PE=3 SV=1	1.85185185	4.66E+01						4.40E+06
Q87S31	Inositol monophosphate family protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0593 PE=4 SV=1	8.98876404	2.91E+01	5.30E+06	4.30E+06	5.30E+06	4.60E+06	6.20E+06	5.20E+06
Q87S40	Isocitrate lyase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0584 PE=4 SV=1	5.04587156	48.039	4.30E+06					
Q87S44	Antioxidant, AhpC/Tsa family OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0580 PE=4 SV=1	50.7389163	2.22E+01	1.70E+08	2.20E+08	1.50E+08	8.30E+07	1.40E+08	1.30E+08
Q87S63	Chaperone protein ClpB OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=clpB PE=3 SV=1	2.10035006	9.58E+01	4.10E+06	4.00E+06	2.40E+06		4.80E+06	3.40E+06
Q87S84	Putative carbon starvation protein A OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0540 PE=4 SV=1	2.4291498	53.283	3.10E+06					4.20E+06
Q87S99	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0525 PE=4 SV=1	16.8831169	4.39E+01	1.30E+07	1.40E+07	1.50E+07	8.60E+06	1.00E+07	8.50E+06
Q87SA8	Oxidoreductase Tas, aldo/keto reductase family OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0516 PE=4 SV=1	19.0340909	3.97E+01	1.90E+07	2.00E+07	2.40E+07	1.60E+07	2.50E+07	2.40E+07
Q87SB4	Thiol:disulfide interchange protein DsbC OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0510 PE=4 SV=1	3.05343511	2.86E+01	9.30E+06	9.90E+06	6.80E+06			
Q87SC7	Autonomous glycyl radical cofactor OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=grcA PE=3 SV=1	5.6	13.92					2.10E+07	
Q87SC8	Threonine synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0496 PE=4 SV=1	6.10328638	4.65E+01	6.80E+06	6.40E+06	3.30E+06	3.30E+06	7.20E+06	5.60E+06
Q87SC9	Homoserine kinase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=thrB PE=3 SV=1	8.17610063	3.44E+01	1.80E+07	2.50E+07	2.70E+07	1.50E+07	3.00E+07	2.60E+07
Q87SD2	Putative 4-hydroxy-4-methyl-2-oxoglutarate aldolase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0492 PE=3 SV=1	6.25	17.697	6.80E+06		5.80E+06			8.50E+06
Q87SD6	Putative DNA polymerase III, beta chain OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0488 PE=4 SV=1	8.44155844	1.73E+01	3.90E+07	4.00E+07	6.90E+07			1.70E+07
Q87SE0	Glutamate synthase, large subunit OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0484 PE=4 SV=1	10.9917877	1.75E+02	1.30E+07	1.10E+07	1.00E+07	1.30E+07	1.50E+07	1.50E+07
Q87SE2	Glutamate synthase, large subunit OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0482 PE=4 SV=1	8.60793544	1.63E+02	9.80E+06	9.40E+06	8.10E+06	3.30E+06	1.10E+07	9.50E+06
Q87SE3	Glutamate synthase, small subunit OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0481 PE=4 SV=1	4.04255319	5.25E+01	4.00E+06	3.90E+06				
Q87SF3	Carbamoyl-phosphate synthase large chain OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=carB PE=3 SV=1	2.13556175	1.18E+02		4.80E+06	4.40E+06	4.90E+06		8.80E+06
Q87SF5	4-hydroxy-tetrahydrodipicolinate reductase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=dapB PE=3 SV=1	41.6356877	2.86E+01	2.80E+07	3.40E+07	3.10E+07	2.10E+07	2.70E+07	2.00E+07
Q87SF7	Protein translocase subunit SecA OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=secA PE=3 SV=1	1.43171806	1.03E+02	4.00E+06		3.30E+06			
Q87SH4	Penicillin-binding protein activator LpoA OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=lpoA PE=3 SV=1	2.48756219	67.514				4.40E+06		
Q87SH9	Stringent starvation protein A OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0444 PE=3 SV=1	16.1137441	2.43E+01	9.20E+06	1.30E+07	1.20E+07	5.40E+06	1.70E+07	1.50E+07
Q87SI4	30S ribosomal protein S9 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpsI PE=3 SV=1	33.8461538	1.46E+01	7.50E+06	7.10E+06	8.10E+06	7.30E+06	1.20E+07	1.30E+07
Q87SI5	50S ribosomal protein L13 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplM PE=3 SV=1	5.63380282	1.60E+01				4.70E+06	8.90E+06	1.00E+07
Q87SJ0	Protease DO OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0433 PE=4 SV=1	16.2637363	4.81E+01	1.40E+07	1.60E+07	1.50E+07	9.80E+06	1.30E+07	1.20E+07
Q87SJ8	Outer membrane protein TolC OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0425 PE=4 SV=1	33.9366516	4.80E+01	1.80E+07	1.70E+07	1.10E+07	1.30E+07	1.20E+07	1.10E+07
Q87SK3	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0420 PE=4 SV=1	8.02348337	59.202	3.20E+06	4.30E+06	8.20E+06	4.50E+06	6.40E+06	5.30E+06
Q87SL6	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0406 PE=4 SV=1	7.4829932	1.61E+01	1.80E+06	2.00E+06				
Q87SR6	Pyruvate kinase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0356 PE=3 SV=1	6.59574468	49.941	1.00E+07	5.30E+06	6.80E+06	5.50E+06	6.60E+06	
Q87SS8	3-isopropylmalate dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=leuB PE=3 SV=1	44.9035813	3.93E+01	4.50E+07	4.90E+07	5.00E+07	3.60E+07	4.50E+07	4.20E+07
Q87ST3	LPS-assembly protein LptD OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=lptD PE=3 SV=1	1.79257362	8.92E+01						2.00E+06
Q87ST4	Chaperone SurA OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=surA PE=3 SV=1	9.3676815	4.74E+01	6.70E+06	9.40E+06	6.40E+06	6.60E+06	1.00E+07	3.90E+06
Q87SU4	50S ribosomal protein L21 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplU PE=3 SV=1	60.1941748	1.15E+01	7.40E+06	7.50E+06	7.00E+06	8.20E+06	2.10E+07	2.10E+07
Q87SU7	Malate dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=mdh PE=3 SV=1	61.7363344	3.22E+01	4.90E+07	5.50E+07	4.50E+07	2.90E+07	4.10E+07	3.40E+07
Q87SV0	Immunogenic protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0323 PE=4 SV=1	70.8074534	3.45E+01	2.50E+08	2.70E+08	2.90E+08	2.20E+08	3.10E+08	2.80E+08
Q87SV6	Thiamin ABC transporter, periplasmic thiamin-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0316 PE=4 SV=1	11.5151515	3.65E+01	1.20E+07	1.50E+07	1.90E+07	1.50E+07	1.70E+07	1.90E+07
Q87SW5	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0307 PE=4 SV=1	3.50877193	6.38E+01						
Q87SW6	Peptide methionine sulfoxide reductase MsrA OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=msrA PE=3 SV=1	8.49056604	23.602	5.10E+06	4.90E+06	3.90E+06		6.20E+06	
Q87SX0	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0302 PE=4 SV=1	3.8277512	23.29	6.40E+07	8.30E+07	5.60E+07	3.50E+07	5.40E+07	4.80E+07
Q87SY2	2',3'-cyclic-nucleotide 2'-phosphodiesterase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0290 PE=3 SV=1	14.5929339	7.21E+01	1.30E+07	1.50E+07	1.60E+07	9.80E+06	1.80E+07	1.00E+07
Q87SY9	50S ribosomal protein L17 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplQ PE=3 SV=1	14.2857143	1.42E+01	1.40E+07	2.10E+07	2.50E+07		2.50E+07	
Q87SZ0	DNA-directed RNA polymerase subunit alpha OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpoA PE=3 SV=1	13.9393939	36.45	1.20E+07	1.60E+07	1.30E+07	7.10E+06	1.70E+07	1.20E+07
Q87SZ1	30S ribosomal protein S4 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpsD PE=3 SV=1	35.9223301	2.33E+01	1.20E+07	3.70E+07	3.20E+07	2.90E+07	4.00E+07	3.50E+07
Q87SZ2	30S ribosomal protein S13 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpsM PE=3 SV=1	63.559322	1.33E+01	1.80E+07	2.50E+07	1.80E+07	1.90E+07	4.00E+07	3.00E+07
Q87SZ4	50S ribosomal protein L15 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplO PE=3 SV=1	6.25	1.49E+01	7.20E+06	1.40E+07	7.60E+06	6.60E+06	1.20E+07	8.70E+06
Q87SZ7	50S ribosomal protein L18 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplR PE=3 SV=1	15.3846154	1.26E+01	6.20E+06	7.40E+06	5.10E+06	6.10E+06	9.60E+06	7.70E+06
Q87SZ8	50S ribosomal protein L6 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplF PE=3 SV=1	6.77966102	1.88E+01				3.90E+06	1.30E+07	
Q87SZ9	30S ribosomal protein S8 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpsH PE=3 SV=1	6.15384615	1.40E+01		6.20E+06			1.50E+07	1.50E+07
Q87T01	50S ribosomal protein L5 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplE PE=3 SV=1	10.6145251	2.01E+01	2.50E+07	1.20E+07	2.00E+07	1.90E+07	2.20E+07	2.00E+07
Q87T02	50S ribosomal protein L24 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplX PE=3 SV=1	9.52380952	1.12E+01						
Q87T03	50S ribosomal protein L14 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplN PE=3 SV=1	20.3252033	1.36E+01				6.40E+06	1.30E+07	3.20E+06
Q87T06	50S ribosomal protein L16 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplP PE=3 SV=1	8.82352941	1.55E+01					1.20E+07	6.00E+06
Q87T07	30S ribosomal protein S3 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpsC PE=3 SV=1	8.62068966	2.56E+01						8.10E+06
Q87T08	50S ribosomal protein L22 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplV PE=3 SV=1	12.7272727	1.21E+01						5.30E+06
Q87T09	30S ribosomal protein S19 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpsS PE=3 SV=1	19.5652174	1.04E+01	1.20E+07	3.10E+07	3.40E+07	1.40E+07	3.30E+07	2.50E+07
Q87T12	50S ribosomal protein L4 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplD PE=3 SV=1	14	2.19E+01					6.30E+06	6.40E+06
Q87T13	50S ribosomal protein L3 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplC PE=3 SV=1	22.9665072	2.24E+01					1.50E+07	2.20E+07
Q87T20	ATP-dependent protease subunit HslV OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=hslV PE=3 SV=2	9.83606557	1.96E+01						2.70E+06
Q87T31	Triosephosphate isomerase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=tpiA PE=3 SV=1	25.390625	26.916	1.70E+07	3.00E+07	4.00E+07	2.60E+07	2.00E+07	2.00E+07
Q87T36	Pilin glycosylation protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0234 PE=3 SV=1	38.6189258	4.34E+01	4.40E+07	5.20E+07	5.30E+07	4.10E+07	5.60E+07	4.90E+07
Q87T41	dTDP-4-dehydrorhamnose 3,5-epimerase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0229 PE=4 SV=1	27.8074866	21.226	6.70E+06	7.60E+06	9.20E+06	6.40E+06	8.80E+06	7.40E+06
Q87T48	dTDP-glucose 4,6-dehydratase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0222 PE=3 SV=1	3.59116022	4.09E+01					1.20E+07	
Q87T51	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0219 PE=4 SV=1	11.7021277	20.591	5.20E+06	6.50E+06	5.60E+06		6.40E+06	
Q87T56	ADP-L-glycero-D-manno-heptose-6-epimerase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=hldD PE=3 SV=1	7.34824281	3.52E+01		5.40E+06	4.40E+06			
Q87T64	Putative amidohydrolase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0206 PE=4 SV=1	3.32103321	3.07E+01	9.20E+06	9.20E+06	8.40E+06	3.90E+06	8.90E+06	
Q87T66	Putative 3-chlorobenzoate-3,4-dioxygenase dyhydrogenase related protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0204 PE=4 SV=1	8.74635569	3.85E+01				6.80E+06	8.90E+06	
Q87T85	50S ribosomal protein L28 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpmB PE=3 SV=1	21.7948718	9.026		1.40E+07	1.30E+07	1.40E+07	1.40E+07	6.40E+06
Q87T94	Putative alpha helix protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0176 PE=4 SV=1	2.08333333	3.32E+01			7.90E+06			6.10E+06
Q87T98	Putative binding protein component of ABC transporter OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0172 PE=4 SV=1	3.45394737	6.96E+01		7.60E+06			4.90E+06	6.00E+06
Q87TA4	Putative TolR OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0166 PE=3 SV=1	5.5187638	49.324		3.50E+06		4.40E+06	5.70E+06	
Q87TB9	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0151 PE=4 SV=1	5.11182109	70.404	6.20E+06	6.70E+06	7.60E+06	6.20E+06	6.80E+06	5.90E+06
Q87TE1	Phosphoenolpyruvate carboxykinase [ATP] OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=pckA PE=3 SV=1	70.295203	6.00E+01	1.30E+08	1.50E+08	1.20E+08	1.10E+08	1.20E+08	1.20E+08
Q87TE6	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0124 PE=4 SV=1	3.28638498	2.42E+01	4.40E+06					
Q87TE8	Glutamine synthetase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0121 PE=3 SV=1	59.9147122	5.15E+01	1.90E+08	2.20E+08	2.50E+08	1.90E+08	2.40E+08	2.30E+08
Q87TG2	DNA polymerase I OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0107 PE=3 SV=1	3.0075188	1.03E+02			2.60E+06	4.10E+06	3.30E+06	
Q87TG5	Delta-aminolevulinic acid dehydratase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0104 PE=3 SV=1	19.8300283	3.92E+01	1.90E+07	1.90E+07	2.00E+07	1.40E+07	1.90E+07	1.60E+07
Q87TJ2	Ferritin OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0077 PE=3 SV=1	5.71428571	1.99E+01	3.90E+06	4.40E+06				
Q87TJ9	Oligopeptidase A OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0070 PE=3 SV=1	27.2058824	7.69E+01	1.40E+08	1.60E+08	5.00E+07	2.70E+07	1.70E+08	3.80E+07
Q87TK1	Glutathione reductase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0068 PE=3 SV=1	37.5824176	4.92E+01	5.50E+07	6.10E+07	6.50E+07	5.00E+07	5.90E+07	5.60E+07
Q87TM1	Peptide ABC transporter, periplasmic peptide-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0048 PE=4 SV=1	71.9535783	5.74E+01	3.40E+08	4.30E+08	4.50E+08	3.50E+08	4.10E+08	3.80E+08
Q87TN4	Ketol-acid reductoisomerase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=ilvC PE=3 SV=1	53.0364372	54.66	8.40E+07	1.10E+08	1.10E+08	8.20E+07	1.20E+08	1.10E+08
Q87TR0	Amino acid ABC transporter, periplasmic amino acid-binding portion OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0008 PE=3 SV=1	46.3709677	2.75E+01	3.50E+07	3.70E+07	3.30E+07	1.60E+07	2.10E+07	2.90E+07
Q99289	Thermolabile hemolysin OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0226 PE=1 SV=2	14.5933014	4.74E+01	4.70E+06	4.30E+06	2.60E+07		2.20E+07	4.50E+06
Q9ALY5	Cyclic AMP receptor protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2793 PE=4 SV=1	48.5714286	23.65	3.10E+07	1.40E+07	3.10E+07	9.30E+06	4.60E+07	3.80E+07
Q9L7P5	60 kDa chaperonin 1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=groL1 PE=3 SV=2	44.9725777	5.75E+01	6.90E+07	7.70E+07	9.00E+07	6.10E+07	1.00E+08	8.30E+07
Q9ZBA2	Polar flagellin E OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=flaE PE=3 SV=2	1.60427807	4.07E+01		1.90E+07	1.40E+07	1.80E+07	9.60E+06	1.50E+07
3rd Experiment (Soulble Fraction)									
Accession	**Description**	**Coverage**	**MW [kDa]**	**Control**	**GlcNAc**	**GlcN**	**(GlcNAc)2**	**(GlcN)2**	**GlcNAc-GlcN**

A7UEM1	Transhydrogenase alpha subunit (Fragment) OS=Vibrio parahaemolyticus GN=pntA PE=4 SV=1	21.6783217	15.485	6.90E+06		1.10E+07	1.00E+07	7.00E+06	7.50E+06
A7UET7	Protein RecA (Fragment) OS=Vibrio parahaemolyticus GN=recA PE=3 SV=1	42.3868313	26.048	1.40E+07	2.50E+07	2.40E+07	1.20E+07	1.50E+07	1.50E+07
A7UEX3	DNA gyrase beta-subunit (Fragment) OS=Vibrio parahaemolyticus GN=gyrB PE=4 SV=1	11.6751269	21.652	7.60E+06	5.70E+06	5.10E+06	9.10E+06	4.60E+06	4.00E+06
A9Q6J2	Protein RecA (Fragment) OS=Vibrio parahaemolyticus GN=recA PE=3 SV=1	42.1800948	22.398	1.30E+07	2.50E+07	2.40E+07	1.20E+07	1.50E+07	1.50E+07
A9Q6M1	DNA gyrase B subunit (Fragment) OS=Vibrio parahaemolyticus GN=gyrB PE=4 SV=1	13.5294118	18.562	7.60E+06	5.70E+06	5.10E+06	9.10E+06	4.60E+06	4.00E+06
A9Q6Q3	Phosphoglucomutase (Fragment) OS=Vibrio parahaemolyticus GN=pgm PE=3 SV=1	26.5306122	21.248	1.60E+07	1.10E+07	2.10E+07	2.20E+07	2.30E+07	2.50E+07
H6BAG3	Protein RecA (Fragment) OS=Vibrio parahaemolyticus GN=recA PE=3 SV=1	35.0877193	18.027	1.20E+07	2.30E+07	2.20E+07	7.00E+06	1.30E+07	1.40E+07
O50286	Dihydrolipoyl dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=lpd PE=3 SV=2	55.7894737	50.956	5.00E+07	5.60E+07	5.60E+07	5.30E+07	6.00E+07	4.80E+07
O51859	DNA gyrase subunit B OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=gyrB PE=3 SV=2	5.59006211	89.386	8.00E+06	3.60E+06	6.00E+06	9.60E+06	2.90E+06	4.00E+06
P0A2W2	Acyl carrier protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=acpP PE=3 SV=2	18.1818182	8.526	1.50E+07	1.40E+07	1.40E+07		1.00E+07	1.00E+07
P0A308	ATP synthase subunit c OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=atpE PE=3 SV=1	8.33333333	8.63	3.90E+07	2.70E+07	4.80E+07		4.00E+07	4.00E+07
P0A481	50S ribosomal protein L20 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplT PE=3 SV=1	29.9145299	13.376	1.80E+07	1.70E+07	1.80E+07	3.70E+07	2.80E+07	3.10E+07
P22095	Tryptophan synthase alpha chain OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=trpA PE=3 SV=2	3.35820896	28.583		2.50E+06				2.90E+06
P22096	Anthranilate phosphoribosyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=trpD PE=3 SV=1	3.01204819	35.393		2.50E+06				
P22097	Tryptophan synthase beta chain 1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=trpB1 PE=3 SV=2	2.27272727	42.999	6.70E+06	9.70E+06	7.50E+06	7.50E+06	1.00E+07	7.40E+06
P22099	Anthranilate synthase component 1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=trpE PE=3 SV=2	2.03327172	59.733			3.10E+06	3.00E+06	1.50E+06	
P40607	Adenylosuccinate synthetase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=purA PE=3 SV=3	37.8995434	47.663	3.20E+07	3.30E+07	3.20E+07	3.40E+07	3.20E+07	2.40E+07
P40611	Ribonuclease R OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rnr PE=3 SV=2	2.75449102	94.978	1.60E+06			3.30E+06	2.10E+06	
P46234	Uncharacterized protein VP2110 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2110 PE=4 SV=2	8.33333333	16.37				1.70E+06		
P59494	Maltoporin OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=lamB PE=3 SV=1	41.2037037	46.933	1.40E+08	6.50E+07	1.20E+08	1.40E+08	1.80E+08	8.70E+07
P59562	UPF0234 protein VP1617 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1617 PE=3 SV=1	5.625	18.142	1.90E+06	2.70E+06				
P59570	Outer membrane protein OmpK OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=ompK PE=3 SV=1	15.4135338	29.857	9.80E+06	6.20E+06	1.00E+07	1.50E+07	1.30E+07	6.10E+06
P59605	Argininosuccinate synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=argG PE=3 SV=1	56.1881188	44.489	7.50E+07	9.20E+07	8.40E+07	8.90E+07	9.70E+07	7.00E+07
P59620	Bifunctional protein ArgH OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=argH PE=3 SV=1	21.3141026	69.314	1.10E+07	1.20E+07	1.20E+07	1.10E+07	1.30E+07	1.20E+07
P65129	Translation initiation factor IF-1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=infA PE=3 SV=1	16.6666667	8.217	9.60E+06		7.20E+06	1.00E+07		
P66346	30S ribosomal protein S10 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpsJ PE=3 SV=1	33.9805825	11.713	1.50E+07	2.00E+07	2.10E+07	2.00E+07	1.80E+07	2.20E+07
P66478	30S ribosomal protein S18 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpsR PE=3 SV=1	50.6666667	8.838	4.00E+07	4.00E+07	4.60E+07	6.90E+07	5.80E+07	5.20E+07
P66533	30S ribosomal protein S21 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpsU PE=3 SV=1	14.084507	8.482	2.30E+06		2.30E+06		3.60E+06	2.80E+06
P74956	Lon protease OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=lon PE=3 SV=2	24.137931	87.757	1.80E+07	2.30E+07	2.20E+07	2.10E+07	2.10E+07	1.60E+07
Q79YV4	OpaR OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2516 PE=4 SV=1	5.88235294	23.62					4.50E+06	
Q79YV5	Hypoxanthine ribosyl transferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2515 PE=4 SV=1	7.95454545	20.048		1.90E+06				
Q79YW1	Flagellar motor switch protein FliG OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2248 PE=3 SV=1	2.56410256	38.641		2.20E+08				
Q79YX4	Chemotaxis protein CheW OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2225 PE=4 SV=1	40.8536585	18.406	3.50E+07	4.70E+07	4.80E+07	1.30E+07	1.30E+07	2.40E+07
Q79YY3	BfdA OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1393 PE=4 SV=1	20.3488372	19.412	2.50E+06		5.00E+06		3.20E+06	
Q877T5	Elongation factor Tu OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=tufA PE=3 SV=1	70.0507614	43.125	3.30E+08	4.60E+08	4.30E+08	4.10E+08	4.30E+08	3.90E+08
Q87FC8	ParB family protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1751 PE=4 SV=1	3.7037037	35.671	5.40E+06	4.80E+06	5.60E+06	5.10E+06	6.20E+06	4.40E+06
Q87FE4	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1735 PE=4 SV=1	3.13971743	72.005	2.60E+06			8.30E+06		
Q87FF3	Putative proline dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1726 PE=3 SV=1	0.86289549	114.924			2.00E+06			
Q87FF4	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1725 PE=4 SV=1	5.10638298	25.459	6.90E+06	6.40E+06	4.50E+06	3.80E+06	4.80E+06	
Q87FL2	PTS system, glucose-specific IIBC component OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1667 PE=4 SV=1	3.95833333	51.126			6.70E+06			2.50E+06
Q87FL7	Putative diaminopimelate decarboxylase protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1662 PE=3 SV=1	35.25	45.284	5.10E+07	5.50E+07	5.00E+07	5.40E+07	5.90E+07	4.50E+07
Q87FL8	Putative AcsD OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1661 PE=4 SV=1	36.2889984	69.443	2.30E+07	3.10E+07	3.00E+07	2.60E+07	3.30E+07	2.00E+07
Q87FM0	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1659 PE=4 SV=1	56.0655738	68.729	1.70E+08	1.80E+08	1.70E+08	1.70E+08	1.70E+08	1.50E+08
Q87FM1	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1658 PE=4 SV=1	40.4466501	44.22	1.00E+08	1.20E+08	1.10E+08	1.00E+08	1.40E+08	8.20E+07
Q87FM2	Ferric siderophore receptor homolog OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1657 PE=3 SV=1	21.8289086	74.942	2.20E+07	9.50E+06	2.30E+07	2.30E+07	2.50E+07	2.20E+07
Q87FM3	Ferric vibrioferrin receptor OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1656 PE=3 SV=1	17.9775281	78.834	1.50E+07	8.50E+06	1.70E+07	1.50E+07	2.30E+07	1.30E+07
Q87FN1	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1648 PE=4 SV=1	6.26086957	62.733	3.90E+06		3.50E+06	6.10E+06	4.50E+06	4.30E+06
Q87FN6	Putative CymC protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1642 PE=4 SV=1	7.14285714	18.564	5.50E+06					
Q87FQ8	Alpha-1,4 glucan phosphorylase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1620 PE=3 SV=1	31.7013464	92.342	4.00E+07	4.00E+07	4.60E+07	2.70E+07	4.80E+07	2.30E+07
Q87FQ9	4-alpha-glucanotransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1619 PE=3 SV=1	26.3085399	81.79	1.80E+07	1.80E+07	2.10E+07	2.00E+07	2.20E+07	1.50E+07
Q87FR0	1,4-alpha-glucan branching enzyme GlgB OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=glgB PE=3 SV=1	3.17880795	87.449	8.50E+06	1.20E+07	1.20E+07	8.80E+06	4.50E+06	6.70E+06
Q87FV6	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1572 PE=4 SV=1	35.5978261	41.766	1.30E+07	1.60E+07	1.20E+07	1.90E+07	1.50E+07	1.10E+07
Q87FW9	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1559 PE=4 SV=1	9.09090909	16.427		4.10E+06				
Q87G18	L-lactate dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=lldD PE=3 SV=1	16.0949868	41.373	1.00E+07	3.80E+06	1.20E+07	4.60E+06	8.60E+06	5.40E+06
Q87G21	Prolyl endopeptidase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1496 PE=4 SV=1	15.5096012	76.045	6.50E+06	1.20E+07	1.10E+07	1.10E+07	1.20E+07	9.50E+06
Q87G42	Purine nucleoside phosphorylase DeoD-type 2 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=deoD2 PE=3 SV=1	37.2881356	25.654	1.50E+07	1.90E+07	1.70E+07	1.90E+07	1.50E+07	1.30E+07
Q87G48	Outer membrane lipoprotein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1469 PE=4 SV=1	28.5714286	8.665	7.60E+06			8.00E+06	7.60E+06	7.80E+06
Q87G77	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1440 PE=3 SV=1	5.64784053	34.37		5.60E+06				
Q87G89	Azurin OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1428 PE=4 SV=1	70.6666667	15.819	5.50E+07	8.20E+07	5.10E+07	5.60E+07	4.90E+07	3.80E+07
Q87GA0	Putative glutathione S-transferase family protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1417 PE=3 SV=1	31.2195122	23.565	1.10E+07	1.50E+07	1.50E+07	1.50E+07	1.30E+07	1.60E+07
Q87GB5	Maltose/maltodextrin import ATP-binding protein MalK OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=malK PE=3 SV=1	2.68817204	41.131			7.30E+06			
Q87GB6	Maltose ABC transporter, periplasmic maltose-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1401 PE=4 SV=1	73.4693878	42.1	1.50E+08	1.60E+08	1.40E+08	1.50E+08	1.40E+08	1.10E+08
Q87GC0	Acyl-CoA thioester hydrolase-related protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1397 PE=4 SV=1	47.826087	17.67	4.10E+07	3.90E+07	4.40E+07	5.40E+07	6.00E+07	3.60E+07
Q87GK7	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1308 PE=4 SV=1	13.9473684	42.312	1.50E+07	6.80E+06	1.70E+07	2.00E+07	2.30E+07	1.40E+07
Q87GL1	Putative 3-oxoacyl-(Acyl carrier protein) reductase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1304 PE=3 SV=1	11.2970711	25.224	1.40E+07		1.40E+07		2.20E+07	
Q87GL7	Putative glutathione S-transferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1298 PE=4 SV=1	18.9473684	32.188	1.20E+07	8.00E+06		8.00E+06	7.60E+06	1.10E+07
Q87GM2	Putative antioxidant OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1293 PE=4 SV=1	9.55414013	16.468	5.00E+06	8.20E+06				
Q87GT5	Glyceraldehyde-3-phosphate dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1230 PE=3 SV=1	26.8343816	52.271	2.50E+07	2.70E+07	9.70E+06	1.90E+07	1.50E+07	1.30E+07
Q87GT9	UPF0265 protein VPA1226 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1226 PE=3 SV=1	11.5384615	12.401						4.60E+06
Q87GW0	Acetoacetyl-CoA reductase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1205 PE=3 SV=1	13.0081301	26.215	1.70E+07	1.10E+07	2.10E+07	1.30E+07	1.70E+07	1.20E+07
Q87GW1	Acetyl-CoA acetyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1204 PE=3 SV=1	24.1293532	41.487	1.10E+07	1.20E+07	1.40E+07		2.10E+07	8.80E+06
Q87GX9	Outer membrane protein OmpA OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1186 PE=3 SV=1	15.8054711	35.991			7.10E+06	4.60E+06	7.80E+06	4.40E+06
Q87GY0	Phospho-2-dehydro-3-deoxyheptonate aldolase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1185 PE=3 SV=1	32.8571429	38.297	1.50E+07	2.30E+07	2.00E+07	2.40E+07	2.20E+07	1.60E+07
Q87GY4	Transketolase 2 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=tkt2 PE=3 SV=1	28.5067873	71.978	1.40E+07	2.00E+07	1.70E+07	1.60E+07	1.70E+07	1.70E+07
Q87GY5	Transaldolase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=tal PE=3 SV=1	61.3924051	34.784	4.70E+07	5.10E+07	4.50E+07	5.90E+07	4.80E+07	4.90E+07
Q87H02	Oxidoreductase, aldo/keto reductase 2 family OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1163 PE=4 SV=1	5.29801325	33.969	5.80E+06	5.80E+06	5.50E+06		6.80E+06	5.40E+06
Q87H16	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1149 PE=4 SV=1	17.1497585	45.331	1.40E+07	2.10E+07	1.20E+07	1.70E+07	1.40E+07	1.20E+07
Q87HD1	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1034 PE=4 SV=1	8.85311871	55.347			5.30E+06		1.60E+07	6.00E+06
Q87HD8	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1027 PE=4 SV=1	22.0125786	17.747	4.00E+06	3.10E+06	7.50E+06		2.40E+07	1.50E+07
Q87HF4	L-allo-threonine aldolase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1011 PE=4 SV=1	22.1556886	36.086	1.90E+07	2.60E+07	2.50E+07	2.60E+07	2.70E+07	2.00E+07
Q87HG0	D-lactate dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1005 PE=4 SV=1	9.15492958	64.257	7.10E+06	6.00E+06	1.00E+07	7.40E+06	4.80E+06	7.20E+06
Q87HI4	Ferric aerobactin receptor OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0979 PE=3 SV=1	3.44827586	79.175	5.10E+06		5.30E+06	5.40E+06	8.20E+06	5.00E+06
Q87HM7	Amino acid biosynthesis aminotransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0936 PE=4 SV=1	29.3969849	43.653	2.00E+07	2.80E+07	2.50E+07	2.00E+07	2.50E+07	1.90E+07
Q87HM8	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0935 PE=4 SV=1	4.84581498	25.657	2.50E+05			4.80E+05		3.50E+05
Q87HP1	NAD(P) transhydrogenase subunit alpha OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0922 PE=3 SV=1	21.8146718	54.772	9.70E+06		1.60E+07	1.40E+07	1.00E+07	8.50E+06
Q87HP2	NAD(P) transhydrogenase subunit beta OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0921 PE=3 SV=1	1.74672489	48.614	4.40E+07					
Q87HP4	Transcriptional regulator OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0919 PE=4 SV=1	23.6363636	24.857	6.60E+06	9.50E+06	8.00E+06	8.50E+06	8.10E+06	2.70E+06
Q87HS4	Heme transport protein HutA OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0882 PE=3 SV=1	18.4704185	77.294	1.90E+07		1.30E+07	1.60E+07	2.10E+07	1.20E+07
Q87HS7	UDP-glucose 4-epimerase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0879 PE=3 SV=1	2.36686391	36.934		5.40E+06				
Q87HV6	UPF0312 protein VPA0850 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0850 PE=3 SV=1	26.984127	20.283	1.90E+07	2.30E+07	2.00E+07	1.80E+07	1.70E+07	1.50E+07
Q87I01	Aminomethyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0805 PE=3 SV=1	11.5591398	40.297	9.80E+06	8.10E+06	1.00E+07		7.90E+06	5.80E+06
Q87I03	Serine hydroxymethyltransferase 2 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=glyA2 PE=3 SV=1	5.56844548	46.478	4.70E+06					
Q87I05	Glycine dehydrogenase (decarboxylating) OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=gcvP PE=3 SV=1	0.94339623	104.056	3.40E+06					
Q87I11	Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta 2 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=accD2 PE=3 SV=1	2.42214533	32.136	6.50E+06		6.90E+06	8.10E+06	7.50E+06	
Q87I38	Catalase-peroxidase 2 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=katG2 PE=3 SV=1	1.65745856	80.653	3.80E+07					
Q87I47	Putative N-acetyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0759 PE=4 SV=1	5.59006211	18.342						
Q87I98	Putative acetyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0708 PE=4 SV=1	14.2857143	20.949	6.30E+06			7.40E+06	9.30E+06	
Q87IE2	Putaive Fe-regulated protein B OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0664 PE=3 SV=1	1.79640719	74.159						
Q87IE9	Iron(III) ABC transporter, periplasmic iron-compound-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0657 PE=4 SV=1	24.1721854	33.51	1.40E+07	4.00E+07	4.40E+07	1.70E+07	5.40E+07	1.60E+07
Q87IG4	Putative glutathione S-transferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0642 PE=4 SV=1	30.6976744	24.317	8.70E+06	9.20E+06	9.10E+06	1.20E+07	9.00E+06	
Q87IG9	Arginine ABC transporter, periplasmic arginine-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0637 PE=3 SV=1	17.4089069	27.324	1.10E+07	9.80E+06	9.20E+06	8.20E+06	1.30E+07	9.40E+06
Q87IH9	Cytochrome o ubiquinol oxidase, subunit II OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0627 PE=4 SV=1	6.82593857	32.726			1.20E+06	5.50E+05		
Q87IJ5	Acetate kinase 2 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=ackA2 PE=3 SV=1	18.1360202	42.621	2.30E+07	2.50E+07	2.40E+07	2.60E+07	2.70E+07	2.20E+07

Q87IL1	ATP-binding component of molybdate transport system OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0595 PE=4 SV=1	1.65289256	55.367		1.60E+07			1.80E+07	
Q87IM1	Tryptophan synthase beta chain 2 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=trpB2 PE=3 SV=1	12.2850123	44.222	9.90E+06	1.00E+07	7.80E+06	1.10E+07	8.10E+06	7.00E+06
Q87IP0	Alcohol dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0566 PE=4 SV=1	29.3193717	40.204	4.10E+07	3.10E+07	1.80E+07	1.30E+07	1.80E+07	1.30E+07
Q87IP4	Putative chemotaxis transducer OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0562 PE=4 SV=1	0.88235294	73.916	3.90E+07	4.00E+07	5.00E+07	5.30E+07	6.20E+07	5.10E+07
Q87IQ4	Cold shock DNA-binding domain protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0552 PE=4 SV=1	36.2318841	7.544	2.70E+07	2.90E+07	3.20E+07	3.30E+07	3.60E+07	2.60E+07
Q87IS1	Putative phosphomannomutase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0535 PE=3 SV=1	40.7801418	61.622	3.30E+07	3.90E+07	3.30E+07	3.70E+07	2.90E+07	3.20E+07
Q87IY2	Spermidine n1-acetyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0474 PE=4 SV=1	8.52272727	21.118		5.00E+06				
Q87IY8	Prolyl endopeptidase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0468 PE=4 SV=1	2.65251989	84.193		1.10E+07	9.10E+06	1.00E+07	1.10E+07	5.30E+06
Q87IZ0	Universal stress protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0466 PE=3 SV=1	8.5106383	16.344	6.20E+06	1.60E+07	1.10E+07	1.40E+07	7.80E+06	1.10E+07
Q87J02	Catalase-peroxidase 1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=katG1 PE=3 SV=1	1.66435506	80.435	3.80E+07					
Q87J24	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0429 PE=4 SV=1	6.81818182	20.192	1.50E+07	2.60E+07	2.50E+07	2.20E+07	1.60E+07	1.30E+07
Q87J25	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0428 PE=4 SV=1	16.374269	19.051	8.40E+06	1.00E+07				4.10E+06
Q87J26	Coproporphyrinogen oxidase homolog PhuW OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0427 PE=4 SV=1	10.5263158	50.44	6.00E+06	9.50E+06	6.00E+06	8.70E+06	8.20E+06	7.60E+06
Q87J30	Hemin ABC transporter, periplasmic hemin-binding protein HutB OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0423 PE=4 SV=1	10.3806228	30.31	4.60E+06	5.00E+06	4.60E+06	5.60E+06	5.30E+06	5.30E+06
Q87J33	LuxT OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0420 PE=1 SV=1	24.1830065	17.491	6.30E+06	1.00E+07	8.50E+06	8.10E+06	5.70E+06	6.10E+06
Q87J41	NH(3)-dependent NAD(+) synthetase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=nadE PE=3 SV=1	5.07246377	30.21	8.20E+06		7.40E+06	7.70E+06	6.90E+06	5.50E+06
Q87J54	Putative aminotransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0399 PE=4 SV=1	1.83246073	42.13	2.60E+06					
Q87J78	Adenylosuccinate synthetase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=purA PE=3 SV=1	3.3492823	45.624	5.90E+06	4.40E+06		6.90E+06		6.20E+06
Q87J81	Phosphoenolpyruvate synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0372 PE=3 SV=1	54.2138365	88.088	1.30E+08	1.50E+08	1.10E+08	1.20E+08	1.10E+08	7.70E+07
Q87J86	Putrescine-binding periplasmic protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0367 PE=3 SV=1	22.9651163	38.671	2.50E+07	2.10E+07	2.20E+07	2.40E+07	2.50E+07	1.80E+07
Q87JD5	Putative outer membrane protein OmpV OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0318 PE=4 SV=1	4.65116279	28.131	1.10E+07		1.10E+07	1.60E+07	1.60E+07	9.70E+06
Q87JF1	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0302 PE=4 SV=1	6.97674419	14.722					2.00E+06	
Q87JG6	60 kDa chaperonin 2 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=groL2 PE=3 SV=1	9.58646617	56.31		8.10E+06	6.50E+06	1.70E+07	5.30E+06	4.20E+06
Q87JN8	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0210 PE=4 SV=1	27.2727273	8.694						
Q87JR8	Phospho-beta-glucosidase B OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0180 PE=3 SV=1	10.7991361	52.96	4.70E+06	9.30E+06	4.10E+06	8.70E+06	6.20E+06	1.50E+06
Q87JS8	Biosynthetic arginine decarboxylase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=speA PE=3 SV=1	6.40625	72.02	8.20E+06	5.80E+06	8.80E+06	1.00E+07	5.70E+06	4.50E+06
Q87JS9	Agmatinase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0169 PE=3 SV=1	5.55555556	33.374		2.00E+06				
Q87JT2	Putative outer membrane protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0166 PE=4 SV=1	14.0401146	37.95	5.20E+07	3.30E+07	4.40E+07	5.60E+07	5.90E+07	3.40E+07
Q87JU6	Biopolymer transport protein ExbB-related protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0152 PE=3 SV=1	3.07692308	49.17			4.10E+06			
Q87JV4	D-lactate dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0144 PE=3 SV=1	12.6888218	36.686	8.00E+06	5.80E+07	1.00E+07		1.50E+07	
Q87JV9	Putative PmbA-related protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0139 PE=4 SV=1	2.9082774	47.661	5.50E+06	6.00E+06			5.60E+06	
Q87JW5	Putative ABC transporter substrate-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0133 PE=4 SV=1	8.86075949	34.726		1.10E+07	5.30E+06	7.90E+06	7.40E+06	3.50E+06
Q87JW6	Putative transcriptional activator OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0132 PE=4 SV=1	3.18181818	24.852		9.40E+06				
Q87JW7	Hydroxyethylthiazole kinase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=thiM PE=3 SV=1	13.3079848	27.713	3.70E+06	1.40E+07	9.70E+06	1.10E+07		
Q87K02	Outer membrane protein OmpW OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0096 PE=4 SV=1	6.54205607	23.453	1.90E+07	8.70E+06	1.50E+07	4.80E+06	2.20E+07	1.30E+07
Q87K60	Glucosamine-6-phosphate deaminase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=nagB PE=3 SV=1	41.3533835	29.639		2.80E+07	1.50E+07	5.30E+07	2.30E+07	2.50E+07
Q87K87	Probable transcriptional regulatory protein VPA0011 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0011 PE=3 SV=1	12.1848739	26.137	4.70E+06	4.30E+06	5.10E+06	3.60E+06	3.50E+06	4.10E+06
Q87K95	Peptide ABC transporter, ATP-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0003 PE=3 SV=1	7.09677419	34.85		5.10E+06			3.00E+06	
Q87KA4	ATP synthase subunit b OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=atpF PE=3 SV=1	43.5897436	17.549	1.00E+07	3.80E+06	1.10E+07	8.80E+06	9.90E+06	6.00E+06
Q87KA5	ATP synthase subunit delta OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=atpH PE=3 SV=1	8.47457627	19.405				4.20E+06	3.40E+06	
Q87KA6	ATP synthase subunit alpha OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=atpA PE=3 SV=1	63.4799235	56.601	1.00E+08	1.20E+08	1.20E+08	1.10E+08	1.10E+08	1.10E+08
Q87KA7	ATP synthase gamma chain OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=atpG PE=3 SV=1	48.6111111	31.839	2.10E+07	2.50E+07	2.40E+07	2.40E+07	1.90E+07	2.10E+07
Q87KA8	ATP synthase subunit beta OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=atpD PE=3 SV=1	56.5310493	50.664	9.80E+07	1.00E+08	9.50E+07	8.20E+07	8.90E+07	8.70E+07
Q87KB5	L-threonine dehydratase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=ilvA PE=3 SV=1	14.9514563	56.568	8.70E+06	1.20E+07	6.60E+06	1.30E+07	9.10E+06	7.10E+06
Q87KB6	Dihydroxy-acid dehydratase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=ilvD PE=3 SV=1	42.903752	65.605	2.90E+07	4.40E+07	3.50E+07	4.40E+07	3.70E+07	3.20E+07
Q87KB7	Branched-chain amino acid amiotransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP3060 PE=3 SV=1	23.7179487	34.277	3.20E+07	3.40E+07	3.10E+07	3.80E+07	3.00E+07	3.20E+07
Q87KB9	Acetolactate synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP3058 PE=3 SV=1	2.73722628	59.194		1.40E+07			1.80E+07	6.70E+06
Q87KC3	Thiol:disulfide interchange protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP3054 PE=3 SV=1	10	22.805	4.70E+06	6.00E+06	6.60E+06	5.20E+06	5.20E+06	5.00E+06
Q87KE1	N5-carboxyaminoimidazole ribonucleotide mutase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=purE PE=3 SV=1	8.07453416	16.588	4.90E+06			6.90E+06		
Q87KF0	Phosphomethylpyrimidine synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=thiC PE=3 SV=1	2.16718266	72.431	1.70E+06	1.80E+06			1.80E+06	
Q87KF6	Aminopeptidase P OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP3021 PE=4 SV=1	4.02684564	65.515	2.40E+06	5.60E+06		8.30E+06	5.60E+06	
Q87KG4	DNA helicase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP3013 PE=4 SV=1	0.82872928	82.398			3.00E+06	1.30E+06		
Q87KH7	Transcription termination factor Rho OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rho PE=3 SV=1	9.06921241	46.789		5.80E+06			8.90E+06	6.10E+06
Q87KI9	Porphobilinogen deaminase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=hemC PE=3 SV=1	3.52564103	34.093	7.50E+06		6.50E+06		7.40E+06	
Q87KJ3	Diaminopimelate decarboxylase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=lysA PE=3 SV=1	27.5779376	45.861	7.50E+06	1.20E+07	7.80E+06	1.30E+07	1.10E+07	7.70E+06
Q87KP9	Transcription termination/antitermination protein NusG OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=nusG PE=3 SV=2	5.49450549	20.696				1.10E+07		
Q87KQ0	50S ribosomal protein L11 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplK PE=3 SV=1	40.8450704	14.693	3.40E+07	8.10E+07	7.60E+07	8.70E+07	7.90E+07	7.40E+07
Q87KQ1	50S ribosomal protein L1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplA PE=3 SV=1	62.6609442	24.676	7.00E+07	7.80E+07	9.80E+07	9.30E+07	9.40E+07	7.70E+07
Q87KQ2	50S ribosomal protein L10 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplJ PE=3 SV=1	36.4197531	17.333		9.30E+06		5.70E+06	9.60E+06	
Q87KQ3	50S ribosomal protein L7/L12 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplL PE=3 SV=1	29.5081967	12.184	2.70E+07	3.20E+07	3.70E+07	3.30E+07	3.90E+07	3.40E+07
Q87KQ4	DNA-directed RNA polymerase subunit beta OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpoB PE=3 SV=1	42.3994039	149.46	3.00E+07	3.50E+07	3.40E+07	3.30E+07	3.60E+07	3.00E+07
Q87KQ5	DNA-directed RNA polymerase subunit beta' OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpoC PE=3 SV=1	38.3571429	154.822	2.90E+07	4.00E+07	4.20E+07	4.40E+07	3.00E+07	3.00E+07
Q87KQ6	Regulator of sigma D OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2920 PE=3 SV=1	9.81595092	18.603	1.30E+07		1.70E+07	1.60E+07	1.50E+07	1.00E+07
Q87KR5	DNA-binding protein HU-2 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2911 PE=3 SV=1	63.7362637	9.562	8.00E+07	1.10E+08	1.10E+08	1.30E+08	1.00E+08	1.00E+08
Q87KS6	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2900 PE=4 SV=1	6.8	57.103	1.70E+06			2.70E+06		
Q87KS8	Phosphoribosylamine--glycine ligase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=purD PE=3 SV=1	2.0979021	45.762		3.90E+06				
Q87KT0	Bifunctional purine biosynthesis protein PurH OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=purH PE=3 SV=1	14.9056604	57.285	7.30E+06	1.20E+07	1.60E+07	1.30E+07	1.70E+07	1.10E+07
Q87KU4	Acetyl-CoA carboxylase, biotin carboxylase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2881 PE=4 SV=1	35.3467562	49.161	1.60E+07	1.90E+07	1.90E+07	1.60E+07	2.00E+07	1.80E+07
Q87KU7	Acetyl-coenzyme A synthetase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=acsA PE=3 SV=1	33.8461538	71.702	7.30E+07	6.60E+07	4.90E+07	5.50E+07	4.80E+07	5.90E+07
Q87KV2	Fumarate hydratase class II OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=fumC PE=3 SV=1	49.6746204	48.703	1.30E+08	1.90E+08	1.70E+08	1.80E+08	1.50E+08	1.40E+08
Q87KW2	Aspartate ammonia-lyase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2863 PE=3 SV=1	13.0434783	52.7	7.10E+06	8.40E+06	6.10E+06	7.20E+06	7.30E+06	5.30E+06
Q87KW5	Superoxide dismutase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2860 PE=3 SV=1	44.5544554	22.973	5.90E+07	6.70E+07	6.20E+07	5.40E+07	6.80E+07	4.90E+07
Q87KX0	ATP-dependent 6-phosphofructokinase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=pfkA PE=3 SV=1	16.5625	34.561	1.40E+07	2.50E+07	2.60E+07	1.60E+07	1.60E+07	1.50E+07
Q87KX9	Elongation factor P OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=efp PE=3 SV=1	17.0212766	20.571	9.20E+06	1.40E+07	1.50E+07	1.40E+07	1.10E+07	1.00E+07
Q87KZ3	Protein-export protein SecB OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=secB PE=3 SV=1	23.3766234	17.162	1.10E+07	1.30E+07	1.40E+07	1.40E+07	1.70E+07	1.50E+07
Q87KZ5	2,3-bisphosphoglycerate-independent phosphoglycerate mutase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=gpmI PE=3 SV=1	24.5098039	55.083	2.30E+07	2.40E+07	2.60E+07	3.20E+07	3.20E+07	2.60E+07
Q87L07	RNA-binding protein Hfq OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=hfq PE=3 SV=1	43.6781609	9.833	2.60E+07	3.70E+07	3.50E+07	3.70E+07	3.10E+07	2.20E+07
Q87L13	Tryptophan--tRNA ligase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=trpS PE=3 SV=1	6.50887574	37.624	6.50E+06	6.80E+06	7.60E+06	6.20E+06	7.20E+06	7.40E+06
Q87L20	Acetylornithine aminotransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=argD PE=3 SV=1	31.7617866	43.334	1.90E+07	1.00E+07	1.70E+07	2.90E+07	1.10E+07	1.90E+07
Q87L21	Arginine N-succinyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2796 PE=4 SV=1	4.42477876	37.689		4.90E+06		5.20E+06	1.90E+06	2.20E+06
Q87L22	N-succinylglutamate 5-semialdehyde dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=astD PE=3 SV=1	6.59793814	52.029	3.80E+06	8.00E+06	5.40E+06	4.30E+06		3.40E+06
Q87L23	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2794 PE=4 SV=1	29.6577947	29.195	2.20E+07	3.10E+07	1.40E+07	3.30E+07	1.90E+07	2.20E+07
Q87L24	Phosphoribulokinase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2792 PE=4 SV=1	4.4982699	32.737						5.10E+06
Q87L38	Peptidyl-prolyl cis-trans isomerase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2778 PE=4 SV=1	19.2307692	28.25	6.20E+06		9.10E+06	1.20E+07	8.30E+06	7.30E+06
Q87L43	30S ribosomal protein S12 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpsL PE=3 SV=1	24.1935484	13.7	8.60E+06	1.10E+07	4.10E+06	6.70E+06	1.10E+07	4.80E+06
Q87L44	30S ribosomal protein S7 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpsG PE=3 SV=1	55.7692308	17.749	7.50E+07	7.60E+07	8.80E+07	8.30E+07	1.00E+08	7.70E+07
Q87L45	Elongation factor G 1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=fusA1 PE=3 SV=1	20.7439199	77.54	1.40E+07	1.50E+07	1.40E+07	1.60E+07	1.60E+07	1.30E+07
Q87L48	Putative malate oxidoreductase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2767 PE=3 SV=1	10.8235294	46.135	7.60E+06	6.90E+06	7.40E+06	7.50E+06	9.40E+06	6.80E+06
Q87L50	Cystathionine gamma-synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2765 PE=3 SV=1	9.58549223	41.835	8.10E+06	1.50E+07	1.20E+07	1.60E+07	1.60E+07	1.10E+07
Q87L51	Aspartokinase II/homoserine dehydrogenase, methionine-sensitive OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2764 PE=4 SV=1	9.72568579	87.764	4.70E+06	7.30E+06	7.40E+06	4.70E+06	6.90E+06	7.70E+06
Q87L52	Methylenetetrahydrofolate reductase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2763 PE=3 SV=1	17.6666667	33.271	1.30E+07	2.10E+07	2.20E+07	2.20E+07	2.40E+07	2.40E+07
Q87L54	Phosphoenolpyruvate carboxylase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=ppc PE=3 SV=2	26.68187	99.211	2.00E+07	2.10E+07	2.50E+07	2.10E+07	2.20E+07	2.00E+07
Q87L55	N-acetyl-gamma-glutamyl-phosphate reductase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=argC PE=3 SV=1	25.4491018	36.154	9.40E+06	8.50E+06	1.20E+07	7.90E+06	5.70E+06	4.80E+06
Q87L56	Acetylglutamate kinase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=argB PE=3 SV=1	23.5741445	27.089	6.90E+06	1.50E+07	1.30E+07	1.80E+07	1.40E+07	1.20E+07
Q87L68	3-dehydroquinate synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=aroB PE=3 SV=1	11.2021858	40.018	7.20E+06	9.10E+06	7.10E+06	1.10E+07	8.80E+06	8.10E+06
Q87L72	30S ribosomal protein S6 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpsF PE=3 SV=1	23.255814	14.974	2.90E+07	2.80E+07	3.90E+07	3.60E+07	4.20E+07	3.50E+07
Q87L75	50S ribosomal protein L9 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplI PE=3 SV=1	61.3333333	15.699	3.70E+07	3.90E+07	4.60E+07	4.80E+07	4.50E+07	4.30E+07
Q87L81	Glucose-6-phosphate isomerase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=pgi PE=3 SV=1	37.8181818	60.874	5.10E+07	7.00E+07	5.40E+07	6.70E+07	7.90E+07	4.70E+07
Q87L90	Sulfite reductase [NADPH] flavoprotein alpha-component OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=cysJ PE=3 SV=1	6.2600321	68.714	5.00E+06	6.20E+06	6.10E+06	6.20E+06	6.70E+06	4.00E+06
Q87L91	Sulfite reductase [NADPH] hemoprotein beta-component OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=cysI PE=3 SV=1	15.5709343	64.834	6.90E+06	9.00E+06	7.80E+06	9.50E+06	9.80E+06	9.20E+06

Q87L96	Aspartokinase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2715 PE=3 SV=1	20.2222222	48.777	8.40E+06	2.10E+07	1.30E+07	1.90E+07	1.20E+07	1.30E+07
Q87L98	Aminotransferase, class V OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2714 PE=3 SV=1	11.5281501	40.759	6.90E+06	1.20E+07				7.20E+06
Q87LA1	UTP--glucose-1-phosphate uridylyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2711 PE=3 SV=1	7.5862069	32.317		6.50E+06			3.30E+06	
Q87LA3	Single-stranded DNA-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=ssb PE=3 SV=1	13.6363636	19.551		1.20E+07	9.70E+06	2.00E+07	1.00E+07	
Q87LB4	Putative V10 pilin OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2698 PE=4 SV=1	31.5151515	16.796	1.80E+07	1.20E+07	2.80E+07	2.40E+07	2.00E+07	2.50E+07
Q87LE1	Putative sigma-54 modulation protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2671 PE=4 SV=1	13.6842105	11.023	1.70E+07	2.50E+07	2.20E+07		1.50E+07	1.40E+07
Q87LF6	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2656 PE=4 SV=1	12.4031008	13.792	5.10E+06		4.80E+06	4.40E+06	5.80E+06	3.50E+06
Q87LF7	Aspartate carbamoyltransferase regulatory chain OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=pyrI PE=3 SV=1	8.49673203	17.394				7.40E+06	7.50E+06	
Q87LF8	Aspartate carbamoyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=pyrB PE=3 SV=1	12.6213592	34.474		3.40E+06	5.50E+06	4.30E+06	4.80E+06	
Q87LF9	Ornithine carbamoyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=argF PE=3 SV=1	38.6227545	37.321	3.50E+07	4.10E+07	3.80E+07	4.90E+07	2.60E+07	3.20E+07
Q87LG6	Valine--tRNA ligase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=valS PE=3 SV=1	2.83613445	108.553	4.60E+06		8.80E+06	5.80E+06	6.20E+06	3.80E+06
Q87LG8	Probable cytosol aminopeptidase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=pepA PE=3 SV=1	19.3227092	54.444	1.10E+07	1.60E+07	1.40E+07	7.20E+06	1.40E+07	9.20E+06
Q87LH4	Deacetylase DA1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2638 PE=4 SV=1	2.81030445	47.005					1.30E+07	1.30E+07
Q87LH6	Permease IIC component OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2636 PE=4 SV=1	12.3042506	48.725					2.70E+07	1.40E+07
Q87LH7	PTS system, cellobiose-specific IIA component OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2635 PE=4 SV=1	48.5436893	11.624					2.50E+07	1.70E+07
Q87LH8	6-phospho-beta-glucosidase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2634 PE=3 SV=1	54.0909091	48.304				9.90E+06	1.40E+08	6.20E+07
Q87LH9	Carbohydrate deacetylase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2633 PE=3 SV=1	13.1474104	28.013					1.60E+07	6.20E+06
Q87LI0	Transcriptional regulator, LacI family OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2632 PE=4 SV=1	3.27380952	37.699					7.80E+06	
Q87LJ5	Pyrroline-5-carboxylate reductase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=proC PE=3 SV=1	4.41176471	29.086		7.70E+06		6.00E+06	7.50E+06	
Q87LK1	Glutathione synthetase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=gshB PE=3 SV=1	22.1518987	35.218	1.40E+07	1.10E+07	1.50E+07	1.30E+07	2.20E+07	1.60E+07
Q87LK2	Ribosomal RNA small subunit methyltransferase E OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2610 PE=3 SV=1	12.345679	27.184				3.80E+06		2.60E+06
Q87LK6	S-adenosylmethionine synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=metK PE=3 SV=1	24.4791667	41.964	1.10E+07	1.40E+07	1.60E+07	1.50E+07	1.50E+07	1.20E+07
Q87LK8	Transketolase 1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=tkt1 PE=3 SV=1	31.626506	71.985	2.20E+07	2.60E+07	2.40E+07	2.10E+07	1.60E+07	2.30E+07
Q87LL1	Phosphoglycerate kinase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=pgk PE=3 SV=1	62.1761658	40.707	7.40E+07	8.80E+07	9.70E+07	1.10E+08	9.90E+07	9.00E+07
Q87LL2	Fructose-bisphosphate aldolase, class II OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2599 PE=4 SV=1	68.4357542	38.856	1.30E+08	1.60E+08	1.70E+08	1.90E+08	1.70E+08	1.60E+08
Q87LL3	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2598 PE=4 SV=1	6.59722222	30.956			3.80E+06			
Q87LL8	D-3-phosphoglycerate dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2593 PE=3 SV=1	50.9756098	44.658	4.30E+07	5.00E+07	4.50E+07	5.30E+07	4.90E+07	4.50E+07
Q87LL9	Ribose-5-phosphate isomerase A OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpiA PE=3 SV=1	16.0550459	23.209	6.80E+06	7.10E+06	6.80E+06	7.00E+06	8.00E+06	4.70E+06
Q87LM8	tRNA-modifying protein YgfZ OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2583 PE=3 SV=1	7.14285714	35.507	3.70E+06	5.90E+06	4.50E+06	5.90E+06	3.80E+06	5.10E+06
Q87LN1	L-aspartate oxidase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2580 PE=3 SV=1	8.88888889	60.918	6.80E+06	9.10E+06	9.90E+06	1.00E+07	9.90E+06	1.00E+07
Q87LP2	Pyridoxine 5'-phosphate synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=pdxJ PE=3 SV=1	8.23045267	26.655	4.80E+06	5.90E+06	6.80E+06	5.50E+06	5.80E+06	
Q87LP9	CTP synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=pyrG PE=3 SV=1	16.4835165	60.089	7.90E+06	5.50E+06	7.70E+06	1.30E+07	1.00E+07	9.30E+06
Q87LQ0	Enolase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=eno PE=3 SV=1	58.1986143	45.533	8.80E+07	1.10E+08	1.10E+08	1.30E+08	1.30E+08	1.20E+08
Q87LQ8	RNA polymerase sigma factor RpoS OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpoS PE=3 SV=1	30.0940439	36.485	1.20E+07	2.10E+07	1.30E+07	2.40E+07	2.20E+07	2.00E+07
Q87LR1	Protein RecA OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=recA PE=3 SV=1	37.1757925	37.409	1.90E+07	2.80E+07	2.60E+07	1.70E+07	2.10E+07	2.00E+07
Q87LR3	Alanine--tRNA ligase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=alaS PE=3 SV=1	11.8604651	93.91	5.70E+06	9.10E+06	9.00E+06	9.20E+06	9.70E+06	5.40E+06
Q87LR5	Carbon storage regulator homolog OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=csrA PE=3 SV=1	18.4615385	7.108	1.50E+07	1.90E+07	1.70E+07	2.10E+07	1.80E+07	1.50E+07
Q87LR7	Oxaloacetate decarboxylase, alpha subunit OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2544 PE=4 SV=1	6.55462185	64.235	6.10E+06		8.70E+06	5.40E+06	7.40E+06	8.60E+06
Q87LS2	Glutamate--cysteine ligase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=gshA PE=3 SV=1	1.72413793	59.048	2.70E+06					
Q87LS4	S-ribosylhomocysteine lyase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=luxS PE=3 SV=1	12.2093023	19.021			5.00E+06	4.60E+06	6.80E+06	3.10E+06
Q87LS7	Signal recognition particle protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=ffh PE=3 SV=1	3.04347826	50.248		5.70E+06	4.60E+06		6.20E+06	3.90E+06
Q87LS8	30S ribosomal protein S16 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpsP PE=3 SV=1	10.9756098	9.058					1.40E+07	
Q87LT1	50S ribosomal protein L19 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplS PE=3 SV=2	56.4102564	13.211	4.50E+07	5.30E+07	6.20E+07	5.20E+07	6.20E+07	6.50E+07
Q87LU2	Pyruvate dehydrogenase E1 component OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2519 PE=4 SV=1	44.6448703	99.601	6.40E+07	8.20E+07	8.20E+07	6.90E+07	7.30E+07	6.50E+07
Q87LU3	Acetyltransferase component of pyruvate dehydrogenase complex OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2518 PE=3 SV=1	27.7511962	64.93	4.70E+07	4.90E+07	5.50E+07	4.90E+07	5.20E+07	3.70E+07
Q87LU4	Carbonic anhydrase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2514 PE=3 SV=1	5.85585586	25.206						
Q87LW3	Aconitate hydratase B OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2495 PE=3 SV=1	31.3294798	94.013	2.60E+07	9.10E+07	2.80E+07	2.90E+07	3.50E+07	3.00E+07
Q87LW7	Iron(III) ABC transporter, periplasmic iron-compound-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2491 PE=4 SV=1	50.7418398	37.673	1.10E+08	1.10E+08	1.00E+08	1.10E+08	1.00E+08	9.00E+07
Q87LX0	Putative phosphoglucomutase/phosphomannomutase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2488 PE=4 SV=1	14.2553191	52.254						7.70E+06
Q87LX1	N,N'-diacetylchitobiose phosphorylase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2487 PE=4 SV=1	23.4413965	90.02				9.90E+06	2.10E+07	3.50E+07
Q87LX9	Peptide ABC transporter, periplasmic peptide-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2479 PE=4 SV=1	21.4285714	62.865				9.80E+06	6.60E+07	8.00E+07
Q87LZ1	Outer membrane protein U OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=ompU PE=3 SV=1	27.8931751	36.263	3.00E+07	2.50E+07	3.00E+07	4.60E+07	2.40E+07	2.50E+07
Q87LZ2	Transcription elongation factor GreA OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=greA PE=3 SV=1	7.00636943	17.487	2.10E+06			2.40E+06		
Q87LZ3	Putative RNA-binding protein containing KH domain OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2465 PE=4 SV=1	9.18367347	10.994				6.10E+06		5.00E+06
Q87LZ5	ATP-dependent zinc metalloprotease FtsH OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=ftsH PE=3 SV=1	5.43806647	72.936			2.60E+06			
Q87M01	Transcription termination/antitermination protein NusA OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=nusA PE=3 SV=1	14.1414141	54.911	8.20E+06	1.10E+07	1.10E+07	1.10E+07	1.00E+07	9.70E+06
Q87M02	Translation initiation factor IF-2 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=infB PE=3 SV=1	14.8066298	99.335	1.70E+07	2.00E+07	2.10E+07	2.00E+07	2.10E+07	1.60E+07
Q87M05	30S ribosomal protein S15 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpsO PE=3 SV=1	13.4831461	10.057	3.90E+07	4.00E+07	5.00E+07	5.60E+07	6.20E+07	5.20E+07
Q87M06	Polyribonucleotide nucleotidyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=pnp PE=3 SV=1	37.6933896	76.691	2.40E+07	2.40E+07	3.60E+07	2.60E+07	1.90E+07	2.60E+07
Q87M22	Deoxyribose-phosphate aldolase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=deoC PE=3 SV=1	4.26356589	27.727	1.10E+07	9.40E+06	1.10E+07	8.50E+06	8.60E+06	8.50E+06
Q87M25	Purine nucleoside phosphorylase DeoD-type 1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=deoD1 PE=3 SV=1	10.460251	25.878	1.00E+07				1.50E+07	1.60E+07
Q87M27	Phosphoserine phosphatase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2431 PE=4 SV=1	19.3251534	35.774	6.20E+06	6.60E+06	7.30E+06	7.80E+06	6.60E+06	7.70E+06
Q87M30	Elongation factor G 2 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=fusA2 PE=3 SV=1	53.1609195	76.319	8.80E+07	1.10E+08	1.00E+08	1.20E+08	1.20E+08	1.00E+08
Q87M78	2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-succinyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=dapD PE=3 SV=1	24.7813411	35.618	2.00E+07	2.80E+07	3.30E+07	3.40E+07	2.80E+07	2.40E+07
Q87MA0	Putative transcriptional activator ChrR OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2357 PE=4 SV=1	8.21917808	23.985						
Q87MC3	Proline--tRNA ligase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=proS PE=3 SV=1	13.3099825	63.216	4.40E+06	5.80E+06	6.60E+06	6.90E+06	9.80E+06	2.60E+06
Q87MD7	Methionine aminopeptidase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=map PE=3 SV=1	2.39726027	32.327		3.60E+06			3.40E+06	3.20E+06
Q87MD8	30S ribosomal protein S2 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpsB PE=3 SV=1	33.4710744	26.791	7.90E+06	1.60E+07	2.20E+07	7.80E+06	1.30E+07	1.50E+07
Q87MD9	Elongation factor Ts OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=tsf PE=3 SV=1	69.0391459	29.755	7.40E+07	7.70E+07	8.00E+07	8.80E+07	9.50E+07	7.10E+07
Q87ME6	Chaperone protein skp OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2309 PE=3 SV=1	28.9156627	18.488	1.10E+07	7.20E+06	1.10E+07	1.40E+07	1.10E+07	9.80E+06
Q87ME8	3-hydroxyacyl-[acyl-carrier-protein] dehydratase FabZ OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=fabZ PE=3 SV=1	18.6666667	16.828	7.50E+06	7.10E+06	5.90E+06	9.30E+06	1.10E+07	7.90E+06
Q87MG7	Phosphoheptose isomerase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=gmhA PE=3 SV=1	16.2303665	20.795	3.30E+07	5.20E+06	4.60E+06	2.80E+07	6.80E+06	
Q87MI2	4-hydroxy-tetrahydrodipicolinate synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=dapA PE=3 SV=1	34.5890411	31.209	4.00E+07	4.30E+07	3.80E+07	4.40E+07	4.30E+07	3.40E+07
Q87MM9	Chorismate synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=aroC PE=3 SV=1	13.0193906	39.04	8.00E+06	7.80E+06	7.80E+06	7.90E+06	7.10E+06	5.80E+06
Q87MN5	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2197 PE=4 SV=1	14.9425287	18.64	1.40E+07	2.50E+07	1.30E+07	2.20E+07	1.60E+07	4.30E+06
Q87MN7	3-oxoacyl-[acyl-carrier-protein] synthase I OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2194 PE=3 SV=1	21.3399504	42.591	1.60E+07	1.80E+08	1.80E+07	2.00E+07	2.10E+07	1.60E+07
Q87MN9	Aspartate-semialdehyde dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=asd PE=3 SV=1	8.01186944	37.243	4.10E+06	7.20E+06	5.90E+06	3.40E+06	6.00E+06	6.30E+06
Q87MP2	Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta 1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=accD1 PE=3 SV=1	9.74025974	34.008	8.00E+06	2.00E+06	1.00E+07	9.50E+06	1.10E+07	5.60E+06
Q87MP6	Amidophosphoribosyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=purF PE=3 SV=1	6.94444444	56.01	2.80E+06	7.80E+06	6.90E+06	6.30E+06	5.40E+06	4.80E+06
Q87MR7	Alkaline phosphatase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2163 PE=3 SV=1	3.23809524	57.343						
Q87MS4	Glyceraldehyde-3-phosphate dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2157 PE=3 SV=1	69.4864048	35.204	2.30E+08	2.60E+08	2.90E+08	3.10E+08	3.30E+08	2.60E+08
Q87MV7	Aspartate-semialdehyde dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=asd PE=3 SV=1	56.8733154	40.185	5.30E+07	6.40E+07	6.20E+07	5.60E+07	6.50E+07	5.40E+07
Q87MW0	Aldehyde-alcohol dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2121 PE=1 SV=1	41.6666667	97.062	4.70E+07	5.50E+07	5.00E+07	6.40E+07	5.00E+07	5.80E+07
Q87MW3	Superoxide dismutase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2118 PE=3 SV=1	6.53266332	22.157			4.30E+06	3.40E+06	7.10E+06	3.80E+06
Q87MY5	Oligopeptide ABC transporter, periplasmic oligopeptide-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2091 PE=4 SV=1	21.5439856	62.342	1.10E+07	7.10E+06	1.80E+07	1.50E+07	1.30E+07	1.40E+07
Q87MZ3	Phosphate acetyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2083 PE=3 SV=1	33.4733894	76.631	1.40E+07	2.00E+07	1.80E+07	2.10E+07	2.10E+07	1.60E+07
Q87MZ4	Acetate kinase 1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=ackA1 PE=3 SV=1	31.9095477	42.986	2.00E+07	2.50E+07	2.50E+07	2.60E+07	2.40E+07	2.00E+07
Q87MZ6	ABC transporter substrate-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2080 PE=4 SV=1	25.5451713	33.175	1.10E+07	1.20E+07	1.00E+07	1.10E+07	1.00E+07	8.60E+06
Q87MZ9	Putative maltodextrin glucosidase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2077 PE=4 SV=1	1.80921053	70.186						
Q87N07	Methionine--tRNA ligase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=metG PE=3 SV=2	4.06976744	77.945	8.00E+06	9.50E+06	8.90E+06	8.80E+06	1.00E+07	8.80E+06
Q87N15	Ribosomal large subunit pseudouridine synthase C OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rluC PE=3 SV=1	2.22222222	36.119						
Q87N18	50S ribosomal protein L32 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpmF PE=3 SV=2	39.2857143	6.294	9.40E+06			1.50E+07	1.00E+07	
Q87N21	Malonyl CoA-acyl carrier protein transacylase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2055 PE=3 SV=1	7.81758958	32.327		1.10E+07	1.20E+07	1.90E+07	1.70E+07	1.60E+07
Q87N23	3-oxoacyl-[acyl-carrier-protein] synthase 2 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2052 PE=3 SV=1	13.2211538	43.395	5.00E+06		1.10E+07	1.00E+07	7.40E+06	1.20E+07
Q87N29	PTS system, glucose-specific IIBC component OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2046 PE=4 SV=1	14.0756303	49.407	1.90E+07	1.20E+07	1.90E+07	1.80E+07	1.30E+07	9.70E+06
Q87N36	Pyruvate kinase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2039 PE=3 SV=1	7.08333333	51.651	1.90E+06	3.00E+06	5.10E+06	3.00E+06	4.00E+06	2.60E+06
Q87N42	Oxidoreductase, short-chain dehydrogenase/reductase family OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2033 PE=3 SV=1	4.03225806	26.994			4.20E+06			2.30E+06
Q87N45	30S ribosomal protein S1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2030 PE=3 SV=1	46.7625899	60.905	8.30E+07	1.10E+08	1.20E+08	1.10E+08	1.10E+08	1.00E+08

Q87N50	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2025 PE=4 SV=1	7.95795796	76.629	9.00E+06	7.10E+06	8.20E+06	9.60E+06	7.30E+06	8.60E+06
Q87N83	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1992 PE=4 SV=1	17.2839506	37.643	8.40E+06	8.80E+06	6.10E+06	5.90E+06	1.00E+07	
Q87N84	5-methyltetrahydropteroyltriglutamate-homocysteine methyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1991 PE=4 SV=1	2.92397661	38.487		6.10E+06	7.00E+06		6.10E+06	3.80E+06
Q87N88	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1987 PE=4 SV=1	6.04395604	19.965	1.10E+07		1.40E+07	1.40E+07	1.40E+07	9.30E+06
Q87N91	Putative two-component sensor OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1984 PE=4 SV=1	2.99539171	48.549						
Q87NA1	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=metE PE=3 SV=1	65.1315789	84.66	1.90E+08	2.20E+08	2.20E+08	2.50E+08	2.60E+08	2.30E+08
Q87NB5	Putative translation factor OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1953 PE=4 SV=1	4.85436893	22.912						4.30E+07
Q87NC0	Elongation factor P-like protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1948 PE=3 SV=1	13.8297872	20.734		4.50E+06			8.90E+06	
Q87NC6	Diaminobutyrate-pyruvate transaminase & L-2,4-diaminobutyrate decarboxylase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1942 PE=1 SV=1	8.14196242	104.32	5.80E+06	1.20E+07			8.20E+06	7.90E+06
Q87NC7	Putative carboxynorspermidine dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1941 PE=4 SV=1	19.4244604	46.471	1.00E+07	1.20E+07	8.60E+06	1.30E+07	8.70E+06	8.50E+06
Q87NC8	Carboxynorspermidine/carboxyspermidine decarboxylase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1940 PE=3 SV=1	4.50928382	42.003	3.30E+06		2.40E+06			
Q87NC9	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1939 PE=4 SV=1	7.05882353	18.444			1.80E+06	3.90E+06		
Q87ND4	Ribonucleoside-diphosphate reductase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1934 PE=3 SV=1	2.10526316	85.622						
Q87ND6	DNA gyrase subunit A OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=gyrA PE=3 SV=1	10.1366743	97.04	1.20E+07	1.70E+07	1.40E+07	1.10E+07	1.80E+07	1.00E+07
Q87NE7	GTP cyclohydrolase-2 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=ribA PE=3 SV=1	5.55555556	22.294	6.20E+06		6.80E+06			
Q87NF7	Extracellular solute-binding protein, family 7 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1911 PE=3 SV=1	17.679558	40.992	7.10E+06	1.30E+07	4.10E+06	1.50E+07		6.10E+06
Q87NG8	Aspartate aminotransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1900 PE=3 SV=1	62.8019324	45.449	1.40E+08	2.30E+08	2.30E+08	2.10E+08	2.20E+08	1.80E+08
Q87NH5	Asparagine--tRNA ligase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=asnS PE=3 SV=1	47.4248927	52.557	6.80E+07	6.60E+07	6.00E+07	6.20E+07	7.30E+07	5.50E+07
Q87NW7	Homoserine O-succinyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=metA PE=3 SV=1	3.83386581	36.249				9.60E+06		
Q87NX4	Thermostable carboxypeptidase 1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1744 PE=4 SV=1	2.16535433	57.33		5.20E+06	4.60E+06	4.50E+06	2.60E+06	
Q87NY3	Histidine kinase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1735 PE=4 SV=1	1.47058824	54.354			3.20E+05			
Q87P08	Glucose-6-phosphate 1-dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=zwf PE=3 SV=1	5.78842315	57.604		7.80E+06	8.50E+06		5.70E+06	4.60E+06
Q87P09	DevB protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1709 PE=4 SV=1	4.20168067	25.977		1.20E+07				
Q87P10	6-phosphogluconate dehydrogenase, decarboxylating OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1708 PE=3 SV=1	24.06639	52.502	1.80E+07	3.00E+07	2.10E+07	2.90E+07	2.80E+07	2.20E+07
Q87P15	Aldehyde dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1703 PE=3 SV=1	20.3557312	55.651		2.30E+07		3.30E+07		
Q87P20	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1698 PE=4 SV=1	14.7590361	38.479	9.20E+06	6.10E+06	6.50E+06	7.50E+06	7.10E+06	6.90E+06
Q87P32	Adenosine monophosphate-protein transferase VopS OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=vopS PE=1 SV=1	28.6821705	41.711	8.80E+06	1.00E+07	8.40E+06	7.50E+06	1.00E+07	4.30E+06
Q87P37	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1682 PE=4 SV=1	27.6315789	17.116	5.10E+06	1.00E+07				
Q87P47	Putative translocation protein in type III secretion OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1671 PE=4 SV=1	6.40243902	36.436	4.60E+06	7.50E+06	4.10E+06	3.50E+06	5.40E+06	
Q87P59	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1659 PE=4 SV=1	20.92257	67.03	2.00E+07	1.90E+07	1.90E+07	1.30E+07	2.20E+07	1.10E+07
Q87P60	Low calcium response locus protein H OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1658 PE=4 SV=1	29.0123457	18.117	1.90E+07	2.20E+07	2.10E+07	1.60E+07	1.80E+07	1.40E+07
Q87P61	Putative translocator protein PopB OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1657 PE=4 SV=1	5.51378446	41.314	6.80E+06	6.60E+06	5.90E+06	7.40E+06	1.10E+07	5.50E+06
Q87P62	Putative translocator protein PopD OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1656 PE=4 SV=1	25.748503	35.286	1.80E+07	2.40E+07	2.40E+07	1.60E+07	2.40E+07	1.50E+07
Q87P63	Immunogenic protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1655 PE=4 SV=1	2.78637771	34.901	5.20E+07	7.40E+07	6.30E+07	7.10E+07	7.40E+07	4.10E+07
Q87PB0	RNA chaperone ProQ OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=proQ PE=3 SV=1	15.3110048	23.23	3.40E+07	8.20E+06	9.60E+06	7.50E+06	3.40E+07	8.50E+06
Q87PB3	Aminopeptidase N OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1604 PE=4 SV=1	4.13793103	98.399	2.70E+06	4.30E+06	2.30E+06		3.00E+06	2.10E+06
Q87PB5	Putative NAD-glutamate dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1602 PE=4 SV=1	0.68195908	183.379	2.80E+06	4.70E+06		3.30E+06		
Q87PB7	Dihydroorotate dehydrogenase (quinone) OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=pyrD PE=3 SV=1	7.44047619	36.859						4.50E+06
Q87PB8	Cell division protein ZapC OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=zapC PE=3 SV=1	30	20.763	7.30E+06	1.20E+07	8.90E+06	6.20E+06	7.60E+06	6.50E+06
Q87PC5	3-hydroxydecanoyl-[acyl-carrier-protein] dehydratase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=fabA PE=3 SV=1	20.3488372	18.985	2.20E+07	3.20E+07	2.80E+07	3.20E+07	2.80E+07	2.50E+07
Q87PE6	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1564 PE=4 SV=1	22.7459016	56.383	9.10E+06	1.10E+07	8.70E+06	8.70E+06	1.00E+07	7.90E+06
Q87PG6	Fumarate and nitrate reduction regulatory protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1536 PE=4 SV=1	4.43548387	27.816	5.20E+06	7.50E+06	6.30E+06	5.40E+06	6.30E+06	5.40E+06
Q87PG7	Putative stress protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1535 PE=4 SV=1	13.3333333	35.308	5.50E+06	5.40E+06	6.10E+06	1.80E+07		5.30E+06
Q87PH6	Putrescine-binding periplasmic protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1526 PE=3 SV=1	18.8732394	39.658	1.00E+07		1.50E+07	1.50E+07		1.40E+07
Q87PH7	Putrescine-binding periplasmic protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1525 PE=3 SV=1	4.05797101	38.974				2.90E+06		
Q87PK2	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1501 PE=1 SV=1	11.3970588	30.055	6.00E+06	6.00E+06	5.30E+06	5.90E+06	4.80E+06	5.80E+06
Q87PK8	N-acetyl-D-glucosamine kinase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=nagK PE=3 SV=1	11.2582781	32.755	1.80E+06	1.60E+06	5.00E+06	1.70E+06	7.80E+06	6.30E+06
Q87PM2	Riboflavin synthase, alpha chain OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1480 PE=4 SV=1	5.41871921	22.027				2.50E+06		
Q87PR5	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1436 PE=4 SV=1	4.54545455	27.73	4.00E+06		5.60E+06		5.40E+06	
Q87PT8	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1413 PE=4 SV=1	4.98866213	49.098	7.40E+06		1.90E+06			
Q87PU8	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1403 PE=4 SV=1	14.2566191	55.542	1.20E+07	5.70E+06	1.10E+07		1.30E+07	
Q87PV5	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1396 PE=4 SV=1	2.33463035	29.853	1.00E+07	9.50E+06		7.40E+06	6.40E+06	9.00E+06
Q87PV8	Putative ClpA/B-type protease OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1392 PE=3 SV=1	2.69662921	97.861	3.70E+06	1.80E+06	4.30E+06		3.50E+06	
Q87Q03	Oligopeptide ABC transporter, periplasmic oligopeptide-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1347 PE=4 SV=1	1.67910448	60.287	7.50E+06		1.20E+07	9.70E+06	9.30E+06	8.70E+06
Q87Q40	Succinylglutamate desuccinylase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=astE PE=1 SV=1	8.47953216	38.813		4.60E+06		4.60E+06		
Q87Q42	Putative oligopeptidase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1308 PE=4 SV=1	2.17028381	67.96		2.40E+06				
Q87Q53	Phosphoribosylglycinamide formyltransferase 2 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=purT PE=3 SV=1	6.39386189	42.864			2.90E+06		3.60E+06	
Q87Q56	Integration host factor subunit alpha OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=ihfA PE=3 SV=1	19.3877551	11.201	1.90E+07	1.80E+07	2.80E+07	1.90E+07	2.00E+07	2.50E+07
Q87Q59	Phenylalanine--tRNA ligase beta subunit OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=pheT PE=3 SV=1	15.7303371	87.044	1.30E+07	1.10E+07	1.40E+07	1.20E+07	1.10E+07	1.10E+07
Q87Q60	Phenylalanine--tRNA ligase alpha subunit OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=pheS PE=3 SV=1	11.9266055	36.85	6.00E+06	8.00E+06	6.80E+06	8.80E+06	7.00E+06	
Q87Q70	Threonine--tRNA ligase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=thrS PE=3 SV=1	8.87850467	73.714	1.00E+07	1.30E+07	1.20E+07	1.20E+07	1.40E+07	1.10E+07
Q87Q81	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1269 PE=4 SV=1	9.73451327	25.259		7.00E+06		6.10E+06	3.80E+06	6.50E+06
Q87Q87	Phosphoribosylaminoimidazole-succinocarboxamide synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=purC PE=3 SV=1	28.6103542	41.031	9.00E+06	1.30E+07	1.50E+07	1.00E+07	1.60E+07	1.20E+07
Q87Q92	NAD-dependent malic enzyme OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=maeA PE=3 SV=1	12.0996441	62.26	8.40E+06		9.20E+06	8.20E+06	1.20E+07	1.00E+07
Q87Q99	Thioredoxin reductase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1251 PE=3 SV=1	10.3448276	34.467	2.10E+07	1.30E+07		6.80E+06		9.10E+06
Q87QA3	Phosphoserine aminotransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=serC PE=3 SV=1	28.021978	40.175	2.50E+07	2.90E+07	2.60E+07	3.30E+07	2.90E+07	2.70E+07
Q87QB9	Putative reductase VP1231 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1231 PE=3 SV=1	46.25	43.941	3.50E+07	4.10E+07	4.20E+07	4.10E+07	4.00E+07	2.90E+07
Q87QD9	50S ribosomal protein L25 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplY PE=3 SV=1	8.69565217	10.408	1.20E+07	1.20E+07	1.50E+07	1.50E+07	1.60E+07	1.30E+07
Q87QE6	Heat shock protein HslJ OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1203 PE=4 SV=1	6.08108108	16.586	3.80E+06				4.60E+06	
Q87QG7	Cystathionine beta-lyase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1182 PE=3 SV=1	7.960199	44.609	1.20E+07	1.40E+07	9.80E+06	1.30E+07	1.40E+07	1.40E+07
Q87QJ9	Cysteine--tRNA ligase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=cysS PE=3 SV=1	11.0869565	52.014	3.80E+06	7.20E+06	3.50E+06	7.60E+06	6.00E+06	4.10E+06
Q87QK5	Histidine biosynthesis bifunctional protein HisIE OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=hisI PE=3 SV=1	15.1658768	23.24		2.60E+06				3.70E+06
Q87QK6	Imidazole glycerol phosphate synthase subunit HisF OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=hisF PE=3 SV=1	6.22568093	28.356						
Q87QK7	1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino] imidazole-4-carboxamide isomerase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=hisA PE=3 SV=1	22.4489796	26.363	6.00E+06	6.90E+06		4.60E+06	6.90E+06	7.00E+06
Q87QK9	Histidine biosynthesis bifunctional protein HisB OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=hisB PE=3 SV=1	2.80112045	39.802						4.10E+06
Q87QL0	Histidinol-phosphate aminotransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=hisC PE=3 SV=1	14.4508671	38.152	1.80E+07	1.70E+07	1.70E+07	1.90E+07	1.90E+07	1.50E+07
Q87QL1	Histidinol dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=hisD PE=3 SV=1	7.65661253	46.07	7.40E+06	1.00E+07	6.50E+06	1.10E+07	8.90E+06	9.60E+06
Q87QL2	ATP phosphoribosyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=hisG PE=3 SV=1	26.8456376	32.824	1.70E+07	1.90E+07	1.70E+07	2.00E+07	2.00E+07	1.80E+07
Q87QM1	Adenylosuccinate lyase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1128 PE=3 SV=1	30.2631579	51.444	1.30E+07	2.10E+07	1.90E+07	2.10E+07	2.40E+07	1.60E+07
Q87QP1	Serine--tRNA ligase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=serS PE=3 SV=1	42.0689655	48.767	2.20E+07	3.90E+07	2.10E+07	2.40E+07	2.60E+07	2.00E+07
Q87QP5	Leucine-responsive regulatory protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1104 PE=4 SV=1	52.4390244	18.793	2.30E+07	2.30E+07	2.60E+07	2.80E+07	2.60E+07	2.00E+07
Q87QP6	Alanine dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1103 PE=3 SV=1	50.5347594	39.857	3.80E+07	7.00E+07	4.40E+07	7.20E+07	2.80E+07	3.90E+07
Q87QP8	Cys regulon transcriptional activator OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1101 PE=4 SV=1	3.7037037	36.075	4.60E+06	4.60E+06	4.20E+06	4.00E+06	3.80E+06	4.90E+06
Q87QS7	Putative helicase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1072 PE=4 SV=1	27.8418451	68.714	1.30E+07	1.50E+07	1.50E+07	1.10E+07	1.50E+07	1.30E+07
Q87QT8	Peptidoglycan-associated lipoprotein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1061 PE=3 SV=1	12.6436782	18.701			3.70E+06	2.60E+06	5.40E+06	3.60E+06
Q87QT9	Protein TolB OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=tolB PE=3 SV=1	16.8888889	49.755	8.10E+06	9.80E+06	8.90E+06	9.90E+06	7.80E+06	8.00E+06
Q87QU6	Cytochrome d ubiquinol oxidase, subunit I OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1053 PE=4 SV=1	1.85873606	60.313					5.50E+06	
Q87QV2	Aspartate--tRNA ligase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=aspS PE=3 SV=1	35.6418919	65.722	2.90E+07	3.30E+07	3.10E+07	2.90E+07	3.60E+07	3.20E+07
Q87QW9	HTH-type transcriptional repressor PurR OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=purR PE=3 SV=1	6.88622754	37.65	2.20E+06		5.20E+06	3.60E+06	5.20E+06	
Q87QX6	Glucose-1-phosphate adenylyltransferase 1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=glgC1 PE=3 SV=1	52.345679	45.454	4.30E+07	4.20E+07	4.60E+07	4.40E+07	5.10E+07	3.60E+07
Q87QX7	DNA topoisomerase 1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=topA PE=3 SV=1	1.71232877	97.95				2.50E+06	3.60E+06	
Q87QX9	3-phosphoshikimate 1-carboxyvinyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=aroA PE=3 SV=1	8.21596244	46.066	5.80E+06	1.00E+07	8.00E+06	8.50E+06	7.80E+06	7.70E+06
Q87QY4	ATP-dependent Clp protease, ATP-binding subunit ClpA OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1014 PE=3 SV=1	6.48148148	83.316	1.00E+06	1.60E+06	2.10E+06	2.20E+06	2.40E+06	
Q87QY7	Isocitrate dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1011 PE=4 SV=1	55.7354926	80.465	5.50E+07	5.40E+07	4.80E+07	4.70E+07	5.70E+07	4.40E+07
Q87QZ9	Amino acid ABC transporter, periplasmic amino acid-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0999 PE=3 SV=1	47.2868217	28.354	2.70E+07	3.20E+07	2.80E+07	2.90E+07	2.70E+07	2.40E+07
Q87R04	Formate acetyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0994 PE=4 SV=1	53.1662269	84.466	5.30E+07	7.30E+07	7.10E+07	8.20E+07	8.70E+07	8.10E+07
Q87R29	UPF0227 protein VP0969 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0969 PE=3 SV=1	4.46927374	20.729		6.10E+06				
Q87R36	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0962 PE=4 SV=1	22.7979275	43.935	1.30E+07	1.10E+07	1.20E+07	1.60E+07	1.70E+07	1.30E+07
Q87R38	Uridine phosphorylase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0960 PE=3 SV=1	16.6666667	26.919	1.20E+07	1.10E+07	1.40E+07	1.20E+07	1.20E+07	9.00E+06

Table S1

Q87R49	Acyl-CoA thioesterase II OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0949 PE=4 SV=1	3.4965035	32.574						
Q87R78	DNA-binding protein HU-beta OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0920 PE=3 SV=1	28.8888889	9.402	1.30E+08	1.30E+08	1.30E+08	1.40E+08	1.40E+08	1.20E+08
Q87R80	ATP-dependent Clp protease proteolytic subunit OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=clpP PE=3 SV=1	30	21.961	3.60E+07	4.10E+07	3.00E+07	4.10E+07	3.60E+07	3.10E+07
Q87R81	Trigger factor OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=tig PE=3 SV=1	56.9124424	48.225	5.00E+07	6.30E+07	6.60E+07	6.20E+07	7.20E+07	5.50E+07
Q87R87	C4-dicarboxylate-binding periplasmic protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0910 PE=4 SV=1	24.3975904	37.109	1.10E+07	1.60E+07	2.00E+07	2.00E+07	2.60E+07	2.00E+07
Q87RB8	Bifunctional protein FolD OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=folD PE=3 SV=1	3.14685315	30.787			3.50E+06			
Q87RD3	Formyltetrahydrofolate deformylase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=purU PE=3 SV=1	2.52707581	31.6						1.10E+07
Q87RD6	Arginine--tRNA ligase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=argS PE=3 SV=1	13.6915078	63.83	2.90E+06	6.60E+06	6.60E+06	4.00E+06	3.30E+06	7.80E+06
Q87RE4	Zinc ABC transporter, periplasmic zinc-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0853 PE=3 SV=1	18.1506849	32.129	7.40E+06	1.00E+07	7.10E+06	8.90E+06	1.30E+07	8.40E+06
Q87RE7	Succinyl-CoA ligase [ADP-forming] subunit alpha OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0850 PE=3 SV=1	48.6206897	29.974	4.70E+07	6.10E+07	4.70E+07	4.90E+07	5.00E+07	4.00E+07
Q87RE8	Succinyl-CoA ligase [ADP-forming] subunit beta OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=sucC PE=3 SV=1	56.7010309	41.516	7.90E+07	1.00E+08	7.80E+07	8.40E+07	8.00E+07	6.00E+07
Q87RE9	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0848 PE=3 SV=1	44.3890274	43.675	7.00E+07	7.10E+07	6.30E+07	6.30E+07	6.40E+07	5.00E+07
Q87RF0	2-oxoglutarate dehydrogenase, E1 component OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0847 PE=4 SV=1	20.8289054	106.016	2.80E+07	2.60E+07	2.80E+07	2.80E+07	2.50E+07	2.10E+07
Q87RF1	Succinate dehydrogenase iron-sulfur subunit OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0846 PE=3 SV=1	5.08474576	26.308			2.90E+06			
Q87RF2	Succinate dehydrogenase flavoprotein subunit OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0845 PE=3 SV=1	12.585034	64.207	1.20E+07	1.20E+07	1.20E+07	6.90E+06	7.30E+06	8.50E+06
Q87RF5	Citrate synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0842 PE=3 SV=1	43.8228438	48.188	1.00E+08	9.80E+07	9.20E+07	9.00E+07	6.80E+07	7.40E+07
Q87RF8	Phosphoglucomutase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0839 PE=3 SV=1	31.0218978	59.243	2.30E+07	2.00E+07	2.50E+07	2.60E+07	2.80E+07	2.60E+07
Q87RG4	Glutamine--tRNA ligase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=glnS PE=3 SV=1	10.4316547	63.929	7.50E+06	8.60E+06	9.70E+06	1.10E+07	1.60E+07	9.40E+06
Q87RG5	PTS system, N-acetylglucosamine-specific IIABC component OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0831 PE=4 SV=1	8.41300191	54.543			1.40E+07	8.70E+06	7.80E+06	1.10E+07
Q87RG7	N-acetylglucosamine-6-phosphate deacetylase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0829 PE=3 SV=1	16.9312169	40.723		1.60E+07		1.80E+07		1.50E+07
Q87RG8	N-acetylglucosamine repressor OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0828 PE=4 SV=1	5.1980198	43.799		2.90E+06	3.40E+06	4.60E+06	4.20E+06	2.60E+06
Q87RH0	Asparagine synthetase B, glutamine-hydrolyzing OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0826 PE=4 SV=1	25.631769	62.273	9.50E+06	8.90E+06	9.70E+06	1.50E+07	1.20E+07	9.50E+06
Q87RH4	Adenylate kinase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=adk PE=3 SV=1	24.7663551	23.28	1.60E+07	1.30E+07	9.40E+06	1.10E+07	9.60E+06	1.10E+07
Q87RH5	Chaperone protein HtpG OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=htpG PE=3 SV=1	13.0914826	72.116	6.30E+06	8.30E+06	8.90E+06	1.20E+07		6.20E+06
Q87RJ7	Cysteine synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0797 PE=3 SV=1	74.8447205	34.112	1.50E+08	1.60E+08	1.50E+08	1.50E+08	1.90E+08	1.50E+08
Q87RJ9	Phosphocarrier protein HPr OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0795 PE=4 SV=1	9.41176471	9.103			2.60E+07		2.30E+07	
Q87RK0	Phosphoenolpyruvate-protein phosphotransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0794 PE=3 SV=1	20.2090592	63.152	4.00E+06	1.20E+07	2.20E+07	2.30E+07	1.80E+07	1.40E+07
Q87RK1	PTS system, glucose-specific IIA component OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0793 PE=4 SV=1	37.2781065	17.943	3.50E+07	3.80E+07	4.10E+07	3.40E+07	4.00E+07	3.80E+07
Q87RL6	Glutamate--tRNA ligase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=gltX PE=3 SV=1	27.4261603	53.42	1.50E+07	2.20E+07	1.50E+07	1.70E+07	1.80E+07	1.30E+07
Q87RL8	Putative chitoporin OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0760 PE=4 SV=1	20.9115282	40.764					2.00E+07	5.40E+07
Q87RL9	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0759 PE=4 SV=1	31.9148936	5.569						4.50E+06
Q87RM3	N,N'-diacetylchitobiase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0755 PE=4 SV=1	2.49150623	97.595						5.10E+06
Q87RN0	2-dehydro-3-deoxyphosphooctonate aldolase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=kdsA PE=3 SV=1	2.82685512	30.79	5.50E+05	6.70E+06	6.40E+06	7.70E+06	6.50E+06	5.40E+06
Q87RN8	Ribose-phosphate pyrophosphokinase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=prs PE=3 SV=1	42.6751592	33.911	1.80E+07	2.30E+07	2.00E+07	2.40E+07	2.10E+07	1.70E+07
Q87RP0	Ribosome-binding ATPase YchF OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=ychF PE=3 SV=1	3.13315927	41.769			4.70E+06	5.40E+06		
Q87RQ0	Leucine--tRNA ligase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=leuS PE=3 SV=1	15.8693116	96.593	1.00E+07	1.70E+07	1.50E+07	1.20E+07	1.50E+07	1.00E+07
Q87RR2	Serine hydroxymethyltransferase 1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=glyA1 PE=3 SV=1	51.9230769	45.476	7.70E+07	1.10E+08	1.10E+08	1.20E+08	1.30E+08	8.40E+07
Q87RS3	Lipoprotein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0704 PE=3 SV=1	44.6096654	29.052	1.60E+07	1.30E+07	2.60E+07	2.00E+07	1.90E+07	1.60E+07
Q87RU3	N utilization substance protein B homolog OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=nusB PE=3 SV=1	7.09677419	17.559	4.70E+06		4.80E+06		4.80E+06	
Q87RU4	6,7-dimethyl-8-ribityllumazine synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=ribH PE=3 SV=1	53.2051282	16.422	1.40E+07	2.00E+07	2.00E+07	2.00E+07	1.90E+07	1.60E+07
Q87RU5	3,4-dihydroxy-2-butanone 4-phosphate synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=ribB PE=3 SV=1	14.6341463	40.086	7.10E+06	8.80E+06	7.00E+06	9.80E+06	9.40E+06	5.40E+06
Q87RU9	Gamma-glutamyl phosphate reductase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=proA PE=3 SV=1	19.7115385	44.665	6.00E+06	9.50E+06	7.40E+06	9.60E+06	1.00E+07	6.90E+06
Q87RV5	Aminoacyl-histidine dipeptidase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0671 PE=4 SV=1	9.79591837	53.592	4.10E+06	2.20E+06	5.40E+06	5.00E+06	5.00E+06	4.40E+06
Q87RV7	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0669 PE=4 SV=1	26.4044944	39.042	1.60E+07	1.90E+07	1.60E+07	1.80E+07	1.60E+07	1.50E+07
Q87RW0	Phosphoribosylformylglycinamidine synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=purL PE=3 SV=1	16.0522273	141.597	4.40E+06	1.40E+07	1.40E+07	1.40E+07	1.40E+07	1.20E+07
Q87RX2	Chaperone protein DnaJ OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=dnaJ PE=3 SV=1	3.1496063	41			4.40E+06	6.90E+06	5.20E+06	
Q87RX3	Chaperone protein DnaK OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=dnaK PE=3 SV=1	59.3406593	69.012	4.50E+07	4.60E+07	4.50E+07	4.90E+07	5.40E+07	4.80E+07
Q87RZ5	Homocysteine synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0629 PE=3 SV=1	12.5592417	45.703	5.60E+06	6.20E+06		7.60E+06	5.70E+06	4.30E+06
Q87S07	GMP synthase [glutamine-hydrolyzing] OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=guaA PE=3 SV=1	10.4448743	57.635	1.10E+07	1.30E+07	1.10E+07	2.10E+07	1.60E+07	1.20E+07
Q87S08	Inosine-5'-monophosphate dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=guaB PE=3 SV=1	34.2857143	51.913	1.40E+07	1.70E+07	1.60E+07	1.70E+07	2.00E+07	1.50E+07
Q87S15	Histidine--tRNA ligase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=hisS PE=3 SV=1	5.45023697	47.116						
Q87S21	Peptidase B OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=pepB PE=3 SV=1	15.9722222	46.582	8.50E+06	8.20E+06	9.30E+06	1.20E+07	9.60E+06	9.50E+06
Q87S24	Chaperone protein HscA homolog OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=hscA PE=3 SV=1	2.10696921	66.054	1.90E+06		2.00E+06	2.00E+06	2.40E+06	
Q87S28	Cysteine desulfurase IscS OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=iscS PE=3 SV=1	8.66336634	44.967	9.30E+06	9.60E+06	6.90E+06	7.40E+06	1.10E+07	7.00E+06
Q87S35	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0589 PE=4 SV=1	11.9266055	11.832	7.30E+06		1.10E+07			
Q87S40	Isocitrate lyase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0584 PE=4 SV=1	7.11009174	48.039		7.00E+06		6.70E+06		1.10E+07
Q87S44	Antioxidant, AhpC/Tsa family OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0580 PE=4 SV=1	67.4876847	22.223	1.30E+08	1.50E+08	1.40E+08	1.40E+08	1.40E+08	1.10E+08
Q87S63	Chaperone protein ClpB OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=clpB PE=3 SV=1	30.6884481	95.813	9.40E+06	1.60E+07	1.30E+07	1.30E+07	1.40E+07	1.30E+07
Q87S68	Putative sigma-54 modulation protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0556 PE=4 SV=1	27.7777778	12.378	7.80E+06	9.00E+06	7.00E+06	9.70E+06	8.10E+06	3.30E+06
Q87S69	Chorismate mutase/prephenate dehydratase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0555 PE=4 SV=1	6.37755102	44.196	1.70E+06	2.60E+06			1.70E+06	
Q87S73	ABC transporter, ATP-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0551 PE=3 SV=1	11.1711712	62.207	3.00E+06	4.30E+06	2.50E+06	4.30E+06	4.20E+06	3.90E+06
Q87S77	T-protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0547 PE=4 SV=1	2.4	41.976		3.10E+06				
Q87S78	Phospho-2-dehydro-3-deoxyheptonate aldolase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0546 PE=3 SV=1	1.96078431	39.669		9.60E+06				
Q87S84	Putative carbon starvation protein A OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0540 PE=4 SV=1	2.4291498	53.283	1.10E+07					
Q87S90	Isoleucine--tRNA ligase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=ileS PE=3 SV=1	6.7940552	105.212	5.10E+06	5.00E+06	4.30E+06	4.90E+06		5.80E+06
Q87S93	30S ribosomal protein S20 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpsT PE=3 SV=1	30.2325581	9.53	4.30E+06	7.90E+06	8.00E+06	1.00E+07	8.70E+06	1.30E+07
Q87S99	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0525 PE=4 SV=1	3.11688312	43.946				6.40E+06		
Q87SA8	Oxidoreductase Tas, aldo/keto reductase family OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0516 PE=4 SV=1	11.3636364	39.659	7.60E+06	4.90E+06	9.80E+06	9.00E+06	1.30E+07	7.30E+06
Q87SB1	Lysine--tRNA ligase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=lysS PE=3 SV=1	29.5049505	57.521	2.20E+07	6.80E+07	5.80E+07	3.00E+07	5.90E+07	2.60E+07
Q87SB3	Single-stranded-DNA-specific exonuclease RecJ OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0511 PE=4 SV=1	3.45423143	64.204						
Q87SC0	UPF0246 protein VP0504 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0504 PE=3 SV=1	4.65116279	29.323					3.60E+06	
Q87SC7	Autonomous glycyl radical cofactor OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=grcA PE=3 SV=1	45.6	13.92	2.00E+07	1.40E+07	1.70E+07	1.60E+07	2.70E+07	2.10E+07
Q87SC8	Threonine synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0496 PE=4 SV=1	38.4976526	46.484	2.50E+07	2.60E+07	2.40E+07	2.40E+07	2.70E+07	2.20E+07
Q87SC9	Homoserine kinase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=thrB PE=3 SV=1	8.17610063	34.413	1.30E+07	1.00E+07	9.80E+06		7.70E+06	
Q87SD0	Aspartokinase I/homoserine dehydrogenase, threonine-sensitive OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0494 PE=4 SV=1	30.7692308	88.447	2.20E+07	2.50E+07	1.90E+07	2.40E+07	2.10E+07	1.90E+07
Q87SD2	Putative 4-hydroxy-4-methyl-2-oxoglutarate aldolase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0492 PE=3 SV=1	6.25	17.697	7.10E+06	9.70E+06	9.90E+06			9.00E+06
Q87SD5	Aerobic respiration control protein FexA OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0489 PE=4 SV=1	19.3277311	26.919	9.70E+06	9.10E+06	9.20E+06	8.20E+06	1.10E+07	9.10E+06
Q87SE0	Glutamate synthase, large subunit OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0484 PE=4 SV=1	11.8130133	175.206	8.60E+06	1.30E+07	1.30E+07	1.70E+07	1.00E+07	1.20E+07
Q87SE1	Glutamate synthase, small subunit OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0483 PE=4 SV=1	15.9509202	53.348	5.70E+06	2.90E+06	1.60E+06	7.30E+06	3.90E+06	4.60E+06
Q87SE2	Glutamate synthase, large subunit OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0482 PE=4 SV=1	5.31271015	162.924	7.90E+06	7.60E+06	7.20E+06	5.80E+06	8.30E+06	8.00E+06
Q87SE3	Glutamate synthase, small subunit OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0481 PE=4 SV=1	2.76595745	52.481	4.60E+06	3.90E+06			3.40E+06	
Q87SF3	Carbamoyl-phosphate synthase large chain OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=carB PE=3 SV=1	27.8551532	117.789	3.20E+07	2.70E+07	4.40E+07	4.80E+07	3.90E+07	2.60E+07
Q87SF4	Carbamoyl-phosphate synthase small chain OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=carA PE=3 SV=1	19.525066	41.001	8.60E+06	1.50E+07	1.60E+07	1.80E+07	1.50E+07	1.20E+07
Q87SF5	4-hydroxy-tetrahydrodipicolinate reductase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=dapB PE=3 SV=1	29.3680297	28.593	1.70E+07	1.50E+07	1.10E+07	1.50E+07	2.00E+07	1.20E+07
Q87SF7	Protein translocase subunit SecA OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=secA PE=3 SV=1	7.92951542	103.108	6.40E+06	7.90E+06	5.30E+06	2.80E+06	5.50E+06	3.50E+06
Q87SG0	Cell division protein FtsZ OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=ftsZ PE=3 SV=1	29.3398533	42.547	1.30E+07	1.60E+07	1.60E+07	1.80E+07	1.90E+07	1.20E+07
Q87SH9	Stringent starvation protein A OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0444 PE=3 SV=1	39.3364929	24.3	2.80E+07	3.60E+07	3.30E+07	3.80E+07	3.50E+07	2.80E+07
Q87SI4	30S ribosomal protein S9 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpsI PE=3 SV=1	60	14.605	6.20E+07	6.30E+07	6.00E+07	7.30E+07	7.90E+07	6.30E+07
Q87SI5	50S ribosomal protein L13 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplM PE=3 SV=1	61.2676056	15.951	5.50E+07	5.70E+07	6.10E+07	6.70E+07	6.60E+07	5.70E+07
Q87SJ0	Protease DO OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0433 PE=4 SV=1	31.6483516	48.119	2.40E+07	2.50E+07	2.70E+07	3.00E+07	2.80E+07	2.20E+07
Q87SJ3	DNA topoisomerase 4 subunit B OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=parE PE=3 SV=1	1.91693291	69.469			1.20E+07		1.50E+07	
Q87SJ8	Outer membrane protein TolC OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0425 PE=4 SV=1	2.26244344	47.954	3.30E+06					
Q87SJ9	Bifunctional protein HldE OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=hldE PE=3 SV=1	2.5210084	50.907		8.50E+06				
Q87SK3	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0420 PE=4 SV=1	5.47945205	59.202	2.40E+06	3.10E+06	2.70E+06			9.90E+05
Q87SL8	RNA polymerase sigma factor RpoD OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpoD PE=3 SV=1	10.483871	70.667	1.00E+07	1.70E+07	8.50E+06	1.40E+07	1.10E+07	6.10E+06
Q87SR3	Glutamine--fructose-6-phosphate aminotransferase [isomerizing] OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=glmS PE=3 SV=2	28.852459	66.799	8.30E+06	2.30E+07	1.90E+07	2.40E+07	8.20E+06	2.00E+07
Q87SR6	Pyruvate kinase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0356 PE=3 SV=1	41.2765957	49.941	1.70E+07	2.90E+07	2.80E+07	3.10E+07	3.20E+07	3.10E+07

Q87SS0	Acetolactate synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0352 PE=3 SV=1	2.26480836	63.006		4.50E+06				
Q87SS7	2-isopropylmalate synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=leuA PE=3 SV=1	30.8737864	56.105	1.30E+07	1.60E+07	1.20E+07	1.80E+07	1.10E+07	1.40E+07
Q87SS8	3-isopropylmalate dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=leuB PE=3 SV=1	42.9752066	39.309	3.20E+07	3.30E+07	3.20E+07	3.90E+07	3.20E+07	3.30E+07
Q87SS9	3-isopropylmalate dehydratase large subunit OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=leuC PE=3 SV=1	3.18471338	50.585				3.80E+06		3.70E+06
Q87ST4	Chaperone SurA OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=surA PE=3 SV=1	2.34192037	47.406		8.00E+06			6.30E+06	
Q87SU3	50S ribosomal protein L27 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpmA PE=3 SV=1	42.3529412	9.202	2.10E+07	2.70E+07	2.90E+07	3.10E+07	2.80E+07	3.30E+07
Q87SU4	50S ribosomal protein L21 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplU PE=3 SV=1	60.1941748	11.514	5.00E+07	4.60E+07	5.90E+07	5.90E+07	6.40E+07	6.70E+07
Q87SU5	Octaprenyl-diphosphate synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0327 PE=3 SV=1	3.3033033	36.368						2.10E+06
Q87SU7	Malate dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=mdh PE=3 SV=1	77.8135048	32.152	1.10E+08	1.40E+08	9.80E+07	1.30E+08	8.80E+07	8.80E+07
Q87SV0	Immunogenic protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0323 PE=4 SV=1	68.9440994	34.529	9.60E+07	1.20E+08	1.00E+08	1.20E+08	1.10E+08	9.10E+07
Q87SW0	Fructose-1,6-bisphosphatase class 1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=fbp PE=3 SV=1	42.3076923	37.276	3.50E+07	3.60E+07	1.40E+07	3.10E+07	1.20E+07	1.30E+07
Q87SW1	Inorganic pyrophosphatase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=ppa PE=3 SV=1	34.6590909	19.632	1.20E+07	1.80E+07	1.60E+07	1.20E+07	7.40E+06	1.20E+07
Q87SW6	Peptide methionine sulfoxide reductase MsrA OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=msrA PE=3 SV=1	19.3396226	23.602	3.30E+06	6.50E+06	5.20E+06	3.50E+06	3.80E+06	3.80E+06
Q87SX0	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0302 PE=4 SV=1	3.8277512	23.29	1.70E+07	2.20E+07	2.00E+07			
Q87SX9	Sulfate adenylyltransferase subunit 1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=cysN PE=3 SV=1	22.6890756	52.562	1.50E+07	1.60E+07	1.60E+07	1.70E+07	2.40E+07	1.40E+07
Q87SY0	Sulfate adenylyltransferase subunit 2 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=cysD PE=3 SV=1	11.2582781	34.961	1.30E+07	1.10E+07	8.20E+06	9.70E+06	1.40E+07	1.50E+07
Q87SY1	Uroporphyrin-III C-methyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0291 PE=3 SV=1	3.61842105	32.997				5.80E+06	7.40E+06	
Q87SY2	2',3'-cyclic-nucleotide 2'-phosphodiesterase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0290 PE=3 SV=1	6.75883257	72.077	1.40E+07		1.90E+07	1.10E+07	3.10E+06	
Q87SY7	Peptidyl-prolyl cis-trans isomerase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0285 PE=4 SV=1	6.31067961	21.826	8.60E+06		1.10E+07		1.20E+07	9.70E+06
Q87SY9	50S ribosomal protein L17 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplQ PE=3 SV=1	46.8253968	14.194	5.00E+07	5.10E+07	5.10E+07	6.10E+07	6.50E+07	6.40E+07
Q87SZ0	DNA-directed RNA polymerase subunit alpha OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpoA PE=3 SV=1	44.2424242	36.45	4.20E+07	4.40E+07	4.80E+07	4.40E+07	5.10E+07	4.10E+07
Q87SZ1	30S ribosomal protein S4 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpsD PE=3 SV=1	65.0485437	23.319	8.50E+07	8.90E+07	1.00E+08	9.40E+07	1.20E+08	9.20E+07
Q87SZ2	30S ribosomal protein S13 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpsM PE=3 SV=1	63.559322	13.282	5.90E+07	5.40E+07	7.80E+07	8.20E+07	8.30E+07	7.60E+07
Q87SZ4	50S ribosomal protein L15 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplO PE=3 SV=1	47.2222222	14.944	3.70E+07	3.70E+07	4.20E+07	5.10E+07	5.50E+07	5.20E+07
Q87SZ5	50S ribosomal protein L30 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpmD PE=3 SV=1	24.137931	6.58	1.50E+07	2.10E+07	2.20E+07	1.90E+07	2.50E+07	1.40E+07
Q87SZ6	30S ribosomal protein S5 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpsE PE=3 SV=1	73.6526946	17.556	7.80E+07	6.50E+07	8.80E+07	9.10E+07	1.00E+08	9.30E+07
Q87SZ7	50S ribosomal protein L18 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplR PE=3 SV=1	57.2649573	12.608	4.20E+07	4.70E+07	5.20E+07	5.40E+07	6.20E+07	4.90E+07
Q87SZ8	50S ribosomal protein L6 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplF PE=3 SV=1	72.3163842	18.767	5.80E+07	6.50E+07	7.50E+07	7.80E+07	8.00E+07	7.80E+07
Q87SZ9	30S ribosomal protein S8 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpsH PE=3 SV=1	40	13.999	3.40E+07	3.50E+07	4.10E+07	5.70E+07	3.90E+07	4.10E+07
Q87T00	30S ribosomal protein S14 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpsN PE=3 SV=1	6.93069307	11.419	8.80E+06	1.50E+07	9.90E+06	1.20E+07	1.60E+07	1.10E+07
Q87T01	50S ribosomal protein L5 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplE PE=3 SV=1	80.4469274	20.118	7.80E+07	8.70E+07	9.70E+07	1.00E+08	9.40E+07	9.50E+07
Q87T02	50S ribosomal protein L24 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplX PE=3 SV=1	20	11.224	6.50E+07	2.70E+07	3.30E+07	6.50E+07	3.60E+07	8.00E+07
Q87T03	50S ribosomal protein L14 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplN PE=3 SV=1	43.902439	13.564	2.10E+07	3.50E+07	4.00E+07	3.70E+07	4.10E+07	2.80E+07
Q87T05	50S ribosomal protein L29 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpmC PE=3 SV=1	46.031746	7.189	1.20E+07	1.80E+07	1.90E+07	2.10E+06	3.50E+06	1.60E+07
Q87T06	50S ribosomal protein L16 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplP PE=3 SV=1	30.1470588	15.516	4.20E+07	4.60E+07	4.60E+07	5.60E+07	5.30E+07	5.70E+07
Q87T07	30S ribosomal protein S3 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpsC PE=3 SV=1	51.2931034	25.565	6.90E+07	6.30E+07	7.40E+07	9.10E+07	8.40E+07	9.00E+07
Q87T08	50S ribosomal protein L22 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplV PE=3 SV=1	60	12.078	3.50E+07	4.50E+07	5.80E+07	5.90E+07	4.80E+07	6.00E+07
Q87T09	30S ribosomal protein S19 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpsS PE=3 SV=1	47.826087	10.421	2.40E+07	1.90E+07	2.50E+07	1.60E+07	2.70E+07	2.70E+07
Q87T10	50S ribosomal protein L2 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplB PE=3 SV=1	13.8686131	29.931		5.40E+06	7.90E+06	8.70E+06	1.30E+07	7.50E+06
Q87T11	50S ribosomal protein L23 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplW PE=3 SV=1	36	11.121	3.60E+07	3.10E+07	4.00E+07	4.30E+07	3.80E+07	4.90E+07
Q87T12	50S ribosomal protein L4 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplD PE=3 SV=1	53	21.875	5.60E+07	7.40E+07	7.30E+07	8.50E+07	7.40E+07	7.20E+07
Q87T13	50S ribosomal protein L3 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplC PE=3 SV=1	49.7607656	22.36	6.40E+07	7.90E+07	8.30E+07	8.50E+07	9.20E+07	6.80E+07
Q87T18	Transcriptional repressor, LacI family OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0252 PE=4 SV=1	5.97014925	36.812					2.70E+06	2.30E+06
Q87T21	ATP-dependent protease ATPase subunit HslU OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=hslU PE=3 SV=1	12.4153499	49.849	7.10E+06	7.60E+06	8.10E+06	1.00E+07	1.10E+07	1.10E+07
Q87T31	Triosephosphate isomerase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=tpiA PE=3 SV=1	23.046875	26.916	2.00E+07	3.20E+07	2.40E+07	2.70E+07	2.90E+07	2.10E+07
Q87T33	UTP--glucose-1-phosphate uridylyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0237 PE=3 SV=1	7.53424658	32.304					5.80E+06	
Q87T34	Nucleotide sugar dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0236 PE=3 SV=1	25.5154639	43.139	1.40E+07	2.30E+07	2.20E+07	2.20E+07	1.90E+07	1.50E+07
Q87T36	Pilin glycosylation protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0234 PE=3 SV=1	45.0127877	43.373	3.90E+07	4.30E+07	4.30E+07	4.30E+07	4.80E+07	3.70E+07
Q87T38	Putative carbamoylphosphate synthase large subunit, short form OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0232 PE=4 SV=1	13.3956386	36.419	9.40E+06	1.90E+07	1.70E+07	8.70E+06	1.60E+07	1.60E+07
Q87T41	dTDP-4-dehydrorhamnose 3,5-epimerase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0229 PE=4 SV=1	22.9946524	21.226	4.80E+06	6.40E+06	4.90E+06	1.30E+07	5.40E+06	
Q87T46	Putative dTDP-4-dehydrorhamnose reductase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0224 PE=4 SV=1	22.0689655	32.437	8.30E+06	6.70E+06	5.60E+06	7.80E+06	5.40E+06	7.80E+06
Q87T47	Glucose-1-phosphate thymidylyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0223 PE=3 SV=1	21.6494845	32.254	6.70E+06	1.00E+07	4.60E+06		5.90E+06	4.00E+06
Q87T48	dTDP-glucose 4,6-dehydratase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0222 PE=3 SV=1	16.8508287	40.888	1.40E+07	2.90E+07	2.70E+07	2.70E+07	7.80E+06	2.10E+07
Q87T56	ADP-L-glycero-D-manno-heptose-6-epimerase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=hldD PE=3 SV=1	7.34824281	35.194	6.20E+06	5.60E+06			9.00E+06	5.30E+06
Q87T63	Putative oxidoreductase (Flagellin modification) OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0207 PE=4 SV=1	7.90513834	27.406				1.10E+07		
Q87T64	Putative amidohydrolase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0206 PE=4 SV=1	3.32103321	30.668	2.90E+06	4.10E+06	4.20E+06	4.50E+06	4.10E+06	
Q87T65	Putative glutamate-1-semialdehyde 2,1-aminomutase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0205 PE=3 SV=1	18.6788155	48.884	9.80E+06	8.00E+06	1.20E+07	9.00E+06	8.70E+06	1.10E+07
Q87T66	Putative 3-chlorobenzoate-3,4-dioxygenase dyhydrogenase related protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0204 PE=4 SV=1	10.787172	38.51	9.80E+06	1.50E+07	1.30E+07	1.20E+07	1.30E+07	8.60E+06
Q87T84	50S ribosomal protein L33 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpmG PE=3 SV=1	26.7857143	6.52	2.10E+06		1.80E+07		1.70E+07	
Q87T85	50S ribosomal protein L28 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpmB PE=3 SV=1	52.5641026	9.026	3.70E+07	3.40E+07	2.90E+07	4.30E+07	4.70E+07	3.70E+07
Q87T93	Ribonuclease PH OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rph PE=3 SV=1	4.62184874	25.637			6.60E+06	5.00E+06		
Q87T98	Putative binding protein component of ABC transporter OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0172 PE=4 SV=1	1.80921053	69.617	7.30E+06	1.00E+07	8.30E+06	7.90E+06	8.30E+06	9.00E+06
Q87TA4	Putative TolR OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0166 PE=3 SV=1	2.64900662	49.324			5.40E+06			
Q87TA8	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0162 PE=4 SV=1	2.72277228	45.497	1.40E+07		7.40E+06	4.90E+06	6.90E+06	1.50E+07
Q87TE1	Phosphoenolpyruvate carboxykinase [ATP] OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=pckA PE=3 SV=1	66.0516605	59.974	1.00E+08	1.30E+08	9.10E+07	1.40E+08	8.90E+07	1.20E+08
Q87TE3	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0127 PE=4 SV=1	3.93442623	34.77	4.00E+06	3.70E+06		4.30E+06		
Q87TE8	Glutamine synthetase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0121 PE=3 SV=1	64.1791045	51.451	1.40E+08	1.50E+08	1.60E+08	1.80E+08	1.60E+08	1.60E+08
Q87TG2	DNA polymerase I OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0107 PE=3 SV=1	4.72610097	103.054	5.00E+06	2.90E+06		2.40E+06		
Q87TG5	Delta-aminolevulinic acid dehydratase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0104 PE=3 SV=1	19.8300283	39.158	1.10E+07	1.50E+07	1.40E+07	1.30E+07	1.50E+07	9.80E+06
Q87TJ2	Ferritin OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0077 PE=3 SV=1	5.71428571	19.939					2.40E+06	
Q87TJ3	Universal stress protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0076 PE=3 SV=1	12.0567376	15.672					3.00E+06	
Q87TJ9	Oligopeptidase A OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0070 PE=3 SV=1	20.8823529	76.939	7.50E+07	9.20E+07	9.80E+07	2.50E+07	2.40E+07	2.10E+07
Q87TK1	Glutathione reductase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0068 PE=3 SV=1	23.5164835	49.246	1.60E+07	2.40E+07	3.30E+07	3.50E+07	1.70E+07	3.00E+07
Q87TM0	Peptide ABC transporter, permease protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0049 PE=3 SV=1	3.50877193	37.92				2.80E+06		
Q87TM1	Peptide ABC transporter, periplasmic peptide-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0048 PE=4 SV=1	63.6363636	57.413	1.20E+08	1.40E+08	1.20E+08	1.40E+08	1.50E+08	1.10E+08
Q87TN4	Ketol-acid reductoisomerase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=ilvC PE=3 SV=1	54.048583	54.66	5.90E+07	7.00E+07	7.80E+07	8.60E+07	9.10E+07	9.20E+07
Q87TP7	Glycine--tRNA ligase alpha subunit OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=glyQ PE=3 SV=1	11.4754098	34.938	5.30E+06		9.80E+06	7.90E+06	9.80E+06	7.30E+06
Q87TP8	Glycine--tRNA ligase beta subunit OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=glyS PE=3 SV=1	26.3081395	76.151	8.30E+06	1.00E+07	9.90E+06	1.00E+07	1.10E+07	9.80E+06
Q87TQ6	DNA polymerase III subunit beta OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0012 PE=4 SV=1	3.00546448	40.631					2.80E+06	
Q87TR0	Amino acid ABC transporter, periplasmic amino acid-binding portion OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0008 PE=3 SV=1	6.0483871	27.485	4.50E+06	6.20E+06	6.60E+06	4.20E+06	4.00E+06	4.00E+06
Q87TR5	Membrane protein insertase YidC OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=yidC PE=3 SV=1	1.85185185	60.35	7.50E+05					
Q8GRF5	Ribosome-recycling factor OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=frr PE=1 SV=1	5.40540541	20.59			2.50E+07		3.20E+07	
Q9ALY5	Cyclic AMP receptor protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2793 PE=4 SV=1	61.4285714	23.65	4.90E+07	7.80E+07	8.60E+07	6.10E+07	8.10E+07	5.50E+07
Q9L5X8	BipA OS=Vibrio parahaemolyticus GN=bipA PE=1 SV=1	8.37438424	66.911	7.90E+06	7.10E+06	6.60E+06	7.70E+06	7.60E+06	6.00E+06
Q9L7P5	60 kDa chaperonin 1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=groL1 PE=3 SV=2	48.9945155	57.537	6.70E+07	8.00E+07	8.50E+07	8.10E+07	9.70E+07	6.00E+07

3rd Experiment (Insoluble Fraction)

Accession	Description	Coverage	MW [kDa]	Control	GlcNAc	GlcN	(GlcNAc)2	(GlcN)2	GlcNAc-GlcN
A7UEM1	Transhydrogenase alpha subunit (Fragment) OS=Vibrio parahaemolyticus GN=pntA PE=4 SV=1	6.99300699	1.55E+01		3.20E+06			2.60E+06	2.40E+06
O50286	Dihydrolipoyl dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=lpd PE=3 SV=2	17.8947368	5.10E+01	1.30E+06	3.00E+06	1.70E+06	3.10E+06	2.50E+06	1.70E+06
P0A308	ATP synthase subunit c OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=atpE PE=3 SV=1	8.33333333	8.63E+00	2.00E+07	2.30E+07	2.50E+07	2.60E+07	2.60E+07	2.60E+07
P40605	Protein HflK OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=hflK PE=3 SV=1	3.25	4.42E+01				3.40E+06	3.40E+06	
P59494	Maltoporin OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=lamB PE=3 SV=1	37.2685185	4.69E+01	9.00E+07	1.00E+08	1.20E+08	9.80E+07	1.00E+08	8.70E+07
P59570	Outer membrane protein OmpK OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=ompK PE=3 SV=1	12.406015	2.99E+01		5.30E+06	8.20E+06	9.20E+06	6.90E+06	8.00E+06
Q877T5	Elongation factor Tu OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=tufA PE=3 SV=1	22.8426396	43.125	3.70E+06	4.40E+06	6.50E+06	6.40E+06	7.60E+06	8.20E+06
Q87FL2	PTS system, glucose-specific IIBC component OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1667 PE=4 SV=1	3.54166667	5.11E+01			4.00E+06			
Q87FM0	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1659 PE=4 SV=1	2.29508197	6.87E+01					1.70E+06	
Q87FM2	Ferric siderophore receptor homolog OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1657 PE=3 SV=1	28.7610619	7.49E+01	1.00E+07	1.70E+07	1.90E+07	1.30E+07	1.40E+07	1.50E+07
Q87FM3	Ferric vibrioferrin receptor OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1656 PE=3 SV=1	15.4494382	7.88E+01	8.00E+06	1.40E+07	1.40E+07	1.20E+07	1.10E+07	1.10E+07
Q87FN5	Putative maltose operon periplasmic protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1643 PE=4 SV=1	9.2936803	2.91E+01		2.80E+06	2.70E+06			
Q87G18	L-lactate dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=lldD PE=3 SV=1	25.3298153	4.14E+01	6.80E+06	9.70E+06	6.30E+06	8.20E+06	7.00E+06	5.90E+06
Q87G48	Outer membrane lipoprotein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1469 PE=4 SV=1	28.5714286	8.67E+00	8.30E+06	8.00E+06	1.10E+07	1.20E+07	1.20E+07	9.70E+06

Q87GB6	Maltose ABC transporter, periplasmic maltose-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1401 PE=4 SV=1	5.6122449	4.21E+01	2.40E+06	3.20E+06	2.60E+06	2.00E+06	2.80E+06	2.50E+06
Q87GK7	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1308 PE=4 SV=1	22.1052632	42.312	1.70E+07	1.90E+07	2.20E+07	1.40E+07	1.40E+07	1.70E+07
Q87GW2	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1203 PE=4 SV=1	49.5652174	1.31E+01	1.50E+07	1.30E+07	2.00E+07	2.00E+07	2.20E+07	1.70E+07
Q87GW3	Polyhydroxyalkanoic acid synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1202 PE=4 SV=1	3.04568528	6.72E+01	4.20E+06	7.30E+06				
Q87GX9	Outer membrane protein OmpA OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1186 PE=3 SV=1	18.2370821	3.60E+01	6.60E+06	9.00E+06	7.80E+06	7.80E+06	7.90E+06	7.40E+06
Q87HI4	Ferric aerobactin receptor OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0979 PE=3 SV=1	5.10344828	7.92E+01	2.50E+06	4.40E+06	3.60E+06	3.40E+06		3.40E+06
Q87HP1	NAD(P) transhydrogenase subunit alpha OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0922 PE=3 SV=1	12.3552124	54.772	5.80E+06	5.40E+06	4.20E+06		4.60E+06	3.90E+06
Q87HS4	Heme transport protein HutA OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0882 PE=3 SV=1	22.6551227	7.73E+01	9.30E+06	1.60E+07	1.60E+07	1.10E+07	1.40E+07	1.30E+07
Q87IE2	Putaive Fe-regulated protein B OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0664 PE=3 SV=1	1.49700599	7.42E+01			5.70E+05			
Q87J28	ExbB-like protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0425 PE=3 SV=1	5.2173913	2.48E+01			1.10E+06			
Q87JD5	Putative outer membrane protein OmpV OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0318 PE=4 SV=1	4.65116279	2.81E+01	5.60E+06	5.80E+06	8.50E+06	6.40E+06	7.90E+06	6.60E+06
Q87JT2	Putative outer membrane protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0166 PE=4 SV=1	11.4613181	3.80E+01	2.70E+07	4.00E+07	3.60E+07	3.50E+07	3.60E+07	2.80E+07
Q87JU6	Biopolymer transport protein ExbB-related protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0152 PE=3 SV=1	5.71428571	4.92E+01	1.50E+06	3.80E+06	2.20E+06	2.00E+06	2.00E+06	3.40E+06
Q87K02	Outer membrane protein OmpW OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0096 PE=4 SV=1	6.54205607	2.35E+01	1.00E+07	8.00E+06	1.40E+07	4.20E+06	1.10E+07	9.20E+06
Q87K95	Peptide ABC transporter, ATP-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA0003 PE=3 SV=1	3.87096774	3.49E+01						
Q87KA3	ATP synthase subunit a OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=atpB PE=3 SV=1	2.96296296	3.01E+01						
Q87KA4	ATP synthase subunit b OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=atpF PE=3 SV=1	43.5897436	1.75E+01	7.00E+06	6.40E+06	8.50E+06	7.70E+06	8.00E+06	7.90E+06
Q87KA6	ATP synthase subunit alpha OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=atpA PE=3 SV=1	31.5487572	5.66E+01	7.30E+06	7.70E+06	7.00E+06	8.10E+06	9.90E+06	6.30E+06
Q87KA8	ATP synthase subunit beta OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=atpD PE=3 SV=1	23.5546039	5.07E+01	5.60E+06	7.40E+06	6.70E+06	9.00E+06	1.00E+07	5.00E+06
Q87KI7	Putative uroporphyrin-III C-methyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2990 PE=4 SV=1	2.48138958	4.51E+01	1.00E+06	1.20E+06	8.00E+05			
Q87KN9	Vitamin B12 transporter BtuB OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=btuB PE=3 SV=1	3.20512821	6.93E+01	7.60E+05	1.60E+06	1.70E+06	1.50E+06	9.70E+05	1.90E+06
Q87KQ1	50S ribosomal protein L1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplA PE=3 SV=1	16.7381974	2.47E+01	5.40E+06	5.40E+06	5.00E+06	5.40E+06	7.90E+06	5.10E+06
Q87KQ2	50S ribosomal protein L10 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplJ PE=3 SV=1	13.5802469	1.73E+01			9.50E+05			1.70E+06
Q87KQ3	50S ribosomal protein L7/L12 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplL PE=3 SV=1	9.01639344	12.184	1.80E+06		1.90E+06			2.00E+06
Q87KQ4	DNA-directed RNA polymerase subunit beta OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpoB PE=3 SV=1	0.96870343	1.49E+02			5.00E+05			
Q87KR5	DNA-binding protein HU-2 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2911 PE=3 SV=1	16.4835165	9.56E+00	3.20E+06					
Q87KV2	Fumarate hydratase class II OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=fumC PE=3 SV=1	9.97830803	4.87E+01		8.50E+05		2.10E+06		1.10E+06
Q87KX4	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2850 PE=4 SV=1	13.6125654	20.214		1.30E+06	3.10E+06	1.70E+06		1.20E+06
Q87L38	Peptidyl-prolyl cis-trans isomerase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2778 PE=4 SV=1	21.1538462	2.83E+01	4.90E+06	6.90E+06	5.50E+06	4.90E+06	8.00E+06	4.00E+06
Q87L72	30S ribosomal protein S6 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpsF PE=3 SV=1	8.52713178	14.974				3.50E+06		
Q87L75	50S ribosomal protein L9 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplI PE=3 SV=1	24.6666667	1.57E+01		1.90E+06	3.00E+06	3.70E+06	4.20E+06	3.90E+06
Q87LB4	Putative V10 pilin OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2698 PE=4 SV=1	31.5151515	1.68E+01	1.80E+07	2.50E+07	2.40E+07	3.00E+07	2.30E+07	2.40E+07
Q87LH6	Permease IIC component OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2636 PE=4 SV=1	10.9619687	4.87E+01					2.10E+07	1.30E+07
Q87LH8	6-phospho-beta-glucosidase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2634 PE=3 SV=1	3.63636364	4.83E+01					2.90E+06	
Q87LL3	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2598 PE=4 SV=1	6.59722222	3.10E+01				8.70E+05		
Q87LQ0	Enolase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=eno PE=3 SV=1	13.3949192	4.55E+01	2.00E+06			2.70E+06	3.10E+06	2.10E+06
Q87LR7	Oxaloacetate decarboxylase, alpha subunit OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2544 PE=4 SV=1	5.21008403	6.42E+01	6.70E+05		7.00E+06	6.70E+06	4.50E+06	6.50E+06
Q87LT1	50S ribosomal protein L19 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplS PE=3 SV=2	10.2564103	1.32E+01				2.70E+06	2.70E+06	1.70E+06
Q87LU2	Pyruvate dehydrogenase E1 component OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2519 PE=4 SV=1	2.367531	99.601	2.60E+06	3.80E+06	2.50E+06	2.40E+06	3.50E+06	
Q87LU3	Acetyltransferase component of pyruvate dehydrogenase complex OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2518 PE=3 SV=1	1.75438596	6.49E+01		4.90E+06		3.80E+06	3.70E+06	2.60E+06
Q87LZ1	Outer membrane protein U OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=ompU PE=3 SV=1	20.4747774	3.63E+01	2.20E+07	3.60E+07	3.30E+07	2.90E+07	1.80E+07	2.10E+07
Q87LZ5	ATP-dependent zinc metalloprotease FtsH OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=ftsH PE=3 SV=1	6.49546828	7.29E+01		3.20E+06	4.70E+06		4.10E+06	2.50E+06
Q87M06	Polyribonucleotide nucleotidyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=pnp PE=3 SV=1	6.89170183	76.691		3.00E+06	9.90E+05		1.70E+06	
Q87MA6	Na(+)-translocating NADH-quinone reductase subunit A OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=nqrA PE=3 SV=1	2.91479821	4.86E+01	1.30E+06		3.00E+06	2.70E+06	2.60E+06	2.90E+06
Q87MD8	30S ribosomal protein S2 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpsB PE=3 SV=1	12.8099174	2.68E+01				1.80E+06	1.00E+06	
Q87MS4	Glyceraldehyde-3-phosphate dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2157 PE=3 SV=1	20.2416918	3.52E+01	4.30E+06	5.90E+06	6.70E+06	7.30E+06	5.50E+06	5.70E+06
Q87MY5	Oligopeptide ABC transporter, periplasmic oligopeptide-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2091 PE=4 SV=1	17.0556553	6.23E+01	6.90E+06	1.30E+07	1.00E+07	1.10E+07	9.90E+06	9.10E+06
Q87N29	PTS system, glucose-specific IIBC component OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2046 PE=4 SV=1	11.3445378	4.94E+01	1.30E+07	1.20E+07	1.30E+07	1.40E+07	9.60E+06	8.80E+06
Q87N45	30S ribosomal protein S1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2030 PE=3 SV=1	5.57553957	6.09E+01		2.80E+06		3.20E+06	3.10E+06	3.50E+06
Q87N76	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1999 PE=4 SV=1	2.65251989	4.02E+01		1.30E+06			1.30E+06	
Q87NA1	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=metE PE=3 SV=1	3.81578947	8.47E+01			2.70E+06	2.00E+06	2.70E+06	2.90E+06
Q87PF9	Cytochrome c oxidase, subunit CcoO OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1543 PE=4 SV=1	4.85436893	2.36E+01						1.00E+06
Q87Q03	Oligopeptide ABC transporter, periplasmic oligopeptide-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1347 PE=4 SV=1	1.67910448	6.03E+01	3.90E+06	7.90E+06	6.40E+06	4.80E+06	5.40E+06	5.80E+06
Q87QA7	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1243 PE=4 SV=1	7.73480663	1.98E+01			3.60E+06	3.80E+06		2.70E+06
Q87QI5	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1164 PE=4 SV=1	1.73267327	43.849			1.80E+06	1.80E+06	1.90E+06	
Q87QP6	Alanine dehydrogenase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1103 PE=3 SV=1	4.01069519	3.99E+01	7.40E+05	1.30E+06				
Q87QT8	Peptidoglycan-associated lipoprotein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1061 PE=3 SV=1	12.6436782	1.87E+01	1.30E+07	1.10E+07	1.90E+07	1.50E+07	1.50E+07	9.80E+06
Q87QU6	Cytochrome d ubiquinol oxidase, subunit I OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP1053 PE=4 SV=1	1.85873606	6.03E+01			2.80E+06		4.20E+06	2.70E+06
Q87R04	Formate acetyltransferase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0994 PE=4 SV=1	1.71503958	8.45E+01					1.00E+06	
Q87R31	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0967 PE=4 SV=1	8.67346939	2.18E+01				4.20E+06		
Q87R78	DNA-binding protein HU-beta OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0920 PE=3 SV=1	12.2222222	9.40E+00	3.00E+06					
Q87R81	Trigger factor OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=tig PE=3 SV=1	6.4516129	4.82E+01					1.80E+06	
Q87RE8	Succinyl-CoA ligase [ADP-forming] subunit beta OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=sucC PE=3 SV=1	2.83505155	4.15E+01		1.40E+06		1.20E+06		
Q87RE9	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0848 PE=3 SV=1	9.22693267	4.37E+01	3.60E+06	5.90E+06	2.50E+06	3.10E+06	3.40E+06	
Q87RI9	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0805 PE=4 SV=1	7.21311475	3.34E+01	5.30E+06	7.60E+06	4.80E+06	7.00E+06	6.70E+06	4.10E+06
Q87RJ7	Cysteine synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0797 PE=3 SV=1	7.14285714	3.41E+01		1.60E+06	1.40E+06	7.90E+05	1.80E+06	
Q87RL8	Putative chitoporin OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0760 PE=4 SV=1	23.0563003	4.08E+01				2.40E+06	1.80E+07	4.10E+07
Q87RR2	Serine hydroxymethyltransferase 1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=glyA1 PE=3 SV=1	3.60576923	4.55E+01					1.10E+06	
Q87RS1	Methionine import ATP-binding protein MetN OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=metN PE=1 SV=1	4.06976744	3.75E+01						
Q87RS3	Lipoprotein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0704 PE=3 SV=1	46.4684015	2.91E+01	1.50E+07	1.70E+07	2.20E+07	2.00E+07	2.10E+07	2.00E+07
Q87RX3	Chaperone protein DnaK OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=dnaK PE=3 SV=1	2.35478807	6.90E+01		4.40E+05				
Q87S35	Uncharacterized protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0589 PE=4 SV=1	11.9266055	1.18E+01	5.60E+06	6.90E+06	7.80E+06	8.80E+06	5.60E+06	7.10E+06
Q87S44	Antioxidant, AhpC/Tsa family OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0580 PE=4 SV=1	12.3152709	2.22E+01	1.70E+06	1.60E+06	1.60E+06	1.50E+06	2.60E+06	2.00E+06
Q87S84	Putative carbon starvation protein A OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0540 PE=4 SV=1	4.8582996	53.283	4.80E+06	4.70E+06	5.30E+06	3.80E+06	4.40E+06	4.00E+06
Q87SI4	30S ribosomal protein S9 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpsI PE=3 SV=1	9.23076923	1.46E+01		2.40E+06			2.80E+06	1.40E+06
Q87SI5	50S ribosomal protein L13 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplM PE=3 SV=1	5.63380282	1.60E+01		4.90E+06				
Q87SJ8	Outer membrane protein TolC OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0425 PE=4 SV=1	9.04977376	4.80E+01		3.70E+06				1.40E+06
Q87SU4	50S ribosomal protein L21 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplU PE=3 SV=1	19.4174757	1.15E+01			3.40E+06		2.30E+06	4.10E+06
Q87SV0	Immunogenic protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0323 PE=4 SV=1	7.45341615	3.45E+01	1.30E+06	2.10E+06				
Q87SZ1	30S ribosomal protein S4 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpsD PE=3 SV=1	9.22330097	2.33E+01		2.70E+06	1.40E+06		2.20E+06	2.10E+06
Q87SZ8	50S ribosomal protein L6 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplF PE=3 SV=1	12.9943503	1.88E+01	5.40E+06	6.00E+06	5.20E+06	5.80E+06	5.80E+06	4.50E+06
Q87T01	50S ribosomal protein L5 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplE PE=3 SV=1	10.6145251	2.01E+01	8.60E+05		1.60E+06			
Q87T07	30S ribosomal protein S3 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rpsC PE=3 SV=1	6.03448276	2.56E+01					1.10E+06	
Q87T12	50S ribosomal protein L4 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplD PE=3 SV=1	13.5	2.19E+01	4.20E+06	5.50E+06		5.60E+06	6.50E+06	5.90E+06
Q87T13	50S ribosomal protein L3 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=rplC PE=3 SV=1	13.3971292	2.24E+01	5.60E+06	7.20E+06			9.00E+06	6.70E+06
Q87T87	Methyl-accepting chemotaxis protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0183 PE=1 SV=1	2.15439856	6.05E+01		9.60E+05				
Q87TA4	Putative TolR OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0166 PE=3 SV=1	9.05077263	4.93E+01			2.30E+06	8.50E+05	1.80E+06	3.20E+06
Q87TE8	Glutamine synthetase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0121 PE=3 SV=1	7.24946695	5.15E+01	2.30E+06	6.90E+06	3.50E+06	5.80E+06	6.00E+06	4.50E+06
Q87TM0	Peptide ABC transporter, permease protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0049 PE=3 SV=1	3.50877193	3.79E+01						
Q87TM1	Peptide ABC transporter, periplasmic peptide-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0048 PE=4 SV=1	4.25531915	5.74E+01	2.10E+06		2.50E+06	2.20E+06	2.30E+06	3.00E+06
Q87TM2	Peptide ABC transporter, ATP-binding protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0047 PE=3 SV=1	4.20315236	6.37E+01		1.30E+06	1.00E+06	1.10E+06	1.40E+06	1.20E+06
Q87TN4	Ketol-acid reductoisomerase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=ilvC PE=3 SV=1	6.47773279	5.47E+01		2.30E+06		2.50E+06	2.50E+06	2.50E+06
Q87TR5	Membrane protein insertase YidC OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=yidC PE=3 SV=1	3.88888889	6.04E+01			2.60E+06			1.00E+06
Q9ALY5	Cyclic AMP receptor protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP2793 PE=4 SV=1	5.71428571	2.37E+01			1.60E+06		2.70E+06	
Q9L7P5	60 kDa chaperonin 1 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=groL1 PE=3 SV=2	6.76416819	5.75E+01				4.00E+06		2.10E+06
Q9LCJ0	Na(+)-translocating NADH-quinone reductase subunit F OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=nqrF PE=3 SV=2	2.94840295	45.054						