**1) OMPLA (Ecoli)**

1QD6, PROTEIN (OUTER MEMBRANE PHOSPHOLIPASE (OMPLA)), [P0A921](http://www.uniprot.org/uniprot/P0A921), Escherichia coli(240aa)

**FTLYPYDTNYLIYTQTSDLNKEAIASYDWAENARKDEVKFQLSLAFPLWRGILGPNSVLGASYTQKSWWQLSNSEESSPFRETNYEPQLFLGFATDYRFAGWTLRDVEMGYNHDSNGRSDPTSRSWNRLYTRLMAENGNWLVEVKPWYVVGNTDDNPDITKYMGYYQLKIGYHLGDAVLSAKGQYNWNTGYGGAELGLSYPITKHVRLYTQVYSGYGESLIDYNFNQTRVGVGVMLNDLF**

**QTY Variant OMPLA [L->Q. I, V->T., F->Y]** 36/240 AA= 15%

**FTLYPYDTNYQTYTQTSDLNKEAIASYDWAENARKDETKYQQSQAYPQWRGILGPNSTQGASYTQKSWWQLSNSEESSPYRETNYEPQQYQGYATDYRFAGWTQRDTEMGYNHDSNGRSDPTSRSWNRQYTRQMAENGNWQTETKPWYTTGNTDDNPDITKYMGYYQQKTGYHLGDATQSAKGQYNWNTGYGGAEQGQSYPITKHTRQYTQTYSGYGESLIDYNFNQTRTGTGTMLNDLF**

**Transmembrane variation in OMPLA (Selected TM amino acids)= 36/141=25.53%**

**YPYQTYTQTDETKYQQSQAYPQWSTQGASYTQKSWWYRETNYEPQQYQGYATDYRWTQRDTEMGYNHDSSWNRQYTRQMAENWQTETKPWYTTYQQKTGYHATQSAKGQYGGAEQGQSYPTRQYTQTYSGYNQTRTGTGTM**

**2) OMPT (Ecoli)**

1I78, Chains A, B, PROTEASE VII, [P09169](http://www.uniprot.org/uniprot/P09169),Escherichia coli (297aa)

**STETLSFTPDNINADISLGTLSGKTKERVYLAEEGGRKVSQLDWKFNNAAIIKGAINWDLMPQISIGAAGWTTLGSRGGNMVDQDWMDSSNPGTWTDEARHPDTQLNYANEFDLNIKGWLLNEPNYRLGLMAGYQESRYSFTARGGSYIYSSEEGFRDDIGSFPNGERAIGYKQRFKMPYIGLTGSYRYEDFELGGTFKYSGWVESSDNDEHYDPKGRITYRSKVKDQNYYSVAVNAGYYVTPNAKVYVEGAWNRVTNKKGNTSLYDHNNNTSDYSKNGAGIENYNFITTAGLKYTF**

**QTY Variant OMPT [L->Q. I, V->T., F->Y]** 42/297 AA=14.14%

**STETLSFTPDNTNADTSQGTQSGKTKERTYQAEEGGRKTSQQDWKYNNAATTKGATNWDLMPQTSTGAAGWTTLGSRGGNMVDQDWMDSSNPGTWTDEARHPDTQQNYANEYDQNTKGWQQNEPNYRQGQMAGYQESRYSYTARGGSYIYSSEEGFRDDIGSFPNGERATGYKQRYKMPYTGQTGSYRYEDYEQGGTYKYSGWTESSDNDEHYDPKGRITYRSKTKDQNYYSTATNAGYYVTPNAKTYTEGAWNRTTNKKGNTSQYDHNNNTSDYSKNGAGTENYNYTTTAGQKYTF**

**Transmembrane variation in OMPT (Selected TM amino acids)= 42/183=22.95%**

**TNADTSQGTQSGKTKERTYQRKTSQQDWKYNNAATTKGATNWTSTGAAGWTTDTQQNYANEYDQNTKGWQQNYRQGQMAGYQESRYSYTARATGYKQRYKMPYTGQTGSYRYEQGGTYKYSGWTESKTKDQNYYSTATNAGYYAKTYTEGAWNRTTNKKGNTSQYDAGTENYNYTTTAGQKYT**

**3) Native PagL** -**Outer membrane lipid A 3-O-deacylase (Pseudomonas aeruginosa**) **(150AA)**

**ADVSAAVGATGQSGMTYRLGLSWDWDKSWWQTSTGRLTGYWDAGYTYWEGGDEGAGKHSLSFAPVFVYEFAGDSIKPFIEAGIGVAAFSGTRVGDQNLGSSLNFEDRIGAGLKFANGQSVGVRAIHYSNAGLKQPNDGIESYSLFYKIPI**

**QTY Variant PagL [L->Q. I, V->T., F->Y]** 29/150 AA=19.33%

**ADTSAATGATGQSGMTYRQGQSWDWDKSWWQTSTGRQTGYWDAGYTYWEGGDEGAGKHSQSYAPTYTYEYAGDSTKPYTEAGTGTAAYSGTRVGDQNLGSSQNYEDRTGAGQKYANGQSTGTRAIHYSNAGLKQPNDGTESYSQYYKTPI**

**Transmembrane variation in PagL (Selected TM amino acids)= 29/94= 30.85%**

**DTSAATGAMTYRQGQSWDGRQTGYWDAGYTYWKHSQSYAPTYTYEYTKPYTEAGTGTAAYQNYEDRTGAGQKYSTGTRAIHYSTESYSQYYKTP**

**4) PagP (Ecoli)**

>1THQ, Chain A, CrcA protein, [P37001](http://www.uniprot.org/uniprot/P37001), Escherichia coli (157aa)

MNADEWM**TTFRENIAQTWQQPEHYDLYIPAITWHARFAYDKEKTDRYNERPWGGGFGLSRWDEKGNWHGLYAMAFKDSWNKWEPIAGYGWESTWRPLADENFHLGLGFTAGVTARDNWNYIPLPVLLPLASVGYGPVTFQMTYIPGTYNNGNVYFAWMRFQFLE**HHHHHH

**QTY Variant PagP [L->Q. I, V->T., F->Y]** 25/157 AA=15.92%

MNADEWM**TTFRENIAQTWQQPEHYDQYTPATTWHARFAYDKEKTDRYNERPWGGGYGQSRWDEKGNWHGQYAMAYKDSWNKWEPTAGYGWESTWRPLADENYHQGQGYTAGTTARDNWNYIPQPTQQPQASTGYGPTTYQMTYIPGTYNNGNTYYAWMRYQYLE**HHHHHH

**Transmembrane variation in PagP (Selected TM amino acids)= 25/84=29.76%**

**HYDQYTPATTWHGGYGQSRWWHGQYAMAYKWEPTAGYGWESTWYHQGQGYTAGTTQPTQQPQASTGYTTYQMTYTYYAWMRYQY**