Global Regulator MorA affects Virulence-associated Protease Secretion in *Pseudomonas aeruginosa* PAO1

Supporting Information

S2 Table. MALDI-ToF-ToF identification of *P. aeruginosa* secreted proteins affected by MorA. Peptide mass tolerance and fragment mass tolerance were 100ppm and 0.2 Da respectively. At the maximum, 1 missed cleavage for trypsin was allowed.

Band No.	**No. of queries matches**	**Nominal Mass**	**Peptide sequences**	**Accession number**	**Genbank Identifier**	**Protein name/function**	**Sequence coverage**
1	35	100615	1. MSLSTTAFPSLQGENMSRSPIPR 2. GLAYGTNVLTQLSGTNAAHAPLLKR 3. LLVLGNGASAASLSATVR 4. SVELGGAYGQDPALVQQIVDGSWR 5. AQNLFALPGTTSLR 6. LWLLWADAVR 7. AADTARFQETFVADAIVGYVR 8. FQETFVADAIVGYVR 9. QQSMPVSGSEETLTLTLPSAQGFTAIGR 10. LSIRIEDAGQASLAVGLNTQR 11. IEDAGQASLAVGLNTQR 12. LQANQSVALVSPYGGLLQLVYSGATPGQTVTVK 13. VTGAASQPFLDIQPGEDSSQAIADFIQALDADK 14. ADWLEIR 15. GWGESHELGHNLQVNR 16. SGEISNQIFPLHK 17. EFGQNLDDTR 18. NAYNLIVAGR 19. AEADPLAGVYK	PA0572	GI:15595769	Hypothetical protein	43%

			20. LWEDPGTYALNGER 21. MAFYTQWVHYWADLK 22. NDPLQGWDIWTLLYLHQR 23. DQRPTFALWGIR 24. TSAAAQAQVAAYGFAEQPAFFYANNR				
2	23	57824	1. SPLLVSTPLGLPR 2. LEDIASLNDGNR 3. AAATPGYQASVDYVK 4. VSVQPFPFTAYYPK 5. GPGSLSATVPQPVTYEWEKDFTYLSQTEAGDVTAK 6. DFTYLSQTEAGDVTAK 7. AENAAAAGAAGVIIFNQGNTDDRK 8. KTETYNVVAETR 9. FAWWGAEEAGLVGSTHYVQNLAPEEK 10. LFEAYFR 11. GQQSEGTEIDFR 12. SDYAEFFNSGIAFGGLFTGAEGLK 13. YGGTAGKAYDECYHSK	PA2939	GI:15598135	Proabable aminopeptidase	39%
3	13	50402	1. SDAYTQVDNFLHAYAR 2. GGDELVNGHPSYTVDQAAEQILR 3. APGDSVLTLSYSFLTKPNDFFNTPWK 4. AYSVMSYWEEQNTGQDFK 5. GAYSSAPLLDDIAAIQK 6. TGDTVYGFNSNTER 7. LVFSVWDAGGNDTLDFSGFSQNQK 8. IDLSGLDAFVNGGLVLQYVDAFAGK	PA1249	GI:15596446	AprA| Alkaline metalloproteinase precursor	34%

4	16	42398	1. AAVAAGGTQALYDWNGVNQGNANGNHQAVVPDGQLCGAGK 2. SDWPSTAIAPDASGNFQFVYK 3. YFDFYITK 4. HVIYNVWQR 5. AQQDLPAGATVTLR 6. LFDAQGR 7. QWPLALAQK 8. VNQDSTLVNIGVLDAYGAVSPVASSQDNQVYVR 9. FQVDIELPVEGGGEQPGGDGK 10. VDFDYPQGLQQYDAGTVVR 11. GWDLYYAPGK	PA0852	GI:116048775	CbpD|Chitin binding protein	49%
5	20	33354	1. IGKYTYGSDYGPLIVNDR 2. YTYGSDYGPLIVNDR 3. FACPTNTYK 4. QVNGAYSPLNDAHFFGGVVFK 5. LYRDWFGTSPLTHK 6. DWFGTSPLTHK 7. GQSGGMNEAFSDMAGEAAEFYMR 8. GKNDFLIGYDIK 9. YMDQPSRDGR 10. YMDQPSR 11. SIDNASQYYNGIDVHHSSGVYNR 12. AFYLLANSPGWDTRK 13. AFYLLANSPGWDTR 14. AFEVFVDANR 15. YYWTATSNYNSGACGVIR 16. NYSAADVTR	PA3724	GI:15598919	LasB| Elastase	51%
6	9	48589	1. MVFTSSADGGSYICTGTLLNNGNSPK 2. TPPAGVFYQGWSATPIANGSLG	PA4175	GI:15599370	PrpL| PvdS regulated endoprotease;	31%

			HDIHHPR 3. YSQGNVSAVGVTYDGHTALTR 4. VDWPSAVVEGGSSGSGLLTVAGDGSYQLR 5. NDYFSDFSGVYSQISR			lysyl class	
7	19	49420	1. ASATQSAVAGTYQIQVNSLATSSK 2. IALQAIADPANAK 3. FNSGTLNISVGDTK 4. LPAITVDSSNNTLAGMR 5. DAINQAGKEAGVSATIITDNSGSR 6. VEVSDDGSGGNTSLSQLAFDPATAPK 7. AANGEITVDGLKR 8. SIASNSVSDVIDGVSFDVK 9. AVTEAGKPITLTVSR 10. LTTQFNLLSAMQDEMTK	PA1094	GI:15596291	FliD| Flagellar capping protein	38%
8	7	45721	1. AVGEDGLNAASAALLGLLREGAK 2. QGYSWQPNGAHSNTGSGYPYSSFDASYDWPR 3. WGSATYSVVAAHAGTVR 4. VTHPSGWATNYYHMDQIQVSNGQQVSADTK 5. YYFYNQSAGTTHCAFRPLYNPGLAL	PA1871	GI:15597068	LasA| Elastase	30%