

# PROTEOMICS

## Supporting Information

### for Proteomics

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**Protein composition of *Paracoccus denitrificans* cells grown on various  
electron acceptors and in the presence of azide**

Supplementary Table 1. List of protein spots in 2-DE gels of *P. denitrificans* TCL, the quantity of which was affected by growth on different terminal electron acceptors and/or by sodium azide

Spot No.	Terminal electron acceptor effects			Azide effect		MS analysis			
	Approx. $M_r$	Approx. pI				Analyzed (PMF)	Database accession.No.	Identified proteins	
0101	27.8	4.0			↑5				
0303	37.9	3.8				↑5	+		
0401	39.4	4.2				↑2			
0601	53.8	4.3	↓2			↓5			
0602	54.0	4.5				↑5			
0701	63.2	4.7	↑5			↑5			
1105	23.6	4.8	↑3	N <sub>2</sub> O		↑5			
1203	24.2	4.5	↓3			↓5			
1207	32.9	4.8	↓3						
1304	33.5	4.1					+		
1309	34.0	4.5	↑5	N <sub>2</sub> O					
1311	35.1	4.7	↑2			↑2	+		
1401	40.1	4.2				↑3	+		
1406	39.2	4.9	↑5						
1408	39.4	4.6		↑3	NO <sub>3</sub> <sup>-</sup>	↓2		+	
1410	39.6	4.8	↑5						
1501	45.7	4.3	↑3		↑2				
1701	61.8	4.0		↑5			+		
1801	77.3	4.1		↓3		↓3			
1805	71.0	4.6	↓5	↓5	↓5	O <sub>2</sub>	↓5		
2001	18.2	5.1					↑5		
2102	20.3	4.9	↓3	↓3	↓3	O <sub>2</sub>	↓5	+	
2103	18.0	4.9	↓3					+	
2104	22.3	4.9	↑3		N <sub>2</sub> O	↓2	↑5	↑2	+
2201	27.6	4.9	↑2						
2202	25.8	4.9	↓3	↓3	↓3	O <sub>2</sub>			+
2205	27.2	4.9		↑5					+
2209	24.8	4.9	↓2	↓3					
2210	23.7	4.7					↑5		
2213	32.1	4.9	↑2						
2214	31.4	4.9					↓5		
2302	35.4	4.8						+	
2306	36.6	4.9					↑5		
2307	36.6	4.9	↓5	↓5	↓3	O <sub>2</sub>	↓5		
2407	41.7	4.8			↓5		↓2	↓5	↓2
2501	48.1	4.8		↓3	↓3				
2608	51.7	4.9		↓2					
2609	49.6	4.9					↓5		
2610	54.9	4.8	↑3				↓2	↓5	+
2701	57.2	4.9	↑2		N <sub>2</sub> O		↑5		+
2702	57.7	5.0	↑5				↑3		++ Q9Z462 60 kDa chaperonin
2703	61.4	4.8		↑5	NO <sub>3</sub> <sup>-</sup>		↑5		+
2708	65.4	4.8		↑2	↑3				++ Q51700 Nitrite reductase (Precursor)
2709	68.4	4.8					↓5		
2804	70.8	4.9	↑2				↓5	↓5	↓5
2805	67.3	4.9						+	
3103	23.5	5.1				↓2			
3202	32.0	5.5					↑5		
3206	31.6	5.2					↑5		
3302	35.6	4.9					↓5		
3304	33.0	5.1					↓5		
3305	33.0	4.9		↓2					
3306	32.3	5.0					↑5		
3307	34.6	4.9	↓5	↓3	↓5	O <sub>2</sub>			
3404	38.2	4.9						↓5	
3405	36.9	5.1	↑5	↑5	↑5	Anaer			+
3407	37.5	5.0	↑5						
3408	41.2	5.3		↓3	↓3				
3409	41.4	5.5					↑5		

Supplementary Table 1. Continued

3716	62.4	5.3					↓5		+		
3717	58.7	5.4					↓5				
3805	70.9	5.0							+		
3810	65.6	5.2	↑5				↑3				
4203	28.4	5.2					↑5				
4204	30.8	5.5	↑5		N <sub>2</sub> O						
4206	25.8	5.5		↓3	↓2						
4303	33.0	5.5					↓5				
4307	34.4	5.5	↑5		N <sub>2</sub> O						
4308	35.7	5.5		↓2			↑2				
4310	37.3	5.5					↑5				
4406	40.0	5.5		↓3							
4504	40.3	5.5	↑3		N <sub>2</sub> O						
4602	55.3	5.4					↑2		+		
4606	53.8	5.5					12				
4713	58.4	5.5							+		
4809	69.5	5.5							+		
4812	74.6	5.5		↓3	↓5						
5003	18.0	5.6							+		
5101	20.0	5.5					↑5				
5207	32.1	5.5		↓3			12				
5303	28.8	5.5					↑5				
5404	40.4	5.5		↑5							
5409	39.9	5.6					↑5				
5510	49.4	5.5					↓5				
5513	50.1	5.6					12				
5809	72.6	5.5					↑3				
6106	24.7	5.5		↓2			12	↑5	↑2	+	
6205	32.2	5.6					12				
6306	37.2	5.5					13	↑3	↑3	+	
6405	39.5	5.6	↓2								
6406	41.0	5.6					12				
6510	42.3	5.6		↑3							
6511	46.8	5.6	↑5	↑5	↑5	Anaer		↓5			
6512	49.8	5.6		↑5	NO <sub>3</sub> <sup>-</sup>			↑5		+	
6709	66.7	5.6		↑2				↓5			
6712	64.5	5.6	↑3	↑3	↑5	Anaer	13	↓5		+	
6713	63.3	5.6						↓2			
6716	62.4	5.6						15			
7105	24.0	5.6						12			
7203	34.6	5.6			↑2			12		+	
7205	32.7	5.6	↓3	↓2							
7308	35.2	5.6						↑5			
7402	39.8	5.6							++	Q9X7H5	Glyceraldehyde-3-phosphate dehydrogenase
7406	39.5	5.6						↑2			
7503	40.7	5.6						12		++	P54810
7506	44.0	5.6	↓2					↓5			Acetyl-CoA acetyltransferase
8115	26.1	5.9						15			
8404	40.5	6.0	↑5		N <sub>2</sub> O	13					
8405	38.5	6.5						13		+	
8502	44.6	6.0			↑2						

## SUMMARY

No. of up-/down-regulated spots							No. of spots typical of individual growth modes							
		N <sub>2</sub> O vs. O <sub>2</sub>	NO <sub>2</sub> vs. O <sub>2</sub>	NO <sub>3</sub> <sup>-</sup> vs. O <sub>2</sub>		O <sub>2</sub> + N <sub>3</sub> <sup>-</sup> vs. O <sub>2</sub>	NO <sub>2</sub> <sup>-</sup> + NO <sub>3</sub> <sup>-</sup> vs. O <sub>2</sub>	common	O <sub>2</sub>	N <sub>2</sub> O	NO <sub>2</sub> <sup>-</sup>	NO <sub>3</sub> <sup>-</sup>	Anaerobic	
Up	> 2-fold	22	8	11		23	29	3	> 2-fold	5	8	0	3	3
	> 3-fold	18	6	8		9	25	1						
	> 5-fold	11	5	5		5	20	0						
Down	< 2-fold	9	19	12		14	12	2	MS analysis					
	< 3-fold	6	12	11		12	12	1	Analyzed (PMF)			Identified		
	< 5-fold	3	2	4		11	12	1	33			4		

((Legend to Supplement Table 1))

The arrows indicate the type of regulation (up ( $\uparrow$ ) or down( $\downarrow$ )). The number behind the arrow indicates how many times the quantity was altered. For example, 5 indicates more than 5-fold alteration, 3 indicates more than 3-fold alteration. In the columns marked terminal electron acceptors effects, the spot quantity under described growth conditions was compared with the one under aerobic growth. If the spot quantity under certain terminal electron acceptor exceeded all others by more than 2-fold, the inducing acceptor is introduced in the column, typical of. In the columns marked, azide effects, we compared the spot quantities under presented terminal electron acceptor ( $\text{NO}_2^-$ ,  $\text{O}_2$ ) with and without  $\text{NaN}_3$  (0.4mM). The + in the column labelled analyzed (PMF) means that the protein spot was subjected to analysis by PMF with good spectrum obtained; if the PMF resulted in successful protein identification, the symbol ++ is present. Accession number and protein name with Swiss-Prot/TrEMBL databases.

Supplementary Table 2. List of protein spots in 2-DE gels of *P. denitrificans* membrane fraction, the quantity of which was affected by growth on different terminal electron acceptors and azide

			Terminal electron acceptor and azide effects		MS analysis			
	Approx. $M_r$	Approx. pI	$\text{NO}_3^-$ vs. $\text{O}_2$	$\text{O}_2 + \text{N}_3^-$ vs. $\text{O}_2$	Common	Analyzed (PMF)	Identified proteins	
							Database accession.No	protein Name
0011	23.6	3.9	↓5			+		
0120	25.7	3.9	↓5			+		
0127	28.3	3.9	↑5					
0207	32.9	3.7	↑2					
0211	32.7	4.0	↑2			+		
0214	34.2	4.1	↑5					
0304	36.8	4.0				+		
0307	39.6	4.5	↓2					
0503	52.6	4.5				++	Q9Z460	F1-ATPase beta-subunit [Fragment]
1016	24.3	4.4		↓2				
1123	28.3	4.6	↑5					
1204	34.5	4.5				+		
1211	31.6	4.7				+		
1213	36.5	4.6	↑5					
1319	38.6	4.5				+		
1702	73.5	4.6	↑5	↑5	↑5	+		
2004	23.6	4.9	↓3					
2117	26.6	4.9	↑5					
2205	35.9	4.8	↑5					
2322	40.5	5.0		↑5				
3107	28.2	5.0	↑5					
3108	31.6	5.0	↓2					
3203	34.0	5.0	↑5					
3618	67.1	5.1	↓5					
4004	19.5	5.2	↓5					
4008	23.2	5.2	↓2					
4011	24.2	5.2				+		
4106	28.4	5.1	↑5			++	P10772	Adenylate kinase
4107	25.3	5.1	↑5					
4113	26.5	5.3	↑5					
5001	24.9	5.3	↑3			+		
5006	23.2	5.5	↓5	↓2	↓2			
5009	18.0	5.5				++	Q9WX81	Granule-associated protein
5103	30.3	5.4	↑3					
5313	34.8	5.3	↑5					
5529	55.2	5.4				+		
5618	60.7	5.5	↓3					
6103	30.5	5.8	↓2	↓2	↓2			
6104	29.5	5.8	↑2					
6204	32.4	5.7	↑5			+		
6206	30.1	5.6		↓5				
6316	39.4	5.7	↑3					
6424	42.2	5.7	↑3					
7101	29.2	5.9	↓3					
8001	18.4	6.6	↓5					
8028	18.4	6.4		↓5				
8101	28.2	6.5	↓3					
8107	30.4	6.8				++	Q59662	Succinate dehydrogenase iron-sulfur protein
8110	27.5	7.0		↑2				
8111	30.5	7.0		↑3				
8115	25.3	6.9		↑5				
8118	27.5	6.6		↑2				
8226	32.8	7.6	↓5					
9103	25.5	~8	↓3					

Supplementary Table 2. Continued

SUMMARY					
No. of up-/down-regulated spots					MS analysis
		$\text{NO}_3^-$ vs. $\text{O}_2$	$\text{O}_2 + \text{N}_3^-$ vs. $\text{O}_2$	Common	Analyzed (PMF)
					Identified
Up	> 2 fold	22	6	1	16
	> 3 fold	19	4	1	4
	> 5 fold	15	3	1	
Down	< 2 fold	15	5	2	
	< 3 fold	11	2	0	
	< 5 fold	6	2	0	

In the columns marked terminal electron acceptors and azide effects, the spot quantity under described growth conditions was compared with the one under aerobic growth. All others notes are as in supplementary Table 1.