

Dataset S1. Annotation of *Nitrospira moscoviensis* and *Nitrospira lenta* genes discussed in this study.

Identifier	Gene	Product	EC number	Best hit in SwissProt database ^a	Best hit in Trembl database ^b
<i>N.moscoviensis</i>					
NITMOv2_1249		conserved protein of unknown function		<i>Escherichia coli</i> K12 (P37177; 748/420; 0.3; 28%)	<i>Nitrospira defluvii</i> (D8PCZ5; 419/420; 0.98; 86%)
NITMOv2_1250		protein of unknown function		no hit	no hit
NITMOv2_1251		putative urea ABC transporter, urea binding protein UrtA		<i>Pseudomonas aeruginosa</i> ATCC 15692 (P27017; 385/449; 0.86; 30%)	<i>Cytophaga hutchinsonii</i> ATCC 33406 (Q11VN9; 445/449; 0.9; 68%)
NITMOv2_1252		exported protein of unknown function		no hit	no hit
NITMOv2_1253	ureA	Urease gamma subunit	3.5.1.5	<i>Azoarcus sp.</i> BH72 (A1KBB7; 100/100; 0.99; 75%)	<i>Caldilinea aerophila</i> DSM 14535 (I0HZB9; 100/100; 1; 75%)
NITMOv2_1254		protein of unknown function		no hit	no hit
NITMOv2_1255	ureB	Urease subunit beta (modular protein)	3.5.1.5	<i>Natronomonas pharaonis</i> ATCC 35678 (<i>Halobacterium pharaonis</i>) (Q3IRZ6; 132/164; 0.73; 60%)	<i>Ethanoligenens harbinense</i> DSM 18485 (E6U7P1; 124/164; 0.71; 62%)
NITMOv2_1256		protein of unknown function		no hit	no hit
NITMOv2_1257		protein of unknown function		no hit	no hit
NITMOv2_1258		exported protein of unknown function		no hit	no hit
NITMOv2_1259		exported protein of unknown function		no hit	no hit
NITMOv2_1260	ureC	Urease alpha subunit	3.5.1.5	<i>Synechococcus sp.</i> (strain JA-2-3B'a(2-13)) (Q2JQ88; 572/575; 1; 73%)	<i>Moorea producens</i> 3L (568/575; 0.99; 73%)
NITMOv2_1261		putative urease accessory protein UreF		<i>Actinobacillus pleuropneumoniae</i> serotype 5b (strain L20) (A3N2R1; 227/228; 0.97; 28%)	<i>Mucilaginibacter paludis</i> DSM 18603 (H1Y7Y1; 228/ 228; 1; 30%)
NITMOv2_1262	ureG	Urease accessory protein UreG		<i>Alkalilimnicola ehrlichii</i> ATCC BAA-1101 (Q0AC95; 211/223; 0.84; 75%)	
NITMOv2_1263		putative urease accessory protein UreD		<i>Cupriavidus pinatubonensis</i> JMP 134 (<i>Ralstonia eutropha</i> JMP 134) (Q473R3; 289/293; 0.91; 31%)	<i>Streptomyces ghanaensis</i> ATCC 14672 (D5ZR9; 292/293; 1; 33%)
NITMOv2_1264		conserved protein of unknown function		<i>Rattus norvegicus</i> (Rat) (O09175; 650/273; 0.2; 27%)	<i>Nitrospira defluvii</i> (D8PCZ8 ; 303/273; 0.9; 37%)
NITMOv2_1265	nadE	Glutamine-dependent NAD(+) synthase	6.3.5.1	<i>Thermotoga maritima</i> ATCC 43589	<i>Nitrospira defluvii</i> (D8PCZ9;

				(Q9X0Y0; 576/590; 1; 48%)	589/590; 1; 74%)
NITMOv2_1266		conserved protein of unknown function		no hit	<i>Nitrospira defluvii</i> (D8PD00; 292/322; 0.93; 71%)
NITMOv2_1267	amtB	Ammonium transporter		<i>Bacillus subtilis</i> 168 (Q07429; 404/441; 0.911; 54%)	<i>Nitrospira defluvii</i> (D8PD01; 442/441; 0.97; 80%)
NITMOv2_1268	glnB	Nitrogen regulatory protein PII		<i>Aquifex aeolicus</i> VF5 (O66513 ; 112/112; 1; 68%)	<i>Nitrospira defluvii</i> (D8PD02 ; 112/112; 1; 90%)
NITMOv2_1269		putative (Protein-PII) uridylyltransferase GlnD	2.7.7.59	<i>Ochrobactrum anthropi</i> ATCC 49188 (A6WV84; 934/891; 0.94; 32%)	<i>Nitrospira defluvii</i> (D8PD03; 894/891; 0.99; 71%)
NITMOv2_1270	glnA	Glutamine synthetase	6.3.1.2	<i>Synechocystis sp.</i> PCC 6803 (P77961; 473/469; 0.99; 63%)	<i>Nitrospira defluvii</i> (D8PD04; 469/469; 1; 93%)
NITMOv2_1271		putative nitrate ABC transporter, nitrate binding protein NrtA		<i>Synechocystis sp.</i> PCC 6803 (P73450; 670/458; 0.56; 34%)	<i>Desulfomonile tiedjei</i> ATCC 49306 (I4C053; 464/458; 0.92; 0.93; 64%)
NITMOv2_1272	nrtB	Nitrate ABC transporter, integral membrane subunit (modular protein)		<i>Synechocystis sp.</i> PCC 6803 (P73451 ; 275/325; 0.68; 37%)	<i>Desulfomonile tiedjei</i> ATCC 49306 (I4C052; 257/325; 0.72; 59%)
NITMOv2_1273		ABC transporter, ATP-binding protein NrtD		<i>Synechococcus elongatus</i> PCC 7942 (<i>Anacystis nidulans</i> R2) (P38046; 274/280; 0.92; 51%)	<i>Desulfomonile tiedjei</i> ATCC 49306 (I4C051; 276/280; 0.9; 66%)
NITMOv2_1274	cynS	Cyanate hydratase	4.2.1.104	<i>Dechloromonas aromatica</i> RCB (Q47G40; 147/146; 1; 39%)	<i>Nitrospira defluvii</i> (D8PD06; 146/146; 1; 79%)
NITMOv2_1275	amtB	Ammonium transporter		<i>Bacillus subtilis</i> 168 (Q07429; 404/462; 0.85; 55%)	<i>Nitrospira defluvii</i> (D8PD01; 442/462; 0.94; 72%)
NITMOv2_1276		protein of unknown function		no hit	no hit
NITMOv2_1277		conserved protein of unknown function		no hit	<i>Nitrospira defluvii</i> (D8PD07; 64/76; 0.78; 46%)
NITMOv2_1278	amtB	Ammonium transporter		<i>Bacillus subtilis</i> 168 (Q07429; 404/387; 0.98; 44%)	<i>Ammonifex degensii</i> DSM 10501 (C9R9J0; 434/387; 0.92; 47%)
NITMOv2_1279		putative quinol-cytochrome <i>c</i> reductase, iron sulfur subunit	1.10.2.2	<i>Chlorobaculum thiosulfatophilum</i> (<i>Chlorobium limicola f.sp. thiosulfatophilum</i>) (Q46136; 181/148; 0.77; 31%)	<i>Caldithrix abyssi</i> DSM 13497 (H1XYE5; 154/148; 0.97; 32%)
NITMOv2_1280		putative quinol-cytochrome <i>c</i> reductase, cytochrome <i>b</i> subunit	1.10.2.2	<i>Spirogyra maxima</i> (Green alga) (Q71KP4; 215/348; 0.56; 42%)	<i>Caldithrix abyssi</i> DSM 13497 (H1XYE4; 348/348; 0.91; 39%)

NITMOv2_1281	putative octaheme cytochrome <i>c</i>		<i>Nitrosomonas europaea</i> ATCC 19718 (Q50925; 570/474; 0.65; 25%)	<i>Desulfomonile tiedjei</i> ATCC 49306 (I4CB31; 453/474; 0.89; 49%)
NITMOv2_1282	conserved protein of unknown function		no hit	<i>Mesorhizobium opportunistum</i> LMG 24607 (F7Y331; 156/176; 0.86; 80%)
NITMOv2_1283	conserved protein of unknown function		<i>Methanopyrus kandleri</i> AV19 (P50100; 196/283; 0.42; 32%)	<i>Nitrospira defluvii</i> (D8PD09; 258/283; 0.89; 65%)
NITMOv2_0254	putative Nitrite oxidoreductase, beta subunit	1.7.99.4	<i>Rhodovulum sulfidophilum</i> (<i>Rhodobacter sulfidophilus</i>) (Q8GPG3; 325/429; 0.82; 36%)	<i>Nitrospira defluvii</i> (D8PI40; 429/429; 1; 97%)
NITMOv2_0255	putative Nitrite oxidoreductase, alpha subunit	1.7.99.4	<i>Thauera selenatis</i> (Q9S1H0; 918/1145; 0.86; 22%)	<i>Nitrospira defluvii</i> (D8PI59; 1147/1145; 1; 88%)
NITMOv2_4027	putative Nitrite oxidoreductase, beta subunit	1.7.99.4	<i>Rhodovulum sulfidophilum</i> (<i>Rhodobacter sulfidophilus</i>) (Q8GPG3; 325/429; 0.82; 36%)	<i>Nitrospira defluvii</i> (D8PI40; 429/429; 1; 97%)
NITMOv2_4028	putative Nitrite oxidoreductase, alpha subunit	1.7.99.4	<i>Thauera selenatis</i> (Q9S1H0; 918/1145; 0.86; 22%)	<i>Nitrospira defluvii</i> (D8PI59; 1147/1145; 1; 88%)
NITMOv2_4030	- Sigma54 dependent transcriptional regulator		<i>Escherichia coli</i> K12 (Q06065; 461/473; 0.72; 45%)	<i>Nitrospira defluvii</i> (D8PI58; 473/473; 1; 69%)
NITMOv2_4032	putative Nitrite oxidoreductase, beta subunit	1.7.99.4	<i>Rhodovulum sulfidophilum</i> (<i>Rhodobacter sulfidophilus</i>) (Q8GPG3; 325/429; 0.82; 36%)	<i>Nitrospira defluvii</i> (D8PI40; 429/429; 1; 97%)
NITMOv2_4033	putative Nitrite oxidoreductase, alpha subunit	1.7.99.4	<i>Thauera selenatis</i> (Q9S1H0; 918/1145; 0.86; 23%)	<i>Nitrospira defluvii</i> (D8PI59; 1147/1145; 1; 87%)
NITMOv2_4035	- Sigma54 dependent transcriptional regulator		<i>Escherichia coli</i> K12 (P14375; 441/488; 0.92; 37%)	<i>Nitrospira defluvii</i> (D8PI58; 473/488; 0.95; 47%)
NITMOv2_4533	putative Nitrite oxidoreductase, beta subunit	1.7.99.4	<i>Rhodovulum sulfidophilum</i> (<i>Rhodobacter sulfidophilus</i>) (Q8GPG3; 325/429; 0.82; 36%)	<i>Nitrospira defluvii</i> (D8PI40; 429/429; 1; 92%)
NITMOv2_4534	putative Nitrite oxidoreductase, alpha subunit	1.7.99.4	<i>Thauera selenatis</i> (Q9S1H0; 918/1145; 0.66; 23%)	<i>Nitrospira defluvii</i> (D8PI59; 1147/1145; 1; 87%)
NITMOv2_4536	Sigma54 dependent transcriptional regulator		<i>Klebsiella oxytoca</i> (Q9APD9; 443/473; 0.87; 40%)	<i>Nitrospira defluvii</i> (D8PI58; 473/473; 1; 64%)
NITMOv2_4537	putative Nitrite oxidoreductase, beta subunit	1.7.99.4	<i>Rhodovulum sulfidophilum</i> (<i>Rhodobacter sulfidophilus</i>) (Q8GPG3; 325/429; 0.82; 36%)	<i>Nitrospira defluvii</i> (D8PI40; 429/429; 1; 97%)

				36%)	
NITMOv2_4538		putative Nitrite oxidoreductase, alpha subunit	1.7.99.4	<i>Thauera selenatis</i> (Q9S1H0 ; 918/1145; 0.86; 22%)	<i>Nitrospira defluvii</i> (D8PI59; 1147/1145; 1; 88%)
NITMOv2_4539		Sigma54 dependent transcriptional regulator		<i>Escherichia coli</i> O157:H7 (Q8X613; 441/472; 0.88; 40%)	<i>Nitrospira defluvii</i> (D8PI58; 473/472; 1; 73%)
NITMOv2_4696	katA	Catalase (hydroperoxidase II)	1.11.1.6	<i>Vibrio fischeri</i> ATCC 700601 (O68146; 482/486; 0.98; 80%)	<i>Azoarcus sp.</i> KH32C (H0PX65; 485/486; 0.98; 82%)
NITMOv2_0085	katA	Catalase	1.11.1.6	<i>Vibrio fischeri</i> ATCC 700601 (O68146; 482/486; 0.98; 80%)	<i>Azoarcus sp.</i> KH32C (H0PX65; 485/486; 0.98; 82%)
NITMOv2_2805	sod	Superoxide dismutase (Fe)	1.15.1.1	<i>Ralstonia metallidurans</i> CH34 (P17550; 197/211; 0.89; 35%)	mine drainage metagenome (E6PDX0 ; 195/211; 0.92; 54%)
NITMOv2_3821	focA	Formate transporter		<i>Escherichia coli</i> K12 (P0AC23; 285/298; 0.93; 43%)	<i>Nitrospira defluvii</i> (D8PEK0; 280/298; 0.9; 72%)
NITMOv2_3822	fdsA	Formate dehydrogenase, alpha subunit	1.2.1.2	<i>Methanocaldococcus jannaschii</i> ATCC 43067 (<i>Methanococcus jannaschii</i>) (P61159; 673/916; 0.74; 40%)	<i>Nitrospira defluvii</i> (D8PEJ9; 908/916; 0.97; 69%)
NITMOv2_3823	fdsB	Formate dehydrogenase, beta subunit	1.2.1.2	<i>Desulfovibrio fructosivorans</i> (Q46507; 490/528; 0.77; 44%)	<i>Nitrospira defluvii</i> (D8PEJ8; 498/528; 0.93; 69%)
NITMOv2_3825	fdsG	Formate dehydrogenase, gamma subunit	1.2.1.2	<i>Pseudomonas aeruginosa</i> ATCC 15692 (Q9I0J8; 166/156; 0.84; 40%)	<i>Nitrospira defluvii</i> (D8PEJ7; 149/156; 0.91; 50%)
NITMOv2_0740		putative Nitrite oxidoreductase, membrane subunit	1.7.99.4	<i>Thauera selenatis</i> (Q9S1G7; 239/279; 0.87; 29%)	<i>Nitrospira defluvii</i> (D8PBQ9; 275/279; 0.88; 69%)
NITMOv2_3617		putative Nitrite oxidoreductase, membrane subunit	1.7.99.4	<i>Thauera selenatis</i> (Q9S1G7; 239/277; 1; 26%)	<i>Nitrospira defluvii</i> (D8PI74; 280/277; 1; 80%)
NITMOv2_3624		putative Nitrite oxidoreductase, membrane subunit	1.7.99.4	<i>Ideonella dechloratans</i> (P60000; 239/316; 0.46; 28%)	<i>Nitrospira defluvii</i> (D8PI81; 317/316; 1; 89%)
NITMOv2_3640		putative Nitrite oxidoreductase, cytochrome <i>c</i> containing membrane subunit		<i>Thauera selenatis</i> (Q9S1G7; 239/591; 0.42; 22%)	<i>Nitrospira defluvii</i> (D8PI95; 594/591; 1; 77%)
NITMOv2_4208		putative Nitrite oxidoreductase, membrane subunit	1.7.99.4	<i>Thauera selenatis</i> (Q9S1G7; 239/262; 1; 27%)	<i>Nitrospira defluvii</i> (D8PI74; 280/262; 0.93; 64%)

Identifier <i>N.lenta</i>	Gene	Product	EC number	Best hit in SwissProt database ^a	Best hit in Trembl database ^b
NITLEN_v1_11 0011		conserved protein of unknown function		<i>Methanopyrus kandleri</i> AV19 (P50100; 196/256; 0.40; 36%)	<i>Nitrospira defluvii</i> (D8PD09; 258/256; 0.98; 63%)
NITLEN_v1_11 0012	<i>nirA</i>	Ferredoxin-nitrite reductase	1.7.7.1	<i>Synechococcus elongatus</i> PCC 794 (<i>Anacystis nidulans</i> R2) (P39661; 512/520; 0.95; 44%)	<i>Nitrospira defluvii</i> (D8PD08; 531/520; 0.98; 73%)
NITLEN_v1_11 0013		protein of unknown function		no hit	no hit
NITLEN_v1_11 0014	<i>cynS</i>	Cyanate hydratase	4.2.1.104	<i>Photorhabdus luminescens</i> TT01 subsp. laumondii (Q7NA33; 156/146; 0.90; 43%)	<i>Nitrospira defluvii</i> (D8PD06; 146/146; 1; 81%)
NITLEN_v1_11 0015	<i>nirC</i>	Nitrite transporter		<i>Escherichia coli</i> K12 (P0AC26; 268/276; 0.88; 47%)	<i>Nitrospira defluvii</i> (D8PD05; 276/276; 1; 76%)
NITLEN_v1_11 0016	<i>glnA</i>	Glutamine synthetase	6.3.1.2	<i>Nostoc</i> sp. PCC 7120/UTEX 2576 (P00964; 474/469; 0.99; 63%)	<i>Nitrospira defluvii</i> (D8PD04; 469/469; 1; 93%)
NITLEN_v1_11 0017		putative (Protein-PII) uridylyltransferase GlnD	2.7.7.59	<i>Azospirillum brasilense</i> (Q8RQD1; 933/894; 0.88; 34%)	<i>Nitrospira defluvii</i> (D8PD03; 894/894; 1; 71%)
NITLEN_v1_11 0018	<i>glnB</i>	Nitrogen regulatory protein P-II		<i>Aquifex aeolicus</i> VF5 (O66513; 112/112; 1; 68%)	<i>Nitrospira defluvii</i> (D8PD02; 112/112; 1; 92%)
NITLEN_v1_11 0019	<i>amtB</i>	Ammonium transporter		<i>Bacillus subtilis</i> 168 (Q07429; 404/444; 0.91; 55%)	<i>Nitrospira defluvii</i> (D8PD01; 442/444; 1; 74%)
NITLEN_v1_11 0020	<i>amtB</i>	Ammonium transporter		<i>Bacillus subtilis</i> 168 (Q07429; 404/462; 0.87; 55)	<i>Ca. Methylomirabilis oxyfera</i> (D5MG60; 458/462; 0.99; 68%)
NITLEN_v1_11 0021		conserved exported protein of unknown function		<i>Neurospora crassa</i> ATCC 24698 (P28349; 1090/449; 0.12; 29%)	<i>Ca. Methylomirabilis oxyfera</i> (D5MG73; 458/449; 0.95; 31%)
NITLEN_v1_11 0022		protein of unknown function		no hit	<i>Pandoraea</i> sp. SD6-2 (R7WZJ2; 806/116; 0.07; 35%)
NITLEN_v1_11 0023		protein of unknown function		<i>Drosophila pseudoobscura</i> (P12348; 1271/657; 0.03; 40%)	no hit
NITLEN_v1_11 0024		exported protein of unknown function		<i>Saccharomyces cerevisiae</i> ATCC 204508/S288c (P41809; 1802/327; 01; 27%)	<i>Nitrospira defluvii</i> (D8PEI4; 348/327; 1.01; 28%)
NITLEN_v1_11	<i>nadE</i>	Glutamine-dependent NAD(+)	6.3.5.1	<i>Thermotoga maritima</i> ATCC	<i>Nitrospira defluvii</i> (D8PCZ9;

0025		synthetase		43589/MSB8 (Q9X0Y0; 576/590; 1; 47%)	589/590; 1; 72%)
NITLEN_v1_11 0026		putative methyl-accepting chemotaxis protein		<i>Alcanivorax borkumensis</i> SK2/ATCC 700651 (Q0VTI9; 675/560; 0.48; 39%)	<i>Pseudomonas pseudoalcaligenes</i> KF707 (L8MRJ5; 566/560; 1.02; 40%)
NITLEN_v1_11 0027		putative urease accessory protein UreD		<i>Streptomyces griseus</i> JCM 4626/NBRC 13350 (B1VSW8; 293/309; 0.9; 34%)	<i>Streptomyces ghanaensis</i> ATCC 14672 (D5ZRX9; 292/309; 0.89; 34%)
NITLEN_v1_11 0028	<i>ureG</i>	Urease accessory protein UreG		<i>Alkalilimnicola ehrlichii</i> ATCC BAA-1101 (Q0AC95; 211/223; 0.84; 76%)	<i>Accumulibacter phosphatis</i> UW-1 (C7RRP5; 220/223; 0.84; 77%)
NITLEN_v1_11 0029		putative urease accessory protein UreF		<i>Actinobacillus pleuropneumoniae</i> (<i>Haemophilus pleuropneumoniae</i>) (O54423; 227/228; 0.97; 27%)	<i>Natrinema versiforme</i> JCM 10478 (L9XMX3; 254/228; 0.98; 33%)
NITLEN_v1_11 0030	<i>ureC</i>	Urease alpha subunit	3.5.1.5	<i>Synechococcus</i> sp. JA-2-3B'a(2-13) (Q2JQ88; 572/575; 1; 73%)	<i>Chroococcidiopsis thermalis</i> PCC 7203 (K9U8V6; 572/575; 1; 75%)
NITLEN_v1_11 0031	<i>ureB</i>	Urease beta subunit (modular protein)	3.5.1.5	<i>Deinococcus radiodurans</i> ATCC 13939 (Q9RYJ3; 228/156; 0.53; 60%)	<i>Natronococcus occultus</i> SP4 (L0JZM2; 1377156; 0.81; 57%)
NITLEN_v1_11 0032	<i>ureA</i>	Urease gamma subunit	3.5.1.5	<i>Azoarcus</i> sp. BH72 (A1KBB7; 100/100; 0.99; 75%)	<i>Actinomyces johnsonii</i> F0542 (U1QF59; 104/100; 0.96; 77%)
NITLEN_v1_11 0033		exported protein of unknown function		<i>Schizosaccharomyces pombe</i> 972/ATCC 24843 (O14207; 1888/142; 0.03; 32%)	<i>Nitrospira defluvii</i> (D8P8T7; 159/142; 0.75; 29%)
NITLEN_v1_11 0034	<i>urtE</i>	Urea ABC transporter, ATP-binding protein UrtE		<i>Salmonella typhi</i> (P0A192; 237/236; 1; 39%)	<i>Microcoleus vaginatus</i> FGP-2 (F5UIY2; 240/236; 0.98; 57%)
NITLEN_v1_11 0035	<i>urtD</i>	Urea ABC transporter, ATP-binding protein UrtD		<i>Escherichia coli</i> O157:H7 (P0A9S8; 255/254; 1; 35%)	<i>Desulfotomaculum carboxydivorans</i> DSM 14880 (F6B8X5; 252/254; 1; 58%)
NITLEN_v1_11 0036		putative urea ABC transporter, permease protein UrtC		<i>Salmonella typhimurium</i> LT2 (P30296; 425/384; 0.76; 25%)	<i>Ca. Entothoonella</i> sp. TSY2 (W4LVW4; 394/384; 0.91; 59%)
NITLEN_v1_11 0037		putative urea ABC transporter, permease protein UrtB		<i>Pseudomonas aeruginosa</i> ATCC 15692/PAO1 (P21627; 307/537; 0.54; 31%)	<i>Curvibacter</i> putative symbiont of <i>Hydra magnipapillata</i> (C9YHE6; 496/537; 0.9; 47%)
NITLEN_v1_11 0038		putative urea ABC transporter, urea binding protein UrtA		<i>Pseudomonas aeruginosa</i> ATCC 15692/PAO1 (P27017; 385/457; 0.85; 29%)	<i>Cytophaga hutchinsonii</i> ATCC 33406 (Q11VN9; 445/457; 0.87; 71%)

NITLEN_v1_11 0039	conserved protein of unknown function	<i>Rattus norvegicus</i> (Q9JIL3; 897/456; 0.21; 25%)	<i>Nitrospira multififormis</i> ATCC 25196 (Q2Y9N1; 474/456; 0.93; 49%)
NITLEN_v1_11 0040	exported protein of unknown function	<i>Mus musculus</i> (Q8CJ40; 2009/278; 0.09; 24%)	<i>Nitrospira defluvii</i> (D8PEI4; 348/278; 0.9; 28%)
NITLEN_v1_11 0041	conserved protein of unknown function	<i>Escherichia coli</i> K12 (P37177; 748/421; 0.23; 28%)	<i>Nitrospira defluvii</i> (D8PCZ5; 419/421; 0.98; 84%)

^a Organism with the highest BLAST e-value in the SwissProt database to the respective *N. moscoviensis* or *N. lenta* protein. In parentheses: SwissProt accession number of BLAST hit; protein length of BLAST hit / length of the homologous *N. moscoviensis* or *N. lenta* protein; alignment ratio (length of alignment / length of longer protein); amino acid identity.

^b Organism with the highest BLAST e-value in the TrEMBL database to the respective *N. moscoviensis* or *N. lenta* protein. In parentheses: TrEMBL accession number of BLAST hit; protein length of BLAST hit / length of the homologous *N. moscoviensis* or *N. lenta* protein; alignment ratio (length of alignment / length of longer protein); amino acid identity.