

Transporter Family	Locus	Gene name	Gene Annotation	Protein length (aa)	Number of TMS (SP)	Functional Domains			Notes	Description	gene neighborhood
						Description	Family	E-value			
1.A.8 Major Intrinsic Protein (MIP) Family	NVIE_020740		Major intrinsic protein	231	6	Major intrinsic protein	PF00230	3.8e-34		Channels in the MIP family transport water, organics (e.g. glycerol), urea, NH <sub>3</sub> , CO <sub>2</sub> , H <sub>2</sub> O <sub>2</sub> and ions.	
1.A.11 (Amt)	NVIE_002420	amt1	Ammonia channel	478	11	Ammonium Transporter Family	PF00909	4.0e-118	ID with each other: 90.07% to amt2, 45.2% to amt3	Channels in the Amt family transport NH <sub>3</sub> , NH <sub>4</sub> <sup>+</sup> , CO <sub>2</sub> , methylammonium	
	NVIE_022110	amt2	Ammonia channel	423	11	Ammonium Transporter Family	PF00909	6.4e-115	ID with each other: 90.07% to amt1, 44.92% to amt3		
	NVIE_023840	amt3	Ammonia channel	410	11	Ammonium Transporter Family	PF00909	2.1e-110			
1.A.22. Large Conductance Mechanosensitive Ion Channel (MscL) Family	NVIE_001630	mscL	Large-conductance mechanosensitive ion channel	129	2	Large-conductance mechanosensitive channel	PF01741	9.70E-21		The MscL channel of E. coli favor the non specific efflux of ions in reponse to hypo-osmotic shock. This transporter has a preference for cations over anions.	
1.A.23. Small Conductance Mechanosensitive Ion Channel (MscS) Family	NVIE_000140	mscS	putative mechanosensitive ion channel MscS	318	3	Mechanosensitive ion channel MscS	PF00924	8.00E-51		The MscS channel of E. coli favor the efflux of ions in reponse to hypo-osmotic shock.	
	NVIE_016970		putative small-conductance mechanosensitive ion channel	320	6	Mechanosensitive ion channel MscS	PF00924	1.50E-10			
	NVIE_020120		putative small-conductance mechanosensitive ion channel protein	280	4	Mechanosensitive ion channel MscS	PF00924	3.20E-12			
	NVIE_022350		putative small-conductance mechanosensitive ion channel protein	236	0	Mechanosensitive ion channel MscS	PF00924	2.70E-07			
1.A.28. Urea Transporter (UT) Family	NVIE_014780		putative urea transporter	370	9	Urea transporter	PF03253	5.30E-21		of urea in mammals and bacteria. Up to now, this family of transporter wasn't known in archaea.	
1.A.35. CorA Metal Ion Transporter (MIT) Family	NVIE_000130		putative CorA ion transporter	311	2	Mg <sup>2+</sup> transporter protein, CorA-like	PF01544	4.50E-61		Characterized transporters of the MIT family favor the uptake and efflux of divalent cations (e.g. Mg <sup>2+</sup> , Co <sup>2+</sup> , Ni <sup>2+</sup> , Zn <sup>2+</sup> , Cd <sup>2+</sup> ).	
	NVIE_016220		putative CorA ion transporter	318	2	Mg <sup>2+</sup> transporter protein, CorA-like	PF01544	8.20E-58			
2.A.1. Major Facilitator Superfamily (MFS)	NVIE_000150		major facilitator superfamily MFS-1	394	8	Major facilitator superfamily, g	SSF103473	8.10E-51		(UMF10) Family (mostly from Archaea but some from bacteria)	
	NVIE_012120		major facilitator superfamily transp	506	14	Major facilitator superfamily, g	SSF103473	6.20E-71		Similarity searches suggest this protein belong to the Drug:H+ Antiporter-2 (14 Spanner) (DHA2) Family (2.A.1.3). This family is involved in the efflux of antibiotics but also in the efflux of siderophores and signalling compounds and in the uptake of basic amino acids and nucleobases for example.	
	NVIE_014470		major facilitator superfamily transp	503	14	Major facilitator superfamily, g	SSF103473	1.50E-61		2.A.1.3	
	NVIE_015090		major facilitator superfamily MFS_1	383	12	Major facilitator superfamily, g	SSF103473	6.00E-50		Best match: The Unknown Major Facilitator-5 (UMF5) Family. 2nd match: The Putative Aromatic Compound/Drug Exporter (ACDE) Family. 3rd match: 2.A.1.2: The Drug:H+ Antiporter-1 (12 Spanner) (DHA1) Family	
	NVIE_017980		major facilitator superfamily transp	435	12	Major facilitator superfamily, g	SSF103473	1.90E-51		partial match to 2.A.1.15: The Aromatic Acid:H+ Symporter (AAHS) Family	
	NVIE_027240		major facilitator superfamily transp	500	14	Major facilitator superfamily, g	SSF103473	6.70E-58		2.A.1.3	
	NVIE_027400		Major facilitator superfamily transporter MFS_1	413	12	Major facilitator superfamily, g Tetracycline resistance protein	SSF103473 PR01035	1.30E-65 9.40E-27		2.A.1.3	
	NVIE_019750		putative SAM-dependent methyltr	833	14	Major facilitator superfamily, g	SSF103473	3.60E-06		containing MFS transporter domain, potentially involved in spermidine biosynthesis.	
2.A.3 (APC) Amino Acid-Polyamine-Organocation Family	NVIE_004030		putative amino acid transporter	445	12	Amino acid permease domain	PF00324	4.00E-34		Transporters of the APC family are involved in the transport of various amino acids, polyamine (e.g. putrescine, spermidine, cadaverine) but also ethanolamine, methylamine, thiamine or choline	
	NVIE_026360		putative amino acid transporter	783	12	Amino acid permease domain	PF00324	2.90E-35			
	NVIE_010720		cation diffusion facilitator family transporter	287	6	Cation efflux protein	PF01545	3.10E-50			

2. A.4. (CDF) Cation Diffusion Facilitator Family	NVIE_012300		cation diffusion facilitator family transporter	472	6	Cation efflux protein	PF01545	1,20E-05		Transporters of the CDF family are involved in the efflux of Zn <sup>2+</sup> , Co <sup>2+</sup> , Cd <sup>2+</sup> , Fe <sup>2+</sup> and Hg <sup>2+</sup> and in the transport of Cu <sup>2+</sup> , Ni <sup>2+</sup> and Mn <sup>2+</sup> .	
	NVIE_023060	czcD	cation diffusion facilitator family transporter	325	5	Cation efflux protein	PF01545	3,70E-72	Cobalt-zinc-cadmium resistance protein CzcD		
	NVIE_027100		cation diffusion facilitator family transporter	300	6	Cation efflux protein	PF01545	8,00E-47			
2. A.5. Zinc (Zn <sup>2+</sup> )-Iron (Fe <sup>2+</sup> ) Permease (ZIP) Family	NVIE_000590		putative Zinc/iron permease	419	9	Zinc/iron permease	PF02535	1,50E-07		Transporters of the ZIP family are involved in the transport of divalent cations, mainly Zn <sup>2+</sup> and Fe <sup>2+</sup> but also Co <sup>2+</sup> , Mn <sup>2+</sup> , Cd <sup>2+</sup> , Pb <sup>2+</sup> , Hg <sup>2+</sup> .	adjacent to a multicopper oxidase - copper uptake gene? no synteny. Putative sensor proteins, transferases, lipases, peptidases etc
	NVIE_001900		putative Zinc/iron permease	254	7	Zinc/iron permease	PF02535	3,50E-07			
	NVIE_026940		putative metal cation transporter (fragment)	135	1						
2. A.7. Drug/Metabolite Transporter (DMT) Superfamily	NVIE_003340		drug/metabolite transporter superfamily protein	313	10	Protein of unknown function DUF6, transmembrane	PF00892	8,50E-15		Transporter of the DMT Superfamily are involved in the uptake/efflux of various drugs and metabolites.	syntenic region
2. A.19. Ca <sup>2+</sup> :Cation Antiporter (CaCA) Family	NVIE_006650			347	10	Sodium/calcium exchanger me	PF01699	8,90E-13		Similarity searches suggest this protein belong to the transporter cluster 2.A.19.5 of Na <sup>+</sup> :Ca <sup>2+</sup> exchanger.	
2. A.20. Inorganic Phosphate Transporter (PIT) Family	NVIE_026480	pit	putative inorganic phosphate transporter	336	8	Phosphate transporter	PF01384	2,80E-97			limited synteny. Adjacent gene is putative phosphate transport regulator.
2. A.21. Solute: Sodium Symporter (SSS) Family	NVIE_014790		urea active transporter, urea/sodium symporter	773	15	Sodium/solute symporter	PF00474	1,90E-23		Similarity searches suggest this protein belong to the transporter cluster 2.A.21.6 of urea, polyamines and antimicrobial peptide uptake systems.	limited synteny. Adjacent to 1.A.28. Urea Transporter (UT) Family NVIE_014780 and the ureABC 1 operon
	NVIE_014880		putative Sodium:solute symporter family protein	507	13	Sodium/solute symporter	PF00474	6,30E-30			no synteny
2. A.37. Monovalent Cation:Proton Antiporter-2 (CPA2) Family	NVIE_002440		putative Na <sup>+</sup> (Li <sup>+</sup> )/H <sup>+</sup> antiporter	388	13	Cation/H <sup>+</sup> exchanger	PF00999	1,60E-62		Similarity searches suggest these proteins belong to the transporter cluster 2.A.37.2 of Na <sup>+</sup> (Li <sup>+</sup> ):H <sup>+</sup> antiporters.	synteny. Next to an amt transporter
	NVIE_006090	napA	putative Na <sup>+</sup> (Li <sup>+</sup> )/H <sup>+</sup> antiporter	433	13	Cation/H <sup>+</sup> exchanger	PF00999	2,30E-68			
	NVIE_010660		putative Na <sup>+</sup> (Li <sup>+</sup> )/H <sup>+</sup> antiporter	411	11	Cation/H <sup>+</sup> exchanger	PF00999	4,90E-64			no synteny
	NVIE_018960		monovalent cation/proton antiporter-2 family protein	411	11	Cation/H <sup>+</sup> exchanger	PF00999	2,20E-57		Transporters of the CPA2 family are mainly involved in K <sup>+</sup> /H <sup>+</sup> antiport, K <sup>+</sup> uniport and Na <sup>+</sup> /H <sup>+</sup> antiport.	partial synteny. Gene neighborhood: succinate-CoA ligase and phosphopyrimidine synthase
2. A.39. Nucleobase:Cation Symporter-1 (NCS1) Family	NVIE_006740	cytX	hydroxymethylpyrimidine transporter	429	12	Permease, cytosine/purines, uracil, thiamine, allantoin	PF02133	1,30E-30			
	NVIE_015860		putative nucleobase-cation symporter family protein	516	12	Permease, cytosine/purines, uracil, thiamine, allantoin	PF02133	4,90E-20			
2. A.52. Ni <sup>2+</sup> - Co <sup>2+</sup> Transporter (NiCoT) Family	NVIE_027900		putative nickel/cobalt transporter	234	4	ABC-type uncharacterized transport system, permease component	COG2215			Transporters of the NiCoT family catalyse the uptake of Ni <sup>2+</sup> and Co <sup>2+</sup> but also the efflux of Ca <sup>2+</sup> and Ni <sup>2+</sup> . Some of these transporters are involved in the incorporation of nickel in urease enzymes.	
2. A.59. Arsenical Resistance-3 (ACR3) Family	NVIE_024440		arsenical resistance-3 family protein	295	10	Bile acid:sodium symporter	PF01758	3,10E-14		Only two representatives of the ACR3 family have been characterized and shown to be arsenite/antimonite efflux systems. This family includes several clusters of phylogenetically distinct protein which have not yet been characterized.	
2. A.64. Twin Arginine Targeting (Tat) Family	NVIE_012240	tatA1	TatA subunit of twin-arginine targeting system	117	1	Bacterial sec-independent trans	PF02416	2,50E-11			
	NVIE_015530	tatA2	TatA subunit of twin-arginine targeting system	110	1	Bacterial sec-independent trans	PF02416	1,70E-08			
	NVIE_015520	tatC	TatC subunit of twin-arginine targeting system	268	6	Sec-independent periplasmic p	PF00902	1,90E-46			
(RhtB)Resistance to Homoserine/ Threonine (RhtB) Family	NVIE_003300	lysE	L-lysine exporter family protein	212	6	Lysine exporter protein (LYSE)	PF01810	1,10E-16		Only two members of this family have been characterized: LysE catalyzes the efflux of L-Lysine and ArgO, the effluxes of arginine.	

2.A.89. Vacuolar Iron Transporter (VIT) Family	NVIE_000910		too short/maybe gene in other reading frame?	95							
	NVIE_003860		vacuolar iron transporter family protein	227	4	Protein of unknown function DL	PF01988	9,00E-66			Transporters of the VIT family are involved in the transport of Fe2+ and Mn2+.
2.A.95. 6TMS Neutral Amino Acid Transporter (NAAT) Family	NVIE_026180		fragment of putative amino acid transporter (part 1)	129	3	Multiple antibiotic resistance (N	PF01914	5,30E-27			The sole NAAT Family protein characterized so far is a neutral amino acid transporter from <i>Thermococcus</i> sp. KS-1. Another member (MarC) might be involved in multidrug resistance but this role is controversial
	NVIE_026190		fragment of putative amino acid transporter (part 2)	89	2	Multiple antibiotic resistance (N	PF01914	1,80E-21			
2.A.102. Putative 4-Toluene Sulfonate Uptake Permease (TSUP) Family	NVIE_005250		putative sulfonate transporter	258	8	Protein of unknown function DL	PF01925	6,10E-51			Transporters of the TSUP family are involved in the uptake and efflux of organo-sulfur compounds such as sulfonates but also sulfite and sulfate.
	NVIE_010680		putative sulfonate transporter	252	7	Protein of unknown function DL	PF01925	8,90E-37			
2.A.108. The Iron/Lead Transporter (ILT) Family	NVIE_013460		putative iron/lead transporter	787	8	Iron permease FTR1	PF03239	1,20E-16			Similarity searches suggest this protein belong to the Lead (Pb2+) Uptake Porter (PbrT) Family. This family is involved in the transport of lead (Pb2+) and ferrous iron (Fe2+).
2.A.109. Tellurium Ion Resistance (TerC) Family	NVIE_019010		tellurium ion resistance family protein	330	9	Integral membrane protein Ter	PF03741	8,60E-52			Some proteins of the TerC family have been implicated in tellurium resistance and some studies suggest that TerC catalyses the efflux of TeO32- ions but this last result has not been consistently reported. Other studies have indicated that some TerC homologues may be involved in membrane biogenesis.
3.A.1.2. The Carbohydrate Uptake Transporter-2 (CUT2) Family	NVIE_015910		ABC uptake transporter, permease protein	311	9	Bacterial inner-membrane tran	PF02653	1,30E-41			of transmembrane subunits (TMs) which belong to a larger group of TMs of Periplasmic Binding Protein (PBP)-dependent ATP-Binding Cassette (ABC) transporters, which are mainly involved in the uptake of branched-chain amino acids (AAs) or in the uptake of monosaccharides including
	NVIE_015920		ABC uptake transporter, permease protein	355	10	Bacterial inner-membrane tran	PF02653	1,10E-40			
	NVIE_015900		putative ABC uptake transporter, substrate-binding protein/surface lipoprotein	485	2	Basic membrane lipoprotein	PF02608	2,40E-53			
	NVIE_015930		ABC uptake transporter, ATP-binding protein	511	0	ABC transporter-like	PF00005	6,40E-21			
3.A.1.5. The Peptide/Opine/Nickel Uptake Transporter (PepT) Family	NVIE_016170	appB	peptide/opine/nickel ABC uptake transporter, permease protein	349	6	Binding-protein-dependent tra	PF00528	3,00E-37			Similarity searches indicate that this transport system belongs to the Peptide/Opine/Nickel Uptake Transporter (PepT) Family (3.A.1.5). This family of transporters also include sugar, glutathione, EDTA, and antibiotic uptake systems.
	NVIE_016180	dppC	peptide/opine/nickel ABC uptake transporter, permease protein	482	6	Binding-protein-dependent tra	PF00528	1,20E-26			
	NVIE_016160		peptide/opine/nickel ABC uptake transporter, substrate-binding protein	1045	6	Bacterial extracellular solute-b	PF00496	1,10E-18			
	NVIE_016150	appF	peptide/opine/nickel ABC uptake transporter, ATP-binding protein	279	0	ABC transporter-like	PF00005	2,60E-20			
	NVIE_003480	oppD	peptide/opine/nickel ABC uptake transporter, putative ATP-binding protein	330	0	Oligopeptide/dipeptide ABC tra	PF08352	7,50E-23			
3.A.1.7. The Phosphate Uptake Transporter (PhoT) Family	NVIE_020860	pstS	ABC phosphate uptake transporter, substrate-binding protein	506	2	Periplasmic phosphate binding	PF01547, TIGR00975	2,60E-84			system belong to the Phosphate Uptake Transporter (PhoT) Family 3.A.1.7. This family include the high affinity phosphate uptake systems pstABC. Interestingly <i>N. gargensis</i> possesses several genes encoding different variant of the phosphate binding protein pstC. One of these variant, RNAR_03306 seems to have arisen from a recombination event between different variant of pstC present in other Thaumarchaeota.
	NVIE_020870	pstS	ABC phosphate uptake transporter, substrate-binding protein	514	1	Periplasmic phosphate binding	PF01547, TIGR00975	9,40E-84			
	NVIE_020880	pstC	phosphate transporter subunit ; membrane component of ABC superfamily	332	6	Phosphate ABC transporter, pe	(PF00528), TIGR02138	3,80E-107			
	NVIE_020890	pstA	ABC phosphate uptake transporter,	305	6	hosphate transport system per	TIGR00974 (PF00528)	1,80E-92			
	NVIE_020900	pstB	ABC phosphat uptake transporter, ATP-binding protein	273	0	Phosphate transport system pe	PF00005, TIGR00972	5,30E-176			
	NVIE_020910	phoU1	Phosphate-specific transport system accessory protein PhoU homolog	219	0	PhoU	PF01895	6,00E-18			
	NVIE_020920	phoU2	Phosphate-specific transport system accessory protein PhoU homolog	363	0	PhoU	PF01895	3,80E-17			

3.A.1 ATP binding cassette (ABC) Superfamily

	NVIE_018300	phoU3	Phosphate-specific transport system accessory protein PhoU homolog	357	0	PhoU	PF01895	7,60E-18		
3.A.1.15. The Manganese/Zinc/Iron Chelate Uptake Transporter (MZT) Family	NVIE_014930	mntC	ABC uptake transporter, permease protein	297	7	ABC-3	PF00950	2,20E-67	Mg transport	Similarity searches suggest these transport systems belong to the Manganese/Zinc/Iron Chelate Uptake Transporter (MZT) Family (3.A.1.15). This family of transporter is involved in the uptake of Mn <sup>2+</sup> , Zn <sup>2+</sup> , Fe <sup>2+</sup> and, to a lower extent, Cu <sup>2+</sup> .
	NVIE_014940	mntB	ABC uptake transporter, ATP-binding protein	243	0	ABC transporter-like	PF00005	4,40E-21	Mg transport	
	NVIE_014950	mntA	ABC uptake transporter, substrate-binding protein	340	1	ABC transporter metal-binding	PF01297	2,60E-78	Mg transport	
	NVIE_021030		Probable Zinc uptake transporter, permease protein	286	8	ABC-3	PF00950	3,40E-66	Zinc transport	
	NVIE_021020		Probable Zinc uptake transporter, ATP-binding protein	243	0	ABC transporter-like	PF00005	5,00E-23	Zinc transport	
3.A.1.17. (TauT)The Taurine Uptake Transporter; 3.A.1.16 (NIT) The Nitrate/Nitrite/Cyanate Uptake Transporter	NVIE_024150		ABC uptake transporter, substrate-binding protein	364	1	NMT1	PF09084	6,80E-16		Similarity searches suggest these two transport systems belong either to the Nitrate/Nitrite/Cyanate Uptake Transporter (NIT) Family (3.A.1.16) or to the Taurine Uptake Transporter (TauT) Family (3.A.1.17).
	NVIE_024160		ABC uptake transporter, ATP-binding protein	284	0	ABC transporter-like	PF00005	9,90E-21		
	NVIE_024170		ABC uptake transporter, permease protein fragment	277	8	Binding-protein-dependent tra	PF00528	1,40E-15		
	NVIE_028050		ABC uptake transporter, substrate-binding protein	351	1	NMT1	PF09084	1,80E-13		
	NVIE_028060		ABC uptake transporter, permease	297	6	Binding-protein-dependent tra	PF00528	8,30E-17		
3.A.1.105. The Drug Exporter-1 (DrugE1) Family	NVIE_025900		ABC uptake transporter, ATP-binding	262	0	ABC transporter-like	PF00005	5,40E-21		
	NVIE_006450		ABC efflux transporter, permease protein	254	6	ABC-2 type transporter	PF01061	3,40E-16		
	NVIE_006460		ABC efflux transporter, ATP-binding protein	303	0	ABC transporter-like	PF00005	6,40E-16	3.6.3.25 EC number: Sulfate-transporting ATPase	
	NVIE_007140		ABC superfamily ATP binding cassette transporter membrane protein, Drug Exporter-1 (DrugE1) Family	274	6	ABC-2 type transporter	PF01061	4,60E-31	no synteny	
	NVIE_007150	drfA	ABC efflux transporter, ATP-binding protein, Drug Exporter-1 (DrugE1) Family	334	0	Daunorubicin resistance ABC tr	TIGR01188	6,90E-131	no synteny	
	NVIE_019690		ABC efflux transporter, permease protein	265	6	ABC-2 type transporter	PF01061	7,30E-38	no synteny	
	NVIE_019700		binding protein, Drug Exporter-1 (DrugE1) Family	386	0	ABC transporter-like	PF00005	8,40E-20	no synteny	
	NVIE_024680		ABC efflux transporter, permease protein	255	6	ABC-2 type transporter	PF01061	5,00E-22	3.A.1.102 The Lipooligosaccharide Ex	
	NVIE_024690		ABC efflux transporter, ATP-binding protein	326	0	ABC transporter-like	PF00005	1,20E-18		
	NVIE_025080		ABC efflux transporter, permease protein, Drug Exporter-1 (DrugE1) Family	259	6	ABC-2 type transporter	PF01061	5,50E-38		
3.A.1.122. The Macrolide Exporter (MacB) Family	NVIE_025090		ABC efflux transporter, ATP-binding protein, Drug Exporter-1 (DrugE1) Family	318	0	Daunorubicin resistance ABC tr	TIGR01188	7,20E-144		Similarity searches suggest this transport system belongs to the Drug Exporter-1 (DrugE1) Family 3.A.1.105 which mainly includes drug/antibiotic efflux systems.
	NVIE_027050		ABC efflux transporter, FtsX-domain permease protein	428	4	Protein of unknown function DU	PF02687	2,50E-30		
	NVIE_027030		ABC efflux transporter, ATP-binding protein	256	0	ABC transporter-like	PF00005	2,30E-25		
	NVIE_028560		ABC efflux transporter, FtsX-domain permease protein	416	4	Protein of unknown function DU	PF02687	3,30E-30		
	NVIE_028580		ABC efflux transporter, ATP-binding protein	247	0	ABC transporter-like	PF00005	1,30E-24		

ABC Transporter Components	NVIE_014380		ABC uptake transporter, putative heme-binding protein	304	0	Periplasmic binding protein	PF01497	9,30E-30		Molecular Function: Iron ion transmembrane transporter activity (GO:0005381), Biological Process: high-affinity iron ion transport (GO:0006827)
3.A.3. (P-ATPase)	NVIE_008380	copA1	Copper-exporting P-type ATPase	817	7	ATPase, P-type, ATPase-associated ATPase, P-type, heavy metal transport ATPase, P type, cation/copper	PF00122 TIGR01525 TIGR01511	3,20E-53 2,90E-230 5,60E-209		Similarity searches suggest this protein belong to the Transporter cluster 3.A.3.5. Proteins within this cluster are involved in the uptake/efflux of Cu <sup>2+</sup> , Cu <sup>+</sup> , Ag <sup>+</sup> , Cd <sup>2+</sup> , Fe <sup>2+</sup> , Fe <sup>3+</sup> , Pb <sup>2+</sup> , Au <sup>2+</sup> .
	NVIE_012900	copA2	Copper-exporting P-type ATPase	720	8	ATPase, P-type, ATPase-associated ATPase, P-type, heavy metal transport ATPase, P type, cation/copper	PF00122 TIGR01525 TIGR01511	3,70E-57 8,40E-240 5,70E-228		
	NVIE_027160	kdpA	potassium translocating ATPase, subunit	544	10	ATPase, K+ transporting, A subunit	PF03814	3,20E-166		
	NVIE_027150	kdpB	potassium translocating ATPase, subunit	718	7	ATPase, P-type, ATPase-associated	PF00122	3,80E-36		
	NVIE_027140	kdpC	potassium translocating ATPase, subunit	158	1	Potassium transporting ATPase	PF02669	6,70E-18		
3.A.4. (ArsAB)	NVIE_023830	arsA	putative arsenical pump-driving ATPase ArsA	391	0	ArsA_ATPase	PF02374	2,90E-67		The membrane component (ArsB) of the ArsAB arsenical pump possesses the pfam domain of the citrate transporters of the 2.A.11. Citrate-Mg <sup>2+</sup> :H <sup>+</sup> (CITM) Citrate-Ca <sup>2+</sup> :H <sup>+</sup> (CITH) Symporter (CITMHS) family.
	NVIE_026090	arsB	putative arsenical pump membrane protein	473	13	Divalent ion symporter	PF03600	2,30E-36		
	NVIE_015840	arsB	putative arsenical pump membrane protein	480	12	Divalent ion symporter	PF03600	1,70E-53		
3.A.5. General Secretory Pathway (Sec) Family	NVIE_013880	SecY	protein translocase subunit SecY	477	10	SecY/SEC61-alpha family (IPR002208)	PF00344	2,60E-82		
	NV_0158	SecB	protein translocase subunit SecB	56	1	Sec61_beta	PF03911	6,00E-13		
	NVIE_029990	SecE	protein translocase SecE subunit	63	1	Protein translocase SEC61 complex, gamma subunit	IPR008158	4,40E-07		
Signal recognition particle	NVIE_006970	srp19	signal recognition particle 19 kDa protein	106	0	SRP19	PF01922	3,00E-17		
	NVIE_016130	srp54	signal recognition particle subunit 54 kDa protein	464	0	Signal recognition particle, SRP	PF02881 PF00448 PF02978	1,20E-14 8,20E-70 3,00E-26		
9.A.58. The Sweet: PO-loop; Saliva; MTN3 (Sweet) Family	NVIE_030100	ftsY	signal recognition particle receptor FtsY	521	0	Signal recognition particle, SRP	PF00448	9,80E-69		
	NVIE_028360		conserved membrane protein of unknown function containing PO-loop domain	123	3	PO-loop	PF04193	7,60E-10		
9.B.20. Putative Mg <sup>2+</sup> Transporter-C (MgtC) Family	NVIE_026040		putative magnesium transporter-C family protein	170	4	MgtC/SapB transporter	PF02308	7,30E-28		The transport function of proteins of the MgtC family has not yet been established. Experimental work with Salmonella typhimurium and Mycobacterium tuberculosis suggests a function in Mg <sup>2+</sup> active transport.
9.B.27. The DedA or YdjX-Z (DedA) Family	NVIE_003220		DedA family protein	226	4	SNARE associated Golgi protein	PF09335	9,30E-16		Protein of the DedA family might be involved in the transport of selenite in bacteria and some fungal homologues might be involved in oxalate efflux. Protein of this family are also related to the SNARE-associated Golgi proteins. The three genes in N. gargensis are only distantly related to each other (id <30%) and only the
	NVIE_019500		DedA family protein	172	4	SNARE associated Golgi protein	PF09335	1,10E-17		
	NVIE_030120		DedA family protein	227	5	SNARE associated Golgi protein	PF09335	1,60E-20		
9.B.45. The Arg/Asp/Asp (RDD) Family	NVIE_004160		RDD family protein	193	2	RDD	PF06271	2,00E-16		The transport function and putative ligands of the RDD family has not yet been established.
	NVIE_011420		RDD family protein	171	3	RDD	PF06271	1,20E-20		
9.B.62. The Copper Resistance (CopD) Family	NVIE_014300		Copper resistance protein CopC/CopI	679	10	Copper resistance protein CopC Copper resistance protein CopI	PF04234 PF05425	4,50E-18 3,20E-18		This protein contain both the CopC and CopD domains of Copper resistance proteins as well as an SMP-30/Gluconolactonase/LRE-like domain in the long (522aa) extracellular C-terminal region. The mechanism of copper resistance is not known.
	NVIE_014310		Copper resistance protein CopC/CopI	988	9	Copper resistance protein CopC Copper resistance protein CopI	PF04234 PF05425	3,60E-23 2,30E-10		
	NVIE_013130		Copper resistance protein CopD	165	4	Copper resistance protein CopI	PF05425	1,40E-14		
9.B.69. Putative Cobalt Transporter (CbtA) Family	NVIE_011340	cbtA	putative cobalt transporter family protein, subunit CbtA	243	6	Probable cobalt transporter subunit	PF09490	1,60E-19		Transporters of the CbtA family might be involved in the uptake of Co <sup>2+</sup> ions with the CbtB subunit having the putative role Co <sup>2+</sup>

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Transporter (CbtAB) Family	NVIE_011350	cbtB	putative cobalt transporter family protein, subunit CbtB	81	1	Cobalt transporter subunit CbtB	PF09489	7,40E-06		binding protein. The function of CbtAB in the Co <sup>2+</sup> uptake has yet to be confirmed.
9.B.71. Camphor Resistance (CrcB) Family	NVIE_010700	crcB	camphor resistance family protein	129	4	Camphor resistance CrcB protein	PF02537	7,80E-23		The CrcB protein of E. coli confer resistance to camphor and it shows similarities on a partial overlap with the lysophospholipid uptake system LpIT of E. coli.
5.A.1 The Disulfide Bond Oxidoreductase D (DsbD) Family	NVIE_014160		Disulfide bond oxidoreductase D family protein	458	7	Cytochrome c assembly protein	PF02683	1,60E-52		Proteins of the DsbD family include thiol-disulfide exchange proteins, cytochrome c-type biogenesis proteins, methylamine utilization proteins, possible Hg <sup>2+</sup> transporters and copper
	NVIE_022760	ccdA	Disulfide bond oxidoreductase D family protein	269	6	Cytochrome c assembly protein	PF02683	4,10E-36		
8.A.5. Voltage-gated K <sup>+</sup> Channel β-subunit (Kvβ) Family	NVIE_029640		Voltage-gated potassium channel β subunit family protein	329	0	Aldo/keto reductase	PF00248	5,80E-09		voltage-gated K <sup>+</sup> channels of the VIC superfamily (1.A.1). These proteins are regulators of the voltage-gated K <sup>+</sup> channels. N. gargensis encodes one transporter of the VIC superfamily.
8.A.21 The Stomatin/Podocin/Band 7/Nephrin.2/SPFH (Stomatin) Family	NVIE_014050		stomatin-like protein	318	0	Stomatin	PR00721	6,90E-29		In prokaryotes, proteins of the stomatin family are often encoded in bicistronic operons that encodes a stomatin homologue and an integral membrane protease. It is thought that the cleavage of the stomatin homologue by the protease lead to the opening of an ion channel.
	NVIE_029810		stomatin-like protein, putative protein	322	2	Stomatin	PR00721	1,60E-59		