

A listing of NCBI GI numbers for all K<sup>+</sup>-channel amino acid sequences found in 270 prokaryotic genomes<sup>1,2</sup>.

Kingdom; Phylum; Class; Order; Family <sup>a</sup>	Total	2TM					6TM			4TM	
		K <sup>+</sup> channel core	Inward rectifier	Glutamate receptor	KTN/RCK domain	Unknown domain	voltage-gated	cNMP-gated	RCK domain	Core only	Core only
<b>Archaea</b>											
<b>Crenarchaeota</b>											
Thermoprotei											
<b>Desulfurococcales</b>											
<u>Desulfurococcaceae</u>											
<i>Aeropyrum pernix</i> K1	1					14601099(295)					
<b>Sulfolobales</b>											
<u>Sulfolobaceae</u>											
<i>Sulfolobus solfataricus</i> P2	1				15898555(336)						
<i>Sulfolobus tokodaii</i> str. 7	1				15922785(336)						
<b>Thermoproteales</b>											
<u>Thermoproteaceae</u>											
<i>Pyrobaculum aerophilum</i> str. IM2	0										
<b>Euryarchaeota</b>											
Archaeoglobi											
<b>Archaeoglobales</b>											
<u>Archaeoglobaceae</u>											
<i>Archaeoglobus fulgidus</i> DSM 4304	2	11498322(141)			11499263(314)						
Halobacteria											
<b>Halobacteriales</b>											
<u>Halobacteriaceae</u>											
<i>Haloarcula marismortui</i> ATCC 43049	3				55379169(544) <sup>d</sup>			55379971(404)			
<i>Halobacterium</i> sp. NRC-1	3				15789819(545) <sup>d</sup>	15790663(584)		55376873(417)		15790750(411)	
Methanobacteria											
<b>Methanobacteriales</b>											
<u>Methanobacteriaceae</u>											
<i>Methanothermobacter thermautotrophicus</i> str. Delta H	2				15679517(336)			15678533(256)			
Methanococci											
<b>Methanococcales</b>											
<u>Methanocaldococcaceae</u>											
<i>Methanocaldococcus jannaschii</i> DSM 2661	3				15668310(333)			15668309(209)			
					15669547(343)						
<u>Methanococcaceae</u>											
<i>Methanococcus maripaludis</i> S2	1				45357590(335)						
Methanopyri											
<b>Methanopyrales</b>											
<u>Methanopyraceae</u>											
<i>Methanopyrus kandleri</i> AV19	1				20094044(375)						
Methanosarcina											
<b>Methanosarcinales</b>											
<u>Methanosarcinaceae</u>											
<i>Methanococcoides burtonii</i> DSM 6242 <sup>*</sup>	3	41718792(115) <sup>b</sup>			46142369(334)			53731195(292)			
<i>Methanosarcina acetivorans</i> C2A	5	20090386(119)			20091279(347)			20090882(279)			
		20091059(136)									
		20090408(140)									
<i>Methanosarcina barkeri</i> str. fusaro <sup>*</sup>	2	48838131(128)			48837563(347)						
<i>Methanosarcina mazei</i> Go1	2	21228960(140)						21229291(279)			
Thermococci											
<b>Thermococcales</b>											
<u>Thermococcaceae</u>											
<i>Pyrococcus abyssi</i> GE5	1				14520711(481)						
<i>Pyrococcus furiosus</i> DSM 3638	1				18978131(481)						
<i>Pyrococcus horikoshii</i> OT3	1				14591442(481)						

Kingdom; Phylum; Class; Order; Family <sup>a</sup>	Total	2TM				6TM			4TM	
		K <sup>+</sup> channel core	Inward rectifier	Glutamate receptor	KTN/RCK domain	Unknown domain	voltage-gated	cNMP-gated	RCK domain	Core only
<b>Archaea</b>										
<b>Euryarchaeota</b> (continued)										
Thermoplasmata										
<b>Thermoplasmatales</b>										
<u>Ferroplasmaceae</u>										
<i>Ferroplasma acidarmanus</i> *	2			48852989(318)						
				48853021(329)						
<u>Picrophilaceae</u>										
<i>Picrophilus torridus</i> DSM 9790	1			48477217(322)						
<u>Thermoplasmataceae</u>										
<i>Thermoplasma acidophilum</i> DSM 1728	1							16082402(341)		
<i>Thermoplasma volcanium</i> GSS1	2			13541819(348)				13540928(342)		
<b>Nanoarchaeota</b>										
<i>Nanoarchaeum equitans</i> Kin4-M	0									
<b>Bacteria</b>										
<b>Actinobacteria</b>										
Actinobacteria										
<b>Actinomycetales</b>										
<u>Corynebacteriaceae</u>										
<i>Corynebacterium diphtheriae</i> NCTC 13129	1			38233330(362)						
<i>Corynebacterium efficiens</i> YS-314	1			25027348(353)						
<i>Corynebacterium glutamicum</i> ATCC 13032	1			19552003(353) <sup>d</sup>						
<u>Cellulomonadaceae</u>										
<i>Tropheryma whipplei</i> TW08/27	0									
<i>Tropheryma whipplei</i> str. Twist	0									
<u>Kineosporiaceae</u>										
<i>Kineococcus radiotolerans</i> SRS30216 *	1			53768531(335) <sup>b</sup>						
<u>Microbacteriaceae</u>										
<i>Leifsonia xyli</i> subsp. <i>Xyli</i> str. CTCB07	0									
<i>Mycobacterium avium</i> subsp. <i>Paratuberculosis</i> str. K10	2			41409397(666)						
				41408577(581) <sup>e</sup>						
<i>Mycobacterium bovis</i> AF2122/97	1			31794377(355)						
<i>Mycobacterium leprae</i> TN	0									
<i>Mycobacterium tuberculosis</i> CDC1551	1			15842786(355)						
<i>Mycobacterium tuberculosis</i> H37Rv	1			15610336(355)						
<u>Nocardiaceae</u>										
<i>Nocardia farcinica</i> IFM 10152	3			54026509(353)			54022815(264)			54026973(174)
<u>Nocardiopsaceae</u>										
<i>Thermobifida fusca</i> *	0									
<u>Propionibacteriaceae</u>										
<i>Propionibacterium acnes</i> KPA171202	1			50842645(364)						
<u>Streptomycetaceae</u>										
<i>Streptomyces avermitilis</i> MA-4680	3			29830910(344)			29832342(275)			29830302(215)
<i>Streptomyces coelicolor</i> A3(2)	5	21225921(160)		21222236(365)			21225475(288)			21224301(191)
										21224644(207)
Unclassified (Actinobacteria)										
<i>Symbiobacterium thermophilum</i> IAM 14863	1								51892846(179)	
<b>Bifidobacteriales</b>										
<u>Bifidobacteriaceae</u>										
<i>Bifidobacterium longum</i> DJO10A *	1						46190713(255)			
<i>Bifidobacterium longum</i> NCC2705	1						23465246(241)			
<b>Rubrobacteriales</b>										
<u>Rubrobacteraceae</u>										
<i>Rubrobacter xylanophilus</i> DSM 9941 *	1						46106887(269)			

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		K <sup>+</sup> channel core	Inward rectifier	Glutamate receptor	KTN/RCK domain	Unknown domain	voltage-gated	cNMP-gated	RCK domain	Core only	Core only
<b>Bacteria</b> (continued)											
<b>Aquificae</b>											
Aquificae											
<b>Aquificales</b>											
<u>Aquificaceae</u>											
<i>Aquifex aeolicus</i> VF5	2				15605833(368)				15606902(455) <sup>f</sup>		
<b>Bacteroidetes</b>											
Bacteroides											
<b>Bacteroidales</b>											
<u>Bacteroidaceae</u>											
<i>Bacteroides fragilis</i> YCH46	1						53714851(299)				
<i>Bacteroides thetaiotaomicron</i> VPI-5482	1						29349894(292)				
<u>Porphyromonadaceae</u>											
<i>Porphyromonas gingivalis</i> W83	2						34541257(240)				34541624(303)
Sphingobacteria											
<b>Sphingobacteriales</b>											
<u>Flexibacteraceae</u>											
<i>Cytophaga hutchinsonii</i> str. ATCC 33406 <sup>*</sup>	1										48854478(277)
<b>Chlamydiae</b>											
Chlamydiae											
<b>Chlamydiales</b>											
<u>Chlamydiaceae</u>											
<i>Chlamydia muridarum</i>	0										
<i>Chlamydia trachomatis</i> D/UW-3/CX	0										
<i>Chlamydomphila caviae</i> GPIC	0										
<i>Chlamydomphila pneumoniae</i> AR39	0										
<i>Chlamydomphila pneumoniae</i> CWL029	0										
<i>Chlamydomphila pneumoniae</i> J138	0										
<i>Chlamydomphila pneumoniae</i> TW-183	0										
<u>Parachlamydiaceae</u>											
<i>Parachlamydia</i> sp. UWE25	0										
<b>Chlorobi</b>											
Chlorobia											
<b>Chlorobiales</b>											
<u>Chlorobiaceae</u>											
<i>Chlorobium tepidum</i> TLS	1										21672962(343)
<b>Chloroflexi</b>											
Chloroflexi											
<b>Chloroflexales</b>											
<u>Chloroflexaceae</u>											
<i>Chloroflexus aurantiacus</i> <sup>*</sup>	1										53796277(242)
<b>Cyanobacteria</b>											
<b>Chroococcales</b>											
<i>Crocospaera watsonii</i> WH 8501 <sup>*</sup>	6		46117626(210)	46119173(368)	53736031(355)			45526586(261)		46119130(217)	46119129(222)
<i>Gloeobacter violaceus</i> PCC 7421	2				37520502(346)						
<i>Synechococcus elongatus</i> PCC 7942 <sup>*</sup>	5	46129756(109)			37523979(677) <sup>f</sup>						
<i>Synechococcus</i> sp. WH 8102	3			33865301(356)	53762840(341)			45513140(277)			
<i>Synechocystis</i> sp. PCC 6803	5			16330443(397)	53763071(384)			53763085(231)			
<i>Thermosynechococcus elongatus</i> BP-1	2				16329750(365)			33864687(274)			
<i>Thermosynechococcus elongatus</i> BP-1	2				16332244(670) <sup>f</sup>						
<i>Thermosynechococcus elongatus</i> BP-1	2				22298921(349)				22299998(452)		

Kingdom; Phylum; Class; Order; Family <sup>a</sup>	Total	2TM				6TM			4TM	
		K <sup>+</sup> channel core	Inward rectifier	Glutamate receptor	KTN/RCK domain	Unknown domain	voltage-gated	cNMP-gated	RCK domain	Core only
<b>Cyanobacteria</b> (continued)										
<b>Nostocales</b>										
<u>Nostocaceae</u>										
<i>Anabaena variabilis</i> ATCC 29413 *	4		53764302(303)		53763731(338)		45506627(263)			
<i>Nostoc punctiforme</i> PCC 73102 *	4		23126456(307)		53763390(683) <sup>e</sup>		23125946(263)			
<i>Nostoc</i> sp. PCC 7120	3		17228449(303)		23127810(687) <sup>e</sup>		17232125(263)			
17228574(338)										
<b>Oscillatoriales</b>										
<i>Trichodesmium erythraeum</i> IMS101 *	4		48893892(299)	48895668(360)			48895851(303)	48892039(454)		
<b>Prochlorales</b>										
<u>Prochlorococcaceae</u>										
<i>Prochlorococcus marinus</i> str. MIT 9313	5	33862649(181)		33862788(359)	33863599(359)		33862490(262)			
33863295(263)										
<i>Prochlorococcus marinus</i> subsp. <i>marinus</i> str. CCMP1375	2				33240677(239)		33240976(255)			
<i>Prochlorococcus marinus</i> subsp. <i>pastoris</i> str. CCMP1986	1				33861261(351)					
<b>Deinococcus-Thermus</b>										
<b>Deinococci</b>										
<b>Deinococcales</b>										
<u>Deinococcaceae</u>										
<i>Deinococcus radiodurans</i> R1	3				15807327(320)	15806910(338)	15805856(280)			
<b>Thermales</b>										
<u>Thermaceae</u>										
<i>Thermus thermophilus</i> HB27	0									
<i>Thermus thermophilus</i> HB8	0									
<b>Firmicutes</b>										
<b>Bacilli</b>										
<b>Bacillales</b>										
<u>Alicyclobacillaceae</u>										
<i>Pasteuria nishizawae</i> str. North American *	0									
<u>Bacillaceae</u>										
<i>Bacillus anthracis</i> str. 'Ames Ancestor'	3	47525805(134)			47530433(331)					
47525956(114)										
<i>Bacillus anthracis</i> str. A2012	4	21398481(134)			21397377(331)					
21397876(146)										
21398638(114)										
<i>Bacillus anthracis</i> str. Ames	3	30260693(134)			30264937(331)					
30260826(114)										
<i>Bacillus anthracis</i> str. Sterne	4	49183531(134)			49187755(331)					
49188231(146)										
49183667(114)										
<i>Bacillus cereus</i> ATCC 10987	3	42779670(134)			42784081(331)					
42779821(114)										
<i>Bacillus cereus</i> ATCC 14579	3	30018722(134)			30023424(334)					
30018851(114)										
<i>Bacillus cereus</i> G9241 *	4	47567092(134)			47570514(317)					
47568805(114)					47566930(331)					
<i>Bacillus cereus</i> ZK	5	52144778(134)			52140173(334)					
52144637(114)					52140628(331)					
52144635(128)										
<i>Bacillus halodurans</i> C-125	3	15613510(141)			15615902(338)					
15614535(102)										
<i>Bacillus licheniformis</i> ATCC 14580	1				52787007(327)					

Kingdom; Phylum; Class; Order; Family <sup>a</sup>	2TM					6TM			4TM		
	Total	K <sup>+</sup> channel core	Inward rectifier	Glutamate receptor	KTN/RCK domain	Unknown domain	voltage-gated	cNMP-gated	RCK domain	Core only	Core only
<b>Bacteria</b>											
<b>Firmicutes</b>											
Bacilli											
Bacillales											
Bacillaceae (continued)											
<i>Bacillus subtilis</i> subsp. <i>subtilis</i> str. 168	2				50812283(438)	16077689(341)					
<i>Bacillus thuringiensis</i> serovar konkukian str. 97-27	4	49480137(134)			49478984(334)						
		49476866(114)			49478804(331)						
<i>Exiguobacterium</i> sp. 255-15 <sup>*</sup>	3	46113983(115)			45532509(317)						
		45532263(108)									
<i>Geobacillus kaustophilus</i> HTA426	2	56419011(134)			56421457 (529)						
<i>Oceanobacillus iheyensis</i> HTE831	3	23098357(150)			23099789(332)						
					23100733(340)						
Listeriaceae											
<i>Listeria innocua</i> Clip11262	1						16801231(247)				
<i>Listeria monocytogenes</i> EGD-e	1						16804098(247)				
<i>Listeria monocytogenes</i> str. 1/2a F6854 <sup>*</sup>	1						47097473(234)				
<i>Listeria monocytogenes</i> str. 4b F2365	1						46908294(234)				
<i>Listeria monocytogenes</i> str. 4b H7858 <sup>*</sup>	1						47094058(234)				
Staphylococcaceae											
<i>Staphylococcus aureus</i> subsp. <i>aureus</i> MRSA252	0										
<i>Staphylococcus aureus</i> subsp. <i>aureus</i> MSSA476	0										
<i>Staphylococcus aureus</i> subsp. <i>aureus</i> MW2	0										
<i>Staphylococcus aureus</i> subsp. <i>aureus</i> Mu50	0										
<i>Staphylococcus aureus</i> subsp. <i>aureus</i> N315	0										
<i>Staphylococcus epidermidis</i> ATCC 12228	0										
Lactobacillales											
Enterococcaceae											
<i>Enterococcus faecalis</i> V583	2	29377477(127)					29377322(242)				
<i>Enterococcus faecium</i> <sup>*</sup>	0										
Lactobacillaceae											
<i>Lactobacillus gasseri</i> <sup>*</sup>	1						52857801(358)				
<i>Lactobacillus johnsonii</i> NCC 533	2						42519024(248)				
							42518512(278)				
<i>Lactobacillus plantarum</i> WCFS1	1						28378402(258)				
<i>Pediococcus pentosaceus</i> ATCC 25745 <sup>*</sup>	1						48870188(233)				
Leuconostocaceae											
<i>Leuconostoc mesenteroides</i> subsp. <i>mesenteroides</i> ATCC 8293 <sup>*</sup>	0										
<i>Oenococcus oeni</i> PSU-1 <sup>*</sup>	0										
Streptococcaceae											
<i>Lactococcus lactis</i> subsp. <i>lactis</i> I11403	1	15672896(140)									
<i>Streptococcus agalactiae</i> 2603V/R	0										
<i>Streptococcus agalactiae</i> NEM316	0										
<i>Streptococcus mutans</i> UA159	1						24380209(234)				
<i>Streptococcus pneumoniae</i> R6	0										
<i>Streptococcus pneumoniae</i> TIGR4	0										
<i>Streptococcus pyogenes</i> M1 GAS	0										
<i>Streptococcus pyogenes</i> MGAS10394	0										
<i>Streptococcus pyogenes</i> MGAS315	0										
<i>Streptococcus pyogenes</i> MGAS8232	0										
<i>Streptococcus pyogenes</i> SSI-1	0										
<i>Streptococcus suis</i> 89/1591 <sup>*</sup>	1						50590667(248)				
<i>Streptococcus thermophilus</i> CNRZ1066	0										
<i>Streptococcus thermophilus</i> LMG 18311	0										

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<b>Firmicutes</b> (continued)										
Clostridia										
Clostridiales										
Clostridiaceae										
<i>Clostridium acetobutylicum</i> ATCC 824	1					15894597(256)				
<i>Clostridium perfringens</i> str. 13	0									
<i>Clostridium tetani</i> E88	0									
<i>Clostridium thermocellum</i> ATCC 27405 *	0									
Peptococcaceae										
<i>Desulfitobacterium hafniense</i> DCB-2 *	2			53682275(239)		53684542(640)				
Thermoanaerobacteriales										
Thermoanaerobacteriaceae										
<i>Moorella thermoacetica</i> ATCC 39073 *	0									
<i>Thermoanaerobacter tengcongensis</i> MB4	0									
Mollicutes										
Acholeplasmatales										
Acholeplasmataceae										
<i>Onion yellows phytoplasma</i> OY-M	0									
Entomoplasmatales										
Entomoplasmataceae										
<i>Mesoplasma florum</i> L1	0									
Mycoplasmatales										
Mycoplasmataceae										
<i>Mycoplasma gallisepticum</i> R	1					31544745(410)				
<i>Mycoplasma genitalium</i> G-37	0									
<i>Mycoplasma hyopneumoniae</i> 232	0									
<i>Mycoplasma mobile</i> 163K	1					47458968(357)				
<i>Mycoplasma mycoides</i> subsp. <i>Mycoides</i> SC str. PG1	0									
<i>Mycoplasma penetrans</i> HF-2	0									
<i>Mycoplasma pneumoniae</i> M129	0									
<i>Mycoplasma pulmonis</i> UAB CTIP	1					15828892(344)				
<i>Ureaplasma parvum</i> serovar 3 str. ATCC 700970	1								13358138(428)	
Fusobacteria										
Fusobacteriales										
Fusobacteriaceae										
<i>Fusobacterium nucleatum</i> subsp. <i>Nucleatum</i> ATCC 25586	0									
<i>Fusobacterium nucleatum</i> subsp. <i>Vincentii</i> ATCC 49256 *	0									
Planctomycetes										
Planctomycetacia										
Planctomycetales										
Planctomycetaceae										
<i>Rhodopirellula baltica</i> SH 1	3			32475291(413)		32477506(317)			32475943(234)	
Proteobacteria										
Alphaproteobacteria										
Caulobacteriales										
Caulobacteraceae										
<i>Caulobacter crescentus</i> CB15	1			16125863(347)						
Rhizobiales										
Bartonellaceae										
<i>Bartonella henselae</i> str. Houston-1	0									
<i>Bartonella uintana</i> str. Toulouse	0									

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<b>Proteobacteria</b>										
Alphaproteobacteria										
<b>Rhizobiales</b> (continued)										
<u>Bradyrhizobiaceae</u>										
<i>Bradyrhizobium japonicum</i> USDA 110	3	27378576(147)						27382967(369)		
								27380860(453)		
<i>Rhodopseudomonas palustris</i> CGA009	3			39933200(546) <sup>d</sup>		39935888(258)		39937293(412)		
<u>Brucellaceae</u>										
<i>Brucella melitensis</i> 16M	0									
<i>Brucella suis</i> 1330	0									
<u>Phyllobacteriaceae</u>										
<i>Mesorhizobium loti</i> MAFF303099	3	13475539(143)				13471010(267)		13472825(355)		
<i>Mesorhizobium</i> sp. BNC1 *	1					45915678(267)				
<u>Rhizobiaceae</u>										
<i>Agrobacterium tumefaciens</i> str. C58	0									
<i>Sinorhizobium meliloti</i> 1021	3	16262824(144)				16264095(265)				
		16263703(146)								
<b>Rhodobacterales</b>										
<u>Rhodobacteraceae</u>										
<i>Rhodobacter sphaeroides</i> 2.4.1 *	0									
<i>Silicibacter</i> sp. TM1040 *	1	52012278(147)								
<b>Rhodospirillales</b>										
<u>Rhodospirillaceae</u>										
<i>Magnetospirillum magnetotacticum</i> MS-1 *	4		46201166(291)			46201458(332)		46202428(389)		46204948(>152) <sup>b</sup>
<i>Rhodospirillum rubrum</i> *	0									
<b>Rickettsiales</b>										
<u>Anaplasmataceae</u>										
<i>Anaplasma marginale</i> str. St. Maries	0									
<i>Ehrlichia canis</i> str. Jake *	0									
<i>Ehrlichia ruminantium</i> str. Welgevonden *	0									
<u>Rickettsiaceae</u>										
<i>Rickettsia akari</i> str. Hartford *	0									
<i>Rickettsia conorii</i> str. Malish 7	0									
<i>Rickettsia prowazekii</i> str. Madrid E	0									
<i>Rickettsia rickettsii</i> *	0									
<i>Rickettsia sibirica</i> 246 *	0									
<i>Rickettsia typhi</i> str. Wilmington	0									
<i>Wolbachia endosymbiont</i> of <i>Drosophila melanogaster</i>	0									
<b>Sphingomonadales</b>										
<u>Sphingomonadaceae</u>										
<i>Novosphingobium aromaticivorans</i> DSM 12444 *	2					48850977(347)				
						48847764(366)				
Betaproteobacteria										
<b>Burkholderiales</b>										
<u>Alcaligenaceae</u>										
<i>Bordetella bronchiseptica</i> RB50	1							33599430(396)		
<i>Bordetella parapertussis</i> 12822	1							33595148(396)		
<i>Bordetella pertussis</i> Tohama I	1							33594472(396)		

Kingdom; Phylum; Class; Order; Family <sup>a</sup>	2TM					6TM			4TM		
	Total	K <sup>+</sup> channel core	Inward rectifier	Glutamate receptor	KTN/RCK domain	Unknown domain	voltage-gated	cNMP-gated	RCK domain	Core only	Core only
<b>Bacteria</b>											
<b>Proteobacteria</b>											
Betaproteobacteria											
<b>Burkholderiales</b> (continued)											
<u>Burkholderiaceae</u>											
<i>Burkholderia cepacia</i> R1808 *	2		46323671(299)		46322434(354)						
<i>Burkholderia cepacia</i> R18194 *	4	46316312(154)	46312337(292)		46312707(354)			46314962(391)			
<i>Burkholderia fungorum</i> LB400 *	2		48781501(323)							48788374(281)	
<i>Burkholderia mallei</i> ATCC 23344	1				53716895(326)						
<i>Burkholderia pseudomallei</i> K96243	2		53717995(333)		53721961(369)						
<i>Ralstonia eutropha</i> JMP134 *	3	45514351(146)					45517078(306)				
		45520045(158)									
<i>Ralstonia metallidurans</i> CH34 *	4	48772513(149)					48768627(307)			48769979(229)	
		48772095(105)									
<i>Ralstonia solanacearum</i> GMI1000	1		17545169(307)								
<u>Comamonadaceae</u>											
<i>Polaromonas</i> sp. JS666 *	1	54029593(139)									
Unclassified (Burkholderiales)											
<i>Rubrivivax gelatinosus</i> PM1 *	2	47573088(143)								47573277(235)	
<b>Hydrogenophilales</b>											
<u>Hydrogenophilaceae</u>											
<i>Thiobacillus denitrificans</i> ATCC 25259 *	0										
<b>Methylophilales</b>											
<u>Methylophilaceae</u>											
<i>Methylobacillus flagellatus</i> KT *	1				53759437(569) <sup>d</sup>						
<b>Neisseriales</b>											
<u>Neisseriaceae</u>											
<i>Chromobacterium violaceum</i> ATCC 12472	2		34496564(296)				34499017(289)				
<i>Neisseria meningitidis</i> MC58	0										
<i>Neisseria meningitidis</i> Z2491	0										
<b>Nitrosomonadales</b>											
<u>Nitrosomonadaceae</u>											
<i>Nitrosomonas europaea</i> ATCC 19718	0										
<b>Rhodocyclales</b>											
<u>Rhodocyclaceae</u>											
<i>Azoarcus</i> sp. EbN1	1				56478421(579) <sup>d</sup>						
<i>Dechloromonas aromatica</i> RCB *	2				41723381(352)						
					53729807(552) <sup>d</sup>						
Deltaproteobacteria											
<b>Bdellovibrionales</b>											
<u>Bdellovibrionaceae</u>											
<i>Bdellovibrio bacteriovorus</i> HD100	0										
<b>Desulfobacterales</b>											
<u>Desulfobulbaceae</u>											
<i>Desulfotalea psychrophila</i> LSv54	3	51246872(167)			51244176(567) <sup>d</sup>		51245114(264)				
<i>Desulfovibrio desulfuricans</i> G20 *	2				23474662(346)		23473800(272)				
<i>Desulfovibrio vulgaris</i> subsp. <i>vulgaris</i> str. Hildenborough	1				46580017(350)						
<b>Desulfuromonadales</b>											
<u>Geobacteraceae</u>											
<i>Geobacter metallireducens</i> GS-15 *	1				48845049(351)						
<i>Geobacter sulfurireducens</i> PCA	1				39995634(564) <sup>d</sup>						

Kingdom; Phylum; Class; Order; Family <sup>a</sup>	Total	2TM				6TM			4TM	
		K <sup>+</sup> channel core	Inward rectifier	Glutamate receptor	KTN/RCK domain	Unknown domain	voltage-gated	cNMP-gated	RCK domain	Core only
<b>Bacteria</b>										
<b>Proteobacteria</b> (continued)										
Epsilonproteobacteria										
<b>Campylobacterales</b>										
<u>Campylobacteraceae</u>										
<i>Campylobacter jejuni</i> subsp. <i>jejuni</i> NCTC 11168	0									
<u>Helicobacteraceae</u>										
<i>Helicobacter hepaticus</i> ATCC 51449	1				32266789(375)					
<i>Helicobacter pylori</i> 26695	1				15645117(378)					
<i>Helicobacter pylori</i> 199	1				15611509(378)					
<i>Wolinella succinogenes</i> DSM 1740	1				34556764(377)					
Gammaproteobacteria										
<b>Alteromonadales</b>										
<u>Alteromonadaceae</u>										
<i>Microbulbifer degradans</i> 2-40 *	2	48863056(102)				48861391(298)				
<u>Idiomarinaceae</u>										
<i>Idiomarina loihiensis</i> L2TR	0									
<u>Shewanellaceae</u>										
<i>Shewanella oneidensis</i> MR-1	2	24376318(131)				24375262(274)				
<b>Enterobacteriales</b>										
<u>Enterobacteriaceae</u>										
<i>Buchnera aphidicola</i> str. APS	0									
<i>Buchnera aphidicola</i> str. Bp	0									
<i>Buchnera aphidicola</i> str. Sg	0									
<i>Blochmannia floridanus</i> ( <i>Candidatus</i> )	0									
<i>Erwinia carotovora</i> subsp. <i>atroseptica</i> SCRI1043	0									
<i>Escherichia coli</i> CFT073	1							26247580(423)		
<i>Escherichia coli</i> K12	1							16129211(417)		
<i>Escherichia coli</i> O157:H7	1							15831004(417)		
<i>Escherichia coli</i> O157:H7 EDL933	1							15801476(417)		
<i>Photorhabdus luminescens</i> subsp. <i>laumondii</i> TTO1	0									
<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar Paratyphi A str. ATCC 9150	1					56413334 (278)				
<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar Typhi Ty2	1					29142089(278)				
<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar Typhi str. CT18	1					16760140(278)				
<i>Salmonella typhimurium</i> LT2	2				16767618(356)	16765085(278)				
<i>Shigella flexneri</i> 2a str. 2457T	1							30062771(417)		
<i>Shigella flexneri</i> 2a str. 301	1							56479865(417)		
<i>Wigglesworthia glossinidia</i> endosymbiont of <i>Glossina brevipalpis</i>	0									
<i>Yersinia pestis</i> CO92	1							16122880(391)		
<i>Yersinia pestis</i> KIM	1							22125147(391)		
<i>Yersinia pestis</i> biovar Mediaevalis str. 91001	1							45442259(391)		
<i>Yersinia pseudotuberculosis</i> IP 32953	1							51597249(391)		
<b>Legionellales</b>										
<u>Coxiellaceae</u>										
<i>Coxiella burnetii</i> RSA 493	0									
<u>Legionellaceae</u>										
<i>Legionella pneumophila</i> str. Lens	0									
<i>Legionella pneumophila</i> str. Paris	0									
<i>Legionella pneumophila</i> subsp. <i>pneumophila</i> str. Philadelphia 1	0									
<b>Methylococcales</b>										
<u>Methylococcaceae</u>										
<i>Methylococcus capsulatus</i> str. Bath	1								53804999(247)	

Kingdom; Phylum; Class; Order; Family <sup>a</sup>	Total	2TM				6TM			4TM	
		K <sup>+</sup> channel core	Inward rectifier	Glutamate receptor	KTN/RCK domain	Unknown domain	voltage-gated	cNMP-gated	RCK domain	Core only
<b>Bacteria</b>										
<b>Proteobacteria</b>										
Gammaproteobacteria (continued)										
Pasteurellales										
Pasteurellaceae										
<i>Actinobacillus pleuropneumoniae</i> serovar 1 str. 4074 <sup>*</sup>	0									
<i>Haemophilus ducreyi</i> 35000HP	0									
<i>Haemophilus influenzae</i> 86-028NP <sup>*</sup>	0									
<i>Haemophilus influenzae</i> R2846 <sup>*</sup>	0									
<i>Haemophilus influenzae</i> R2866 <sup>*</sup>	0									
<i>Haemophilus influenzae</i> Rd KW20	0									
<i>Haemophilus somnus</i> 129PT <sup>*</sup>	0									
<i>Haemophilus somnus</i> 2336 <sup>*</sup>	0									
<i>Mannheimia succiniciproducens</i> MBEL55E	0									
<i>Pasteurella multocida</i> Pm70	0									
Pseudomonadales										
Moraxellaceae										
<i>Acinetobacter</i> sp. ADP1	1					50085477(281)				
<i>Psychrobacter</i> sp. 273-4 <sup>*</sup>	2					46141646(276)				
						41689524(287)				
Pseudomonadaceae										
<i>Azotobacter vinelandi</i> <sup>*</sup>	3	23103946(149)				53610543(-281) <sup>b</sup>			53610407(220)	
<i>Pseudomonas aeruginosa</i> PA01	2	15595939(102)				15596693(283)				
<i>Pseudomonas aeruginosa</i> UCBPP-PA14 <sup>*</sup>	2					53727716(283)			53727304(214)	
<i>Pseudomonas fluorescens</i> PfO-1 <sup>*</sup>	1					48729526(274)				
<i>Pseudomonas putida</i> KT2440	2	26990011(141)				26990995(273)				
<i>Pseudomonas syringae</i> pv. <i>syringae</i> B728a <sup>*</sup>	1					46187362(-249) <sup>b</sup>				
<i>Pseudomonas syringae</i> pv. <i>tomato</i> str. DC3000	3	28868871(149)			28870939(341)	28870782(277)				
Vibrionales										
Vibrionaceae										
<i>Photobacterium profundum</i> SS9	4				54301734(341)	54308294(272)			54308754(203)	
						54307659(271)				
<i>Vibrio cholerae</i> O1 biovar <i>eltor</i> str. N16961	1					15600964(280)				
<i>Vibrio parahaemolyticus</i> RIMD 2210633	4				28897838(347)	28897195(272)			28901437(232)	
						28898897(285)				
<i>Vibrio vulnificus</i> CMCP6	4				27365504(346)	27363880(325)	27364075(250)			
						27366380(286)				
<i>Vibrio vulnificus</i> YJ016	5				37680454(346)	37678966(325)	37678762(250)		37678323(226)	
						37679357(286)				
Xanthomonadales										
Xanthomonadaceae										
<i>Xanthomonas axonopodis</i> pv. <i>citri</i> str. 306	2				21243733(384)		21244155(290)			
<i>Xanthomonas campestris</i> pv. <i>campestris</i> str. ATCC 33913	2				21232268(360)		21232712(290)			
<i>Xylella fastidiosa</i> 9a5c	1						15838027(297)			
<i>Xylella fastidiosa</i> Ann-1 <sup>*</sup>	1						52856624(289)			
<i>Xylella fastidiosa</i> Dixon <sup>*</sup>	1						53801245(289) <sup>b</sup>			
<i>Xylella fastidiosa</i> Temecula1	1						28198561(297)			
Unclassified (Proteobacteria)										
<i>Magnetococcus</i> sp. MC-1 <sup>*</sup>	3					48832141(399)		48833229(509) <sup>c</sup>		
						48832392(564) <sup>d</sup>				

Kingdom; Phylum; Class; Order; Family <sup>a</sup>	Total	2TM				6TM			4TM	
		K <sup>+</sup> channel core	Inward rectifier	Glutamate receptor	KTN/RCK domain	Unknown domain	voltage-gated	cNMP-gated	RCK domain	Core only
<b>Bacteria</b> (continued)										
<b>Spirochaetes</b>										
Spirochaetes										
<b>Spirochaetales</b>										
<u>Leptospiraceae</u>										
<i>Leptospira interrogans</i> serovar Copenhageni str. Fiocruz L1-130	0									
<i>Leptospira interrogans</i> serovar Lai str. 56601	0									
<u>Spirochaetaceae</u>										
<i>Borrelia burgdorferi</i> B31	0									
<i>Borrelia garinii</i> PB1	0									
<i>Treponema denticola</i> ATCC 35405	1				42527939(430)					
<i>Treponema pallidum</i> subsp. <i>pallidum</i> str. Nichols	0									
<b>Thermotogae</b>										
Thermotogae										
<b>Thermotogales</b>										
<u>Thermotogaceae</u>										
<i>Thermotoga maritima</i> MSB8	1				15643815(363)					

<sup>1</sup> Organisms that do not carry any annotated K<sup>+</sup>-channel gene are highlighted in gray.

<sup>2</sup> Channels that have altered K<sup>+</sup>-filter sequence (GYG) are highlighted in pink (also see Section 6.1).

\* Completed whole genome-shotgun sequences that are not yet assembled as of December 2004.

<sup>a</sup> The classification of the organisms is based on the NCBI Taxonomy database. Family names are underlined.

<sup>b</sup> The assigned ORF of these genes may not be correct. Assembly of the DNA sequences is not finished.

<sup>c</sup> KTN/RCK domain at both N- and C-termini.

<sup>d</sup> Tandem KTN/RCK repeat at C-terminus.

<sup>e</sup> Also has a voltage-sensing S4.