TableS:

manX gcc11 gcc12 gcc13 gcc14 gcc15			lass	Type of variation
gcc12 gcc13 gcc14	145 K027	PTS-Aga-EllA; PTS system, N-acetylgalactosamine-specific IIA component [EC.2.7.1] env hypothetical protein	ıv	Gene absent Point mutations
gcc14	190 55	hypothetical protein hypothetical protein		Gene absent Gene absent
	188 374	hypothetical protein hypothetical protein		Gene absent Gene absent
gcc16	108 45	hypothetical protein		Gene absent Gene absent
gcc17 gcc18	531	hypothetical protein hypothetical protein		Gene absent
phd doc	86 K191 124 K073	Toxin; death on curing protein		Gene absent Gene absent
gcc19 gcc110	109 133	hypothetical protein hypothetical protein		Gene absent Gene absent
lytG gcc111	469 176	hypothetical protein hypothetical protein		Gene absent Gene absent
gcc112	63 K077	putative transcriptional regulator		Gene absent
gcc113 Tn916	284	hypothetical protein hypothetical protein		Gene absent Gene absent
xerD gcc114	409 65	hypothetical protein hypothetical protein		Gene absent Gene absent
gcc115 gcc116	273 470	hypothetical protein hypothetical protein		Gene absent Gene absent
gcc117 gcc118	146 71	hypothetical protein hypothetical protein		Gene absent Gene absent
gcc119	131	hypothetical protein		Gene absent Gene absent
gcc120 gcc121	97	hypothetical protein hypothetical protein		Gene absent
gcc122 gcc123	248 98	hypothetical protein hypothetical protein		Gene absent Gene absent
gcc124 gcc125	105 102	hypothetical protein hypothetical protein		Gene absent Gene absent
gcc126	197	hypothetical protein		Gene absent Point mutations
mdf gcc127	1166 K037	hypothetical protein		Gene absent
gcc128	196 62	HTH-type transcriptional regulator Xre hypothetical protein		Gene absent Gene absent
gcc129 gcc130	201 151	hypothetical protein hypothetical protein		Gene absent Gene absent
gcc131 gcc132	111	hypothetical protein hypothetical protein		Gene absent Gene absent
gcc133	64	hypothetical protein		Gene absent
gcc134 gcc135	91 465	hypothetical protein hypothetical protein		Gene absent Gene absent
gcc136 gcc137	86 186	hypothetical protein hypothetical protein		Gene absent Gene absent
gcc138 gcc139	163 126	hypothetical protein		Gene absent Gene absent
gcc140	96	hypothetical protein hypothetical protein		Gene absent
gcc141 acpP	116 55 K020	hypothetical protein net Acyl carrier protein net	et	Gene absent Point mutations
gcc142	73	hypothetical protein		Truncated protein
gcc101	102	hypothetical protein		Truncated protein
gcc102 gcc103	113 687	hypothetical protein putative licABCH operon regulator		Gene absent Gene absent
gatB_1 gatC_1	93 K027 446 K027	PTS-Gat-EIIC; PTS system, galactitol-specific IIC component met	et/env et/env	Gene absent Gene absent
rhaD gatA	277 K016 155 K027	Rhamnulose-1-phosphate aldolase [EC:4.1.2.19] mei		Gene absent Gene absent
gatC 2	444 K027	PTS-Gat-EIIC; PTS system, galactitol-specific IIC component mel	et/env	Gene absent
gatB 2 soxS	95 K027 277	Regulatory protein	et/env	Gene absent Gene absent
yesO lacF	426 K020 297 K020			Gene absent Gene absent
araQ gcc104	278 K020 734 K074	ABC.MS.P1; multiple sugar transport system permease protein - L-arabinose transport system permease protein		Gene absent
galK	391 K008	Galactokinase [EC:2.7.1.6] met	et	Gene absent Gene absent
galT galE	383 K009 332 K017	UDP-glucose 4-epimerase [EC:5.1.3.2] mei	et	Gene absent Synonimous point mutations
galM csd2	334 K017		et	Gene absent Gene absent
cas4 cas2	224 K074 98 K099	CRISPR-associated exonuclease		Gene absent Gene absent
gcc105	70	hypothetical protein		Gene absent
gcc106 galK_2	385 317 K008	hypothetical protein mel	et	Truncated protein Gene absent
gcc107 ydfK	58 239 K071	hypothetical protein  Putative membrane protein		Gene absent Point mutations
phoB baeS	218 447	Phosphate regulon transcriptional regulatory protein Signal transduction histidine-protein kinase		Gene absent Gene absent
gcc108	176 1159	hypothetical protein		Gene absent
gcc109 gcc1010	341	IgA FC receptor hypothetical protein		Gene absent Gene absent
gcc1011 gcc1012	303 501 K069			Gene absent Gene absent
gcc1013 gcc1014	286 66	hypothetical protein hypothetical protein		Gene absent Gene absent
gcc1015 gcc1016	103 388	hypothetical protein hypothetical protein		Gene absent Point mutations
veiL	215	Regulatory protein		Point mutations
gcc1017 gcc1018	205 K070 252	27-O-demethylrifamycin SV methyltransferase		Synonimous point mutations Truncated protein
lacC	311 K009	Tagatose 6-phosphale kinase [EC:2.7.1.144] met	et	Truncated protein
mdtH	411 K081: 273 K037	MFS transporter, DHA1 family, multidrug resistance protein B		Point mutations
pncC gcc191	390	hypothetical protein	et	Point mutations Point mutations
xerC	235 76	Tyrosine recombinase hypothetical protein		Gene absent Gene absent
gcc192	75	HTH-type transcriptional regulator hypothetical protein		
gcc192 immR	122			Gene absent Gene absent
gcc192 immR gcc193 gcc194	122 96	hypothetical protein  Cd2+/7g2-ayropting ATPass - putative cadmium-transporting ATPass (EC:3.6.3.3.3.6.3.5)		Gene absent Gene absent
gcc192 immR gcc193 gcc194 ztnA cadC	122 96 710 K015 123 K219	Cd2+/Zn2+-exporting ATPase - putative cadmium-transporting ATPase [EC:3.6.3.3 3.6.3.5]  ArsR family transcriptional regulator, heavy-metals responsive transcriptional repressor - Cadmium resistance transcriptional regulatory protein		Gene absent Gene absent Gene absent Gene absent Gene absent
gcc192 immR gcc193 gcc194 ztnA cadC gcc195 gcc196	96 710 K015 123 K219 100 263	Cd2*2722+exporting ATPase - putative cadmium-transporting ATPase [EC.3.8.3.3.8.6.5] ARSR family transcriptional regulator, heavy-metals responsive transcriptional repressor - Cadmium resistance transcriptional regulatory protein hypothetical protein hypothetical protein hypothetical protein		Gene absent
gcc192 immR gcc193 gcc194 ztnA cadC gcc195	122 96 710 K015 123 K219 100	Cd2*2722+exporting ATPase - putative cadmium-transporting ATPase [EC3.8.3.3.3.8.3.5] ARRI family transcriptional regulator, heavy-metals responsive transcriptional repressor - Cadmium resistance transcriptional regulatory protein hypothetical protein hypothetic		Gene absent Gene absent Gene absent Gene absent Gene absent Gene absent
gcc192 immR gcc193 gcc194 ztnA cadC gcc195 gcc196 gcc197 gcc198 gcc198	122 96 710 K015: 123 K219 100 263 199 69 159 K176	Cd2*-27c2+-exporting ATPase - putathe cadmium-transporting ATPase [EC3.8.3.3.8.6.3.5]  Arst Earnly transcriptional regulator, heavy-metals responsive transcriptional repressor - Cadmium resistance transcriptional regulatory protein hypothetical protein	nv	Gene absent
gcc192 immR gcc193 gcc194 ztnA cadC gcc195 gcc196 gcc197 gcc198 copA gcc199 gcc199 gcc1910	122 96 710 K015: 123 K219 100 263 199 69 159 K176 130 76	Cd2+2-2r24-exporting ATPese - putative cadmium-transporting ATPese [EC.3.6.3.3.3.6.3.5]  ARRI family transcriptional regulator, heavy-metals responsive transcriptional repressor - Cadmium resistance transcriptional regulatory protein hypothetical protein hypothetical protein hypothetical protein Cut-exporting ATPese (EC.3.6.3.54) hypothetical protein hypothetical protein	ıv	Gene absent
gcc192 immR gcc193 gcc194 ztnA gcc196 gcc196 gcc197 gcc197 gcc198 copA gcc199 gcc1910 gcc19110 gcc19111	122 96 710 K015: 123 K219 100 263 199 69 159 K176: 130 76	Cd2*-2724-exporting ATP8ee - putative cadmism-transporting ATPsee [EC.3.6.3.3.3.6.3.5]  ARSI Sanis) transcriptional regulator, heavy-metals responsive transcriptional repressor - Cadmism resistance transcriptional regulatory protein hypothetical protein hypothe	nv	Gene absent
gcc192 ImmR gcc193 gcc194 ztnA cadC gcc196 gcc196 gcc196 gcc197 gcc196 gcc198 gcc199 gcc1910 gcc1910 gcc1911 gcc1912 gcc1913	122 96 710 K015: 123 K219 100 263 199 69 159 K176: 130 76 164 184 64 197	Cd2*-2724exporting ATPase - putative cadmism-transporting ATPase [EC.3.6.3.3.3.6.3.5]  ARSR family transcriptional regulator, heavy-metals responsive transcriptional repressor - Cadmism resistance transcriptional regulatory protein hypothetical protein hypoth	)V	Gene absent
goc192 ImmR goc193 goc194 ztnA eadC goc196 goc196 goc196 goc197 goc196 goc199 goc1910 goc1911 goc1912 goc1913 goc1913 goc1916 goc1916 goc1916	122 96 710 K015: 123 K219: 100 263 199 69 159 K176: 130 76 164 184 64 1977 282; 994	Cd2*2/22+exporting ATPase – putative cadmium-transporting ATPase [EC3.8.3.3.8.3.5.5]  ARSI family transcriptional regulator, heavy-metals responsive transcriptional repressor - Cadmium resistance transcriptional regulatory protein hypothetical protein hypotheti	1V	Gene absent
goc192 immR goc193 goc194 zzhA aadC goc196 goc196 goc197 goc197 goc197 goc197 goc199 goc197 goc199 goc191 goc1911 goc1912 goc1911 goc1912 goc1914 goc1914 goc1916 goc1916	122 96 710 K015: 123 K219: 100 263 199 69 159 K176: 130 76 164 184 44 197 282 934 118	Cd2+-2/224-exporting ATPese - putative cadmini-rearraporting ATPese (EC.3.6.3.3.8.6.3.5)  ARRI Entiry Interactiforoni regulator, heavy-metals responsive transcriptional repressor - Cadmium resistance transcriptional regulatory protein hypothetical protein hypothetical protein typothetical protein Cut-exporting ATPese (EC.3.6.3.54) hypothetical protein	IV	Gene absent
goc192 immR goc193 goc194 zbA cadC goc195 goc196 goc197 goc1971 goc1971 goc1971 goc1971 goc1971 goc1971 goc1971	122 96 (515) 710 (6015) 123 (8219) 100 263 199 159 (4176) 176 184 184 184 197 197 282 934 118 285 81	Cd2*-2724exporting ATPese - putative cadminim-transporting ATPese (EC.3.6.3.3.8.6.3.5)  ARSI Ranity Inarcoptional regulator, heavy-metals responsive transcriptional repressor - Cadmium resistance transcriptional regulatory protein hypothetical protein hypothe	IV	Gene absent
goc192 immR goc193 goc194 zbA cadC goc195 goc196 goc197 goc199 goc199 goc199 goc191 goc191 goc191 goc191 goc191 goc191 goc191 goc1911 goc1911 goc1911 goc1911 goc1911 goc1911 goc1911	122 96   123   124   12	Cd2*-2724exporting ATPese - putative cadmini-framporting ATPese (EC.3.6.3.3.8.6.3.5)  ARSI Sanity Incorporational regulator, heavy-metals responsive transcriptional repressor - Cadmium resistance transcriptional regulatory protein hypothetical protein	10	Gene absent
goc192 immR goc193 goc194 zen4 zen5 goc195 goc196 goc196 goc197 goc197 goc197 goc199 goc199 goc191 goc1919 goc1919 goc1919 goc1919	122 96 97 to Kots 1 123 K2191 100 263 199 69 199 199 199 199 199 199	Cd2+2/22+-exporting ATPase - putative cadmium-transporting ATPase [EC.3.8.3.3.8.6.3.5]  ARSR family transcriptional regulator, heavy-metals responsive transcriptional repressor - Cadmium resistance transcriptional regulatory protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein (CG+-exporting ATPase [EC.3.6.3.54])  Beny CG+-exporting ATPase [EC.3.6.3.54]  Beny CG+-	IV IV	Gene absent
goc192 mmR goc193 goc194 zhA zhA goc193 goc196 zhA zhA goc196 goc196 goc196 goc196 goc197 goc197 goc197 goc198 goc198 goc198 goc199 goc	122 96   710   K015   710   K01	Cd2+2/224-exporting ATPese - putative cadmin-rearraporting ATPese (EC.3.6.3.3.8.6.3.5)  ARRS family transcriptional regulator, heavy-metals responsive transcriptional repressor - Cadmium resistance transcriptional regulatory protein hypothetical protein hypothetical protein hypothetical protein Cd2+-exporting ATPese (EC.3.6.3.54) hypothetical protein	IV	Gene absent
goc192 mmR goc193 goc194 zhrA goc193 goc194 zhrA goc195 goc196 goc196 goc196 goc196 goc196 goc196 goc196 goc197 goc196 goc197 go	122 96 710 KO15 123 K2191 100 100 100 100 100 100 100	Cd2+-2/224-exporting ATPese - putative cadmini-rearraporting ATPese (EC.3.6.3.3.86.3.5)  ARRI Starily Interactifolional regulator, heavy-metals responsive transcriptional regressor - Cadmium resistance transcriptional regulatory protein hypothetical protein		Gene absent
pcc192 mmR gcc193 gcc194 gcc193 gcc194 zhvA gcc193 gcc194 zhvA gcc195 gcc196 gcc196 gcc197 gc	122 96   9710   Kolts   123   K2191   100	Cd2+2r23+-exporting ATPsee - putative cadminim-transporting ATPsee [EC.3.6.3.3.86.3.5]  ARRI Starily Interactioptional regulator, heavy-metals responsive transcriptional regressor - Cadmium resistance transcriptional regulatory protein hypothetical protein		Gene absent
pcc192 mmR gcc193 gcc194 gcc193 gcc194 dbA	122 96 97 10 Kot15 123 K219 100 100 1263 199 199 190 176 180 180 180 180 180 180 180 180 180 180	Cd2**C2**-apporting ATPase - putative cadminim-transporting ATPase [EC.3.6.3.3.6.5.5]  ARSR Samily transcriptional regulator, heavy-metals responsive transcriptional repressor - Cadmium resistance transcriptional regulatory protein hypothetical protein hypothet		Gene absent
pcc192 mmR gcc193 gcc194 gcc193 gcc193 gcc194 zmA  zmA  gcc193 gcc194 zmA  gcc196 gcc196 gcc196 gcc196 gcc196 gcc196 gcc196 gcc196 gcc197 gcc196 gcc197 gcc191 gcc197 gcc191 gcc1	122 96 710 K015 123 K219 100 100 100 100 100 100 100 100 100 1	Cd2+2v22+apporting ATPase - putative cadminim-transporting ATPase [EC.3 6.3 3 8 6 3.5]  ARRS family transcriptional regulator, heavy-metals responsive transcriptional repressor - Cadmium resistance transcriptional regulatory protein hypothetical protein hypothetical protein hypothetical protein Cut-exporting ATPase [EC.3 6 3 54] hypothetical protein hypothetical p		Gene absent
pcc192 mmR gcc193 gcc194 gcc193 gcc194 zhnA gcc193 gcc194 zhnA gcc195 gcc196 gcc197 gcc197 gcc198	122 96 97 10 Kot15 123 K219 100 100 1263 199 199 190 176 180 180 180 180 180 180 180 180 180 180	Cd2**C2**-apporting ATPase - putative cadminim-transporting ATPase [EC.3.6.3.3.6.5.5]  ARSR Samily transcriptional regulator, heavy-metals responsive transcriptional repressor - Cadmium resistance transcriptional regulatory protein hypothetical protein hypothet		Gene absent
pcc192   mmmPr   pcc192   mmmPr   pcc192   mmmPr   pcc193   pcc193   pcc193   pcc193   pcc193   pcc194   pcc193   pcc194   pcc195   pcc195	122 96 9710 KO15-1 123 K2191 100 100 263 199 98 99 100 100 100 100 100 100 100 100 100	Cd2**272**-exporting ATPase - putative cadminim-transporting ATPase (EC.3.6.3.3.8.6.3.5)  ARSR family transcriptional regulator, heavy-metals responsive transcriptional repressor - Cadmium resistance transcriptional regulatory protein hypothetical protein		Gene absent
pcc192 mmR gcc193 gcc194 gcc193 gcc194 dbA	122 96 9710 KO15-1 123 K2191 100 263 199 189 189 180 180 180 180 180 180 180 180 180 180	Cd2**272**-exporting ATPase - putative cadmism*-samporting ATPase [EC.3.6.3.3.8.6.3.5]  ARSR family transcriptional regulator, heavy-metals responsive transcriptional repressor - Cadmism resistance transcriptional regulatory protein hypothetical protein	et	Gene absent
pcc192 pcc192 pcc192 pcc193 pcc193 pcc194 pcc193 pcc194 pcc193 pcc194 pcc193 pcc194 pcc195 pcc196 pc	122 96 9710 Ko15-2	CG2+V224-seporting ATPese - putative cadminim-transporting ATPese (EC.3.6.3.3.8.6.3.5)  ARRS family transcriptional regulator, heavy-metals responsive transcriptional repressor - Cadmium resistance transcriptional regulatory protein hypothetical protein hypothe	et	Gene absent Gene a
pcc192 mmR gcc193 gcc194 gcc193 gcc194 zhvA gcc193 gcc194 zhvA gcc195 gcc196 gcc196 gcc196 gcc197 gc	122 96 9710 KO15-2	Cd2+2r23+-exporting ATPase - putative cadmini-framporting ATPase (EC3.6.3.3.3.6.3.5)  ARSR family transcriptional regulator, heavy-metals responsive transcriptional regressor - Cadmium resistance transcriptional regulatory protein hypothetical protein hypotheti	et	Gene absent
pcc192 mmR gcc193 gcc194 gcc193 gcc194 zhrA gcc193 gcc194 zhrA gcc195 gcc196 gcc197 gcc198 gc	122 96 97 10 Kot15 123 K2191 100 100 100 100 100 100 100 100 100	Cd2**C2**Paperting ATPase - putative cadminim-transporting ATPase (EC.3.6.3.3.6.5.5)  ARSR Samily transcriptional regulator, heavy-metals responsive transcriptional represent - Cadmium resistance transcriptional regulatory protein hypothetical protein hypotheti	et	Gene absent
pcc192 mmR gcc193 gcc194 gcc193 gcc194 dbA	122 96 7710 K015 22 96 7710 K015 23 7710 K015 23 123 K2191 100 100 100 100 100 100 100 100 100	Cd2**C2**2-exporting ATPase - putative cadminim-transporting ATPase (EC.3.6.3.3.6.5.5) ARSR family transcriptional regulator, heavy-metals responsive transcriptional repressor - Cadmium resistance transcriptional regulatory protein hypothetical protein hypothet	et 114 114 114 114 114 114 114 114 114 11	Gene absent
pcc192 mmR gcc193 gcc193 gcc193 gcc193 gcc193 gcc194 dbA dbA dbA dbA gcc193 gcc196 gcc196 gcc196 gcc196 gcc196 gcc197 gcc197 gcc197 gcc198 gcc196 gcc197 gcc	122 96 9710 Ko15-2	Cd2+2v22+apporting ATPase - putative cadminim-transporting ATPase [EC.3 6.3 3 8 6 3.5]  ARRS family transcriptional regulator, heavy-metals responsive transcriptional regressor - Cadmium resistance transcriptional regulatory protein hypothetical protein hypothe	et  NY  NY  NY  NY  NY  NY  NY  NY  NY  N	Gene absent
pcc192   mmR   pcc192   pcc192   pcc192   pcc192   pcc193   pcc193   pcc193   pcc193   pcc193   pcc193   pcc194   pcc194   pcc194   pcc196   pcc196	122 96 9710 KO15-2	Cd2+2v22+apporting ATPase - putative cadminim-transporting ATPase [EC.3 6.3 3 8 6 3.5]  ARRS family transcriptional regulator, heavy-metals responsive transcriptional regressor - Cadmium resistance transcriptional regulatory protein hypothetical protein hypothe	et  NY  NY  NY  NY  NY  NY  NY  NY  NY  N	Gene absent

degV ysnE efrB gdh	283	Garma-polyglutamate biosynthesis protein - Capsule biosynthesis protein - Lapsule biosynthesis protein - Capsule biosynthesi		Point mutations
gdh	66 K03828	hypothetical protein (contaning DegV domain)  Putative acetyltransferase [EC:2.3.1]		Synonimous point mutations Point mutations
yun	590 K18888 450 K00262	ATP-binding cassette, subfamily B, multidrug efflux pump Glutamate dehydrogenase (NADP+ specific) [EC:1.4.1.4]	env met	Point mutations Point mutations
yhcR	691 K01081	5'-nucleotidase [EC:3.1.3.5]	met	Point mutations
qldA	363 K00005	Glycerol dehydrogenase [EC:1.1.1.6]	met	Point mutations
gcc175 gcc176	163 K02755 535 K01992	PTS-Bgl-EIIA; PTS system, beta-glucoside-specific IIA component [EC:2.7.1]  ABC-2 type transport system permease protein	env	Point mutations Point mutations
gcc177 natA	77 108 K01990	hypothetical protein		Truncated protein
dinG	836 K03722	ABC-2 type transport system ATP-binding protein ATP-dependent DNA helicase [EC:3.6.4.12]	env met	Point mutations Point mutations
nikE	132 K10824	Nickel transport system ATP-binding protein [EC:3.6.3.24]		Truncated protein
nikD gspA	263 K15587 402	Nickel transport system ATP-binding protein [EC:3.6.3.24] General stress protein A	env	Point mutations Gene absent
isaA	235	Putative transglycosylase		Truncated protein
lytN gcc178	57 586 K00382	hypothetical protein DLD; dihydrolipoamide dehydrogenase [EC:1.8.1.4]	met/cell	Synonimous point mutations Synonimous point mutations
pdhC	463 K00627	DLAT; pyruvate dehydrogenase E2 component (dihydrolipoamide acetyltransferase) [EC:2.3.1.12]	met	Point mutations
acoA	323 K00161 107 K00975	PDHA; pyruvate dehydrogenase E1 component alpha subunit [EC:1.2.4.1]	met/env met/cell	Synonimous point mutations
glgD glgC	380 K00975	glgC; glucose-1-phosphate adenylyltransferase [EC:2.7.7.27] Glucose-1-phosphate adenylyltransferase	met/cell	Point mutations Point mutations
metN	245 K02071	Methionine import ATP-binding protein MetN	env	Point mutations
gcc179 yhjX	230 407 K08177	hypothetical protein oxIT; MFS transporter, OFA family, oxalate/formate antiporter	env	Truncated protein Point mutations
luxA	348	Alkanal monooxygenase alpha chain		Point mutations
gcc1710 gcc1711	58 95	hypothetical protein hypothetical protein		Gene absent Truncated protein
gcc1712	134	hypothetical protein		Gene absent
gcc1713 gcc1714	406 359	hypothetical protein hypothetical protein		Gene absent Point mutations
cadR	320	Topput consists processing Color Col		Synonimous point mutations
gcc1715 gcc1716	282 415	hypothetical protein hypothetical protein		Gene absent Gene absent
lacC	270 K00917	insponence process Tagatose 6-phosphate kinase [EC:2.7.1.144]	met	Point mutations
gcc1717	66 370 K02346	FMN-binding protein  DNA polymerase IV [EC:2.7.7.7]		Truncated protein
dinB mta 2	58	Once polymense by [CC.2.7.7.] hypothetical protein	met	Point mutations Point mutations
glpF_1	238 K02440	GLPF; glycerol uptake facilitator protein	env	Point mutations
gcc1718 endA	92 118 K15051	hypothetical protein  DNA-entry nuclease		Gene absent Gene absent
gcc1719	67	hypothetical protein		Gene absent
panE	318 K00077	2-dehydropantoate 2-reductase [EC:1.1.1.169]	met	Gene absent
gcc1720 puuD	235 230 K07010	hypothetical protein  Putative qlutamine amidotransferase	met	Gene absent Point mutations
yxeM 1	278 K02030	ABC; polar amino acid transport system substrate-binding protein	env	Point mutations
speG 1 cas3	195 480 K07012	Spermidine N(1)-acetyltransferase  CRISPR-associated endonuclease/helicase [EC:3.1 3.6.4]	cell	Gene absent Gene absent
gcc1721	271	Putative phosphatase		Point mutations
gcc1722 cpdA	895 K01537 102	Ca2+-transporting ATPase [EC:3.6.3.8] hypothetical protein	-	Synonimous point mutations Synonimous point mutations
gpp1723	205	hypothetical protein		Point mutations
gpp1724	288 K07052 419	hypothetical protein	<u> </u>	Point mutations
leuS	834 K01869	Sensor histidine kinase  LARS; leucyl-tRNA synthetase [EC:6.1.1.4]	met	Point mutations Point mutations
pta	331 K00625	Phosphate acetyltransferase [EC:2.3.1.8]	met	Point mutations
ydfG pyrB	197 308 K00609	NADP-dependent 3-hydroxy acid dehydrogenase Aspartate carbamoyltransferase catalytic subunit [EC:2.1.3.2]	met	Truncated protein Point mutations
smc_1	825	Proposition of the Control of the Co	mex	Truncated protein
gpp1725 gpp1726	177 159	hypothetical protein hypothetical protein		Gene absent
gpp1727	136	Inypotnetical protein  hypothetical protein		Gene absent Gene absent
gpp1728	89	hypothetical protein		Gene absent
gpp1729 lytS	127 580 K07704	hypothetical protein Two-component system, LytTR family, sensor histidine kinase [EC:2.7.13.3]	met/env	Gene absent Point mutations
lytR	486	Transcriptional regulator LyfR		Point mutations
pepS	680 414 K19689	Acylamidase Aminopeptidase [EC:3.4.11]	met	Truncated protein Point mutations
uvrB	664 K03702	Point Superposed   Eco. Sect. 11:7    Exclinic Legislane ABC subunit B - UvrABC system protein	met	Point mutations
prtP 2	1386 354	PIII-type proteinase		Gene absent
gcc1730 mutT	175 K03574	hypothetical protein 8-oxo-dGTP diphosphatase [EC:3.6.1.55]	met	Gene absent Truncated protein
gcc1731	56 370 K03086	hypothetical protein	met	Truncated protein
sigA gcc1732	91	RNA polymerase primary sigma factor hypothetical protein	met	Synonimous point mutations Gene absent
lepB	190 K03100	Signal peptidase I [EC:3.4.21.89]	met/cell	Gene absent
inIA_2 gcc1733	1435 503	Internalin-A Fimbrial subunit type 1		Gene absent Gene absent
rgpB	303 K12997	Rhamnosyltransferase [EC:2.4.1]	met	Point mutations
scpA	457 K01361 292 K07284	C5a peptidase - lactocepin [EC:3.4.21.96] Sortase A [EC:3.4.22.70]	met met	Truncated protein Gene absent
		hypothetical protein	mex	Gene absent
strA gcc1734	224			
gcc1734 rsmH 1	189	hypothetical protein		Point mutations
gcc1734		hypothetical protein putative NTE family protein		Point mutations Point mutations
gcc1734 rsmH_1 gcc1735	189 282 207	putative NTE family protein  hypothetical protein		Point mutations  Gene absent
gcc1734 rsmH_1 gcc1735 gcc231 gcc232	189 282			Point mutations  Gene absent Gene absent
gcc1734 rsmH_1 gcc1735 gcc231 gcc232 gcc233 comR	282 207 86 368 301 K20342	Dutative NTE smilty protein  hypothetical pr	cell	Point mutations  Gene absent Gene absent Gene absent Gene absent
gcc1734 rsmH_1 gcc1735 gcc231 gcc232 gcc232 gcc233 ccomR yvgN_2	189 282 207 86 368 301 K20342 115	Dutative NTE family protein  hypothetical pr	cell	Point mutations  Gene absent Gene absent Gene absent Gene absent Point mutations
gcc1734 rsmH_1 gcc1735 gcc231 gcc232 gcc233 comR yvgN_2 gcc234 gcc234 gcc235	189 282 207 86 368 301 K20342 115 132 389	putative NTE tamily protein  hypothetical protein	cell	Point mutations  Gene absent Gene absent Gene absent Gene absent Point mutations Truncated protein Gene absent
gcc1734 rsmH_1 gcc1735 gcc231 gcc232 gcc233 comR yygN_2 gcc234 gcc234 gcc236	189 282 207 86 368 301 K20342 115 132 389 173	Dutative NTE family protein  hypothetical protein	cell	Point mutations  Gene absent Gene absent Gene absent Gene absent Point mutations Truncated protein Gene absent Gene absent
gcc1734 rsmH_1 gcc1735 gcc231 gcc232 gcc233 comR yvgN_2 gcc234 gcc234 gcc235	189 282 207 86 368 301 K20342 115 132 389 173 95 285	putative NTE tamily protein  hypothetical protein	cell	Point mutations  Gene absent Gene absent Gene absent Gene absent Point mutations Truncated protein Gene absent
gcc1734 rsmH_1 gcc1735 gcc231 gcc232 gcc232 gcc233 gcc233 gcc234 gcc235 gcc236 gcc236 gcc237 gcc238 gcc239	189 282 207 86 368 301 115 132 389 173 95 285	hypothetical protein  putative coddreductane  typothetical protein  hypothetical protein	cell	Point mutations  Gene absent Gene absent Gene absent Gene absent Point mutations Truncated protein Gene absent
gcc1734 rsmH_1 gcc1735 gcc231 gcc232 gcc233 ccomR yvgN_2 gcc234 gcc235 gcc236 gcc236 gcc236	189 282 207 86 368 301 K20342 115 132 389 173 95 285	hypothetical protein	cell	Point mutations  Gene absent Gene absent Gene absent Gene absent Point mutations Truncated protein Gene absent
gec1734 mmH 1 gec1735 gec231 gec231 gec232 gec232 comR yygN 2 gec236 gec236 gec236 gec237 gec236 gec237 gec237 gec231 gec231 gec231 gec231 gec2310 gec2311 hadS	189 282 207 86 368 368 361 173 173 95 285 97 135 119 462 K01154	hypothetical protein	cell	Point mutations  Gene absent Gene absent Gene absent Gene absent Gene absent Point mutations Truncated protein Gene absent
goc1734 ramH 1 goc1735 goc231 goc232 goc233 comR yugh 2 goc234 goc234 goc234 goc236 goc237 goc236 goc231 goc231 goc231 goc231 goc231 goc231 goc231 goc231	189 282 207 86 368 368 301 K20342 115 132 389 173 95 285 97 135	hypothetical protein	cell	Point mutations  Gene absent Gene absent Gene absent Gene absent Point mutations Truncated protein Gene absent
geof734 ramH 1 geof735 geo231 geo232 geo233 geo233 geo233 geo233 geo234 geo234 geo234 geo236 geo237 geo231 geo231 geo231 geo231 geo231 geo231 geo231 geo231 geo231	189   189   207   186   207   186   207   186   207	byochetical protein  hypochetical protein	cell	Gene absent Forit mutations Truncated protein Gene absent Forit mutations Forit mutations Forit mutations
gcc1734 ssmH 1 gcc1734 ssmH 1 gcc1735 gcc231 gcc231 gcc233 gcc231	189 282 207 86 368 301 K20342 115 132 389 173 95 97 135 119 462 K01154 524 107	hypothetical protein  Oxidaty D-Selentranian protein  Oxidaty D-Selentranian protein protein EC-3.1.21.31  hypothetical protein  Oxidaty D-Selentranian proteins pototical eC-1.1.1.100  Oxidaty D-Selentranian proteins proteins (EC-1.1.1.100  Oxidaty D-Selentranian proteins proteins (EC-1.1.1.100	cell	Point mutations  Gene absent Gene absent Gene absent Gene absent Gene absent Gene absent Funcated protein Gene absent
geot734 smith 1 geot734 geot734 geot735 geot371 geot372 geot372 geot372 geot372 geot372 geot372 geot373 geot373 geot373 geot373 geot373 geot374 geot37	189   282   207   207   208	hypothetical protein hypotheti	cell met env met	Point mutations  Gene absent G
geot734 ssmH 1 geot734 ssmH 1 geot735 geo231 geo233 geo233 geo233 geo233 geo233 geo234 geo236 geo236 geo236 geo237	189   282   207   86   86   86   87   87   87   87   8	hypothetical protein hypotheti	cell	Gene absent Point mutations Truncated protein Gene absent
goe1734 ramH 1 gec1735 gec231 gec231 gec231 gec232 gec233 gec234 gec236 gec237 gec236 gec237 gec238	189   282   207   86   86   86   86   87   87   87   8	hypothetical protein hypotheti	cell met env met	Point mutations  Gene absent Truncated protein Gene absent Fort mutations Point mutations
gee1734 rsmH 1 per1735 gee231 gee231 gee232 gee233 ceemR yvgN 2 gee236 gee233 ceemR yvgN 2 gee236 gee237 see237 see231 gee231 gee2310 gee231 gee2311 hed5 gee231 gee2311 fibit fill fill fill fill fill fill fill fi	189   189   207   86   207   86   86   207   86   96   207   97   97   97   97   97   97   97	hypothetical protein Gey uncharacteried protein hypothetical protein Oyfk uncharacteried protein hypothetical protein Oyfk uncharacteried protein hypothetical protein	cell met env met met	Gene absent Truncated protein Gene absent Forit mutations Proint mutations Proint mutations Point mutations
goc1734 ramH 1 goc1734 ramH 1 goc1734 ramH 1 goc1735 goc231 goc233 goc233 goc233 goc233 goc233 goc233 goc233 goc2310 goc2310 goc2310 goc2310 goc2310 goc2311 had goc317 goc2312 goc2311 goc231	189   189   282	hypothetical protein Gyt uncharacteried protein hypothetical protein	cell met env met met env	Gene absent Gene a
ger1734 rsmH 1 ger1735 ger231 ger231 ger232 ger233 comm 2 ger233 ger233 ger233 ger233 ger233 ger233 ger234 ger234 ger234 ger234 ger236 ger236 ger237 ger238	189   189   282   207   86   688   301   X20342   115   132   115   132   115   132   115   132   115   132   115   132   134	hypothetical protein O-alenyP-D-alenine-carboxypoptideselendopeptidese 3-axeao(-jacy-t-arrier-protein) productase (Ec.1.1.1.100 CylE uncharacterised protein hypothetical protein	cell met env met met	Point mutations  Gene absent G
goc1734 rsmH 1 goc1734 rsmH 1 goc1735 goc231 goc231 goc232 goc233 comR 2 goc332 goc233 goc333 goc336 goc337 goc238 goc337 goc238 goc337 goc231 goc2310 goc2310 goc37 goc	189   282   207   207   207   208	hypothetical protein D-alany-b-alanine-carboxypeptidaseindopeptidase D-alany-b-alanine-carboxypeptidaseindopeptidase D-alany-b-alanine-carboxypeptidaseindopeptidase D-alany-b-alanine-carboxypeptidaseindopeptidase D-alany-b-alanine-carboxypeptidaseindopeptidase D-alany-b-alanine-carboxyperidaseindopeptidase D-alany-b-alanine-carboxyperidaseindopeptidase D-alany-b-alanine-carboxyperidaseindopeptidase D-alany-b-alanine-carboxyperidaseindopeptidase D-alany-b-alanine-carboxyperidaseindopeptidase D-alany-b-alanine-carboxyperidaseindopeptidase D-alany-b-alanine-carboxyperidaseindopeptidase D-alany-b-alanine-carboxyperidaseindopeptidas	cell met env met met env	Point mutations  Gene absent G
goe1734 ramH 1 goe2735 goe237	189   282   207   86   86   86   86   86   86   86   8	hypothetical protein hypotheti	cell met env met met env	Point mutations  Gene absent Gene absent Gene absent Gene absent Gene absent Gene absent Fort musicins Truncated protein Gene absent Fort mutations Point mutations
goe1734 ramH 1 gec21735 gec231 gec231 gec231 gec231 gec233 gec231	189   282   207   86   86   86   86   87   87   87   8	hypothetical protein hypotheti	cell met env met env env env	Gene absent Funcated protein Gene absent Funcated protein Gene absent Gene absent Funcations Foirt mutations F
geot734   geot3734   geot3735   geot373   geot374   geot	189   189   282   282   282   282   282   282   282   282   297   86   86   875   87	hypothetical protein	cell met env met env env env env	Gene absent Tuntations Point mutations From mutations Tuncated protein Gene absent Gene absent Gene absent Gene absent
goc1734 rsmH 1 goc2373 goc2373 goc2373 goc2373 goc2373 goc2373 goc2374 goc2374 goc2374 goc2374 goc2374 goc2371	189   282	hypothetical protein	cell met env met env env env	Gene absent Turustons Point mutations Point mutations Point mutations Point mutations Point mutations Point mutations Form mutations Form mutations Form mutations Form mutations Synonimous point mutations Synonimous point mutations Synonimous point mutations Form mutations Synonimous point mutations Synonimous point mutations Turuscated protein Turuscated protein Turuscated protein Turuscated protein Gene absent Gene absent
goc1734 rsmH 1 goc21734 rsmH 1 goc21735 goc2371 goc2371 goc2371 goc2372 goc2373 goc2373 goc2373 goc2373 goc2373 goc2373 goc2373 goc2371 goc237	189   189   282   207   86   86   87   87   88   180   87   88   180   87   88   87   87   87   88   87	hypothetical protein  O-alany-D-alanine-rarboxypeptidaseelenoseptidasee 3-xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx	cell met env met env env env env	Point mutations  Gene absent Thurations Point mutations Point mutations Point mutations Froit mutations Gene absent Gene absent
goe1734 rsmH 1 gec1314 gec13735 gec2317 gec237 gec2	189   189   282	hypothetical protein	cell met env met env env env env	Gene absent Fort mutations Truncated protein Gene absent Fort mutations Froit mutations Froit mutations Point mutations Point mutations Point mutations Point mutations Point mutations Froit mutations Fr
goc1734 ramH 1 goc2311 goc2323 goc232 goc2323 goc232 go	189   189   282	hypothetical protein	cell met env met env env env env	Point mutations  Gene absent Tuncate Gene absent Gene absent Tuncate Gene absent Tuncate Gene absent Foot mutations Point mutations Cene absent Gene absent Gene absent Gene absent Gene absent Gene absent
goc1734 rsmH 1 goc1734 rsmH 1 goc1735 goc1735 goc1735 goc237 goc2	189   189   282   282   282   282   282   282   282   282   297   86   686   282   2	hypothetical protein Challey D- daintine-carboxypotidisaelendopoptidisae  (D-dainty D- daintine-carboxypotidisaelendopoptidisael (D-dainty D- daintine-carboxypotidisaelendopoptidisael (D-dainty D- daintine-carboxypotidisaelendopoptidisael (D-dainty D- daintine-carboxypotidisaelendopoptidisael (D-dainty D- daintine-carboxypotidisaelendopoptidis	cell met env met env env env env	Gene absent
goe1734 ramin 1 goe2373 goe2373 goe2373 goe2373 goe2373 goe2373 goe2373 goe2373 goe2374 goe2374 goe2374 goe2374 goe2374 goe2374 goe2371 goe237	189   189   282	hypothetical protein	cell met env met env env env env	Gene absent Form mutations Truncated protein Gene absent Four mutations Point mutations Form absent Gene absent
goe1734 ramH 1 geo1735 geo231 geo231 geo233 com8	189   189   282   282   282   282   282   282   282   283	hypothetical protein O-alenyl-D-alanine-carboxypeptidaselendopeptidasel 3-axoao/i-qa/c-rairer protein protein peduchase (Ec.1.1.100 Cylic uncharacterised protein hypothetical pr	cell met env met env env env env	Point mutations  Gene absent Truccated protein Gene absent Truccate Gene absent Gene absent Gene absent Truccate Gene absent Truccate Gene absent Gene absent Gene absent Truccate Gene absent Truccate Truc
goe1734 rsmH 1 gec131 gec131 gec131 gec131 gec231 gec232 gec332 gec332 gec334 gec236 gec236 gec236 gec236 gec236 gec236 gec237 gec2311 had s gec2312 gec2314 gec2315 gec2316 gec2316 gec2316 gec2317 gec2316 gec2317 g	189   189   282	hypothetical protein	cell met env met env env env env	Gene absent Fort mutations Truncated protein Gene absent Fort mutations Froir mutations Froir mutations Proir mutations Froir mutations Gene absent
goc1734 ramH 1 goc2735 goc2373 goc2371	189   189   282	hypothetical protein	cell met env met env env env env	Point mutations  Gene absent Form mutations Point mutations Form mutations Gene absent
goe1734 rsmH 1 goe2734 rsmH 1 goe2735 goe2735 goe2327 goe2324 goe2324 goe2326	189   189   282   282   282   282   282   282   282   282   297   86   686   282   2	hypothetical protein	cell met env met env env env env	Point mutations  Gene absent Tunutations Point mutations Point mutations Point mutations Point mutations Point mutations Point mutations Fort mutations Tunucated protein Tunucated protein Tunucated protein Tunucated protein Tunucated protein Gene absent
goe1734 rsmH 1 goe2735 goe2735 goe2735 goe2737	189   189   282   282   282   282   282   282   282   282   297   86   686   282   2	hypothetical protein	cell met env met env env env env	Point mutations  Gene absent Gene absent Gene absent Gene absent Gene absent Gene absent Fort mutations Truncated protein Gene absent Forti mutations Point mutations Point mutations Point mutations Point mutations Point mutations Forti mutations Fort
goc1734 rsmH 1 goc2734 goc2735 goc2371 goc2371 goc2371 goc2373 goc2373 goc2373 goc2373 goc2373 goc2373 goc2373 goc2373 goc2373 goc2374 goc2374 goc2374 goc2374 goc2374 goc2737	189   189   282   282   282   282   282   282   282   283	hypothetical protein hypotheti	cell met env met env env env env	Point mutations  Gene absent
goe1734 rsmH 1 goe2131 goe231 goe232 goe233	189   189   282   282   282   282   282   282   282   282   283	hypothetical protein	cell met env met env env env env	Gene absent Form mutations Truncated protein Gene absent Ford mutations Point mutations Point mutations Point mutations Point mutations Ford mutations Gene absent
goe1734 ramiH 1 goe21735 goe21735 goe2273 goe2237 goe2	189   189   282	hypothetical protein hypotheti	cell met env env env env env env	Point mutations  Gene absent Fort mutations Point
goe1734 rsmH 1 goe2734 rsmH 1 goe2735 goe1735 goe2737 goe2737 goe2736 goe2737 goe2736 goe2737	189   189   282   282   282   282   282   282   282   283	hypothetical protein hypotheti	cell met env env env env env env	Point mutations  Gene absent Funcated protein Gene absent Funcated protein Gene absent Gene absent Funcated protein Gene absent Funcated protein Gene absent
goe1734 ramin 1 goe2313 goe2323 goe2324 goe2324 goe2326 goe2321 goe2324 goe2326 goe2327 goe232	189   189   2207   186   2207   186   2207   186   2207   186   2207   186   2207   186   2208   220	hypothetical protein hypotheti	cell  met env	Gene absent Foot mutations Point mutations Point mutations Point mutations Point mutations Point mutations Point mutations Fort mutations Gene absent
goc1734 ramH 1 goc2731 goc2321 goc2321 goc2323 goc2323 goc233 goc2333 goc2333 goc2333 goc2333 goc2333 goc2333 goc2333 goc2333 goc2334 goc2336 goc2331 goc2336 goc2331 goc2336 goc2331 goc2332 goc2332 goc2333 goc2333 goc2333 goc2333 goc23331	189   189   282   282   282   282   282   282   282   282   282   283	hypothetical protein hypotheti	cell met env met met env	Point mutations Gene absent
goc1734 rsmH 1 goc1734 rsmH 1 goc1734 rsmH 1 goc1735 goc231 goc231 goc232 goc233 goc23	189   189   282   282   282   282   282   282   282   282   282   282   282   282   282   283	hypothetical protein hypotheti	cell  met env	Gene absent
goe1734 ramiH 1 goe2373 goe2371 goe237	189   189   282   207   186   282	hypothetical protein hypotheti	cell met met met met env	Gene absent