

1 **Table S1: Annotated genomes utilised to facilitate an *in silico* screen for sulphite reducing genes**

Species	Strain	GC %	Size Mb
<i>Bacillus cereus</i>	ATCC 14579	35.3	5.42
<i>Bacillus licheniformis</i>	DSM 13	46.2	4.22
<i>Clostridium acetireducens</i>	DSM 10703	26.7	2.4
<i>Clostridium algidcarnis</i>	B3	3.06	30.3
<i>Clostridium beijerickii</i>	ATCC 35702	30	6.49
<i>Clostridium botulinum</i>	B str Eklund	27.47	3.8
<i>Clostridium botulinum</i>	ATCC 3502	28.19	3.9
<i>Clostridium botulinum</i>	D str 16868	28.17	3.08
<i>Clostridium botulinum</i>	E1 str BoNT E Beluga	27	3.99
<i>Clostridium botulinum</i>	F str Langeland	28.29	4.01
<i>Clostridium butyricum</i>	DSM 10702	28.5	4.59
<i>Clostridium butyricum</i>	KNU L09	32	3.82
<i>Clostridium celerecens</i>	AAU1	27.9	3.98
<i>Clostridium celluovorans</i>	743B	31.2	5.26
<i>Clostridium intestinale</i>	DSM 6191	30.1	4.6
<i>Clostridium kluyveri</i>	DSM 555	32.02	4.02
<i>Clostridium magnum</i>	DSM 2767	32.1	6.63
<i>Clostridium noyvi</i>	ATCC 27606	27.57	2.61
<i>Clostridium pasteurianum</i>	DSM 525	29.9	4.35
<i>Clostridium perfringens</i>	ATCC 13124	28.4	3.26
<i>Clostridium sartagoforme</i>	AAU1	27.9	3.98
<i>Clostridium sporogenes</i>	ATCC 15579	28	4.1
<i>Clostridium sporogenes</i>	ATCC 19494	27.9	4.06
<i>Clostridium sporogenes</i>	DSM 795	28	4.14
<i>Clostridium sulfidigenes</i>	113A c1	30	3.72
<i>Clostridium tetani</i>	E88	28.8	2.87
<i>Clostridium tunisiense</i>	TJ C661	31.2	4.31
<i>Clostridium tyrobutyricum</i>	KCTC	31.1	3.13
<i>Clostridioides difficile</i>	630	29.1	4.2
<i>Paenibacillus lactis</i>	154	51.8	6.8
<i>Proteus mirabilis</i>	HI4320	38.8	4.09
<i>Paraclostridium bifermentans</i>	ATCC 638	28.4	3.6
<i>Clostridium amygdalinum</i>	DPC 7176	40	5.3
<i>Clostridium peptidovorans</i>	DPC 7177	33	3.4
<i>Clostridium aminovelericum</i>	DPC 7173	35	4.4
<i>Clostridium thiosulfatireducens</i>	DPC 7172	28.3	6.7
<i>Clostridium cochlearium</i>	DPC 7174	29.2	2.6
<i>Clostridium tertium</i>	DPC 7175	28.9	3.6
<i>Salmonella enterica</i> LT2	LT2	52.2	4.95

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3 **Table S1: Roary core genes of SRC phenotype**

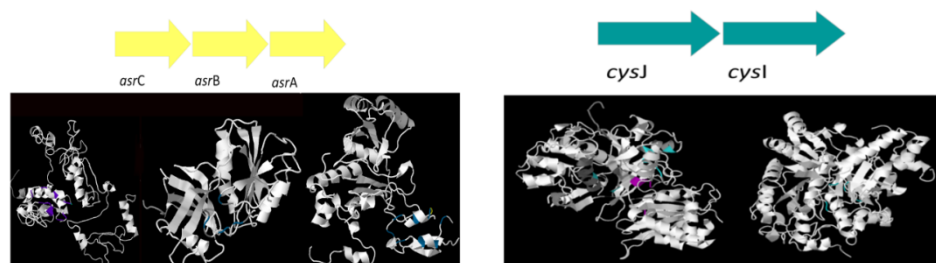
Gene	Annotation	No. isolates
<i>accB</i>	Biotin carboxyl carrier protein of acetyl-CoA carboxylase	33
<i>lon1</i>	Lon protease 1	33
<i>clpC</i>	Negative regulator of genetic competence ClpC/MecB	33
<i>mraY</i>	Phospho-N-acetylmuramoyl-pentapeptide-transferase	33
<i>rpe</i>	Ribulose-phosphate 3-epimerase	33
<i>clpP</i>	ATP-dependent Clp protease proteolytic subunit	33
<i>fmt</i>	Methionyl-tRNA formyltransferase	33
<i>pnp</i>	Polyribonucleotide nucleotidyltransferase	33
<i>trmD</i>	tRNA (guanine-N(1)-)-methyltransferase	33
<i>murB</i>	UDP-N-acetylenolpyruvoylglucosamine reductase	33
group_2420	Radical SAM superfamily protein	33
<i>prkC</i>	Serine/threonine-protein kinase PrkC	33
<i>mazG</i>	Nucleoside triphosphate pyrophosphohydrolase	33
<i>fabD</i>	Malonyl CoA-acyl carrier protein transacylase	33
<i>fabG_2</i>	3-oxoacyl-[acyl-carrier-protein] reductase FabG	33
<i>fabF</i>	3-oxoacyl-[acyl-carrier-protein] synthase 2	33
<i>accC</i>	Biotin carboxylase	33
<i>uppS</i>	Ditrans, polycis-undecaprenyl-diphosphate synthase ((2E,6E)-farnesyl-diphosphate specific)	33
<i>ispG</i>	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase	33
<i>uvrC</i>	UvrABC system protein C	33
<i>clpX</i>	ATP-dependent Clp protease ATP-binding subunit ClpX	33
<i>prfB</i>	Peptide chain release factor 2	33
<i>rlmN</i>	putative dual-specificity RNA methyltransferase RlmN	33
<i>miaA</i>	tRNA dimethylallyltransferase	33
<i>pgsA</i>	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase	33
<i>rimO</i>	Ribosomal protein S12 methylthiotransferase RimO	33
group_2719	dihydrolipoamide dehydrogenase	33
<i>dxr</i>	1-deoxy-D-xylulose 5-phosphate reductoisomerase	33
group_2821	glmZ(sRNA)-inactivating NTPase	33
<i>ispH</i>	hypothetical protein	33
<i>dxs_1</i>	1-deoxy-D-xylulose-5-phosphate synthase	33
group_2882	hypothetical protein	33
<i>yrrK</i>	Putative Holliday junction resolvase	33
<i>dnaK_1</i>	Chaperone protein DnaK	33
<i>rpsT</i>	30S ribosomal protein S20	33
<i>gpmI</i>	2,3-bisphosphoglycerate-independent phosphoglycerate mutase	33
<i>topA</i>	DNA topoisomerase 1	33
<i>mnmG</i>	tRNA uridine 5-carboxymethylaminomethyl modification enzyme MnmG	33
<i>rsmG</i>	Ribosomal RNA small subunit methyltransferase G	33

<i>rsmH</i>	Ribosomal RNA small subunit methyltransferase H	33
<i>engB</i>	putative GTP-binding protein EngB	33
group_2983	Nucleoid-associated protein	33
<i>yvyD</i>	Putative sigma-54 modulation protein	33
<i>tepA</i>	Translocation-enhancing protein TepA	33
<i>mdeA</i>	methionine gamma-lyase	33
group_3095	alanine racemase	33
<i>rpsR</i>	30S ribosomal protein S18	33
<i>hpt_2</i>	Hypoxanthine-guanine phosphoribosyltransferase	33
<i>tpiA</i>	Triosephosphate isomerase	33
<i>rex</i>	Redox-sensing transcriptional repressor Rex	33
<i>frr</i>	Ribosome-recycling factor	33
group_3184	R3H domain protein	33
<i>tig</i>	Trigger factor	33
<i>recR</i>	Recombination protein RecR	33
<i>prfA</i>	Peptide chain release factor 1	33
<i>greA_1</i>	Transcription elongation factor GreA	33
<i>rpsP</i>	30S ribosomal protein S16	33
<i>sigF_2</i>	RNA polymerase sigma-F factor	33
<i>ssbB</i>	Single-stranded DNA-binding protein SsbB	33
group_3473	hypothetical protein	33
<i>tsf</i>	Elongation factor Ts	33
<i>dnaA</i>	Chromosomal replication initiator protein DnaA	33
<i>sigE</i>	RNA polymerase sigma-E factor precursor	33
<i>pyrB</i>	Aspartate carbamoyltransferase catalytic chain	33
<i>rpoB</i>	DNA-directed RNA polymerase subunit beta	33
group_3678	hypothetical protein	33
<i>rpsO</i>	30S ribosomal protein S15	33
<i>ffh</i>	Signal recognition particle protein	33
<i>lepA</i>	Elongation factor 4	33
<i>fabZ</i>	3-hydroxyacyl-[acyl-carrier-protein] dehydratase FabZ	33
<i>rpmF</i>	50S ribosomal protein L32	33
<i>sigF_1</i>	RNA polymerase sigma-F factor	33
<i>rplK</i>	50S ribosomal protein L11	33
group_4134	hypothetical protein	33
<i>glyQS</i>	Glycine--tRNA ligase	33
group_4434	hypothetical protein	33
group_4475	hypothetical protein	33
<i>rpmB</i>	50S ribosomal protein L28	33
<i>def</i>	Peptide deformylase	33
<i>ftsH_2</i>	ATP-dependent zinc metalloprotease FtsH	33
<i>accD</i>	Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta	33

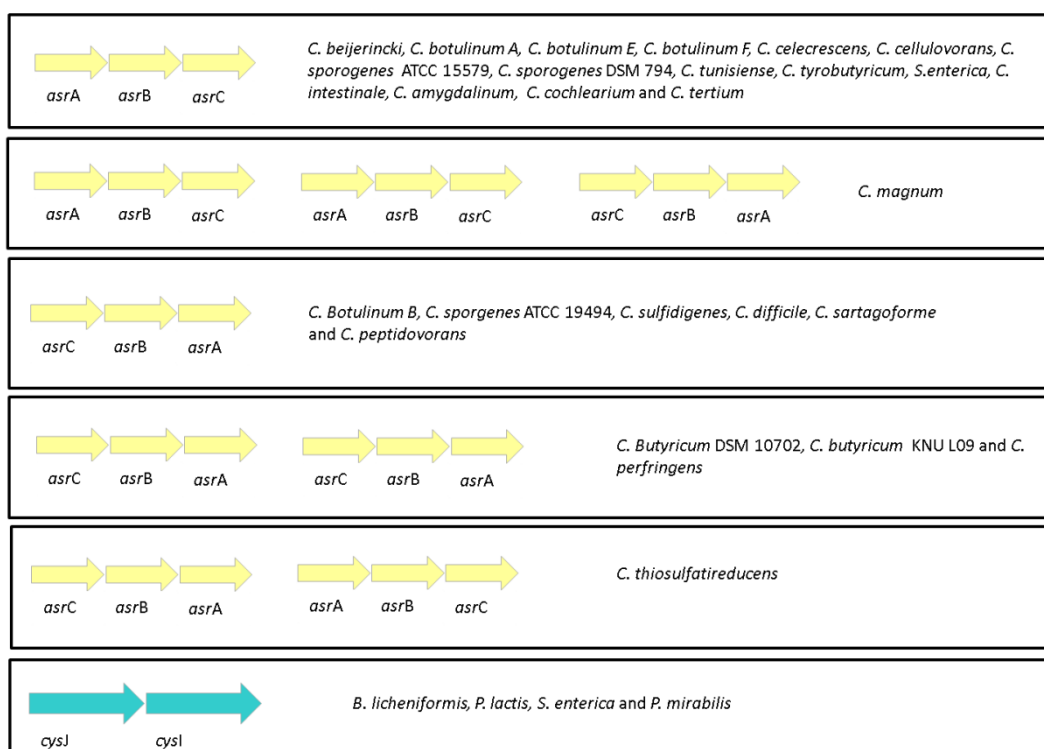
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A



B



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Fig.S1: (A) *asrABC* and *cysJI* sulphite reducing operons, with tertiary structures of proteins, (B) annotated complete sulphite reducing gene clusters in SRBs

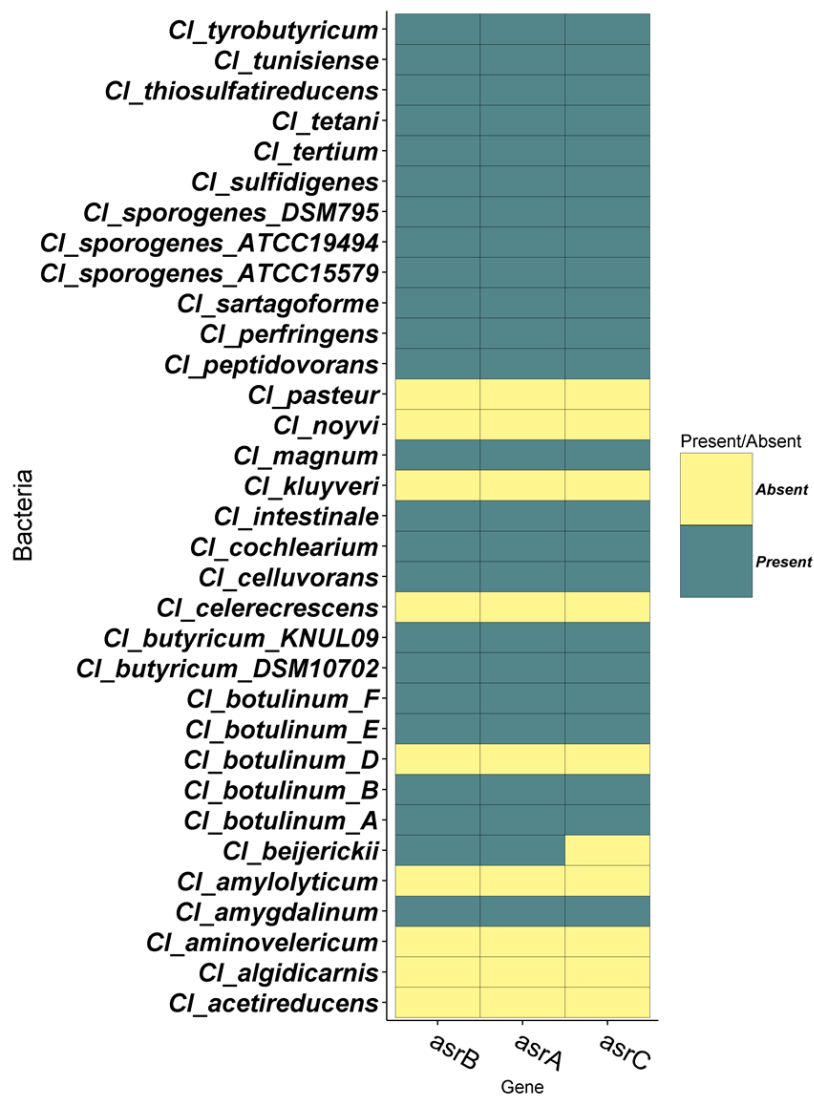
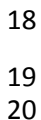


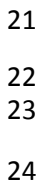
Fig.S2: Roary results for sulphite reducing genes



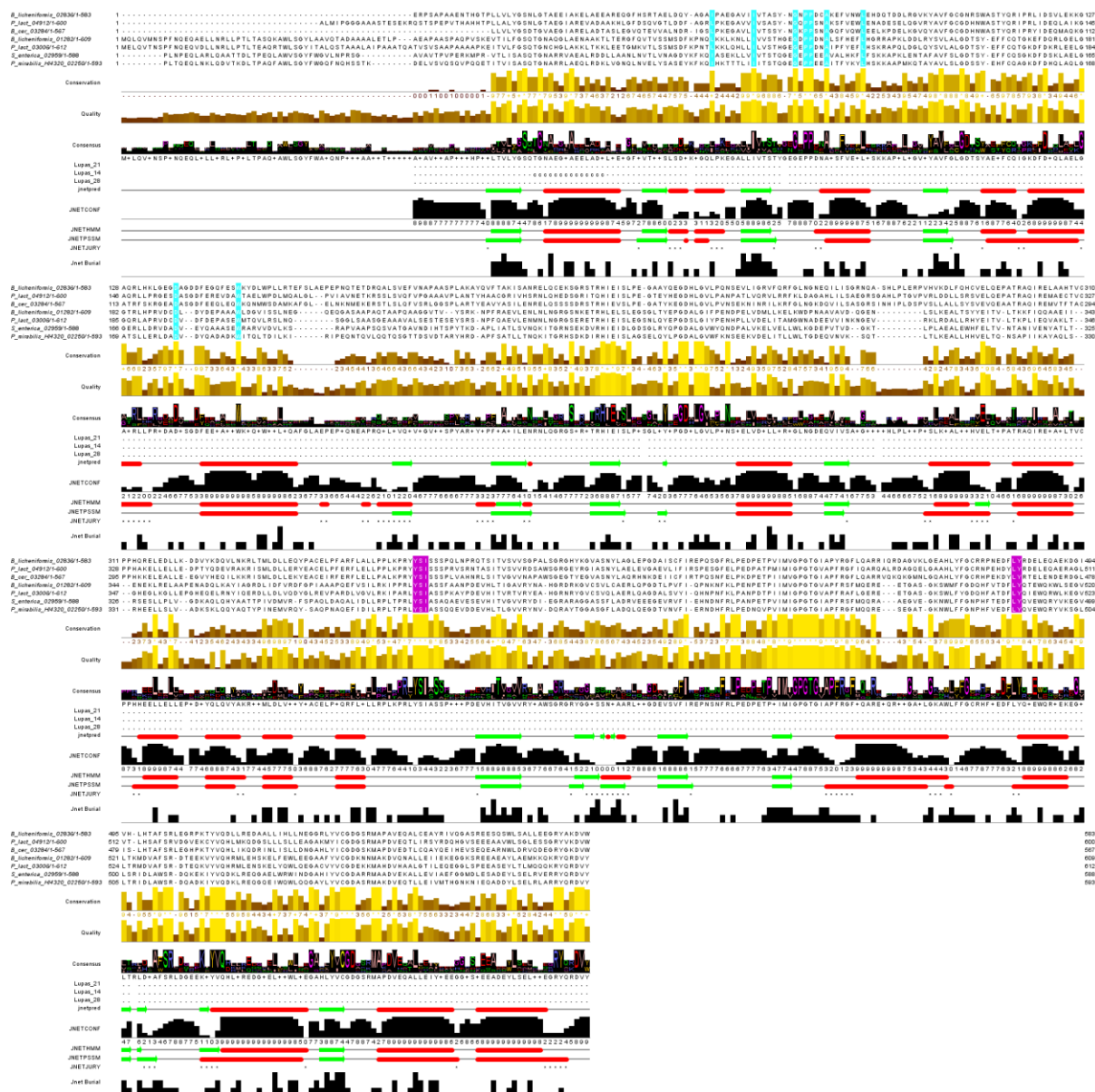
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Fig.S6: Jalview alignment of *cysJ* gene based on blastp results; conserved amino acids in the mononucleotide binding domains, highlighted in the light blue

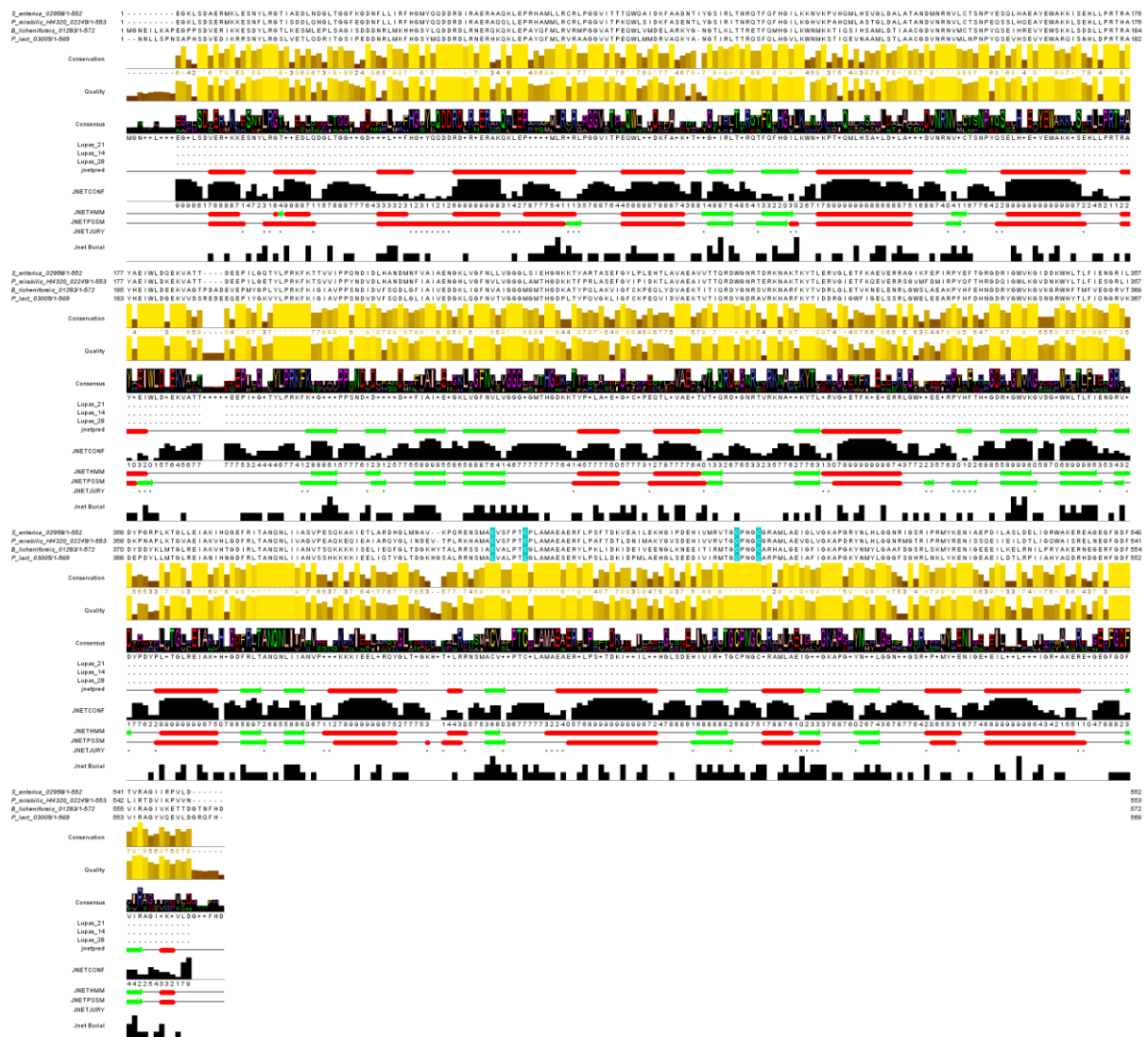


Fig.S7: Jalview alignment of *cysI* gene based on blastp results; conserved cysteine residues in this amino acid sequence are highlighted