

Table S2: Proteins identified in detergent resistant fraction of *R. leguminosarum*

| Gene | Protein | Accession ¹ | Score ² | Mw ³ | pI ⁴ | Sc ⁵ | Np ⁶ | Location ⁷ |
|--------------|--|------------------------|--------------------|-----------------|-----------------|-----------------|-----------------|-----------------------|
| <i>ropA</i> | Outer membrane protein IIIA | OM3A_RHILV | 172.6 | 39.1 | 3.9 | 9.8 | 2 | M |
| <i>rpoB</i> | DNA-directed RNA polymerase subunit beta | RPOB_RHIL3 | 93.9 | 153.6 | 4.9 | 12.5 | 16 | C |
| <i>mutS</i> | DNA mismatch repair protein MutS | MUTS_RHIL3 | 67.5 | 98.6 | 5.3 | 13.7 | 10 | C |
| <i>acdS</i> | 1-aminocyclopropane-1-carboxylate deaminase | 1A1D_RHILV | 65 | 36.8 | 5.1 | 18.6 | 5 | C |
| <i>atpA</i> | ATP synthase subunit alpha | ATPA_RHIL3 | 63.1 | 54.8 | 6 | 18.9 | 8 | M |
| <i>alaS</i> | Alanine--tRNA ligase | SYA_RHIL3 | 60.6 | 95.4 | 5.2 | 14.1 | 12 | C |
| <i>mnmG</i> | tRNA uridine 5-carboxymethylaminomethyl modification enzyme MnmG | MNMG_RHIL3 | 58.9 | 67.9 | 5.7 | 16.5 | 8 | C |
| <i>gltX</i> | Glutamate--tRNA ligase | SYE_RHIL3 | 56.8 | 55.1 | 5.7 | 25.8 | 10 | C |
| <i>katG</i> | Catalase-peroxidase | KATG_RHIL3 | 55.3 | 79.7 | 5.4 | 6.9 | 3 | C |
| <i>groL1</i> | 60 kDa chaperonin 1 | CH601_RHIL3 | 55.1 | 57.9 | 4.9 | 24.9 | 10 | C |
| <i>tsf</i> | Elongation factor Ts | EFTS_RHIL3 | 53.9 | 32.2 | 4.9 | 20.8 | 7 | C |
| <i>glnD</i> | Bifunctional uridylyltransferase/uridylyl-removing enzyme | GLND_RHILV | 51.5 | 106.7 | 6.9 | 9.5 | 8 | C |
| <i>dnaK</i> | Chaperone protein DnaK | DNAK_RHIL3 | 51.1 | 68.5 | 4.7 | 22.6 | 11 | C |
| <i>infB</i> | Translation initiation factor IF-2 | IF2_RHIL3 | 50.7 | 99.6 | 7.9 | 8.8 | 7 | C |
| <i>trmD</i> | tRNA (guanine-N(1)-)-methyltransferase | TRMD_RHIL3 | 50.2 | 26.6 | 5.8 | 30.3 | 5 | C |
| <i>hslV</i> | ATP-dependent protease subunit HslV | HSLV_RHIL3 | 47.3 | 18.7 | 5.7 | 24.6 | 7 | C |
| <i>ilvD</i> | Dihydroxy-acid dehydratase | ILVD_RHIL3 | 46.4 | 66 | 5.7 | 24.7 | 10 | C |
| <i>argG1</i> | Argininosuccinate synthase 1 | ASSY1_RHIL3 | 45.7 | 44.4 | 5.6 | 17.9 | 9 | C |
| <i>RL450</i> | UPF0235 protein RL4503 | Y4503_RHIL3 | 45.5 | 11.1 | 9.7 | 62.1 | 6 | N. d. |

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|--------------|---|------------------------|--------------------|-----------------|-----------------|-----------------|-----------------|-----------------------|
| <i>ispDF</i> | Bifunctional enzyme IspD/IspF | ISPDF_RHIL3 | 44.6 | 43.5 | 6 | 11.6 | 5 | N. d. |
| <i>modC</i> | Molybdenum import ATP-binding protein ModC | MODC_RHIL3 | 42.8 | 38.8 | 7.9 | 14.6 | 4 | M |
| <i>rpoC</i> | DNA-directed RNA polymerase subunit beta' | RPOC_RHIL3 | 42.3 | 156.3 | 6.6 | 10 | 13 | C |
| <i>prfA</i> | Peptide chain release factor 1 | RF1_RHIL3 | 41.4 | 40 | 4.9 | 28.7 | 8 | C |
| <i>miaB</i> | (Dimethylallyl)adenosin e tRNA methylthiotransferase MiaB | MIAB_RHIL3 | 40 | 53.2 | 5.7 | 17.3 | 8 | C |
| <i>rplA</i> | 50S ribosomal protein L1 | NDVA_RHIL3 | 39.6 | 24.1 | 10.1 | 29.2 | 6 | C |
| <i>ndvA</i> | Beta-(1-->2)glucan export ATP- binding/permease protein NdvA | RL1_RHIL3 | 39.6 | 64.8 | 9.1 | 10.2 | 5 | M |
| <i>xseA</i> | Exodeoxyribonuclease 7 large subunit | EX7L_RHIL3 | 39.2 | 57.4 | 10.4 | 18.6 | 8 | C |
| <i>glsA</i> | Glutaminase | GLSA_RHIL3 | 37.8 | 33.1 | 6.9 | 19.4 | 5 | C |
| <i>pyrD</i> | Dihydroorotate dehydrogenase (quinone) | PYRD_RHIL3 | 37.4 | 38.9 | 9.4 | 11.3 | 4 | M |
| <i>fhs</i> | Formate-- tetrahydrofolate ligase | FTHS_RHIL3 | 36.5 | 60.2 | 6.8 | 11.8 | 5 | C |
| <i>groL</i> | 60 kDa chaperonin | CH60_RHILV | 35.9 | 57.8 | 5 | 25.5 | 10 | C |
| <i>recA</i> | Protein RecA | RECA_RHILV | 35.6 | 37.8 | 5.2 | 21.9 | 5 | C |
| <i>rbsA1</i> | Ribose import ATP- binding protein RbsA 1 | RBSA1_RHIL3 | 35.5 | 55.9 | 6.8 | 17 | 7 | M |
| <i>rplI</i> | 50S ribosomal protein L9 | RL9_RHIL3 | 35.2 | 21.1 | 4.6 | 28.6 | 4 | C |
| <i>glyS</i> | Glycine--tRNA ligase beta subunit | SYGB_RHIL3 | 35 | 77.3 | 5.6 | 9.9 | 6 | C |
| <i>proB</i> | Glutamate 5-kinase | PROB_RHIL3 | 34.8 | 40.9 | 9.4 | 13.9 | 5 | C |
| <i>rbsA2</i> | Ribose import ATP- binding protein RbsA 2 | RBSA2_RHIL3 | 34.5 | 55.6 | 6.4 | 12.9 | 7 | M |

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| <i>ureC</i> | Urease subunit alpha | URE1_RHIL3 | 34 | 61 | 5.6 | 4 | 4 | C |
| <i>accA</i> | Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha | ACCA_RHIL3 | 33.9 | 34.6 | 6.1 | 21.8 | 4 | C |
| <i>ruvB</i> | Holliday junction ATP-dependent DNA helicase RuvB | RUVB_RHIL3 | 33.9 | 38.4 | 5.3 | 23.7 | 6 | C |
| <i>purA</i> | Adenylosuccinate synthetase | PURA_RHIL3 | 33.6 | 46.6 | 5.4 | 13 | 5 | C |
| <i>rplQ</i> | 50S ribosomal protein L17 | RL17_RHIL3 | 33.4 | 15.3 | 11.1 | 21.4 | 5 | C |
| <i>rbsA3</i> | Ribose import ATP-binding protein RbsA 3 | RBSA3_RHIL3 | 32.9 | 55.5 | 6 | 6.2 | 4 | M |
| <i>rpsF</i> | 30S ribosomal protein S6 | RS6_RHIL3 | 32.3 | 17.8 | 9.6 | 32.9 | 4 | C |
| <i>mutL</i> | DNA mismatch repair protein MutL | MUTL_RHIL3 | 32 | 64.6 | 6.3 | 9.7 | 3 | C |
| <i>ropB</i> | 22 kDa outer membrane protein | MASZ_RHILV | 31.9 | 22.5 | 4.2 | 9 | 2 | M |
| <i>glcB</i> | Malate synthase G | ROPB_RHILV | 31.9 | 80 | 5.6 | 9.4 | 8 | C |
| <i>ttcA</i> | tRNA 2-thiocytidine biosynthesis protein TtcA | TTCA_RHIL3 | 31.5 | 32.8 | 6.9 | 12.1 | 5 | C |
| <i>tdh</i> | L-threonine 3-dehydrogenase | TDH_RHIL3 | 31.2 | 37.8 | 5.9 | 20.9 | 5 | C |
| <i>nodT</i> | Nodulation protein T | NODT_RHILV | 30.9 | 51.5 | 6.6 | 11.2 | 5 | M |
| <i>hypD</i> | Hydrogenase expression/formation protein HypD | HYPD_RHILV | 30.8 | 42.6 | 6.5 | 6.2 | 3 | C |
| <i>betA</i> | Oxygen-dependent choline dehydrogenase | BETA_RHIL3 | 30.8 | 0 | 6.9 | 6.2 | 2 | M |
| <i>leuC</i> | 3-isopropylmalate dehydratase large subunit | LEUC_RHIL3 | 30.6 | 51.1 | 5.6 | 19.6 | 8 | C |
| <i>groL</i> | 60 kDa chaperonin | CH60_RHIL3 | 30.5 | 57.3 | 4.9 | 14.2 | 7 | C |

¹UniProt accession number;

²MASCOT protein score (index for determining accuracy identification by Mascot software);

³Calculated molecular weight. kDa;

⁴Calculated isoelectric point;

⁵Protein sequence coverage (%);

⁶Number of unique peptides matched to mass peaks;

⁷Protein location according to UniProt (<https://www.uniprot.org/>) database (M – membrane, C – cytoplasmic, n.d. – no data).