Table S1. TATPred analyses of putative Tat-substrates from *S. meliloti*.

Systematic identifier	Annotation	S. meliloti locus tag	Cleavage site	Prediction	Reliability Score
gi|16262454|ref|NP_435247.1|	FdoG formate dehydrogenase-O alpha subunit	SMa0002	Most likely cleavage site: 1- 38 [AEA-AV]	Tat signal peptide predicted.	Reliability score: 0.998
gi|193782528|ref|NP_435258.2|	hypothetical protein SMa0025	SMa0025	Most likely cleavage site: 1 - 30 [ARA-EE]	Tat signal peptide predicted.	Reliability score: 1.000
gi|16262474|ref|NP_435267.1|	carbonic anhydrase Cah	SMa0045	Most likely cleavage site: 1 - 25 [AYA-AE]	Tat signal peptide predicted.	Reliability score: 0.965
gi|16262498|ref|NP_435291.1|	hypothetical protein SMa0089	SMa0089		No signal peptide predicted	Reliability score: 0.177
gi|16262550|ref|NP_435343.1|	transmembrane-transport protein	SMa0185		TM segment predicted: 17 - 45	Reliability score: 0.724
gi|16262620|ref|NP_435413.1|	hypothetical protein SMa0308	SMa0308	Most likely cleavage site: 1 - 28 [TFA-KA]	Tat signal peptide predicted.	Reliability score: 0.974
gi|16262656|ref|NP_435449.1|	hydrolase	Sma0380	Most likely cleavage site: 1 - 25 [AKA-AD]	Tat signal peptide predicted.	Reliability score: 0.998
gi|193782564|ref|NP_435453.2|	short chain alcohol dehydrogenase-related dehydrogenase	SMa0389	Most likely cleavage site: 1 - 37 [AHV-AV]	Tat signal peptide predicted.	Reliability score: 0.974
gi|16262662|ref|NP_435455.1|	ABC transporter periplasmic solute-binding protein	SMa0392	Most likely cleavage site: 1 - 39 [AFA-QE]	Tat signal peptide predicted.	Reliability score: 1.000
gi|16262696|ref|NP_435489.1|	ABC transporter periplasmic solute-binding protein	SMa0514	Most likely cleavage site: 1 - 35 [AKA-AE]	Tat signal peptide predicted.	Reliability score: 0.996
gi|16262724|ref|NP_435517.1|	IdnK gluconate kinase IdnK	SMa0513	Most likely cleavage site: 1 - 33 [LGA-TY]	Tat signal peptide predicted.	Reliability score: 0.917
gi|16262760|ref|NP_435553.1|	nitrate ABC transporter substrate-binding protein	SMa0585	Most likely cleavage site: 1 - 37 [AFA-QG]	Tat signal peptide predicted.	Reliability score: 0.999
gi|193782589|ref|NP_435561.2|	hypothetical protein	SMa0604	Most likely cleavage site: 1 - 37 [SRA-QS]	Tat signal peptide predicted.	Reliability score: 0.690
gi|16262963|ref|NP_435756.1|	arylsulfatase	SMa0943	Most likely cleavage site: 1 - 40 [AKA-QT]	Tat signal peptide predicted.	Reliability score: 0.998
gi|193782626|ref|NP_435790.2|	hypothetical protein	SMa1008	Most likely cleavage site: 1 - 24 [ARA-AN]	Tat signal peptide predicted.	Reliability score: 0.998
gi|16263016|ref|NP_435809.1|	putative copper-containing oxidase	SMa1038	Most likely cleavage site: 1 - 21 [AWA-KT]	Tat signal peptide predicted.	Reliability score: 0.897
gi|16263096|ref|NP_435889.1|	nitrous-oxide reductase	SMa1182	Most likely cleavage site: 1 - 46 [ARA-QE]	Tat signal peptide predicted.	Reliability score: 1.000
gi|16263101|ref|NP_435894.1|	NosX accesory protein	SMa1188	Most likely cleavage site: 1 - 34 [AVA-AV]	Tat signal peptide predicted.	Reliability score: 0.981
gi|16263127|ref|NP_435920.1|	nitrate reductase catalytic subunit	SMA1236	Most likely cleavage site: 1 - 31 [AAA-QP]	Tat signal peptide predicted.	Reliability score: 0.990
gi|16263129|ref|NP_435922.1|	NapF ferrexdoxin component of periplasmic nitrate reductase	SMa1240	Most likely cleavage site: 1 - 31 [ATA-EG]	Tat signal peptide predicted.	Reliability score: 0.999
gi|16263134|ref|NP_435927.1|	NirK nitrite reductase	SMa1250	Most likely cleavage site: 1 - 33 [AHA-EE]	Tat signal peptide predicted.	Reliability score: 1.000
gi|193782652|ref|NP_435945.2|	Carboxylase	SMa1288	Most likely cleavage site: 1 - 44 [VDA-SG]	Tat signal peptide predicted.	Reliability score: 0.798
gi|16263198|ref|NP_435991.1|	putative inner-membrane permease	SMa1362		TM segment predicted: 33 - 56	Reliability score: 0.797
gi|16263232|ref|NP_436025.1|	ABC transporter periplasmic solute-binding protein	SMa1427	Most likely cleavage site: 1 - 44 [ARA-AL]	Tat signal peptide predicted.	Reliability score: 0.999
gi|16263240|ref|NP_436033.1|	5-dehydro-4-deoxyglucarate dehydratase	SMa1440	Most likely cleavage site: 1 - 72 [RAA-KD]	Tat signal peptide predicted.	Reliability score: 0.799
gi|193782675|ref|NP_436035.2|	hypothetical protein	SMa1445	Most likely cleavage site: 1 - 36 [SQA-DE]	Tat signal peptide predicted.	Reliability score: 0.999
gi|16263252|ref|NP_436045.1|	putative ABC transporter permease	SMa1465	Most likely cleavage site: 1 - 40 [GMA-EE]	Tat signal peptide predicted.	Reliability score: 0.792
gi|16263263|ref|NP_436056.1|	putative oxidoreductase	SMa1488	Most likely cleavage site: 1 - 50 [AQA-AA]	Tat signal peptide predicted.	Reliability score: 0.986
gi|16263273|ref|NP_436066.1|	hypothetical protein	SMa1507	Most likely cleavage site: 1 - 31 [AGA-EE]	Tat signal peptide predicted.	Reliability score: 0.999
gi|16263349|ref|NP_436142.1|	NreB protein	SMa1641	Most likely cleavage site: 1 - 41 [AGA-DA]	Tat signal peptide predicted.	Reliability score: 0.989
gi|16263356|ref|NP_436149.1|	ABC transporter	SMa1615	Most likely cleavage site: 1 - 31 [VYA-QG]	Tat signal peptide predicted.	Reliability score: 0.995
gi|16263391|ref|NP_436184.1|	MUCR family transcriptional regulatory protein IN SYRB 5'region	SMa1705	Most likely cleavage site: 1 - 28 [VIA-PD]	Tat signal peptide predicted.	Reliability score: 0.790
gi|16263442|ref|NP_436235.1|	hypothetical protein	SMa1793	Most likely cleavage site: 1 - 30 [AAA-QT]	Tat signal peptide predicted.	Reliability score: 0.974
gi|16263451|ref|NP_436244.1|	hypothetical protein	SMa1811	Most likely cleavage site: 1 - 33 [AKA-QQ]	Tat signal peptide predicted.	Reliability score: 0.992
gi|16263454|ref|NP_436247.1|	hypothetical protein	SMa1819	Most likely cleavage site: 1 - 25 [ARA-AD]	Tat signal peptide predicted.	Reliability score: 0.999
gi|16263476|ref|NP_436269.1|	ABC transporter periplasmic solute-binding protein	SMa1860	Most likely cleavage site: 1 - 55 [AVA-AT]	Tat signal peptide predicted.	Reliability score: 0.998
gi|16263511|ref|NP_436304.1|	hypothetical protein	SMa1927	Most likely cleavage site: 1 - 30 [AKA-QD]	Tat signal peptide predicted.	Reliability score: 0.984
gi|16263586|ref|NP_436379.1|	extracellular solute-binding protein	SMa2075	Most likely cleavage site: 1 - 38 [SFA-AE]	Tat signal peptide predicted.	Reliability score: 0.999
gi|16263591|ref|NP_436384.1|	ABC transporter permease	SMa2085	Most likely cleavage site: 1 - 40 [GDA-AD]	Tat signal peptide predicted.	Reliability score: 0.750
gi|193782744|ref|NP_436406.2|	hypothetical protein	SMa2129	Most likely cleavage site: 1 - 28 [TFA-AG]	Tat signal peptide predicted.	Reliability score: 0.994
gi|193782748|ref|NP_436418.2|	oxidoreductase	SMa2157	Most likely cleavage site: 1 - 36 [AGA-QQ]	Tat signal peptide predicted.	Reliability score: 0.992
gi|16263650|ref|NP_436443.1|	decarboxylase	SMa2219	Most likely cleavage site: 1 - 28 [AQA-AG]	Tat signal peptide predicted.	Reliability score: 0.993
gi|193782759|ref|NP_436487.2|	ABC transporter	SMa2305	Most likely cleavage site: 1 - 35 [ALA-QS]	Tat signal peptide predicted.	Reliability score: 0.999
gi|16263724|ref|NP_436517.1|	putative xanthine dehydrogenase iron-sulfur-binding subunit	SMa2349	Most likely cleavage site: 1 - 37 [GHA-QT]	Tat signal peptide predicted.	Reliability score: 0.983
gi|16263730|ref|NP_436523.1|	hypothetical protein	SMa2361	Most likely cleavage site: 1 - 41 [VHA-SP]	Tat signal peptide predicted.	Reliability score: 0.981
gi|15963755|ref|NP_384108.1|	Maf-like protein	SMc02792	Most likely cleavage site: 1 - 24 [GLA-FE]	Sec signal peptide predicted.	Reliability score: 0.903
gi|15963773|ref||NP_384126.1|	ABC transporter periplasmic-binding protein	SMc02774	Most likely cleavage site: 1 - 32 [SFA-QD]	Tat signal peptide predicted.	Reliability score: 0.996
gi|15963870|ref|NP_384223.1|	putative periplasmic binding ABC transporter protein	SMc04135	Most likely cleavage site: 1 - 28 [AFA-QE]	Tat signal peptide predicted.	Reliability score: 0.996
gi|15963937|ref|NP_384290.1|	hypothetical protein	SMc02859	Most likely cleavage site: 1 - 38 [LAA-AM]	Tat signal peptide predicted.	Reliability score: 0.971
gi|15963966|ref|NP_384319.1|	putative transcription regulator protein	SMc02888	Most likely cleavage site: 1 - 31 [ASA-QP]	Tat signal peptide predicted.	Reliability score: 1.000
gi|15964071|ref|NP_384424.1|	hypothetical protein	SMc00460	Most likely cleavage site: 1 - 31 [AFA-LE]	Tat signal peptide predicted.	Reliability score: 1.000
gi|15964180|ref|NP_384533.1|	putative multidrug efflux system transmembrane protein	SMc01094	Most likely cleavage site: 1 - 39 [ADA-AT]	Tat signal peptide predicted.	Reliability score: 0.982
gi|15964193|ref|NP_384546.1|	hypothetical protein	SMc01725		No signal peptide predicted	Reliability score: 0.164
gi|15964194|ref|NP_384547.1|	hypothetical protein	SMc01724	Most likely cleavage site: 1 - 31 [AVA-GE]	Tat signal peptide predicted.	Reliability score: 0.997
gi|15964223|ref|NP_384576.1|	hypothetical protein	SMc02177	Most likely cleavage site: 1 - 28 [TAA-AP]	Sec signal peptide predicted.	Reliability score: 0.980
gi|15964300|ref|NP_384653.1|	hypothetical protein	SMc02243	Most likely cleavage site: 1 - 35 [LLS-PD]	Tat signal peptide predicted.	Reliability score: 0.983
gi|15964339|ref|NP_384692.1|	putative copper-containing oxidoreductase protein	SMc02282	Most likely cleavage site: 1 - 32 [EAA-IM]	Tat signal peptide predicted.	Reliability score: 0.940
gi|15964375|ref|NP_384728.1|	hypothetical protein	SMc02316	Most likely cleavage site: 1 - 49 [AIA-KS]	Tat signal peptide predicted.	Reliability score: 0.998
gi|15964418|ref|NP_384771.1|	MotE	SMc03033	Most likely cleavage site: 1 - 33 [AFA-QD]	Sec signal peptide predicted.	Reliability score: 0.978
gi|15964471|ref|NP_384824.1|	hypothetical protein	SMc00838	Most likely cleavage site: 1 - 48 [ARA-TM]	Tat signal peptide predicted.	Reliability score: 0.987
gi|15964512|ref|NP_384865.1|	putative signal peptide protein	SMc00814	Most likely cleavage site: 1 - 30 [AGA-QE]	Tat signal peptide predicted.	Reliability score: 0.999
gi|15964515|ref|NP_384868.1|	putative carboxymethylenebutenolidase (dienelactone hydrolase)	SMc00817	Most likely cleavage site: 1 - 55 [AKA-EM]	Tat signal peptide predicted.	Reliability score: 0.997
gi|15964691|ref|NP_385044.1|	hypothetical protein	SMc00028	Most likely cleavage site: 1 - 45 [ALA-QE]	Tat signal peptide predicted.	Reliability score: 0.584
gi|15964733|ref|NP_385086.1|	putative BETA-lactamase signal peptide protein	SMc00047	Most likely cleavage site: 1 - 29 [ALA-SG]	Tat signal peptide predicted.	Reliability score: 0.988
gi|15964842|ref|NP_385195.1|	hypothetical protein	SMc02634	Most likely cleavage site: 1 - 76 [ARA-EG]	Tat signal peptide predicted.	Reliability score: 0.985
gi|15964900|ref|NP_385253.1|	guanylate kinase	SMc00577	Most likely cleavage site: 1 - 38 [LEA-DP]	Tat signal peptide predicted.	Reliability score: 0.843
gi|15964954|ref|NP_385307.1|	hypothetical protein	SMc01763	Most likely cleavage site: 1 - 34 [RSA-DG]	Tat signal peptide predicted.	Reliability score: 0.720
gi|15964960|ref|NP_385313.1|	hypothetical protein	SMc01769	Most likely cleavage site: 1 - 33 [AGA-QD]	Tat signal peptide predicted.	Reliability score: 0.999
gi|15964970|ref|NP_385323.1|	putative transport transmembrane protein	SMc01779		No signal peptide predicted	Reliability score: 0.397
gi|15965136|ref|NP_385489.1|	putative sulfite oxidase subunit YedY	SMc01281	Most likely cleavage site: 1 - 46 [AAA-LE]	Tat signal peptide predicted.	Reliability score: 0.995
gi|15965344|ref|NP_385697.1|	hypothetical protein	SMc01200	Most likely cleavage site: 1 - 29 [RSA-DS]	Tat signal peptide predicted.	Reliability score: 0.847
gi|15965362|ref|NP_385715.1|	hypothetical protein	SMc01184	Most likely cleavage site: 1 - 50 [ANA-AQ]	Tat signal peptide predicted.	Reliability score: 0.976
gi|15965379|ref|NP_385732.1|	bifunctional 2'3'-cyclic nucleotide 2'-phosphodiesterase 3'-nucleotidase periplasmic precursor protein	SMc04449	Most likely cleavage site: 1 - 33 [RAA-AN]	Tat signal peptide predicted.	Reliability score: 0.994
gi|15965446|ref|NP_385799.1|	putative periplasmic binding protein	SMc00496	Most likely cleavage site: 1 - 27 [AHA-AD]	Tat signal peptide predicted.	Reliability score: 1.000
gi|15965524|ref|NP_385877.1|	hypothetical protein	SMc00496	Most likely cleavage site: 1 - 50 [AYA-SE]	Tat signal peptide predicted.	Reliability score: 0.954
gi|15965553|ref|NP_385906.1|	putative carbohydrate kinase protein	SMc00473		No signal peptide predicted	Reliability score: 0.202
gi|15965572|ref|NP_385925.1|	ubiquinol-cytochrome C reductase IRON-sulfur subunit protein	SMc00187	Most likely cleavage site: 1 - 53 [ALA-SI]	Tat signal peptide predicted.	Reliability score: 0.996
gi|15965674|ref|NP_386027.1|	putative mannitol-binding periplasmic signal peptide protein	SMc04251	Most likely cleavage site: 1 - 29 [AIA-QT]	Tat signal peptide predicted.	Reliability score: 0.999
gi|15965749|ref|NP_386102.1|	putative histidine-rich transporter transmembrane protein	SMc04167	Most likely cleavage site: 1 - 53 [SMA-LV]	Tat signal peptide predicted.	Reliability score: 0.916

<table>
<tr><td>gi|15965789|ref|NP_386142.1|</td><td>putative toxin secretion transmembrane protein</td><td>SMc04208</td><td>Most likely cleavage site: 1 - 43 [AGA-VV]</td><td>Tat signal peptide predicted.</td><td>Reliability score: 0.989</td></tr>
<tr><td>gi|195970155|ref|NP_386154.2|</td><td>hypothetical protein</td><td>SMc04289</td><td>Most likely cleavage site: 1 - 35 [VRA-QG]</td><td>Tat signal peptide predicted.</td><td>Reliability score: 1.000</td></tr>
<tr><td>gi|15965868|ref|NP_386221.1|</td><td>hypothetical protein</td><td>SMc01432</td><td></td><td>No signal peptide predicted</td><td>Reliability score: 0.20</td></tr>
<tr><td>gi|15965895|ref|NP_386248.1|</td><td>hypothetical protein</td><td>SMc01459</td><td>Most likely cleavage site: 1 - 44 [ALA-AG]</td><td>Tat signal peptide predicted.</td><td>Reliability score: 0.994</td></tr>
<tr><td>gi|15965942|ref|NP_386295.1|</td><td>hypothetical protein</td><td>SMc01853</td><td></td><td>No signal peptide predicted</td><td>Reliability score: 0.316</td></tr>
<tr><td>gi|15965993|ref|NP_386346.1|</td><td>putative periplasmic binding ABC transporter protein</td><td>SMc01628</td><td>Most likely cleavage site: 1 - 49 [ALA-AD]</td><td>Tat signal peptide predicted.</td><td>Reliability score: 1.000</td></tr>
<tr><td>gi|15965997|ref|NP_386350.1|</td><td>putative periplasmic binding ABC transporter protein</td><td>SMc01632</td><td>Most likely cleavage site: 1 - 59 [AYA-AG]</td><td>Tat signal peptide predicted.</td><td>Reliability score: 0.996</td></tr>
<tr><td>gi|195970151|ref|NP_386360.2|</td><td>putative periplasmic binding protein</td><td>SMc01642</td><td>Most likely cleavage site: 1 - 46 [AAA-QE]</td><td>Tat signal peptide predicted.</td><td>Reliability score: 0.997</td></tr>
<tr><td>gi|15966012|ref|NP_386365.1|</td><td>putative periplasmic binding protein</td><td>SMc01647</td><td>Most likely cleavage site: 1 - 46 [ARA-QE]</td><td>Tat signal peptide predicted.</td><td>Reliability score: 1.000</td></tr>
<tr><td>gi|15966169|ref|NP_386522.1|</td><td>hypothetical protein</td><td>SMc01522</td><td>Most likely cleavage site: 1 - 42 [SQA-AG]</td><td>Tat signal peptide predicted.</td><td>Reliability score: 0.988</td></tr>
<tr><td>gi|15966231|ref|NP_386584.1|</td><td>putative haloperoxidase protein</td><td>SMc01944</td><td>Most likely cleavage site: 1 - 51 [AGA-AT]</td><td>Tat signal peptide predicted.</td><td>Reliability score: 0.977</td></tr>
<tr><td>gi|15966253|ref|NP_386606.1|</td><td>spermidine/putrescine ABC transporter periplasmic protein</td><td>SMc01966</td><td>Most likely cleavage site: 1 - 30 [LRA-QD]</td><td>Tat signal peptide predicted.</td><td>Reliability score: 0.997</td></tr>
<tr><td>gi|15966286|ref|NP_386639.1|</td><td>putative periplasmic binding ABC transporter protein</td><td>SMc02021</td><td>Most likely cleavage site: 1 - 44 [ALA-TG]</td><td>Tat signal peptide predicted.</td><td>Reliability score: 0.996</td></tr>
<tr><td>gi|15966325|ref|NP_386678.1|</td><td>putative periplasmic binding protein</td><td>SMc02344</td><td>Most likely cleavage site: 1 - 33 [ASA-GE]</td><td>Tat signal peptide predicted.</td><td>Reliability score: 0.977</td></tr>
<tr><td>gi|15966387|ref|NP_386740.1|</td><td>hypothetical protein</td><td>SMc00738</td><td>Most likely cleavage site: 1 - 31 [ALG-FE]</td><td>Tat signal peptide predicted.</td><td>Reliability score: 0.982</td></tr>
<tr><td>gi|15966410|ref|NP_386763.1|</td><td>hypothetical protein</td><td>SMc00715</td><td></td><td>TM segment predicted 22-44</td><td>Reliability score: 0.775</td></tr>
<tr><td>gi|15966492|ref|NP_386845.1|</td><td>translocation protein TolB</td><td>SMc04461</td><td>Most likely cleavage site: 1 - 28 [ANA-LV]</td><td>Tat signal peptide predicted.</td><td>Reliability score: 0.960</td></tr>
<tr><td>gi|15966501|ref|NP_386854.1|</td><td>hypothetical protein</td><td>SMc03964</td><td>Most likely cleavage site: 1 - 27 [AFG-IE]</td><td>Tat signal peptide predicted.</td><td>Reliability score: 0.993</td></tr>
<tr><td>gi|15966561|ref|NP_386914.1|</td><td>putative membrane-bound lytic murein transglycosylase protein</td><td>SMc04024</td><td>Most likely cleavage site: 1 - 29 [ARA-DQ]</td><td>Tat signal peptide predicted.</td><td>Reliability score: 0.812</td></tr>
<tr><td>gi|15966585|ref|NP_386938.1|</td><td>putative sulfite oxidase protein</td><td>SMc04049</td><td>Most likely cleavage site: 1 - 31 [AEA-KE]</td><td>Tat signal peptide predicted.</td><td>Reliability score: 1.000</td></tr>
<tr><td>gi|15966680|ref|NP_387033.1|</td><td>molybdate ABC transporter periplasmic molybdate-binding protein</td><td>SMc03196</td><td>Most likely cleavage site: 1 - 29 [AQA-AE]</td><td>Tat signal peptide predicted.</td><td>Reliability score: 0.998</td></tr>
<tr><td>gi|15966722|ref|NP_387075.1|</td><td>putative periplasmic binding ABC transporter protein</td><td>SMc03124</td><td>Most likely cleavage site: 1 - 28 [AFS-QG]</td><td>Tat signal peptide predicted.</td><td>Reliability score: 0.999</td></tr>
<tr><td>gi|15966844|ref|NP_387197.1|</td><td>putative alkaline phosphatase transmembrane protein</td><td>SMc03243</td><td>Most likely cleavage site: 1 - 34 [FYA-RG]</td><td>Tat signal peptide predicted.</td><td>Reliability score: 0.981</td></tr>
<tr><td>gi|15966861|ref|NP_387214.1|</td><td>putative antikinase protein</td><td>SMc03254</td><td>Most likely cleavage site: 1 - 23 [AFA-LD]</td><td>Tat signal peptide predicted.</td><td>Reliability score: 0.893</td></tr>
<tr><td>gi|15966886|ref|NP_387239.1|</td><td>putative oxidoreductase protein</td><td>SMc03287</td><td>Most likely cleavage site: 1 - 29 [ARA-QA]</td><td>Tat signal peptide predicted.</td><td>Reliability score: 0.997</td></tr>
<tr><td>gi|15966945|ref|NP_387298.1|</td><td>hypothetical protein</td><td>SMc03809</td><td>Most likely cleavage site: 1 - 42 [AQA-SA]</td><td>Tat signal peptide predicted.</td><td>Reliability score: 0.989</td></tr>
<tr><td>gi|15966988|ref|NP_387341.1|</td><td>hypothetical protein</td><td>SMc03852</td><td>Most likely cleavage site: 1 - 32 [VLV-QH]</td><td>Tat signal peptide predicted.</td><td>Reliability score: 0.878</td></tr>
<tr><td>gi|16263875|ref|NP_436667.1|</td><td>hypothetical protein</td><td>SM_b20127</td><td>Most likely cleavage site: 1 - 25 [AFA-EG]</td><td>Tat signal peptide predicted.</td><td>Reliability score: 0.987</td></tr>
<tr><td>gi|16263957|ref|NP_436749.1|</td><td>putative epoxide hydrolase protein</td><td>SM_b20216</td><td>Most likely cleavage site: 1 - 53 [SFA-AI]</td><td>Tat signal peptide predicted.</td><td>Reliability score: 0.881</td></tr>
<tr><td>gi|16263961|ref|NP_436753.1|</td><td>putative epoxide hydrolase protein</td><td>SM_b20221</td><td>Most likely cleavage site: 1 - 46 [AQA-GT]</td><td>Tat signal peptide predicted.</td><td>Reliability score: 0.997</td></tr>
<tr><td>gi|16263970|ref|NP_436762.1|</td><td>putative ABC transporter sugar-binding protein</td><td>SM_b20231</td><td>Most likely cleavage site: 1 - 43 [VRA-QE]</td><td>Tat signal peptide predicted.</td><td>Reliability score: 0.999</td></tr>
<tr><td>gi|16264022|ref|NP_436814.1|</td><td>putative ABC transporter periplasmic spermidine putrescine-binding protein</td><td>SM_b20284</td><td>Most likely cleavage site: 1 - 33 [AFS-QS]</td><td>Tat signal peptide predicted.</td><td>Reliability score: 0.951</td></tr>
<tr><td>gi|16264054|ref|NP_436846.1|</td><td>TRAP-type large permease component</td><td>SM_b20320</td><td>Most likely cleavage site: 1 - 28 [VRA-QE]</td><td>Tat signal peptide predicted.</td><td>Reliability score: 1.000</td></tr>
<tr><td>gi|16264065|ref|NP_436857.1|</td><td>hypothetical protein</td><td>SM_b20331</td><td>Most likely cleavage site: 1 - 36 [AEA-AP]</td><td>Sec signal peptide predicted</td><td>Reliability score: 0.959</td></tr>
<tr><td>gi|16264076|ref|NP_436868.1|</td><td>putative isoquinoline 1-oxidoreductase</td><td>SM_b20342</td><td>Most likely cleavage site: 1 - 48 [ALA-GE]</td><td>Tat signal peptide predicted.</td><td>Reliability score: 0.998</td></tr>
<tr><td>gi|16264117|ref|NP_436909.1|</td><td>putative ABC transporter periplasmic solute-binding protein</td><td>SM_b20383</td><td>Most likely cleavage site: 1 - 38 [ASA-EE]</td><td>Tat signal peptide predicted.</td><td>Reliability score: 1.000</td></tr>
<tr><td>gi|16264138|ref|NP_436930.1|</td><td>putative aldehyde dehydrogenase protein</td><td>SM_b20404</td><td>Most likely cleavage site: 1 - 31 [AFA-QE]</td><td>Tat signal peptide predicted.</td><td>Reliability score: 1.000</td></tr>
<tr><td>gi|16264191|ref|NP_436983.1|</td><td>hypothetical protein</td><td>SM_b20461</td><td>Most likely cleavage site: 1 - 40 [ASA-EV]</td><td>Tat signal peptide predicted.</td><td>Reliability score:0.781</td></tr>
<tr><td>gi|16264243|ref|NP_437035.1|</td><td>putative protein-glutamate methyltransferase protein</td><td>SM_b20514</td><td>Most likely cleavage site: 1 - 84 [FAA-AV]</td><td>Tat signal peptide predicted.</td><td>Reliability score: 0.890</td></tr>
<tr><td>gi|16264265|ref|NP_437057.1|</td><td>putative solute-binding protein</td><td>SM_b20538</td><td>Most likely cleavage site: 1 - 28 [ALA-AE]</td><td>Tat signal peptide predicted.</td><td>Reliability score: 1.000</td></tr>
<tr><td>gi|16264420|ref|NP_437212.1|</td><td>putative transcriptional regulator</td><td>SM_b21093</td><td>Most likely cleavage site: 1 - 30 [AAA-ES]</td><td>Tat signal peptide predicted.</td><td>Reliability score: 0.965</td></tr>
<tr><td>gi|16264513|ref|NP_437305.1|</td><td>putative mureinpeptideoligopeptide ABC transporter periplasmic solute-binding protein precursor</td><td>SM_b21261</td><td>Most likely cleavage site: 1 - 31 [ALA-TL]</td><td>Tat signal peptide predicted.</td><td>Reliability score: 0.978</td></tr>
<tr><td>gi|16264540|ref|NP_437332.1|</td><td>xanthine dehydrogenase protein</td><td>SM_b21288</td><td>Most likely cleavage site: 1 - 28 [ASA-AG]</td><td>Tat signal peptide predicted.</td><td>Reliability score: 0.953</td></tr>
<tr><td>gi|16264630|ref|NP_437422.1|</td><td>putative dipeptide uptake ABC transporter periplasmic solute-binding protein precursor</td><td>SM_b21215</td><td>Most likely cleavage site: 1 - 52 [ARA-SG]</td><td>Tat signal peptide predicted.</td><td>Reliability score: 0.999</td></tr>
<tr><td>gi|16264653|ref|NP_437445.1|</td><td>hypothetical protein</td><td>SM_b21329</td><td>Most likely cleavage site: 1 - 34 [AIA-AV]</td><td>Tat signal peptide predicted.</td><td>Reliability score: 0.936</td></tr>
<tr><td>gi|16264661|ref|NP_437453.1|</td><td>iron-sulfur-binding protein</td><td>SM_b21337</td><td>Most likely cleavage site: 1 - 43 [AVA-AP]</td><td>Tat signal peptide predicted.</td><td>Reliability score: 0.994</td></tr>
<tr><td>gi|16264669|ref|NP_437461.1|</td><td>putative sugar uptake ABC transporter periplasmic solute-binding protein precursor</td><td>SM_b21345</td><td>Most likely cleavage site: 1 - 28 [AFA-EL]</td><td>Tat signal peptide predicted.</td><td>Reliability score: 0.999</td></tr>
<tr><td>gi|16264672|ref|NP_437464.1|</td><td>putative 2-deoxy-D-gluconate 3-dehydrogenase protein</td><td>SM_b21348</td><td>Most likely cleavage site: 1 - 34 [ARA-GG]</td><td>Tat signal peptide predicted.</td><td>Reliability score: 0.979</td></tr>
<tr><td>gi|16264706|ref|NP_437498.1|</td><td>catechol 1, 2-dioxygenase</td><td>SM_b21380</td><td>Most likely cleavage site: 1 - 30 [VWA-QL]</td><td>Tat signal peptide predicted.</td><td>Reliability score: 0.985</td></tr>
<tr><td>gi|16264709|ref|NP_437501.1|</td><td>SDR family dehydrogenase protein</td><td>SM_b21383</td><td>Most likely cleavage site: 1 - 39 [AQA-QS]</td><td>Tat signal peptide predicted.</td><td>Reliability score: 0.987</td></tr>
<tr><td>gi|16264733|ref|NP_437525.1|</td><td>hypothetical protein</td><td>SM_b21544</td><td>Most likely cleavage site: 1 - 28 [VAA-QS]</td><td>Tat signal peptide predicted.</td><td>Reliability score: 0.996</td></tr>
<tr><td>gi|16264746|ref|NP_437538.1|</td><td>putative aldehyde or xanthine dehydrogenase iron-sulfur subunit protein</td><td>SM_b21558</td><td>Most likely cleavage site: 1 - 41 [AAA-DS]</td><td>Tat signal peptide predicted.</td><td>Reliability score: 0.990</td></tr>
<tr><td>gi|16264829|ref|NP_437621.1|</td><td>putative glucosyltransferase protein</td><td>SM_b20956</td><td></td><td>No signal peptide predicted</td><td>Reliability score: 0.173</td></tr>
<tr><td>gi|16264923|ref|NP_437715.1|</td><td>hypothetical protein</td><td>SM_b20881</td><td>Most likely cleavage site: 1 - 26 [AFA-AG]</td><td>Tat signal peptide predicted.</td><td>Reliability score: 1.000</td></tr>
<tr><td>gi|16264956|ref|NP_437748.1|</td><td>hypothetical protein</td><td>SM_b20910</td><td>Most likely cleavage site: 1 - 48 [AIA-KS]</td><td>Tat signal peptide predicted.</td><td>Reliability score: 0.998</td></tr>
<tr><td>gi|16264962|ref|NP_437754.1|</td><td>putative arylsulfatase protein</td><td>SM_b20915</td><td>Most likely cleavage site: 1 - 46 [AQA-AS]</td><td>Tat signal peptide predicted.</td><td>Reliability score: 0.997</td></tr>
<tr><td>gi|16265069|ref|NP_437861.1|</td><td>hypothetical protein</td><td>SM_b21492</td><td>Most likely cleavage site: 1 - 42 [AAA-RA]</td><td>Sec signal peptide predicted.</td><td>Reliability score: 0.965</td></tr>
<tr><td>gi|16265094|ref|NP_437886.1|</td><td>hypothetical protein</td><td>SM_b21516</td><td>Most likely cleavage site: 1 - 35 [AER-AP]</td><td>Tat signal peptide predicted.</td><td>Reliability score: 0.983</td></tr>
<tr><td>gi|16265099|ref|NP_437891.1|</td><td>hypothetical protein</td><td>SM_b21521</td><td>Most likely cleavage site: 1 - 30 [ALS-GS]</td><td>Tat signal peptide predicted.</td><td>Reliability score: 0.925</td></tr>
<tr><td>gi|16265115|ref|NP_437907.1|</td><td>putative sugar uptake ABC transporter periplasmic solute-binding protein precursor</td><td>SM_b20660</td><td>Most likely cleavage site: 1 - 30 [AQA-EP]</td><td>Tat signal peptide predicted.</td><td>Reliability score: 0.996</td></tr>
<tr><td>gi|16265126|ref|NP_437918.1|</td><td>putative sugar uptake ABC transporter periplasmic solute-binding protein precursor</td><td>SM_b20671</td><td>Most likely cleavage site: 1 - 30 [ALA-QD]</td><td>Tat signal peptide predicted.</td><td>Reliability score: 0.998</td></tr>
<tr><td>gi|16265216|ref|NP_438008.1|</td><td>putative adenylate cyclase protein</td><td>SM_b20776</td><td>Most likely cleavage site: 1 - 43 [LRA-YD]</td><td>Tat signal peptide predicted.</td><td>Reliability score: 0.622</td></tr>
<tr><td>gi|16265268|ref|NP_438060.1|</td><td>putative transcriptional regulator ArsR family protein</td><td>SM_b20608</td><td>Most likely cleavage site: 1 - 34 [ELA-AP]</td><td>Tat signal peptide predicted.</td><td>Reliability score: 0.807</td></tr>
<tr><td>gi|16265272|ref|NP_438064.1|</td><td>C4-dicarboxylate transport sensor protein</td><td>SM_b20612</td><td>Most likely cleavage site: 1 - 55 [ALA-GL]</td><td>Tat signal peptide predicted.</td><td>Reliability score: 0.961</td></tr>
<tr><td>gi|16265274|ref|NP_438066.1|</td><td>hypothetical protein</td><td>SM_b20614</td><td>Most likely cleavage site: 1 - 44 [GMA-GY]</td><td>Tat signal peptide predicted.</td><td>Reliability score: 0.839</td></tr>
<tr><td>gi|16265280|ref|NP_438072.1|</td><td>putative sugar uptake ABC transporter periplasmic solute-binding protein precursor</td><td>SM_b20620</td><td>Most likely cleavage site: 1 - 27 [SLA-AD]</td><td>Tat signal peptide predicted.</td><td>Reliability score: 0.975</td></tr>
</table>

The 145 proteins predicted to contain twin arginine leaders were downloaded (http://www.compgen.org/tools/PRED-TAT/supplement/genomes) and reanalyzed using TAT-PRED. The results are tabulated such that, systematic identifers, locus tags, most likely cleavage sites, and reliability scores are presented. Coloured fonts were used to denote proteins that were not bonafide predictions. Font colours are used as follows; Green, No signal petide; Red, sec signal peptide; Blue, Transmembrane segment.

Table S2. Bacterial Strains and Plasmids

Strain or plasmid	Relevant characteristics*	Reference or source
Strains		
S. meliloti		
Rm1021	SU47 *str-21*, Sm^r	(4)
SRmA691	Rm1021, Δ*SMa1236*	This work
SRmA693	Rm1021, Δ*SMb20660*	This work
SRmA703	Rm1021, Δ*SMb21337*	This work
SRmA709	Rm1021, Δ*SMc01724*	This work
SRmA720	Rm1021, Δ*SMa2125*	This work
SRmA722	Rm1021, Δ*SMa1507*	This work
SRmA725	Rm1021, Δ*SMa1038*	This work
SRmA729	Rm1021, Δ*SMc03063*	This work
SRmA730	Rm1021, Δ*SMc04137*	This work
SRmA731	Rm1021, Δ*SMc01632*	This work
SRmA821	Rm1021, Δ*SMa2129*	This work
SRmA823	Rm1021, Δ*SMb20383*	This work
SRmA862	Rm1021, Δ*SMb20231*	This work
SRmA961	Rm1021, Δ*SMa1641*	This work
SRmD212	Rm1021, Δ*SMb20404*	This work
SRmD214	Rm1021, Δ*SMb20671*	This work
SRmD216	Rm1021, Δ*SMb21558*	This work
SRmD218	Rm1021, Δ*SMc04218*	This work
SRmD220	Rm1021, Δ*SMc00577*	This work
SRmD222	Rm1021, Δ*SMc04167*	This work
SRmD224	Rm1021, Δ*SMc00817*	This work
SRmD226	Rm1021, Δ*SMc04049*	This work
SRmD228	Rm1021, Δ*SMc02021*	This work
SRmD230	Rm1021, Δ*SMb21380*	This work
SRmD232	Rm1021, Δ*SMc00187*	This work
SRmD234	Rm1021, Δ*SMa0943*	This work
SRmD236	Rm1021, Δ*SMa1182*	This work
SRmD238	Rm1021, Δ*SMa1819*	This work
SRmD240	Rm1021, Δ*SMa2157*	This work
SRmD242	Rm1021, Δ*SMb20342*	This work
E. coli		
DB3.1	F$^-$*gyrA462 endA1* Δ(*sr1-recA*) *mcrB mrr hsdS20* (r_B^- m_B^-) *supE44 ara-14 galK2 lacY1proA2 rpsL20 (Sm^r) xyl-5 Δleu mtl-1*	(3)
DB3.1 λ*pir*	λ*pir* lysogen of DB3.1	(3)
DH5αR λ*pir*	Rif^r derivative of DH5α λ*pir*	(3)
DH5α	λ$^-$ Φ80d*lacZ*°M15 °(*lacZYA-argF*)*U169 recA1 endA1 hsdR17*(r_K^- m_K^-) *supE44 thi-1 gyrA relA1*	(2)

DH5α λpir	λpir lysogen of DH5α	(3)
HMS17-1	Rif^r derivative of S17-1	(3)
S17-1	*recA* derivative of MM294A with integrated RP4-2 (Tc::Mu::Kan::Tn*7*)	(5)
MM294A	*pro-82 thi-1 hsdR17 supE44*	(1)
MT607	MM294A *recA56*	(1)
MT616	MT607(pRK600)	(1)
Plasmids		
pRK600	pRK2013 *npt*::Tn*9*, Cm^r	(1)
pBH474	Suc^s derivative of pTH474	(3)
pMK2016	Spc^r Sm^r *oriV oriT*ColE1 with FRT cassette from pMK2014	(3)
pMK2017	Tet^r *oriV* R6K *oriT*RP4 with FRT cassette from pMK2015	(3)
pXINT129	Kan^r; λ *int* and *xis* driven by P$_{lac}$	(3)
pBP152	*SMa1041* in pMK2017 destination vector	This work
pBP153	*SMa1183* in pMK2017 destination vector	This work
pBP154	*SMc04048* in pMK2017 destination vector	This work
pBP156	*SMa2153* in pMK2017 destination vector	This work
pBP157	*SMb20670* in pMK2017 destination vector	This work
pBP158	*SMc00578* in pMK2017 destination vector	This work
pBP161	*SMc04217* in pMK2017 destination vector	This work
pBP163	*SMc00186* in pMK2017 destination vector	This work
pBP164	*SMc02020* in pMK2017 destination vector	This work
pBP165	*SMa945* in pMK2017 destination vector	This work
pBP166	*SMc01724* in pMK2017 destination vector	This work
pBP167	*SMc00818* in pMK2017 destination vector	This work
pBP168	*SMc01633* in pMK2017 destination vector	This work
pBP169	*SMb20341* in pMK2017 destination vector	This work
pBP170	*SMb20405* in pMK2017 destination vector	This work
pBP171	*SMb21559* in pMK2017 destination vector	This work
pBP193	*SMa2159* in pMK2016 destination vector	This work
pBP197	*SMc01631* in pMK2016 destination vector	This work
pBP199	*SMc00576* in pMK2016 destination vector	This work
pBP201	*SMb21380* in pMK2017 destination vector	This work
pBP203	*SMa1820* in pMK2017 destination vector	This work
pBP204	*SMc04168* in pMK2017 destination vector	This work
pBP205	*SMc01723* in pMK2016 destination vector	This work
pBP213	*SMa941* in pMK2016 destination vector	This work
pBP216	*SMb20434* in pMK2016 destination vector	This work
pBP218	*SMb21557* in pMK2016 destination vector	This work
pBP219	*SMb20672* in pMK2016 destination vector	This work
pBP220	*SMc04050* in pMK2016 destination vector	This work
pBP221	*SMa816* in pMK2016 destination vector	This work
pBP223	*SMb20403* in pMK2016 destination vector	This work
pBP226	*SMc04166* in pMK2016 destination vector	This work
pBP229	*SMb21381* in pMK2016 destination vector	This work
pBP231	*SMc00188* in pMK2016 destination vector	This work
pBP234	*SMa1817* in pMK2016 destination vector	This work
pBP236	*SMc04219* in pMK2016 destination vector	This work
pBP238	*SMc02022* in pMK2016 destination vector	This work

pBP240	*SMa1179* in pMK2016 destination vector	This work
pBP258	*SMa2131* in pMK2017 destination vector	This work
pBP259	*SMa2127* in pMK2016 destination vector	This work
pBP260	*SMa1639* in pMK2016 destination vector	This work
pBP261	*SMa1643* in pMK2017 destination vector	This work
pHY1	*SMb20230* in pMK2017 destination vector	This work
pHY2	*SMb20232* in pMK2016 destination vector	This work
pHY8	*SMb20661* in pMK2017 destination vector	This work
pHY12	*SMb21338* in pMK2017 destination vector	This work
pHY16	*SMa1239* in pMK2017 destination vector	This work
pHY20	*SMa1509* in pMK2017 destination vector	This work
pHY24	*SMb21336* in pMK2016 destination vector	This work
pHY28	*SMa1233* in pMK2016 destination vector	This work
pHY32	*SMb20659* in pMK2016 destination vector	This work
pHY40	*SMa1505* in pMK2016 destination vector	This work
pHY64	*SMc03064* in pMK2017 destination vector	This work
pHY66	*SMc04138* in pMK2017 destination vector	This work
pHY72	*SMb20384* in pMK2017 destination vector	This work
pHY74	*SMa2127* in pMK2017 destination vector	This work
pHY76	*SMa1037* in pMK2016 destination vector	This work
pHY88	*SMc03062* in pMK2016 destination vector	This work
pHY90	*SMc04136* in pMK2016 destination vector	This work
pHY96	*SMb20382* in pMK2016 destination vector	This work
pHY98	*SMa2123* in pMK2016 destination vector	This work

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[*] Antibiotic abbreviations: Cm, chloramphenicol; Tc, tetracycline; Kan, kanamycin; Sm, streptomycin; Spc, spectinomycin; Rif, rifampin; Suc, sucrose.

Table S3. Primers used in this work

No.	Primer name	Sequence (5'→ 3')
1	sma0943 Fwd	ACCCGCATACAGGAAGTGTC
2	sma0943 Rvs	AGGATGAACTTCCCGAGGAT
3	sma1038 Fwd	CCCTCCTCACATACAACGCG
4	sma1038 Rvs	TGGGTGGCCTGGGCTTTCTT
5	sma1182 Fwd	GCGCCAAGGAGTGTCCGG
6	sma1182 Rvs	CTTTGCCGTTGCCCATGACA
7	sma1236 Fwd	GGCGTGTCTCTCCGCCAG
8	sma1236 Rvs	GCTGGTCGGGATAGGCGC
9	sma1507 Fwd	AGGTCTTTCCGGAGCTGAC
10	sma1507 Rvs	ATTGTGCGCTTCGATCCGTC
11	sma1641 Fwd	GGCATCTGAAAAGCGTCATT
12	sma1641 Rvs	GCCATCCAGCTGAGGAGTAG
13	sma1819 Fwd	GAATGACGATGAAGATGTATCTC
14	sma1819 Rvs	GAAGGTCTTCGCCGTCCTC
15	sma2021 Fwd	CAACCAGAGGCTGAGGTTTC
16	sma2021 Rvs	TTGCGTCGGCTTATAGGTTC
17	sma2125 Fwd	GAAGATCCTGGAAAAGCGTGC
18	sma2125 Rvs	AGGTTCAGGGCCAGACCGG
19	sma2129 Fwd	CTCTGCAGCCTATCGTCGATG
20	sma 2129 Rvs	GCGCGGTAGTATCCGTAAAGAC
21	sma2157 Fwd	CATTTGGACGCCCCGTCGC
22	sma2157 Rvs	GCGTTCCCAGCCGCTTCCC
23	smb20231 Fwd	ATCGCGCGTGTCGGCAAC
24	smb20231 Rvs	CAGCGGGTCGTTCCACATG
25	smb20342 Fwd	CGGTCCTGTCAAACCTTCAT
26	smb20342 Rvs	ACCCGTTCTTCTGGACAAGC
27	smb20383 Fwd	ATGTCGTCGGGATCAGCTT
28	smb20383 Rvs	ATGGGACCTATTGCCCCTAC
29	smb20404 Fwd	GGAGATCACCACCATCGAG
30	smb20404 Rvs	AGGCCTCGCTGATCCTTT
31	smb20660 Fwd	GACCGGCTACGAGACGCA
32	smb20660 Rvs	GATCAGAAAGACGGCTGCC
33	smb20671 Fwd	GTGCTCTATGTGGCGCAGTA
34	smb20671 Rvs	CATGTTGCTGACGCTGAAAT
35	smb21337 Fwd	CTCGAGGAACGCATCCGG
36	smb21337 Rvs	CTGAGACAGAGCCGGGTA
37	smb21380 Fwd	ACGCTGCACATGTCGTCGG
38	smb21380 Rvs	TGGCGAGCGCTCGAAGAATG
39	smb21558 Fwd	GCTTTTGCCGCTAGCTTTC
40	smb21558 Rvs	AATCTGCGCACATCCTGATT
41	smc00187 Fwd	CTATAACCCGTCAAGTCCTTG
42	smc00187 Rvs	CGGTGAGGATCTGCACGATC
43	smc00817 Fwd	CTATCGCCAGCCGCTGTTC
44	smc00817 Rvs	CGGCGCCACGTCGATGGC
45	smc01632 Fwd	CCGGTCATGGTGGCGCTGC
46	smc01632 Rvs	CAACGCCGCCGTAACCAGG
47	smc01724 Fwd	TGGTGACGATCCGCCGGT
48	smc01724 Rvs	ACGGCATCGACGACGACTT
49	smc02021 Fwd	CCTCTGGGCCACACCATG
50	smc02021 Rvs	ATGTGGACCTGTTTGCCATT
51	smc04049 Fwd	CAAGCTTCCTGCTTGTAGCC
52	smc04049 Rvs	GGGTTTGAGTTCGTCGAGAT

53	smc03063 Fwd	ACGGCGCCAATGGCTGGC
54	smc03063 Rvs	GCGCCGAGCCCTGCAATG
55	smc04137 Fwd	GGCGTCCAAGTTCCGTCAGT
56	smc04137 Rvs	TCCTCTGCCGTCGCGATGC
57	smc4167 Fwd	GTCGAGCGTGCGCTCGAAG
58	smc4167 Rvs	CGCGGCCTTGCCGAAGTTG
59	smc04218 Fwd	CAGCGGCGAGATACTGCTCG
60	smc04218 Rvs	GCACTTGCGGCCCCGGTCA
61	orf conf. Fwd	GGGGACAAGTTTGTACAAAAAACCAGGCT
62	orf conf. Rvs	GGGGACCACTTTGTACAAGAAAGCTGGGT

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