| Locus tag | Function | 42 fold regulation | 44 fold regulation | 47 fold regulation | 50 fold regulation | EtOH fold regulation | Osmo fold regulation |
|---|---|---|---|---|---|---|---|
| Bbr_0001 | dnaA Chromosomal replication initiator protein dnaA 1:1467 forward MW:54102 | 1.1 | 1.2 | 0.7 | 0.2 | 0.7 | 1.6 |
| Bbr_0002 | dnaN DNA polymerase III, beta chain 2043:3167 forward MW:41023 | 1.0 | 1.0 | 0.5 | 0.4 | 0.6 | 2.2 |
| Bbr_0003 | recF DNA replication and repair protein recF 3243:4349 forward MW:39964 | 1.0 | 1.0 | 0.4 | 0.7 | 0.4 | 1.0 |
| Bbr_0004 | Bbr_0004 Conserved hypothetical protein 4346:4816 forward MW:17466 | 0.8 | 0.8 | 0.5 | 1.1 | 0.4 | 0.5 |
| Bbr_0005 | gyrB1 DNA gyrase subunit B 4999:7089 forward MW:76955 | 0.9 | 1.4 | 1.0 | 1.0 | 1.1 | 0.7 |
| Bbr_0006 | gyrA1 DNA gyrase subunit A 7264:9954 forward MW:99717 | 0.9 | 1.5 | 0.8 | 0.3 | 1.4 | 0.8 |
| Bbr_0007 | Bbr_0007 Conserved hypothetical membrane spanning protein 10023:10574 forward MW:19588 | 1.0 | 1.0 | 0.9 | 0.7 | 1.0 | 0.6 |
| Bbr_0008 | Bbr_0008 Transcriptional regulator, LacI family 10649:11662 reverse MW:37244 | 0.9 | 0.8 | 5.4 | 4.1 | 0.9 | 1.2 |
| Bbr_0009 | Bbr_0009 Lactose permease 11931:12332 reverse MW:14358 | 1.6 | 2.4 | 1.7 | 2.6 | 0.5 | 0.5 |
| Bbr_0010 | lacZ1 Beta-galactosidase 12675:15806 forward MW:115182 | 0.7 | 0.3 | 0.9 | 0.3 | 0.9 | 1.0 |
| Bbr_0011 | Bbr_0011 Conserved hypothetical membrane spanning protein 16239:17324 forward MW:40582 | 0.9 | 1.0 | 1.4 | 1.9 | 0.7 | 0.9 |
| Bbr_0012 | gdhA NADP-specific glutamate dehydrogenase 17872:19218 reverse MW:48550 | 0.7 | 0.3 | 0.1 | 0.2 | 0.4 | 0.3 |
| Bbr_0013 | Bbr_0013 Narrowly conserved hypothetical membrane spanning protein 19324:20316 reverse MW:37242 | 0.8 | 0.3 | 0.8 | 0.6 | 0.2 | 2.8 |
| Bbr_0014 | Bbr_0014 Conserved hypothetical protein with DUF45 domain 20861:21592 forward MW:27184 | 1.0 | 1.1 | 1.5 | 2.2 | 0.3 | 2.4 |
| Bbr_0015 | Bbr_0015 Conserved hypothetical protein 22369:23682 reverse MW:50219 | 0.7 | 0.7 | 0.6 | 0.5 | 1.0 | 0.5 |
| Bbr_0016 | Bbr_0016 Conserved hypothetical protein in DPS family 23917:24396 reverse MW:17806 | 0.8 | 1.1 | 2.8 | 1.9 | 9.3 | 0.9 |
| Bbr_0018 | Bbr_0018 Narrowly conserved hypothetical membrane spanning protein 26215:26880 forward MW:23736 | 0.8 | 1.0 | 4.7 | 4.1 | 0.7 | 2.9 |
| Bbr_0019 | Bbr_0019 Transcriptional regulator, LacI family 26884:27945 forward MW:38188 | 1.0 | 1.1 | 1.2 | 2.4 | 0.8 | 1.2 |
| Bbr_0020 | Bbr_0020 Glycosyl hydrolases family 32, Beta-fructosidase 28215:29612 forward MW:53786 | 0.8 | 0.8 | 4.3 | 3.6 | 0.3 | 3.4 |
| Bbr_0021 | Bbr_0021 Solute-binding protein ABC transporter (MalE family) 29817:31130 forward MW:48498 | 0.9 | 0.7 | 2.6 | 4.0 | 0.4 | 1.0 |
| Bbr_0022 | agl1 Glycosyl hydrolases family 31, Alpha-glucosidase 31622:34195 reverse MW:95887 | 0.8 | 0.5 | 0.7 | 1.2 | 0.8 | 0.9 |
| Bbr_0023 | Bbr_0023 Transcriptional regulator, LacI family 34350:35363 reverse MW:36432 | 0.7 | 0.5 | 2.0 | 2.6 | 1.2 | 0.4 |
| Bbr_0024 | Bbr_0024 Transposase 35527:36633 reverse MW:42308 | 0.9 | 1.1 | 2.6 | 6.2 | 1.0 | 0.8 |
| Bbr_0026 | Bbr_0026 Permease protein of ABC transporter system for sugars 39047:39883 reverse MW:31119 | 0.8 | 0.2 | 0.6 | 0.3 | 0.6 | 0.4 |
| Bbr_0027 | Bbr_0027 Permease protein of ABC transporter system for sugars 39880:40734 reverse MW:31408 | 0.6 | 0.2 | 0.5 | 0.7 | 0.5 | 0.7 |
| Bbr_0030 | Bbr_0030 Conserved hypothetical protein 44050:45150 reverse MW:41928 | 0.8 | 0.4 | 3.3 | 1.0 | 0.7 | 0.6 |
| Bbr_0032 | Bbr_0032 Transcriptional regulator, LacI family 46942:47976 reverse MW:37146 | 1.0 | 1.2 | 8.6 | 25.4 | 1.0 | 1.1 |
| Bbr_0033 | Bbr_0033 Solute binding protein of ABC transporter system (MalE family) 48339:49724 forward MW:51649 | 0.5 | 0.1 | 1.2 | 2.4 | 1.0 | 0.3 |
| Bbr_0034 | Bbr_0034 Conserved hypothetical protein in DPS family 50113:50592 reverse MW:17822 | 0.6 | 1.0 | 2.6 | 1.3 | 7.8 | 0.7 |
| Bbr_0035 | Bbr_0035 Conserved hypothetical membrane spanning protein with duf21 and CBS domains 50755:52020 reverse MW:45786 | 1.0 | 1.3 | 0.8 | 0.5 | 1.1 | 0.7 |
| Bbr_0036 | Bbr_0036 Conserved hypothetical protein 52334:53470 forward MW:40680 | 0.8 | 0.9 | 2.6 | 6.0 | 0.9 | 1.3 |
| Bbr_0037 | icfA Carbonic anhydrase 53486:54169 reverse MW:24902 | 0.8 | 0.7 | 1.2 | 1.4 | 1.5 | 2.2 |
| Bbr_0038 | ahpC Alkyl hydroperoxide reductase C22 protein 54436:54999 forward MW:21257 | 0.5 | 0.3 | 0.3 | 0.1 | 3.9 | 0.8 |
| Bbr_0039 | trxB1 Thioredoxin reductase/Thioredoxin/Glutaredoxin family protein 55153:57066 forward MW:66176 | 0.6 | 0.4 | 0.8 | 0.3 | 3.6 | 1.2 |
| Bbr_0040 | Bbr_0040 Nucleoside-diphosphate-sugar epimerase 57372:59579 forward MW:83005 | 1.1 | 1.3 | 1.5 | 2.0 | 0.5 | 0.8 |
| Bbr_0041 | Bbr_0041 Conserved hypothetical membrane spanning protein 59591:60490 forward MW:34115 | 1.3 | 1.5 | 0.1 | 0.4 | 0.4 | 0.3 |
| Bbr_0042 | Bbr_0042 Conserved hypothetical protein 60487:61089 forward MW:21905 | 1.2 | 1.2 | 0.3 | 0.8 | 0.2 | 0.3 |
| Bbr_0043 | Bbr_0043 Conserved hypothetical protein 61208:62365 forward MW:42746 | 1.0 | 1.2 | 1.3 | 4.7 | 0.2 | 1.3 |
| Bbr_0044 | Bbr_0044 Glycosyl transferase (group 1) 62362:63780 forward MW:53848 | 1.1 | 1.2 | 0.9 | 2.0 | 0.1 | 1.3 |
| Bbr_0045 | Bbr_0045 Conserved hypothetical membrane spanning protein 63782:65329 forward MW:57331 | 1.2 | 1.3 | 2.1 | 18.5 | 0.2 | 1.2 |
| Bbr_0046 | Bbr_0046 Conserved hypothetical protein 65333:67147 forward MW:68877 | 1.5 | 1.1 | 0.5 | 1.3 | 0.2 | 0.9 |
| Bbr_0047 | Bbr_0047 Conserved hypothetical protein 67137:67961 forward MW:32012 | 1.5 | 1.3 | 0.9 | 2.4 | 0.4 | 1.1 |
| Bbr_0048 | Bbr_0048 Conserved hypothetical membrane spanning protein 68039:68704 forward MW:24610 | 0.9 | 1.7 | 15.5 | 53.0 | 0.6 | 20.4 |
| Bbr_0049 | Bbr_0049 Conserved hypothetical protein containing diguanylate cyclase/phosphodiesterase (EAL/GGDEF) domain 68729:70993 forward MW:853 | 1.5 | 1.5 | 1.2 | 1.1 | 0.2 | 1.3 |
| Bbr_0050 | Bbr_0050 Conserved hypothetical protein containing ATP-binding domain 71215:71907 forward MW:25531 | 1.4 | 1.6 | 2.5 | 3.9 | 0.3 | 2.2 |
| Bbr_0051 | Bbr_0051 Conserved hypothetical protein similar to ATP-dependent DNA helicases 71894:73543 forward MW:60432 | 1.5 | 2.9 | 15.4 | 2.5 | 0.5 | 2.3 |
| Bbr_0052 | ppc Phosphoenolpyruvate carboxylase 73711:76464 reverse MW:102591 | 0.5 | 0.4 | 0.2 | 0.2 | 1.1 | 1.5 |
| Bbr_0053 | Bbr_0053 Conserved hypothetical membrane spanning protein with DUF1212 domain 76760:78748 forward MW:71987 | 1.2 | 1.1 | 0.9 | 2.2 | 0.6 | 0.7 |
| Bbr_0054 | opuE Sodium/proline symporter 78982:80622 forward MW:58749 | 1.0 | 0.9 | 0.7 | 1.0 | 0.4 | 0.8 |
| Bbr_0055 | Bbr_0055 Conserved hypothetical protein 81110:82099 reverse MW:37410 | 0.9 | 0.5 | 0.6 | 1.3 | 0.4 | 3.3 |
| Bbr_0056 | Bbr_0056 Conserved hypothetical protein 82546:84168 forward MW:57854 | 1.0 | 0.9 | 0.8 | 1.0 | 1.3 | 1.5 |
| Bbr_0057 | trpS Tryptophanyl-tRNA synthetase 84703:85794 reverse MW:39952 | 1.1 | 1.1 | 0.8 | 0.5 | 0.9 | 0.6 |
| Bbr_0058 | Bbr_0058 Narrowly conserved hypothetical protein 85928:86311 forward MW:13459 | 1.1 | 1.6 | 7.5 | 12.2 | 2.6 | 1.9 |
| Bbr_0059 | Bbr_0059 Conserved hypothetical protein 86524:87093 reverse MW:20022 | 0.9 | 1.1 | 0.9 | 1.7 | 1.3 | 0.8 |
| Bbr_0060 | glgP1 Glycogen phosphorylase 87237:89759 forward MW:94070 | 0.7 | 0.5 | 0.4 | 0.3 | 1.0 | 1.2 |
| Bbr_0061 | Bbr_0061 Narrowly conserved hypothetical protein 90062:90289 reverse MW:8161 | 0.6 | 0.4 | 0.8 | 1.0 | 0.6 | 0.7 |
| Bbr_0062 | Bbr_0062 Conserved hypothetical membrane spanning protein in rhomboid family 90455:91195 forward MW:27190 | 0.9 | 1.3 | 2.2 | 1.3 | 1.7 | 1.5 |
| Bbr_0063 | Bbr_0063 Conserved hypothetical membrane spanning protein in uncharacterised protein family (UPF0233) 91725:92186 reverse MW:17029 | 1.0 | 1.0 | 1.7 | 2.2 | 1.0 | 0.3 |
| Bbr_0064 | Bbr_0064 Conserved hypothetical secreted protein with DUF881 domain 92275:93063 forward MW:28198 | 0.9 | 1.0 | 1.1 | 0.7 | 2.4 | 0.6 |
| Bbr_0065 | Bbr_0065 Conserved hypothetical membrane spanning protein in sortase family 93060:94265 forward MW:44248 | 0.9 | 0.8 | 0.2 | 0.3 | 1.4 | 0.4 |
| Bbr_0066 | pabA Para-aminobenzoate synthase glutamine amidotransferase component II 94344:94988 forward MW:22891 | 1.1 | 1.0 | 0.7 | 0.7 | 1.1 | 0.4 |
| Bbr_0067 | pknB Serine/threonine protein kinase 95061:97112 reverse MW:72190 | 0.9 | 0.7 | 0.3 | 0.6 | 0.7 | 0.6 |
| Bbr_0068 | pknA1 Serine/threonine protein kinase 97109:98059 reverse MW:34650 | 0.9 | 0.7 | 0.1 | 0.5 | 0.6 | 0.7 |
| Bbr_0069 | pbp1 Penicillin-binding protein 98056:99522 reverse MW:51062 | 0.9 | 0.7 | 0.2 | 0.4 | 0.7 | 0.6 |
| Bbr_0070 | rodA Cell division protein ftsW 99519:101126 reverse MW:57720 | 0.8 | 0.8 | 0.2 | 0.3 | 0.6 | 0.6 |
| Bbr_0071 | pp2c Protein phosphatase 2C 101123:102742 reverse MW:57144 | 0.9 | 0.9 | 0.2 | 0.3 | 0.5 | 1.4 |
| Bbr_0072 | Bbr_0072 Conserved hypothetical secreted protein with FHA domain 102747:103271 reverse MW:19126 | 1.0 | 0.9 | 0.9 | 0.5 | 0.8 | 1.9 |
| Bbr_0073 | Bbr_0073 Conserved hypothetical protein with FHA domain 103302:104003 reverse MW:25371 | 0.9 | 0.8 | 0.8 | 0.9 | 0.9 | 1.2 |
| Bbr_0074 | pepX Xaa-Pro dipeptidyl-peptidase 104456:107326 reverse MW:103920 | 0.9 | 1.0 | 0.3 | 0.7 | 1.4 | 0.7 |
| Bbr_0075 | pldB Lysophospholipase L2 107631:108722 forward MW:40589 | 1.1 | 1.1 | 0.8 | 1.2 | 0.8 | 1.4 |
| Bbr_0076 | Bbr_0076 Hsp20-family heat shock chaperone 108922:109425 forward MW:18730 | 19.4 | 26.7 | 51.8 | 119.3 | 1.8 | 5.4 |
| Bbr_0077 | Bbr_0077 Conserved hypothetical membrane spanning protein with DUF6 domain 109799:110779 forward MW:33702 | 1.4 | 2.2 | 7.8 | 17.3 | 0.9 | 1.1 |
| Bbr_0078 | Bbr_0078 Hypothetical protein 111019:111228 forward MW:7287 | 0.9 | 1.2 | 4.2 | 6.1 | 0.8 | 1.3 |
| Bbr_0079 | Bbr_0079 Conserved hypothetical membrane spanning protein 111452:112807 forward MW:47922 | 1.1 | 1.3 | 1.2 | 1.5 | 0.9 | 1.5 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| Bbr_0080 | lysX Lysylcardiolipin synthase/Lysyltransferase 112804:115428 forward MW:94747 | 1.0 | 1.1 | 0.4 | 0.6 | 0.7 | 0.9 |
| Bbr_0081 | msrA/msrB1 Peptide methionine sulfoxide reductase msrA/msrB 116027:117043 forward MW:37863 | 0.9 | 0.9 | 0.9 | 1.0 | 2.0 | 1.2 |
| Bbr_0082 | Bbr_0082 Antibiotic resistance protein 117122:117841 forward MW:25569 | 0.9 | 0.8 | 1.1 | 2.1 | 1.2 | 1.5 |
| Bbr_0083 | Bbr_0083 Fic family protein 117882:118943 reverse MW:39573 | 0.9 | 0.6 | 1.1 | 0.5 | 0.8 | 0.6 |
| Bbr_0084 | Bbr_0084 Glycosyltransferase 119122:120180 forward MW:36887 | 0.7 | 0.8 | 1.1 | 1.8 | 0.4 | 2.6 |
| Bbr_0085 | Bbr_0085 DNA/RNA helicase (DEAD/DEAH box family) 120187:123393 reverse MW:121321 | 0.8 | 0.5 | 0.8 | 1.3 | 0.5 | 0.4 |
| Bbr_0086 | Bbr_0086 Conserved hypothetical protein with DUF74 domain 123744:124436 forward MW:24864 | 0.8 | 1.1 | 1.0 | 1.6 | 0.4 | 1.0 |
| Bbr_0087 | Bbr_0087 Conserved hypothetical membrane spanning protein (hemolysin III homolog) 124497:125354 reverse MW:30125 | 1.5 | 2.4 | 13.8 | 9.6 | 1.4 | 30.1 |
| Bbr_0088 | tgt Queuine tRNA-ribosyltransferase 125839:127152 reverse MW:48353 | 1.1 | 0.9 | 0.6 | 1.0 | 1.0 | 1.6 |
| Bbr_0089 | degP DO serine protease containing PDZ domain 127555:129510 forward MW:65678 | 1.0 | 1.7 | 4.9 | 1.0 | 3.6 | 1.9 |
| Bbr_0090 | Bbr_0090 Lead, cadmium, zinc and mercury transporting ATPase 130071:132536 forward MW:85779 | 0.6 | 0.6 | 3.0 | 2.0 | 0.8 | 3.0 |
| Bbr_0091 | fprA Ferredoxin--NADP reductase 132924:134375 forward MW:53046 | 1.3 | 1.5 | 0.5 | 0.5 | 0.8 | 0.8 |
| Bbr_0092 | htpX Endopeptidase htpX (EC 3.4.24.-) 134772:135695 forward MW:33155 | 0.7 | 0.8 | 1.0 | 1.2 | 1.4 | 0.9 |
| Bbr_0093 | Bbr_0093 Transporter, drug/metabolite exporter family 135961:136896 forward MW:33393 | 1.1 | 1.4 | 1.3 | 1.1 | 0.7 | 5.7 |
| Bbr_0094 | fba Fructose-bisphosphate aldolase 136959:138026 forward MW:38248 | 1.0 | 1.1 | 1.2 | 1.0 | 1.9 | 0.9 |
| Bbr_0095 | purA Adenylosuccinate synthetase 138194:139480 forward MW:46508 | 1.1 | 1.0 | 0.8 | 0.5 | 0.8 | 0.6 |
| Bbr_0096 | Bbr_0096 Chloride channel protein 139504:141087 forward MW:56028 | 0.9 | 0.9 | 0.9 | 0.5 | 0.7 | 0.8 |
| Bbr_0097 | crcb1 CrcB family protein 141275:142339 forward MW:37025 | 0.7 | 0.7 | 1.8 | 2.8 | 0.7 | 1.0 |
| Bbr_0098 | crcb2 CrcB family protein 142339:142734 forward MW:14204 | 0.8 | 0.6 | 1.1 | 1.1 | 0.5 | 0.7 |
| Bbr_0099 | scrR1 Transcriptional regulator, LacI family 143009:144094 forward MW:39358 | 1.1 | 0.8 | 1.2 | 3.4 | 0.6 | 0.7 |
| Bbr_0100 | scrP Sucrose phosphorylase 144521:146047 forward MW:56412 | 0.8 | 0.5 | 1.7 | 1.2 | 0.6 | 3.2 |
| Bbr_0101 | scrT Sucrose transporter 146252:147886 forward MW:57196 | 0.9 | 1.4 | 1.8 | 0.9 | 1.2 | 0.9 |
| Bbr_0102 | scrR2 Transcriptional regulator, LacI family 147956:149008 forward MW:37473 | 1.0 | 1.0 | 1.8 | 1.9 | 1.2 | 1.0 |
| Bbr_0103 | Bbr_0103 Transporter, MFS superfamily 149996:151363 forward MW:49288 | 1.0 | 1.1 | 0.4 | 1.3 | 0.4 | 1.7 |
| Bbr_0104 | ilvC1 Ketol-acid reductoisomerase/2-dehydropantoate 2-reductase 151758:152810 forward MW:38550 | 0.6 | 0.2 | 0.1 | 0.3 | 0.5 | 0.1 |
| Bbr_0105 | cebR Cellobiose transport system transcriptional regulator 153080:154084 forward MW:36674 | 0.8 | 0.6 | 0.9 | 0.7 | 0.5 | 0.7 |
| Bbr_0106 | cebE Cellobiose/cellotriose binding protein 154265:155572 forward MW:47291 | 0.5 | 0.1 | 1.7 | 0.5 | 0.3 | 0.6 |
| Bbr_0107 | cebF Cellobiose/cellotriose transport system permease protein CebF 155651:156772 forward MW:41448 | 0.5 | 0.2 | 0.9 | 0.2 | 0.1 | 0.6 |
| Bbr_0108 | cebG Cellobiose/cellotriose transport system permease protein CebG 156780:157727 forward MW:33983 | 0.6 | 0.2 | 0.5 | 0.3 | 0.2 | 0.6 |
| Bbr_0109 | bgl1 Beta-glucosidase 157834:159234 forward MW:52130 | 0.5 | 0.2 | 0.6 | 1.4 | 0.2 | 0.8 |
| Bbr_0110 | ilvC2 Ketol-acid reductoisomerase/2-dehydropantoate 2-reductase 159499:160551 forward MW:38576 | 0.6 | 0.4 | 0.8 | 1.0 | 0.7 | 0.5 |
| Bbr_0111 | agl2 Alpha-glucosidase 160736:162553 reverse MW:67086 | 0.9 | 1.0 | 1.1 | 2.5 | 1.1 | 0.6 |
| Bbr_0112 | Bbr_0112 Transcriptional regulator, LacI family 162825:163856 reverse MW:36478 | 1.2 | 1.4 | 1.7 | 1.6 | 1.3 | 0.5 |
| Bbr_0113 | Bbr_0113 Cell surface protein precursor with Cna protein B-type domain and Gram-positive cocci surface proteins LPxTG motif profile 164585:169 | 0.9 | 1.0 | 1.2 | 2.1 | 0.9 | 1.1 |
| Bbr_0114 | Bbr_0114 Cell surface protein with Gram positive anchor and Cna protein B-type domain 169274:171112 forward MW:64651 | 0.8 | 0.7 | 0.7 | 1.3 | 0.8 | 0.3 |
| Bbr_0115 | Bbr_0115 Sortase 171366:172325 forward MW:34714 | 0.9 | 0.5 | 0.4 | 1.0 | 1.0 | 0.5 |
| Bbr_0116 | malQ1 4-alpha-glucanotransferase 172642:174846 reverse MW:81226 | 0.5 | 0.2 | 0.3 | 0.3 | 1.1 | 0.8 |
| Bbr_0117 | agl3 Alpha-glucosidase 175102:176991 reverse MW:69871 | 0.8 | 0.2 | 0.2 | 0.2 | 0.4 | 1.0 |
| Bbr_0118 | malE Maltose/maltodextrin-binding protein 177248:178489 forward MW:43955 | 0.3 | 0.1 | 0.1 | 0.2 | 0.3 | 3.1 |
| Bbr_0119 | malC Maltodextrin transport system permease protein malC 178830:180233 forward MW:52448 | 0.3 | 0.1 | 0.1 | 0.2 | 0.3 | 1.2 |
| Bbr_0120 | malG Maltose transport system permease protein malG 180230:181150 forward MW:34676 | 0.3 | 0.1 | 0.1 | 0.2 | 0.4 | 1.1 |
| Bbr_0121 | Bbr_0121 Conserved hypothetical membrane spanning protein 181335:182138 forward MW:29528 | 0.3 | 0.1 | 0.3 | 0.6 | 0.6 | 1.2 |
| Bbr_0122 | Bbr_0122 Transcriptional regulator, LacI family 182139:183164 reverse MW:37603 | 1.1 | 1.5 | 2.4 | 1.3 | 0.7 | 7.1 |
| Bbr_0123 | apuB Amylopullulanase 183482:188608 forward MW:182362 | 0.3 | 0.1 | 0.3 | 0.5 | 0.9 | 0.8 |
| Bbr_0124 | dnaK Chaperone protein dnaK 188855:190735 forward MW:66873 | 3.5 | 7.0 | 10.2 | 29.3 | 3.6 | 16.7 |
| Bbr_0125 | grpE GrpE protein 190735:191418 forward MW:24387 | 3.2 | 6.7 | 7.8 | 22.8 | 3.6 | 13.1 |
| Bbr_0126 | dnaJ1 Chaperone protein dnaJ 191597:192610 forward MW:35328 | 3.6 | 8.2 | 10.2 | 24.9 | 1.6 | 16.2 |
| Bbr_0127 | Bbr_0127 Heat shock regulatory protein hspR 192766:193353 forward MW:21844 | 2.6 | 6.1 | 8.8 | 23.8 | 1.9 | 15.4 |
| Bbr_0129 | fabG 3-oxoacyl-[acyl-carrier protein] reductase 194593:195396 forward MW:27638 | 1.0 | 1.2 | 2.8 | 8.1 | 0.5 | 14.3 |
| Bbr_0130 | Bbr_0130 Haloacid dehalogenase-like hydrolase (HAD superfamily) 195509:196180 forward MW:24169 | 1.1 | 1.0 | 2.0 | 2.1 | 1.5 | 1.6 |
| Bbr_0131 | dedA1 DedA family protein 196332:197057 forward MW:26511 | 0.9 | 1.2 | 1.3 | 0.7 | 0.7 | 0.7 |
| Bbr_0132 | Bbr_0132 Septum site-determining protein minD 197244:198182 forward MW:33175 | 0.7 | 0.9 | 1.6 | 7.5 | 0.4 | 6.5 |
| Bbr_0133 | Bbr_0133 Conserved hypothetical secreted protein similar to type II/IV secretion system protein 198223:199218 forward MW:35414 | 0.9 | 1.0 | 1.9 | 8.0 | 0.3 | 6.4 |
| Bbr_0134 | Bbr_0134 Conserved hypothetical membrane spanning protein 199230:199940 forward MW:25118 | 0.8 | 1.1 | 1.4 | 2.4 | 0.3 | 0.8 |
| Bbr_0135 | Bbr_0135 Conserved hypothetical secreted protein with prokaryotic membrane lipoprotein lipid attachment site 199963:200619 forward MW:22778 | 0.7 | 0.9 | 0.9 | 4.8 | 0.4 | 2.0 |
| Bbr_0136 | Bbr_0136 Conserved hypothetical protein 200911:201198 forward MW:10118 | 1.0 | 1.1 | 1.2 | 3.4 | 0.4 | 1.3 |
| Bbr_0137 | Bbr_0137 Conserved hypothetical protein 201215:201595 forward MW:13173 | 0.9 | 0.6 | 1.3 | 4.8 | 0.3 | 0.6 |
| Bbr_0138 | Bbr_0138 Narrowly conserved hypothetical secreted protein 201627:202016 forward MW:13243 | 0.9 | 0.9 | 1.7 | 4.2 | 0.5 | 0.6 |
| Bbr_0139 | Bbr_0139 Conserved hypothetical protein 202081:203211 forward MW:40736 | 1.0 | 1.5 | 3.6 | 5.4 | 1.3 | 0.3 |
| Bbr_0140 | Bbr_0140 Transcriptional regulator, TetR family 203290:203889 reverse MW:22583 | 1.0 | 1.1 | 2.1 | 0.9 | 0.8 | 0.4 |
| Bbr_0141 | dnaX DNA polymerase III subunit gamma/tau 204111:206843 forward MW:93748 | 1.0 | 0.9 | 0.6 | 0.6 | 1.0 | 0.6 |
| Bbr_0142 | recR Recombination protein recR 206888:207490 forward MW:21734 | 0.9 | 0.9 | 1.0 | 1.3 | 0.7 | 0.5 |
| Bbr_0144 | Bbr_0144 Sortase 208177:209400 reverse MW:43499 | 0.7 | 0.5 | 0.2 | 0.3 | 0.4 | 0.2 |
| Bbr_0145 | Bbr_0145 Conserved hypothetical protein 209419:209808 reverse MW:14525 | 0.7 | 1.0 | 0.6 | 3.0 | 0.3 | 1.6 |
| Bbr_0146 | Bbr_0146 DNA-binding protein 210101:211093 reverse MW:36765 | 1.1 | 1.6 | 2.2 | 11.8 | 0.6 | 1.2 |
| Bbr_0147 | askA Aspartokinase 211317:212081 forward MW:26848 | 1.2 | 1.2 | 1.3 | 1.7 | 0.9 | 0.3 |
| Bbr_0148 | askB Aspartokinase 212173:212715 forward MW:18704 | 1.6 | 1.4 | 0.4 | 0.3 | 0.8 | 0.2 |
| Bbr_0149 | asd Aspartate-semialdehyde dehydrogenase 213112:214206 reverse MW:40258 | 0.8 | 0.6 | 1.0 | 0.5 | 0.8 | 0.4 |
| Bbr_0150 | Bbr_0150 Conserved hypothetical protein 214440:215060 forward MW:22624 | 1.0 | 0.9 | 0.5 | 0.9 | 0.8 | 0.3 |
| Bbr_0153 | Bbr_0153 Solute binding protein of ABC transporter system 219293:220417 forward MW:40056 | 1.1 | 1.7 | 10.3 | 24.9 | 0.7 | 5.0 |
| Bbr_0154 | Bbr_0154 Permease protein of ABC transporter system 220457:221356 forward MW:32281 | 1.3 | 1.7 | 3.6 | 3.8 | 0.4 | 3.9 |
| Bbr_0155 | Bbr_0155 Permease protein of ABC transporter system 221344:222270 forward MW:32673 | 1.4 | 1.5 | 0.8 | 0.6 | 0.4 | 1.3 |
| Bbr_0156 | Bbr_0156 ATP-binding protein of ABC transporter system 222267:223385 forward MW:39614 | 1.4 | 1.6 | 0.6 | 1.8 | 0.3 | 1.0 |
| Bbr_0157 | Bbr_0157 Phosphodiesterase I/nucleotide pyrophosphatase 223456:224283 forward MW:30264 | 1.3 | 1.6 | 4.5 | 3.7 | 0.7 | 1.1 |
| Bbr_0158 | Bbr_0158 Hypothetical protein 224277:224708 reverse MW:16084 | 1.0 | 1.4 | 1.3 | 3.0 | 0.8 | 0.4 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| Bbr_0160 | Bbr_0160 Conserved hypothetical protein 228001:228909 forward MW:32703 | 0.6 | 0.4 | 2.1 | 2.3 | 1.7 | 1.0 |
| Bbr_0161 | Bbr_0161 Conserved hypothetical protein in ROK family 228906:229913 forward MW:33361 | 0.8 | 0.8 | 2.3 | 2.0 | 1.4 | 0.9 |
| Bbr_0162 | Bbr_0162 N-acetylmannosamine-6-phosphate 2-epimerase 229943:230611 forward MW:23429 | 0.7 | 0.7 | 1.1 | 4.2 | 0.7 | 1.2 |
| Bbr_0163 | Bbr_0163 Hydrolase 230626:231444 forward MW:30155 | 0.7 | 0.7 | 0.9 | 1.8 | 0.8 | 0.7 |
| Bbr_0164 | oppA1 Oligopeptide-binding protein oppA 231641:233203 forward MW:57416 | 0.4 | 0.1 | 1.8 | 1.4 | 0.6 | 0.6 |
| Bbr_0165 | oppB1 Oligopeptide transport system permease protein oppB 233314:234270 forward MW:34607 | 0.3 | 0.1 | 0.4 | 0.3 | 0.5 | 0.7 |
| Bbr_0166 | oppD1 Oligopeptide transport ATP-binding protein oppD 234272:236302 forward MW:73167 | 0.5 | 0.2 | 4.0 | 3.7 | 0.9 | 0.9 |
| Bbr_0167 | oppF1 Oligopeptide transport ATP-binding protein oppF 236299:237123 forward MW:29549 | 0.5 | 0.4 | 1.5 | 1.7 | 1.0 | 1.0 |
| Bbr_0168 | dapA1/nanA Dihydrodipicolinate synthase/N-acetylneuraminate lyase 237232:238194 forward MW:33993 | 0.6 | 0.5 | 1.1 | 0.9 | 0.9 | 0.9 |
| Bbr_0169 | nagB1 Glucosamine-6-phosphate isomerase 238233:239045 forward MW:28653 | 0.6 | 0.7 | 2.3 | 1.6 | 0.7 | 0.7 |
| Bbr_0171 | Bbr_0171 Sialidase A 239422:241713 forward MW:83102 | 0.6 | 0.5 | 1.3 | 2.3 | 0.6 | 0.8 |
| Bbr_0172 | Bbr_0172 ATPase 241753:243114 forward MW:50737 | 1.0 | 1.3 | 4.0 | 7.2 | 1.4 | 1.1 |
| Bbr_0173 | Bbr_0173 Transcriptional regulator, GntR family 243163:244014 reverse MW:31028 | 0.7 | 0.9 | 3.8 | 0.5 | 2.8 | 2.2 |
| Bbr_0174 | Bbr_0174 Conserved hypothetical protein 244877:246349 reverse MW:53071 | 1.1 | 1.4 | 1.7 | 1.7 | 2.3 | 0.6 |
| Bbr_0175 | leuA 2-isopropylmalate synthase 246581:248497 forward MW:70335 | 1.1 | 0.9 | 1.2 | 0.5 | 1.5 | 0.7 |
| Bbr_0176 | pbp2 Penicillin binding protein 248656:251010 reverse MW:84324 | 1.2 | 1.4 | 0.8 | 0.8 | 2.5 | 1.7 |
| Bbr_0177 | Bbr_0177 Conserved hypothetical membrane spanning protein containing phosphatase domain 251394:252572 forward MW:40269 | 1.0 | 1.0 | 1.1 | 1.7 | 1.6 | 2.3 |
| Bbr_0178 | topA DNA topoisomerase I 252676:255726 forward MW:109674 | 1.2 | 1.0 | 0.3 | 0.4 | 1.4 | 0.8 |
| Bbr_0179 | tmk Thymidylate kinase 255994:256665 forward MW:24418 | 1.0 | 1.2 | 0.6 | 1.1 | 1.8 | 2.1 |
| Bbr_0180 | Bbr_0180 DNA polymerase III, delta' subunit 256662:257813 forward MW:41499 | 0.8 | 0.9 | 0.8 | 1.4 | 1.3 | 0.8 |
| Bbr_0181 | Bbr_0181 Transcriptional regulator, LacI family 257965:258594 reverse MW:22133 | 0.6 | 0.3 | 1.2 | 1.5 | 0.5 | 2.9 |
| Bbr_0182 | Bbr_0182 Phosphocarrier protein HPr 258718:258978 reverse MW:8576 | 0.4 | 0.1 | 0.1 | 0.2 | 0.1 | 0.4 |
| Bbr_0183 | Bbr_0183 Phosphoenolpyruvate-protein phosphotransferase 259236:260885 forward MW:56897 | 0.6 | 0.3 | 0.5 | 0.7 | 0.6 | 0.8 |
| Bbr_0184 | Bbr_0184 Hypothetical protein 261203:261751 reverse MW:19814 | 1.0 | 1.5 | 4.7 | 11.4 | 0.9 | 2.1 |
| Bbr_0185 | Bbr_0185 Hypothetical protein 261897:262544 forward MW:22842 | 0.7 | 0.7 | 7.0 | 7.5 | 0.4 | 6.8 |
| Bbr_0186 | Bbr_0186 Conserved hypothetical protein 262694:263248 forward MW:20490 | 1.1 | 1.2 | 1.1 | 1.4 | 1.1 | 0.6 |
| Bbr_0187 | pepD Dipeptidase A (EC 3.4.13.-) 263391:264992 forward MW:59751 | 1.4 | 1.2 | 0.7 | 0.5 | 1.6 | 1.0 |
| Bbr_0188 | fhs Formate--tetrahydrofolate ligase 265106:266623 forward MW:53928 | 1.4 | 1.6 | 0.9 | 0.5 | 1.5 | 1.0 |
| Bbr_0189 | Bbr_0189 Conserved hypothetical protein 267061:267408 reverse MW:12657 | 0.9 | 0.6 | 0.5 | 0.4 | 0.7 | 0.4 |
| Bbr_0190 | Bbr_0190 Conserved hypothetical membrane spanning protein with GtrA-like domain 267653:268189 forward MW:20384 | 1.2 | 1.5 | 1.6 | 1.1 | 0.6 | 1.1 |
| Bbr_0191 | Bbr_0191 Conserved hypothetical membrane spanning protein 268512:269963 reverse MW:52048 | 1.3 | 1.1 | 2.1 | 1.4 | 0.7 | 0.5 |
| Bbr_0192 | gpm1 Phosphoglycerate mutase 270203:270862 forward MW:24627 | 1.1 | 0.9 | 1.0 | 0.8 | 1.6 | 1.0 |
| Bbr_0193 | Bbr_0193 Narrowly conserved hypothetical protein 271127:272095 forward MW:34019 | 0.7 | 0.4 | 0.5 | 0.7 | 0.9 | 0.7 |
| Bbr_0194 | Bbr_0194 Conserved hypothetical protein 272292:273476 forward MW:41738 | 0.6 | 0.2 | 0.9 | 3.1 | 0.9 | 1.3 |
| Bbr_0195 | Bbr_0195 Conserved hypothetical membrane spanning protein with DUF805 domain 273595:274944 reverse MW:46542 | 0.7 | 0.4 | 0.3 | 0.3 | 0.6 | 0.6 |
| Bbr_0196 | gltX1 Glutamyl-tRNA synthetase 275365:276885 forward MW:56516 | 1.0 | 1.4 | 0.6 | 0.3 | 1.3 | 0.5 |
| Bbr_0197 | Bbr_0197 Narrowly conserved hypothetical protein 277748:278245 reverse MW:17374 | 1.3 | 1.6 | 4.7 | 4.4 | 1.1 | 1.8 |
| Bbr_0198 | Bbr_0198 Conserved hypothetical membrane spanning protein with DUF1275 domain 278411:279226 reverse MW:28701 | 1.1 | 1.5 | 4.4 | 2.0 | 1.6 | 2.7 |
| Bbr_0199 | Bbr_0199 Transcriptional regulator, MarR family 279593:279922 reverse MW:12346 | 1.6 | 2.0 | 6.5 | 8.9 | 0.8 | 2.8 |
| Bbr_0200 | Bbr_0200 Conserved hypothetical protein 280120:280581 forward MW:16013 | 1.3 | 1.4 | 1.7 | 3.1 | 0.4 | 1.5 |
| Bbr_0201 | Bbr_0201 DNA-binding protein 280706:282331 forward MW:60050 | 1.0 | 1.2 | 1.0 | 1.9 | 0.5 | 1.8 |
| Bbr_0202 | Bbr_0202 Hypothetical secreted protein 282676:283200 reverse MW:18979 | 0.9 | 1.2 | 1.8 | 5.9 | 1.5 | 2.1 |
| Bbr_0203 | Bbr_0203 Conserved hypothetical membrane spanning protein 283376:284944 forward MW:55182 | 1.0 | 1.2 | 1.8 | 1.7 | 0.4 | 1.2 |
| Bbr_0204 | Bbr_0204 Multi-domain protein possibly involved in fatty acids or polyketide biosynthesis 284960:289324 forward MW:159700 | 1.1 | 1.3 | 1.6 | 2.0 | 0.5 | 0.7 |
| Bbr_0205 | Bbr_0205 Multi-domain protein possibly involved in fatty acids or polyketide biosynthesis 289321:291855 forward MW:91039 | 1.1 | 2.1 | 12.3 | 21.8 | 0.4 | 0.7 |
| Bbr_0208 | Bbr_0208 Transcriptional regulator, TetR family 294719:295354 forward MW:23652 | 0.8 | 0.8 | 5.4 | 9.7 | 0.7 | 0.4 |
| Bbr_0209 | Bbr_0209 Phosphopantetheinyl transferase component of siderophore synthetase 295303:295986 reverse MW:24530 | 1.0 | 1.3 | 5.7 | 7.5 | 1.6 | 0.8 |
| Bbr_0210 | Bbr_0210 Hypothetical protein 296425:297024 reverse MW:22191 | 1.1 | 0.9 | 1.1 | 3.7 | 0.6 | 1.0 |
| Bbr_0211 | Bbr_0211 Hypothetical protein 297021:297281 reverse MW:9407 | 1.6 | 2.2 | 1.3 | 3.6 | 0.4 | 1.3 |
| Bbr_0212 | Bbr_0212 Hypothetical membrane spanning protein 297620:298123 reverse MW:18531 | 0.5 | 0.5 | 1.3 | 1.2 | 0.3 | 2.6 |
| Bbr_0213 | Bbr_0213 Hypothetical protein 298636:299040 reverse MW:15544 | 0.6 | 0.3 | 0.2 | 0.2 | 0.3 | 0.3 |
| Bbr_0214 | Bbr_0214 Type II restriction-modification system restriction subunit 299276:300067 reverse MW:30003 | 0.7 | 0.6 | 0.4 | 1.1 | 0.3 | 0.5 |
| Bbr_0215 | Bbr_0215 Conserved hypothetical protein 302123:303040 reverse MW:33910 | 0.9 | 1.3 | 1.2 | 0.3 | 1.1 | 0.6 |
| Bbr_0216 | Bbr_0216 Modification methylase (EC 2.1.1.73) 303053:304231 reverse MW:43207 | 0.8 | 1.3 | 5.3 | 3.1 | 0.9 | 1.9 |
| Bbr_0217 | Bbr_0217 Conserved hypothetical protein 304322:305830 reverse MW:57427 | 1.3 | 1.3 | 0.5 | 0.6 | 0.4 | 0.4 |
| Bbr_0218 | Bbr_0218 Hypothetical protein 306004:306408 reverse MW:15407 | 0.9 | 0.9 | 2.8 | 2.7 | 0.7 | 4.7 |
| Bbr_0219 | tnpY TnpY-like protein 306530:308701 reverse MW:77991 | 0.8 | 1.1 | 2.2 | 4.1 | 1.4 | 1.1 |
| Bbr_0220 | Bbr_0220 DNA integration/recombination/inversion protein 309355:311028 reverse MW:60997 | 1.4 | 1.3 | 1.7 | 0.9 | 1.0 | 5.1 |
| Bbr_0221 | Bbr_0221 Conserved hypothetical membrane spanning protein with iron permease FTR1 family domain 311843:313759 forward MW:68402 | 0.7 | 0.4 | 0.3 | 1.0 | 0.6 | 0.6 |
| Bbr_0222 | Bbr_0222 Conserved hypothetical secreted protein 313876:314571 forward MW:24422 | 0.8 | 0.5 | 0.4 | 0.8 | 0.6 | 0.4 |
| Bbr_0223 | Bbr_0223 Conserved hypothetical membrane spanning protein 314838:316106 forward MW:45520 | 1.1 | 1.0 | 0.7 | 1.0 | 1.0 | 0.5 |
| Bbr_0224 | Bbr_0224 Permease protein of ABC transporter system 316129:317433 forward MW:46076 | 1.2 | 1.1 | 0.6 | 1.7 | 0.8 | 0.4 |
| Bbr_0225 | Bbr_0225 Permease protein of ABC transporter system 317466:318860 forward MW:48923 | 1.2 | 1.1 | 0.3 | 0.3 | 0.6 | 0.5 |
| Bbr_0226 | Bbr_0226 ATP-binding protein of ABC transporter system 318876:319673 forward MW:28730 | 1.2 | 1.2 | 0.6 | 0.7 | 0.9 | 0.8 |
| Bbr_0227 | Bbr_0227 Conserved hypothetical protein 319739:320290 forward MW:19058 | 1.1 | 1.1 | 0.9 | 0.6 | 1.0 | 0.8 |
| Bbr_0228 | Bbr_0228 Transcriptional regulator, TetR family 320549:321142 reverse MW:22269 | 1.2 | 1.5 | 1.3 | 1.9 | 0.9 | 1.1 |
| Bbr_0229 | Bbr_0229 Conserved hypothetical membrane spanning protein with similarity to phage infection protein 321237:323399 reverse MW:76775 | 0.9 | 1.5 | 1.3 | 2.9 | 2.1 | 0.7 |
| Bbr_0230 | Bbr_0230 Conserved hypothetical membrane spanning protein with similarity to phage infection protein 323396:326020 reverse MW:93342 | 1.6 | 2.7 | 0.9 | 0.7 | 0.9 | 1.3 |
| Bbr_0231 | Bbr_0231 Conserved hypothetical membrane spanning protein with DUF1113 domain 326495:327853 forward MW:50285 | 0.7 | 0.4 | 0.2 | 0.3 | 0.8 | 3.8 |
| Bbr_0232 | gnt 6-phosphogluconate dehydrogenase 328054:329508 forward MW:52396 | 0.9 | 0.9 | 0.8 | 0.8 | 1.2 | 0.8 |
| Bbr_0233 | pgl 6-phosphogluconolactonase 329709:330551 reverse MW:30625 | 0.8 | 1.0 | 0.2 | 0.2 | 2.6 | 0.5 |
| Bbr_0234 | Bbr_0234 Oxppcycle protein OpcA 330674:331696 reverse MW:37408 | 0.9 | 1.1 | 0.2 | 0.2 | 3.1 | 0.5 |
| Bbr_0235 | zwf Glucose-6-phosphate 1-dehydrogenase 331693:333399 reverse MW:63765 | 1.0 | 1.2 | 0.5 | 0.5 | 4.0 | 0.5 |
| Bbr_0236 | Bbr_0236 Conserved hypothetical protein 333544:335397 forward MW:66102 | 1.0 | 1.1 | 0.3 | 0.4 | 1.6 | 0.5 |
| Bbr_0237 | pepDB Dipeptidase A 335624:337144 forward MW:56237 | 1.1 | 1.1 | 0.6 | 0.4 | 0.5 | 2.8 |

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|---|---|---|---|---|---|---|---|
| Bbr_0238 | Bbr_0238 Glycosyltransferase 337208:338242 reverse MW:39152 | 0.8 | 0.6 | 0.4 | 0.4 | 0.6 | 0.5 |
| Bbr_0239 | Bbr_0239 Transcriptional regulator, TetR family 338266:339114 reverse MW:31254 | 1.0 | 1.0 | 1.0 | 1.3 | 1.5 | 0.6 |
| Bbr_0240 | ftsY Cell division protein ftsY 339196:340446 forward MW:43043 | 1.0 | 1.2 | 1.2 | 1.7 | 2.2 | 0.7 |
| Bbr_0241 | amtP Ammonium transporter 340754:342049 forward MW:44784 | 1.2 | 1.1 | 0.8 | 0.9 | 0.9 | 0.9 |
| Bbr_0242 | glnB Nitrogen regulatory protein P-II 342051:342389 forward MW:11723 | 1.0 | 0.9 | 2.1 | 1.2 | 0.9 | 1.1 |
| Bbr_0243 | glnD [protein-PII] uridylyltransferase 342720:344546 forward MW:67572 | 1.1 | 0.7 | 0.5 | 0.5 | 0.6 | 1.4 |
| Bbr_0244 | Bbr_0244 Na+ driven multidrug efflux pump (MatE domain) 344625:345995 reverse MW:47172 | 1.4 | 1.4 | 0.6 | 1.2 | 0.5 | 0.5 |
| Bbr_0245 | dnaB Replicative DNA helicase 346378:347838 forward MW:53009 | 1.3 | 1.3 | 0.5 | 0.2 | 1.0 | 1.0 |
| Bbr_0246 | murE UDP-N-acetylmuramoylalanyl-D-glutamate--2, 6-diaminopimelate ligase 347841:349268 forward MW:50499 | 1.2 | 1.2 | 0.5 | 2.0 | 1.3 | 0.6 |
| Bbr_0247 | Bbr_0247 CobB/CobQ-like glutamine amidotransferase domain 349378:350130 forward MW:27563 | 1.1 | 1.1 | 0.8 | 1.9 | 0.8 | 0.9 |
| Bbr_0248 | Bbr_0248 Conserved hypothetical protein 350279:350563 forward MW:9676 | 0.6 | 0.3 | 0.6 | 1.2 | 0.5 | 0.4 |
| Bbr_0249 | Bbr_0249 ABC1 family protein kinase 350560:352380 forward MW:66824 | 0.6 | 0.5 | 0.3 | 0.4 | 0.4 | 0.6 |
| Bbr_0252 | Bbr_0252 Conserved hypothetical protein with alanine racemase, N-terminal domain 355136:356023 forward MW:30636 | 1.1 | 1.1 | 1.6 | 1.5 | 1.2 | 1.0 |
| Bbr_0254 | rpsF SSU ribosomal protein S6P 357583:357873 forward MW:11042 | 1.0 | 0.8 | 0.7 | 0.4 | 0.6 | 1.1 |
| Bbr_0255 | ssb Single-strand DNA binding protein 357922:358566 forward MW:22288 | 1.1 | 0.9 | 0.8 | 0.3 | 0.6 | 1.1 |
| Bbr_0256 | rpsR SSU ribosomal protein S18P 358624:358872 forward MW:9418 | 1.1 | 0.9 | 0.8 | 0.4 | 0.7 | 1.0 |
| Bbr_0257 | rplI LSU ribosomal protein L9P 358892:359338 forward MW:15528 | 1.1 | 0.9 | 0.8 | 0.3 | 0.7 | 1.0 |
| Bbr_0258 | Bbr_0258 Hypothetical membrane spanning protein 360155:360847 reverse MW:24222 | 1.2 | 0.9 | 0.8 | 1.1 | 0.3 | 2.0 |
| Bbr_0259 | Bbr_0259 ATP-binding protein of ABC transporter system 360873:361604 reverse MW:26624 | 1.3 | 0.9 | 1.0 | 2.9 | 0.9 | 2.6 |
| Bbr_0260 | Bbr_0260 Hypothetical protein 361730:362038 forward MW:11389 | 0.6 | 1.1 | 1.6 | 3.2 | 0.7 | 18.1 |
| Bbr_0261 | Bbr_0261 Two-component response regulator 362135:362764 forward MW:22976 | 0.8 | 0.8 | 1.4 | 2.6 | 1.1 | 2.8 |
| Bbr_0262 | Bbr_0262 Two-component sensor protein 362776:363942 forward MW:43134 | 0.9 | 0.8 | 0.3 | 0.4 | 0.5 | 0.6 |
| Bbr_0263 | Bbr_0263 MFS transporter 365435:366640 forward MW:42247 | 0.8 | 0.6 | 0.5 | 0.6 | 1.3 | 0.3 |
| Bbr_0264 | Bbr_0264 Hypothetical protein 366860:367117 forward MW:9955 | 0.9 | 1.0 | 3.1 | 17.5 | 1.4 | 7.7 |
| Bbr_0265 | Bbr_0265 Hypothetical protein 367133:367498 forward MW:13341 | 1.0 | 1.1 | 2.8 | 12.9 | 1.3 | 9.3 |
| Bbr_0266 | Bbr_0266 DNA integration/recombination/inversion protein 367740:368417 reverse MW:25188 | 0.5 | 0.6 | 0.8 | 2.4 | 0.8 | 0.6 |
| Bbr_0267 | glpF Glycerol uptake facilitator protein 368856:369590 forward MW:26301 | 0.9 | 0.6 | 0.6 | 0.7 | 0.3 | 0.7 |
| Bbr_0268 | silP Copper-transporting ATPase 369674:372310 reverse MW:92144 | 1.2 | 1.1 | 0.7 | 0.3 | 0.9 | 0.4 |
| Bbr_0269 | Bbr_0269 Conserved hypothetical protein 372420:372701 forward MW:10156 | 0.9 | 0.9 | 5.3 | 19.8 | 0.8 | 0.7 |
| Bbr_0270 | Bbr_0270 DNA recombination protein rmuC homolog 372981:374255 forward MW:46793 | 1.2 | 1.3 | 1.0 | 0.8 | 0.6 | 0.7 |
| Bbr_0271 | pyrE1 Orotate phosphoribosyltransferase 374252:374881 forward MW:22312 | 1.1 | 1.2 | 1.0 | 0.4 | 0.8 | 0.3 |
| Bbr_0272 | Bbr_0272 23S rRNA methyltransferase 374970:375908 forward MW:33286 | 1.0 | 1.0 | 1.6 | 3.3 | 0.6 | 0.6 |
| Bbr_0273 | Bbr_0273 ATP-binding protein of ABC transporter system 376109:377047 forward MW:33508 | 0.9 | 0.8 | 0.2 | 0.3 | 0.6 | 1.5 |
| Bbr_0274 | Bbr_0274 Permease protein of ABC transporter system 377044:378090 forward MW:36416 | 0.8 | 0.7 | 0.2 | 0.7 | 0.3 | 1.2 |
| Bbr_0275 | Bbr_0275 Conserved hypothetical protein 378166:379128 reverse MW:35557 | 0.8 | 0.9 | 0.7 | 3.7 | 0.3 | 1.0 |
| Bbr_0276 | gatC Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit C 379824:380282 forward MW:16174 | 1.3 | 1.8 | 1.2 | 0.9 | 1.3 | 0.4 |
| Bbr_0277 | gatA Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit A 380286:381827 forward MW:54230 | 1.3 | 1.4 | 0.2 | 0.3 | 1.1 | 0.8 |
| Bbr_0278 | gatB Glutamyl-tRNA(Gln) amidotransferase subunit B 381852:383351 forward MW:55122 | 1.1 | 1.1 | 0.4 | 0.4 | 1.3 | 0.7 |
| Bbr_0279 | Bbr_0279 Acetyltransferase (GNAT) family 383492:384538 forward MW:38345 | 0.8 | 1.0 | 1.8 | 1.1 | 1.1 | 1.2 |
| Bbr_0280 | Bbr_0280 Conserved hypothetical protein 384545:384859 forward MW:12399 | 0.9 | 1.0 | 1.4 | 0.5 | 1.6 | 2.0 |
| Bbr_0281 | Bbr_0281 Conserved hypothetical protein 385030:386643 forward MW:60764 | 0.9 | 1.0 | 0.6 | 0.3 | 0.7 | 0.9 |
| Bbr_0282 | rho Transcription termination factor rho 387003:388973 forward MW:73389 | 1.2 | 1.5 | 1.7 | 1.0 | 2.2 | 2.1 |
| Bbr_0283 | Bbr_0283 Transcriptional regulator, LacI family 389206:390324 reverse MW:40697 | 1.0 | 0.8 | 1.3 | 1.9 | 1.0 | 0.2 |
| Bbr_0284 | Bbr_0284 Sugar/Sodium symporter 390487:391932 reverse MW:52921 | 1.1 | 0.4 | 1.2 | 0.4 | 0.6 | 0.6 |
| Bbr_0285 | lacZ2 Beta-galactosidase 392006:393826 reverse MW:69008 | 1.2 | 0.4 | 1.5 | 0.9 | 0.5 | 0.7 |
| Bbr_0287 | tyrA1 Chorismate mutase 398025:398414 forward MW:14110 | 1.0 | 0.8 | 0.7 | 1.0 | 0.7 | 0.6 |
| Bbr_0288 | Bbr_0288 Conserved hypothetical secreted protein 398561:400546 forward MW:67705 | 1.1 | 0.8 | 0.5 | 1.0 | 1.3 | 0.5 |
| Bbr_0289 | valS Valyl-tRNA synthetase 400579:403314 reverse MW:102184 | 1.2 | 1.4 | 2.3 | 4.3 | 2.0 | 0.7 |
| Bbr_0290 | Bbr_0290 Solute binding protein of ABC transporter system for peptides 403366:404895 reverse MW:54980 | 1.1 | 1.2 | 1.1 | 1.6 | 0.6 | 3.7 |
| Bbr_0291 | nth Endonuclease III 404930:405598 reverse MW:24754 | 1.0 | 1.2 | 1.7 | 0.7 | 0.7 | 4.1 |
| Bbr_0292 | glnR Transcriptional regulatory protein glnR 405623:406411 reverse MW:28255 | 0.8 | 0.9 | 1.1 | 1.7 | 0.9 | 2.7 |
| Bbr_0293 | Bbr_0293 Narrowly conserved hypothetical membrane spanning protein 406569:407273 reverse MW:24678 | 0.7 | 0.7 | 0.5 | 1.0 | 1.0 | 1.4 |
| Bbr_0294 | Bbr_0294 Conserved hypothetical membrane spanning protein 407333:407911 reverse MW:20302 | 0.6 | 0.7 | 1.0 | 0.5 | 0.7 | 1.4 |
| Bbr_0295 | ppa Inorganic pyrophosphatase 408145:408639 reverse MW:18352 | 0.8 | 0.6 | 0.3 | 0.2 | 0.9 | 0.3 |
| Bbr_0296 | Bbr_0296 Alpha-amylase family protein 408725:410992 reverse MW:83874 | 1.0 | 0.7 | 0.1 | 0.2 | 0.8 | 0.5 |
| Bbr_0297 | Bbr_0297 Narrowly conserved hypothetical secreted protein with prokaryotic membrane lipoprotein lipid attachment site and Gram-positive cocci s | 0.8 | 1.0 | 0.7 | 2.6 | 0.6 | 3.3 |
| Bbr_0299 | Bbr_0299 Holin 413888:414217 forward MW:11758 | 1.4 | 4.9 | 23.6 | 23.4 | 1.9 | 10.3 |
| Bbr_0300 | Bbr_0300 Hypothetical secreted protein 414474:414842 forward MW:13347 | 0.9 | 1.5 | 2.1 | 1.2 | 1.8 | 0.6 |
| Bbr_0302 | Bbr_0302 Transposase 416651:418111 reverse MW:53506 | 0.8 | 0.9 | 1.1 | 6.5 | 0.5 | 1.3 |
| Bbr_0303 | Bbr_0303 Permease protein of ABC transporter system for sugars 419418:420401 forward MW:36938 | 0.6 | 0.4 | 2.4 | 1.2 | 0.5 | 0.6 |
| Bbr_0304 | Bbr_0304 Permease protein of ABC transporter system for sugars 420416:421348 forward MW:34373 | 0.6 | 0.3 | 0.8 | 0.3 | 0.3 | 0.4 |
| Bbr_0305 | Bbr_0305 Solute binding protein of ABC transporter system for sugars 421440:423065 forward MW:61079 | 0.4 | 0.2 | 0.2 | 0.2 | 0.4 | 0.3 |
| Bbr_0306 | Bbr_0306 Glycosyl hydrolases family 30, Glucosylceramidase 423197:424528 forward MW:49294 | 0.4 | 0.2 | 0.4 | 0.8 | 0.2 | 0.5 |
| Bbr_0307 | Bbr_0307 Narrowly conserved hypothetical membrane spanning protein with DUF624 domain 424534:425223 forward MW:25324 | 0.7 | 0.8 | 1.7 | 1.3 | 0.6 | 0.5 |
| Bbr_0308 | Bbr_0308 Transcriptional regulator, TetR family 425220:425894 forward MW:25230 | 0.7 | 0.7 | 0.9 | 0.9 | 0.5 | 0.6 |
| Bbr_0310 | lacZ3 Beta-galactosidase 428396:430156 forward MW:66554 | 0.9 | 0.8 | 1.1 | 2.3 | 0.4 | 0.5 |
| Bbr_0311 | Bbr_0311 Transposase 430953:432110 reverse MW:44527 | 0.8 | 1.1 | 2.6 | 5.1 | 0.8 | 2.1 |
| Bbr_0312 | Bbr_0312 Transposase 432337:433626 forward MW:47884 | 0.7 | 0.6 | 1.4 | 3.0 | 0.7 | 7.5 |
| Bbr_0313 | Bbr_0313 Hypothetical protein 433872:434507 forward MW:23504 | 1.0 | 1.1 | 4.2 | 11.0 | 0.8 | 1.0 |
| Bbr_0315 | Bbr_0315 Conserved hypothetical protein 436179:437522 forward MW:51004 | 1.3 | 2.6 | 0.9 | 1.5 | 0.5 | 0.4 |
| Bbr_0316 | Bbr_0316 Narrowly conserved hypothetical protein 437734:438225 forward MW:18283 | 0.8 | 0.9 | 1.4 | 2.1 | 0.7 | 0.6 |
| Bbr_0317 | Bbr_0317 Phage major head 438235:439134 forward MW:31554 | 0.8 | 0.9 | 1.4 | 2.0 | 0.6 | 0.7 |
| Bbr_0318 | Bbr_0318 Predicted hypothetical protein 439440:439673 forward MW:8347 | 1.1 | 1.3 | 2.3 | 1.8 | 1.6 | 0.6 |
| Bbr_0319 | Bbr_0319 Phage transcriptional regulator 439760:440137 reverse MW:13557 | 1.1 | 2.0 | 11.1 | 44.4 | 1.9 | 15.7 |
| Bbr_0320 | Bbr_0320 Hypothetical protein 440134:440328 reverse MW:7373 | 1.0 | 1.6 | 10.5 | 60.4 | 1.2 | 11.1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| Bbr_0321 | Bbr_0321 Phage integrase 440392:441216 reverse MW:30334 | 0.9 | 0.9 | 2.6 | 4.1 | 0.8 | 24.0 |
| Bbr_0322 | metA Homoserine O-succinyltransferase 441619:442653 forward MW:39915 | 1.2 | 1.7 | 1.5 | 0.7 | 1.0 | 2.3 |
| Bbr_0323 | atpB ATP synthase A chain 442998:443807 forward MW:29693 | 1.4 | 1.9 | 2.2 | 0.9 | 0.4 | 1.6 |
| Bbr_0324 | atpE ATP synthase C chain 443905:444132 forward MW:7660 | 1.3 | 1.0 | 0.6 | 0.2 | 0.3 | 0.9 |
| Bbr_0325 | atpF ATP synthase B chain 444189:444707 forward MW:18624 | 1.3 | 1.0 | 0.6 | 0.2 | 0.4 | 0.9 |
| Bbr_0326 | atpH ATP synthase delta chain 444742:445578 forward MW:31599 | 1.3 | 1.1 | 0.7 | 0.4 | 0.4 | 1.0 |
| Bbr_0327 | atpA ATP synthase alpha chain 445647:447278 forward MW:58415 | 1.3 | 1.1 | 0.6 | 0.3 | 0.3 | 0.9 |
| Bbr_0328 | atpG ATP synthase gamma chain 447282:448205 forward MW:33710 | 1.3 | 1.2 | 0.6 | 0.3 | 0.4 | 1.1 |
| Bbr_0329 | atpD ATP synthase beta chain 448214:449686 forward MW:53334 | 1.3 | 1.3 | 0.7 | 0.3 | 0.4 | 0.9 |
| Bbr_0330 | atpC ATP synthase epsilon chain 449686:449979 forward MW:10373 | 1.5 | 1.8 | 0.9 | 0.5 | 0.5 | 1.0 |
| Bbr_0331 | Bbr_0331 Conserved hypothetical protein with DUF91 domain 450012:450767 forward MW:27810 | 1.2 | 1.4 | 1.7 | 0.6 | 0.7 | 2.2 |
| Bbr_0332 | fkbP1 Peptidyl-prolyl cis-trans isomerase 450815:451768 reverse MW:33420 | 1.0 | 0.9 | 0.4 | 0.3 | 1.1 | 0.7 |
| Bbr_0333 | Bbr_0333 Narrowly conserved hypothetical membrane spanning protein 451870:453108 forward MW:43338 | 1.0 | 1.3 | 1.2 | 0.3 | 1.7 | 1.8 |
| Bbr_0334 | Bbr_0334 Conserved hypothetical secreted protein 453108:454112 forward MW:36230 | 1.0 | 1.3 | 0.9 | 0.4 | 1.3 | 1.5 |
| Bbr_0335 | Bbr_0335 Conserved hypothetical protein with marginal similarity to thioredoxin 454335:455306 forward MW:33911 | 0.9 | 1.2 | 2.2 | 0.5 | 2.3 | 1.3 |
| Bbr_0336 | Bbr_0336 Conserved hypothetical protein with CYTH domain 455445:456071 reverse MW:23589 | 0.7 | 0.5 | 1.1 | 2.1 | 2.2 | 0.5 |
| Bbr_0337 | Bbr_0337 Hypothetical protein 456466:456603 forward MW:5247 | 1.0 | 1.4 | 3.0 | 4.2 | 1.2 | 2.8 |
| Bbr_0338 | psp1 Translation initiation inhibitor 456749:457138 forward MW:13482 | 0.9 | 0.4 | 0.5 | 0.7 | 1.0 | 0.4 |
| Bbr_0339 | plsC1 1-acyl-sn-glycerol-3-phosphate acyltransferase 457264:458217 forward MW:35814 | 1.1 | 0.9 | 0.4 | 1.2 | 0.8 | 0.3 |
| Bbr_0340 | gpsA Glycerol-3-phosphate dehydrogenase [NAD(P)+] 458411:459412 forward MW:34831 | 1.0 | 0.8 | 0.4 | 0.4 | 1.0 | 0.3 |
| Bbr_0341 | ddlA D-alanine--D-alanine ligase 459458:460645 forward MW:42213 | 1.1 | 0.9 | 0.5 | 0.9 | 1.0 | 0.6 |
| Bbr_0342 | Bbr_0342 Solute binding protein of ABC transporter system 460910:462076 forward MW:41573 | 1.1 | 1.1 | 1.8 | 1.7 | 0.7 | 1.8 |
| Bbr_0343 | Bbr_0343 Permease protein of ABC transporter system 462088:463026 forward MW:32939 | 1.2 | 1.3 | 0.5 | 1.2 | 0.3 | 2.2 |
| Bbr_0344 | Bbr_0344 Permease protein of ABC transporter system 463023:463934 forward MW:32698 | 1.1 | 1.1 | 1.2 | 0.9 | 0.8 | 1.4 |
| Bbr_0345 | Bbr_0345 ATP-binding protein of ABC transporter system 463931:465250 forward MW:46850 | 1.0 | 0.8 | 0.5 | 0.9 | 0.8 | 1.0 |
| Bbr_0346 | Bbr_0346 Conserved hypothetical membrane spanning protein in CAAX amino terminal protease family 465667:466704 forward MW:38283 | 0.9 | 0.8 | 1.3 | 2.3 | 0.9 | 1.0 |
| Bbr_0347 | Bbr_0347 Conserved hypothetical membrane spanning protein with mechanosensitive ion channel 466836:467627 reverse MW:27673 | 0.6 | 0.6 | 1.1 | 1.9 | 1.2 | 0.4 |
| Bbr_0348 | ansB Aspartate ammonia-lyase 467808:469241 reverse MW:51199 | 1.2 | 1.4 | 0.6 | 0.7 | 1.2 | 0.4 |
| Bbr_0349 | Bbr_0349 Conserved hypothetical membrane spanning protein with DUF81 domain 469959:470762 reverse MW:27440 | 0.7 | 0.3 | 0.1 | 0.6 | 1.5 | 0.4 |
| Bbr_0350 | Bbr_0350 Arylsulfatase regulator (Fe-S oxidoreductase) 470841:472133 reverse MW:48895 | 0.9 | 0.5 | 0.4 | 1.1 | 0.6 | 0.4 |
| Bbr_0351 | Bbr_0351 Transcriptional regulatory protein 472206:473267 reverse MW:37930 | 0.8 | 0.4 | 0.3 | 0.3 | 1.0 | 0.3 |
| Bbr_0352 | Bbr_0352 Sulfatase family protein 473316:474797 reverse MW:55062 | 1.1 | 1.5 | 3.8 | 5.9 | 0.3 | 1.1 |
| Bbr_0353 | Bbr_0353 Sugar-binding protein 475319:476662 forward MW:48964 | 1.1 | 0.6 | 0.8 | 0.9 | 0.3 | 0.4 |
| Bbr_0354 | Bbr_0354 Permease of ABC transporter for sugars 476735:477646 forward MW:34158 | 0.9 | 0.6 | 0.3 | 0.5 | 0.3 | 0.3 |
| Bbr_0355 | Bbr_0355 Permease of ABC transporter for sugars 477648:478622 forward MW:36322 | 1.0 | 0.6 | 0.7 | 0.9 | 0.3 | 1.6 |
| Bbr_0356 | Bbr_0356 Conserved hypothetical protein 478785:480008 reverse MW:45968 | 1.0 | 1.2 | 1.2 | 2.3 | 1.0 | 3.2 |
| Bbr_0358 | Bbr_0358 Conserved hypothetical protein 481393:482730 reverse MW:49069 | 0.9 | 1.2 | 1.9 | 0.5 | 2.4 | 1.1 |
| Bbr_0359 | ogt O6-methylguanine-DNA methyltransferase 483000:483554 reverse MW:20461 | 1.1 | 0.9 | 1.3 | 3.1 | 1.3 | 0.6 |
| Bbr_0360 | Bbr_0360 Holo-[acyl-carrier protein] synthase 483835:484293 forward MW:16507 | 0.9 | 1.0 | 1.1 | 2.4 | 0.9 | 1.3 |
| Bbr_0361 | Bbr_0361 Amylosucrase 484548:485000 forward MW:17180 | 0.7 | 1.4 | 1.4 | 4.8 | 0.2 | 7.3 |
| Bbr_0362 | Bbr_0362 Conserved hypothetical membrane spanning protein 484980:485678 reverse MW:24662 | 1.5 | 2.5 | 4.9 | 6.2 | 0.7 | 9.9 |
| Bbr_0363 | Bbr_0363 Hypothetical protein 486053:486697 forward MW:24354 | 0.9 | 0.8 | 0.7 | 1.4 | 0.8 | 5.2 |
| Bbr_0364 | Bbr_0364 Hypothetical protein 487097:487321 forward MW:8215 | 0.8 | 1.1 | 2.3 | 7.0 | 0.5 | 14.7 |
| Bbr_0365 | Bbr_0365 Narrowly conserved hypothetical secreted protein with Gram-positive cocci surface proteins LPxTG motif profile 487381:491109 forward | 0.4 | 0.1 | 0.2 | 0.8 | 0.4 | 0.4 |
| Bbr_0366 | Bbr_0366 Narrowly conserved hypothetical secreted protein with Gram positive anchor and Cna protein B-type domain 491317:492864 forward M | 0.5 | 0.3 | 0.9 | 1.4 | 1.0 | 0.5 |
| Bbr_0367 | Bbr_0367 Hypothetical protein 492973:493647 forward MW:24682 | 0.7 | 0.6 | 0.8 | 2.5 | 0.8 | 0.6 |
| Bbr_0368 | Bbr_0368 Conserved hypothetical protein 493926:494420 forward MW:18295 | 0.4 | 0.1 | 0.3 | 1.2 | 0.4 | 0.9 |
| Bbr_0369 | Bbr_0369 Narrowly conserved hypothetical membrane spanning protein 494728:495414 forward MW:24493 | 1.0 | 1.2 | 1.6 | 0.7 | 1.5 | 0.6 |
| Bbr_0370 | rpsO SSU ribosomal protein S15P 495544:495813 forward MW:10455 | 0.8 | 0.9 | 1.2 | 2.4 | 0.9 | 1.0 |
| Bbr_0371 | pnp Polyribonucleotide nucleotidyltransferase 496090:498801 forward MW:100370 | 0.6 | 0.7 | 0.8 | 0.3 | 1.4 | 1.0 |
| Bbr_0372 | Bbr_0372 ATP-binding protein of ABC transporter system 499238:499948 reverse MW:25823 | 0.9 | 1.3 | 2.0 | 2.6 | 0.8 | 0.6 |
| Bbr_0373 | Bbr_0373 Hypothetical protein 500083:500997 reverse MW:30423 | 1.2 | 1.7 | 1.9 | 4.9 | 0.9 | 0.8 |
| Bbr_0374 | lemA LemA protein 501459:502046 forward MW:21229 | 0.8 | 0.3 | 0.1 | 0.4 | 0.6 | 0.2 |
| Bbr_0375 | Bbr_0375 Conserved hypothetical membrane spanning protein 502112:504367 forward MW:80432 | 0.6 | 0.2 | 0.4 | 0.7 | 0.5 | 0.5 |
| Bbr_0376 | Bbr_0376 Narrowly conserved hypothetical membrane spanning protein 504710:506185 forward MW:52873 | 0.8 | 1.8 | 2.2 | 8.2 | 0.6 | 4.6 |
| Bbr_0377 | Bbr_0377 Oxidoreductase, aldo/keto reductase family 506813:507676 forward MW:31765 | 1.1 | 0.8 | 0.8 | 0.6 | 1.2 | 0.4 |
| Bbr_0378 | iunH1 Inosine-uridine preferring nucleoside hydrolase 507942:508997 forward MW:37351 | 1.0 | 0.8 | 0.8 | 0.4 | 1.7 | 0.5 |
| Bbr_0379 | rimM 16S rRNA processing protein rimM 509071:509670 reverse MW:21989 | 1.1 | 1.3 | 2.9 | 0.9 | 1.2 | 1.6 |
| Bbr_0380 | Bbr_0380 RNA binding protein 509708:509941 reverse MW:8654 | 0.9 | 0.9 | 0.3 | 0.3 | 1.4 | 0.5 |
| Bbr_0381 | rpsP SSU ribosomal protein S16P 509965:510438 reverse MW:16900 | 0.9 | 0.8 | 0.6 | 0.4 | 1.4 | 0.5 |
| Bbr_0382 | Bbr_0382 Conserved hypothetical membrane spanning protein 510658:511989 reverse MW:47390 | 1.2 | 2.1 | 1.2 | 0.7 | 0.7 | 1.6 |
| Bbr_0383 | ffh Signal recognition particle, subunit FFH/SRP54 512241:513896 reverse MW:58665 | 1.2 | 1.9 | 1.1 | 0.5 | 1.8 | 1.0 |
| Bbr_0384 | Bbr_0384 Conserved hypothetical membrane spanning protein in cation efflux family 514092:515159 forward MW:39617 | 0.8 | 1.1 | 3.0 | 2.3 | 0.7 | 7.4 |
| Bbr_0385 | cysS Cysteinyl-tRNA synthetase 515408:517057 reverse MW:59443 | 1.2 | 1.3 | 0.6 | 0.4 | 1.2 | 0.4 |
| Bbr_0386 | guaA1 GMP synthase [glutamine-hydrolyzing] 517130:517996 forward MW:31057 | 1.3 | 1.3 | 0.7 | 1.6 | 0.9 | 0.4 |
| Bbr_0387 | Bbr_0387 ATP-binding protein of ABC transporter system 518231:520444 forward MW:80925 | 1.1 | 1.2 | 0.4 | 0.7 | 1.6 | 0.5 |
| Bbr_0388 | Bbr_0388 Plasmid stability protein 520585:521007 reverse MW:15684 | 1.4 | 1.6 | 4.3 | 3.0 | 0.8 | 1.5 |
| Bbr_0389 | Bbr_0389 Hypothetical protein 521017:521295 reverse MW:10767 | 1.5 | 1.8 | 7.6 | 3.9 | 0.8 | 1.5 |
| Bbr_0390 | ilvN Acetolactate synthase small subunit 521463:522020 reverse MW:20083 | 1.0 | 1.1 | 0.5 | 0.5 | 0.9 | 0.7 |
| Bbr_0391 | ilvB Acetolactate synthase large subunit 522036:524000 reverse MW:69747 | 1.1 | 1.3 | 0.7 | 0.4 | 1.1 | 0.9 |
| Bbr_0392 | rncS Ribonuclease III 524160:524903 reverse MW:26684 | 0.9 | 0.9 | 2.6 | 0.7 | 0.8 | 1.6 |
| Bbr_0393 | rpmF LSU ribosomal protein L32P 525074:525268 reverse MW:6888 | 0.9 | 1.2 | 2.3 | 4.4 | 0.7 | 0.5 |
| Bbr_0394 | Bbr_0394 Conserved hypothetical protein 525358:525978 reverse MW:22163 | 0.9 | 0.8 | 0.4 | 0.3 | 0.9 | 0.6 |
| Bbr_0395 | Bbr_0395 Conserved hypothetical protein 526094:526879 reverse MW:28362 | 0.9 | 0.6 | 0.1 | 0.1 | 1.3 | 0.2 |
| Bbr_0396 | coaD Phosphopantetheine adenylyltransferase 526885:527385 reverse MW:17769 | 1.0 | 0.7 | 0.3 | 0.7 | 0.6 | 0.2 |

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|---|---|---|---|---|---|---|---|
| Bbr_0397 | Bbr_0397 Conserved hypothetical protein 527490:527771 forward MW:10319 | 1.0 | 1.0 | 1.0 | 2.0 | 1.3 | 0.8 |
| Bbr_0398 | Bbr_0398 Oxidoreductase 527967:528977 reverse MW:37205 | 1.4 | 0.7 | 0.3 | 0.5 | 0.8 | 0.7 |
| Bbr_0399 | Bbr_0399 Transcriptional regulator, MerR family 529236:529664 forward MW:16832 | 1.9 | 3.0 | 5.9 | 4.9 | 0.9 | 4.4 |
| Bbr_0400 | Bbr_0400 Conserved hypothetical membrane spanning protein 529672:530298 reverse MW:23481 | 1.1 | 1.1 | 0.6 | 0.7 | 0.6 | 0.4 |
| Bbr_0401 | pncB Nicotinate phosphoribosyltransferase 530406:531728 forward MW:47539 | 0.8 | 0.7 | 0.5 | 0.3 | 1.1 | 0.7 |
| Bbr_0402 | rph Ribonuclease PH 532153:532929 forward MW:28206 | 1.0 | 1.0 | 0.5 | 0.3 | 1.2 | 0.8 |
| Bbr_0403 | Bbr_0403 Conserved hypothetical protein with HAM1 family domain 533054:533827 forward MW:26608 | 1.0 | 1.0 | 0.4 | 0.3 | 1.1 | 0.8 |
| Bbr_0404 | Bbr_0404 Conserved hypothetical membrane spanning protein with auxin efflux carrier domain 533953:534954 reverse MW:35789 | 1.2 | 1.3 | 1.5 | 1.7 | 1.0 | 2.0 |
| Bbr_0405 | gpi Glucose-6-phosphate isomerase 535829:537529 forward MW:62928 | 1.0 | 0.6 | 0.2 | 0.2 | 0.5 | 0.5 |
| Bbr_0406 | Bbr_0406 ATP-binding protein of ABC transporter system 538133:539551 reverse MW:51451 | 1.1 | 1.1 | 1.3 | 1.7 | 1.2 | 7.0 |
| Bbr_0407 | Bbr_0407 Permease protein of ABC transporter system 539673:541463 reverse MW:65627 | 1.0 | 1.0 | 1.1 | 0.9 | 0.9 | 8.4 |
| Bbr_0408 | rplS LSU ribosomal protein L19P 542254:542619 forward MW:13613 | 1.0 | 1.3 | 1.9 | 2.0 | 1.7 | 0.7 |
| Bbr_0409 | lepB Signal peptidase I 542788:543711 forward MW:33165 | 1.1 | 1.0 | 0.8 | 1.0 | 0.8 | 1.3 |
| Bbr_0410 | rnhB Ribonuclease HII 543739:544596 forward MW:30035 | 1.0 | 0.9 | 0.5 | 0.5 | 0.7 | 1.1 |
| Bbr_0411 | Bbr_0411 Transcriptional regulator, LacI family 544758:545873 forward MW:40625 | 0.9 | 0.7 | 0.9 | 1.0 | 0.4 | 1.1 |
| Bbr_0413 | fadD1 Long-chain-fatty-acid--CoA ligase 546437:548260 reverse MW:65844 | 1.1 | 1.0 | 1.2 | 0.8 | 1.8 | 0.8 |
| Bbr_0414 | Bbr_0414 Hypothetical protein 548497:549180 reverse MW:24245 | 0.9 | 2.3 | 0.6 | 1.8 | 0.5 | 1.1 |
| Bbr_0415 | Bbr_0415 ATP-binding protein of ABC transporter system 549994:554055 forward MW:143360 | 1.3 | 1.0 | 0.9 | 2.1 | 0.9 | 1.1 |
| Bbr_0417 | Bbr_0417 Solute-binding protein of ABC transporter system for sugars 555378:556727 forward MW:48864 | 1.2 | 1.2 | 1.7 | 3.8 | 0.4 | 0.6 |
| Bbr_0418 | Bbr_0418 Permease protein of ABC transporter system for sugars 556948:557910 forward MW:35404 | 1.5 | 1.2 | 3.9 | 5.4 | 1.3 | 0.3 |
| Bbr_0419 | Bbr_0419 Permease protein of ABC transporter system for sugars 557963:558961 forward MW:36140 | 1.2 | 1.0 | 1.8 | 0.5 | 1.2 | 0.6 |
| Bbr_0420 | lacZ4 Beta-galactosidase 559129:561261 forward MW:79032 | 1.4 | 1.8 | 1.6 | 3.9 | 0.9 | 0.6 |
| Bbr_0421 | Bbr_0421 Transcriptional regulator, LacI family 561305:562360 forward MW:38068 | 1.0 | 1.2 | 1.9 | 1.8 | 1.7 | 0.6 |
| Bbr_0422 | galA Glycosyl hydrolases family 53, Endogalactanase 562556:565249 forward MW:93937 | 0.8 | 1.0 | 4.3 | 6.7 | 0.8 | 2.3 |
| Bbr_0423 | Bbr_0423 Narrowly conserved hypothetical protein 565599:565853 reverse MW:8999 | 1.0 | 1.7 | 2.0 | 4.3 | 1.0 | 7.1 |
| Bbr_0424 | Bbr_0424 2,5-diketo-D-gluconic acid reductase 565923:566792 forward MW:31693 | 1.0 | 1.0 | 1.7 | 1.4 | 0.8 | 1.5 |
| Bbr_0425 | Bbr_0425 Conserved hypothetical secreted protein 566792:567550 forward MW:27346 | 1.1 | 1.3 | 1.1 | 0.8 | 0.6 | 2.1 |
| Bbr_0427 | mntH Manganese transport protein mntH 567971:569296 forward MW:46626 | 1.6 | 1.8 | 2.1 | 0.9 | 1.0 | 1.4 |
| Bbr_0428 | Bbr_0428 Conserved hypothetical membrane spanning protein 569337:570863 reverse MW:54761 | 1.2 | 1.8 | 0.9 | 0.5 | 1.1 | 1.2 |
| Bbr_0429 | Bbr_0429 Conserved hypothetical protein 571411:573063 forward MW:59229 | 1.0 | 1.0 | 0.9 | 0.4 | 0.6 | 2.1 |
| Bbr_0430 | rfbP Undecaprenyl-phosphate galactosephosphotransferase 573157:574875 reverse MW:63312 | 0.9 | 0.8 | 0.3 | 0.7 | 0.7 | 0.7 |
| Bbr_0431 | Bbr_0431 Protein tyrosine phosphatase 575151:575756 forward MW:22476 | 0.9 | 0.6 | 0.7 | 1.2 | 1.0 | 5.0 |
| Bbr_0434 | Bbr_0434 Oligosaccharide repeat unit transporter 579996:581459 reverse MW:53488 | 0.9 | 0.7 | 0.1 | 0.2 | 0.6 | 0.3 |
| Bbr_0435 | Bbr_0435 Beta-1,6-N-acetylglucosaminyltransferase 581509:582393 reverse MW:34174 | 0.9 | 0.6 | 0.1 | 0.3 | 0.5 | 0.3 |
| Bbr_0436 | Bbr_0436 Hypothetical membrane spanning protein 582390:583616 reverse MW:45756 | 1.0 | 0.7 | 0.3 | 0.6 | 0.5 | 0.2 |
| Bbr_0437 | Bbr_0437 Acetyltransferase 583627:584091 reverse MW:16505 | 1.1 | 0.8 | 0.1 | 0.2 | 0.6 | 0.2 |
| Bbr_0438 | Bbr_0438 Glycosyltransferase 584084:585094 reverse MW:37920 | 1.2 | 0.9 | 0.1 | 0.2 | 0.7 | 0.3 |
| Bbr_0439 | Bbr_0439 Capsular polysaccharide biosynthesis protein 585091:586026 reverse MW:35753 | 1.2 | 1.1 | 0.1 | 0.8 | 0.8 | 0.2 |
| Bbr_0440 | Bbr_0440 Polysaccharide biosynthesis protein 586013:586843 reverse MW:31166 | 1.3 | 1.0 | 0.2 | 0.4 | 0.9 | 0.2 |
| Bbr_0441 | Bbr_0441 Capsular polysaccharide biosynthesis protein 586871:587977 reverse MW:41124 | 1.1 | 1.1 | 0.6 | 0.3 | 1.5 | 0.4 |
| Bbr_0442 | Bbr_0442 Capsular polysaccharide biosynthesis protein 588370:589491 forward MW:41871 | 1.1 | 0.9 | 0.6 | 1.0 | 0.4 | 0.2 |
| Bbr_0443 | Bbr_0443 Glycosyltransferase 589488:590762 forward MW:47768 | 1.1 | 0.8 | 0.3 | 1.3 | 0.3 | 0.1 |
| Bbr_0444 | Bbr_0444 Membrane spanning polysaccharide biosynthesis protein 590767:592182 forward MW:52215 | 1.1 | 1.2 | 1.5 | 2.1 | 0.3 | 0.9 |
| Bbr_0445 | Bbr_0445 Glycosyltransferase 592179:593219 forward MW:39673 | 1.1 | 1.2 | 2.0 | 2.9 | 0.9 | 1.0 |
| Bbr_0446 | Bbr_0446 Acetyltransferase (cell wall biosynthesis) 593224:593937 forward MW:27145 | 1.0 | 1.3 | 1.5 | 3.7 | 1.6 | 2.1 |
| Bbr_0447 | Bbr_0447 Conserved hypothetical protein 593961:595070 forward MW:41988 | 1.3 | 1.5 | 1.1 | 0.8 | 1.0 | 0.8 |
| Bbr_0448 | Bbr_0448 Glycosyltransferase 595067:596038 forward MW:36641 | 1.1 | 1.3 | 1.0 | 1.6 | 1.0 | 0.7 |
| Bbr_0449 | Bbr_0449 Hypothetical membrane spanning protein 596124:596360 forward MW:8710 | 1.1 | 1.3 | 1.9 | 3.1 | 1.0 | 0.7 |
| Bbr_0450 | Bbr_0450 Membrane spanning protein involved in polysaccharide biosynthesis 596467:597525 forward MW:40498 | 1.1 | 1.6 | 1.2 | 1.3 | 1.9 | 2.5 |
| Bbr_0451 | Bbr_0451 Acyltransferase 597655:598722 forward MW:39337 | 1.0 | 1.4 | 1.8 | 1.7 | 1.3 | 4.9 |
| Bbr_0452 | Bbr_0452 Hypothetical protein 599217:599465 forward MW:9172 | 0.9 | 1.3 | 3.0 | 9.5 | 1.6 | 7.6 |
| Bbr_0453 | Bbr_0453 Transposase 599649:600455 reverse MW:29992 | 1.2 | 1.2 | 7.9 | 3.0 | 0.5 | 3.7 |
| Bbr_0454 | Bbr_0454 Conserved hypothetical protein 600462:600734 reverse MW:9499 | 1.1 | 1.5 | 6.2 | 3.6 | 1.2 | 1.9 |
| Bbr_0457 | Bbr_0457 Transposase 603258:604586 reverse MW:49522 | 0.8 | 0.9 | 1.6 | 4.3 | 0.2 | 2.2 |
| Bbr_0458 | Bbr_0458 Hypothetical protein 604738:605295 reverse MW:21414 | 1.6 | 1.8 | 0.6 | 0.8 | 0.5 | 2.6 |
| Bbr_0459 | Bbr_0459 Conserved hypothetical protein 605359:606660 reverse MW:48075 | 1.6 | 1.7 | 0.6 | 0.4 | 0.7 | 0.6 |
| Bbr_0460 | Bbr_0460 Hypothetical membrane spanning protein 606669:606914 reverse MW:9020 | 1.5 | 1.3 | 1.6 | 3.1 | 0.8 | 3.7 |
| Bbr_0461 | Bbr_0461 Hypothetical protein 608189:608569 reverse MW:14611 | 1.2 | 1.4 | 1.2 | 0.9 | 4.4 | 0.5 |
| Bbr_0464 | Bbr_0464 Hypothetical protein 612759:615563 forward MW:105773 | 0.7 | 0.5 | 0.2 | 0.2 | 0.7 | 0.3 |
| Bbr_0465 | Bbr_0465 Hypothetical protein 615744:616904 reverse MW:45279 | 1.3 | 1.5 | 1.4 | 1.4 | 0.7 | 0.5 |
| Bbr_0466 | Bbr_0466 Hypothetical protein 618065:618601 forward MW:20366 | 1.2 | 1.2 | 1.2 | 0.6 | 1.4 | 1.2 |
| Bbr_0467 | Bbr_0467 Conserved hypothetical protein with a helix-turn-helix motif 618665:619159 forward MW:18446 | 1.1 | 1.3 | 6.8 | 6.1 | 1.5 | 1.0 |
| Bbr_0468 | Bbr_0468 Hypothetical protein 619156:619545 forward MW:14432 | 1.1 | 1.3 | 5.3 | 1.3 | 1.0 | 1.1 |
| Bbr_0469 | Bbr_0469 Conserved hypothetical membrane spanning protein 619690:620079 reverse MW:14892 | 0.9 | 1.0 | 1.4 | 2.0 | 0.7 | 4.6 |
| Bbr_0470 | Bbr_0470 Conserved hypothetical membrane spanning protein 620087:620773 reverse MW:26418 | 1.3 | 1.7 | 2.9 | 6.1 | 0.6 | 9.4 |
| Bbr_0471 | Bbr_0471 Hypothetical protein 621595:622311 forward MW:27727 | 1.1 | 1.0 | 2.7 | 2.8 | 0.9 | 3.1 |
| Bbr_0472 | Bbr_0472 Narrowly conserved hypothetical membrane spanning protein 622785:624176 reverse MW:51663 | 1.3 | 1.3 | 0.5 | 0.3 | 0.5 | 1.7 |
| Bbr_0473 | Bbr_0473 Narrowly conserved hypothetical protein 624483:624917 reverse MW:15467 | 1.0 | 1.1 | 4.6 | 6.2 | 1.6 | 3.3 |
| Bbr_0474 | Bbr_0474 Chain length regulator (capsular polysaccharide biosynthesis) / Tyrosine-protein kinase (capsular polysaccharide biosynthesis) 625219: | 1.3 | 1.5 | 1.5 | 0.5 | 1.0 | 1.2 |
| Bbr_0475 | Bbr_0475 Narrowly conserved hypothetical protein 626877:628220 forward MW:47240 | 1.1 | 1.0 | 0.6 | 0.6 | 0.7 | 1.2 |
| Bbr_0476 | Bbr_0476 Conserved hypothetical secreted protein with G5 domain 628566:629549 reverse MW:34635 | 1.1 | 1.3 | 1.4 | 0.9 | 1.4 | 1.2 |
| Bbr_0477 | Bbr_0477 Thioredoxin 629722:630093 reverse MW:13071 | 0.8 | 1.4 | 2.7 | 0.8 | 4.0 | 0.3 |
| Bbr_0478 | Bbr_0478 Conserved hypothetical protein 630291:630923 forward MW:22972 | 0.9 | 1.0 | 0.8 | 1.0 | 1.6 | 1.1 |
| Bbr_0479 | Bbr_0479 Hydrolase 631058:631903 forward MW:30145 | 0.8 | 0.7 | 0.4 | 0.3 | 1.7 | 1.1 |
| Bbr_0480 | Bbr_0480 Phosphohydrolase (MutT/nudix family protein) 632037:633293 forward MW:44419 | 0.7 | 0.5 | 0.2 | 0.2 | 1.7 | 0.9 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| Bbr_0481 | gcvH Glycine cleavage system H protein 633309:633710 forward MW:14751 | 0.8 | 0.7 | 0.5 | 0.5 | 1.2 | 1.0 |
| Bbr_0482 | Bbr_0482 Conserved hypothetical protein 633757:635013 forward MW:46149 | 0.9 | 0.8 | 0.5 | 0.2 | 0.9 | 1.2 |
| Bbr_0483 | ptrB Protease II 635036:637792 forward MW:101491 | 1.1 | 1.1 | 1.3 | 3.4 | 0.7 | 1.1 |
| Bbr_0484 | leuB 3-isopropylmalate dehydrogenase 637859:638890 forward MW:37175 | 0.9 | 0.5 | 0.1 | 0.2 | 0.5 | 0.4 |
| Bbr_0485 | lplA Lipoate-protein ligase A 638942:640105 forward MW:41674 | 1.1 | 1.0 | 0.5 | 0.7 | 0.8 | 1.0 |
| Bbr_0486 | Bbr_0486 Transcription regulator, crp family 640217:640936 forward MW:26977 | 1.0 | 0.8 | 1.6 | 2.5 | 1.1 | 0.9 |
| Bbr_0487 | pbp3 Penicillin-binding protein 641065:643335 forward MW:81703 | 1.0 | 0.9 | 0.4 | 0.4 | 1.1 | 1.2 |
| Bbr_0488 | baiC NADH-dependent flavin oxidoreductase 643669:644784 forward MW:39761 | 1.1 | 1.1 | 1.6 | 1.4 | 1.2 | 1.3 |
| Bbr_0489 | pyrD2 Dihydroorotate dehydrogenase 644930:645946 reverse MW:37371 | 0.9 | 0.9 | 0.5 | 0.5 | 2.0 | 0.6 |
| Bbr_0490 | Bbr_0490 Transcriptional regulator, DeoR family 646369:647190 forward MW:29282 | 0.9 | 0.8 | 0.6 | 0.5 | 1.0 | 1.5 |
| Bbr_0491 | galT1 Galactose-1-phosphate uridylyltransferase 647196:648446 forward MW:46874 | 1.1 | 0.7 | 0.1 | 0.2 | 1.0 | 0.7 |
| Bbr_0492 | galK Galactokinase 648464:649714 forward MW:44271 | 0.9 | 0.7 | 0.2 | 0.3 | 1.3 | 0.7 |
| Bbr_0493 | Bbr_0493 Conserved hypothetical protein 650483:650755 forward MW:10140 | 1.1 | 1.0 | 1.0 | 0.8 | 0.9 | 0.6 |
| Bbr_0494 | Bbr_0494 Conserved hypothetical protein 650897:652261 forward MW:47489 | 1.1 | 1.0 | 0.5 | 0.3 | 0.9 | 0.8 |
| Bbr_0495 | Bbr_0495 RNA methyltransferase 652920:653429 reverse MW:18740 | 1.3 | 1.9 | 1.6 | 0.8 | 0.8 | 0.6 |
| Bbr_0496 | mutY A/G-specific adenine DNA glycosylase 653603:654565 forward MW:35459 | 1.1 | 2.3 | 2.5 | 0.6 | 3.9 | 1.7 |
| Bbr_0497 | Bbr_0497 Narrowly conserved hypothetical protein 654729:655547 forward MW:29026 | 0.9 | 1.3 | 1.5 | 0.8 | 1.6 | 2.6 |
| Bbr_0498 | rpoB DNA-directed RNA polymerase beta chain 655782:659345 forward MW:131711 | 1.5 | 2.5 | 1.6 | 0.7 | 1.4 | 1.2 |
| Bbr_0499 | rpoC DNA-directed RNA polymerase beta' chain 659436:663473 forward MW:149006 | 1.7 | 2.8 | 1.4 | 1.0 | 1.7 | 1.0 |
| Bbr_0500 | Bbr_0500 Conserved hypothetical membrane spanning protein 663573:666002 reverse MW:87729 | 0.9 | 1.7 | 0.7 | 0.9 | 0.5 | 0.4 |
| Bbr_0501 | Bbr_0501 Conserved hypothetical protein with DUF58 domain 665999:667294 reverse MW:47092 | 0.8 | 1.4 | 0.5 | 1.0 | 0.2 | 0.4 |
| Bbr_0502 | moxR1 MoxR protein 667302:668492 reverse MW:43530 | 0.9 | 1.8 | 0.5 | 0.8 | 0.2 | 0.5 |
| Bbr_0503 | Bbr_0502 Fused conserved hypothetical protein with a fibronectin type III domain and MoxR protein 667302:673826 reverse MW:229538 | 0.8 | 1.6 | 0.7 | 0.9 | 0.2 | 0.7 |
| Bbr_0504 | Bbr_0504 Serine/threonine protein kinase 673798:674946 reverse MW:41889 | 0.6 | 0.9 | 0.3 | 0.6 | 0.1 | 1.4 |
| Bbr_0505 | Bbr_0505 ATP-dependent DNA helicase, UvrD/REP family 675082:679179 forward MW:146313 | 1.4 | 1.3 | 0.5 | 0.8 | 0.8 | 0.6 |
| Bbr_0506 | Bbr_0506 ATP-dependent DNA helicase, UvrD/REP family 679176:683111 forward MW:143284 | 1.1 | 1.0 | 1.2 | 4.8 | 1.1 | 0.8 |
| Bbr_0507 | Bbr_0507 Conserved hypothetical membrane spanning protein 683283:684602 forward MW:46634 | 1.1 | 0.9 | 0.9 | 0.5 | 1.2 | 0.9 |
| Bbr_0508 | dapB Dihydrodipicolinate reductase 684690:685445 forward MW:26286 | 1.1 | 1.0 | 0.8 | 1.0 | 1.1 | 0.6 |
| Bbr_0509 | dapA2 Dihydrodipicolinate synthase 685551:686456 forward MW:31881 | 1.0 | 1.0 | 0.6 | 0.6 | 1.0 | 0.6 |
| Bbr_0510 | Bbr_0510 Metal-dependent hydrolase 686692:688392 forward MW:62023 | 1.2 | 1.3 | 0.2 | 0.1 | 1.4 | 0.7 |
| Bbr_0511 | pepN Membrane alanine aminopeptidase 688434:691043 forward MW:97270 | 1.1 | 1.0 | 0.2 | 0.3 | 1.1 | 0.8 |
| Bbr_0512 | mrsA Phosphoglucosamine mutase 691530:692915 forward MW:48616 | 0.9 | 0.8 | 0.4 | 0.4 | 0.7 | 0.7 |
| Bbr_0513 | Bbr_0513 Peptide deformylase 693059:693712 forward MW:24365 | 0.9 | 0.8 | 0.5 | 0.3 | 0.9 | 0.8 |
| Bbr_0514 | Bbr_0514 Narrowly conserved hypothetical protein 693709:695163 forward MW:53216 | 0.8 | 0.8 | 0.8 | 1.1 | 1.0 | 1.0 |
| Bbr_0515 | prfB Bacterial Peptide Chain Release Factor 2 (RF-2) 695515:696639 forward MW:41706 | 1.0 | 1.4 | 1.9 | 1.0 | 2.3 | 1.5 |
| Bbr_0516 | ftsE Cell division ATP-binding protein ftsE 696642:697838 forward MW:42665 | 1.1 | 1.5 | 0.6 | 0.4 | 2.4 | 1.1 |
| Bbr_0517 | ftsX Cell division protein ftsX 697842:698765 forward MW:33894 | 1.1 | 1.4 | 0.7 | 0.3 | 2.2 | 1.0 |
| Bbr_0518 | Bbr_0518 Conserved hypothetical secreted protein with CHAP domain 698844:700190 forward MW:47180 | 0.7 | 0.6 | 0.4 | 0.3 | 1.9 | 2.1 |
| Bbr_0519 | smpB SsrA-binding protein 700304:700780 forward MW:18217 | 1.2 | 1.3 | 3.3 | 4.9 | 1.6 | 3.6 |
| Bbr_0520 | Bbr_0520 Solute-binding protein of ABC transporter system 700902:701855 forward MW:32695 | 1.5 | 1.3 | 2.1 | 1.3 | 1.4 | 3.5 |
| Bbr_0521 | Bbr_0521 Solute binding protein of ABC transporter system 701989:702930 forward MW:32826 | 1.2 | 1.3 | 2.5 | 3.5 | 0.9 | 2.2 |
| Bbr_0522 | Bbr_0522 Permease protein of ABC transporter system 703075:704058 forward MW:36005 | 1.3 | 1.2 | 0.8 | 0.6 | 1.4 | 0.9 |
| Bbr_0523 | Bbr_0523 ATP-binding protein of ABC transporter system 704074:704904 forward MW:29961 | 1.2 | 1.1 | 0.6 | 0.8 | 1.2 | 0.9 |
| Bbr_0524 | glmS Glucosamine--fructose-6-phosphate aminotransferase [isomerizing] 705149:707041 forward MW:68633 | 1.0 | 0.9 | 0.8 | 0.9 | 1.1 | 1.2 |
| Bbr_0525 | Bbr_0525 Ribosomal large subunit pseudouridine synthase D 707085:707819 forward MW:27886 | 1.0 | 1.1 | 0.4 | 0.3 | 1.2 | 2.6 |
| Bbr_0526 | Bbr_0526 Transcriptional regulator, LacI family 707812:708822 reverse MW:36374 | 1.4 | 1.0 | 2.1 | 0.9 | 1.3 | 0.4 |
| Bbr_0527 | Bbr_0527 Permease protein of ABC transporter system for sugars 709038:709964 forward MW:34164 | 1.6 | 1.2 | 2.6 | 4.6 | 1.3 | 0.3 |
| Bbr_0528 | Bbr_0528 Permease protein of ABC transporter system for sugars 710017:711015 forward MW:36167 | 1.2 | 1.0 | 1.7 | 0.5 | 1.2 | 0.6 |
| Bbr_0529 | lacZ5 Beta-galactosidase 711195:713270 forward MW:77363 | 1.6 | 1.2 | 2.2 | 0.4 | 2.3 | 0.6 |
| Bbr_0530 | Bbr_0530 Solute-binding protein of ABC transporter system for sugars 713526:714872 forward MW:48177 | 1.1 | 0.4 | 1.5 | 0.6 | 0.9 | 0.5 |
| Bbr_0531 | Bbr_0531 Solute-binding protein of ABC transporter system for sugars 715035:716456 forward MW:52388 | 0.9 | 0.8 | 1.0 | 0.2 | 1.8 | 1.0 |
| Bbr_0532 | Bbr_0532 Tanscriptional regulator, homologs of Bvg accessory factor 716550:717320 reverse MW:27603 | 1.4 | 1.7 | 4.4 | 5.3 | 2.2 | 1.1 |
| Bbr_0533 | Bbr_0533 Solute-binding protein of ABC transporter system for peptides 717447:719081 forward MW:58684 | 2.5 | 4.1 | 4.1 | 1.7 | 6.1 | 1.3 |
| Bbr_0534 | Bbr_0534 Permease protein of ABC transporter system for peptides 719268:720245 forward MW:34105 | 1.1 | 1.2 | 1.9 | 1.9 | 3.0 | 0.9 |
| Bbr_0535 | Bbr_0535 Permease protein of ABC transporter system for peptides 720242:721228 forward MW:34289 | 0.9 | 1.0 | 0.3 | 0.5 | 1.7 | 0.6 |
| Bbr_0536 | Bbr_0536 ATP-binding protein of ABC transporter system for peptides 721218:722009 forward MW:27633 | 0.9 | 1.0 | 0.1 | 0.2 | 2.4 | 0.5 |
| Bbr_0537 | Bbr_0537 ATP-binding protein of ABC transporter system for peptides 722002:722787 forward MW:27967 | 0.9 | 0.8 | 0.2 | 0.3 | 1.6 | 0.4 |
| Bbr_0538 | cysK cysteine synthase 723180:724202 forward MW:36515 | 0.8 | 1.0 | 1.4 | 2.4 | 1.5 | 8.6 |
| Bbr_0539 | metB Cystathionine gamma-synthase 724392:725576 forward MW:41761 | 1.0 | 0.8 | 0.8 | 0.8 | 1.0 | 6.5 |
| Bbr_0540 | recQ ATP-dependent DNA helicase recQ 725882:727801 forward MW:70164 | 0.8 | 0.6 | 0.2 | 0.8 | 1.5 | 1.1 |
| Bbr_0541 | luxS Autoinducer-2 production protein luxS 727915:728409 forward MW:18491 | 0.9 | 1.1 | 1.4 | 0.5 | 3.2 | 0.2 |
| Bbr_0542 | cysE Serine O-acetyltransferase 728533:729075 forward MW:20512 | 1.0 | 1.1 | 2.1 | 0.5 | 2.0 | 0.3 |
| Bbr_0543 | aap1 Amino acid permease 729132:730589 reverse MW:52733 | 1.8 | 2.8 | 4.2 | 5.9 | 1.5 | 0.4 |
| Bbr_0544 | alr Alanine racemase 730781:732139 forward MW:48202 | 1.3 | 1.2 | 0.6 | 0.5 | 1.1 | 0.6 |
| Bbr_0545 | dgt Deoxyguanosinetriphosphate triphosphohydrolase 732179:733465 forward MW:47740 | 0.7 | 0.5 | 0.2 | 0.3 | 1.3 | 0.8 |
| Bbr_0546 | dnaG DNA primase 733649:735751 forward MW:77105 | 1.1 | 1.3 | 0.5 | 0.8 | 2.0 | 0.6 |
| Bbr_0547 | Bbr_0547 Conserved hypothetical protein with PIN domain 735800:736222 reverse MW:15248 | 1.3 | 1.4 | 3.6 | 11.9 | 1.5 | 6.6 |
| Bbr_0548 | Bbr_0548 Conserved hypothetical protein 736219:736572 reverse MW:13335 | 1.2 | 1.4 | 2.0 | 5.9 | 1.1 | 5.8 |
| Bbr_0549 | Bbr_0549 Pyridoxine biosynthesis protein 736660:737535 forward MW:31122 | 1.7 | 1.0 | 0.4 | 1.0 | 0.6 | 0.7 |
| Bbr_0550 | Bbr_0550 Pyridoxine biosynthesis amidotransferase 737562:738200 forward MW:22742 | 1.7 | 0.9 | 0.3 | 0.9 | 0.5 | 0.7 |
| Bbr_0551 | Bbr_0551 Multiple substrate aminotransferase (MsaT) containing domain of GntR family 738258:739781 forward MW:56937 | 1.1 | 0.8 | 0.6 | 1.0 | 1.3 | 0.7 |
| Bbr_0552 | Bbr_0552 Conserved hypothetical membrane spanning protein 739862:741040 forward MW:43091 | 1.0 | 0.9 | 2.1 | 3.3 | 0.8 | 1.3 |
| Bbr_0553 | Bbr_0553 Conserved hypothetical protein 741044:741319 reverse MW:9804 | 0.9 | 0.8 | 1.8 | 3.0 | 0.8 | 1.8 |
| Bbr_0555 | Bbr_0555 Transcriptional regulator, RpiR family 742164:743033 forward MW:31199 | 1.1 | 1.3 | 5.1 | 11.9 | 1.6 | 9.2 |
| Bbr_0556 | Bbr_0556 Hypothetical protein 743271:743699 forward MW:15465 | 1.1 | 1.1 | 3.0 | 2.7 | 0.5 | 7.0 |

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|---|---|---|---|---|---|---|---|
| Bbr_0557 | Bbr_0557 Solute-binding protein of ABC transporter system for sugars 743897:745228 forward MW:47748 | 0.7 | 0.2 | 0.1 | 0.2 | 0.7 | 0.5 |
| Bbr_0558 | Bbr_0558 Transcriptional regulator, LacI family 745240:746484 forward MW:44779 | 0.8 | 0.3 | 0.3 | 0.5 | 0.6 | 0.5 |
| Bbr_0559 | agl4 Alpha-glucosidase 746465:748279 forward MW:68320 | 0.8 | 0.3 | 0.4 | 0.8 | 0.4 | 0.7 |
| Bbr_0560 | dppA1 Solute-binding protein of ABC transporter system for peptides 748793:750412 forward MW:58923 | 1.5 | 1.1 | 0.7 | 2.0 | 0.3 | 0.4 |
| Bbr_0561 | msrA2/mrsB2 Peptide methionine sulfoxide reductase msrA/msrB 750414:750905 forward MW:18035 | 1.4 | 1.3 | 3.5 | 6.3 | 1.9 | 0.9 |
| Bbr_0562 | Bbr_0562 ATP-binding protein of ABC transporter system 751600:752412 forward MW:29531 | 0.3 | 0.1 | 0.1 | 0.1 | 0.4 | 0.8 |
| Bbr_0563 | Bbr_0563 Conserved hypothetical membrane spanning protein 752424:753719 forward MW:44567 | 0.3 | 0.1 | 0.1 | 0.1 | 0.5 | 0.9 |
| Bbr_0564 | Bbr_0564 Permease protein of ABC transporter system 753731:755260 forward MW:54176 | 0.4 | 0.2 | 0.2 | 0.4 | 0.3 | 1.1 |
| Bbr_0565 | dxs 1-deoxy-D-xylulose 5-phosphate synthase 755244:757322 reverse MW:73420 | 1.2 | 1.5 | 0.9 | 0.8 | 0.7 | 0.9 |
| Bbr_0566 | adh3 Alcohol dehydrogenase 757549:758541 forward MW:34536 | 0.7 | 0.5 | 0.8 | 0.8 | 1.4 | 1.3 |
| Bbr_0567 | purE Phosphoribosylaminoimidazole carboxylase carboxyltransferase subunit 758602:759108 forward MW:17663 | 1.0 | 1.0 | 1.0 | 0.5 | 1.2 | 0.7 |
| Bbr_0568 | purK Phosphoribosylaminoimidazole carboxylase NCAIR mutase subunit 759092:760270 forward MW:42878 | 1.1 | 1.0 | 0.8 | 0.9 | 1.0 | 0.8 |
| Bbr_0569 | Bbr_0569 Ferric uptake regulation protein 760267:760707 forward MW:16201 | 0.9 | 0.9 | 0.5 | 0.8 | 1.0 | 0.9 |
| Bbr_0571 | Bbr_0571 ATP-binding protein of ABC transporter system 761886:762446 reverse MW:20684 | 0.8 | 1.1 | 1.2 | 5.7 | 0.8 | 5.2 |
| Bbr_0572 | Bbr_0572 Hypothetical protein 762713:763060 reverse MW:12606 | 1.1 | 1.3 | 1.6 | 1.0 | 0.7 | 11.2 |
| Bbr_0573 | Bbr_0573 Ferric uptake regulation protein 763409:763909 reverse MW:18701 | 1.2 | 1.6 | 1.5 | 1.2 | 0.7 | 2.4 |
| Bbr_0574 | Bbr_0574 Conserved hypothetical membrane spanning protein 764168:764923 reverse MW:27149 | 1.3 | 1.4 | 0.5 | 1.3 | 1.5 | 0.6 |
| Bbr_0575 | Bbr_0575 Conserved hypothetical membrane spanning protein 764926:766053 reverse MW:39674 | 1.1 | 1.3 | 2.8 | 9.3 | 1.9 | 1.5 |
| Bbr_0576 | Bbr_0576 Hypothetical protein 766050:766412 reverse MW:12918 | 1.1 | 1.9 | 3.4 | 6.7 | 1.3 | 1.5 |
| Bbr_0577 | rpmE1 LSU ribosomal protein L31P 766409:766633 reverse MW:8175 | 1.0 | 1.0 | 0.6 | 0.6 | 0.7 | 0.5 |
| Bbr_0579 | Bbr_0579 Solute binding protein of ABC transporter system 767162:768085 forward MW:32596 | 1.2 | 1.5 | 0.8 | 0.8 | 0.7 | 1.5 |
| Bbr_0580 | Bbr_0580 Phosphoglycerol transferase 768380:770455 forward MW:76780 | 0.7 | 0.6 | 0.3 | 0.3 | 1.2 | 0.7 |
| Bbr_0581 | aldH Aldehyde dehydrogenase (NAD(P)+) 770574:772133 forward MW:55913 | 0.5 | 0.4 | 0.4 | 0.3 | 1.4 | 1.3 |
| Bbr_0582 | purD Phosphoribosylamine--glycine ligase 772510:773778 reverse MW:45202 | 1.0 | 1.2 | 0.6 | 0.9 | 1.2 | 0.3 |
| Bbr_0583 | purM Phosphoribosylformylglycinamidine cyclo-ligase 773805:774842 reverse MW:36134 | 1.0 | 1.1 | 0.7 | 0.4 | 0.8 | 0.5 |
| Bbr_0584 | purF Amidophosphoribosyltransferase 774959:776470 reverse MW:55334 | 1.3 | 1.9 | 1.3 | 0.2 | 1.0 | 0.4 |
| Bbr_0585 | Bbr_0585 ImpB/MucB/SamB family protein involved in DNA repair 776781:778361 forward MW:58112 | 1.3 | 4.3 | 33.0 | 18.3 | 1.9 | 4.7 |
| Bbr_0586 | Bbr_0586 Conserved hypothetical protein 778358:778576 forward MW:7971 | 0.9 | 1.9 | 3.6 | 3.7 | 1.2 | 1.5 |
| Bbr_0588 | Bbr_0588 Conserved hypothetical protein 778914:779528 reverse MW:22540 | 1.2 | 1.4 | 1.5 | 1.3 | 0.3 | 2.1 |
| Bbr_0589 | Bbr_0589 Hypothetical protein 779577:780164 forward MW:21141 | 1.0 | 1.2 | 6.6 | 18.4 | 0.6 | 5.6 |
| Bbr_0590 | Bbr_0590 Hypothetical protein 780161:781102 forward MW:36412 | 1.2 | 1.8 | 0.8 | 0.6 | 0.4 | 4.0 |
| Bbr_0591 | Bbr_0591 Hypothetical protein 781067:781699 reverse MW:23456 | 1.4 | 2.0 | 4.6 | 1.8 | 0.5 | 3.7 |
| Bbr_0592 | Bbr_0592 Hypothetical protein 781992:782264 forward MW:10220 | 1.1 | 2.2 | 2.6 | 4.4 | 1.1 | 14.6 |
| Bbr_0593 | Bbr_0593 Hypothetical secreted protein 782391:783203 forward MW:29930 | 1.0 | 1.1 | 5.5 | 7.5 | 1.4 | 6.7 |
| Bbr_0594 | Bbr_0594 Narrowly conserved hypothetical membrane spanning protein 783287:783946 reverse MW:24422 | 1.1 | 0.8 | 0.2 | 0.2 | 0.6 | 0.5 |
| Bbr_0595 | Bbr_0595 Predicted conserved hypothetical protein 783943:785313 reverse MW:50658 | 1.1 | 0.9 | 0.3 | 0.3 | 1.3 | 0.6 |
| Bbr_0596 | Bbr_0596 Carboxylesterase or lipase 785286:786623 reverse MW:47266 | 1.1 | 1.0 | 0.8 | 1.2 | 1.1 | 1.0 |
| Bbr_0597 | purL Phosphoribosylformylglycinamidine synthase 786761:790495 reverse MW:134329 | 1.1 | 1.0 | 0.7 | 0.8 | 1.2 | 0.8 |
| Bbr_0598 | purC Phosphoribosylamidoimidazole-succinocarboxamide synthase 790703:791455 reverse MW:28293 | 1.0 | 0.9 | 0.6 | 0.2 | 0.9 | 0.3 |
| Bbr_0599 | purT Phosphoribosylglycinamide formyltransferase 791537:792838 reverse MW:45169 | 1.0 | 0.9 | 0.9 | 0.7 | 2.3 | 0.8 |
| Bbr_0600 | Bbr_0600 Aminotransferase 793338:794588 forward MW:43507 | 1.1 | 1.1 | 5.2 | 57.5 | 0.9 | 7.3 |
| Bbr_0601 | Bbr_0601 Glycosyltransferase 794705:795865 forward MW:42740 | 0.6 | 0.4 | 0.2 | 0.4 | 0.9 | 1.3 |
| Bbr_0602 | Bbr_0602 Low specificity-threonine aldolase 796006:797031 reverse MW:37501 | 1.1 | 0.9 | 0.9 | 0.2 | 1.2 | 1.7 |
| Bbr_0603 | Bbr_0603 Transporter, Sodium/bile acid symporter family 797476:798549 forward MW:38592 | 1.5 | 0.9 | 0.2 | 0.4 | 1.1 | 0.5 |
| Bbr_0604 | rpsL SSU ribosomal protein S12P 799133:799504 forward MW:13547 | 1.5 | 1.4 | 1.5 | 1.9 | 0.7 | 1.4 |
| Bbr_0605 | rpsG SSU ribosomal protein S7P 799510:799980 forward MW:17553 | 1.5 | 1.5 | 1.0 | 0.4 | 0.7 | 1.3 |
| Bbr_0606 | fusA Protein Translation Elongation Factor G (EF-G) 800014:802137 forward MW:78116 | 1.8 | 1.9 | 1.0 | 0.2 | 0.9 | 1.3 |
| Bbr_0607 | tuf Protein Translation Elongation Factor Tu (EF-TU) 802311:803510 forward MW:43938 | 0.8 | 0.6 | 0.5 | 0.3 | 0.5 | 0.6 |
| Bbr_0608 | Bbr_0608 Conserved hypothetical protein 803718:804449 forward MW:26247 | 0.7 | 0.5 | 1.4 | 0.3 | 1.4 | 4.4 |
| Bbr_0609 | Bbr_0609 Transcriptional regulator, LysR family 804467:805282 forward MW:29611 | 0.8 | 0.6 | 0.5 | 0.7 | 0.9 | 2.8 |
| Bbr_0610 | Bbr_0610 Conserved hypothetical membrane spanning protein 805397:806461 forward MW:37509 | 1.8 | 1.5 | 0.5 | 0.6 | 0.9 | 0.7 |
| Bbr_0611 | Bbr_0611 Narrowly conserved hypothetical protein 806836:807039 reverse MW:7112 | 1.2 | 1.1 | 2.9 | 4.2 | 1.3 | 0.4 |
| Bbr_0612 | crcB3 CrcB family protein 807114:807479 reverse MW:12869 | 1.1 | 1.1 | 1.5 | 1.2 | 0.7 | 0.4 |
| Bbr_0613 | crcB4 CrcB family protein 807479:808015 reverse MW:17749 | 1.3 | 1.8 | 7.3 | 9.3 | 1.8 | 0.4 |
| Bbr_0614 | Bbr_0614 Transcriptional regulator, MerR family 808223:808687 forward MW:17317 | 1.1 | 0.9 | 0.7 | 1.1 | 1.3 | 0.5 |
| Bbr_0615 | adh1 Alcohol dehydrogenase 808728:809771 forward MW:36732 | 1.1 | 0.8 | 0.3 | 0.6 | 1.4 | 0.4 |
| Bbr_0616 | Bbr_0616 Conserved hypothetical protein 810000:811361 forward MW:52589 | 1.4 | 1.6 | 4.7 | 2.3 | 1.1 | 3.6 |
| Bbr_0617 | Bbr_0617 Conserved hypothetical protein 811470:812087 reverse MW:22888 | 1.4 | 2.5 | 4.7 | 2.1 | 1.4 | 1.5 |
| Bbr_0618 | uvrA1 Excinuclease ABC subunit A 812292:814805 forward MW:88825 | 1.0 | 1.0 | 0.7 | 1.1 | 1.5 | 0.7 |
| Bbr_0619 | Bbr_0619 Na+ driven multidrug efflux pump 814981:816339 forward MW:47579 | 1.4 | 1.5 | 0.4 | 0.6 | 1.0 | 0.8 |
| Bbr_0620 | Bbr_0620 DNA-(apurinic or apyrimidinic site) lyase 816347:817039 forward MW:25355 | 1.6 | 1.6 | 1.6 | 3.1 | 1.1 | 0.5 |
| Bbr_0621 | Bbr_0621 Conserved hypothetical protein 817249:817485 forward MW:8244 | 1.0 | 1.1 | 1.4 | 1.3 | 1.7 | 0.7 |
| Bbr_0622 | lacA Galactoside O-acetyltransferase 817525:818199 forward MW:25102 | 0.8 | 0.5 | 0.6 | 1.3 | 0.8 | 0.7 |
| Bbr_0624 | Bbr_0624 Transporter 818640:819710 forward MW:37958 | 1.4 | 1.6 | 1.5 | 1.8 | 0.9 | 0.7 |
| Bbr_0625 | Bbr_0625 Conserved hypothetical protein 819742:820014 reverse MW:9784 | 0.5 | 0.6 | 6.7 | 4.4 | 1.5 | 3.7 |
| Bbr_0626 | Bbr_0626 Glycosyltransferase 820371:822644 reverse MW:86210 | 0.7 | 0.5 | 0.2 | 0.1 | 0.9 | 0.7 |
| Bbr_0627 | Bbr_0627 Secreted glycosyl hydrolase 822877:824190 forward MW:48069 | 0.7 | 0.7 | 0.3 | 0.2 | 0.8 | 0.4 |
| Bbr_0628 | Bbr_0628 Sensory box/GGDEF family protein 824279:826732 forward MW:90266 | 0.6 | 0.3 | 0.3 | 0.8 | 1.1 | 0.5 |
| Bbr_0629 | Bbr_0629 Conserved hypothetical membrane spanning protein in uncharacterised protein family (UPF0014) 826950:827738 reverse MW:28009 | 0.8 | 0.8 | 0.6 | 1.3 | 2.8 | 0.6 |
| Bbr_0630 | Bbr_0630 ATP-binding protein of ABC transporter system 827735:828451 reverse MW:25768 | 0.9 | 1.0 | 3.2 | 5.0 | 2.0 | 0.9 |
| Bbr_0631 | efp Protein Translation Elongation Factor P (EF-P) 828579:829142 forward MW:20563 | 1.2 | 1.2 | 1.5 | 1.3 | 0.8 | 0.5 |
| Bbr_0632 | nusB N utilization substance protein B 829197:829727 forward MW:19218 | 1.0 | 1.0 | 0.5 | 0.8 | 0.7 | 0.6 |
| Bbr_0633 | carA Carbamoyl-phosphate synthase small chain 829915:831138 forward MW:44210 | 1.1 | 0.9 | 0.6 | 0.3 | 0.7 | 0.4 |
| Bbr_0634 | carB Carbamoyl-phosphate synthase large chain 831140:834523 forward MW:123028 | 1.1 | 1.1 | 0.5 | 0.5 | 1.0 | 0.7 |
| Bbr_0635 | pyrF2 Orotidine 5'-phosphate decarboxylase 834523:835443 forward MW:32615 | 1.0 | 1.0 | 0.5 | 0.4 | 0.9 | 0.8 |

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|---|---|---|---|---|---|---|---|
| Bbr_0636 | gmk Guanylate kinase 835480:836070 forward MW:21594 | 0.9 | 1.0 | 0.4 | 0.3 | 0.7 | 1.1 |
| Bbr_0637 | dnaQ DNA polymerase III alpha subunit 836104:836811 reverse MW:26220 | 1.5 | 1.7 | 2.1 | 1.5 | 1.1 | 0.6 |
| Bbr_0638 | Bbr_0638 Conserved hypothetical protein 836936:837367 reverse MW:15695 | 1.1 | 1.9 | 4.5 | 23.9 | 0.5 | 21.6 |
| Bbr_0639 | Bbr_0639 Tetracycline resistance protein 837575:839761 forward MW:79583 | 1.8 | 1.3 | 0.2 | 0.2 | 0.7 | 0.8 |
| Bbr_0640 | Bbr_0640 Phospholipase/carboxylesterase 839742:840392 reverse MW:23591 | 1.1 | 1.0 | 0.6 | 0.8 | 1.3 | 0.4 |
| Bbr_0641 | metC1 Cystathionine beta-lyase 840559:841791 forward MW:44313 | 1.2 | 1.4 | 4.8 | 12.9 | 1.2 | 2.9 |
| Bbr_0642 | Bbr_0642 Glutaredoxin 842199:842450 forward MW:9065 | 1.1 | 1.3 | 0.7 | 0.3 | 2.0 | 0.4 |
| Bbr_0643 | Bbr_0643 Conserved hypothetical protein 843444:844355 forward MW:33663 | 0.7 | 0.4 | 0.4 | 0.3 | 1.4 | 0.8 |
| Bbr_0645 | Bbr_0645 Phospholipase 845212:846042 reverse MW:30930 | 1.5 | 1.2 | 1.3 | 0.8 | 2.2 | 0.8 |
| Bbr_0646 | murI Glutamate racemase 846184:846978 reverse MW:29060 | 1.1 | 1.1 | 1.9 | 1.2 | 1.4 | 1.0 |
| Bbr_0647 | dapF Diaminopimelate epimerase 847109:848008 forward MW:32346 | 1.0 | 0.8 | 0.6 | 0.5 | 0.9 | 0.6 |
| Bbr_0648 | Bbr_0648 Conserved hypothetical membrane spanning protein 848077:848796 reverse MW:25866 | 1.1 | 1.2 | 0.8 | 0.7 | 2.8 | 0.7 |
| Bbr_0649 | Bbr_0649 PHP domain containing protein (TRPH) 848923:849816 forward MW:32173 | 1.0 | 1.0 | 2.8 | 14.3 | 2.6 | 0.6 |
| Bbr_0650 | Bbr_0650 Conserved hypothetical protein 849873:850097 reverse MW:7662 | 0.8 | 0.9 | 1.1 | 1.0 | 2.6 | 0.4 |
| Bbr_0651 | Bbr_0651 Conserved hypothetical secreted protein 850203:851834 reverse MW:57815 | 1.1 | 1.1 | 0.6 | 0.6 | 1.5 | 0.6 |
| Bbr_0652 | Bbr_0652 DNA helicase II homolog 851917:853464 forward MW:55970 | 1.0 | 1.0 | 0.7 | 1.2 | 2.1 | 1.0 |
| Bbr_0653 | Bbr_0653 Conserved hypothetical protein 853535:855265 reverse MW:61344 | 0.8 | 1.0 | 0.4 | 0.2 | 3.3 | 0.9 |
| Bbr_0654 | Bbr_0654 Conserved hypothetical protein 855346:856356 forward MW:35034 | 1.2 | 1.8 | 1.3 | 0.9 | 4.4 | 1.4 |
| Bbr_0655 | Bbr_0655 Conserved hypothetical protein 856448:856864 forward MW:14954 | 1.2 | 1.5 | 1.2 | 1.2 | 1.4 | 0.7 |
| Bbr_0656 | Bbr_0656 Conserved hypothetical protein 857189:858787 forward MW:55876 | 1.1 | 1.1 | 1.5 | 0.2 | 1.6 | 1.3 |
| Bbr_0657 | ispC 1-deoxy-D-xylulose 5-phosphate reductoisomerase 858784:859974 forward MW:42078 | 1.1 | 1.2 | 0.5 | 0.2 | 0.9 | 0.9 |
| Bbr_0658 | ispG 1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate synthase 859971:861194 forward MW:43058 | 1.2 | 1.4 | 0.5 | 0.5 | 1.0 | 1.1 |
| Bbr_0659 | Bbr_0659 Narrowly conserved hypothetical membrane spanning protein 861242:863017 forward MW:64428 | 1.0 | 1.4 | 0.3 | 0.1 | 1.2 | 1.0 |
| Bbr_0660 | recO DNA repair protein recO 863050:863769 forward MW:26488 | 0.8 | 0.9 | 0.4 | 0.6 | 1.1 | 2.0 |
| Bbr_0661 | uppS Undecaprenyl pyrophosphate synthetase 863766:864560 forward MW:30220 | 1.2 | 1.2 | 0.4 | 0.4 | 1.8 | 0.9 |
| Bbr_0662 | Bbr_0662 Permease protein of ABC transporter system 864680:865459 reverse MW:27765 | 0.9 | 1.0 | 1.0 | 0.3 | 1.1 | 0.6 |
| Bbr_0663 | Bbr_0663 Solute binding protein of ABC transporter system 865524:866591 reverse MW:37841 | 1.0 | 0.9 | 0.8 | 0.5 | 0.8 | 0.7 |
| Bbr_0664 | Bbr_0664 Aminotransferase 866857:868062 forward MW:43194 | 1.2 | 1.6 | 0.9 | 0.4 | 2.3 | 0.7 |
| Bbr_0665 | Bbr_0665 ATP-binding protein of ABC transporter system 868062:868856 forward MW:28770 | 1.2 | 1.3 | 1.8 | 2.5 | 2.8 | 0.7 |
| Bbr_0666 | Bbr_0666 Narrowly conserved hypothetical membrane spanning protein 869251:871500 reverse MW:82691 | 1.1 | 0.9 | 0.4 | 0.4 | 0.9 | 0.4 |
| Bbr_0667 | Bbr_0667 Narrowly conserved hypothetical protein 871620:874922 forward MW:121048 | 0.8 | 1.1 | 0.2 | 0.2 | 3.6 | 0.5 |
| Bbr_0668 | ligA NAD-dependent DNA ligase 874961:877753 forward MW:100655 | 1.0 | 1.1 | 0.3 | 0.3 | 2.8 | 0.6 |
| Bbr_0669 | mrp ATP-binding Mrp-like protein 878009:879130 forward MW:39669 | 1.1 | 1.2 | 1.5 | 1.4 | 3.2 | 0.6 |
| Bbr_0670 | glnA1 Glutamine synthetase 879609:881045 reverse MW:53222 | 1.5 | 0.9 | 0.3 | 0.4 | 0.4 | 0.8 |
| Bbr_0671 | Bbr_0671 Conserved hypothetical membrane spanning protein 881349:882131 reverse MW:29279 | 0.9 | 0.8 | 1.3 | 1.1 | 1.3 | 0.8 |
| Bbr_0672 | pdhD Dihydrolipoamide dehydrogenase 882196:883689 reverse MW:52280 | 0.7 | 0.4 | 0.3 | 0.2 | 1.8 | 0.5 |
| Bbr_0673 | Bbr_0673 Conserved hypothetical membrane spanning protein 883813:884328 reverse MW:19944 | 1.1 | 1.3 | 0.9 | 0.2 | 2.1 | 0.4 |
| Bbr_0674 | Bbr_0674 Peptidase family M20A protein 884525:885892 forward MW:48328 | 1.3 | 1.6 | 1.9 | 1.8 | 1.9 | 1.0 |
| Bbr_0675 | Bbr_0675 Permease protein of ABC transporter system 886463:887062 forward MW:21139 | 1.3 | 1.7 | 4.7 | 12.9 | 1.3 | 1.7 |
| Bbr_0676 | Bbr_0676 ATP-binding protein of ABC transporter system 887062:888534 forward MW:52548 | 1.4 | 1.9 | 0.9 | 1.1 | 1.0 | 1.4 |
| Bbr_0677 | Bbr_0677 Permease protein of ABC transporter system for cobalt 888531:889469 forward MW:33002 | 1.4 | 2.0 | 0.4 | 0.8 | 1.0 | 1.0 |
| Bbr_0678 | Bbr_0678 rRNA methylase 889500:890384 forward MW:32109 | 1.0 | 1.2 | 0.9 | 0.7 | 2.6 | 0.8 |
| Bbr_0679 | pheS Phenylalanyl-tRNA synthetase alpha chain 890381:891505 forward MW:40973 | 1.2 | 1.3 | 1.4 | 0.6 | 1.4 | 0.5 |
| Bbr_0680 | pheT Phenylalanyl-tRNA synthetase beta chain 891513:894122 forward MW:94441 | 1.1 | 1.2 | 0.3 | 0.2 | 1.4 | 0.7 |
| Bbr_0681 | Bbr_0681 Narrowly conserved hypothetical membrane spanning protein 894150:894806 forward MW:23563 | 1.0 | 0.9 | 0.2 | 0.1 | 0.9 | 0.8 |
| Bbr_0682 | argC N-acetyl-gamma-glutamyl-phosphate reductase 894903:895997 forward MW:37883 | 1.2 | 1.4 | 1.8 | 2.6 | 1.6 | 1.7 |
| Bbr_0683 | argJ Glutamate N-acetyltransferase/Amino-acid acetyltransferase 895994:897169 forward MW:39839 | 1.3 | 1.6 | 1.3 | 0.2 | 1.6 | 1.3 |
| Bbr_0684 | argB Acetylglutamate kinase 897398:898354 forward MW:33795 | 1.4 | 1.8 | 1.4 | 1.1 | 1.3 | 1.3 |
| Bbr_0685 | argD Acetylornithine aminotransferase 898344:899639 forward MW:45599 | 1.4 | 1.9 | 0.9 | 0.9 | 1.4 | 1.0 |
| Bbr_0686 | argF Ornithine carbamoyltransferase 899668:900633 forward MW:35244 | 1.4 | 1.7 | 0.8 | 0.6 | 1.0 | 0.9 |
| Bbr_0687 | argR Arginine repressor, argR 900630:901142 forward MW:17750 | 1.4 | 1.9 | 0.6 | 0.6 | 1.4 | 0.8 |
| Bbr_0688 | argG Argininosuccinate synthase 901298:902536 forward MW:45535 | 1.0 | 1.1 | 1.2 | 0.3 | 0.8 | 0.7 |
| Bbr_0690 | Bbr_0690 Transposase 903896:905377 forward MW:55460 | 1.3 | 1.8 | 3.7 | 9.7 | 0.2 | 3.9 |
| Bbr_0691 | Bbr_0691 Transposase 905380:906165 forward MW:29886 | 1.1 | 1.3 | 3.0 | 3.6 | 0.1 | 2.9 |
| Bbr_0692 | argH Argininosuccinate lyase 907967:909439 forward MW:53252 | 1.0 | 1.0 | 1.0 | 0.3 | 1.5 | 0.7 |
| Bbr_0693 | thiS ThiS protein 909879:910073 forward MW:7117 | 1.1 | 1.2 | 3.4 | 5.4 | 1.9 | 2.6 |
| Bbr_0694 | thiG Thiazole biosynthesis protein thiG 910085:910954 forward MW:30708 | 1.1 | 1.0 | 1.6 | 1.5 | 2.2 | 2.4 |
| Bbr_0695 | thiF ThiF protein 911093:911902 forward MW:28257 | 1.0 | 1.0 | 2.4 | 1.6 | 1.3 | 2.5 |
| Bbr_0696 | Bbr_0696 Conserved hypothetical protein 912047:912439 forward MW:14423 | 1.1 | 0.7 | 2.5 | 5.1 | 1.3 | 3.0 |
| Bbr_0697 | Bbr_0697 Hydrolase (HAD superfamily) 912673:913206 forward MW:20790 | 1.0 | 0.9 | 0.9 | 1.2 | 1.3 | 0.6 |
| Bbr_0698 | Bbr_0698 Transporter 913216:913983 forward MW:28775 | 0.9 | 0.8 | 0.4 | 0.2 | 1.4 | 0.6 |
| Bbr_0699 | Bbr_0699 Transporter 914004:915824 reverse MW:67002 | 0.9 | 0.6 | 0.7 | 1.2 | 1.1 | 0.6 |
| Bbr_0700 | tyrS Tyrosyl-tRNA synthetase 915985:917307 forward MW:48452 | 1.3 | 0.8 | 0.8 | 0.5 | 1.4 | 0.8 |
| Bbr_0701 | Bbr_0701 Conserved hypothetical protein 917335:919167 forward MW:70005 | 1.1 | 0.9 | 0.3 | 0.2 | 1.7 | 0.8 |
| Bbr_0702 | Bbr_0702 Haloacid dehalogenase-like hydrolase (HAD superfamily) 919176:920222 forward MW:37821 | 1.1 | 1.0 | 0.4 | 0.4 | 1.7 | 0.9 |
| Bbr_0703 | Bbr_0703 Hemolysin-like protein with S4 and FtsJ-like methyltransferase domains 920378:921151 forward MW:27338 | 1.1 | 1.1 | 0.2 | 0.4 | 1.3 | 1.4 |
| Bbr_0704 | Bbr_0704 Narrowly conserved hypothetical protein 921133:921807 reverse MW:24402 | 0.9 | 0.7 | 5.1 | 7.0 | 1.5 | 22.4 |
| Bbr_0707 | Bbr_0707 ATP-NAD kinase (EC 2.7.1.23) 923048:924028 forward MW:35324 | 1.0 | 1.1 | 1.8 | 3.2 | 1.5 | 1.4 |
| Bbr_0708 | recN DNA repair protein recN 924028:925878 forward MW:65196 | 1.0 | 1.0 | 0.3 | 0.2 | 1.5 | 1.0 |
| Bbr_0709 | Bbr_0709 Haloacid dehalogenase-like hydrolase (HAD superfamily) 925875:926522 forward MW:23784 | 1.0 | 1.0 | 0.2 | 0.4 | 1.5 | 0.7 |
| Bbr_0711 | Bbr_0711 Transcriptional regulator, GntR family 927411:927785 forward MW:13698 | 0.8 | 0.6 | 1.8 | 11.8 | 1.3 | 1.5 |
| Bbr_0712 | Bbr_0712 ATP-binding protein of ABC transporter system 927801:928727 forward MW:33978 | 0.8 | 0.7 | 1.2 | 2.8 | 0.5 | 1.3 |
| Bbr_0713 | Bbr_0713 Narrowly conserved hypothetical membrane spanning protein 928734:929447 forward MW:25627 | 0.9 | 0.8 | 0.8 | 0.6 | 0.5 | 0.8 |
| Bbr_0714 | Bbr_0714 Narrowly conserved hypothetical protein 929362:930141 reverse MW:28462 | 1.2 | 1.8 | 1.1 | 0.6 | 0.4 | 6.5 |
| Bbr_0715 | thrC Threonine synthase 931295:932785 reverse MW:54021 | 0.9 | 0.8 | 0.9 | 0.3 | 2.3 | 0.8 |

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|---|---|---|---|---|---|---|---|
| Bbr_0716 | proA Gamma-glutamyl phosphate reductase 933164:934468 forward MW:46193 | 1.0 | 0.7 | 0.2 | 0.2 | 1.3 | 0.5 |
| Bbr_0717 | Bbr_0717 Narrowly conserved hypothetical protein 934465:935028 forward MW:21052 | 0.9 | 0.7 | 0.2 | 0.2 | 1.4 | 0.5 |
| Bbr_0718 | nadD Nicotinate-nucleotide adenylyltransferase 935025:935753 forward MW:26635 | 0.9 | 0.7 | 0.2 | 0.2 | 0.8 | 0.6 |
| Bbr_0720 | Bbr_0720 Conserved hypothetical membrane spanning protein in uncharacterised protein family (UPF0182) 937221:940478 forward MW:116952 | 0.7 | 0.7 | 0.1 | 0.2 | 3.1 | 1.2 |
| Bbr_0721 | Bbr_0721 Phosphinothricin N-acetyltransferase 940624:941121 forward MW:18169 | 0.9 | 1.1 | 0.6 | 0.6 | 2.4 | 2.0 |
| Bbr_0722 | pth Peptidyl-tRNA hydrolase 941170:941769 forward MW:21790 | 1.2 | 1.5 | 2.6 | 1.4 | 1.9 | 1.5 |
| Bbr_0723 | mfd Transcription-repair coupling factor 941759:945349 forward MW:131439 | 1.1 | 1.0 | 0.2 | 0.3 | 1.2 | 0.4 |
| Bbr_0724 | Bbr_0724 Oxidoreductase, aldo-keto reductase family 945346:946257 forward MW:33916 | 1.1 | 0.8 | 0.1 | 0.2 | 1.2 | 0.3 |
| Bbr_0725 | eno Enolase 946408:947706 forward MW:46563 | 0.7 | 0.6 | 0.4 | 0.2 | 0.8 | 0.4 |
| Bbr_0726 | Bbr_0726 Conserved hypothetical membrane spanning protein with septum formation initiator domain 947773:948381 forward MW:21936 | 1.2 | 1.7 | 3.3 | 0.4 | 1.5 | 1.7 |
| Bbr_0727 | Bbr_0727 Conserved hypothetical protein with DUF501 domain 948378:948944 forward MW:20187 | 1.1 | 1.4 | 3.7 | 0.8 | 1.0 | 3.0 |
| Bbr_0728 | Bbr_0728 Exopolyphosphatase 949003:950004 forward MW:35800 | 1.0 | 1.2 | 3.2 | 0.9 | 0.9 | 2.4 |
| Bbr_0729 | Bbr_0729 Narrowly conserved hypothetical membrane spanning protein 950244:950813 forward MW:20133 | 1.1 | 1.4 | 3.1 | 4.7 | 1.4 | 1.9 |
| Bbr_0730 | sdaA L-serine dehydratase 950945:952402 forward MW:51867 | 1.1 | 1.1 | 1.6 | 1.6 | 2.3 | 0.9 |
| Bbr_0731 | fkbP Peptidyl-prolyl cis-trans isomerase 952463:952870 forward MW:14348 | 1.0 | 0.8 | 0.4 | 0.4 | 0.7 | 1.7 |
| Bbr_0732 | greA Transcription elongation factor greA 952968:953447 forward MW:17136 | 1.3 | 1.0 | 0.7 | 0.3 | 1.1 | 2.6 |
| Bbr_0733 | Bbr_0733 Conserved hypothetical membrane spanning protein (hemolysin III homolog) 953532:954476 reverse MW:34787 | 1.8 | 1.6 | 2.8 | 4.3 | 1.3 | 8.1 |
| Bbr_0734 | Bbr_0734 Sensory transduction protein kinase 954639:956126 forward MW:54520 | 0.9 | 1.0 | 0.6 | 0.4 | 2.7 | 1.2 |
| Bbr_0735 | Bbr_0735 Cell division transcription factor WhmD 956186:956464 reverse MW:10419 | 1.1 | 1.9 | 4.4 | 6.0 | 3.4 | 1.2 |
| Bbr_0736 | Bbr_0736 DNA segregation ATPase and related proteins (FtsK/SpoIIIE family) 956579:958399 reverse MW:65413 | 1.0 | 1.2 | 1.3 | 2.9 | 2.4 | 1.9 |
| Bbr_0737 | Bbr_0737 Transcriptional regulator 958501:959835 reverse MW:46346 | 1.0 | 0.9 | 0.4 | 0.3 | 0.8 | 1.4 |
| Bbr_0738 | whiB2 Transcription factor WhiB 960096:960395 forward MW:11538 | 0.9 | 0.9 | 0.8 | 1.7 | 0.9 | 4.3 |
| Bbr_0739 | Bbr_0739 Conserved hypothetical membrane spanning protein 960441:963533 forward MW:111780 | 1.0 | 1.0 | 0.2 | 0.3 | 1.9 | 1.0 |
| Bbr_0740 | Bbr_0740 Conserved hypothetical secreted protein 963530:965071 forward MW:52709 | 1.0 | 0.9 | 0.3 | 0.5 | 1.9 | 1.0 |
| Bbr_0741 | Bbr_0741 Conserved hypothetical protein 965093:965521 reverse MW:16366 | 0.9 | 1.0 | 1.1 | 1.9 | 2.4 | 0.6 |
| Bbr_0742 | Bbr_0742 Phosphomannomutase 965607:966410 forward MW:28989 | 0.9 | 0.9 | 1.4 | 1.4 | 2.4 | 2.0 |
| Bbr_0743 | Bbr_0743 Conserved hypothetical protein with phosphoribosylpyrophosphate transferase domain 966542:967156 forward MW:22127 | 1.0 | 1.2 | 3.2 | 2.1 | 2.0 | 3.1 |
| Bbr_0744 | Bbr_0744 Sensory transduction protein kinase 967214:968287 reverse MW:39245 | 0.9 | 0.8 | 0.2 | 0.4 | 0.6 | 0.8 |
| Bbr_0745 | Bbr_0745 Two-component response regulator 968287:969009 reverse MW:26385 | 0.8 | 0.7 | 0.4 | 0.8 | 0.8 | 0.7 |
| Bbr_0746 | glgB 1,4-alpha-glucan branching enzyme 969040:971292 reverse MW:84364 | 0.7 | 0.3 | 0.1 | 0.2 | 0.9 | 0.6 |
| Bbr_0747 | Bbr_0747 CarD-like transcriptional regulator 971470:972063 forward MW:21763 | 1.3 | 1.8 | 4.2 | 5.4 | 1.3 | 1.0 |
| Bbr_0748 | ispF 2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase 972060:972575 forward MW:17292 | 1.3 | 2.5 | 4.5 | 3.0 | 1.5 | 1.3 |
| Bbr_0749 | Bbr_0749 Permease protein of ABC transporter system for metals 972648:973481 reverse MW:28674 | 1.2 | 1.4 | 0.4 | 0.3 | 0.6 | 0.6 |
| Bbr_0750 | Bbr_0750 ATP-binding protein of ABC transporter system for metals 973572:974444 reverse MW:31370 | 1.2 | 1.6 | 0.3 | 0.2 | 0.6 | 0.6 |
| Bbr_0751 | Bbr_0751 Solute-binding protein of ABC transporter system for metals 974602:975774 reverse MW:40754 | 0.9 | 0.7 | 0.4 | 0.4 | 1.7 | 0.5 |
| Bbr_0752 | folD Bifunctional methylenetetrahydrofolate dehydrogenase/cyclohydrolase 975879:976757 forward MW:31036 | 1.2 | 1.4 | 1.2 | 1.3 | 1.4 | 0.4 |
| Bbr_0753 | rpsA SSU ribosomal protein S1P 977007:978482 forward MW:54615 | 0.9 | 0.7 | 0.2 | 0.2 | 0.9 | 0.4 |
| Bbr_0754 | coaE Dephospho-CoA kinase 978597:979256 forward MW:24187 | 0.9 | 0.8 | 0.9 | 0.8 | 2.2 | 0.4 |
| Bbr_0755 | uvrB Excinuclease ABC subunit B 979422:981533 forward MW:79720 | 0.9 | 0.8 | 0.2 | 0.4 | 1.8 | 0.3 |
| Bbr_0756 | terC Tellurium resistance protein terC 981567:982553 forward MW:36441 | 1.1 | 1.1 | 0.3 | 0.1 | 1.4 | 0.4 |
| Bbr_0757 | pyk Pyruvate kinase 982723:984165 forward MW:52001 | 0.8 | 0.8 | 0.4 | 0.4 | 0.9 | 0.6 |
| Bbr_0758 | aspA ADP-ribose pyrophosphatase 984289:984888 reverse MW:22678 | 0.8 | 0.7 | 0.5 | 0.5 | 1.5 | 0.4 |
| Bbr_0759 | Bbr_0759 Transcriptional regulator 985223:986011 forward MW:29168 | 0.9 | 0.7 | 1.8 | 0.6 | 1.4 | 1.4 |
| Bbr_0760 | polA DNA polymerase I 986050:988905 forward MW:104270 | 0.7 | 0.6 | 0.2 | 0.3 | 0.9 | 1.1 |
| Bbr_0761 | Bbr_0761 NIF3-related protein 989043:989963 forward MW:33486 | 1.1 | 1.0 | 0.6 | 0.5 | 1.8 | 2.2 |
| Bbr_0762 | Bbr_0762 Phosphohydrolase (MutT/nudix family protein) 990006:990680 forward MW:25218 | 1.1 | 1.1 | 0.7 | 1.3 | 1.8 | 1.3 |
| Bbr_0763 | glgX1 Glycogen operon protein glgX 990733:992865 forward MW:80951 | 1.0 | 0.7 | 0.2 | 0.1 | 1.4 | 0.6 |
| Bbr_0764 | Bbr_0764 Narrowly conserved hypothetical protein 993003:993203 forward MW:7351 | 1.0 | 1.0 | 0.2 | 0.4 | 1.2 | 1.1 |
| Bbr_0765 | Bbr_0765 Conserved hypothetical protein with helix-turn-helix motif 993352:993837 forward MW:18249 | 0.3 | 0.2 | 0.3 | 0.8 | 2.2 | 0.7 |
| Bbr_0766 | Bbr_0766 Conserved hypothetical protein 993841:994491 forward MW:24430 | 0.3 | 0.2 | 0.2 | 0.3 | 1.8 | 0.6 |
| Bbr_0768 | Bbr_0768 Narrowly conserved hypothetical protein 995488:996180 forward MW:26788 | 0.7 | 0.6 | 1.4 | 1.5 | 0.6 | 3.9 |
| Bbr_0769 | Bbr_0769 Conserved hypothetical membrane spanning protein 996342:997514 forward MW:42675 | 1.3 | 1.3 | 0.8 | 0.7 | 1.1 | 0.6 |
| Bbr_0770 | aroA 3-phosphoshikimate 1-carboxyvinyltransferase 997542:998876 forward MW:47118 | 1.2 | 1.6 | 0.9 | 1.0 | 1.4 | 0.7 |
| Bbr_0771 | ack Acetate kinase 999104:1000333 reverse MW:44169 | 1.0 | 0.8 | 0.5 | 0.2 | 0.8 | 0.5 |
| Bbr_0772 | pta Phosphate acetyltransferase 1000465:1002135 reverse MW:59459 | 0.7 | 0.3 | 0.4 | 0.2 | 1.2 | 0.7 |
| Bbr_0773 | prsA Ribose-phosphate pyrophosphokinase 1002556:1003578 reverse MW:36891 | 1.0 | 1.1 | 1.2 | 1.5 | 1.6 | 0.7 |
| Bbr_0774 | Bbr_0774 Acyltransferase family protein 1003719:1005650 reverse MW:69971 | 2.0 | 3.1 | 1.4 | 0.8 | 1.7 | 0.7 |
| Bbr_0775 | guaA2 GMP synthase [glutamine-hydrolyzing] 1005794:1007356 reverse MW:56251 | 1.2 | 1.3 | 0.7 | 0.4 | 0.8 | 0.9 |
| Bbr_0776 | Bbr_0776 Xylulose-5-phosphate/Fructose-6-phosphate phosphoketolase 1007804:1010281 forward MW:92395 | 0.8 | 0.6 | 0.1 | 0.1 | 0.6 | 0.5 |
| Bbr_0777 | glmU UDP-N-acetylglucosamine pyrophosphorylase 1010465:1011847 forward MW:49207 | 1.0 | 1.2 | 0.9 | 1.1 | 1.0 | 0.8 |
| Bbr_0778 | Bbr_0778 iojap protein family 1011851:1012237 forward MW:14301 | 1.1 | 1.3 | 0.4 | 0.2 | 1.8 | 0.8 |
| Bbr_0779 | Bbr_0779 Phosphoglycerate mutase family protein 1012234:1012935 forward MW:26565 | 1.1 | 1.3 | 0.4 | 0.4 | 1.4 | 0.7 |
| Bbr_0780 | Bbr_0780 Hydrolase (HAD superfamily) 1013345:1014154 reverse MW:29877 | 1.3 | 1.6 | 2.0 | 1.1 | 1.8 | 0.4 |
| Bbr_0781 | Bbr_0781 Solute-binding protein of ABC transporter system 1014403:1015383 forward MW:35186 | 1.2 | 1.2 | 1.6 | 1.7 | 0.8 | 3.5 |
| Bbr_0782 | Bbr_0782 ATP-binding protein of ABC transporter system 1015552:1016754 forward MW:43568 | 1.1 | 1.0 | 1.5 | 2.3 | 1.7 | 2.4 |
| Bbr_0783 | Bbr_0783 Permease protein of ABC transporter system 1016751:1017437 forward MW:24493 | 1.4 | 1.3 | 0.7 | 0.6 | 1.0 | 1.6 |
| Bbr_0784 | Bbr_0784 N-acyl-L-amino acid amidohydrolase 1017516:1018667 forward MW:41599 | 1.0 | 1.0 | 0.9 | 1.0 | 2.3 | 0.5 |
| Bbr_0785 | nadE Glutamine-dependent NAD(+) synthetase 1018766:1020463 forward MW:60957 | 1.0 | 1.0 | 0.6 | 0.7 | 1.7 | 0.6 |
| Bbr_0786 | Bbr_0786 Predicted hypothetical protein 1020483:1020713 forward MW:9022 | 1.0 | 0.8 | 0.3 | 0.3 | 1.3 | 0.4 |
| Bbr_0787 | pfl Formate acetyltransferase 1020988:1023363 forward MW:88964 | 0.3 | 0.1 | 0.0 | 0.1 | 0.5 | 0.3 |
| Bbr_0788 | pflA1 Pyruvate formate-lyase activating enzyme 1023476:1024357 forward MW:32867 | 0.6 | 0.2 | 0.2 | 0.2 | 1.3 | 0.4 |
| Bbr_0789 | Bbr_0789 Conserved hypothetical protein 1024539:1025171 forward MW:22943 | 0.9 | 0.6 | 0.3 | 1.5 | 1.1 | 0.5 |
| Bbr_0790 | Bbr_0790 Ribonuclease D 1025168:1026469 forward MW:48838 | 1.3 | 1.9 | 2.1 | 3.9 | 1.1 | 0.9 |
| Bbr_0791 | tig Trigger factor, ppiase 1026524:1027897 forward MW:49381 | 1.0 | 1.4 | 2.8 | 1.8 | 1.5 | 0.7 |
| Bbr_0792 | Bbr_0792 Chloride channel protein 1028081:1029481 forward MW:47738 | 1.1 | 1.6 | 4.2 | 1.2 | 1.7 | 1.3 |

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|---|---|---|---|---|---|---|---|
| Bbr_0793 | Bbr_0793 Conserved hypothetical protein 1029526:1029903 forward MW:13803 | 1.2 | 1.6 | 3.3 | 1.4 | 1.8 | 1.1 |
| Bbr_0794 | clp1 ATP-dependent Clp protease proteolytic subunit 1 1030055:1030678 forward MW:22648 | 1.0 | 1.2 | 1.0 | 0.7 | 3.4 | 0.4 |
| Bbr_0795 | clpP2 ATP-dependent Clp protease proteolytic subunit 2 1030684:1031367 forward MW:25150 | 0.9 | 1.2 | 0.7 | 0.3 | 3.3 | 0.6 |
| Bbr_0796 | clpX ATP-dependent Clp protease ATP-binding subunit clpX 1031541:1032902 forward MW:49588 | 1.0 | 1.2 | 2.3 | 0.9 | 1.8 | 1.6 |
| Bbr_0797 | metC2 Cystathionine beta-lyase 1033295:1034500 forward MW:45200 | 1.3 | 1.1 | 3.0 | 1.5 | 0.5 | 9.2 |
| Bbr_0798 | nhaA Na+/H+ antiporter nhaA 1034581:1035969 forward MW:48773 | 1.2 | 2.1 | 1.4 | 0.4 | 4.0 | 2.3 |
| Bbr_0799 | Bbr_0799 Lysine decarboxylase family 1036008:1036910 forward MW:32456 | 0.7 | 0.6 | 0.7 | 0.5 | 1.7 | 2.2 |
| Bbr_0800 | safC Caffeoyl-CoA O-methyltransferase 1036950:1037615 reverse MW:23604 | 1.0 | 0.9 | 0.9 | 0.9 | 1.0 | 0.4 |
| Bbr_0801 | sdhB Succinate dehydrogenase iron-sulfur protein 1037678:1038628 reverse MW:34230 | 1.1 | 1.2 | 1.0 | 1.1 | 1.6 | 0.4 |
| Bbr_0802 | sdhA Succinate dehydrogenase flavoprotein subunit 1038701:1040563 reverse MW:66957 | 1.2 | 1.2 | 0.3 | 0.5 | 1.6 | 0.5 |
| Bbr_0803 | Bbr_0803 Smf protein 1040665:1042284 reverse MW:58183 | 1.2 | 1.3 | 0.5 | 1.2 | 0.5 | 0.5 |
| Bbr_0804 | Bbr_0804 ATPase related to magnesium chelatase subunit ChlI 1042281:1043816 reverse MW:54858 | 1.2 | 1.1 | 0.9 | 3.3 | 0.4 | 0.7 |
| Bbr_0805 | Bbr_0805 Endonuclease 1043831:1044205 reverse MW:14358 | 1.0 | 1.0 | 1.3 | 2.0 | 1.1 | 0.5 |
| Bbr_0806 | Bbr_0806 Pyridoxine kinase 1045220:1046092 reverse MW:31108 | 0.8 | 0.6 | 0.2 | 0.3 | 0.6 | 0.2 |
| Bbr_0807 | metY O-acetylhomoserine aminocarboxypropyltransferase 1046706:1048022 forward MW:47551 | 1.2 | 1.2 | 0.5 | 0.7 | 1.1 | 0.5 |
| Bbr_0808 | Bbr_0808 ATP-binding protein of ABC transporter system 1048480:1049406 forward MW:33304 | 1.2 | 1.4 | 0.4 | 0.8 | 0.7 | 0.6 |
| Bbr_0809 | Bbr_0809 Permease protein of ABC transporter system 1049438:1052176 forward MW:94844 | 1.3 | 1.7 | 0.5 | 0.5 | 1.2 | 0.6 |
| Bbr_0810 | Bbr_0810 Two-component response regulator 1052465:1053271 reverse MW:28433 | 1.1 | 0.8 | 0.3 | 0.2 | 0.8 | 0.3 |
| Bbr_0811 | Bbr_0811 Two component system histidine kinase 1053293:1055767 reverse MW:89325 | 0.9 | 0.9 | 0.1 | 0.4 | 2.0 | 0.6 |
| Bbr_0812 | pap Proline iminopeptidase 1055843:1057321 forward MW:54686 | 0.9 | 0.7 | 0.2 | 0.3 | 1.2 | 0.5 |
| Bbr_0813 | proC Pyrroline-5-carboxylate reductase 1057468:1058289 forward MW:28713 | 0.8 | 0.8 | 0.5 | 1.4 | 1.4 | 0.7 |
| Bbr_0814 | glnH Glutamine-binding protein glnH 1058432:1059283 reverse MW:30364 | 1.1 | 1.2 | 1.1 | 0.6 | 2.1 | 1.4 |
| Bbr_0815 | glnQ Glutamine transport ATP-binding protein glnQ 1059353:1060117 reverse MW:28733 | 1.3 | 1.9 | 1.6 | 0.4 | 3.6 | 3.5 |
| Bbr_0816 | glnP1 Glutamine transport system permease protein glnP 1060134:1060841 reverse MW:25577 | 1.3 | 1.9 | 2.3 | 0.7 | 3.4 | 3.2 |
| Bbr_0817 | glnP2 Glutamine transport system permease protein glnP 1060819:1061481 reverse MW:24197 | 1.2 | 1.8 | 2.4 | 1.9 | 2.6 | 4.7 |
| Bbr_0818 | Bbr_0818 GTP-binding protein, probable translation factor 1061923:1063023 forward MW:39777 | 1.4 | 1.5 | 0.4 | 0.3 | 1.8 | 0.3 |
| Bbr_0819 | Bbr_0819 Transcriptional regulator, AraC family 1063204:1064064 reverse MW:32559 | 0.9 | 1.3 | 3.2 | 1.9 | 1.8 | 8.9 |
| Bbr_0820 | Bbr_0820 Conserved hypothetical protein 1064120:1064350 reverse MW:8480 | 1.0 | 1.2 | 6.1 | 3.9 | 2.5 | 9.9 |
| Bbr_0821 | Bbr_0821 Na+ driven multidrug efflux pump 1064738:1066120 forward MW:48440 | 1.4 | 1.9 | 2.9 | 1.8 | 1.4 | 5.0 |
| Bbr_0822 | drrC Daunorubicin resistance DNA-binding protein drrC 1066125:1068368 forward MW:82093 | 0.9 | 1.0 | 3.2 | 3.0 | 1.3 | 1.7 |
| Bbr_0823 | Bbr_0823 Hypothetical protein 1068931:1069221 reverse MW:10568 | 1.2 | 1.3 | 1.8 | 0.8 | 1.4 | 5.3 |
| Bbr_0824 | Bbr_0824 Fic family protein 1069232:1070497 reverse MW:47303 | 1.4 | 1.3 | 3.4 | 1.3 | 3.5 | 5.9 |
| Bbr_0825 | Bbr_0825 Narrowly conserved hypothetical protein 1070941:1071381 reverse MW:16542 | 0.9 | 1.0 | 2.3 | 1.0 | 1.1 | 2.5 |
| Bbr_0826 | Bbr_0826 Conserved hypothetical protein 1071642:1072511 forward MW:31932 | 0.8 | 0.6 | 1.1 | 1.7 | 8.2 | 0.8 |
| Bbr_0827 | Bbr_0827 Conserved hypothetical protein 1072605:1073219 forward MW:21863 | 0.8 | 0.9 | 1.4 | 1.1 | 4.4 | 0.4 |
| Bbr_0828 | Bbr_0828 PEMK-like protein 1073436:1073759 reverse MW:11859 | 1.1 | 1.3 | 3.8 | 2.8 | 2.8 | 5.7 |
| Bbr_0829 | Bbr_0829 Hypothetical protein 1073746:1073991 reverse MW:9339 | 1.0 | 1.2 | 4.8 | 5.1 | 3.2 | 5.8 |
| Bbr_0830 | Bbr_0830 Conserved hypothetical protein 1074163:1075419 forward MW:46846 | 0.9 | 1.0 | 2.6 | 2.9 | 4.3 | 3.8 |
| Bbr_0831 | Bbr_0831 Hypothetical protein 1075495:1075863 forward MW:13812 | 1.1 | 1.6 | 10.8 | 4.5 | 3.1 | 9.8 |
| Bbr_0832 | Bbr_0832 Macrolide-efflux protein 1076047:1077318 reverse MW:44136 | 0.9 | 0.8 | 0.8 | 0.7 | 2.0 | 3.5 |
| Bbr_0836 | Bbr_0836 Narrowly conserved hypothetical protein 1081006:1081533 reverse MW:19713 | 0.9 | 0.8 | 1.3 | 1.0 | 0.5 | 0.8 |
| Bbr_0837 | Bbr_0837 Narrowly conserved hypothetical protein 1081745:1082044 reverse MW:11027 | 1.1 | 2.0 | 2.8 | 4.5 | 1.1 | 3.1 |
| Bbr_0838 | Bbr_0838 Multidrug resistance protein B 1082072:1084123 forward MW:71358 | 1.2 | 2.0 | 1.4 | 1.4 | 1.1 | 3.6 |
| Bbr_0839 | Bbr_0839 Serine/threonine protein kinase 1084252:1085910 reverse MW:59000 | 1.0 | 0.8 | 0.3 | 0.9 | 1.0 | 0.4 |
| Bbr_0840 | Bbr_0840 Conserved hypothetical protein 1085960:1086400 reverse MW:16740 | 1.1 | 1.0 | 1.7 | 2.5 | 1.0 | 1.0 |
| Bbr_0841 | Bbr_0841 Narrowly conserved hypothetical membrane spanning protein 1086835:1088382 forward MW:54639 | 1.5 | 1.3 | 1.5 | 1.7 | 0.8 | 1.8 |
| Bbr_0842 | Bbr_0842 Conserved hypothetical membrane spanning protein 1088755:1089918 forward MW:41680 | 1.3 | 1.1 | 0.9 | 1.1 | 0.9 | 0.5 |
| Bbr_0843 | Bbr_0843 Conserved hypothetical secreted protein with excalibur domain 1090093:1090806 forward MW:25334 | 0.8 | 0.5 | 1.6 | 2.4 | 2.6 | 0.2 |
| Bbr_0844 | Bbr_0844 Predicted hypothetical protein 1090828:1091382 reverse MW:19838 | 0.9 | 0.9 | 2.8 | 2.1 | 1.9 | 0.7 |
| Bbr_0845 | glgP2 Glycogen phosphorylase 1092031:1093464 forward MW:53445 | 0.8 | 0.7 | 1.1 | 0.7 | 0.8 | 1.9 |
| Bbr_0846 | nagA1 N-acetylglucosamine-6-phosphate deacetylase 1093779:1095023 reverse MW:44068 | 0.9 | 1.3 | 6.3 | 4.1 | 3.1 | 1.1 |
| Bbr_0847 | nagB2 Glucosamine-6-phosphate isomerase 1095117:1095929 reverse MW:28349 | 0.9 | 1.2 | 4.5 | 5.0 | 2.3 | 1.3 |
| Bbr_0848 | Bbr_0848 Sugar kinase, ROK family 1096015:1096989 reverse MW:32552 | 1.0 | 1.6 | 4.2 | 6.4 | 3.2 | 2.0 |
| Bbr_0849 | Bbr_0849 NagC/XylR-type transciptional regulator 1097045:1098229 reverse MW:42346 | 1.1 | 1.9 | 15.8 | 27.7 | 4.6 | 4.0 |
| Bbr_0850 | Bbr_0850 Aldose 1-epimerase family protein 1098548:1099387 forward MW:29735 | 1.1 | 2.0 | 7.7 | 13.5 | 1.8 | 2.6 |
| Bbr_0851 | Bbr_0851 Glucose/fructose transport protein 1099640:1101067 forward MW:50693 | 0.8 | 0.7 | 5.0 | 1.2 | 0.9 | 0.8 |
| Bbr_0852 | Bbr_0852 Sulfatase family protein 1101157:1102683 forward MW:57933 | 0.9 | 0.9 | 5.1 | 1.0 | 1.0 | 0.9 |
| Bbr_0853 | atsB Arylsulfatase regulator (Fe-S oxidoreductase) 1102770:1104149 forward MW:51860 | 1.0 | 1.1 | 5.9 | 0.7 | 1.5 | 0.7 |
| Bbr_0854 | Bbr_0854 Conserved hypothetical membrane spanning protein with DUF81 domain 1104198:1104998 forward MW:26847 | 0.9 | 1.0 | 5.2 | 1.6 | 1.3 | 1.0 |
| Bbr_0855 | Bbr_0855 Hypothetical protein 1105111:1105461 forward MW:13350 | 0.8 | 1.0 | 2.9 | 2.2 | 1.7 | 1.2 |
| Bbr_0856 | Bbr_0856 Conserved hypothetical membrane spanning protein 1105531:1106049 forward MW:18262 | 0.9 | 1.3 | 3.3 | 1.8 | 2.3 | 2.9 |
| Bbr_0857 | Bbr_0857 Glyoxalase family protein 1106189:1106551 reverse MW:12579 | 1.1 | 0.9 | 1.2 | 0.9 | 1.6 | 0.7 |
| Bbr_0858 | Bbr_0858 Hypothetical protein 1106766:1106942 forward MW:6363 | 1.2 | 1.9 | 2.2 | 3.1 | 1.7 | 4.0 |
| Bbr_0859 | Bbr_0859 Macrolide-efflux protein 1107012:1108382 forward MW:48121 | 1.0 | 1.1 | 2.3 | 2.7 | 1.8 | 1.3 |
| Bbr_0860 | Bbr_0860 Narrowly conserved hypothetical protein 1108502:1109083 forward MW:22664 | 0.9 | 1.0 | 3.3 | 4.3 | 2.0 | 1.3 |
| Bbr_0861 | Bbr_0861 Conserved hypothetical protein in phosphoglycerate mutase family 1109134:1109964 forward MW:32135 | 1.0 | 1.1 | 3.9 | 2.2 | 1.7 | 1.2 |
| Bbr_0862 | pyrP Uracil permease 1110072:1111361 forward MW:44995 | 0.9 | 0.7 | 0.8 | 0.7 | 1.3 | 0.7 |
| Bbr_0863 | Bbr_0863 ATP-dependent RNA helicase 1111735:1113762 forward MW:76116 | 0.7 | 1.1 | 5.9 | 9.1 | 1.4 | 1.5 |
| Bbr_0864 | Bbr_0864 Cyclomaltodextrinase 1113802:1115097 reverse MW:48077 | 1.3 | 1.2 | 0.8 | 0.7 | 0.8 | 0.5 |
| Bbr_0865 | Bbr_0865 Low-affinity inorganic phosphate transporter 1115336:1116400 forward MW:37288 | 0.8 | 0.5 | 0.8 | 1.0 | 0.9 | 0.7 |
| Bbr_0866 | Bbr_0866 Conserved hypothetical protein with DUF47 domain 1116418:1117041 forward MW:24054 | 0.7 | 0.5 | 0.5 | 1.0 | 1.1 | 1.0 |
| Bbr_0867 | Bbr_0867 Response regulatorof two-component system 1117068:1117721 reverse MW:23160 | 0.9 | 0.6 | 0.3 | 0.4 | 0.8 | 0.4 |
| Bbr_0868 | Bbr_0868 Histidine kinase sensor of two-component system 1117718:1119064 reverse MW:48492 | 0.8 | 0.7 | 0.6 | 0.9 | 1.1 | 0.4 |
| Bbr_0869 | pacL1 Calcium-transporting ATPase 1119112:1120062 forward MW:35229 | 0.8 | 1.5 | 0.7 | 1.1 | 0.5 | 10.7 |
| Bbr_0870 | Bbr_0870 ATP-binding protein of ABC transporter system 1120213:1121196 forward MW:36120 | 1.0 | 0.4 | 0.4 | 0.5 | 0.7 | 0.3 |

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|---|---|---|---|---|---|---|---|
| Bbr_0871 | Bbr_0871 Narrowly conserved hypothetical membrane spanning protein 1121313:1122551 forward MW:44541 | 0.8 | 0.4 | 0.7 | 1.5 | 1.8 | 0.5 |
| Bbr_0872 | Bbr_0872 Narrowly conserved hypothetical membrane spanning protein 1122538:1123977 forward MW:49623 | 0.7 | 0.2 | 0.2 | 0.3 | 1.0 | 0.6 |
| Bbr_0873 | Bbr_0873 DNA-binding protein 1123982:1125460 reverse MW:54129 | 0.8 | 0.5 | 0.5 | 0.5 | 2.2 | 1.1 |
| Bbr_0874 | Bbr_0874 Hypothetical protein 1125636:1126241 forward MW:22052 | 1.0 | 1.7 | 3.6 | 5.7 | 2.2 | 5.3 |
| Bbr_0875 | Bbr_0875 Hypothetical membrane spanning protein 1126276:1127496 forward MW:42530 | 1.0 | 1.3 | 3.4 | 5.1 | 2.4 | 1.2 |
| Bbr_0876 | Bbr_0876 Peptidase E 1127690:1128313 reverse MW:22723 | 1.2 | 1.8 | 4.9 | 4.3 | 4.1 | 0.8 |
| Bbr_0877 | pncA Pyrazinamidase/Nicotinamidase 1128405:1129019 reverse MW:21920 | 1.0 | 1.0 | 1.0 | 1.0 | 2.0 | 1.0 |
| Bbr_0878 | Bbr_0878 Conserved hypothetical secreted protein 1129129:1130061 reverse MW:33445 | 1.3 | 1.6 | 1.9 | 1.5 | 1.3 | 1.6 |
| Bbr_0879 | Bbr_0879 Hydrolase, alpha/beta fold family 1130588:1131409 forward MW:30223 | 1.1 | 1.3 | 2.2 | 3.5 | 1.6 | 0.8 |
| Bbr_0880 | Bbr_0880 Conserved hypothetical protein 1131550:1131810 forward MW:9442 | 1.3 | 1.6 | 9.3 | 11.3 | 2.0 | 1.5 |
| Bbr_0881 | Bbr_0881 Transcriptional regulator 1131817:1132026 forward MW:7586 | 1.3 | 1.6 | 7.1 | 8.0 | 1.5 | 1.8 |
| Bbr_0882 | pbuX Xanthine permease 1132156:1133520 reverse MW:47265 | 0.7 | 0.4 | 0.3 | 0.3 | 0.9 | 0.5 |
| Bbr_0883 | xpt Xanthine phosphoribosyltransferase 1133668:1134249 reverse MW:20740 | 0.7 | 0.5 | 0.5 | 0.4 | 2.0 | 0.2 |
| Bbr_0884 | pcrA ATP-dependent DNA helicase pcrA 1134494:1137169 forward MW:97456 | 1.8 | 2.1 | 0.4 | 0.3 | 0.8 | 0.6 |
| Bbr_0885 | Bbr_0885 Narrowly conserved hypothetical membrane spanning protein 1137290:1137685 forward MW:13658 | 1.5 | 1.6 | 0.8 | 0.7 | 0.6 | 1.2 |
| Bbr_0886 | Bbr_0886 Permease protein of ABC transporter system 1137782:1138999 forward MW:43393 | 1.5 | 1.5 | 0.5 | 0.3 | 0.6 | 1.4 |
| Bbr_0887 | Bbr_0887 ATP-binding protein of ABC transporter system 1139001:1139912 forward MW:32577 | 1.5 | 1.8 | 2.1 | 2.3 | 1.0 | 1.4 |
| Bbr_0888 | rpsD SSU ribosomal protein S4P 1140109:1140735 forward MW:23659 | 0.9 | 0.7 | 1.7 | 1.2 | 1.3 | 0.9 |
| Bbr_0889 | Bbr_0889 Glutamine amidotransferase, class I 1141072:1141854 reverse MW:28450 | 1.1 | 1.3 | 3.8 | 4.3 | 1.9 | 1.8 |
| Bbr_0890 | Bbr_0890 Conserved hypothetical protein 1141997:1142482 reverse MW:17952 | 1.1 | 1.3 | 4.0 | 1.9 | 1.5 | 2.2 |
| Bbr_0891 | Bbr_0891 Hypothetical membrane spanning protein 1142573:1142929 forward MW:12654 | 1.1 | 1.4 | 1.2 | 1.2 | 1.3 | 1.5 |
| Bbr_0892 | Bbr_0892 Conserved hypothetical protein 1143034:1143636 forward MW:22788 | 1.1 | 1.1 | 1.6 | 1.3 | 1.3 | 1.2 |
| Bbr_0893 | Bbr_0893 Hypothetical protein 1143813:1144169 reverse MW:13316 | 0.9 | 1.2 | 2.6 | 4.6 | 1.9 | 2.7 |
| Bbr_0894 | Bbr_0894 Hypothetical protein 1144156:1144449 reverse MW:10866 | 0.9 | 1.2 | 4.2 | 6.2 | 2.7 | 2.7 |
| Bbr_0895 | Bbr_0895 Phosphoglycerate mutase family protein 1144864:1145538 forward MW:24580 | 1.0 | 1.0 | 0.5 | 0.4 | 1.7 | 1.1 |
| Bbr_0896 | Bbr_0896 Conserved hypothetical protein 1145621:1146025 forward MW:13947 | 1.1 | 0.9 | 0.9 | 0.7 | 1.0 | 0.8 |
| Bbr_0897 | Bbr_0897 Narrowly conserved hypothetical secreted protein 1146025:1146261 forward MW:8756 | 1.0 | 0.9 | 0.6 | 0.6 | 0.9 | 0.9 |
| Bbr_0898 | alaS Alanyl-tRNA synthetase 1146357:1149035 forward MW:97339 | 1.2 | 1.3 | 0.3 | 0.4 | 2.1 | 0.8 |
| Bbr_0899 | Bbr_0899 Endonuclease involved in recombination 1149032:1149496 forward MW:17075 | 1.1 | 1.1 | 0.3 | 0.4 | 1.3 | 0.8 |
| Bbr_0900 | Bbr_0900 Conserved hypothetical protein with aminodeoxychorismate lyase domain 1149509:1150696 forward MW:42372 | 0.9 | 0.7 | 0.3 | 0.8 | 0.9 | 0.8 |
| Bbr_0901 | Bbr_0901 Conserved hypothetical membrane spanning protein 1150796:1151209 reverse MW:14595 | 0.8 | 0.9 | 0.8 | 1.7 | 1.5 | 0.5 |
| Bbr_0902 | aroC Chorismate synthase 1151318:1152505 forward MW:42289 | 1.0 | 1.1 | 1.3 | 0.9 | 2.5 | 0.9 |
| Bbr_0903 | aroB Shikimate kinase/3-dehydroquinate synthase 1152540:1154162 forward MW:58715 | 1.1 | 0.9 | 0.4 | 0.3 | 1.8 | 0.8 |
| Bbr_0904 | aroQ 3-dehydroquinate dehydratase 1154314:1154760 forward MW:16510 | 1.1 | 0.9 | 0.4 | 0.5 | 1.3 | 0.8 |
| Bbr_0905 | pyrG CTP synthase 1154880:1156544 forward MW:61204 | 1.0 | 0.9 | 0.3 | 0.4 | 1.0 | 1.0 |
| Bbr_0906 | Bbr_0906 Narrowly conserved hypothetical protein with ErfK/YbiS/YcfS/YnhG domain 1156705:1158333 forward MW:57762 | 1.0 | 1.3 | 0.7 | 0.4 | 1.8 | 0.7 |
| Bbr_0907 | Bbr_0907 ABC transporter-associated protein 1158512:1160011 forward MW:55565 | 1.1 | 1.2 | 1.3 | 0.8 | 3.2 | 0.5 |
| Bbr_0908 | Bbr_0908 ATP-binding protein of ABC transporter system 1160017:1161252 forward MW:44600 | 1.0 | 1.3 | 0.3 | 0.2 | 2.2 | 0.6 |
| Bbr_0909 | Bbr_0909 ATP-binding protein of ABC transporter system 1161279:1162058 forward MW:28219 | 1.0 | 1.1 | 0.3 | 0.2 | 2.2 | 0.7 |
| Bbr_0910 | iscS/sufS Cysteine desulfurase/Selenocysteine lyase 1162227:1163501 forward MW:45559 | 1.0 | 1.4 | 0.4 | 0.7 | 3.1 | 0.8 |
| Bbr_0911 | iscU IscU protein 1163513:1164067 forward MW:19978 | 1.1 | 1.2 | 1.4 | 1.4 | 1.6 | 0.6 |
| Bbr_0912 | Bbr_0912 Conserved hypothetical protein with DUF59 domain 1164075:1164659 forward MW:21296 | 1.1 | 1.2 | 1.4 | 1.1 | 1.6 | 0.6 |
| Bbr_0913 | glgC Glucose-1-phosphate adenylyltransferase 1164783:1166027 reverse MW:45756 | 0.7 | 0.4 | 0.3 | 0.1 | 0.8 | 0.5 |
| Bbr_0914 | Bbr_0914 SpoU rRNA methylase family protein 1166233:1167111 reverse MW:32397 | 1.0 | 1.6 | 2.5 | 1.5 | 1.0 | 11.8 |
| Bbr_0915 | Bbr_0915 Conserved hypothetical protein with DUF558 domain 1167354:1168151 forward MW:28430 | 0.9 | 0.9 | 0.7 | 0.8 | 2.4 | 2.6 |
| Bbr_0916 | Bbr_0916 HIT family protein 1168262:1168600 forward MW:12219 | 1.0 | 1.1 | 1.7 | 0.5 | 2.1 | 0.7 |
| Bbr_0917 | phoH PhoH protein 1168619:1169803 forward MW:43242 | 1.1 | 1.6 | 1.2 | 0.5 | 1.9 | 1.2 |
| Bbr_0918 | Bbr_0918 Conserved hypothetical protein in uncharacterized protein family UPF0054 1169793:1170344 forward MW:20307 | 1.1 | 1.7 | 0.4 | 0.3 | 2.1 | 0.8 |
| Bbr_0919 | Bbr_0919 Conserved hypothetical membrane spanning protein with CBS and transporter associated domains 1170369:1171802 forward MW:5216 | 1.1 | 1.6 | 0.2 | 0.2 | 1.5 | 0.6 |
| Bbr_0920 | era GTP-binding protein era 1171804:1172811 forward MW:36996 | 1.0 | 1.4 | 0.3 | 0.4 | 2.2 | 0.5 |
| Bbr_0921 | fadD2 Long-chain-fatty-acid--CoA ligase 1172885:1174942 reverse MW:75063 | 0.9 | 0.6 | 0.5 | 0.2 | 1.1 | 0.6 |
| Bbr_0922 | pntA1 NAD(P) transhydrogenase subunit alpha part 1 1175311:1176474 forward MW:39742 | 0.7 | 0.4 | 0.3 | 0.4 | 1.0 | 0.5 |
| Bbr_0923 | pntA NAD(P) transhydrogenase alpha subunit 1176490:1176795 forward MW:10626 | 0.7 | 0.4 | 0.2 | 0.5 | 1.3 | 0.9 |
| Bbr_0924 | pntB NAD(P) transhydrogenase subunit beta 1176795:1178219 forward MW:49069 | 0.8 | 0.5 | 0.3 | 0.4 | 1.0 | 0.9 |
| Bbr_0925 | Bbr_0925 Permease MFS superfamily 1178323:1179606 reverse MW:45737 | 1.1 | 1.0 | 0.8 | 1.6 | 4.2 | 0.5 |
| Bbr_0926 | rplY LSU ribosomal protein L25P 1180004:1180633 forward MW:22307 | 1.2 | 1.2 | 2.4 | 2.2 | 0.5 | 0.9 |
| Bbr_0927 | ilvE Branched-chain amino acid aminotransferase 1180857:1181984 forward MW:41488 | 1.2 | 1.1 | 2.2 | 1.0 | 0.9 | 1.1 |
| Bbr_0928 | Bbr_0928 Conserved hypothetical protein similar to MazG 1182183:1183064 forward MW:32100 | 1.3 | 1.5 | 2.7 | 2.3 | 1.6 | 1.3 |
| Bbr_0929 | Bbr_0929 Conserved hypothetical membrane spanning protein in uncharacterised protein family UPF0126 1183362:1184132 forward MW:27568 | 1.1 | 1.2 | 1.4 | 0.5 | 1.9 | 0.5 |
| Bbr_0930 | rpsT SSU ribosomal protein S20P 1184383:1184643 reverse MW:8898 | 0.9 | 1.0 | 1.9 | 2.5 | 1.4 | 0.5 |
| Bbr_0931 | lepA GTP-binding protein lepA 1184790:1186670 forward MW:69289 | 1.2 | 1.5 | 0.8 | 0.3 | 2.7 | 0.6 |
| Bbr_0932 | hemN Coproporphyrinogen oxidase (NAD) 1186670:1187983 forward MW:47125 | 1.1 | 1.6 | 0.5 | 0.3 | 2.5 | 0.5 |
| Bbr_0933 | Bbr_0933 Hypothetical membrane spanning protein 1188198:1188659 forward MW:17736 | 1.2 | 1.9 | 1.3 | 1.2 | 8.7 | 1.0 |
| Bbr_0934 | Bbr_0934 Transcriptional regulator, LacI family 1188693:1189721 forward MW:37460 | 0.8 | 0.5 | 0.5 | 0.9 | 2.8 | 1.1 |
| Bbr_0935 | Bbr_0935 Hypothetical protein 1189843:1190181 forward MW:12400 | 0.8 | 1.0 | 1.1 | 2.2 | 2.1 | 2.4 |
| Bbr_0936 | gltB Glutamate synthase [NADPH] large chain 1190781:1195352 forward MW:167305 | 1.5 | 1.4 | 0.3 | 0.3 | 1.1 | 0.9 |
| Bbr_0937 | gltD Glutamate synthase [NADPH] small chain 1195354:1196892 forward MW:56365 | 1.6 | 1.3 | 0.3 | 0.4 | 1.6 | 0.8 |
| Bbr_0938 | Bbr_0938 Hypothetical membrane spanning protein 1197651:1197947 reverse MW:11205 | 0.8 | 0.6 | 1.8 | 4.0 | 1.8 | 10.0 |
| Bbr_0939 | Bbr_0939 Solute binding protein of ABC transporter system for peptides 1198201:1199841 forward MW:58798 | 1.0 | 0.6 | 0.2 | 0.3 | 0.9 | 1.8 |
| Bbr_0940 | Bbr_0940 Narrowly conserved hypothetical protein 1199998:1201893 forward MW:71903 | 1.0 | 0.7 | 0.6 | 0.7 | 0.8 | 1.3 |
| Bbr_0941 | Bbr_0941 Narrowly conserved hypothetical membrane spanning protein 1202001:1202465 forward MW:17264 | 0.9 | 0.9 | 2.6 | 4.0 | 2.1 | 0.9 |
| Bbr_0942 | Bbr_0942 Glycosyltransferase 1202594:1203844 forward MW:45419 | 1.0 | 0.6 | 0.7 | 0.5 | 0.9 | 0.6 |
| Bbr_0943 | Bbr_0943 ATP-binding protein of ABC transporter system 1203924:1204886 forward MW:35543 | 0.9 | 0.7 | 0.7 | 0.4 | 1.2 | 0.8 |
| Bbr_0944 | Bbr_0944 Hydrolase (HAD superfamily) 1204982:1205827 forward MW:30541 | 1.2 | 1.1 | 1.0 | 0.9 | 1.2 | 1.2 |
| Bbr_0945 | Bbr_0945 Hypothetical protein 1205925:1206092 forward MW:6439 | 1.0 | 1.1 | 2.4 | 4.7 | 2.4 | 1.5 |

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|---|---|---|---|---|---|---|---|
| Bbr_0946 | Bbr_0946 Narrowly conserved hypothetical protein 1206106:1206429 forward MW:12003 | 1.0 | 1.3 | 3.2 | 3.9 | 2.4 | 1.7 |
| Bbr_0947 | bcp Thioredoxin peroxidase 1206469:1207056 forward MW:21147 | 1.0 | 1.2 | 3.4 | 1.8 | 3.1 | 2.1 |
| Bbr_0948 | Bbr_0948 Narrowly conserved hypothetical protein 1207121:1207945 reverse MW:29941 | 0.9 | 0.5 | 0.4 | 0.3 | 1.5 | 0.1 |
| Bbr_0949 | Bbr_0949 Narrowly conserved hypothetical protein 1208365:1208691 reverse MW:12178 | 1.2 | 2.0 | 3.4 | 5.3 | 0.9 | 6.1 |
| Bbr_0953 | Bbr_0953 Narrowly conserved hypothetical protein 1212030:1212551 reverse MW:18990 | 1.2 | 1.0 | 1.0 | 0.3 | 2.0 | 2.3 |
| Bbr_0954 | Bbr_0954 Conserved hypothetical protein with YfbU domain 1212576:1213310 reverse MW:28916 | 1.1 | 0.9 | 1.4 | 0.3 | 1.8 | 3.0 |
| Bbr_0955 | Bbr_0955 Narrowly conserved hypothetical protein 1213717:1214475 forward MW:29518 | 0.7 | 0.8 | 1.0 | 0.7 | 1.4 | 2.0 |
| Bbr_0956 | Bbr_0956 Narrowly conserved hypothetical protein 1214801:1215118 forward MW:12277 | 0.7 | 0.9 | 0.9 | 2.1 | 1.5 | 2.2 |
| Bbr_0957 | rarD Chloramphenicol-sensitive protein rarD 1215230:1215673 reverse MW:16351 | 1.1 | 1.3 | 3.7 | 5.4 | 1.1 | 3.1 |
| Bbr_0958 | Bbr_0958 Conserved hypothetical protein 1215893:1216528 forward MW:25033 | 0.7 | 0.5 | 1.1 | 1.1 | 2.9 | 1.6 |
| Bbr_0959 | Bbr_0959 Narrowly conserved hypothetical protein 1216695:1217378 forward MW:26454 | 0.6 | 0.3 | 1.9 | 1.2 | 1.0 | 2.1 |
| Bbr_0960 | Bbr_0960 Narrowly conserved hypothetical protein 1217473:1217826 reverse MW:13441 | 0.9 | 1.2 | 3.7 | 2.7 | 0.9 | 0.4 |
| Bbr_0961 | Bbr_0961 Lipase 1217995:1218930 reverse MW:34315 | 1.1 | 0.9 | 1.0 | 0.9 | 0.9 | 0.8 |
| Bbr_0962 | Bbr_0962 ATPase associated with chromosome architecture/replication 1219005:1219514 reverse MW:17889 | 1.1 | 0.8 | 0.3 | 0.5 | 0.7 | 0.7 |
| Bbr_0963 | Bbr_0963 Conserved hypothetical protein 1219535:1220278 reverse MW:27577 | 0.9 | 0.8 | 0.9 | 1.1 | 1.4 | 0.6 |
| Bbr_0964 | tenA Transcriptional activator tenA 1220575:1221312 forward MW:28556 | 1.6 | 2.1 | 5.2 | 1.9 | 1.9 | 0.8 |
| Bbr_0965 | Bbr_0965 Narrowly conserved hypothetical protein 1221325:1221621 forward MW:10672 | 1.4 | 1.9 | 4.1 | 2.2 | 1.1 | 0.8 |
| Bbr_0966 | Bbr_0966 Conserved hypothetical protein with phospholipase/carboxylesterase domain 1222050:1222670 reverse MW:22734 | 1.1 | 0.8 | 1.5 | 0.6 | 2.9 | 0.8 |
| Bbr_0967 | Bbr_0967 tRNA (adenine-N(1)-)-methyltransferase 1222851:1223921 forward MW:39973 | 1.1 | 1.2 | 1.3 | 1.1 | 2.0 | 1.2 |
| Bbr_0968 | Bbr_0968 Phosphohistidine phosphatase sixA 1224010:1224567 forward MW:20287 | 1.0 | 1.0 | 2.0 | 4.0 | 1.5 | 0.8 |
| Bbr_0969 | metE 5-methyltetrahydropteroyltriglutamate-- homocysteine methyltransferase 1224816:1227119 forward MW:85569 | 1.9 | 2.0 | 1.0 | 0.5 | 1.6 | 0.7 |
| Bbr_0970 | metF Methylenetetrahydrofolate reductase 1227265:1228119 forward MW:31390 | 1.7 | 1.8 | 0.6 | 0.4 | 1.5 | 0.6 |
| Bbr_0971 | cbh Choloylglycine hydrolase 1228254:1229207 forward MW:35124 | 0.7 | 0.6 | 0.6 | 0.4 | 3.6 | 0.8 |
| Bbr_0972 | glnE Glutamate-ammonia-ligase adenylyltransferase 1229264:1232446 forward MW:118794 | 1.0 | 1.5 | 0.8 | 0.5 | 2.2 | 1.1 |
| Bbr_0973 | pyrB Aspartate carbamoyltransferase 1232739:1233719 forward MW:35819 | 1.0 | 0.6 | 0.3 | 1.2 | 0.6 | 0.3 |
| Bbr_0974 | pyrI Aspartate carbamoyltransferase 1233719:1234138 forward MW:15550 | 0.9 | 0.5 | 0.2 | 0.2 | 0.4 | 0.3 |
| Bbr_0975 | pyrC Dihydroorotase 1234135:1235649 forward MW:53656 | 0.8 | 0.5 | 0.1 | 0.2 | 0.6 | 0.4 |
| Bbr_0976 | pyrF1 Orotidine 5'-phosphate decarboxylase 1235667:1236620 forward MW:33854 | 0.8 | 0.5 | 0.2 | 0.3 | 0.4 | 0.6 |
| Bbr_0977 | pyrK Dihydroorotate dehydrogenase electron transfer subunit 1236772:1237596 forward MW:30091 | 0.9 | 0.8 | 0.5 | 0.4 | 1.2 | 0.8 |
| Bbr_0978 | pyrD1 Dihydroorotate dehydrogenase, catalytic subunit 1237599:1238570 forward MW:34048 | 1.0 | 0.8 | 0.3 | 0.3 | 1.5 | 0.8 |
| Bbr_0979 | pyrE2 Orotate phosphoribosyltransferase 1238574:1239269 forward MW:24943 | 1.0 | 0.9 | 1.2 | 1.1 | 1.1 | 0.6 |
| Bbr_0980 | Bbr_0980 Conserved hypothetical protein 1239933:1241054 forward MW:41286 | 0.9 | 0.6 | 0.6 | 1.6 | 2.1 | 1.4 |
| Bbr_0981 | Bbr_0981 Transcriptional regulator, LysR family 1241211:1242134 reverse MW:35113 | 1.0 | 1.1 | 0.8 | 0.3 | 1.3 | 0.6 |
| Bbr_0982 | Bbr_0982 Haloacid dehalogenase-like hydrolase (HAD superfamily) 1242175:1242804 reverse MW:23420 | 0.9 | 0.8 | 1.9 | 2.6 | 3.2 | 0.8 |
| Bbr_0983 | Bbr_0983 Sugar kinase 1242996:1244759 reverse MW:60626 | 0.8 | 0.7 | 2.0 | 1.1 | 6.1 | 0.6 |
| Bbr_0984 | Bbr_0984 ATP-binding protein of ABC transporter system 1244931:1246532 forward MW:58672 | 1.3 | 1.4 | 1.5 | 0.6 | 1.6 | 0.6 |
| Bbr_0985 | Bbr_0985 Conserved hypothetical protein with short chain dehydrogenase domain 1246594:1247301 forward MW:25480 | 1.0 | 0.9 | 0.8 | 0.5 | 1.7 | 0.5 |
| Bbr_0986 | Bbr_0986 ATP-binding protein of ABC transporter system 1247367:1248068 reverse MW:25472 | 1.3 | 1.6 | 1.2 | 2.5 | 1.3 | 9.1 |
| Bbr_0988 | Bbr_0988 Aminotransferase 1248944:1250134 reverse MW:43201 | 1.0 | 0.7 | 0.4 | 0.6 | 1.4 | 0.9 |
| Bbr_0989 | uvrA2 Excinuclease ABC subunit A 1250330:1253359 forward MW:111503 | 1.2 | 1.7 | 0.3 | 0.3 | 1.7 | 0.6 |
| Bbr_0990 | uvrC Excinuclease ABC subunit C 1253513:1255930 forward MW:88948 | 1.1 | 1.5 | 0.9 | 2.6 | 3.4 | 0.8 |
| Bbr_0991 | aroE Shikimate 5-dehydrogenase 1256166:1257146 forward MW:35626 | 0.9 | 0.9 | 1.3 | 2.4 | 1.9 | 0.7 |
| Bbr_0992 | Bbr_0992 ATP-binding protein (contains P-loop) 1257146:1258111 forward MW:35335 | 1.0 | 0.8 | 0.4 | 0.2 | 1.3 | 0.6 |
| Bbr_0993 | Bbr_0993 Conserved hypothetical protein 1258268:1259218 forward MW:34404 | 1.5 | 1.7 | 4.6 | 4.3 | 1.6 | 0.8 |
| Bbr_0994 | pgk Phosphoglycerate kinase 1259377:1260582 forward MW:41777 | 1.0 | 0.8 | 0.9 | 0.8 | 1.3 | 0.5 |
| Bbr_0995 | tpi Triosephosphate isomerase 1260733:1261536 forward MW:29200 | 1.1 | 1.1 | 1.8 | 0.8 | 2.6 | 0.6 |
| Bbr_0996 | secG Protein translocase subunit secG 1261600:1261848 forward MW:8696 | 1.0 | 1.1 | 1.3 | 2.1 | 1.0 | 0.5 |
| Bbr_0997 | ldh1 L-lactate dehydrogenase 1261940:1262890 forward MW:33973 | 0.9 | 0.9 | 0.9 | 0.3 | 0.6 | 1.0 |
| Bbr_0998 | Bbr_0998 DNA polymerase III, beta chain 1262887:1263738 forward MW:31663 | 1.0 | 0.9 | 0.6 | 0.2 | 0.6 | 0.8 |
| Bbr_0999 | Bbr_0999 Aminotransferase 1263857:1265392 forward MW:57072 | 1.0 | 1.2 | 2.4 | 0.4 | 0.6 | 1.7 |
| Bbr_1000 | Bbr_1000 Narrowly conserved hypothetical membrane spanning protein 1265893:1267077 reverse MW:41708 | 1.2 | 0.8 | 0.6 | 0.6 | 0.5 | 0.7 |
| Bbr_1001 | Bbr_1001 Branched chain amino acid transport system II carrier protein 1267250:1268587 reverse MW:47322 | 1.0 | 0.9 | 0.6 | 0.3 | 1.1 | 1.2 |
| Bbr_1002 | tal Transaldolase 1268714:1269817 reverse MW:39704 | 0.8 | 0.6 | 0.2 | 0.2 | 0.8 | 0.6 |
| Bbr_1003 | tkt Transketolase 1269891:1271999 reverse MW:75804 | 1.0 | 0.7 | 0.2 | 0.3 | 1.0 | 1.0 |
| Bbr_1004 | hrcA Heat-inducible transcription repressor hrcA 1272260:1273357 forward MW:38624 | 2.0 | 5.2 | 11.2 | 3.5 | 5.7 | 6.9 |
| Bbr_1005 | dnaJ2 Chaperone protein dnaJ 1273412:1274557 forward MW:40659 | 1.4 | 2.4 | 2.0 | 0.2 | 3.8 | 1.5 |
| Bbr_1006 | Bbr_1006 Fructosamine kinase family protein 1274702:1275493 reverse MW:29262 | 1.0 | 0.9 | 2.0 | 1.8 | 1.8 | 2.1 |
| Bbr_1007 | bacA Bacitracin resistance protein (Putative undecaprenol kinase) 1275644:1276528 forward MW:31753 | 1.0 | 0.9 | 0.3 | 0.2 | 0.9 | 0.7 |
| Bbr_1009 | thrS Threonyl-tRNA synthetase 1278335:1280368 forward MW:76935 | 1.1 | 1.0 | 0.2 | 0.2 | 0.9 | 0.6 |
| Bbr_1010 | Bbr_1010 HIT family hydrolase 1280380:1280964 forward MW:21862 | 1.1 | 1.0 | 0.3 | 0.2 | 0.6 | 0.7 |
| Bbr_1011 | Bbr_1011 Conserved hypothetical protein with DUF28 1281104:1281859 forward MW:27092 | 1.1 | 1.4 | 0.6 | 0.5 | 0.9 | 0.6 |
| Bbr_1012 | ruvC Crossover junction endodeoxyribonuclease ruvC 1281865:1282449 forward MW:20895 | 1.0 | 1.4 | 1.2 | 0.6 | 1.4 | 1.0 |
| Bbr_1013 | ruvA Holliday junction DNA helicase ruvA 1282493:1283119 forward MW:21855 | 1.1 | 2.0 | 5.7 | 6.7 | 2.6 | 1.5 |
| Bbr_1014 | ruvB Holliday junction DNA helicase ruvB 1283119:1284183 forward MW:38718 | 1.0 | 1.9 | 2.2 | 0.4 | 2.4 | 1.0 |
| Bbr_1015 | YajC Protein translocase subunit YajC 1284248:1284694 forward MW:16359 | 1.1 | 1.2 | 1.2 | 0.5 | 1.0 | 0.4 |
| Bbr_1016 | apt Adenine phosphoribosyltransferase 1284745:1285326 forward MW:20199 | 1.1 | 1.1 | 0.9 | 0.3 | 0.9 | 0.4 |
| Bbr_1017 | sucC Succinyl-CoA synthetase beta chain 1285411:1286613 forward MW:42753 | 1.1 | 1.3 | 0.6 | 0.3 | 0.8 | 0.5 |
| Bbr_1018 | sucD Succinyl-CoA synthetase alpha chain 1286613:1287524 forward MW:30877 | 1.1 | 1.3 | 0.3 | 0.2 | 0.8 | 0.5 |
| Bbr_1019 | Bbr_1019 Narrowly conserved hypothetical membrane spanning protein 1287544:1288929 forward MW:49627 | 1.0 | 0.9 | 0.4 | 0.6 | 1.0 | 0.6 |
| Bbr_1020 | purH Phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase 1288877:1290514 forward MW:58421 | 1.0 | 0.8 | 0.8 | 0.9 | 1.7 | 0.7 |
| Bbr_1021 | Bbr_1021 Major intrinsic protein 1290870:1291808 reverse MW:32325 | 0.9 | 1.0 | 0.5 | 0.6 | 0.9 | 0.6 |
| Bbr_1022 | rluB Ribosomal large subunit pseudouridine synthase B 1291997:1292767 forward MW:28845 | 1.3 | 1.9 | 6.3 | 10.2 | 3.1 | 2.4 |
| Bbr_1023 | Bbr_1023 GTP-binding protein 1292764:1294890 forward MW:77627 | 1.3 | 2.2 | 2.0 | 0.5 | 4.6 | 1.0 |
| Bbr_1024 | Bbr_1024 Hydrolase (HAD superfamily) 1295153:1295992 forward MW:31377 | 1.2 | 1.5 | 5.2 | 2.4 | 0.9 | 4.9 |
| Bbr_1025 | ugpA UTP--glucose-1-phosphate uridylyltransferase 1296090:1297592 forward MW:56511 | 1.0 | 0.5 | 0.2 | 0.3 | 0.7 | 0.3 |

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|---|---|---|---|---|---|---|---|
| Bbr_1026 | Bbr_1026 Conserved hypothetical protein 1297733:1299646 forward MW:70296 | 0.9 | 0.8 | 1.1 | 0.3 | 1.2 | 0.9 |
| Bbr_1027 | Bbr_1027 Narrowly conserved hypothetical secreted protein 1299659:1299976 forward MW:12038 | 0.8 | 0.8 | 0.6 | 0.2 | 1.2 | 0.7 |
| Bbr_1028 | helY Helicase helY 1299997:1302585 forward MW:96592 | 1.0 | 1.1 | 0.3 | 0.5 | 1.1 | 0.9 |
| Bbr_1029 | Bbr_1029 Conserved hypothetical protein 1302699:1303046 forward MW:13245 | 1.5 | 2.3 | 13.9 | 87.7 | 3.6 | 0.5 |
| Bbr_1030 | Bbr_1030 Hydrolase or phosphatase 1303155:1303874 forward MW:26841 | 1.7 | 2.1 | 16.8 | 47.0 | 2.9 | 0.5 |
| Bbr_1031 | Bbr_1031 Narrowly conserved hypothetical membrane spanning protein 1303898:1304122 forward MW:8536 | 1.6 | 2.2 | 17.6 | 20.1 | 3.1 | 0.5 |
| Bbr_1032 | Bbr_1032 Predicted hypothetical protein 1304173:1304580 reverse MW:15083 | 1.3 | 1.8 | 2.7 | 2.8 | 1.6 | 17.8 |
| Bbr_1033 | Bbr_1033 Transcriptional regulator 1304697:1305329 reverse MW:23470 | 1.1 | 1.3 | 1.6 | 1.2 | 1.5 | 6.0 |
| Bbr_1034 | garA Signal transduction protein gara 1305408:1305851 reverse MW:15981 | 1.1 | 1.1 | 0.7 | 0.5 | 1.3 | 1.2 |
| Bbr_1035 | Bbr_1035 Conserved hypothetical protein with DUF881 domain 1305858:1306679 reverse MW:30135 | 1.1 | 1.1 | 0.5 | 0.3 | 0.8 | 0.7 |
| Bbr_1036 | Bbr_1036 Small basic protein 1306681:1307013 reverse MW:11789 | 1.1 | 1.2 | 0.7 | 1.2 | 1.2 | 0.5 |
| Bbr_1037 | Bbr_1037 Conserved hypothetical protein with DUF881 domain 1307013:1307990 reverse MW:35546 | 1.2 | 1.4 | 0.2 | 0.2 | 1.0 | 0.9 |
| Bbr_1038 | pgsA1 CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase 1307980:1308597 reverse MW:22539 | 1.2 | 1.3 | 0.5 | 0.9 | 1.8 | 0.8 |
| Bbr_1039 | hisG ATP phosphoribosyltransferase 1308620:1309471 reverse MW:30917 | 1.3 | 1.1 | 0.4 | 0.3 | 1.1 | 0.6 |
| Bbr_1040 | hisE Phosphoribosyl-ATP pyrophosphatase 1309597:1309860 reverse MW:9945 | 1.2 | 1.1 | 0.4 | 0.3 | 1.0 | 0.7 |
| Bbr_1041 | rpe1 Ribulose-phosphate 3-epimerase 1309910:1310578 reverse MW:24106 | 1.3 | 1.3 | 0.4 | 0.3 | 1.1 | 0.5 |
| Bbr_1042 | lgt Prolipoprotein diacylglyceryl transferase 1310658:1311608 reverse MW:35621 | 1.4 | 1.3 | 0.7 | 1.0 | 0.8 | 0.7 |
| Bbr_1043 | trpA Tryptophan synthase alpha chain (EC 4.2.1.20) 1311843:1312718 reverse MW:30944 | 1.3 | 1.1 | 0.3 | 0.3 | 1.1 | 0.5 |
| Bbr_1044 | trpBC TrpB/TrpC bifunctional protein, includes tryptophan synthase beta chain and indole-3-glycerol phosphate synthase 1312735:1314822 revers | 1.3 | 1.1 | 0.4 | 0.5 | 1.5 | 0.6 |
| Bbr_1045 | Bbr_1045 Conserved hypothetical protein 1315022:1315714 forward MW:25961 | 0.9 | 0.9 | 1.6 | 2.4 | 1.4 | 1.3 |
| Bbr_1046 | nfo Endonuclease IV 1315844:1316698 reverse MW:30656 | 1.1 | 1.7 | 8.9 | 18.1 | 5.0 | 1.9 |
| Bbr_1047 | aap2 Amino acid permease 1316831:1318231 forward MW:50324 | 1.3 | 1.7 | 2.1 | 2.1 | 1.2 | 1.0 |
| Bbr_1048 | Bbr_1048 Narrowly conserved hypothetical membrane spanning protein, MFS superfamily 1318594:1319202 forward MW:20902 | 1.0 | 1.3 | 1.8 | 3.6 | 1.0 | 5.9 |
| Bbr_1049 | Bbr_1049 VanZ family protein 1319386:1320405 reverse MW:37847 | 1.1 | 0.8 | 1.1 | 1.3 | 1.2 | 1.2 |
| Bbr_1050 | Bbr_1050 Narrowly conserved hypothetical protein 1320730:1320996 reverse MW:10497 | 0.7 | 0.6 | 0.4 | 0.5 | 1.4 | 1.1 |
| Bbr_1051 | Bbr_1051 Abortive infection protein AbiEi 1321053:1321466 reverse MW:15614 | 0.8 | 0.8 | 0.3 | 0.2 | 1.1 | 0.9 |
| Bbr_1052 | Bbr_1052 Conserved hypothetical protein with DUF984 domain 1321716:1322174 reverse MW:16885 | 0.8 | 0.8 | 1.0 | 1.0 | 2.0 | 1.4 |
| Bbr_1053 | Bbr_1053 Acetyltransferase (GNAT) family 1322314:1322868 forward MW:20436 | 1.0 | 1.0 | 0.2 | 0.2 | 1.5 | 0.4 |
| Bbr_1054 | Bbr_1054 Conserved hypothetical protein 1323026:1323208 forward MW:6970 | 0.9 | 1.0 | 0.8 | 0.4 | 4.1 | 0.5 |
| Bbr_1055 | Bbr_1055 Acetyltransferase (GNAT) family 1323249:1323782 reverse MW:19784 | 1.1 | 1.1 | 1.0 | 0.9 | 0.8 | 0.8 |
| Bbr_1056 | Bbr_1056 Narrowly conserved hypothetical membrane spanning protein 1323918:1324247 reverse MW:12148 | 1.0 | 0.9 | 1.2 | 3.8 | 1.9 | 3.0 |
| Bbr_1057 | Bbr_1057 Conserved hypothetical protein with DUF1526 domain 1324657:1325463 reverse MW:31305 | 1.5 | 1.4 | 0.6 | 1.6 | 1.1 | 1.6 |
| Bbr_1058 | Bbr_1058 Narrowly conserved hypothetical protein 1325647:1325952 forward MW:11067 | 0.9 | 1.2 | 33.2 | 110.4 | 1.8 | 43.1 |
| Bbr_1059 | Bbr_1059 Narrowly conserved hypothetical protein 1326044:1326280 forward MW:8527 | 1.0 | 1.1 | 3.9 | 10.1 | 1.1 | 25.7 |
| Bbr_1060 | Bbr_1060 Hypothetical membrane spanning protein 1327393:1328556 reverse MW:42936 | 1.1 | 1.0 | 1.4 | 1.5 | 1.4 | 0.8 |
| Bbr_1061 | Bbr_1061 Two-component response regulator 1328532:1329218 reverse MW:24742 | 1.2 | 1.2 | 1.3 | 2.1 | 0.9 | 0.9 |
| Bbr_1062 | Bbr_1062 Hypothetical secreted protein 1329356:1329868 forward MW:18891 | 1.0 | 0.8 | 1.7 | 3.4 | 1.5 | 1.1 |
| Bbr_1063 | Bbr_1063 Hypothetical secreted protein 1329865:1330755 forward MW:30036 | 0.9 | 0.7 | 1.0 | 2.1 | 1.2 | 0.9 |
| Bbr_1064 | Bbr_1064 ATP-binding protein of ABC transporter system 1330752:1331432 forward MW:24812 | 0.9 | 0.7 | 0.9 | 2.1 | 1.2 | 0.6 |
| Bbr_1065 | Bbr_1065 Conserved hypothetical protein 1331429:1332448 forward MW:36306 | 0.9 | 0.7 | 1.0 | 1.3 | 0.8 | 0.7 |
| Bbr_1066 | Bbr_1066 Conserved hypothetical protein with RelB antitoxin domain 1332782:1333051 forward MW:9860 | 1.0 | 0.9 | 3.9 | 12.4 | 1.7 | 4.4 |
| Bbr_1067 | yafQ DNA damage inducible protein yafQ 1333055:1333348 forward MW:11189 | 1.0 | 0.9 | 3.0 | 3.5 | 1.8 | 4.9 |
| Bbr_1068 | Bbr_1068 RNA polymerase sigma-E factor 1334017:1334568 forward MW:20158 | 1.1 | 0.9 | 1.5 | 5.0 | 3.5 | 2.7 |
| Bbr_1069 | Bbr_1069 Hypothetical membrane spanning protein 1334602:1335429 forward MW:28168 | 0.9 | 0.9 | 1.7 | 2.3 | 2.0 | 2.8 |
| Bbr_1070 | Bbr_1070 Hypothetical membrane spanning protein 1335561:1336187 forward MW:21653 | 0.9 | 1.0 | 2.3 | 4.4 | 2.4 | 1.7 |
| Bbr_1071 | Bbr_1071 Hypothetical membrane spanning protein 1336184:1336966 forward MW:27090 | 1.4 | 1.4 | 1.1 | 2.5 | 3.1 | 1.0 |
| Bbr_1072 | Bbr_1072 ATP-binding protein of ABC transporter system 1337018:1337893 forward MW:32239 | 0.9 | 0.9 | 1.8 | 1.5 | 1.9 | 1.2 |
| Bbr_1073 | Bbr_1073 Hypothetical protein 1337947:1338345 forward MW:13995 | 0.8 | 0.7 | 1.0 | 1.4 | 1.5 | 1.0 |
| Bbr_1074 | Bbr_1074 Hypothetical membrane spanning protein 1338440:1338802 reverse MW:13566 | 0.9 | 0.8 | 2.6 | 3.1 | 2.7 | 1.5 |
| Bbr_1075 | Bbr_1075 Transporter, drug/metabolite exporter family 1338926:1339801 reverse MW:29364 | 0.9 | 1.3 | 4.0 | 3.0 | 3.3 | 1.6 |
| Bbr_1076 | Bbr_1076 Hypothetical membrane spanning protein 1340005:1340628 reverse MW:22544 | 1.1 | 1.3 | 0.5 | 0.3 | 1.4 | 1.1 |
| Bbr_1077 | Bbr_1077 Hypothetical membrane spanning protein 1340625:1341353 reverse MW:25891 | 1.2 | 1.4 | 2.1 | 0.9 | 2.2 | 1.6 |
| Bbr_1078 | Bbr_1078 Lantibiotic transport ATP-binding protein 1341358:1342014 reverse MW:23595 | 1.0 | 1.5 | 4.3 | 4.4 | 3.3 | 2.0 |
| Bbr_1079 | Bbr_1079 Two-component response regulator 1343775:1344443 reverse MW:24664 | 0.9 | 0.7 | 2.3 | 5.7 | 1.1 | 1.8 |
| Bbr_1080 | Bbr_1080 Two component system histidine kinase 1344440:1345669 reverse MW:43920 | 1.0 | 1.3 | 2.5 | 6.8 | 2.9 | 1.4 |
| Bbr_1081 | Bbr_1081 Permease protein of ABC transporter system 1345702:1347126 reverse MW:49594 | 0.7 | 0.7 | 1.2 | 1.5 | 2.2 | 1.7 |
| Bbr_1082 | Bbr_1082 ATP-binding protein of ABC transporter system 1347119:1348021 reverse MW:32209 | 0.8 | 0.8 | 1.7 | 3.9 | 1.9 | 2.1 |
| Bbr_1083 | Bbr_1083 Hypothetical membrane spanning protein 1348216:1348749 reverse MW:19471 | 0.8 | 0.8 | 1.7 | 7.6 | 1.8 | 2.5 |
| Bbr_1084 | Bbr_1084 Conserved hypothetical protein with helix-turn-helix motif 1349081:1349383 forward MW:11668 | 0.8 | 0.6 | 3.7 | 38.3 | 0.9 | 4.5 |
| Bbr_1085 | Bbr_1085 Hypothetical membrane spanning protein 1349386:1349730 forward MW:12652 | 0.8 | 0.5 | 3.6 | 6.2 | 1.0 | 3.9 |
| Bbr_1086 | Bbr_1086 Hypothetical protein 1349829:1350437 forward MW:21832 | 1.0 | 1.0 | 15.7 | 10.8 | 1.9 | 15.5 |
| Bbr_1087 | Bbr_1087 Narrowly conserved hypothetical secreted protein 1350706:1351347 forward MW:22759 | 1.1 | 1.2 | 1.0 | 1.2 | 2.1 | 2.2 |
| Bbr_1088 | Bbr_1088 Conserved hypothetical protein 1351597:1352217 forward MW:23613 | 1.1 | 1.1 | 1.5 | 2.3 | 0.8 | 1.7 |
| Bbr_1090 | aap3 Amino acid permease 1353490:1355070 forward MW:57602 | 1.8 | 1.9 | 1.4 | 1.6 | 1.6 | 0.3 |
| Bbr_1091 | Bbr_1091 Hypothetical protein 1355237:1355620 forward MW:13798 | 1.5 | 2.6 | 0.8 | 0.9 | 2.6 | 4.0 |
| Bbr_1092 | Bbr_1092 Conserved hypothetical protein with DUF488 domain 1355839:1356201 forward MW:13705 | 1.2 | 1.3 | 2.8 | 13.0 | 3.9 | 3.2 |
| Bbr_1093 | Bbr_1093 Narrowly conserved hypothetical protein 1356267:1356695 reverse MW:15800 | 1.0 | 0.7 | 0.8 | 1.1 | 1.2 | 0.3 |
| Bbr_1094 | Bbr_1094 Conserved hypothetical membrane spanning protein 1356893:1357909 forward MW:37607 | 1.1 | 0.9 | 0.8 | 0.5 | 1.0 | 0.7 |
| Bbr_1095 | Bbr_1095 Conserved hypothetical protein 1357893:1358495 reverse MW:21969 | 1.0 | 1.0 | 1.2 | 2.0 | 1.0 | 2.0 |
| Bbr_1096 | trpE Anthranilate synthase component I 1358618:1360174 reverse MW:56645 | 1.1 | 1.0 | 0.8 | 0.9 | 2.6 | 0.6 |
| Bbr_1097 | hisI Phosphoribosyl-AMP cyclohydrolase 1360380:1360775 reverse MW:14611 | 1.2 | 1.1 | 1.0 | 1.1 | 1.7 | 0.7 |
| Bbr_1098 | hisF Imidazole glycerol phosphate synthase, cyclase subunit 1360858:1361628 reverse MW:27481 | 1.3 | 1.2 | 1.4 | 1.7 | 3.1 | 0.8 |
| Bbr_1100 | Bbr_1100 Radical SAM family enzyme 1362346:1363515 reverse MW:42540 | 1.0 | 0.8 | 0.2 | 0.1 | 1.0 | 0.5 |
| Bbr_1101 | cdsA Phosphatidate cytidylyltransferase 1363541:1364527 reverse MW:35419 | 1.0 | 0.8 | 0.4 | 0.2 | 1.0 | 0.4 |
| Bbr_1102 | frr Ribosome Recycling Factor (RRF) 1364552:1365103 reverse MW:20113 | 1.0 | 0.8 | 0.5 | 0.4 | 0.9 | 0.4 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| Bbr_1103 | pyrH Uridylate kinase 1365166:1365906 reverse MW:26585 | 1.1 | 1.0 | 0.6 | 0.5 | 1.0 | 0.5 |
| Bbr_1104 | tsf Protein Translation Elongation Factor Ts (EF-Ts) 1366082:1366933 reverse MW:29892 | 1.0 | 0.9 | 1.0 | 0.9 | 1.5 | 0.9 |
| Bbr_1105 | rpsB SSU ribosomal protein S2P 1367015:1367854 reverse MW:30754 | 0.9 | 1.0 | 1.9 | 2.1 | 1.3 | 0.8 |
| Bbr_1106 | def Peptide deformylase 1368190:1368675 reverse MW:18236 | 1.1 | 1.4 | 0.3 | 0.2 | 1.7 | 0.5 |
| Bbr_1107 | fadD3 Long-chain-fatty-acid--CoA ligase 1368682:1370742 reverse MW:74612 | 1.0 | 1.1 | 0.3 | 0.1 | 1.7 | 0.4 |
| Bbr_1108 | Bbr_1108 Narrowly conserved hypothetical protein 1370818:1371039 reverse MW:8389 | 0.7 | 0.8 | 1.5 | 2.2 | 1.4 | 1.1 |
| Bbr_1109 | guaC GMP reductase 1371452:1372576 reverse MW:39504 | 1.2 | 1.3 | 0.5 | 0.4 | 1.8 | 0.3 |
| Bbr_1110 | icdA Isocitrate dehydrogenase [NADP] 1372705:1373925 forward MW:45446 | 1.1 | 0.7 | 0.2 | 0.4 | 0.8 | 0.4 |
| Bbr_1111 | Bbr_1111 Narrowly conserved hypothetical secreted protein 1374066:1375751 forward MW:58852 | 1.0 | 0.9 | 0.4 | 0.1 | 0.7 | 0.3 |
| Bbr_1112 | Bbr_1112 Peptidoglycan-specific endopeptidase, M23 family 1375764:1376387 reverse MW:22715 | 0.9 | 1.0 | 1.1 | 2.6 | 1.2 | 2.3 |
| Bbr_1113 | Bbr_1113 DNA integration/recombination/inversion protein 1376932:1377315 forward MW:14844 | 0.7 | 0.9 | 0.5 | 1.3 | 0.8 | 1.1 |
| Bbr_1114 | Bbr_1114 Transposase 1377490:1378983 forward MW:54591 | 1.0 | 1.4 | 2.8 | 8.3 | 2.8 | 1.0 |
| Bbr_1115 | Bbr_1115 Transposase 1378980:1379759 forward MW:29564 | 1.1 | 1.5 | 3.4 | 6.1 | 0.5 | 1.6 |
| Bbr_1117 | Bbr_1117 Hypothetical protein 1380659:1381726 forward MW:40214 | 1.0 | 2.3 | 0.8 | 0.7 | 0.8 | 0.5 |
| Bbr_1118 | Bbr_1118 Type II restriction-modification system restriction subunit 1382030:1382977 reverse MW:36630 | 1.0 | 1.0 | 0.5 | 0.6 | 1.3 | 0.7 |
| Bbr_1119 | Bbr_1119 Modification methylase 1382959:1384362 reverse MW:52108 | 1.0 | 1.0 | 0.7 | 0.8 | 1.6 | 0.8 |
| Bbr_1120 | Bbr_1120 Conserved hypothetical protein with Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase motifs 1384500:1386587 reverse MW:79 | 0.8 | 0.5 | 0.1 | 0.3 | 0.9 | 0.5 |
| Bbr_1121 | dcm Cytosine methyl transferase 1386593:1387642 reverse MW:38881 | 1.0 | 0.8 | 0.4 | 0.3 | 1.4 | 0.7 |
| Bbr_1122 | topB DNA topoisomerase III 1387901:1389832 reverse MW:71083 | 0.9 | 1.4 | 1.3 | 1.4 | 1.0 | 7.9 |
| Bbr_1123 | gcp O-sialoglycoprotein endopeptidase 1390463:1391506 reverse MW:36044 | 1.2 | 1.1 | 0.5 | 0.4 | 0.7 | 0.6 |
| Bbr_1124 | rimI Ribosomal-protein-S18-alanine acetyltransferase 1391503:1392102 reverse MW:21945 | 1.2 | 1.2 | 1.0 | 1.0 | 1.7 | 1.0 |
| Bbr_1125 | Bbr_1125 Glycoprotease protein family 1392124:1393005 reverse MW:31354 | 1.3 | 1.5 | 2.1 | 1.8 | 2.0 | 0.9 |
| Bbr_1126 | Bbr_1126 Glycoprotease protein family 1393145:1393579 reverse MW:16417 | 1.2 | 1.0 | 0.6 | 0.7 | 1.8 | 0.8 |
| Bbr_1127 | Bbr_1127 DNA polymerase III, delta subunit 1393637:1394512 reverse MW:31352 | 1.3 | 1.3 | 0.5 | 0.6 | 0.9 | 1.2 |
| Bbr_1128 | Bbr_1128 COME operon protein 3 1394687:1396324 reverse MW:58989 | 1.1 | 1.5 | 5.2 | 11.5 | 1.5 | 5.8 |
| Bbr_1129 | Bbr_1129 COME operon protein 1 1396390:1397157 reverse MW:27191 | 1.2 | 1.6 | 0.4 | 0.5 | 0.7 | 10.4 |
| Bbr_1130 | leuS Leucyl-tRNA synthetase 1397243:1400206 reverse MW:110497 | 1.3 | 1.1 | 0.6 | 0.9 | 1.0 | 1.0 |
| Bbr_1131 | Bbr_1131 Predicted solute binding protein of ABC transporter system 1400249:1401130 reverse MW:31315 | 1.2 | 1.4 | 2.7 | 0.6 | 2.0 | 1.7 |
| Bbr_1132 | corA Magnesium and cobalt transport protein corA 1401143:1402093 reverse MW:36267 | 1.3 | 1.4 | 2.6 | 0.8 | 1.3 | 1.0 |
| Bbr_1133 | Bbr_1133 Phosphoglycerate mutase family protein 1402273:1403118 reverse MW:31317 | 1.0 | 0.9 | 1.4 | 0.6 | 1.9 | 1.1 |
| Bbr_1134 | Bbr_1134 Methyltransferase 1403187:1404458 forward MW:46596 | 1.0 | 0.8 | 0.5 | 0.7 | 2.0 | 0.5 |
| Bbr_1135 | Bbr_1135 Conserved hypothetical protein (Pyridoxamine 5'-phosphate oxidase pdxH (EC 1.4.3.5)) 1404542:1404961 reverse MW:15438 | 0.7 | 0.8 | 1.8 | 1.6 | 3.9 | 0.5 |
| Bbr_1136 | Bbr_1136 Transporter, drug/metabolite exporter family 1405181:1406116 forward MW:33658 | 1.2 | 1.2 | 0.5 | 0.4 | 2.9 | 0.6 |
| Bbr_1137 | Bbr_1137 Conserved hypothetical protein 1406191:1406889 forward MW:24900 | 1.4 | 1.7 | 2.5 | 3.2 | 1.7 | 1.1 |
| Bbr_1138 | Bbr_1138 Hypothetical protein 1407252:1408196 reverse MW:32815 | 0.9 | 1.2 | 1.2 | 4.5 | 1.5 | 1.4 |
| Bbr_1139 | Bbr_1139 Conserved hypothetical protein with DUF1237 domain 1408739:1410037 forward MW:48780 | 0.8 | 0.5 | 0.7 | 0.8 | 0.5 | 0.4 |
| Bbr_1140 | Bbr_1140 N-acylglucosamine 2-epimerase family protein 1410104:1411339 forward MW:45264 | 0.8 | 0.3 | 0.4 | 0.3 | 1.0 | 0.5 |
| Bbr_1141 | Bbr_1141 Transcriptional regulator, LacI family 1411461:1412567 reverse MW:40501 | 0.6 | 0.2 | 0.3 | 0.4 | 1.9 | 0.4 |
| Bbr_1142 | Bbr_1142 Endo-beta-N-acetylglucosaminidase 1412863:1415676 reverse MW:101790 | 1.2 | 0.9 | 0.4 | 0.6 | 0.8 | 0.4 |
| Bbr_1143 | agl5 Alpha-glucosidase 1415724:1418213 reverse MW:93301 | 0.9 | 0.9 | 2.5 | 5.4 | 0.5 | 2.5 |
| Bbr_1144 | Bbr_1144 Conserved hypothetical protein 1418491:1419780 reverse MW:47471 | 0.8 | 1.0 | 3.1 | 4.0 | 2.4 | 0.9 |
| Bbr_1145 | Bbr_1145 Transporter 1419794:1420651 reverse MW:31429 | 0.9 | 0.9 | 1.0 | 1.1 | 1.0 | 1.1 |
| Bbr_1146 | Bbr_1146 Sugar transport system permease protein 1420651:1421589 reverse MW:34503 | 0.9 | 0.7 | 0.7 | 1.0 | 0.7 | 0.8 |
| Bbr_1147 | Bbr_1147 Sugar-binding protein 1421592:1422863 reverse MW:46078 | 0.9 | 0.5 | 0.5 | 0.7 | 0.7 | 0.4 |
| Bbr_1148 | Bbr_1148 Alpha-mannosidase 1423059:1426163 reverse MW:115049 | 1.1 | 1.0 | 1.4 | 6.1 | 1.4 | 1.1 |
| Bbr_1149 | Bbr_1149 Alpha-mannosidase 1426433:1429573 reverse MW:116103 | 0.9 | 1.1 | 1.1 | 2.8 | 1.0 | 0.6 |
| Bbr_1150 | Bbr_1150 Alpha-mannosidase 1429695:1432814 reverse MW:115364 | 1.2 | 1.2 | 1.8 | 1.5 | 0.9 | 0.7 |
| Bbr_1151 | Bbr_1151 Hypothetical protein 1432975:1433388 reverse MW:15268 | 1.0 | 1.1 | 7.8 | 33.6 | 1.0 | 1.7 |
| Bbr_1152 | Bbr_1152 Hypothetical protein 1433823:1434056 reverse MW:8863 | 0.9 | 1.0 | 1.4 | 1.8 | 2.4 | 1.2 |
| Bbr_1153 | Bbr_1153 Fic family protein 1434141:1435058 reverse MW:34399 | 1.0 | 1.0 | 1.7 | 2.2 | 2.9 | 1.4 |
| Bbr_1154 | Bbr_1154 Conserved hypothetical protein 1435119:1436432 reverse MW:49464 | 1.0 | 1.2 | 5.5 | 3.3 | 2.3 | 1.7 |
| Bbr_1155 | Bbr_1155 Hypothetical secreted protein 1436768:1437172 forward MW:14585 | 0.7 | 0.5 | 0.6 | 0.6 | 1.2 | 0.4 |
| Bbr_1156 | Bbr_1156 Peptidyl-prolyl cis-trans isomerase 1437288:1437827 forward MW:19476 | 0.9 | 1.0 | 0.6 | 0.5 | 1.2 | 0.3 |
| Bbr_1157 | relA1 GTP pyrophosphokinase/Guanosine-3',5'-bis(Diphosphate) 3'-pyrophosphohydrolase 1437928:1440270 reverse MW:86826 | 0.9 | 0.7 | 0.1 | 0.1 | 0.7 | 0.3 |
| Bbr_1158 | dut Deoxyuridine 5'-triphosphate nucleotidohydrolase 1440346:1440822 reverse MW:16794 | 1.2 | 0.8 | 0.4 | 0.6 | 0.4 | 0.4 |
| Bbr_1159 | Bbr_1159 Conserved hypothetical protein 1440822:1441115 reverse MW:10654 | 1.3 | 0.9 | 0.5 | 0.8 | 0.5 | 0.3 |
| Bbr_1160 | Bbr_1160 Conserved hypothetical protein 1441267:1442340 forward MW:38130 | 1.2 | 1.4 | 2.3 | 3.1 | 2.0 | 0.5 |
| Bbr_1161 | Bbr_1161 Nucleotide pyrophosphatase 1442446:1443687 reverse MW:44337 | 0.9 | 1.1 | 0.6 | 1.2 | 1.9 | 1.1 |
| Bbr_1162 | gyrA2 DNA gyrase subunit A 1443940:1446660 forward MW:97613 | 1.1 | 1.2 | 0.3 | 0.3 | 2.2 | 0.6 |
| Bbr_1163 | Bbr_1163 Hypothetical protein 1446830:1447213 reverse MW:14199 | 0.9 | 0.7 | 0.6 | 1.5 | 0.6 | 1.2 |
| Bbr_1164 | Bbr_1164 Conserved hypothetical protein 1447480:1448439 reverse MW:35776 | 0.9 | 0.6 | 0.9 | 2.7 | 0.7 | 1.4 |
| Bbr_1167 | lhr ATP-dependent helicase lhr 1451875:1456926 reverse MW:181729 | 1.3 | 1.9 | 0.3 | 1.4 | 1.9 | 0.7 |
| Bbr_1168 | rbsK1 Ribokinase 1457121:1458083 reverse MW:33003 | 0.8 | 0.9 | 1.0 | 1.5 | 1.6 | 1.3 |
| Bbr_1169 | Bbr_1169 Multidrug resistance protein 1458157:1459365 reverse MW:43022 | 0.7 | 0.7 | 1.3 | 4.9 | 0.9 | 1.8 |
| Bbr_1170 | gyrB2 DNA gyrase subunit B 1459532:1461883 reverse MW:85718 | 1.1 | 1.6 | 0.5 | 1.5 | 2.0 | 0.8 |
| Bbr_1171 | Bbr_1171 RNA polymerase principal sigma factor hrdB 1462010:1463503 reverse MW:55569 | 1.1 | 1.7 | 5.8 | 13.8 | 1.7 | 1.3 |
| Bbr_1172 | Bbr_1172 Narrowly conserved hypothetical protein 1463631:1464272 reverse MW:23720 | 1.2 | 1.7 | 0.8 | 0.8 | 0.7 | 1.3 |
| Bbr_1173 | idsA Polyprenyl synthase 1464450:1465559 forward MW:39707 | 1.0 | 1.1 | 1.2 | 1.1 | 1.2 | 2.2 |
| Bbr_1174 | pknA2 Serine/threonine protein kinase 1465674:1467821 forward MW:76683 | 1.1 | 1.1 | 0.2 | 0.1 | 0.8 | 0.4 |
| Bbr_1175 | plsC2 1-acyl-sn-glycerol-3-phosphate acyltransferase 1467862:1468572 reverse MW:25844 | 0.9 | 0.8 | 0.7 | 0.8 | 1.0 | 0.4 |
| Bbr_1176 | Bbr_1176 Narrowly conserved hypothetical membrane spanning protein 1468603:1469322 forward MW:25260 | 1.0 | 1.0 | 1.1 | 1.2 | 1.0 | 0.5 |
| Bbr_1177 | trpD Anthranilate phosphoribosyltransferase 1469416:1470462 reverse MW:36086 | 1.1 | 1.0 | 2.1 | 1.1 | 1.5 | 0.5 |
| Bbr_1178 | secA Protein translocase subunit secA 1470616:1473498 reverse MW:107004 | 1.5 | 2.0 | 1.0 | 0.4 | 1.3 | 0.8 |
| Bbr_1179 | Bbr_1179 Ribosome-associated factor Y 1473661:1474323 reverse MW:24797 | 0.5 | 0.4 | 1.2 | 1.2 | 3.7 | 0.6 |
| Bbr_1180 | recX RecX-like protein 1475046:1475645 reverse MW:22297 | 1.2 | 2.9 | 17.7 | 10.9 | 3.5 | 2.6 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| Bbr_1181 | recA RecA protein 1475648:1476826 reverse MW:41404 | 1.4 | 3.3 | 10.2 | 12.0 | 4.3 | 2.4 |
| Bbr_1182 | Bbr_1182 Conserved hypothetical protein 1477133:1477435 reverse MW:11361 | 1.0 | 1.7 | 9.1 | 66.9 | 3.6 | 1.2 |
| Bbr_1183 | Bbr_1183 Transcriptional regulator 1477473:1477991 reverse MW:19149 | 1.6 | 3.6 | 57.2 | 416.3 | 7.1 | 3.3 |
| Bbr_1184 | cinA Competence-damage protein cinA 1478051:1478608 reverse MW:19399 | 0.8 | 0.7 | 0.5 | 0.5 | 2.3 | 2.4 |
| Bbr_1185 | pgsA2 CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase 1478709:1479368 reverse MW:24534 | 0.9 | 0.8 | 0.5 | 0.3 | 1.4 | 0.6 |
| Bbr_1186 | ftsK Cell division protein ftsK 1479522:1482377 reverse MW:101119 | 1.2 | 1.4 | 0.3 | 0.1 | 2.3 | 0.8 |
| Bbr_1187 | fic Cell filamentation protein fic 1482409:1483338 forward MW:34344 | 1.0 | 0.8 | 0.7 | 1.4 | 1.6 | 0.6 |
| Bbr_1188 | miaA tRNA delta(2)-isopentenylpyrophosphate transferase 1483381:1484364 reverse MW:36530 | 1.1 | 1.2 | 0.7 | 0.4 | 1.3 | 0.9 |
| Bbr_1189 | Bbr_1189 tRNA 2-methylthioadenosine synthase 1484487:1485926 reverse MW:53007 | 1.0 | 1.2 | 0.8 | 0.4 | 2.5 | 0.5 |
| Bbr_1190 | relA2 GTP pyrophosphokinase 1486011:1486811 forward MW:30362 | 1.0 | 1.0 | 1.3 | 1.2 | 0.9 | 0.5 |
| Bbr_1191 | Bbr_1191 Transporter, drug/metabolite exporter family 1486808:1487755 reverse MW:33275 | 1.3 | 1.8 | 4.3 | 0.5 | 1.0 | 1.8 |
| Bbr_1192 | Bbr_1192 Conserved hypothetical membrane spanning protein in uncharacterised protein family UPF0005 1487878:1488699 reverse MW:29575 | 0.8 | 0.8 | 0.7 | 0.7 | 1.7 | 0.7 |
| Bbr_1193 | Bbr_1193 Transcriptional regulatory protein 1488904:1489563 forward MW:23564 | 0.9 | 1.9 | 1.6 | 3.6 | 1.6 | 8.8 |
| Bbr_1194 | Bbr_1194 Narrowly conserved hypothetical protein in acetyl transferase family 1489596:1490264 forward MW:24824 | 0.9 | 1.7 | 4.0 | 2.5 | 2.6 | 0.9 |
| Bbr_1195 | acn Aconitate hydratase 1490383:1493082 reverse MW:97673 | 1.1 | 0.9 | 0.6 | 0.7 | 1.4 | 1.0 |
| Bbr_1196 | ctpE Cation-transporting ATPase 1493201:1495813 reverse MW:93081 | 1.0 | 0.9 | 0.2 | 0.3 | 1.2 | 0.8 |
| Bbr_1197 | Bbr_1197 Narrowly conserved hypothetical secreted protein 1495878:1496462 reverse MW:20407 | 0.7 | 0.7 | 0.2 | 0.4 | 0.6 | 1.4 |
| Bbr_1198 | Bbr_1198 tRNA (Uracil-5-) -methyltransferase 1496474:1497733 reverse MW:45984 | 0.7 | 0.7 | 0.2 | 0.2 | 1.4 | 0.8 |
| Bbr_1199 | Bbr_1199 Conserved hypothetical membrane spanning protein 1497723:1498499 reverse MW:27659 | 0.7 | 0.5 | 0.2 | 0.1 | 0.9 | 0.8 |
| Bbr_1200 | Bbr_1200 Conserved hypothetical protein 1498515:1499360 reverse MW:30602 | 0.8 | 0.6 | 0.3 | 0.4 | 0.7 | 0.3 |
| Bbr_1201 | xth Exodeoxyribonuclease III 1499485:1500345 forward MW:32131 | 1.2 | 1.2 | 1.6 | 1.8 | 1.2 | 0.3 |
| Bbr_1202 | oppD2 Oligopeptide transport ATP-binding protein oppD 1500654:1502663 reverse MW:73124 | 1.1 | 1.2 | 0.4 | 0.7 | 1.5 | 1.1 |
| Bbr_1203 | oppC1 Oligopeptide transport system permease protein oppC 1502686:1503690 reverse MW:35726 | 1.2 | 1.2 | 0.3 | 0.3 | 0.7 | 1.0 |
| Bbr_1204 | oppB2 Oligopeptide transport system permease protein oppB 1503709:1504635 reverse MW:33853 | 1.4 | 1.4 | 0.6 | 0.4 | 0.8 | 0.7 |
| Bbr_1205 | oppA2 Oligopeptide-binding protein oppA 1505025:1506665 reverse MW:59272 | 1.0 | 0.5 | 0.1 | 0.2 | 0.3 | 0.7 |
| Bbr_1206 | Bbr_1206 Integrase/recombinase 1506919:1507938 reverse MW:37633 | 1.1 | 1.2 | 0.3 | 0.2 | 1.8 | 0.8 |
| Bbr_1207 | Bbr_1207 ATP-binding protein of ABC transporter system 1508110:1508922 forward MW:29467 | 1.1 | 1.5 | 1.4 | 0.7 | 2.9 | 2.4 |
| Bbr_1208 | Bbr_1208 Permease protein of ABC transporter system 1508919:1511777 forward MW:99607 | 1.0 | 1.1 | 0.2 | 0.3 | 2.4 | 0.5 |
| Bbr_1209 | Bbr_1209 Narrowly conserved hypothetical protein 1512030:1512287 reverse MW:9507 | 0.7 | 0.5 | 1.3 | 1.6 | 1.9 | 1.1 |
| Bbr_1210 | tyrA2 Prephenate dehydrogenase 1512373:1513389 reverse MW:36753 | 0.9 | 0.7 | 0.4 | 0.7 | 1.6 | 1.3 |
| Bbr_1211 | pheA Prephenate dehydratase 1513383:1514363 reverse MW:35636 | 1.0 | 1.0 | 0.7 | 0.2 | 0.9 | 1.9 |
| Bbr_1212 | Bbr_1212 Narrowly conserved hypothetical membrane spanning protein 1514422:1514838 reverse MW:15050 | 1.0 | 1.7 | 4.9 | 1.0 | 1.5 | 2.4 |
| Bbr_1213 | Bbr_1213 GTP-binding protein TypA/BipA 1514995:1516926 reverse MW:70233 | 1.2 | 1.6 | 3.3 | 1.0 | 1.4 | 1.3 |
| Bbr_1214 | Bbr_1214 Transcriptional regulator 1517316:1517921 forward MW:22415 | 0.9 | 0.9 | 1.7 | 0.7 | 1.0 | 0.8 |
| Bbr_1215 | Bbr_1215 ATP-binding protein of ABC transporter system 1517938:1518699 forward MW:27109 | 1.0 | 1.0 | 1.2 | 0.4 | 1.1 | 0.6 |
| Bbr_1216 | Bbr_1216 Hypothetical membrane spanning protein 1518696:1521818 forward MW:109904 | 1.1 | 1.2 | 0.9 | 0.8 | 1.3 | 1.1 |
| Bbr_1218 | iscS Cysteine desulfurase 1522245:1523543 reverse MW:45854 | 1.3 | 2.0 | 1.3 | 1.0 | 1.4 | 1.0 |
| Bbr_1219 | nadC Nicotinate-nucleotide pyrophosphorylase [carboxylating] 1523546:1524439 reverse MW:31768 | 1.5 | 2.3 | 4.2 | 1.3 | 1.7 | 1.3 |
| Bbr_1220 | nadB L-aspartate oxidase 1524443:1526047 reverse MW:56757 | 1.3 | 2.2 | 12.6 | 2.0 | 1.8 | 1.8 |
| Bbr_1221 | nadA Quinolinate synthetase A 1526196:1527476 reverse MW:46653 | 1.3 | 1.9 | 7.2 | 2.0 | 2.3 | 1.9 |
| Bbr_1222 | Bbr_1222 Phosphohydrolase (MutT/nudix family protein) 1527529:1528365 reverse MW:30583 | 1.2 | 2.0 | 22.4 | 26.2 | 2.1 | 4.0 |
| Bbr_1223 | scpB Segregation and condensation protein ScpB 1528498:1529172 reverse MW:24399 | 0.9 | 1.1 | 1.4 | 1.5 | 1.9 | 1.1 |
| Bbr_1224 | scpA Segregation and condensation protein ScpA 1529185:1530036 reverse MW:31260 | 1.1 | 1.3 | 0.4 | 0.4 | 1.9 | 1.6 |
| Bbr_1225 | parA1 Chromosome partitioning protein parA 1530036:1530875 reverse MW:30223 | 1.0 | 1.0 | 0.8 | 0.6 | 1.2 | 1.2 |
| Bbr_1226 | Bbr_1226 Integrase/recombinase (XerD/RipX family) 1531100:1532029 reverse MW:33686 | 0.8 | 1.0 | 2.0 | 3.5 | 1.5 | 4.9 |
| Bbr_1227 | glxK Glycerate kinase 1532065:1533219 reverse MW:39680 | 1.2 | 1.8 | 3.6 | 0.5 | 2.3 | 5.1 |
| Bbr_1228 | rplT LSU ribosomal protein L20P 1533290:1533673 reverse MW:14606 | 1.1 | 1.2 | 1.0 | 0.5 | 0.7 | 1.7 |
| Bbr_1229 | rpmI LSU ribosomal protein L35P 1533725:1533919 reverse MW:6994 | 1.1 | 1.2 | 1.7 | 0.6 | 0.7 | 1.9 |
| Bbr_1230 | infC Bacterial Protein Translation Initiation Factor 3 (IF-3) 1533900:1534700 reverse MW:29696 | 1.2 | 1.5 | 3.5 | 2.6 | 0.9 | 2.6 |
| Bbr_1231 | Bbr_1231 Hypothetical protein 1535072:1535560 reverse MW:18572 | 1.8 | 3.0 | 6.3 | 15.0 | 1.3 | 2.0 |
| Bbr_1232 | Bbr_1232 Thiamin pyrophosphokinase 1535653:1536378 forward MW:25569 | 1.1 | 1.2 | 0.9 | 0.5 | 2.3 | 2.3 |
| Bbr_1233 | gap Glyceraldehyde 3-phosphate dehydrogenase 1536612:1537670 forward MW:37793 | 0.9 | 0.9 | 0.5 | 0.5 | 1.2 | 1.0 |
| Bbr_1234 | Bbr_1234 Conserved hypothetical protein with YbaK / prolyl-tRNA synthetases associated domain 1537764:1538270 forward MW:17781 | 1.0 | 1.3 | 1.0 | 0.5 | 1.4 | 2.3 |
| Bbr_1235 | ispH 4-hydroxy-3-methylbut-2-enyl diphosphate reductase 1538311:1539303 reverse MW:35543 | 0.9 | 0.9 | 2.9 | 15.3 | 3.0 | 1.7 |
| Bbr_1236 | Bbr_1236 Aldose 1-epimerase 1539594:1540550 forward MW:34839 | 0.9 | 0.4 | 0.2 | 0.2 | 0.5 | 0.5 |
| Bbr_1237 | Bbr_1237 Aldose 1-epimerase 1540685:1541629 forward MW:34695 | 1.0 | 0.4 | 0.3 | 0.3 | 0.4 | 0.5 |
| Bbr_1238 | Bbr_1238 Narrowly conserved hypothetical protein 1541891:1542199 reverse MW:11149 | 0.9 | 1.2 | 8.5 | 15.9 | 4.2 | 1.3 |
| Bbr_1239 | sigH RNA polymerase ECF-type sigma factor 1542196:1542990 reverse MW:29499 | 0.9 | 0.8 | 1.0 | 1.6 | 1.7 | 0.9 |
| Bbr_1240 | mur UDP-N-acetylmuramoyl-L-alanyl-D-glutamate-- lysine ligase 1543108:1544655 forward MW:56404 | 1.3 | 1.3 | 0.5 | 0.4 | 1.5 | 0.6 |
| Bbr_1241 | Bbr_1241 Cell wall biosynthesis-associated protein 1544716:1545723 forward MW:38043 | 1.1 | 1.0 | 0.5 | 0.7 | 0.8 | 0.5 |
| Bbr_1242 | Bbr_1242 Cell wall biosynthesis-associated protein 1545875:1546444 forward MW:20659 | 1.1 | 1.4 | 1.6 | 1.7 | 2.0 | 0.8 |
| Bbr_1243 | smc Chromosome partition protein smc 1546364:1550011 reverse MW:133838 | 1.0 | 2.0 | 1.1 | 1.7 | 3.6 | 0.5 |
| Bbr_1244 | folC Folylpolyglutamate synthase/Dihydrofolate synthase 1550056:1551621 reverse MW:55924 | 1.1 | 1.9 | 2.9 | 1.2 | 4.8 | 1.0 |
| Bbr_1245 | pepP Xaa-Pro aminopeptidase 1552228:1553823 forward MW:58519 | 1.0 | 1.0 | 0.6 | 0.4 | 1.5 | 0.5 |
| Bbr_1246 | Bbr_1246 Phosphohydrolase (MutT/nudix family protein) 1553961:1554482 forward MW:19113 | 1.0 | 0.9 | 0.4 | 0.4 | 1.6 | 0.5 |
| Bbr_1247 | nagA2 N-acetylglucosamine-6-phosphate deacetylase 1554580:1555857 reverse MW:44696 | 0.7 | 0.9 | 3.3 | 1.2 | 2.0 | 0.6 |
| Bbr_1248 | nagB3 Glucosamine-6-phosphate isomerase 1555912:1556724 reverse MW:28705 | 0.8 | 0.9 | 2.2 | 1.4 | 0.7 | 0.4 |
| Bbr_1249 | Bbr_1249 Transcriptional regulator, ROK family 1557061:1558185 forward MW:39987 | 1.0 | 1.4 | 5.4 | 2.8 | 2.7 | 1.3 |
| Bbr_1250 | Bbr_1250 Sugar kinase, ROK family 1558213:1559127 reverse MW:31020 | 0.7 | 1.0 | 7.8 | 3.3 | 0.8 | 1.2 |
| Bbr_1251 | Bbr_1251 N-acetylglucosamine repressor 1559353:1560567 forward MW:43368 | 1.5 | 0.8 | 1.3 | 0.6 | 0.5 | 1.2 |
| Bbr_1252 | Bbr_1252 Fructokinase 1560637:1561533 forward MW:32284 | 1.7 | 1.1 | 0.4 | 0.4 | 0.5 | 0.3 |
| Bbr_1254 | Bbr_1254 D-tyrosyl-tRNA(Tyr) deacylase 1562872:1563360 reverse MW:17863 | 1.0 | 1.0 | 1.8 | 2.6 | 1.3 | 2.5 |
| Bbr_1255 | ftsQ Cell division protein ftsQ 1563950:1564984 reverse MW:37104 | 1.0 | 1.1 | 0.8 | 1.6 | 1.4 | 1.8 |
| Bbr_1256 | murC UDP-N-acetylmuramate--alanine ligase 1564984:1566522 reverse MW:53569 | 1.0 | 0.9 | 0.5 | 0.2 | 1.9 | 1.2 |
| Bbr_1257 | murG UDP-N-acetylglucosamine--N-acetylmuramyl- (pentapeptide) pyrophosphoryl-undecaprenol N-acetylglucosamine transferase 1566625:1567 | 1.0 | 1.0 | 0.8 | 0.9 | 1.1 | 1.5 |

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|---|---|---|---|---|---|---|---|
| Bbr_1258 | fstW Cell division protein ftsW 1567814:1569031 reverse MW:43395 | 1.0 | 1.0 | 0.2 | 0.3 | 0.7 | 1.3 |
| Bbr_1259 | murD UDP-N-acetylmuramoylalanine--D-glutamate ligase 1569018:1570463 reverse MW:50947 | 1.0 | 0.9 | 0.4 | 0.3 | 1.0 | 1.0 |
| Bbr_1260 | murX Phospho-N-acetylmuramoyl-pentapeptide- transferase 1570519:1571625 reverse MW:40267 | 1.0 | 0.8 | 0.4 | 0.4 | 0.9 | 1.1 |
| Bbr_1261 | murF UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D- alanine ligase 1571669:1573114 reverse MW:50209 | 1.0 | 0.9 | 0.4 | 0.3 | 0.9 | 1.1 |
| Bbr_1262 | Bbr_1262 Narrowly conserved hypothetical protein 1573175:1574047 reverse MW:30538 | 1.1 | 1.0 | 0.7 | 0.6 | 1.1 | 1.4 |
| Bbr_1263 | ftsI Peptidoglycan synthetase FtsI, penicillin-binding protein 1574074:1575864 reverse MW:63509 | 0.9 | 0.8 | 0.3 | 0.4 | 1.3 | 1.1 |
| Bbr_1264 | Bbr_1264 Narrowly conserved hypothetical protein 1575861:1576313 reverse MW:16262 | 0.9 | 0.8 | 0.8 | 0.4 | 1.7 | 1.6 |
| Bbr_1265 | mraW S-adenosyl-methyltransferase mraW 1576316:1577368 reverse MW:38938 | 0.9 | 1.0 | 1.3 | 1.5 | 2.2 | 3.3 |
| Bbr_1266 | mraZ Cell division protein mraZ 1577368:1577889 reverse MW:19129 | 0.9 | 0.9 | 2.5 | 2.3 | 2.3 | 3.2 |
| Bbr_1267 | Bbr_1267 ATP-dependent DNA helicase 1578216:1580495 forward MW:84139 | 0.9 | 0.9 | 0.4 | 0.3 | 1.1 | 0.5 |
| Bbr_1268 | serA1 D-3-phosphoglycerate dehydrogenase 1580506:1581705 forward MW:43229 | 0.8 | 0.7 | 2.3 | 4.5 | 1.3 | 0.4 |
| Bbr_1269 | Bbr_1269 Conserved hypothetical protein with ATP cone domain 1581780:1582220 reverse MW:16483 | 1.0 | 1.9 | 4.8 | 11.3 | 2.4 | 15.7 |
| Bbr_1270 | Bbr_1270 LysM domain protein 1582274:1582657 reverse MW:13427 | 1.0 | 4.0 | 16.5 | 39.8 | 6.0 | 28.9 |
| Bbr_1271 | lexA LexA repressor 1582808:1583521 forward MW:25626 | 1.1 | 1.9 | 2.8 | 7.0 | 3.4 | 6.8 |
| Bbr_1272 | czcD Cobalt-zinc-cadmium resistance protein czcD 1583672:1584616 forward MW:33255 | 1.3 | 2.6 | 9.1 | 1.9 | 2.1 | 33.2 |
| Bbr_1273 | ldh2 L-lactate dehydrogenase 1584870:1585832 reverse MW:34055 | 0.9 | 0.8 | 0.5 | 0.2 | 1.2 | 0.4 |
| Bbr_1274 | hflX GTP-binding protein hflX 1586017:1587522 reverse MW:54478 | 1.1 | 1.5 | 0.8 | 1.0 | 1.1 | 1.0 |
| Bbr_1275 | Bbr_1275 16S RNA methylase 1587646:1588302 forward MW:23459 | 1.3 | 1.4 | 3.1 | 1.4 | 2.5 | 0.6 |
| Bbr_1276 | hrpA ATP-dependent helicase hrpA 1588292:1592428 forward MW:153018 | 1.0 | 1.6 | 0.8 | 1.5 | 3.2 | 0.5 |
| Bbr_1277 | Bbr_1277 Conserved hypothetical membrane spanning protein 1592437:1593657 reverse MW:43737 | 1.2 | 1.4 | 0.4 | 0.3 | 1.6 | 2.5 |
| Bbr_1278 | glnA2 Glutamine synthetase 1593853:1595190 reverse MW:49960 | 1.2 | 1.2 | 0.2 | 0.3 | 1.6 | 0.7 |
| Bbr_1279 | Bbr_1279 Conserved hypothetical protein 1595292:1596728 forward MW:53942 | 1.0 | 0.8 | 0.6 | 0.5 | 0.6 | 0.3 |
| Bbr_1280 | hisA 1-(5-phosphoribosyl)-5-[(5- phosphoribosylamino)methylideneamino] imidazole-4-carboxamide isomerase 1596896:1597621 reverse MW:257 | 1.0 | 1.1 | 0.2 | 0.3 | 1.9 | 1.9 |
| Bbr_1281 | hisH Imidazole glycerol phosphate synthase subunit hisH 1597645:1598292 reverse MW:23233 | 1.0 | 1.0 | 0.3 | 0.3 | 1.1 | 2.1 |
| Bbr_1282 | Bbr_1282 Narrowly conserved hypothetical protein 1598323:1599072 reverse MW:26077 | 1.0 | 1.1 | 0.4 | 0.2 | 1.5 | 2.3 |
| Bbr_1283 | hisB Imidazoleglycerol-phosphate dehydratase 1599069:1599668 reverse MW:21575 | 1.1 | 1.0 | 0.3 | 0.5 | 1.0 | 1.8 |
| Bbr_1284 | hisC Histidinol-phosphate aminotransferase 1599746:1600906 reverse MW:42477 | 1.1 | 1.0 | 0.3 | 0.3 | 1.5 | 2.2 |
| Bbr_1285 | hisD Histidinol dehydrogenase 1600903:1602300 reverse MW:49604 | 1.2 | 1.1 | 0.2 | 0.2 | 1.8 | 2.1 |
| Bbr_1286 | acyP Acylphosphatase 1602388:1602711 reverse MW:12155 | 0.8 | 0.9 | 1.9 | 4.1 | 2.7 | 5.7 |
| Bbr_1287 | Bbr_1287 Aldo/keto reductase family 1602826:1603653 forward MW:30233 | 0.7 | 0.7 | 0.8 | 0.4 | 3.8 | 0.4 |
| Bbr_1288 | Bbr_1288 Conserved hypothetical protein (Glycosyl hydrolases family 95) 1603792:1606143 reverse MW:87653 | 1.8 | 1.5 | 0.8 | 0.4 | 2.5 | 18.8 |
| Bbr_1289 | dapA3 Dihydrodipicolinate synthase 1606170:1607063 reverse MW:32003 | 1.6 | 1.4 | 2.0 | 1.2 | 1.4 | 38.8 |
| Bbr_1290 | Bbr_1290 Conserved hypothetical protein 1607060:1607881 reverse MW:30615 | 0.6 | 0.7 | 3.8 | 1.7 | 1.5 | 50.0 |
| Bbr_1291 | Bbr_1291 Short chain dehydrogenase 1607892:1608683 reverse MW:28810 | 0.6 | 0.9 | 4.4 | 2.4 | 1.8 | 39.5 |
| Bbr_1293 | Bbr_1293 Myosin-crossreactive antigen 1615696:1617573 reverse MW:70536 | 0.7 | 0.3 | 0.1 | 0.1 | 0.5 | 0.4 |
| Bbr_1294 | dkgV 2,5-diketo-D-gluconic acid reductase A 1617751:1618632 reverse MW:32351 | 1.5 | 1.2 | 0.9 | 0.9 | 0.8 | 0.8 |
| Bbr_1295 | Bbr_1295 Conserved hypothetical protein 1618723:1619109 reverse MW:14730 | 1.2 | 1.7 | 3.0 | 3.2 | 1.5 | 1.5 |
| Bbr_1296 | dnaE DNA polymerase III alpha subunit 1619121:1622735 reverse MW:133161 | 0.9 | 0.9 | 0.1 | 0.5 | 1.5 | 0.5 |
| Bbr_1297 | Bbr_1297 Narrowly conserved hypothetical protein with helix turn helix motif 1622973:1624022 forward MW:39873 | 2.3 | 2.1 | 3.8 | 1.3 | 1.2 | 2.7 |
| Bbr_1298 | Bbr_1298 Ribosomal large subunit pseudouridine synthase D 1624033:1624977 reverse MW:34352 | 1.0 | 1.0 | 0.6 | 0.5 | 0.8 | 1.5 |
| Bbr_1299 | lspA Lipoprotein signal peptidase 1624977:1625531 reverse MW:19343 | 0.8 | 0.8 | 0.6 | 1.3 | 0.7 | 1.1 |
| Bbr_1300 | Bbr_1300 Conserved hypothetical protein containing a repeated sequence found in lipoprotein LPP 1625548:1626897 reverse MW:49281 | 0.8 | 0.5 | 0.2 | 0.2 | 1.0 | 0.9 |
| Bbr_1301 | Bbr_1301 Conserved hypothetical membrane spanning protein with YGGT family 1627038:1627340 reverse MW:11584 | 0.8 | 0.9 | 0.4 | 0.2 | 1.6 | 1.3 |
| Bbr_1302 | Bbr_1302 Conserved hypothetical protein with DUF552 domain 1627452:1627928 reverse MW:17138 | 1.0 | 1.0 | 0.7 | 0.2 | 1.6 | 0.6 |
| Bbr_1303 | ftsZ Cell division protein ftsZ 1627941:1629143 reverse MW:41192 | 1.1 | 1.1 | 1.5 | 1.6 | 1.8 | 0.8 |
| Bbr_1304 | Bbr_1304 tRNA-dihydrouridine synthase 1629264:1630499 reverse MW:45762 | 1.4 | 1.5 | 0.9 | 0.4 | 1.7 | 3.4 |
| Bbr_1305 | glyS Glycyl-tRNA synthetase 1630642:1632114 reverse MW:55842 | 1.3 | 1.2 | 1.5 | 0.5 | 0.7 | 2.0 |
| Bbr_1306 | Bbr_1306 Hypothetical membrane spanning protein 1632189:1632902 reverse MW:25790 | 1.6 | 2.4 | 9.0 | 6.0 | 1.8 | 20.2 |
| Bbr_1307 | Bbr_1307 ATP-binding protein of ABC transporter system 1632922:1633686 reverse MW:28292 | 1.7 | 2.5 | 14.3 | 8.3 | 1.8 | 26.8 |
| Bbr_1308 | Bbr_1308 Hypothetical membrane spanning protein 1633785:1634429 reverse MW:22379 | 1.3 | 1.8 | 4.7 | 7.9 | 1.5 | 13.0 |
| Bbr_1309 | Bbr_1309 Transcriptional regulator 1634429:1634815 reverse MW:13954 | 1.6 | 2.0 | 7.5 | 11.2 | 2.8 | 17.5 |
| Bbr_1310 | Bbr_1310 Hypothetical membrane spanning protein 1634812:1635342 reverse MW:19878 | 1.6 | 2.1 | 7.2 | 11.8 | 2.6 | 15.8 |
| Bbr_1311 | thiM Hydroxyethylthiazole kinase 1635656:1636600 forward MW:32442 | 0.8 | 1.2 | 5.2 | 2.3 | 2.0 | 7.1 |
| Bbr_1312 | thiE/thiC Thiamine biosynthesis protein thiC 1636683:1639436 forward MW:100181 | 0.8 | 0.9 | 0.8 | 0.6 | 1.8 | 0.8 |
| Bbr_1313 | Bbr_1313 AAA family ATPase 1639474:1640679 reverse MW:44354 | 1.0 | 1.2 | 2.3 | 1.8 | 2.6 | 1.3 |
| Bbr_1314 | thiD Phosphomethylpyrimidine kinase/Hydroxymethylpyrimidine kinase 1640881:1641615 forward MW:25957 | 1.1 | 1.3 | 1.3 | 0.9 | 1.9 | 0.5 |
| Bbr_1315 | Bbr_1315 Conserved hypothetical protein with DUF77 domain 1641679:1642056 forward MW:13445 | 1.0 | 1.1 | 0.9 | 0.5 | 2.0 | 0.4 |
| Bbr_1316 | Bbr_1316 Transporter, MFS superfamily 1642581:1643960 forward MW:48660 | 1.4 | 1.1 | 1.3 | 0.7 | 0.8 | 2.8 |
| Bbr_1317 | Bbr_1317 Hypothetical membrane spanning protein 1643970:1645382 reverse MW:48787 | 0.9 | 0.7 | 2.0 | 2.3 | 1.0 | 1.2 |
| Bbr_1318 | Bbr_1318 Two-component response regulator 1645436:1646128 reverse MW:24477 | 0.8 | 0.6 | 1.9 | 6.2 | 0.8 | 0.8 |
| Bbr_1319 | Bbr_1319 Narrowly conserved hypothetical membrane spanning protein 1646275:1647291 forward MW:37574 | 0.8 | 0.4 | 1.9 | 2.6 | 0.5 | 0.4 |
| Bbr_1320 | Bbr_1320 Neuroserpin precursor 1647330:1648763 forward MW:51458 | 0.8 | 0.8 | 1.1 | 1.8 | 0.7 | 0.5 |
| Bbr_1321 | Bbr_1321 Transcriptional regulator, LacI family 1648816:1649847 forward MW:36912 | 1.1 | 1.2 | 3.6 | 12.0 | 1.6 | 1.3 |
| Bbr_1322 | fosA Conserved hypothetical protein 1649956:1650519 forward MW:22220 | 0.7 | 0.7 | 4.2 | 5.7 | 0.4 | 1.1 |
| Bbr_1323 | fosB Sucrose permease 1650566:1651036 forward MW:17334 | 0.8 | 0.7 | 1.8 | 1.2 | 0.3 | 3.2 |
| Bbr_1324 | fosC Beta-fructofuranosidase 1651048:1652604 forward MW:58360 | 0.8 | 0.9 | 1.5 | 2.8 | 0.7 | 0.7 |
| Bbr_1325 | ppgK Polyphosphate glucokinase/Transcriptional regulator 1652748:1653515 reverse MW:27153 | 0.6 | 0.3 | 0.2 | 0.2 | 0.5 | 0.4 |
| Bbr_1326 | Bbr_1326 Nitroreductase family protein 1653735:1654526 forward MW:29183 | 1.0 | 0.7 | 0.3 | 0.5 | 0.8 | 0.1 |
| Bbr_1327 | Bbr_1327 dTDP-rhamnosyl transferase rfbF 1654665:1655687 reverse MW:38489 | 1.1 | 1.2 | 1.5 | 1.1 | 1.7 | 0.3 |
| Bbr_1328 | Bbr_1328 Conserved hypothetical membrane spanning protein 1655969:1656625 forward MW:23067 | 0.8 | 1.5 | 8.6 | 1.3 | 2.4 | 1.6 |
| Bbr_1329 | Bbr_1329 Fused ATP binding protein and permease of ABC transporter 1656639:1658990 forward MW:83894 | 0.9 | 1.5 | 1.5 | 0.3 | 0.8 | 1.0 |
| Bbr_1330 | Bbr_1330 Hypothetical RNA binding protein 1659055:1659360 forward MW:11275 | 1.1 | 1.1 | 1.6 | 1.0 | 1.0 | 0.4 |
| Bbr_1331 | Bbr_1331 Conserved hypothetical membrane spanning protein 1659444:1659809 reverse MW:12904 | 0.6 | 0.7 | 3.1 | 6.6 | 0.8 | 2.0 |
| Bbr_1332 | Bbr_1332 Narrowly conserved hypothetical protein 1660242:1660652 reverse MW:15075 | 1.3 | 1.7 | 0.7 | 0.9 | 0.6 | 2.9 |
| Bbr_1333 | Bbr_1333 Hypothetical protein 1660651:1661682 forward MW:37972 | 0.9 | 1.3 | 1.3 | 0.8 | 0.5 | 12.7 |

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|---|---|---|---|---|---|---|---|
| Bbr_1334 | Bbr_1334 Transporter 1661919:1663379 forward MW:50490 | 1.2 | 1.7 | 2.1 | 0.2 | 1.1 | 0.5 |
| Bbr_1337 | Bbr_1337 AAA family ATPase 1664022:1665401 reverse MW:49517 | 1.1 | 1.6 | 3.4 | 5.2 | 3.3 | 1.5 |
| Bbr_1338 | Bbr_1338 DEAD/DEAH box-like helicase 1665504:1668074 reverse MW:95731 | 1.0 | 1.1 | 0.5 | 0.3 | 1.6 | 0.7 |
| Bbr_1339 | Bbr_1339 Conserved hypothetical protein with DUF344 domain 1668162:1669235 reverse MW:40697 | 0.8 | 0.8 | 0.9 | 0.3 | 1.8 | 0.6 |
| Bbr_1340 | Bbr_1340 Multiple substrate aminotransferase (MsaT) containing domain of GntR family 1669295:1670776 reverse MW:54303 | 2.4 | 4.9 | 3.5 | 13.7 | 2.9 | 1.4 |
| Bbr_1341 | Bbr_1341 Lysine exporter protein 1671057:1671716 forward MW:23364 | 2.0 | 1.0 | 0.5 | 0.8 | 0.7 | 0.3 |
| Bbr_1342 | Bbr_1342 Conserved hypothetical secreted protein 1671700:1673253 reverse MW:55167 | 1.1 | 1.0 | 0.7 | 0.9 | 0.6 | 1.8 |
| Bbr_1343 | gluD Glutamate transport system permease protein gluD 1673340:1674440 reverse MW:40432 | 1.0 | 0.8 | 0.9 | 1.1 | 1.7 | 1.6 |
| Bbr_1344 | gluC Glutamate transport system permease protein gluC 1674446:1675123 reverse MW:24380 | 1.0 | 1.0 | 0.4 | 0.5 | 0.9 | 1.4 |
| Bbr_1345 | gluB Glutamate-binding protein gluB 1675123:1675923 reverse MW:28512 | 1.1 | 1.2 | 0.4 | 0.5 | 1.6 | 1.5 |
| Bbr_1346 | gluA Glutamate transport ATP-binding protein gluA 1675981:1676823 reverse MW:31011 | 1.1 | 1.2 | 1.7 | 1.8 | 1.5 | 1.5 |
| Bbr_1347 | Bbr_1347 Conserved hypothetical protein with YbaK / prolyl-tRNA synthetases associated domain 1676876:1677427 reverse MW:19433 | 1.1 | 1.3 | 1.4 | 2.3 | 1.6 | 2.0 |
| Bbr_1348 | aspS Aspartyl-tRNA synthetase 1677631:1679430 reverse MW:66824 | 1.1 | 1.1 | 0.3 | 0.4 | 1.0 | 0.7 |
| Bbr_1349 | hisS Histidyl-tRNA synthetase 1679466:1680857 reverse MW:50173 | 1.2 | 1.2 | 0.5 | 0.6 | 1.0 | 0.6 |
| Bbr_1350 | Bbr_1350 Conserved hypothetical protein with DUF349 domain 1680957:1682402 forward MW:53220 | 1.0 | 1.1 | 1.6 | 0.9 | 1.7 | 0.6 |
| Bbr_1351 | Bbr_1351 Calcineurin-like phosphoesterase 1682563:1684326 reverse MW:61357 | 0.9 | 1.4 | 1.1 | 1.6 | 1.3 | 1.1 |
| Bbr_1352 | Bbr_1352 Creatininase 1684436:1685194 reverse MW:27125 | 1.4 | 1.4 | 3.7 | 6.7 | 1.0 | 0.7 |
| Bbr_1353 | proP Proline/betaine transporter 1685302:1686678 reverse MW:48836 | 1.1 | 0.8 | 1.0 | 1.8 | 0.6 | 2.2 |
| Bbr_1354 | Bbr_1354 Transcriptional regulator 1686866:1688368 reverse MW:53972 | 1.1 | 0.7 | 0.9 | 2.9 | 1.0 | 2.3 |
| Bbr_1355 | codA Cytosine deaminase 1688511:1689833 forward MW:48253 | 1.4 | 1.1 | 2.1 | 4.6 | 0.9 | 0.8 |
| Bbr_1356 | clpC Negative regulator of genetic competence clpC/mecB 1689990:1692599 reverse MW:95437 | 0.9 | 1.2 | 0.8 | 0.4 | 2.4 | 0.6 |
| Bbr_1357 | Bbr_1357 Universal stress protein family 1692752:1693717 forward MW:34393 | 1.0 | 1.0 | 1.9 | 1.0 | 1.9 | 0.6 |
| Bbr_1358 | Bbr_1358 Conserved hypothetical protein 1693869:1694918 reverse MW:38904 | 1.2 | 1.1 | 0.3 | 0.3 | 1.2 | 1.3 |
| Bbr_1359 | cspB Cold shock protein 1694927:1695316 reverse MW:14022 | 1.1 | 0.9 | 0.6 | 1.0 | 1.2 | 0.7 |
| Bbr_1360 | Bbr_1360 Two component system histidine kinase 1695410:1697335 reverse MW:69129 | 0.6 | 0.7 | 0.2 | 0.5 | 0.7 | 0.9 |
| Bbr_1361 | Bbr_1361 Two-component response regulator 1697412:1698143 reverse MW:27189 | 0.9 | 1.0 | 1.4 | 0.7 | 0.9 | 0.7 |
| Bbr_1362 | Bbr_1362 Narrowly conserved hypothetical membrane spanning protein 1698136:1698972 reverse MW:29624 | 1.0 | 1.0 | 1.8 | 0.6 | 1.8 | 1.0 |
| Bbr_1363 | Bbr_1363 Conserved hypothetical protein with DUF909 domain 1699049:1699339 forward MW:10396 | 1.4 | 1.4 | 1.3 | 1.8 | 2.0 | 0.5 |
| Bbr_1364 | groEL 60 kDa chaperonin GroEL 1699522:1701147 reverse MW:56846 | 2.1 | 3.6 | 3.8 | 1.1 | 3.8 | 1.1 |
| Bbr_1365 | cspA Cold shock protein 1701385:1701624 reverse MW:8637 | 0.9 | 1.3 | 5.2 | 10.8 | 2.1 | 1.8 |
| Bbr_1366 | Bbr_1366 Conserved hypothetical protein 1701848:1702504 reverse MW:22726 | 1.0 | 1.1 | 1.4 | 0.6 | 1.1 | 1.4 |
| Bbr_1367 | ung Uracil-DNA glycosylase 1702621:1703310 forward MW:25056 | 1.3 | 1.8 | 2.2 | 0.5 | 1.5 | 0.9 |
| Bbr_1368 | moxR2 MoxR protein 1703340:1704428 forward MW:38698 | 1.2 | 1.9 | 1.3 | 0.3 | 1.7 | 1.5 |
| Bbr_1369 | Bbr_1369 Conserved hypothetical protein 1704473:1705369 forward MW:33272 | 1.1 | 1.5 | 0.6 | 0.5 | 0.8 | 1.7 |
| Bbr_1370 | Bbr_1370 Narrowly conserved hypothetical protein 1705366:1705908 forward MW:19431 | 1.0 | 1.2 | 0.5 | 0.4 | 1.0 | 1.2 |
| Bbr_1371 | Bbr_1371 Conserved hypothetical membrane spanning protein 1705908:1706963 forward MW:38396 | 0.9 | 0.9 | 1.2 | 1.2 | 0.9 | 1.1 |
| Bbr_1372 | Bbr_1372 Conserved hypothetical membrane spanning protein with a von Willebrand factor type A domain 1706960:1707997 forward MW:36261 | 0.8 | 0.8 | 0.3 | 0.3 | 0.4 | 0.8 |
| Bbr_1373 | Bbr_1373 Narrowly conserved hypothetical secreted protein 1707994:1708566 forward MW:19825 | 0.8 | 0.8 | 1.0 | 1.7 | 0.7 | 1.0 |
| Bbr_1374 | Bbr_1374 Narrowly conserved hypothetical protein 1708693:1709001 forward MW:10698 | 0.9 | 1.1 | 2.1 | 2.6 | 0.8 | 6.1 |
| Bbr_1375 | Bbr_1375 Conserved hypothetical protein 1708998:1710578 forward MW:56012 | 0.8 | 1.2 | 1.0 | 2.1 | 1.3 | 7.2 |
| Bbr_1376 | Bbr_1376 Permease protein of ABC transporter system 1710605:1711249 reverse MW:22984 | 1.3 | 1.5 | 2.6 | 3.1 | 1.2 | 1.4 |
| Bbr_1377 | purB Adenylosuccinate lyase 1711373:1712818 forward MW:53870 | 1.2 | 1.5 | 0.7 | 0.3 | 1.0 | 0.7 |
| Bbr_1378 | Bbr_1378 Conserved hypothetical membrane spanning protein in uncharacterised protein UPF0104 family 1712891:1715455 forward MW:91572 | 0.9 | 1.3 | 0.8 | 0.8 | 1.2 | 0.7 |
| Bbr_1379 | Bbr_1379 DNA-binding protein HU 1715593:1715874 forward MW:9929 | 0.8 | 0.4 | 0.2 | 0.7 | 0.9 | 0.2 |
| Bbr_1380 | Bbr_1380 Conserved hypothetical protein with DUF275 domain 1715986:1717473 reverse MW:55009 | 1.1 | 1.1 | 0.3 | 0.3 | 1.0 | 0.5 |
| Bbr_1381 | Bbr_1381 Conserved hypothetical protein with DUF797 domain 1717473:1717670 reverse MW:7203 | 1.1 | 1.0 | 0.5 | 0.3 | 1.0 | 0.5 |
| Bbr_1382 | Bbr_1382 Inositol monophosphatase family protein 1717780:1718685 reverse MW:33576 | 1.0 | 1.2 | 0.9 | 0.7 | 1.2 | 0.6 |
| Bbr_1383 | Bbr_1383 Conserved hypothetical protein with DUF275 domain 1718688:1720352 reverse MW:60990 | 1.2 | 1.1 | 1.2 | 3.1 | 1.3 | 0.5 |
| Bbr_1384 | rpe2 Ribulose-phosphate 3-epimerase 1720464:1721180 reverse MW:27013 | 1.9 | 1.3 | 1.0 | 0.4 | 0.3 | 0.7 |
| Bbr_1385 | Bbr_1385 PTS system, fructose-like enzyme IIC component 1721358:1722476 reverse MW:38440 | 1.2 | 0.4 | 0.9 | 0.8 | 0.2 | 0.5 |
| Bbr_1386 | Bbr_1386 PTS system, fructose-like IIB component 1722528:1722839 reverse MW:10957 | 1.1 | 0.5 | 0.9 | 1.2 | 0.7 | 0.5 |
| Bbr_1387 | Bbr_1387 PTS system, fructose-like IIA component 1722890:1723360 reverse MW:17051 | 1.2 | 0.8 | 0.6 | 0.8 | 0.3 | 0.9 |
| Bbr_1388 | Bbr_1388 Nitrogen regulatory IIA (Enzyme IIA-NTR) (Phosphotransferase enzyme II, A component) transcription regulator protein 1723404:17238 | 1.2 | 1.8 | 0.8 | 1.6 | 0.4 | 1.9 |
| Bbr_1389 | Bbr_1389 Transcription antiterminator, BglG family 1723829:1725322 reverse MW:56310 | 1.0 | 1.3 | 0.6 | 0.6 | 0.3 | 4.7 |
| Bbr_1390 | Bbr_1390 Haloacid dehalogenase-like hydrolase (HAD superfamily) 1725542:1726279 forward MW:27338 | 1.4 | 1.3 | 2.5 | 2.5 | 0.9 | 0.5 |
| Bbr_1391 | Bbr_1391 AAA family ATPase 1726339:1727913 reverse MW:56804 | 0.8 | 0.7 | 1.3 | 3.0 | 1.2 | 1.4 |
| Bbr_1392 | dedA2 DedA family protein 1727967:1728662 reverse MW:24781 | 0.9 | 1.0 | 0.4 | 0.4 | 1.7 | 1.8 |
| Bbr_1393 | serB1 Phosphoserine phosphatase 1728683:1729435 forward MW:27023 | 1.5 | 2.0 | 1.5 | 2.9 | 1.3 | 1.4 |
| Bbr_1394 | priA Primosomal protein N' 1729483:1731792 forward MW:83024 | 0.9 | 0.9 | 0.4 | 0.7 | 1.4 | 1.5 |
| Bbr_1395 | Bbr_1395 Haloacid dehalogenase-like hydrolase (HAD superfamily) 1732037:1732741 forward MW:25739 | 0.9 | 0.8 | 2.0 | 2.4 | 1.2 | 0.4 |
| Bbr_1396 | fmt Methionyl-tRNA formyltransferase 1732881:1733894 forward MW:35450 | 0.9 | 0.8 | 1.0 | 0.9 | 1.6 | 0.7 |
| Bbr_1397 | ilvD Dihydroxy-acid dehydratase 1734190:1736052 reverse MW:66445 | 0.9 | 0.7 | 0.3 | 0.3 | 1.3 | 0.6 |
| Bbr_1398 | rpoZ DNA-directed RNA polymerase omega chain 1736219:1736503 forward MW:10396 | 1.1 | 1.0 | 1.2 | 0.6 | 0.8 | 0.6 |
| Bbr_1399 | metK S-adenosylmethionine synthetase 1736789:1738009 forward MW:43701 | 1.2 | 1.4 | 1.9 | 1.2 | 1.9 | 0.9 |
| Bbr_1400 | Bbr_1400 Fic family protein 1738194:1739048 forward MW:32653 | 0.9 | 0.7 | 1.3 | 1.4 | 0.7 | 0.9 |
| Bbr_1401 | Bbr_1401 Transposase 1739449:1740210 reverse MW:28249 | 1.0 | 1.2 | 3.6 | 4.0 | 0.7 | 5.5 |
| Bbr_1402 | Bbr_1402 Transposase 1740666:1742165 forward MW:56251 | 0.8 | 1.2 | 0.8 | 2.3 | 0.7 | 1.7 |
| Bbr_1403 | Bbr_1403 Transposase 1742162:1742941 forward MW:29538 | 1.1 | 1.4 | 3.0 | 4.3 | 0.3 | 2.2 |
| Bbr_1404 | Bbr_1404 Transposase 1742984:1744141 reverse MW:44053 | 0.7 | 0.8 | 1.2 | 2.0 | 1.1 | 1.6 |
| Bbr_1405 | cas2 CRISPR-associated protein Cas2 1748791:1749081 reverse MW:11077 | 0.5 | 0.4 | 0.7 | 1.4 | 0.7 | 0.8 |
| Bbr_1406 | cas1 CRISPR-associated protein Cas1 1749138:1750169 reverse MW:39037 | 0.5 | 0.3 | 0.5 | 0.6 | 0.4 | 0.7 |
| Bbr_1407 | cas4 CRISPR-associated protein Cas4 1750171:1750860 reverse MW:25998 | 0.5 | 0.3 | 0.2 | 0.3 | 0.5 | 0.5 |
| Bbr_1408 | Bbr_1408 CRISPR-associated protein 1750899:1751750 reverse MW:31325 | 0.5 | 0.2 | 0.1 | 0.1 | 0.3 | 0.4 |
| Bbr_1409 | Bbr_1409 CRISPR-associated protein 1751754:1753712 reverse MW:74091 | 0.5 | 0.3 | 0.1 | 0.1 | 0.3 | 0.4 |
| Bbr_1410 | Bbr_1410 CRISPR-associated protein 1753715:1754419 reverse MW:27630 | 0.7 | 0.4 | 0.2 | 0.3 | 0.4 | 0.5 |

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|---|---|---|---|---|---|---|---|
| Bbr_1411 | cas3 CRISPR-associated helicase Cas3 1754426:1756864 reverse MW:90834 | 0.8 | 0.6 | 0.2 | 1.0 | 0.5 | 0.4 |
| Bbr_1414 | ileS Isoleucyl-tRNA synthetase 1761037:1764345 reverse MW:124150 | 1.4 | 2.5 | 2.1 | 0.7 | 1.3 | 0.8 |
| Bbr_1415 | rbsK2 Ribokinase 1765018:1766019 reverse MW:34449 | 0.8 | 0.9 | 6.5 | 6.3 | 0.7 | 2.9 |
| Bbr_1416 | rbsD1 Ribose transport system permease protein rbsD 1766059:1766454 reverse MW:14291 | 0.6 | 0.7 | 4.0 | 3.0 | 0.7 | 3.6 |
| Bbr_1417 | rbsB1 D-ribose-binding protein rbsB 1766586:1767533 reverse MW:32226 | 0.4 | 0.2 | 0.3 | 0.4 | 0.7 | 0.4 |
| Bbr_1418 | rbsC1 Ribose transport system permease protein rbsC 1767610:1768617 reverse MW:34348 | 0.5 | 0.2 | 0.4 | 0.4 | 0.2 | 0.5 |
| Bbr_1419 | rbsA1 Ribose transport ATP-binding protein rbsA 1768614:1770134 reverse MW:54075 | 0.5 | 0.2 | 0.9 | 1.0 | 0.5 | 0.9 |
| Bbr_1420 | Bbr_1420 Transcriptional regulator, LacI family 1770394:1771413 reverse MW:36710 | 0.8 | 0.5 | 0.8 | 0.5 | 0.4 | 0.5 |
| Bbr_1421 | Bbr_1421 Conserved hypothetical membrane spanning protein 1772681:1774126 reverse MW:51319 | 0.8 | 0.4 | 0.4 | 0.6 | 0.7 | 0.3 |
| Bbr_1422 | rbsK3 Ribokinase 1774166:1775068 reverse MW:31998 | 1.0 | 0.6 | 0.9 | 1.3 | 0.4 | 0.6 |
| Bbr_1423 | bdhA NADH-dependent butanol dehydrogenase 1 1775068:1776273 reverse MW:43204 | 1.1 | 0.6 | 0.7 | 0.7 | 0.4 | 0.6 |
| Bbr_1424 | gph Phosphoglycolate phosphatase 1776270:1776956 reverse MW:25670 | 1.0 | 0.4 | 0.1 | 0.6 | 0.3 | 0.4 |
| Bbr_1425 | iunH2 Inosine-uridine preferring nucleoside hydrolase 1777080:1778063 reverse MW:35334 | 1.2 | 0.5 | 0.2 | 0.2 | 0.3 | 0.3 |
| Bbr_1426 | Bbr_1426 Fructokinase 1778119:1779075 reverse MW:34192 | 1.1 | 0.7 | 0.8 | 1.5 | 0.6 | 0.4 |
| Bbr_1427 | trpF N-(5'-phosphoribosyl)anthranilate isomerase 1779068:1779769 reverse MW:25215 | 1.2 | 0.5 | 0.5 | 1.2 | 0.4 | 0.4 |
| Bbr_1428 | CbiO1 Cobalt transport ATP-binding protein cbiO 1779762:1780577 reverse MW:29731 | 1.2 | 0.6 | 0.4 | 0.3 | 0.4 | 0.4 |
| Bbr_1429 | cbiO2 Cobalt transport ATP-binding protein cbiO 1780574:1781404 reverse MW:30063 | 1.2 | 0.7 | 0.8 | 0.7 | 0.4 | 0.6 |
| Bbr_1430 | cbiQ Cobalt transport protein cbiQ 1781405:1782217 reverse MW:29035 | 1.2 | 0.8 | 0.8 | 1.0 | 0.4 | 0.7 |
| Bbr_1431 | Bbr_1431 Conserved hypothetical membrane spanning protein 1782221:1782874 reverse MW:22864 | 1.1 | 0.6 | 0.9 | 1.9 | 0.5 | 1.4 |
| Bbr_1432 | rbsK4 Ribokinase 1783131:1785032 forward MW:68958 | 1.1 | 1.0 | 1.4 | 1.1 | 0.6 | 1.6 |
| Bbr_1433 | Bbr_1433 ATP-binding protein of ABC transporter system 1785140:1787155 reverse MW:74122 | 1.5 | 2.7 | 4.4 | 1.1 | 0.6 | 0.8 |
| Bbr_1434 | Bbr_1434 ATP-binding protein of ABC transporter system 1787152:1789113 reverse MW:71033 | 2.0 | 3.5 | 4.8 | 2.7 | 0.8 | 0.7 |
| Bbr_1435 | Bbr_1435 Transcriptional regulator, MarR family 1789110:1789643 reverse MW:20034 | 1.6 | 2.7 | 22.3 | 27.5 | 0.6 | 1.3 |
| Bbr_1437 | Bbr_1437 Narrowly conserved hypothetical protein 1791100:1791390 reverse MW:9989 | 0.7 | 0.9 | 1.6 | 6.6 | 1.5 | 1.2 |
| Bbr_1438 | Bbr_1438 Glucan 1,3-beta-glucosidase 1791447:1792661 reverse MW:46464 | 0.6 | 0.5 | 0.3 | 0.3 | 0.8 | 0.7 |
| Bbr_1439 | Bbr_1439 Conserved hypothetical protein 1792667:1793068 reverse MW:15580 | 0.7 | 0.6 | 1.8 | 0.9 | 1.4 | 0.6 |
| Bbr_1440 | Bbr_1440 Nucleotidyltransferase 1793055:1793342 reverse MW:10616 | 0.8 | 0.8 | 1.8 | 3.6 | 2.4 | 0.7 |
| Bbr_1441 | Bbr_1441 Narrowly conserved hypothetical protein 1793390:1793755 reverse MW:13290 | 0.9 | 1.0 | 1.4 | 2.3 | 1.2 | 1.7 |
| Bbr_1442 | bgl2 Beta-glucosidase 1793779:1796142 reverse MW:84674 | 0.8 | 0.8 | 1.4 | 2.3 | 1.4 | 0.9 |
| Bbr_1443 | Bbr_1443 Transcriptional regulator, TetR family 1796338:1797069 reverse MW:27646 | 0.8 | 0.8 | 0.8 | 0.9 | 0.6 | 1.2 |
| Bbr_1444 | gshA Glutamate--cysteine ligase 1797129:1798406 reverse MW:48755 | 0.6 | 0.6 | 0.2 | 0.1 | 1.8 | 0.5 |
| Bbr_1445 | Bbr_1445 Activator of (R)-2-hydroxyglutaryl-CoA dehydratase 1798569:1803674 reverse MW:185175 | 1.2 | 1.9 | 0.3 | 0.2 | 1.7 | 0.6 |
| Bbr_1446 | nrdG Anaerobic ribonucleoside-triphosphate reductase activating protein 1803904:1804632 reverse MW:27586 | 0.7 | 0.6 | 0.5 | 0.3 | 1.1 | 2.7 |
| Bbr_1447 | nrdD Anaerobic ribonucleoside-triphosphate reductase 1804787:1807195 reverse MW:90399 | 0.8 | 0.7 | 0.4 | 0.3 | 1.2 | 1.1 |
| Bbr_1448 | xseA Exodeoxyribonuclease VII large subunit 1807597:1808964 forward MW:49212 | 1.4 | 1.7 | 0.4 | 0.3 | 0.6 | 0.9 |
| Bbr_1449 | xseB Exodeoxyribonuclease VII small subunit 1809026:1809310 forward MW:10260 | 1.0 | 1.0 | 0.6 | 0.8 | 0.8 | 0.5 |
| Bbr_1450 | Bbr_1450 NAD(P)H oxidoreductase 1809377:1809901 forward MW:19354 | 1.0 | 0.9 | 0.3 | 0.4 | 0.9 | 0.6 |
| Bbr_1451 | Bbr_1451 Hypothetical protein 1810085:1811905 forward MW:64367 | 1.6 | 2.0 | 3.1 | 7.2 | 1.0 | 0.3 |
| Bbr_1452 | Bbr_1452 Large-conductance mechanosensitive channel 1812030:1812536 reverse MW:17475 | 1.0 | 0.8 | 1.1 | 1.6 | 0.4 | 8.3 |
| Bbr_1453 | Bbr_1453 Conserved hypothetical protein with nucleoside deoxyribosyltransferase (ntd) domain 1812724:1813152 reverse MW:15968 | 1.1 | 0.9 | 1.9 | 2.0 | 0.8 | 3.5 |
| Bbr_1454 | Bbr_1454 Conserved hypothetical membrane spanning protein with Endonuclease/Exonuclease/phosphatase family domain 1813693:1814646 for | 1.0 | 1.1 | 1.2 | 1.8 | 0.5 | 0.9 |
| Bbr_1455 | ppx Exopolyphosphatase 1814680:1815648 reverse MW:35117 | 0.9 | 0.8 | 0.6 | 0.9 | 0.8 | 0.4 |
| Bbr_1456 | Bbr_1456 Aminotransferase 1815702:1816913 reverse MW:44215 | 1.0 | 0.8 | 0.7 | 0.3 | 0.9 | 0.2 |
| Bbr_1457 | Bbr_1457 NAD-dependent oxidoreductase 1817012:1818067 forward MW:38177 | 1.1 | 0.4 | 0.5 | 0.3 | 0.7 | 0.5 |
| Bbr_1458 | vsr DNA mismatch endonuclease, patch repair protein 1818147:1818599 reverse MW:17781 | 1.1 | 1.0 | 1.3 | 3.0 | 0.6 | 0.6 |
| Bbr_1459 | Bbr_1459 Acetyltransferase 1818754:1819317 forward MW:20630 | 1.0 | 0.6 | 0.3 | 0.3 | 0.5 | 0.5 |
| Bbr_1460 | Bbr_1460 Helicase 1819323:1823387 reverse MW:148417 | 1.0 | 1.2 | 11.3 | 57.9 | 1.7 | 4.5 |
| Bbr_1461 | dapD 2,3,4,5-tetrahydropyridine-2-carboxylate N-succinyltransferase 1823565:1824584 forward MW:35603 | 1.0 | 0.9 | 0.7 | 0.6 | 2.1 | 0.4 |
| Bbr_1462 | gltA Citrate synthase 1824959:1826251 reverse MW:48240 | 1.1 | 1.0 | 0.9 | 0.5 | 2.1 | 3.6 |
| Bbr_1463 | map Methionine aminopeptidase 1826463:1827245 reverse MW:28441 | 1.0 | 1.1 | 0.7 | 0.8 | 0.9 | 0.9 |
| Bbr_1464 | Bbr_1464 Conserved hypothetical membrane spanning protein 1827409:1828293 reverse MW:31617 | 1.2 | 1.5 | 1.3 | 1.9 | 1.1 | 0.7 |
| Bbr_1465 | pepO Zinc metalloprotease 1828458:1830641 forward MW:80317 | 0.8 | 0.9 | 0.2 | 0.2 | 1.0 | 0.6 |
| Bbr_1466 | Bbr_1466 Single-strand DNA binding protein 1830711:1831385 reverse MW:23769 | 0.8 | 1.0 | 1.1 | 3.5 | 1.3 | 2.1 |
| Bbr_1467 | proS Prolyl-tRNA synthetase 1831648:1833462 reverse MW:66930 | 1.3 | 1.4 | 0.4 | 0.4 | 1.4 | 0.6 |
| Bbr_1468 | pflA2 Pyruvate formate-lyase activating enzyme 1833601:1834470 reverse MW:31555 | 0.9 | 1.2 | 2.6 | 6.5 | 0.6 | 9.8 |
| Bbr_1470 | Bbr_1470 Helicase 1834794:1836212 reverse MW:51659 | 0.9 | 0.8 | 0.6 | 0.4 | 0.8 | 1.4 |
| Bbr_1471 | orn Oligoribonuclease 1836337:1836987 reverse MW:24300 | 1.0 | 0.9 | 0.7 | 0.5 | 0.6 | 0.7 |
| Bbr_1472 | guaB Inosine-5'-monophosphate dehydrogenase 1837155:1838708 reverse MW:55017 | 1.0 | 0.7 | 0.4 | 0.6 | 0.9 | 0.7 |
| Bbr_1473 | rfe Undecaprenyl-phosphate alpha-N-acetylglucosaminephosphotransferase 1838797:1840044 reverse MW:44539 | 1.0 | 0.9 | 0.1 | 0.2 | 1.1 | 1.1 |
| Bbr_1474 | Bbr_1474 Sua5/YciO/YrdC/YwlC family protein 1840041:1840703 reverse MW:23209 | 1.0 | 1.0 | 0.6 | 0.5 | 1.1 | 0.7 |
| Bbr_1475 | Bbr_1475 Branched-chain amino acid transport ATP-binding protein livF 1840862:1841566 reverse MW:25439 | 1.4 | 1.3 | 1.8 | 2.1 | 0.7 | 0.6 |
| Bbr_1476 | Bbr_1476 Branched-chain amino acid transport ATP-binding protein livG 1841566:1842429 reverse MW:31523 | 1.4 | 1.3 | 1.2 | 1.6 | 0.5 | 0.5 |
| Bbr_1477 | Bbr_1477 Branched-chain amino acid transport system permease protein livM 1842426:1843502 reverse MW:37831 | 1.4 | 1.2 | 0.6 | 0.5 | 0.5 | 0.6 |
| Bbr_1478 | Bbr_1478 Branched-chain amino acid transport system permease protein livH 1843519:1844442 reverse MW:31851 | 1.5 | 1.1 | 0.3 | 0.4 | 0.4 | 0.5 |
| Bbr_1479 | Bbr_1479 Leucine-, isoleucine-, valine-, threonine-, and alanine-binding protein 1844604:1845791 reverse MW:41422 | 1.5 | 1.0 | 0.2 | 0.2 | 0.4 | 0.5 |
| Bbr_1480 | hemK Peptide release factor-glutamine N5-methyltransferase 1846064:1846948 reverse MW:32015 | 1.0 | 1.6 | 1.7 | 2.2 | 1.1 | 1.7 |
| Bbr_1481 | prfA Bacterial Peptide Chain Release Factor 1 (RF-1) 1847091:1848179 reverse MW:40100 | 1.1 | 1.4 | 1.1 | 0.5 | 1.0 | 0.8 |
| Bbr_1482 | rpmE2 LSU ribosomal protein L31P 1848289:1848540 reverse MW:9640 | 0.9 | 1.2 | 2.7 | 2.7 | 0.8 | 0.5 |
| Bbr_1483 | Bbr_1483 Multidrug resistance protein B 1848790:1849401 forward MW:22326 | 1.0 | 1.4 | 6.8 | 13.3 | 0.6 | 4.1 |
| Bbr_1484 | Bbr_1484 Narrowly conserved hypothetical protein 1849504:1850295 reverse MW:29678 | 0.7 | 0.6 | 2.1 | 1.3 | 0.7 | 3.0 |
| Bbr_1485 | fms Peptide deformylase 1850684:1851103 reverse MW:15583 | 0.9 | 0.9 | 2.1 | 1.5 | 1.5 | 0.9 |
| Bbr_1486 | dkg 2,5-diketo-D-gluconic acid reductase 1851103:1851951 reverse MW:31640 | 0.9 | 0.8 | 2.2 | 1.6 | 0.8 | 0.7 |
| Bbr_1487 | Bbr_1487 Narrowly conserved hypothetical protein 1852384:1852926 reverse MW:19674 | 1.5 | 2.2 | 4.1 | 3.3 | 0.7 | 2.0 |
| Bbr_1488 | glk Glucokinase/Xylose repressor 1853171:1854121 reverse MW:32905 | 1.0 | 1.1 | 0.7 | 0.5 | 1.1 | 0.6 |
| Bbr_1489 | Bbr_1489 Conserved hypothetical membrane spanning protein 1854657:1856396 reverse MW:59400 | 0.8 | 0.9 | 0.6 | 0.8 | 1.5 | 0.7 |

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|---|---|---|---|---|---|---|---|
| Bbr_1490 | Bbr_1490 ATP-binding protein of ABC transporter system 1856997:1858676 forward MW:61958 | 1.0 | 1.5 | 1.7 | 1.0 | 1.3 | 1.0 |
| Bbr_1491 | tesB Acyl-CoA thioesterase 1858893:1859798 forward MW:33309 | 1.1 | 1.3 | 1.5 | 0.6 | 1.2 | 0.9 |
| Bbr_1492 | Bbr_1492 Narrowly conserved hypothetical membrane spanning protein 1859839:1860366 reverse MW:18786 | 0.8 | 0.9 | 2.7 | 2.3 | 3.0 | 1.5 |
| Bbr_1493 | sulD Dihydroneopterin aldolase/2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase/Hypothetical protein 1860461:1862071 re | 0.7 | 0.8 | 1.0 | 2.1 | 2.8 | 0.9 |
| Bbr_1494 | folP Dihydropteroate synthase 1862188:1863063 reverse MW:30603 | 0.7 | 0.7 | 0.9 | 1.4 | 3.0 | 1.4 |
| Bbr_1495 | folE GTP cyclohydrolase I 1863261:1863920 reverse MW:24129 | 0.7 | 0.8 | 0.7 | 0.7 | 2.0 | 1.4 |
| Bbr_1496 | ftsH Cell division protein ftsH 1864017:1866116 reverse MW:76507 | 0.8 | 1.0 | 0.6 | 0.3 | 3.6 | 0.9 |
| Bbr_1497 | hprT Hypoxanthine-guanine phosphoribosyltransferase 1866113:1866676 reverse MW:20730 | 0.9 | 1.2 | 1.7 | 1.8 | 1.4 | 0.6 |
| Bbr_1498 | tilS tRNA(Ile)-lysidine synthetase TilS 1866663:1867814 reverse MW:40778 | 0.7 | 0.6 | 0.9 | 1.8 | 1.2 | 1.1 |
| Bbr_1499 | Bbr_1499 Conserved hypothetical secreted protein with D-Ala-D-Ala carboxypeptidase 3 (S13) domain 1867850:1869346 reverse MW:51131 | 0.7 | 0.6 | 0.4 | 0.5 | 1.9 | 0.7 |
| Bbr_1500 | Bbr_1500 Conserved hypothetical membrane spanning protein 1869371:1871041 reverse MW:59148 | 0.5 | 0.4 | 0.3 | 0.4 | 0.9 | 2.2 |
| Bbr_1501 | Bbr_1501 ATP-binding protein of ABC transporter system 1871041:1872123 reverse MW:38204 | 0.5 | 0.5 | 0.4 | 0.5 | 0.8 | 3.6 |
| Bbr_1502 | Bbr_1502 N-acetylglucosaminyltransferase 1872556:1873779 reverse MW:45918 | 0.9 | 0.8 | 0.1 | 0.1 | 0.9 | 0.6 |
| Bbr_1503 | Bbr_1503 Conserved hypothetical membrane spanning protein with DUF20 domain 1873779:1875371 reverse MW:58058 | 1.0 | 1.0 | 0.3 | 0.4 | 0.7 | 1.0 |
| Bbr_1504 | Bbr_1504 Glycosyltransferase 1875449:1876375 forward MW:35135 | 1.4 | 1.6 | 0.6 | 0.7 | 1.6 | 0.3 |
| Bbr_1505 | fucO Lactaldehyde reductase 1876511:1877662 reverse MW:40625 | 0.5 | 0.2 | 0.4 | 0.2 | 0.7 | 0.6 |
| Bbr_1506 | Bbr_1506 Cyclopropane-fatty-acyl-phospholipid synthase 1878014:1879318 forward MW:48753 | 0.9 | 1.0 | 2.6 | 0.8 | 1.1 | 0.8 |
| Bbr_1507 | Bbr_1507 tRNA (m(7)G46) methyltransferase 1879859:1880728 forward MW:31868 | 0.8 | 0.9 | 0.7 | 0.4 | 1.3 | 1.5 |
| Bbr_1508 | Bbr_1508 Hypothetical protein 1880960:1881481 forward MW:18194 | 0.8 | 1.2 | 5.9 | 11.4 | 2.5 | 7.7 |
| Bbr_1509 | Bbr_1509 Narrowly conserved hypothetical protein 1881858:1883120 forward MW:46421 | 0.9 | 1.0 | 6.7 | 8.3 | 2.6 | 25.6 |
| Bbr_1510 | Bbr_1510 WhiB-like transcription factor 1883117:1883539 forward MW:15711 | 0.8 | 0.6 | 2.2 | 4.6 | 1.0 | 7.4 |
| Bbr_1513 | parA2 Chromosome partitioning protein parA 1886245:1886844 forward MW:21454 | 0.9 | 0.8 | 1.7 | 1.9 | 0.7 | 4.9 |
| Bbr_1514 | Bbr_1514 Narrowly conserved hypothetical protein 1886841:1887092 forward MW:9027 | 0.6 | 0.5 | 1.3 | 1.8 | 0.7 | 5.6 |
| Bbr_1515 | Bbr_1515 ATP-binding protein of ABC transporter system 1887457:1888968 forward MW:55532 | 1.1 | 1.1 | 3.0 | 3.5 | 0.7 | 29.7 |
| Bbr_1516 | Bbr_1516 Acetyltransferase (GNAT) family 1889047:1889652 forward MW:22005 | 1.1 | 1.5 | 7.2 | 9.8 | 0.8 | 7.1 |
| Bbr_1517 | serB2 Phosphoserine phosphatase 1890002:1890649 reverse MW:23057 | 1.0 | 1.0 | 1.2 | 2.6 | 1.8 | 1.0 |
| Bbr_1518 | Bbr_1518 Cell surface protein 1890938:1895320 forward MW:158568 | 0.9 | 1.1 | 1.5 | 4.1 | 0.6 | 1.2 |
| Bbr_1519 | Bbr_1519 Multidrug-efflux transporter 2 regulator 1895631:1896416 forward MW:29939 | 1.0 | 1.3 | 3.1 | 3.0 | 1.3 | 1.4 |
| Bbr_1520 | pacB Penicillin acylase 1896548:1897549 forward MW:36695 | 1.1 | 0.6 | 0.3 | 0.5 | 0.6 | 1.0 |
| Bbr_1521 | Bbr_1521 Hypothetical secreted protein 1897581:1898120 forward MW:19043 | 1.2 | 0.7 | 0.4 | 0.4 | 0.7 | 1.1 |
| Bbr_1522 | Bbr_1522 Hypothetical protein 1898295:1898720 forward MW:15763 | 1.1 | 1.8 | 7.3 | 5.5 | 1.0 | 3.2 |
| Bbr_1523 | Bbr_1523 MerR family regulatory protein 1899018:1899470 forward MW:16525 | 1.4 | 3.1 | 7.3 | 18.1 | 3.6 | 11.5 |
| Bbr_1524 | Bbr_1524 Conserved hypothetical protein 1899481:1900050 forward MW:21579 | 1.3 | 2.3 | 5.1 | 5.5 | 2.4 | 11.9 |
| Bbr_1525 | Bbr_1525 Hypothetical protein 1900083:1901351 forward MW:48506 | 1.4 | 2.0 | 0.8 | 1.1 | 1.1 | 6.1 |
| Bbr_1527 | Bbr_1527 Narrowly conserved hypothetical membrane spanning protein 1902893:1903099 forward MW:7028 | 0.9 | 1.2 | 1.6 | 3.4 | 1.0 | 2.0 |
| Bbr_1528 | Bbr_1528 Conserved hypothetical membrane spanning protein 1903128:1903973 forward MW:30161 | 0.9 | 0.9 | 2.0 | 3.7 | 0.9 | 3.0 |
| Bbr_1529 | Bbr_1529 Hypothetical protein 1904002:1904139 forward MW:4981 | 0.8 | 0.8 | 1.4 | 3.5 | 0.6 | 2.4 |
| Bbr_1530 | Bbr_1530 Conserved hypothetical protein with CHAP and transglycosylase SLT domains 1904190:1905299 forward MW:39251 | 0.6 | 0.7 | 0.9 | 2.2 | 0.7 | 5.8 |
| Bbr_1531 | Bbr_1531 Narrowly conserved hypothetical protein 1905333:1906628 forward MW:46132 | 0.9 | 1.0 | 1.7 | 6.2 | 0.8 | 3.7 |
| Bbr_1532 | Bbr_1532 DNA processing chain A 1906897:1907901 forward MW:36834 | 0.9 | 1.2 | 4.2 | 4.5 | 1.7 | 0.8 |
| Bbr_1533 | Bbr_1533 Hypothetical protein 1907898:1908722 forward MW:30174 | 0.9 | 1.2 | 2.7 | 1.4 | 0.6 | 1.5 |
| Bbr_1534 | rep ATP-dependent DNA helicase rep 1908898:1910601 reverse MW:64414 | 0.8 | 0.6 | 0.2 | 0.2 | 0.4 | 0.2 |
| Bbr_1535 | Bbr_1535 Conserved hypothetical protein with ABC transporter domain 1910588:1912180 reverse MW:57719 | 1.1 | 1.0 | 0.3 | 0.4 | 0.8 | 0.3 |
| Bbr_1536 | Bbr_1536 TraG/TraD family 1912368:1914032 reverse MW:61956 | 0.8 | 1.0 | 0.5 | 1.2 | 1.2 | 0.5 |
| Bbr_1537 | Bbr_1537 Hypothetical protein 1914029:1914409 reverse MW:13272 | 1.0 | 1.2 | 2.3 | 2.6 | 1.1 | 1.2 |
| Bbr_1538 | Bbr_1538 Hypothetical protein 1914406:1914726 reverse MW:11307 | 1.0 | 1.0 | 2.3 | 3.9 | 1.1 | 0.9 |
| Bbr_1539 | Bbr_1539 Conserved hypothetical protein 1914716:1915864 reverse MW:42295 | 0.9 | 1.6 | 7.0 | 6.8 | 0.9 | 0.8 |
| Bbr_1542 | Bbr_1542 Hypothetical protein 1918715:1919422 reverse MW:25837 | 1.2 | 1.5 | 1.6 | 3.1 | 0.9 | 0.4 |
| Bbr_1543 | Bbr_1543 Hypothetical protein 1919450:1920319 reverse MW:31978 | 0.9 | 1.7 | 1.4 | 4.5 | 0.9 | 0.4 |
| Bbr_1544 | Bbr_1544 Relaxase 1920388:1921818 reverse MW:52910 | 0.9 | 1.2 | 1.8 | 2.7 | 0.9 | 0.6 |
| Bbr_1545 | Bbr_1545 Mobilisation protein 1921809:1922240 reverse MW:16636 | 0.9 | 1.3 | 1.1 | 3.4 | 0.7 | 0.5 |
| Bbr_1546 | parB1 Chromosome partitioning protein parB 1923319:1924893 reverse MW:57021 | 0.8 | 0.8 | 1.7 | 3.8 | 0.7 | 0.6 |
| Bbr_1547 | Bbr_1547 Narrowly conserved hypothetical protein 1924971:1925585 reverse MW:22743 | 1.0 | 1.4 | 2.0 | 3.7 | 0.9 | 1.5 |
| Bbr_1548 | Bbr_1548 Integrase protein 1926025:1927389 reverse MW:52282 | 0.8 | 1.4 | 0.6 | 2.5 | 0.4 | 1.1 |
| Bbr_1549 | Bbr_1549 DNA integration/recombination/inversion protein 1927798:1928061 reverse MW:9712 | 0.8 | 1.0 | 1.9 | 2.2 | 0.7 | 0.8 |
| Bbr_1550 | Bbr_1550 Hypothetical protein 1928217:1928495 reverse MW:9430 | 0.8 | 0.9 | 1.9 | 2.8 | 1.0 | 0.8 |
| Bbr_1551 | lacS Galactoside symporter 1928562:1929977 reverse MW:51532 | 1.2 | 1.0 | 2.6 | 1.0 | 1.5 | 0.6 |
| Bbr_1552 | LacZ6 Beta-galactosidase 1930411:1933548 forward MW:116684 | 1.0 | 0.7 | 7.4 | 5.5 | 0.7 | 0.8 |
| Bbr_1553 | Bbr_1553 Transcriptional regulator, LacI family 1933748:1934758 reverse MW:36889 | 1.0 | 1.0 | 1.9 | 2.6 | 1.7 | 0.8 |
| Bbr_1554 | Bbr_1554 Solute-binding protein of ABC transporter system (lactose) 1935263:1936588 reverse MW:48060 | 0.7 | 0.6 | 0.4 | 0.4 | 0.4 | 0.5 |
| Bbr_1555 | Bbr_1555 NagC/XylR-type transciptional regulator 1936818:1937993 forward MW:42087 | 1.1 | 1.3 | 4.7 | 7.4 | 0.6 | 3.2 |
| Bbr_1556 | nagZ Beta-N-acetylhexosaminidase 1938241:1940262 forward MW:75974 | 1.0 | 1.0 | 1.6 | 2.2 | 1.4 | 0.6 |
| Bbr_1558 | Bbr_1558 Permease protein of ABC transporter system 1940897:1942264 forward MW:48867 | 0.7 | 0.3 | 0.2 | 0.3 | 0.2 | 2.3 |
| Bbr_1559 | Bbr_1559 ATP-binding protein of ABC transporter system 1942261:1943484 forward MW:42950 | 0.7 | 0.3 | 0.2 | 0.2 | 0.3 | 1.8 |
| Bbr_1560 | Bbr_1560 ATP-binding protein of ABC transporter system 1943497:1944132 forward MW:22903 | 0.7 | 0.3 | 0.1 | 0.2 | 0.4 | 1.3 |
| Bbr_1562 | ptpA Protein tyrosine phosphatase 1944578:1945096 reverse MW:19888 | 1.0 | 1.0 | 0.6 | 0.4 | 0.7 | 0.7 |
| Bbr_1563 | dfrA Dihydrofolate reductase 1945212:1945874 reverse MW:24233 | 1.1 | 1.1 | 0.7 | 0.5 | 1.0 | 0.6 |
| Bbr_1564 | thyA Thymidylate synthase 1945992:1946792 reverse MW:30597 | 1.1 | 0.9 | 0.2 | 0.1 | 0.9 | 0.6 |
| Bbr_1565 | Bbr_1565 Conserved hypothetical protein 1946997:1947410 forward MW:14904 | 0.8 | 0.6 | 0.6 | 1.2 | 0.7 | 0.3 |
| Bbr_1566 | Bbr_1566 Universal stress protein family 1947557:1948594 reverse MW:36536 | 0.6 | 0.3 | 0.4 | 0.3 | 1.8 | 0.7 |
| Bbr_1567 | Bbr_1567 Conserved hypothetical secreted protein with NlpC/P60 family domain 1948815:1949537 reverse MW:24210 | 1.1 | 1.1 | 0.3 | 0.3 | 1.1 | 1.3 |
| Bbr_1568 | Bbr_1568 Conserved hypothetical secreted protein with NlpC/P60 family domain 1949700:1950437 reverse MW:24911 | 0.8 | 0.7 | 0.4 | 0.5 | 1.2 | 4.3 |
| Bbr_1569 | Bbr_1569 Conserved hypothetical protein with CHAP domain 1950539:1951498 reverse MW:33436 | 0.9 | 1.0 | 0.5 | 0.5 | 1.5 | 7.4 |
| Bbr_1570 | serC Phosphoserine aminotransferase 1951752:1952888 forward MW:40113 | 1.2 | 1.1 | 0.5 | 0.6 | 1.9 | 1.3 |
| Bbr_1571 | Bbr_1571 Narrowly conserved hypothetical membrane spanning protein 1952978:1953238 forward MW:9562 | 1.1 | 1.6 | 3.2 | 2.2 | 1.1 | 2.6 |

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|---|---|---|---|---|---|---|---|
| Bbr_1572 | senX3 Sensor-like histidine kinase senX3 1953239:1954432 reverse MW:42979 | 1.0 | 0.8 | 0.7 | 0.9 | 0.9 | 1.0 |
| Bbr_1573 | Bbr_1573 Phosphate transport system protein phoU homolog 1954624:1955298 forward MW:24659 | 0.8 | 0.7 | 1.0 | 1.0 | 0.9 | 0.8 |
| Bbr_1574 | gpm2 Phosphoglycerate mutase 1955668:1956438 reverse MW:28737 | 1.0 | 1.1 | 1.0 | 0.6 | 1.4 | 1.1 |
| Bbr_1575 | menA 1,4-dihydroxy-2-naphthoate polyprenyltransferase 1956546:1957511 reverse MW:33883 | 1.0 | 1.2 | 1.3 | 0.6 | 1.3 | 1.8 |
| Bbr_1576 | lysS Lysyl-tRNA synthetase 1957669:1959351 reverse MW:62039 | 1.1 | 1.3 | 1.0 | 0.4 | 1.8 | 0.6 |
| Bbr_1577 | Bbr_1577 AraJ-like protein probably involved in transport of arabinose polymers 1960100:1961290 forward MW:41642 | 1.6 | 1.9 | 1.6 | 0.6 | 1.0 | 1.7 |
| Bbr_1578 | Bbr_1578 Conserved hypothetical protein with TPR domain 1961374:1963575 forward MW:79692 | 1.0 | 0.8 | 0.4 | 0.5 | 1.9 | 0.2 |
| Bbr_1579 | Bbr_1579 Conserved hypothetical protein 1963585:1964217 forward MW:24042 | 1.0 | 0.9 | 0.4 | 0.8 | 1.3 | 0.2 |
| Bbr_1580 | Bbr_1580 Narrowly conserved hypothetical membrane spanning protein 1964235:1965959 reverse MW:62047 | 0.9 | 0.9 | 0.4 | 0.3 | 1.5 | 2.5 |
| Bbr_1581 | Bbr_1581 Narrowly conserved hypothetical membrane spanning protein 1966080:1966799 reverse MW:24743 | 0.7 | 0.6 | 0.1 | 0.1 | 0.3 | 0.8 |
| Bbr_1582 | Bbr_1582 Narrowly conserved hypothetical membrane spanning protein with PspC domain 1966796:1968562 reverse MW:63070 | 0.8 | 0.6 | 0.1 | 0.1 | 0.2 | 0.8 |
| Bbr_1583 | Bbr_1583 Histidine kinase sensor of two component system 1968607:1969893 forward MW:46430 | 1.0 | 0.9 | 0.5 | 0.2 | 0.6 | 0.6 |
| Bbr_1584 | Bbr_1584 undefined product 1969890:1970573 forward MW:24058 | 0.9 | 0.8 | 0.5 | 0.5 | 1.4 | 0.8 |
| Bbr_1585 | galE UDP-glucose 4-epimerase 1970699:1971721 reverse MW:37212 | 1.0 | 0.7 | 0.7 | 0.5 | 0.9 | 1.3 |
| Bbr_1586 | Bbr_1586 Mucin desulfatase 1971860:1972930 reverse MW:39759 | 0.8 | 0.8 | 1.9 | 0.4 | 0.6 | 0.7 |
| Bbr_1587 | lnbP lacto-N-biose phorylase 1973307:1975559 reverse MW:84104 | 0.7 | 0.5 | 0.5 | 0.4 | 1.2 | 0.7 |
| Bbr_1588 | Bbr_1588 Permease protein of ABC transporter system for sugars 1975773:1976723 reverse MW:34659 | 0.9 | 0.7 | 0.3 | 0.3 | 0.8 | 0.6 |
| Bbr_1589 | Bbr_1589 Permease protein of ABC transporter system for sugars 1976723:1977694 reverse MW:34750 | 0.8 | 0.6 | 0.3 | 0.3 | 0.5 | 0.5 |
| Bbr_1590 | Bbr_1590 Solute-binding protein of ABC transporter system for sugars 1977885:1979201 reverse MW:46135 | 0.6 | 0.3 | 0.5 | 1.0 | 0.5 | 0.5 |
| Bbr_1591 | serS Seryl-tRNA synthetase 1979677:1981035 reverse MW:50571 | 1.1 | 1.2 | 0.7 | 0.4 | 1.1 | 0.6 |
| Bbr_1592 | Bbr_1592 Conserved hypothetical secreted protein with presumed diacylglycerol kinase catalytic domain 1981134:1982384 forward MW:44674 | 0.9 | 0.9 | 0.5 | 0.2 | 1.1 | 1.2 |
| Bbr_1593 | Bbr_1593 Transcription antiterminator, BglG family 1982386:1983279 reverse MW:32857 | 0.7 | 0.3 | 0.7 | 0.6 | 1.5 | 1.5 |
| Bbr_1594 | ptsG PTS system, glucose-specific IIABC component 1983331:1985421 reverse MW:72713 | 0.9 | 0.4 | 0.5 | 0.7 | 1.3 | 1.0 |
| Bbr_1595 | pgm Phosphoglucomutase 1985917:1987593 forward MW:60212 | 0.9 | 0.7 | 0.3 | 0.3 | 1.3 | 0.8 |
| Bbr_1596 | Bbr_1596 Conserved hypothetical protein 1988177:1989244 reverse MW:39556 | 0.8 | 1.0 | 4.7 | 2.9 | 1.3 | 36.2 |
| Bbr_1597 | Bbr_1597 Rrf2 family protein 1989440:1989871 forward MW:15132 | 1.7 | 2.3 | 4.8 | 5.7 | 1.9 | 9.6 |
| Bbr_1598 | Bbr_1598 Pyridine nucleotide-disulphide oxidoreductase family protein 1990154:1991662 forward MW:53281 | 1.9 | 3.0 | 3.7 | 1.8 | 1.9 | 17.0 |
| Bbr_1599 | rnh Ribonuclease HI 1991717:1992880 forward MW:40821 | 1.2 | 2.5 | 5.8 | 2.0 | 1.6 | 7.1 |
| Bbr_1600 | rpi Ribose 5-phosphate isomerase 1992946:1993644 forward MW:25365 | 1.1 | 1.3 | 4.3 | 2.5 | 1.1 | 2.3 |
| Bbr_1601 | Bbr_1601 Narrowly conserved hypothetical membrane spanning protein 1993822:1994094 forward MW:9890 | 1.6 | 2.8 | 12.3 | 1.2 | 1.9 | 7.4 |
| Bbr_1602 | Bbr_1602 Narrowly conserved hypothetical secreted protein 1994073:1994696 reverse MW:21892 | 1.2 | 1.1 | 0.6 | 0.6 | 0.9 | 0.2 |
| Bbr_1603 | radA DNA repair protein radA 1994816:1996315 forward MW:52197 | 1.3 | 1.0 | 1.3 | 3.6 | 1.5 | 1.7 |
| Bbr_1604 | ribF Riboflavin kinase/FMN adenylyltransferase 1996325:1997449 reverse MW:41075 | 1.0 | 1.0 | 0.8 | 0.8 | 1.4 | 0.7 |
| Bbr_1605 | truB tRNA pseudouridine synthase B 1997504:1998691 reverse MW:42673 | 0.7 | 0.9 | 1.0 | 2.1 | 1.6 | 1.4 |
| Bbr_1606 | rbfA Ribosome-binding factor A 1998751:1999236 reverse MW:18143 | 0.7 | 0.8 | 0.8 | 0.8 | 1.8 | 0.9 |
| Bbr_1607 | infB Bacterial Protein Translation Initiation Factor 2 (IF-2) 1999507:2002329 reverse MW:99700 | 0.9 | 1.1 | 1.4 | 0.6 | 1.8 | 0.9 |
| Bbr_1608 | nusA N utilization substance protein A 2002605:2003660 reverse MW:37764 | 0.9 | 0.9 | 3.4 | 2.9 | 1.5 | 1.0 |
| Bbr_1609 | Bbr_1609 Narrowly conserved hypothetical protein 2003864:2004592 forward MW:24952 | 1.3 | 1.6 | 1.0 | 1.0 | 1.1 | 0.7 |
| Bbr_1610 | Bbr_1610 Transcriptional regulator, LacI family 2004650:2005450 reverse MW:29215 | 0.9 | 1.0 | 25.5 | 20.6 | 0.9 | 8.1 |
| Bbr_1611 | Bbr_1611 Conserved hypothetical protein in transglutaminase family 2005663:2006463 reverse MW:29748 | 1.0 | 1.2 | 1.8 | 1.7 | 1.0 | 2.5 |
| Bbr_1612 | Bbr_1612 Conserved hypothetical protein with DUF404 and DUF407 domains 2006609:2008789 reverse MW:81940 | 1.1 | 0.7 | 0.2 | 0.3 | 0.5 | 5.3 |
| Bbr_1613 | truA tRNA pseudouridine synthase A 2008950:2009861 reverse MW:32974 | 1.1 | 1.3 | 1.9 | 1.2 | 0.9 | 14.1 |
| Bbr_1614 | rplQ 50S ribosomal protein L17 2010030:2010563 reverse MW:19166 | 1.1 | 1.3 | 0.7 | 0.5 | 1.0 | 1.8 |
| Bbr_1615 | rpoA DNA-directed RNA polymerase alpha chain 2010660:2011655 reverse MW:36127 | 1.1 | 1.0 | 0.4 | 0.4 | 0.8 | 1.6 |
| Bbr_1616 | rpsK SSU ribosomal protein S11P 2011735:2012133 reverse MW:13916 | 0.9 | 0.9 | 0.6 | 0.6 | 0.7 | 1.3 |
| Bbr_1617 | rpsM SSU ribosomal protein S13P 2012221:2012598 reverse MW:14257 | 0.9 | 0.9 | 1.0 | 1.6 | 0.7 | 1.4 |
| Bbr_1618 | rpmJ LSU ribosomal protein L36P 2012747:2012860 reverse MW:4372 | 0.9 | 0.8 | 0.9 | 2.3 | 0.6 | 1.2 |
| Bbr_1619 | infA Bacterial Protein Translation Initiation Factor 1 (IF-1) 2012884:2013102 reverse MW:8378 | 1.0 | 0.8 | 0.7 | 2.8 | 0.7 | 1.2 |
| Bbr_1620 | adk Adenylate kinase 2013255:2013815 reverse MW:20499 | 1.1 | 0.9 | 0.3 | 0.3 | 0.8 | 0.9 |
| Bbr_1621 | secY Protein translocase subunit secY 2013967:2015304 reverse MW:49064 | 1.0 | 1.0 | 0.5 | 0.2 | 0.7 | 1.0 |
| Bbr_1622 | rplO 50S ribosomal protein L15 2015621:2016073 reverse MW:15923 | 1.1 | 1.2 | 1.0 | 0.5 | 1.2 | 1.1 |
| Bbr_1623 | rpmD 50S ribosomal protein L30 2016076:2016261 reverse MW:6723 | 1.1 | 1.1 | 1.0 | 0.3 | 1.1 | 1.0 |
| Bbr_1624 | rpsE 30S ribosomal protein S5 2016267:2016965 reverse MW:24590 | 1.1 | 0.9 | 0.9 | 0.4 | 1.1 | 1.0 |
| Bbr_1625 | rplR 50S ribosomal protein L18 2016992:2017363 reverse MW:12999 | 1.0 | 1.0 | 0.9 | 0.4 | 1.0 | 1.0 |
| Bbr_1626 | rplF 50S ribosomal protein L6 2017365:2017904 reverse MW:18854 | 1.1 | 1.1 | 0.9 | 0.4 | 1.1 | 1.1 |
| Bbr_1627 | rpsH 30S ribosomal protein S8 2017922:2018320 reverse MW:14444 | 1.1 | 1.1 | 1.2 | 0.6 | 1.0 | 1.1 |
| Bbr_1628 | rpsN 30S ribosomal protein S14-1 2018410:2018595 reverse MW:6920 | 1.1 | 1.1 | 1.1 | 0.7 | 1.0 | 1.1 |
| Bbr_1629 | rplE 50S ribosomal protein L5 2018597:2019169 reverse MW:21380 | 1.1 | 1.1 | 0.9 | 0.8 | 0.9 | 1.1 |
| Bbr_1630 | rplX 50S ribosomal protein L24 2019166:2019501 reverse MW:12102 | 1.1 | 1.1 | 1.5 | 1.5 | 1.0 | 1.1 |
| Bbr_1631 | rplN 50S ribosomal protein L14 2019503:2019871 reverse MW:13151 | 1.1 | 1.1 | 1.2 | 1.6 | 1.1 | 1.2 |
| Bbr_1632 | rpsQ 30S ribosomal protein S17 2019966:2020226 reverse MW:10090 | 1.1 | 1.2 | 1.1 | 2.0 | 1.0 | 1.1 |
| Bbr_1633 | rpmC 50S ribosomal protein L29 2020229:2020480 reverse MW:9387 | 1.2 | 1.2 | 0.8 | 0.3 | 1.0 | 1.1 |
| Bbr_1634 | rplP 50S ribosomal protein L16 2020480:2020899 reverse MW:15587 | 1.2 | 1.3 | 0.8 | 0.3 | 1.0 | 1.1 |
| Bbr_1635 | rpsC 30S ribosomal protein S3 2020906:2021706 reverse MW:30157 | 1.3 | 1.4 | 1.0 | 0.3 | 1.1 | 1.3 |
| Bbr_1636 | rplV 50S ribosomal protein L22 2021709:2022068 reverse MW:13217 | 1.3 | 1.4 | 1.2 | 0.4 | 1.1 | 1.3 |
| Bbr_1637 | rpsS 30S ribosomal protein S19 2022085:2022363 reverse MW:10511 | 1.3 | 1.3 | 1.1 | 0.4 | 0.9 | 1.2 |
| Bbr_1638 | rplB 50S ribosomal protein L2 2022379:2023209 reverse MW:30206 | 1.2 | 1.3 | 1.0 | 0.3 | 1.0 | 1.2 |
| Bbr_1639 | rplW 50S ribosomal protein L23 2023246:2023542 reverse MW:10867 | 1.2 | 1.3 | 1.0 | 0.4 | 1.0 | 1.1 |
| Bbr_1640 | rplD 50S ribosomal protein L4 2023548:2024204 reverse MW:23559 | 1.2 | 1.2 | 1.3 | 0.4 | 1.0 | 1.1 |
| Bbr_1641 | rplC 50S ribosomal protein L3 2024211:2024852 reverse MW:22631 | 1.1 | 1.1 | 1.4 | 0.5 | 0.9 | 1.1 |
| Bbr_1642 | rpsJ 30S ribosomal protein S10 2024869:2025177 reverse MW:11554 | 1.1 | 1.2 | 1.3 | 0.9 | 0.8 | 1.1 |
| Bbr_1643 | aldB Alpha-acetolactate decarboxylase 2025626:2026399 forward MW:28071 | 1.1 | 0.9 | 0.9 | 1.1 | 1.0 | 0.7 |
| Bbr_1644 | Bbr_1644 Narrowly conserved hypothetical membrane spanning protein 2026758:2027654 forward MW:32445 | 1.1 | 1.0 | 1.0 | 2.4 | 1.3 | 2.1 |
| Bbr_1645 | adh2 Aldehyde-alcohol dehydrogenase 2 2027945:2030674 reverse MW:98753 | 1.4 | 1.8 | 1.6 | 0.8 | 0.7 | 2.2 |
| Bbr_1646 | Bbr_1646 Transcriptional regulator, ROK family 2031195:2032337 forward MW:42163 | 1.4 | 1.4 | 1.4 | 1.7 | 1.6 | 2.4 |

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|---|---|---|---|---|---|---|---|
| Bbr_1647 | glgX2 Glycogen operon protein glgX 2032395:2034911 forward MW:94568 | 1.0 | 1.0 | 0.6 | 0.6 | 1.0 | 0.3 |
| Bbr_1648 | rpsI 30S ribosomal protein S9 2035734:2036225 reverse MW:17607 | 0.9 | 0.8 | 1.2 | 0.6 | 1.0 | 1.0 |
| Bbr_1649 | rplM 50S ribosomal protein L13 2036248:2036697 reverse MW:16576 | 0.9 | 0.9 | 1.0 | 0.9 | 1.0 | 1.1 |
| Bbr_1650 | malQ2 4-alpha-glucanotransferase 2036985:2039150 reverse MW:79586 | 0.8 | 0.5 | 0.2 | 0.3 | 0.7 | 2.0 |
| Bbr_1651 | Bbr_1651 Narrowly conserved hypothetical protein with leucine rich repeat variant 2039273:2039956 reverse MW:24626 | 1.2 | 1.3 | 1.3 | 1.1 | 0.9 | 4.9 |
| Bbr_1652 | Bbr_1652 Thymidylate synthase 2039953:2040594 reverse MW:22955 | 1.4 | 1.5 | 0.6 | 0.4 | 1.0 | 4.9 |
| Bbr_1653 | serA2 D-3-phosphoglycerate dehydrogenase 2040618:2041634 reverse MW:36828 | 1.5 | 1.9 | 1.2 | 1.2 | 0.9 | 4.5 |
| Bbr_1655 | bgl3 Beta-glucosidase 2042986:2044176 reverse MW:44643 | 0.5 | 0.4 | 0.7 | 0.8 | 0.2 | 0.5 |
| Bbr_1656 | Bbr_1656 Sugar ABC transporter, permease protein 2044207:2045094 reverse MW:32362 | 0.5 | 0.3 | 0.8 | 0.4 | 0.3 | 0.5 |
| Bbr_1657 | Bbr_1657 Sugar-binding protein of ABC transporter system 2045106:2046023 reverse MW:33668 | 0.5 | 0.3 | 1.2 | 0.6 | 0.4 | 0.6 |
| Bbr_1658 | Bbr_1658 Sugar-binding protein of ABC transporter system 2046044:2047339 reverse MW:45772 | 0.5 | 0.2 | 2.9 | 8.3 | 0.2 | 0.6 |
| Bbr_1659 | Bbr_1659 Transcriptional regulator 2047522:2048649 reverse MW:40915 | 0.9 | 0.8 | 0.5 | 0.7 | 0.9 | 3.0 |
| Bbr_1660 | Bbr_1660 Hypothetical protein 2048795:2049175 reverse MW:13831 | 0.9 | 1.6 | 7.8 | 12.1 | 2.1 | 11.3 |
| Bbr_1662 | Bbr_1662 DNA polymerase IV 2050258:2051532 forward MW:46150 | 1.0 | 1.1 | 1.1 | 1.6 | 0.6 | 1.0 |
| Bbr_1663 | Bbr_1663 Aminotransferase 2051533:2052720 reverse MW:41678 | 1.0 | 1.0 | 1.9 | 1.1 | 1.2 | 2.0 |
| Bbr_1664 | fdxC Ferredoxin 2052813:2053133 reverse MW:11449 | 1.2 | 1.3 | 1.9 | 0.7 | 1.4 | 1.5 |
| Bbr_1665 | aap4 Amino acid permease 2053198:2054724 reverse MW:54508 | 1.2 | 1.3 | 2.5 | 2.1 | 0.8 | 6.2 |
| Bbr_1666 | murB UDP-N-acetylenolpyruvoylglucosamine reductase 2054886:2056109 reverse MW:42493 | 1.0 | 1.4 | 4.4 | 3.2 | 1.3 | 21.0 |
| Bbr_1667 | rpmG LSU ribosomal protein L33P 2056231:2056404 reverse MW:6668 | 0.9 | 1.0 | 2.2 | 2.2 | 0.5 | 2.1 |
| Bbr_1668 | Hsp10 10 kDa chaperonin GROES 2057116:2057409 reverse MW:10583 | 1.5 | 2.3 | 3.3 | 3.3 | 3.3 | 1.8 |
| Bbr_1669 | Bbr_1669 Narrowly conserved hypothetical membrane spanning protein 2057566:2058744 reverse MW:42445 | 1.0 | 1.0 | 1.1 | 1.1 | 1.0 | 1.4 |
| Bbr_1670 | Bbr_1670 Ribosomal-protein-S5-alanine acetyltransferase 2058817:2059482 reverse MW:25106 | 1.4 | 1.6 | 2.2 | 2.0 | 0.6 | 2.2 |
| Bbr_1672 | Bbr_1672 Conserved hypothetical secreted protein with Flp pilus assembly protein CpaB domain 2060516:2061139 forward MW:21552 | 1.3 | 1.3 | 11.1 | 7.3 | 1.0 | 4.4 |
| Bbr_1673 | Bbr_1673 DNA and RNA helicase related protein 2061582:2065202 reverse MW:133073 | 1.0 | 1.0 | 0.4 | 0.4 | 0.7 | 0.9 |
| Bbr_1674 | Bbr_1674 Narrowly conserved hypothetical protein with FHA domain 2065211:2066566 reverse MW:48801 | 1.2 | 1.1 | 1.5 | 0.6 | 1.3 | 2.0 |
| Bbr_1675 | rplL LSU ribosomal protein L12P (L7/L12) 2066780:2067160 reverse MW:13187 | 1.1 | 0.9 | 0.5 | 0.3 | 0.3 | 0.5 |
| Bbr_1676 | rplJ LSU ribosomal protein L10P 2067270:2067791 reverse MW:18702 | 1.4 | 1.1 | 0.7 | 0.6 | 0.3 | 0.5 |
| Bbr_1677 | Bbr_1677 Narrowly conserved hypothetical protein 2068138:2068929 reverse MW:28442 | 1.1 | 1.2 | 1.4 | 1.0 | 0.6 | 1.0 |
| Bbr_1678 | Bbr_1678 Guanine-hypoxanthine permease 2069171:2070565 forward MW:48773 | 1.2 | 1.1 | 0.8 | 0.5 | 0.7 | 0.9 |
| Bbr_1679 | pstB Phosphate transport ATP-binding protein pstB 2071206:2071985 reverse MW:28843 | 1.2 | 1.4 | 0.9 | 1.5 | 0.9 | 0.8 |
| Bbr_1680 | pstA Phosphate transport system permease protein pstA 2072031:2072996 reverse MW:34294 | 1.4 | 1.6 | 1.0 | 0.6 | 1.0 | 0.6 |
| Bbr_1681 | pstC Phosphate transport system permease protein pstC 2073029:2073982 reverse MW:33712 | 1.5 | 1.7 | 0.9 | 0.4 | 0.8 | 0.6 |
| Bbr_1682 | pstS Phosphate-binding protein 2074189:2075319 reverse MW:39202 | 1.8 | 1.6 | 1.7 | 0.8 | 0.8 | 0.4 |
| Bbr_1683 | Bbr_1683 Two-component response regulator 2075573:2076343 reverse MW:28780 | 1.2 | 1.0 | 0.9 | 1.0 | 1.2 | 0.6 |
| Bbr_1684 | Bbr_1684 Phosphate regulon sensor protein phoR 2076396:2077691 reverse MW:46713 | 1.1 | 1.3 | 0.8 | 0.6 | 1.1 | 0.8 |
| Bbr_1685 | Bbr_1685 Transporter, MFS superfamily 2077829:2079136 reverse MW:46719 | 2.1 | 2.2 | 0.4 | 0.4 | 0.6 | 1.3 |
| Bbr_1686 | pfs 5'-methylthioadenosine nucleosidase/S-adenosylhomocysteine nucleosidase 2079404:2080117 reverse MW:24883 | 1.1 | 1.2 | 1.1 | 0.5 | 1.2 | 1.4 |
| Bbr_1687 | aroG1 3-deoxy-7-phosphoheptulonate synthase 2080258:2081490 reverse MW:44208 | 1.3 | 1.7 | 1.7 | 1.3 | 2.2 | 1.8 |
| Bbr_1688 | aroG2 3-deoxy-7-phosphoheptulonate synthase, Phe-sensitive 2081555:2082691 reverse MW:41445 | 1.2 | 1.3 | 2.7 | 1.8 | 1.1 | 2.4 |
| Bbr_1689 | ebgB Evolved beta-galactosidase beta-subunit 2082916:2083389 reverse MW:17448 | 1.2 | 0.7 | 0.7 | 0.9 | 0.8 | 1.0 |
| Bbr_1690 | ebgA Evolved beta-galactosidase alpha subunit 2083389:2086553 reverse MW:118479 | 1.1 | 0.8 | 1.1 | 1.6 | 0.5 | 1.3 |
| Bbr_1691 | Bbr_1691 Beta-phosphoglucomutase 2086692:2087333 reverse MW:23640 | 0.6 | 0.9 | 1.4 | 1.9 | 0.2 | 1.5 |
| Bbr_1692 | Bbr_1692 Transporter, drug/metabolite exporter family 2087396:2088304 reverse MW:32061 | 0.7 | 0.7 | 5.5 | 6.4 | 0.6 | 3.8 |
| Bbr_1693 | kojP Glycosyl hydrolases family 65, Kojibiose phosphorylase 2088301:2090634 reverse MW:88154 | 0.8 | 1.3 | 3.4 | 4.1 | 0.4 | 1.0 |
| Bbr_1694 | Bbr_1694 Sugar-binding protein of ABC transporter system, permease 2090797:2091618 reverse MW:31191 | 0.7 | 0.6 | 0.3 | 0.6 | 0.2 | 0.6 |
| Bbr_1695 | Bbr_1695 Sugar-binding protein of ABC transporter system, permease 2091615:2092559 reverse MW:34929 | 0.6 | 0.5 | 0.2 | 0.2 | 0.1 | 0.7 |
| Bbr_1696 | Bbr_1696 Sugar-binding protein of ABC transporter system 2092584:2093816 reverse MW:45334 | 0.8 | 0.5 | 1.1 | 2.0 | 0.2 | 0.6 |
| Bbr_1697 | Bbr_1697 Transcriptional regulator, LacI family 2094021:2095037 forward MW:37263 | 0.7 | 0.3 | 0.5 | 1.1 | 0.3 | 0.5 |
| Bbr_1698 | Bbr_1698 Multiple antibiotic transport protein marC 2095136:2095750 forward MW:21807 | 0.7 | 0.4 | 1.0 | 2.5 | 0.4 | 0.4 |
| Bbr_1699 | pepC1 Aminopeptidase C 2095831:2097168 reverse MW:50861 | 0.8 | 0.8 | 1.8 | 0.3 | 0.9 | 0.2 |
| Bbr_1700 | pepC2 Aminopeptidase C 2097570:2098913 reverse MW:50128 | 1.3 | 1.9 | 3.3 | 1.2 | 1.1 | 0.4 |
| Bbr_1701 | Bbr_1701 Narrowly conserved hypothetical protein 2099031:2100470 reverse MW:52466 | 0.8 | 0.7 | 0.9 | 1.0 | 0.6 | 0.6 |
| Bbr_1702 | pcp Pyrrolidone-carboxylate peptidase 2100609:2101286 reverse MW:24318 | 1.1 | 1.1 | 0.8 | 0.8 | 0.6 | 0.4 |
| Bbr_1703 | ispD 2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase 2101325:2102170 reverse MW:30195 | 1.2 | 1.2 | 0.6 | 0.7 | 1.0 | 0.5 |
| Bbr_1704 | Bbr_1704 Conserved hypothetical protein 2102241:2103305 reverse MW:37557 | 1.1 | 1.2 | 0.8 | 0.8 | 0.8 | 0.5 |
| Bbr_1705 | Bbr_1705 Peptidase family U32 2103316:2104929 reverse MW:59656 | 1.3 | 1.6 | 0.8 | 0.4 | 0.6 | 0.6 |
| Bbr_1706 | trmD tRNA (Guanine-N1) -methyltransferase 2104988:2105878 forward MW:31900 | 0.9 | 1.0 | 1.3 | 1.7 | 0.7 | 0.5 |
| Bbr_1707 | Bbr_1707 Methyltransferase 2105880:2106461 reverse MW:20851 | 1.0 | 1.3 | 1.9 | 2.9 | 1.1 | 2.0 |
| Bbr_1708 | recG ATP-dependent DNA helicase recG 2106797:2109403 reverse MW:92635 | 0.8 | 0.7 | 0.5 | 0.7 | 1.3 | 3.8 |
| Bbr_1709 | rpmB LSU ribosomal protein L28P 2109502:2109696 reverse MW:6999 | 0.9 | 1.1 | 1.2 | 3.1 | 1.0 | 1.8 |
| Bbr_1710 | rbsK5 Ribokinase 2110100:2111116 forward MW:36008 | 0.7 | 0.5 | 2.1 | 1.1 | 1.2 | 1.7 |
| Bbr_1711 | Bbr_1711 Transporter, MFS superfamily 2111270:2112571 forward MW:46991 | 0.9 | 1.0 | 1.2 | 0.3 | 0.7 | 2.4 |
| Bbr_1712 | Bbr_1712 Transcriptional regulator, MerR family 2112752:2113324 reverse MW:20992 | 0.9 | 1.2 | 6.7 | 4.6 | 0.6 | 5.8 |
| Bbr_1713 | Bbr_1713 Hypothetical protein 2113362:2113751 reverse MW:14615 | 0.8 | 1.0 | 5.5 | 16.6 | 0.9 | 5.0 |
| Bbr_1714 | Bbr_1714 Conserved hypothetical protein with RelB antitoxin domain 2113741:2114064 reverse MW:11595 | 0.8 | 1.1 | 7.8 | 20.5 | 0.6 | 4.7 |
| Bbr_1715 | Bbr_1715 Hypothetical protein 2114061:2114288 reverse MW:8511 | 0.9 | 0.9 | 1.1 | 2.2 | 0.8 | 1.1 |
| Bbr_1716 | Bbr_1716 Transcriptional regulator 2114528:2115598 reverse MW:38117 | 0.9 | 0.8 | 0.7 | 0.7 | 0.7 | 1.4 |
| Bbr_1717 | Bbr_1717 Conserved hypothetical protein 2116302:2116934 reverse MW:24195 | 0.9 | 0.9 | 3.3 | 4.6 | 0.5 | 20.1 |
| Bbr_1718 | Bbr_1718 Hypothetical protein 2117954:2118301 reverse MW:11701 | 0.9 | 1.2 | 2.0 | 3.0 | 1.5 | 0.9 |
| Bbr_1719 | fas Type I multifunctional fatty acid synthase 2119256:2128738 reverse MW:336398 | 1.8 | 1.7 | 0.9 | 1.1 | 1.1 | 1.0 |
| Bbr_1720 | accD Acetyl-/propionyl-CoA carboxylase beta chain 2128778:2130400 reverse MW:57472 | 1.5 | 1.4 | 0.4 | 0.6 | 0.6 | 0.8 |
| Bbr_1721 | accC Acetyl-/propionyl-CoA carboxylase alpha chain 2130393:2132273 reverse MW:67923 | 1.6 | 1.7 | 0.9 | 0.7 | 0.7 | 0.5 |
| Bbr_1722 | BioY BioY protein 2132786:2133385 forward MW:19512 | 0.9 | 1.3 | 3.6 | 5.4 | 0.9 | 0.4 |
| Bbr_1723 | Bbr_1723 Conserved hypothetical protein with possible biotin-(acetyl-CoA carboxylase) ligase domain 2133387:2134349 reverse MW:34252 | 0.4 | 0.1 | 0.2 | 0.8 | 1.3 | 0.3 |
| Bbr_1724 | Bbr_1724 Narrowly conserved hypothetical membrane spanning protein 2134521:2136626 forward MW:78060 | 0.8 | 0.6 | 0.2 | 0.2 | 0.6 | 0.3 |

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|---|---|---|---|---|---|---|---|
| Bbr_1725 | Bbr_1725 Transcriptional regulator 2136705:2137562 forward MW:30298 | 0.9 | 1.0 | 1.6 | 1.1 | 1.8 | 0.5 |
| Bbr_1726 | rlpA LSU ribosomal protein L1P 2137836:2138528 reverse MW:24872 | 1.1 | 1.4 | 2.1 | 2.1 | 1.5 | 0.5 |
| Bbr_1727 | rplK LSU ribosomal protein L11P 2138544:2138975 reverse MW:15245 | 1.0 | 1.0 | 1.6 | 3.1 | 1.0 | 0.5 |
| Bbr_1728 | Bbr_1728 Conserved hypothetical protein 2139592:2140545 forward MW:35899 | 0.9 | 0.7 | 1.3 | 1.1 | 0.5 | 1.1 |
| Bbr_1729 | nusG Transcription antitermination protein nusG 2140901:2141728 reverse MW:29836 | 1.2 | 1.4 | 1.5 | 0.7 | 1.0 | 2.2 |
| Bbr_1730 | secE Protein translocase subunit secE 2141761:2141988 reverse MW:8308 | 0.9 | 1.0 | 1.9 | 0.7 | 1.2 | 3.2 |
| Bbr_1731 | aspC Aspartate aminotransferase 2142318:2143523 reverse MW:42835 | 1.1 | 0.9 | 0.3 | 0.2 | 0.6 | 0.5 |
| Bbr_1732 | Bbr_1732 Polysaccharide deacetylase 2143665:2144927 forward MW:45555 | 1.3 | 1.0 | 0.5 | 0.4 | 0.8 | 0.4 |
| Bbr_1733 | proB Glutamate 5-kinase 2145023:2146156 reverse MW:39218 | 1.2 | 1.7 | 2.4 | 1.3 | 2.0 | 6.4 |
| Bbr_1734 | Bbr_1734 GTP-binding protein, GTP1/OBG family 2146263:2147954 reverse MW:61288 | 1.3 | 1.8 | 3.3 | 1.2 | 2.2 | 8.8 |
| Bbr_1735 | rpmA LSU ribosomal protein L27P 2148021:2148272 reverse MW:8796 | 1.1 | 1.2 | 2.2 | 2.3 | 1.3 | 2.6 |
| Bbr_1736 | rplU LSU ribosomal protein L21P 2148295:2148603 reverse MW:10901 | 1.1 | 1.2 | 2.1 | 3.6 | 1.4 | 2.4 |
| Bbr_1737 | rne Ribonuclease G 2148790:2151852 reverse MW:116212 | 1.1 | 1.4 | 1.1 | 0.2 | 2.7 | 2.3 |
| Bbr_1738 | dapE Succinyl-diaminopimelate desuccinylase 2152295:2153500 reverse MW:43325 | 0.9 | 0.9 | 1.2 | 1.9 | 0.9 | 0.9 |
| Bbr_1739 | Bbr_1739 Transporter 2153606:2154550 forward MW:33588 | 1.2 | 1.0 | 0.6 | 0.5 | 0.6 | 1.1 |
| Bbr_1740 | dapA4 Dihydrodipicolinate synthase 2154626:2155519 reverse MW:31874 | 0.8 | 1.0 | 3.8 | 7.4 | 0.4 | 1.2 |
| Bbr_1741 | Bbr_1741 Conserved hypothetical protein 2155631:2156398 reverse MW:28541 | 0.8 | 0.9 | 2.8 | 3.7 | 0.3 | 1.1 |
| Bbr_1742 | Bbr_1742 L-fucose permease 2156400:2157662 reverse MW:44117 | 0.8 | 0.9 | 2.5 | 3.2 | 0.3 | 1.1 |
| Bbr_1743 | Bbr_1743 Short chain dehydrogenase 2157852:2158679 reverse MW:30388 | 0.6 | 0.6 | 4.0 | 4.5 | 0.4 | 3.9 |
| Bbr_1744 | Bbr_1744 Mandelate racemase 2158784:2160067 reverse MW:47455 | 0.6 | 0.5 | 0.7 | 1.9 | 0.3 | 1.7 |
| Bbr_1745 | Bbr_1745 Transcriptional regulator, LacI family 2160279:2161307 forward MW:37323 | 1.1 | 1.1 | 1.8 | 1.5 | 0.3 | 0.7 |
| Bbr_1746 | Bbr_1746 Transporter 2161289:2162737 reverse MW:50775 | 1.0 | 1.3 | 0.3 | 0.3 | 1.6 | 0.7 |
| Bbr_1747 | Bbr_1747 ATP-binding protein of ABC transporter system 2162734:2163594 reverse MW:29933 | 1.0 | 1.3 | 1.7 | 1.8 | 0.8 | 0.8 |
| Bbr_1748 | Bbr_1748 Acetyltransferase 2164186:2164695 forward MW:18673 | 1.4 | 2.0 | 5.0 | 2.0 | 0.4 | 2.0 |
| Bbr_1749 | Bbr_1749 Maf protein 2164758:2166209 reverse MW:51582 | 0.9 | 0.9 | 0.4 | 0.7 | 0.8 | 0.6 |
| Bbr_1750 | thrB Homoserine kinase 2166347:2167459 reverse MW:38529 | 1.0 | 1.0 | 0.7 | 0.3 | 0.9 | 0.6 |
| Bbr_1751 | thrA Homoserine dehydrogenase 2167554:2168870 reverse MW:45803 | 1.0 | 0.8 | 0.3 | 0.4 | 0.8 | 0.4 |
| Bbr_1753 | lysA Diaminopimelate decarboxylase 2170154:2171776 reverse MW:57299 | 1.1 | 1.0 | 0.4 | 0.5 | 0.9 | 0.9 |
| Bbr_1754 | argS Arginyl-tRNA synthetase 2171779:2173641 reverse MW:67361 | 1.3 | 1.4 | 0.6 | 0.6 | 1.5 | 1.0 |
| Bbr_1755 | Bbr_1755 Transcriptional regulator, TetR family 2173849:2174556 forward MW:26666 | 0.8 | 0.7 | 0.3 | 0.2 | 2.6 | 8.6 |
| Bbr_1756 | Bbr_1756 Macrolide-efflux protein 2174553:2175821 forward MW:45002 | 0.6 | 0.4 | 0.4 | 0.8 | 1.6 | 3.0 |
| Bbr_1757 | murA UDP-N-acetylglucosamine 1-carboxyvinyltransferase 2175870:2177195 reverse MW:47250 | 0.8 | 1.0 | 1.5 | 0.5 | 1.2 | 1.7 |
| Bbr_1758 | nox NADH oxidase H2O-forming 2177489:2178835 forward MW:47798 | 0.4 | 0.1 | 0.1 | 0.3 | 0.6 | 0.4 |
| Bbr_1759 | Bbr_1759 Solute binding protein of ABC transporter system for amino acids 2179275:2180126 forward MW:31371 | 1.0 | 0.8 | 1.3 | 1.4 | 0.8 | 12.6 |
| Bbr_1760 | Bbr_1760 Permease protein of ABC transporter system for amino acids 2180178:2180867 forward MW:25189 | 1.1 | 1.0 | 0.6 | 0.4 | 0.4 | 5.6 |
| Bbr_1761 | Bbr_1761 Permease protein of ABC transporter system for amino acids 2180872:2181660 forward MW:29212 | 1.1 | 1.1 | 1.0 | 1.1 | 0.5 | 2.7 |
| Bbr_1762 | Bbr_1762 Conserved hypothetical protein 2181750:2182304 forward MW:20845 | 1.1 | 1.1 | 0.7 | 0.6 | 0.5 | 1.0 |
| Bbr_1763 | Bbr_1763 ATP-binding protein of ABC transporter system for amino acids 2182359:2183108 forward MW:27092 | 1.3 | 1.1 | 0.5 | 1.2 | 0.6 | 0.6 |
| Bbr_1764 | pyr Dihydroorotate dehydrogenase 2183230:2184393 reverse MW:40963 | 1.0 | 1.1 | 1.3 | 2.8 | 1.5 | 1.0 |
| Bbr_1765 | Bbr_1765 Hypothetical membrane spanning protein 2184456:2185025 reverse MW:19587 | 1.0 | 0.9 | 1.6 | 3.7 | 0.4 | 2.0 |
| Bbr_1766 | leuD 3-isopropylmalate dehydratase small subunit 2185892:2186581 reverse MW:26005 | 1.3 | 0.8 | 0.1 | 0.3 | 0.6 | 0.5 |
| Bbr_1767 | leuC 3-isopropylmalate dehydratase large subunit 2186729:2188132 reverse MW:50313 | 1.3 | 0.7 | 0.2 | 0.3 | 0.6 | 0.4 |
| Bbr_1768 | Bbr_1768 Transcriptional regulator, IclR family 2188329:2189138 forward MW:28582 | 1.1 | 1.8 | 2.3 | 3.2 | 0.7 | 2.3 |
| Bbr_1769 | Bbr_1769 Phosphoesterase 2189272:2190615 reverse MW:48562 | 0.8 | 0.9 | 1.8 | 3.7 | 1.1 | 2.4 |
| Bbr_1770 | ppk Polyphosphate kinase 2191147:2193384 forward MW:83874 | 1.0 | 1.0 | 0.7 | 0.6 | 1.8 | 0.8 |
| Bbr_1771 | Bbr_1771 Phosphohydrolase (MutT/nudix family protein) 2193524:2194954 forward MW:50999 | 0.9 | 1.3 | 3.6 | 9.1 | 2.2 | 2.1 |
| Bbr_1772 | Bbr_1772 Conserved hypothetical protein 2195091:2195765 forward MW:24136 | 0.8 | 1.2 | 2.9 | 3.8 | 2.0 | 1.5 |
| Bbr_1775 | Bbr_1775 Conserved hypothetical protein (possible glycogen debranching enzyme) 2199245:2201194 reverse MW:70355 | 0.9 | 1.0 | 2.3 | 8.2 | 0.3 | 2.5 |
| Bbr_1776 | Bbr_1776 Glucose transport system permease protein 2201246:2201566 reverse MW:11492 | 0.9 | 0.9 | 1.2 | 4.8 | 0.5 | 5.6 |
| Bbr_1777 | upp Uracil phosphoribosyltransferase 2201996:2202637 forward MW:23283 | 0.8 | 0.6 | 0.3 | 0.3 | 1.0 | 0.2 |
| Bbr_1778 | Bbr_1778 Conserved hypothetical protein 2202873:2203352 forward MW:17960 | 0.8 | 0.7 | 0.3 | 0.3 | 1.2 | 0.6 |
| Bbr_1779 | glpQ Glycerophosphoryl diester phosphodiesterase 2203394:2204503 reverse MW:39938 | 0.9 | 0.6 | 0.3 | 0.3 | 1.0 | 0.5 |
| Bbr_1780 | gltX2 Glutamyl-tRNA synthetase 2204529:2205626 reverse MW:40710 | 0.9 | 1.1 | 3.1 | 7.6 | 0.7 | 3.3 |
| Bbr_1781 | clpB ClpB protein 2206094:2208763 reverse MW:96454 | 4.2 | 12.2 | 27.3 | 94.6 | 4.4 | 8.0 |
| Bbr_1782 | Bbr_1782 Permease 2209186:2210115 forward MW:34028 | 0.8 | 0.5 | 0.6 | 0.7 | 0.6 | 0.4 |
| Bbr_1783 | Bbr_1783 Fumarylacetoacetate hydrolase family protein 2210132:2210953 reverse MW:29661 | 0.9 | 1.1 | 1.0 | 0.6 | 1.7 | 1.1 |
| Bbr_1784 | Bbr_1784 Conserved hypothetical membrane spanning protein 2211043:2211768 reverse MW:25911 | 0.8 | 0.6 | 2.0 | 3.3 | 1.0 | 1.6 |
| Bbr_1785 | Bbr_1785 Hypothetical secreted protein 2211921:2212856 forward MW:33891 | 0.5 | 0.3 | 1.9 | 4.4 | 1.0 | 2.2 |
| Bbr_1786 | gif UDP-galactopyranose mutase 2212964:2214220 reverse MW:48065 | 1.2 | 0.9 | 2.2 | 1.5 | 0.8 | 0.8 |
| Bbr_1788 | Bbr_1788 Glycosyltransferase involved in cell wall biogenesis 2214947:2215996 forward MW:39265 | 1.0 | 1.1 | 1.4 | 0.9 | 0.8 | 0.6 |
| Bbr_1789 | Bbr_1789 Conserved hypothetical membrane spanning protein 2216027:2217379 reverse MW:48752 | 1.0 | 0.9 | 0.6 | 1.6 | 0.3 | 0.7 |
| Bbr_1790 | Bbr_1790 Phosphoglycerol transferase 2217524:2219776 forward MW:83788 | 1.0 | 0.7 | 0.3 | 0.7 | 0.2 | 0.2 |
| Bbr_1791 | Bbr_1791 Phosphoglycerol transferase 2219845:2222148 forward MW:85509 | 1.0 | 1.1 | 0.5 | 0.6 | 0.3 | 0.3 |
| Bbr_1792 | Bbr_1792 Glycosyltransferase 2222175:2223698 reverse MW:55897 | 0.7 | 0.5 | 0.2 | 0.4 | 0.3 | 0.4 |
| Bbr_1793 | Bbr_1793 ATP-binding protein ABC transporter system for polysaccharides 2223723:2224967 reverse MW:46081 | 0.7 | 0.6 | 0.2 | 0.3 | 0.3 | 0.3 |
| Bbr_1794 | Bbr_1794 Permease protein of ABC transporter systemfor polysaccharides 2224991:2225824 reverse MW:32031 | 0.8 | 0.7 | 0.1 | 0.3 | 0.4 | 0.3 |
| Bbr_1795 | Bbr_1795 Alpha-L-Rha alpha-1,2-L-rhamnosyltransferase/alpha-L-Rha alpha-1,3-L-rhamnosyltransferase 2225846:2227846 reverse MW:76790 | 0.8 | 0.7 | 0.2 | 0.3 | 0.4 | 0.3 |
| Bbr_1796 | Bbr_1796 Glycosyltransferase 2227884:2229203 reverse MW:49927 | 0.9 | 1.0 | 0.9 | 0.9 | 0.5 | 1.0 |
| Bbr_1797 | rmlA Glucose-1-phosphate thymidylyltransferase 2229216:2230112 reverse MW:33041 | 0.9 | 0.8 | 1.3 | 1.0 | 0.8 | 0.8 |
| Bbr_1798 | rmlC/rmlD dTDP-4-dehydrorhamnose 3,5-epimerase/dTDP-4-dehydrorhamnose reductase 2230253:2231704 reverse MW:53258 | 1.0 | 1.0 | 0.5 | 0.3 | 1.2 | 1.0 |
| Bbr_1799 | rmlB dTDP-glucose 4,6-dehydratase 2231712:2232734 reverse MW:38590 | 1.1 | 1.2 | 0.9 | 0.8 | 1.2 | 0.6 |
| Bbr_1800 | Bbr_1800 Conserved hypothetical membrane spanning protein 2232784:2234988 reverse MW:80510 | 1.2 | 1.3 | 0.5 | 1.0 | 0.6 | 0.8 |
| Bbr_1801 | Bbr_1801 Glycosyltransferase involved in cell wall biogenesis 2235043:2235984 forward MW:34737 | 1.0 | 0.9 | 0.3 | 0.3 | 0.7 | 0.3 |
| Bbr_1802 | lytC Glycosyl hydrolases family 25,lysozyme 2236025:2237884 reverse MW:66383 | 1.0 | 1.0 | 0.7 | 0.9 | 0.8 | 1.3 |
| Bbr_1803 | Bbr_1803 Transcriptional regulator, LytR family 2238159:2239565 reverse MW:49495 | 1.0 | 1.0 | 0.5 | 0.7 | 0.6 | 1.8 |

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|---|---|---|---|---|---|---|---|
| Bbr_1804 | Bbr_1804 Permease protein of ABC transporter system 2239969:2241429 forward MW:51414 | 0.8 | 0.7 | 0.6 | 0.4 | 0.6 | 0.5 |
| Bbr_1805 | Bbr_1805 ATP-binding protein of ABC transporter system 2241426:2242610 forward MW:41369 | 0.9 | 0.8 | 0.5 | 0.4 | 0.6 | 0.5 |
| Bbr_1806 | Bbr_1806 Phosphohydrolase 2242971:2243735 forward MW:28574 | 1.2 | 1.2 | 1.2 | 2.5 | 1.2 | 0.7 |
| Bbr_1807 | Bbr_1807 Conserved hypothetical protein 2243853:2244713 reverse MW:31251 | 1.2 | 1.5 | 0.7 | 0.9 | 0.8 | 2.6 |
| Bbr_1808 | Bbr_1808 Kup system potassium uptake protein 2244997:2247408 reverse MW:88711 | 1.2 | 0.9 | 0.1 | 0.1 | 0.5 | 0.5 |
| Bbr_1809 | Bbr_1809 DNase, TatD family 2247607:2248566 reverse MW:35159 | 1.2 | 1.5 | 6.7 | 13.2 | 1.2 | 2.7 |
| Bbr_1810 | Bbr_1810 ATP-binding and permease protein of ABC transporter system 2248821:2250626 reverse MW:67770 | 0.4 | 0.2 | 0.7 | 0.7 | 0.3 | 1.0 |
| Bbr_1811 | Bbr_1811 ATP-binding and permease protein of ABC transporter system 2250826:2252736 reverse MW:70237 | 0.4 | 0.2 | 0.6 | 1.7 | 0.7 | 1.2 |
| Bbr_1812 | Bbr_1812 ATPase 2253444:2254760 reverse MW:50223 | 1.1 | 1.2 | 5.0 | 3.4 | 0.6 | 7.8 |
| Bbr_1814 | oppA3 Oligopeptide-binding protein oppA 2255781:2257514 reverse MW:63159 | 1.9 | 2.7 | 1.6 | 2.7 | 0.5 | 0.8 |
| Bbr_1815 | oppD3 Oligopeptide transport ATP-binding protein oppD 2257546:2259615 reverse MW:75760 | 1.1 | 1.1 | 2.1 | 2.7 | 0.8 | 1.5 |
| Bbr_1816 | oppC2 Oligopeptide transport system permease protein oppC 2259702:2260700 reverse MW:35767 | 0.9 | 1.2 | 5.7 | 8.2 | 1.1 | 3.2 |
| Bbr_1817 | oppB3 Oligopeptide transport system permease protein oppB 2260725:2261708 reverse MW:36021 | 1.1 | 1.5 | 10.1 | 7.0 | 0.6 | 7.9 |
| Bbr_1818 | pepC3 Aminopeptidase C 2262000:2263502 forward MW:57099 | 1.7 | 1.8 | 0.6 | 0.7 | 1.0 | 0.6 |
| Bbr_1819 | Bbr_1819 Narrowly conserved hypothetical protein 2263583:2263876 reverse MW:10774 | 0.9 | 0.7 | 12.5 | 18.9 | 0.9 | 2.4 |
| Bbr_1820 | metG Methionyl-tRNA synthetase 2264386:2266251 reverse MW:69114 | 1.1 | 1.2 | 0.5 | 0.3 | 1.0 | 0.6 |
| Bbr_1821 | Bbr_1821 Narrowly conserved hypothetical protein 2266528:2267160 forward MW:23080 | 0.6 | 0.7 | 0.3 | 0.5 | 0.5 | 0.2 |
| Bbr_1822 | Bbr_1822 Narrowly conserved hypothetical protein 2267151:2267498 forward MW:12580 | 0.6 | 0.5 | 0.3 | 1.2 | 0.3 | 0.4 |
| Bbr_1823 | Bbr_1823 Tetrapyrrole (Corrin/Porphyrin) methylase family protein 2267618:2268637 reverse MW:36544 | 1.1 | 1.4 | 1.3 | 0.9 | 1.7 | 2.8 |
| Bbr_1824 | Bbr_1824 Melibiose carrier protein 2269297:2270715 reverse MW:50387 | 1.1 | 1.1 | 2.8 | 0.7 | 0.9 | 0.7 |
| Bbr_1825 | Bbr_1825 Conserved hypothetical protein 2270820:2271761 forward MW:33178 | 1.0 | 1.3 | 2.0 | 1.7 | 0.9 | 1.1 |
| Bbr_1826 | Bbr_1826 ATP-binding and permease protein of ABC transporter system 2271770:2273584 reverse MW:66099 | 1.9 | 9.1 | 23.9 | 2.8 | 2.4 | 2.4 |
| Bbr_1827 | Bbr_1827 ATP-binding and permease protein of ABC transporter system 2273731:2275599 reverse MW:68162 | 2.0 | 8.8 | 34.5 | 5.9 | 3.3 | 5.4 |
| Bbr_1828 | Bbr_1828 Transcriptional regulator, MarR family 2275783:2276304 reverse MW:19720 | 1.8 | 6.0 | 39.6 | 47.6 | 1.1 | 3.3 |
| Bbr_1830 | maa Maltose O-acetyltransferase 2279495:2280061 reverse MW:20557 | 1.0 | 0.8 | 0.5 | 0.4 | 0.6 | 0.4 |
| Bbr_1831 | Bbr_1831 Transcriptional regulator, LacI family 2280153:2281226 reverse MW:39509 | 1.1 | 0.9 | 0.9 | 0.6 | 0.6 | 0.4 |
| Bbr_1832 | Bbr_1832 Hypothetical protein 2281349:2282128 reverse MW:29401 | 0.8 | 0.5 | 0.3 | 0.5 | 0.2 | 2.4 |
| Bbr_1833 | lacZ7 Beta-galactosidase 2282195:2284291 reverse MW:78187 | 0.9 | 0.7 | 2.0 | 1.2 | 0.2 | 3.1 |
| Bbr_1834 | rbsC2 Ribose transport system permease protein rbsC 2284353:2285294 reverse MW:32417 | 0.8 | 0.7 | 0.8 | 1.3 | 0.2 | 1.2 |
| Bbr_1835 | rbsA2 Ribose transport ATP-binding protein rbsA 2285299:2286858 reverse MW:56349 | 1.0 | 0.8 | 1.3 | 2.2 | 0.3 | 1.7 |
| Bbr_1836 | Bbr_1836 Sugar-binding protein of ABC transporter system 2286883:2288061 reverse MW:41473 | 0.9 | 0.6 | 1.1 | 1.0 | 0.3 | 2.3 |
| Bbr_1839 | aap5 Amino acid permease 2293243:2294766 reverse MW:55942 | 1.1 | 1.3 | 1.1 | 1.4 | 0.8 | 0.8 |
| Bbr_1840 | Bbr_1840 Permease protein of ABC transporter system 2295021:2298779 reverse MW:135013 | 0.6 | 0.4 | 0.1 | 0.1 | 0.7 | 0.2 |
| Bbr_1841 | Bbr_1841 ATP-binding protein of ABC transporter system 2298789:2299490 reverse MW:25434 | 0.8 | 0.7 | 1.5 | 3.6 | 1.5 | 2.5 |
| Bbr_1842 | aap6 Amino acid permease 2299973:2301445 forward MW:52803 | 1.5 | 1.2 | 0.6 | 0.5 | 0.4 | 0.3 |
| Bbr_1843 | Bbr_1843 Narrowly conserved hypothetical membrane spanning protein 2301497:2302102 reverse MW:22483 | 0.5 | 0.1 | 0.2 | 0.2 | 0.5 | 0.6 |
| Bbr_1844 | Bbr_1844 Permease protein of ABC transporter system for sugars 2302253:2303095 reverse MW:31025 | 0.4 | 0.1 | 0.2 | 0.1 | 0.5 | 0.7 |
| Bbr_1845 | Bbr_1845 Permease protein of ABC transporter system for sugars 2303095:2303949 reverse MW:31311 | 0.4 | 0.1 | 0.2 | 0.2 | 0.5 | 0.9 |
| Bbr_1846 | Bbr_1846 Transcriptional regulator, LacI family 2304320:2305336 forward MW:36993 | 0.8 | 0.7 | 1.7 | 0.7 | 1.0 | 2.0 |
| Bbr_1847 | Bbr_1847 Solute binding protein of ABC transporter system for sugars 2305544:2306872 reverse MW:48699 | 0.4 | 0.1 | 0.0 | 0.1 | 0.2 | 0.6 |
| Bbr_1848 | Bbr_1848 Phosphoglycerate mutase family protein 2307285:2307998 reverse MW:26063 | 0.5 | 0.4 | 0.8 | 1.2 | 1.2 | 1.2 |
| Bbr_1849 | Bbr_1849 Narrowly conserved hypothetical protein 2308070:2308447 forward MW:13266 | 0.8 | 0.8 | 1.2 | 1.4 | 1.3 | 0.3 |
| Bbr_1850 | Bbr_1850 Chromate reductase/NADPH-dependent FMN reductase/Oxygen-insensitive NADPH nitroreductase 2308543:2309310 forward MW:283 | 0.8 | 0.6 | 0.3 | 0.3 | 2.5 | 0.2 |
| Bbr_1851 | pip1 Phage infection protein 2309476:2312223 forward MW:99153 | 0.6 | 0.4 | 0.1 | 0.1 | 1.6 | 0.2 |
| Bbr_1852 | pip2 Phage infection protein 2312220:2314559 forward MW:82509 | 0.6 | 0.4 | 0.1 | 0.1 | 1.4 | 0.3 |
| Bbr_1853 | Bbr_1853 SIR2 family protein 2321043:2321693 forward MW:23996 | 1.3 | 1.7 | 0.8 | 0.5 | 1.9 | 3.4 |
| Bbr_1854 | tdcB Threonine dehydratase 2321873:2323120 reverse MW:44000 | 1.2 | 1.3 | 1.4 | 0.5 | 1.6 | 0.4 |
| Bbr_1855 | Bbr_1855 Oligo-1,6-glucosidase 2323400:2325223 reverse MW:68221 | 0.5 | 0.2 | 0.6 | 0.6 | 0.5 | 0.5 |
| Bbr_1856 | Bbr_1856 Raffinose synthase or seed imbibition protein Sip1/Alpha-galactosidase 2325344:2327206 reverse MW:68201 | 1.1 | 0.9 | 0.7 | 1.1 | 0.4 | 0.7 |
| Bbr_1857 | Bbr_1857 Alpha-1,4-glucosidase 2327238:2328908 reverse MW:62456 | 1.2 | 1.5 | 1.3 | 2.0 | 1.1 | 1.2 |
| Bbr_1858 | Bbr_1858 Permease protein of ABC transporter system for sugars 2329009:2329833 reverse MW:30009 | 1.0 | 1.4 | 2.7 | 1.9 | 0.5 | 0.6 |
| Bbr_1859 | Bbr_1859 Permease protein of ABC transporter system for sugars 2329836:2330858 reverse MW:37053 | 1.1 | 1.9 | 2.5 | 0.7 | 0.7 | 0.6 |
| Bbr_1860 | Bbr_1860 Solute binding protein of ABC transporter system for sugars 2330880:2332205 reverse MW:46740 | 1.1 | 2.2 | 8.8 | 15.6 | 0.4 | 0.7 |
| Bbr_1861 | Bbr_1861 Conserved hypothetical protein 2332453:2333571 reverse MW:42141 | 1.4 | 3.6 | 7.1 | 1.8 | 0.6 | 0.5 |
| Bbr_1862 | Bbr_1862 Solute binding protein of ABC transporter system for sugars 2333633:2334961 reverse MW:47169 | 1.7 | 4.1 | 12.9 | 3.7 | 0.7 | 0.8 |
| Bbr_1863 | Bbr_1863 Transcriptional regulator, LacI family 2335171:2336199 forward MW:37001 | 1.4 | 2.3 | 3.6 | 2.4 | 0.3 | 1.0 |
| Bbr_1864 | Bbr_1864 Transcriptional regulator, LacI family 2336316:2337335 forward MW:36670 | 1.5 | 2.1 | 1.8 | 1.6 | 0.6 | 0.6 |
| Bbr_1865 | Bbr_1865 Raffinose transport system permease protein 2337392:2338258 reverse MW:31991 | 0.5 | 0.5 | 0.5 | 0.5 | 0.4 | 0.4 |
| Bbr_1866 | Bbr_1866 Raffinose transport system permease protein 2338277:2339224 reverse MW:35136 | 0.3 | 0.3 | 0.9 | 0.8 | 0.3 | 0.6 |
| Bbr_1867 | Bbr_1867 Raffinose-binding protein 2339246:2340535 reverse MW:47102 | 0.5 | 0.5 | 2.8 | 3.0 | 0.5 | 0.7 |
| Bbr_1868 | Bbr_1868 Transcriptional repressor, ROK family 2340708:2341916 forward MW:42332 | 1.1 | 0.8 | 1.5 | 3.2 | 0.6 | 0.7 |
| Bbr_1869 | aga Alpha-galactosidase 2342029:2344344 reverse MW:84110 | 0.7 | 0.4 | 0.6 | 0.7 | 0.4 | 0.5 |
| Bbr_1870 | mesJ tRNA-specific adenosine deaminase 2344461:2344892 reverse MW:14923 | 1.0 | 1.2 | 3.2 | 11.0 | 0.8 | 0.7 |
| Bbr_1871 | nhaP Na+/H+ antiporter nhaP 2345344:2347416 forward MW:75710 | 1.1 | 1.3 | 1.0 | 1.1 | 0.6 | 0.5 |
| Bbr_1872 | Bbr_1872 Conserved hypothetical membrane spanning protein with DUF81 domain 2347458:2348261 reverse MW:27973 | 1.0 | 1.0 | 1.9 | 3.7 | 0.4 | 2.8 |
| Bbr_1873 | Bbr_1873 Phospholipase/carboxylesterase 2348373:2349131 reverse MW:27629 | 0.7 | 0.4 | 0.8 | 0.7 | 0.6 | 0.6 |
| Bbr_1874 | Bbr_1874 Narrowly conserved hypothetical membrane spanning protein 2349189:2350058 reverse MW:30340 | 0.7 | 0.6 | 2.9 | 7.9 | 0.8 | 0.5 |
| Bbr_1875 | dcd Deoxycytidine triphosphate deaminase 2350415:2350996 forward MW:21490 | 1.1 | 1.2 | 1.4 | 1.0 | 0.8 | 0.5 |
| Bbr_1876 | Bbr_1876 Conserved hypothetical protein 2351059:2352438 forward MW:47442 | 1.0 | 1.1 | 0.7 | 0.4 | 0.9 | 0.7 |
| Bbr_1877 | pacL2 Calcium-transporting ATPase 2352528:2355518 reverse MW:105423 | 0.5 | 0.3 | 1.1 | 1.2 | 0.6 | 0.8 |
| Bbr_1878 | Bbr_1878 Hypothetical protein 2355671:2355838 reverse MW:5710 | 0.4 | 0.2 | 1.1 | 1.2 | 1.6 | 0.8 |
| Bbr_1879 | Bbr_1879 PTS system, glucose-specific IIABC component 2355886:2356398 reverse MW:16795 | 0.5 | 0.2 | 0.9 | 1.3 | 0.7 | 0.8 |
| Bbr_1880 | Bbr_1880 PTS system, N-acetylglucosamine-specific IIBC component 2356508:2358046 reverse MW:54407 | 0.4 | 0.1 | 0.4 | 0.2 | 1.7 | 0.6 |
| Bbr_1881 | Bbr_1881 Transporter 2358348:2359562 reverse MW:42736 | 1.0 | 0.9 | 1.0 | 0.8 | 0.8 | 0.6 |
| Bbr_1882 | Bbr_1882 SpoU rRNA methylase family protein 2359650:2360648 forward MW:35331 | 0.9 | 0.9 | 1.1 | 0.6 | 1.8 | 0.4 |

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|---|---|---|---|---|---|---|---|
| Bbr_1883 | Bbr_1883 Aldose 1-epimerase family protein 2360700:2361560 reverse MW:31113 | 1.0 | 0.9 | 2.6 | 2.9 | 0.7 | 0.6 |
| Bbr_1884 | galT2 Galactose-1-phosphate uridylyltransferase 2361615:2363126 reverse MW:55795 | 1.0 | 0.9 | 3.6 | 7.9 | 0.5 | 0.5 |
| Bbr_1885 | Bbr_1885 Conserved hypothetical protein 2363304:2364716 reverse MW:53440 | 1.0 | 0.8 | 0.6 | 0.5 | 0.8 | 0.5 |
| Bbr_1886 | Bbr_1886 Narrowly conserved hypothetical secreted protein 2364707:2365567 reverse MW:30152 | 1.0 | 0.8 | 0.4 | 0.7 | 0.3 | 0.6 |
| Bbr_1887 | Bbr_1887 Sortase 2365551:2366534 reverse MW:36059 | 1.2 | 1.0 | 1.0 | 3.1 | 0.3 | 0.6 |
| Bbr_1888 | Bbr_1888 Cell surface protein with gram positive anchor and Cna protein B-type domains 2366615:2368213 reverse MW:55040 | 1.2 | 0.9 | 0.3 | 0.6 | 0.3 | 0.3 |
| Bbr_1889 | Bbr_1889 Cell surface protein with gram positive anchor domain 2368278:2376299 reverse MW:274479 | 1.3 | 1.2 | 0.3 | 0.7 | 0.5 | 0.4 |
| Bbr_1890 | Bbr_1890 ATP-binding protein of ABC transporter system for sugars 2376743:2377870 reverse MW:40697 | 0.4 | 0.1 | 0.1 | 0.3 | 0.4 | 0.2 |
| Bbr_1891 | Bbr_1891 Transcriptional regulator, GntR family 2378191:2378931 reverse MW:27498 | 0.6 | 0.3 | 1.7 | 0.7 | 0.5 | 1.1 |
| Bbr_1892 | Bbr_1892 PTS system, IIC component 2379059:2380438 reverse MW:47425 | 0.4 | 0.1 | 0.8 | 0.3 | 0.2 | 0.8 |
| Bbr_1893 | Bbr_1893 PTS system, IIB component 2380535:2380831 reverse MW:10259 | 0.4 | 0.1 | 1.0 | 0.5 | 0.3 | 0.9 |
| Bbr_1894 | Bbr_1894 PTS system, IIA component 2380880:2381320 reverse MW:15373 | 0.4 | 0.1 | 0.9 | 1.7 | 0.4 | 1.3 |
| Bbr_1895 | Bbr_1895 Glycosyltransferase 2381593:2382753 reverse MW:43621 | 1.1 | 1.0 | 0.7 | 0.5 | 1.2 | 0.5 |
| Bbr_1896 | virR Two-component response regulator virR 2382856:2383647 forward MW:29456 | 0.8 | 0.8 | 2.5 | 4.6 | 1.3 | 0.9 |
| Bbr_1897 | virS Two-component sensor kinase virS 2383647:2384969 forward MW:48021 | 0.9 | 0.8 | 1.2 | 1.4 | 1.1 | 0.5 |
| Bbr_1898 | nrdF Ribonucleoside-diphosphate reductase beta chain 2384973:2385965 reverse MW:37711 | 0.8 | 0.7 | 1.1 | 0.8 | 0.8 | 1.2 |
| Bbr_1899 | nrdE Ribonucleoside-diphosphate reductase alpha chain 2386270:2388465 reverse MW:81826 | 0.7 | 0.6 | 0.6 | 0.5 | 0.6 | 2.8 |
| Bbr_1900 | nrdI NrdI protein 2388474:2388974 reverse MW:17948 | 0.7 | 0.7 | 1.4 | 0.7 | 0.7 | 3.7 |
| Bbr_1901 | nrdH Glutaredoxin nrdH 2388971:2389237 reverse MW:9514 | 0.7 | 0.6 | 1.3 | 0.9 | 1.0 | 2.3 |
| Bbr_1902 | Bbr_1902 Hypothetical membrane spanning protein 2389787:2390440 reverse MW:24584 | 1.5 | 3.8 | 1.7 | 1.5 | 0.5 | 0.6 |
| Bbr_1903 | bgl4 Beta-glucosidase 2390433:2392934 reverse MW:88406 | 1.5 | 4.1 | 2.2 | 1.0 | 0.7 | 0.8 |
| Bbr_1904 | Bbr_1904 Narrowly conserved hypothetical protein with helix-turn-helix motif 2393233:2393883 reverse MW:24201 | 0.9 | 1.1 | 2.3 | 2.9 | 0.3 | 4.1 |
| Bbr_1905 | Bbr_1905 Narrowly conserved hypothetical protein 2393864:2394547 reverse MW:25787 | 1.1 | 1.2 | 1.6 | 1.5 | 0.2 | 11.5 |
| Bbr_1906 | Bbr_1906 Potassium channel protein 2394741:2395307 forward MW:20757 | 1.0 | 1.2 | 1.8 | 3.5 | 0.3 | 10.6 |
| Bbr_1907 | bgl5 Beta-glucosidase 2395432:2398335 reverse MW:105871 | 1.4 | 1.8 | 2.3 | 5.7 | 0.3 | 2.0 |
| Bbr_1908 | Bbr_1908 Serine/threonine protein kinase 2398852:2401044 forward MW:76574 | 0.9 | 1.1 | 0.3 | 0.3 | 1.7 | 1.1 |
| Bbr_1909 | Bbr_1909 Conserved hypothetical protein 2401157:2402134 forward MW:34974 | 1.2 | 1.7 | 1.2 | 0.3 | 1.3 | 0.9 |
| Bbr_1910 | Bbr_1910 Conserved hypothetical secreted protein with G5 and DUF348 domains 2402655:2404145 forward MW:52943 | 1.2 | 1.3 | 0.5 | 0.2 | 0.6 | 1.1 |
| Bbr_1911 | ksgA Dimethyladenosine transferase 2404166:2405095 forward MW:33027 | 1.1 | 1.2 | 0.4 | 0.3 | 0.6 | 0.8 |
| Bbr_1912 | ispE 4-diphosphocytidyl-2-C-methyl-D-erythritol kinase 2405092:2406039 forward MW:32932 | 1.0 | 1.0 | 0.2 | 0.4 | 0.5 | 0.7 |
| Bbr_1913 | Bbr_1913 Narrowly conserved hypothetical protein 2406085:2406714 forward MW:22490 | 0.9 | 0.8 | 0.5 | 0.3 | 0.6 | 0.5 |
| Bbr_1914 | pcnA tRNA nucleotidyltransferase 2406843:2408285 reverse MW:54544 | 1.1 | 1.2 | 3.2 | 2.4 | 0.8 | 0.6 |
| Bbr_1915 | Bbr_1915 Phosphohydrolase (MutT/nudix family protein) 2408348:2409319 forward MW:35334 | 0.9 | 1.0 | 1.0 | 0.7 | 1.4 | 0.9 |
| Bbr_1916 | Bbr_1916 Narrowly conserved hypothetical secreted protein 2409316:2411469 forward MW:76262 | 1.0 | 1.0 | 0.2 | 0.5 | 0.6 | 0.6 |
| Bbr_1917 | Bbr_1917 Conserved hypothetical membrane spanning protein with virulence factor mviN domain 2411466:2415245 forward MW:134567 | 1.0 | 0.9 | 0.3 | 0.2 | 0.7 | 0.2 |
| Bbr_1918 | trxB2 Thioredoxin reductase 2415447:2416466 forward MW:35202 | 0.9 | 1.4 | 4.3 | 0.8 | 0.8 | 1.1 |
| Bbr_1919 | parB2 Chromosome partitioning protein parB 2416583:2417848 reverse MW:45472 | 1.1 | 1.0 | 0.5 | 0.3 | 0.5 | 0.4 |
| Bbr_1920 | parA3 Chromosome partitioning protein parA 2417848:2418816 reverse MW:34972 | 0.9 | 1.0 | 1.8 | 1.3 | 0.4 | 0.6 |
| Bbr_1921 | gidB Methyltransferase gidB (Glucose inhibited division protein B) 2419069:2419734 reverse MW:24378 | 0.8 | 0.6 | 1.2 | 0.8 | 0.2 | 0.3 |
| Bbr_1922 | jag Jag protein 2419858:2420394 reverse MW:20274 | 0.8 | 0.5 | 0.7 | 0.4 | 0.4 | 0.3 |
| Bbr_1923 | YidC Inner membrane protein (Preprotein translocase subunit YidC) 2420517:2421527 reverse MW:38467 | 1.0 | 0.8 | 1.1 | 0.3 | 0.5 | 1.6 |
| Bbr_1924 | Bbr_1924 Conserved hypothetical protein with DUF37 domain 2421524:2421841 reverse MW:12274 | 1.0 | 1.0 | 1.1 | 0.7 | 0.5 | 2.8 |
| Bbr_1925 | rnpA Ribonuclease P protein component 2421845:2422195 reverse MW:13121 | 1.1 | 1.3 | 1.5 | 1.1 | 0.7 | 2.0 |
| Bbr_1926 | rpmH LSU ribosomal protein L34P 2422227:2422361 reverse MW:5377 | 1.1 | 1.1 | 1.0 | 0.9 | 0.7 | 1.6 |
| rRNA16s | rRNA16s | 2.1 | 3.6 | 1.2 | 1.1 | 5.3 | 0.4 |
| tRNA-Ala | tRNA-Ala | 0.9 | 1.1 | 1.6 | 2.3 | 0.6 | 2.3 |
| tRNA-Arg | tRNA-Arg | 0.9 | 1.4 | 5.1 | 2.4 | 1.3 | 1.9 |
| tRNA-Asn | tRNA-Asn | 0.9 | 1.5 | 7.3 | 17.7 | 0.6 | 3.7 |
| tRNA-Asp | tRNA-Asp | 0.8 | 1.1 | 2.3 | 3.0 | 0.5 | 2.1 |
| tRNA-Cys | tRNA-Cys | 0.8 | 1.5 | 2.6 | 1.3 | 0.8 | 3.2 |
| tRNA-Gln | tRNA-Gln | 0.9 | 0.8 | 0.3 | 0.5 | 0.3 | 0.8 |
| tRNA-Glu | tRNA-Glu | 0.6 | 0.7 | 0.5 | 0.4 | 0.3 | 0.8 |
| tRNA-Gly | tRNA-Gly | 0.6 | 0.9 | 2.4 | 0.6 | 0.9 | 4.8 |
| tRNA-His | tRNA-His | 0.7 | 0.8 | 1.0 | 2.4 | 0.5 | 2.2 |
| tRNA-Leu | tRNA-Leu | 0.8 | 1.0 | 2.1 | 2.1 | 1.2 | 11.3 |
| tRNA-Lys | tRNA-Lys | 0.8 | 1.1 | 5.6 | 29.4 | 0.5 | 3.8 |
| tRNA-Met | tRNA-Met | 0.8 | 1.0 | 2.8 | 3.1 | 0.6 | 10.3 |
| tRNA-Phe | tRNA-Phe | 0.8 | 1.2 | 6.4 | 6.1 | 1.0 | 3.1 |
| tRNA-Pro | tRNA-Pro | 1.1 | 2.1 | 7.5 | 3.6 | 1.0 | 2.3 |
| tRNA-Ser | tRNA-Ser | 0.7 | 1.1 | 1.5 | 3.1 | 1.1 | 3.3 |
| tRNA-Thr | tRNA-Thr | 1.0 | 1.3 | 1.1 | 0.7 | 0.6 | 0.9 |
| tRNA-Trp | tRNA-Trp | 0.9 | 1.2 | 2.2 | 2.1 | 1.0 | 5.3 |
| tRNA-Tyr | tRNA-Tyr | 0.8 | 1.1 | 0.9 | 2.1 | 0.5 | 0.8 |
| tRNA-unknown | tRNA-Val | 0.9 | 1.3 | 3.3 | 6.2 | 0.6 | 4.0 |
| tRNA-Val | tRNA-unknown | 1.0 | 1.4 | 1.5 | 1.4 | 1.1 | 1.2 |