

## Misc. parameters

<b>WID</b>	<b>Name</b>
<u>Parameter_0001</u>	<u>equilibriumSuperhelicalDensity</u>
<u>Parameter_0002</u>	<u>relaxedBasesPerTurn</u>
<u>Parameter_0003</u>	<u>supercoiledSuperhelicalDensityTolerance</u>
<u>Parameter_0004</u>	<u>numFtsZSubunitsPerFilament</u>
<u>Parameter_0005</u>	<u>numFtsZSubunitsPerNm</u>
<u>Parameter_0006</u>	<u>density</u>
<u>Parameter_0007</u>	<u>cellInitialDryWeight</u>
<u>Parameter_0008</u>	<u>dryWeightFractionCarbohydrate</u>
<u>Parameter_0009</u>	<u>dryWeightFractionDNA</u>
<u>Parameter_0010</u>	<u>dryWeightFractionIon</u>
<u>Parameter_0011</u>	<u>dryWeightFractionLipid</u>
<u>Parameter_0012</u>	<u>dryWeightFractionPolyamine</u>
<u>Parameter_0013</u>	<u>dryWeightFractionProtein</u>
<u>Parameter_0014</u>	<u>dryWeightFractionRNA</u>
<u>Parameter_0015</u>	<u>dryWeightFractionVitamin</u>
<u>Parameter_0016</u>	<u>fractionWetWeight</u>
<u>Parameter_0017</u>	<u>initialBiomassConcentration</u>
<u>Parameter_0018</u>	<u>initialFractionAAsInMonomers</u>
<u>Parameter_0019</u>	<u>initialFractionNTPsInRNAs</u>
<u>Parameter_0020</u>	<u>timeAveragedCellWeight</u>
<u>Parameter_0021</u>	<u>geneExpressionRobustness</u>
<u>Parameter_0022</u>	<u>weightFractionMRNA</u>
<u>Parameter_0023</u>	<u>weightFractionRRNA16S</u>
<u>Parameter_0024</u>	<u>weightFractionRRNA23S</u>
<u>Parameter_0025</u>	<u>weightFractionRRNA5S</u>
<u>Parameter_0026</u>	<u>weightFractionSRNA</u>
<u>Parameter_0027</u>	<u>weightFractionTRNA</u>
<u>Parameter_0028</u>	<u>stateExpectations_activelyTranscribing</u>
<u>Parameter_0029</u>	<u>stateExpectations_specificallyBound</u>
<u>Parameter_0030</u>	<u>stateExpectations_nonSpecificallyBound</u>
<u>Parameter_0031</u>	<u>stateExpectations_free</u>

<u>Parameter_0036</u>	<u>cellCycleLength</u>
<u>Parameter_0037</u>	<u>cytokinesisDuration</u>
<u>Parameter_0038</u>	<u>replicationDuration</u>
<u>Parameter_0039</u>	<u>replicationInitiationDuration</u>
<u>Parameter_0040</u>	<u>smcSepNt</u>
<u>Parameter_0041</u>	<u>smcSepProbCenter</u>
<u>Parameter_0042</u>	<u>gtpCost</u>
<u>Parameter_0043</u>	<u>rateFilamentBindingMembrane</u>
<u>Parameter_0044</u>	<u>rateFilamentDissociation</u>
<u>Parameter_0045</u>	<u>rateFtsZGtpHydrolysis</u>
<u>Parameter_0046</u>	<u>strandBreakClassification_doubleStrandBreakSeparation</u>
<u>Parameter_0047</u>	<u>strandBreakClassification_segmentLength</u>
<u>Parameter_0048</u>	<u>doubleStrandBreakSeparation</u>
<u>Parameter_0049</u>	<u>HR_PoIA_ResectionLength</u>
<u>Parameter_0050</u>	<u>HR_RecA_Spacing</u>
<u>Parameter_0051</u>	<u>HR_RecU_CleavagePosition</u>
<u>Parameter_0052</u>	<u>HR_RecU_CleavageSequence</u>
<u>Parameter_0053</u>	<u>HR_RuvAB_JunctionMigrationHop</u>
<u>Parameter_0054</u>	<u>NER_PcrA_StepSize</u>
<u>Parameter_0055</u>	<u>NER_UvrABC_IncisionMargin3</u>
<u>Parameter_0056</u>	<u>NER_UvrABC_IncisionMargin5</u>
<u>Parameter_0057</u>	<u>RM_EcoD_MethylationPosition</u>
<u>Parameter_0058</u>	<u>RM_EcoD_RecognitionSequence</u>
<u>Parameter_0059</u>	<u>RM_EcoD_RestrictionPosition</u>
<u>Parameter_0060</u>	<u>RM_MunI_MethylationPosition</u>
<u>Parameter_0061</u>	<u>RM_MunI_RecognitionSequence</u>
<u>Parameter_0062</u>	<u>RM_MunI_RestrictionPosition</u>
<u>Parameter_0063</u>	<u>foldChangeIntercepts_gyrase</u>
<u>Parameter_0064</u>	<u>foldChangeIntercepts_topoIV</u>
<u>Parameter_0065</u>	<u>foldChangeIntercepts_topoI</u>
<u>Parameter_0066</u>	<u>foldChangeLowerSigmaLimit</u>
<u>Parameter_0067</u>	<u>foldChangeSlopes_gyrase</u>
<u>Parameter_0068</u>	<u>foldChangeSlopes_topoIV</u>

<u>Parameter_0069</u>	<u>foldChangeSlopes_topol</u>
<u>Parameter_0070</u>	<u>foldChangeUpperSigmaLimit</u>
<u>Parameter_0071</u>	<u>gyraseActivityRate</u>
<u>Parameter_0072</u>	<u>gyraseATPCost</u>
<u>Parameter_0073</u>	<u>gyraseDeltaLK</u>
<u>Parameter_0074</u>	<u>gyraseMeanDwellTime</u>
<u>Parameter_0075</u>	<u>gyraseSigmaLimit</u>
<u>Parameter_0076</u>	<u>topoIActivityRate</u>
<u>Parameter_0077</u>	<u>topoIATPCost</u>
<u>Parameter_0078</u>	<u>topoIDeltaLK</u>
<u>Parameter_0079</u>	<u>topoISigmaLimit</u>
<u>Parameter_0080</u>	<u>topoIVActivityRate</u>
<u>Parameter_0081</u>	<u>topoIVATPCost</u>
<u>Parameter_0082</u>	<u>topoIVDeltaLK</u>
<u>Parameter_0083</u>	<u>topoIVSigmaLimit</u>
<u>Parameter_0084</u>	<u>activationFwd</u>
<u>Parameter_0085</u>	<u>activationRev</u>
<u>Parameter_0086</u>	<u>elongationFwd</u>
<u>Parameter_0087</u>	<u>elongationRev</u>
<u>Parameter_0088</u>	<u>exchangeFwd</u>
<u>Parameter_0089</u>	<u>exchangeRev</u>
<u>Parameter_0090</u>	<u>nucleationFwd</u>
<u>Parameter_0091</u>	<u>nucleationRev</u>
<u>Parameter_0092</u>	<u>growthAssociatedMaintenance</u>
<u>Parameter_0093</u>	<u>nonGrowthAssociatedMaintenance</u>
<u>Parameter_0094</u>	<u>ftsHProteaseEnergyCost</u>
<u>Parameter_0095</u>	<u>ftsHProteaseFragmentLength</u>
<u>Parameter_0096</u>	<u>ftsHProteaseSpecificRate</u>
<u>Parameter_0097</u>	<u>lonProteaseEnergyCost</u>
<u>Parameter_0098</u>	<u>lonProteaseFragmentLength</u>
<u>Parameter_0099</u>	<u>lonProteaseSpecificRate</u>
<u>Parameter_0100</u>	<u>oligoendopeptidaseFSpecificRate</u>
<u>Parameter_0101</u>	<u>proteinMisfoldingRate</u>

<u>Parameter_0102</u>	<u>deformylaseSpecificRate</u>
<u>Parameter_0103</u>	<u>methionineAminoPeptidaseSpecificRate</u>
<u>Parameter_0104</u>	<u>lipoproteinDiacylglycerylTransferaseSpecificRate</u>
<u>Parameter_0105</u>	<u>lipoproteinSignalPeptidaseSpecificRate</u>
<u>Parameter_0106</u>	<u>preproteinTranslocase_aaTranslocatedPerATP</u>
<u>Parameter_0107</u>	<u>SRP_GTPUsedPerMonomer</u>
<u>Parameter_0108</u>	<u>translocaseSpecificRate</u>
<u>Parameter_0109</u>	<u>dnaPolymeraseElongationRate</u>
<u>Parameter_0110</u>	<u>laggingBackupClampReloadingLength</u>
<u>Parameter_0111</u>	<u>ligaseRate</u>
<u>Parameter_0112</u>	<u>okazakiFragmentMeanLength</u>
<u>Parameter_0113</u>	<u>primerLength</u>
<u>Parameter_0114</u>	<u>ssbComplexSpacing</u>
<u>Parameter_0115</u>	<u>startingOkazakiLoopLength</u>
<u>Parameter_0116</u>	<u>k_inact</u>
<u>Parameter_0117</u>	<u>k_Regen</u>
<u>Parameter_0118</u>	<u>K_Regen_P4</u>
<u>Parameter_0119</u>	<u>kb1ADP</u>
<u>Parameter_0120</u>	<u>kb1ATP</u>
<u>Parameter_0121</u>	<u>kb2ADP</u>
<u>Parameter_0122</u>	<u>kb2ATP</u>
<u>Parameter_0123</u>	<u>kd1ADP</u>
<u>Parameter_0124</u>	<u>kd1ATP</u>
<u>Parameter_0125</u>	<u>siteCooperativity</u>
<u>Parameter_0126</u>	<u>stateCooperativity</u>
<u>Parameter_0127</u>	<u>peptidylTRNAHydrolaseSpecificRate</u>
<u>Parameter_0128</u>	<u>ribonucleaseRFragmentLength</u>
<u>Parameter_0129</u>	<u>enzymeEnergyCost_DeaD</u>
<u>Parameter_0130</u>	<u>enzymeEnergyCost_RsgA</u>
<u>Parameter_0131</u>	<u>enzymeSpecificRate_DeaD</u>
<u>Parameter_0132</u>	<u>enzymeSpecificRate_RNAseIII</u>
<u>Parameter_0133</u>	<u>enzymeSpecificRate_RNAseJ</u>
<u>Parameter_0134</u>	<u>enzymeSpecificRate_RNAseP</u>

<u>Parameter_0135</u>	<u>enzymeSpecificRate_RsgA</u>
<u>Parameter_0136</u>	<u>rnaPolymeraseElongationRate</u>
<u>Parameter_0137</u>	<u>ribosomeElongationRate</u>
<u>Parameter_0138</u>	<u>tmRNABindingProbability</u>
<u>Parameter_0139</u>	<u>exchangeRateUpperBound_carbon</u>
<u>Parameter_0140</u>	<u>exchangeRateUpperBound_noncarbon</u>
<u>Parameter_0141</u>	<u>minimumAverageExpression</u>
<u>Parameter_0142</u>	<u>nInitMax</u>
<u>Parameter_0143</u>	<u>nSpecBoundMax</u>
<u>Parameter_0144</u>	<u>minTRnaCnt</u>
<u>Parameter_0145</u>	<u>rnaPolymeraseCollisionMeanDwellTime</u>
<u>Parameter_0146</u>	<u>topoLogisiticConst</u>
<u>Parameter_0147</u>	<u>gyrLogisiticConst</u>
<u>Parameter_0148</u>	<u>macromoleculeStateInitializationVariation</u>
<u>Parameter_0149</u>	<u>macromoleculeStateInitializationGrowthFactor</u>
<u>Parameter_0150</u>	<u>initialGrowthFilterWidth</u>
<u>Parameter_0151</u>	<u>meanInitialGrowthRate</u>
<u>Parameter_0152</u>	<u>ssbDissociationRate</u>
<u>Parameter_0153</u>	<u>minimumAverageExpression</u>
<u>Parameter_0154</u>	<u>dryWeightFractionNucleotide</u>
<u>Parameter_0155</u>	<u>cellInitialMassVariation</u>
<u>Parameter_0156</u>	<u>meanNTPConcentration</u>
<u>Parameter_0157</u>	<u>meanNDPCConcentration</u>
<u>Parameter_0158</u>	<u>meanNMPCConcentration</u>