

CORRIGENDUM

Methods for predicting bacterial protein subcellular localization

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In the above article, there was an error in the true negative (TN) values provided in Table 2 for the PSORTb and Proteome Analyst programs. This error had no impact on the article's arguments or conclusions, however the authors wish to apologise to readers for any confusion caused. The correct values are shown below.

Table 2 | Comparison of the performance of available bacterial protein subcellular localization prediction methods*

Actual localization	Performance statistics						
	Total	TP	FP	FN	TN	Precision	Recall
PSORTb							
C	145	110	1	35	153	99.1%	75.9%
CM	69	55	2	14	228	96.5%	79.7%
P	29	18	0	11	270	100.0%	62.1%
OM	38	30	0	8	261	100.0%	78.9%
EC	18	6	3	12	278	66.7%	33.3%
Total	299	219	6	80	1,190	97.3%	73.2%
Proteome Analyst							
C	145	94	0	51	154	100.0%	64.8%
CM	69	59	2	10	228	96.7%	85.5%
P	29	19	3	10	267	86.4%	65.5%
OM	38	31	0	7	261	100.0%	81.6%
EC	18	9	6	9	275	60.0%	50.0%
Total	299	212	11	87	1,185	95.1%	70.9%

*A test set of 299 proteins from Gram-negative bacteria was used. For the detailed results of the analysis, see Supplementary information S1 (table). C, cytoplasm; CM, cytoplasmic membrane; EC, extracellular; FN, false negative; FP, false positive; N/A, not applicable; OM, outer membrane; P, periplasm; TN, true negative; TP, true positive.