

Table 4. Genes known to be induced during flagellar regeneration

<u>Gene</u> <u>identification</u>	<u>30 min, %</u>	<u>45 min, %</u>	<u>120 min, %</u>
167398 DLC5	-20.88	-15.26	-11.58
168923 PF6	-5.69	34.6	-30.05
158670	-4.1	16.43	7.14
159590	-1.86	-27.63	-1.13
165162 ODA5	-0.4	-11.64	2.73
169516 DHC2	1.63	4.81	-7.89
159662 FA1	10.92	0.2	-0.61
157246	19.49	20.12	27.04
157793	23.53	26.8	6.53
163484	24.01	15.86	-4.08
169293	25.39	9.84	-16.11
165004	25.85	31.32	5.78
168565	30.25	-4.18	-14.56
153422	31.21	6.02	-6.38
169882	41.2	13.25	9.73
153053	47.19	23.29	-1.24
159155	54.96	27.24	-13.87
158615	60.01	40.31	8.66
158194 FLA10	61.09	45.16	0.6
158033	71.88	66.67	-8.88
163664	74.46	23.13	1.15
157052 MBO2	76.19	40.82	-5.26
153708 LF4	81.06	27.19	12.12
163277	91.26	41.44	-14.82
165115	91.7	79.72	11.98
166736 IDA7	92.65	42.85	3.51
164264	100	22.26	-23.52
167776	110.06	37.1	33.84
156043	116.06	48.75	9.94
164149	117.95	77.94	6.19
166131 PF20	118.52	43.45	31.97
157798 ODA3	127.93	33.57	1
164561	129.22	93.45	24.46
158863	134.99	49.99	-2.5
162279 RSP3	143.86	56.65	6.06
171911	153.4	43.84	-9.11
163193	161.35	80.24	-6.28
154393 IFT52	168.36	81.09	5.86
164100 ODA6	170.31	81	4.73
153853	196.25	75.98	7.61
159749	212.19	180.48	37.7

153658		220.27	157.04	-1.71
161253		221.12	27.38	2.99
156948	IFT57	232.55	56.82	19
171602		302.64	147.04	109.3
159247		334.95	35.71	-20.73
164620	TUA1	345.71	192.45	114.43
171096	PF16	367.77	123.03	-4.21
160297		371.12	219.34	83.35
157967	RSP4	382.67	240.87	30.47
165606		389.99	208.84	67.13
170055	TUB2	418.67	214.58	97.42
171102		431.1	197.22	16.93
168339		443.1	126.61	-7.46
160952	ODA-DC3	676.09	213.18	43.84
162703		724.23	436.64	87.7

Data set used to validate microarray detection of induction of transcripts and the strategy of flagellar gene identification based on induction during flagellar regeneration. Entries in bold type indicate at least 75% induction at either 30 or 45 min after initiation of flagellar regeneration. Plain text indicates genes classified as not induced according to this same criterion. Within each list, entries are sorted in increasing order of induction at $t = 30$ min. The gene list consists of the strongly induced genes from the RT-PCR analysis of Li *et al.* (1), plus 20 *Chlamydomonas* genes (as indicated) whose induction has been reported in the literature based on Northern blot analysis.

1. Li, J. B., Gerdes, J. M., Haycraft, C. J., Fan, Y., Teslovich, T. M., May-Simera, H., Li, H., Blacque, O. E., Li, L., Leitch, C. C., *et al.* (2004) *Cell* **117**, 541-552.