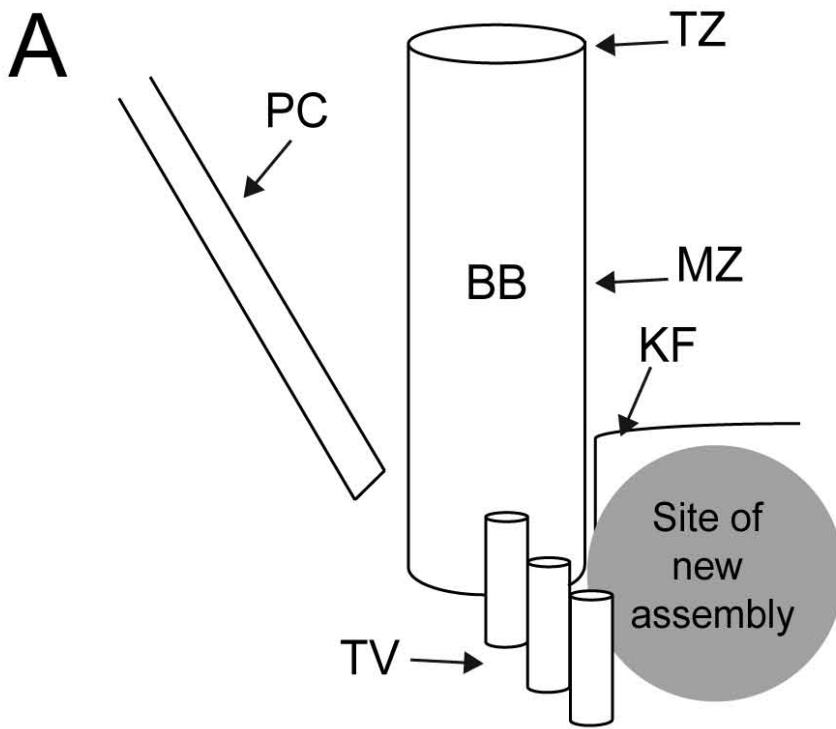
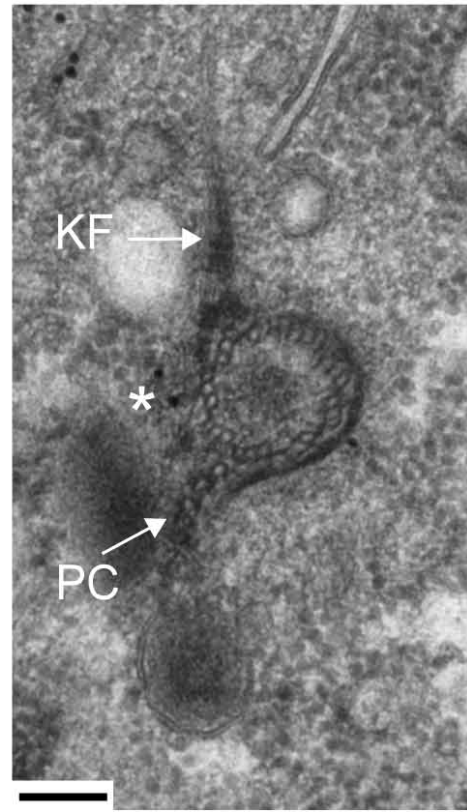
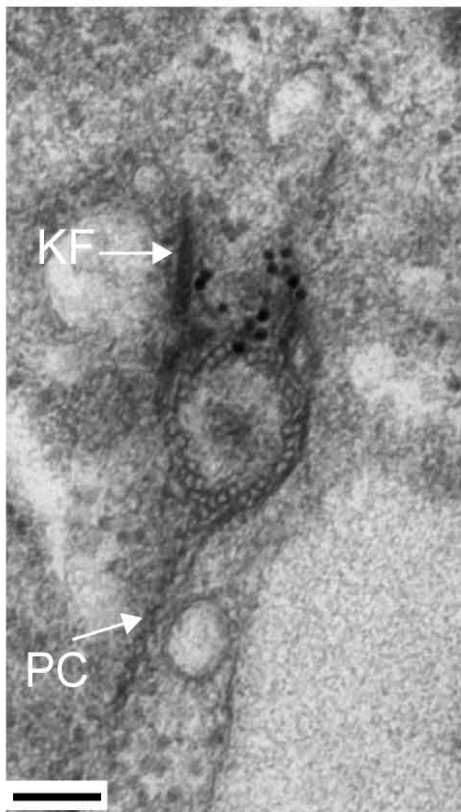
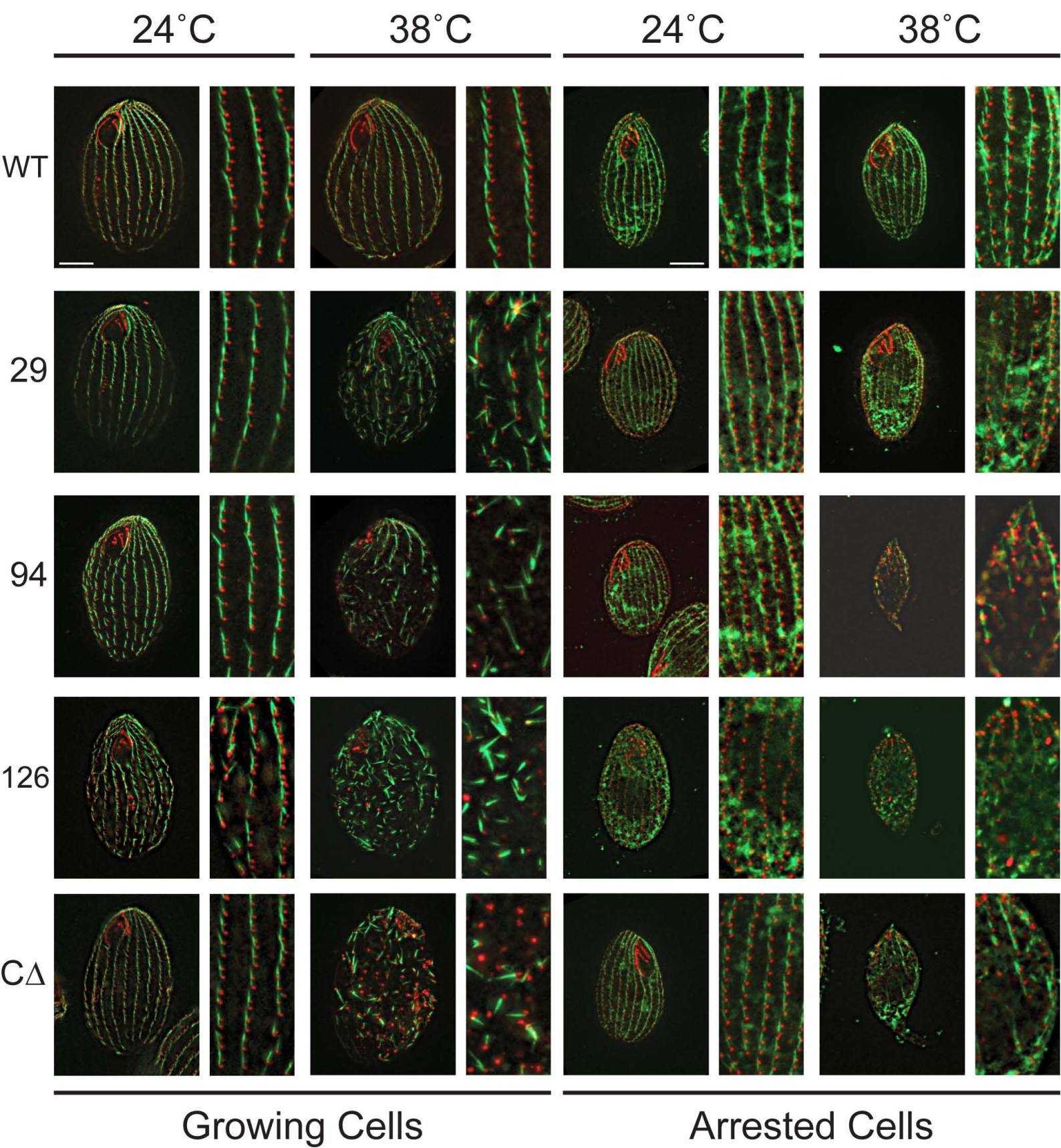


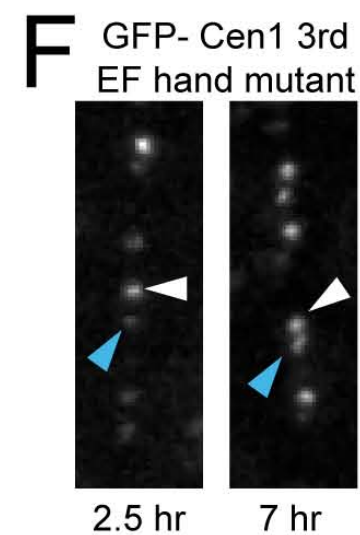
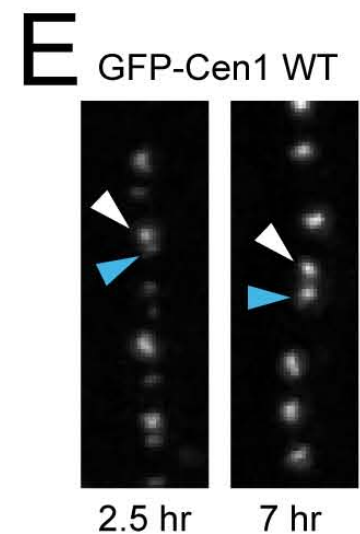
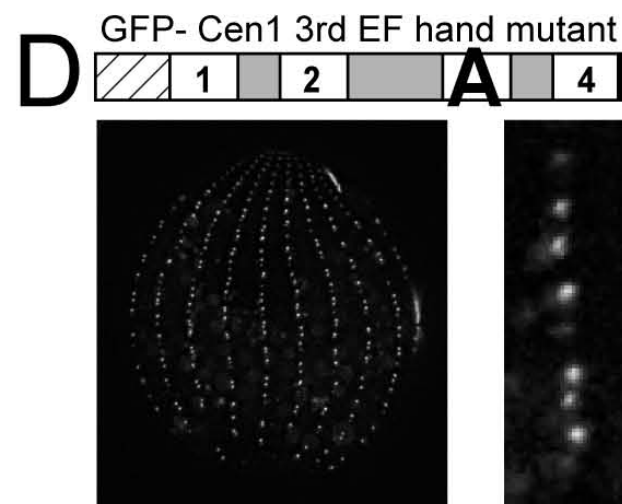
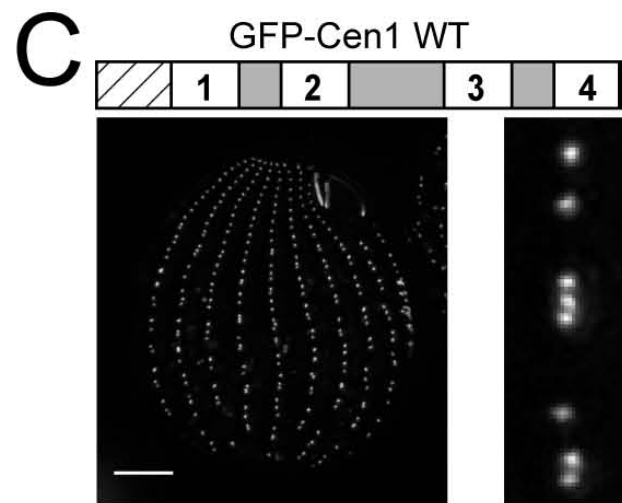
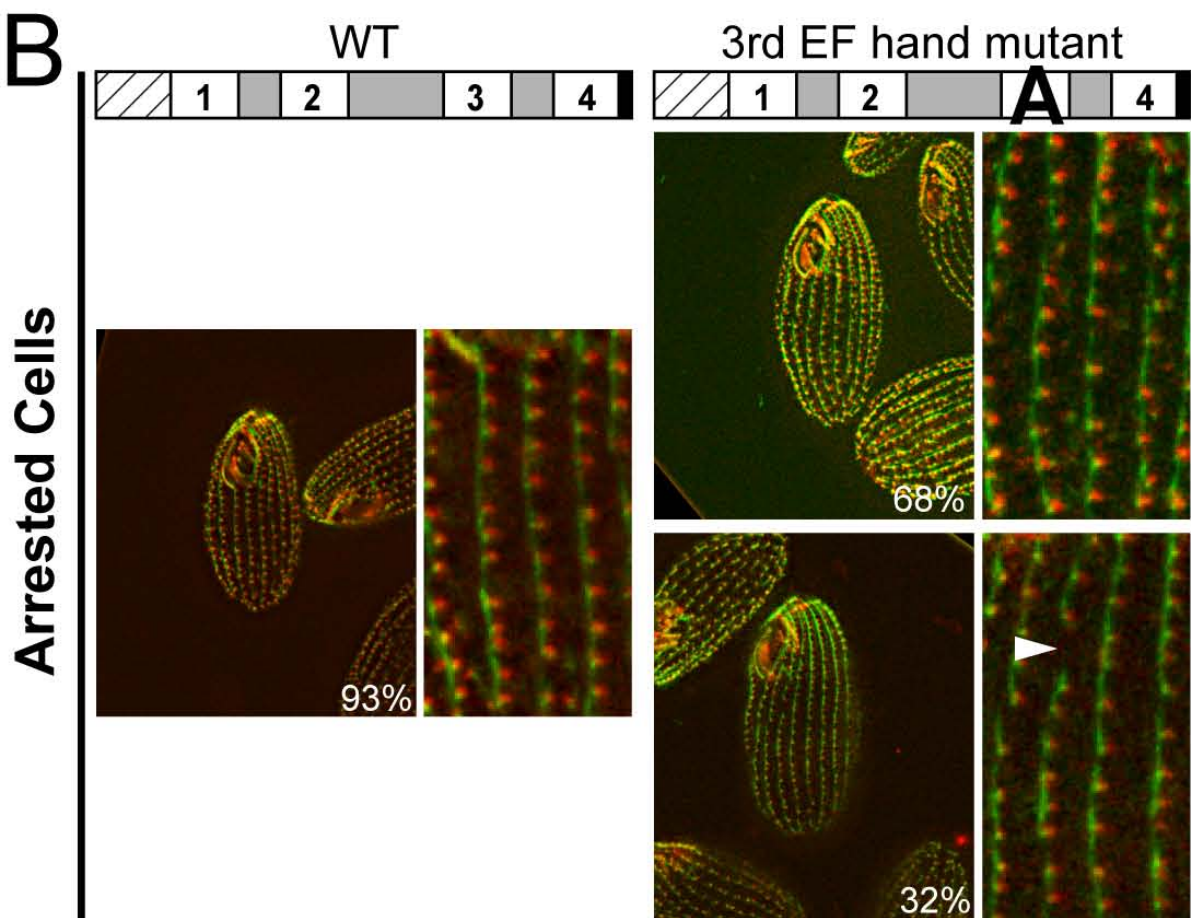
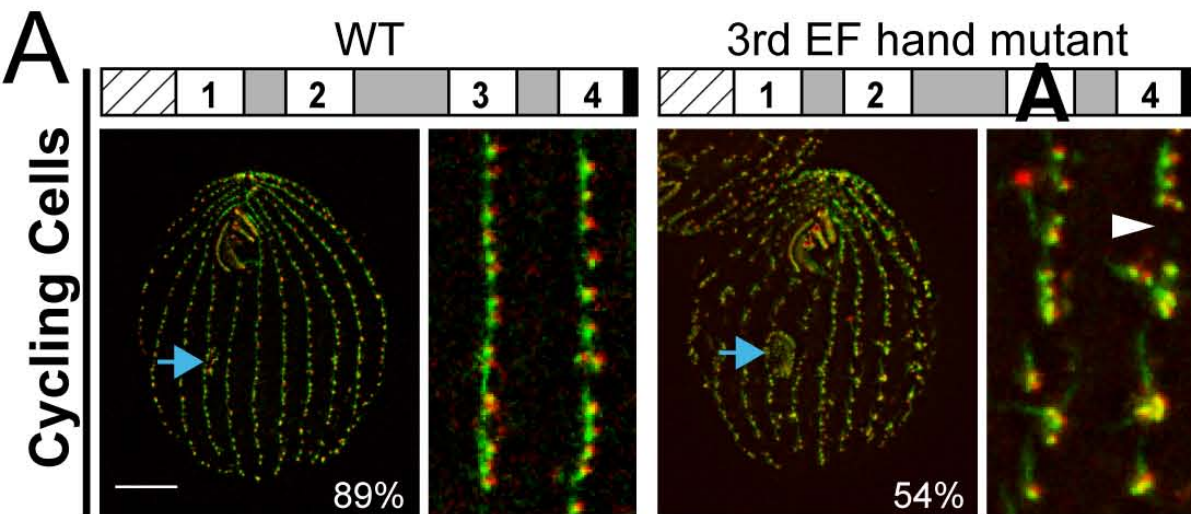
MUTANT ALLELE	MUTATION	PHENOTYPE
DOMAIN DELETIONS		
N-terminal domain deletion	Residues 1-92 deleted	Lethal
C-terminal domain deletion	Residues 93-167 deleted	Lethal
EF HAND MUTATIONS		
1 st EF hand	D36A	None
2 nd EF hand	D72A	None
1 st and 2nd EF hand	D36A, D72A	Basal body disorganization (TS)
3 rd EF hand	D109A	Slight defects in basal body organization and stability (TS)
4 th EF hand	D145A	Basal body disorganization and stability defects (TS)
3 rd and 4th EF hand	D109A, D145A	Lethal
4x EF hand	D36A, D72A, D109A, D145A (all 4 EF hands)	Lethal
OTHER DELETIONS		
N-terminal tail deletion	Residues 2-26 deleted	Lethal
Linker deletion 1	Residues 92-95 deleted	Lethal
Linker deletion 2	Residues 96-99 deleted	Lethal
C-terminal tail deletion	Residues 165-167 deleted	Basal body disorganization and stability defects (TS)
CHARGED RESIDUES TO ALANINE MUTATIONS		
14	R14A, R17A	Lethal
22	E22A, E23A, K25A	Mild basal body disorganization (TS)
27	E27A, K29A, E30A	Lethal
29	K29A, E30A, D33A	Basal body disorganization (TS)
49	K49A, R53A	Mild basal body disorganization (TS)
58	E58A, K60A, K61A	Basal body disorganization (TS)
60	K60A, K61A, E62A, E63A	Basal body disorganization (TS)
86	D86A	None
94	E94A, R95A, D96A	Basal body disorganization and stability defects (TS)
98	R98A, D99A, E100A	Lethal
103	K103A, R106A	Basal body disorganization and stability defects (TS)
126	R126A, E127A, E130A	Basal body disorganization and stability defects (TS)
134	E134A, E135A, E136A	Basal body disorganization and stability defects (TS)
142	E142A, E143A	Lethal
159	K159A, K162A, K163A	Lethal



	Particles per BB	TZ	MZ	TV	Site of new assembly	Proximal other	Other
WT	44.5 (N=15 BBs)	2.1 (4.7%)	5.9 (13.3%)	9 (20.2%)	25.6 (57.5%)	1.9 (4.3%)	0 (0%)
NTD double EF hand	34.1 (N=22 BBs)	2.8 (8.2%)	4.5 (13.2%)	6.7 (19.6%)	19.3 (56.6%)	0.8 (2.3%)	0 (0%)
4th EF hand	17.5 (N=11 BBs)	2.4 (13.7%)	5 (28.6%)	0.5 (2.9%)	1.6 (9.1%)	6.5 (37.1%)	1.5 (8.6%)

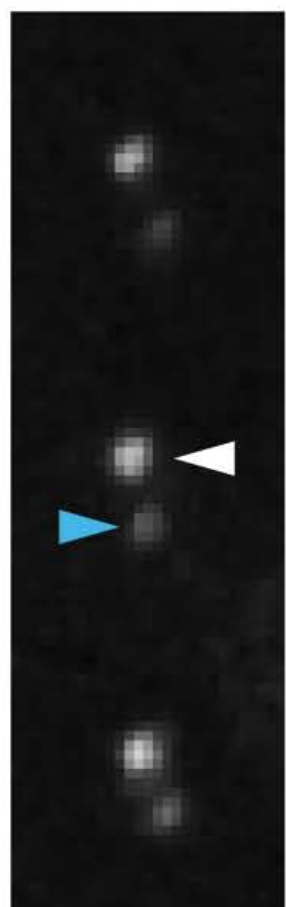
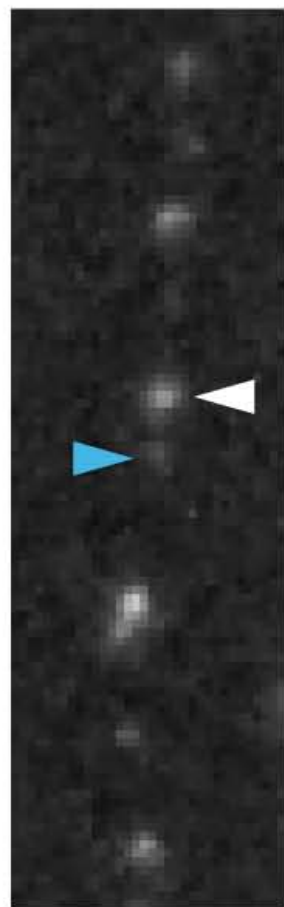




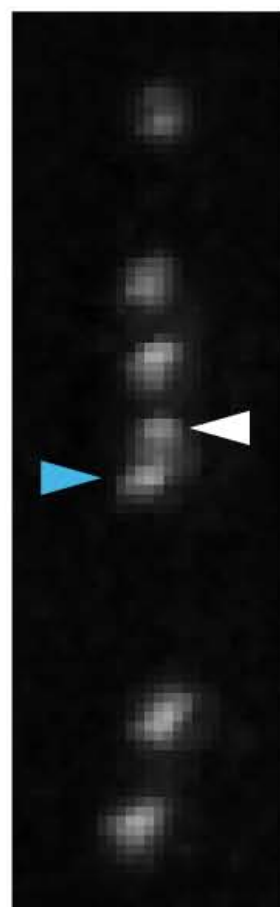
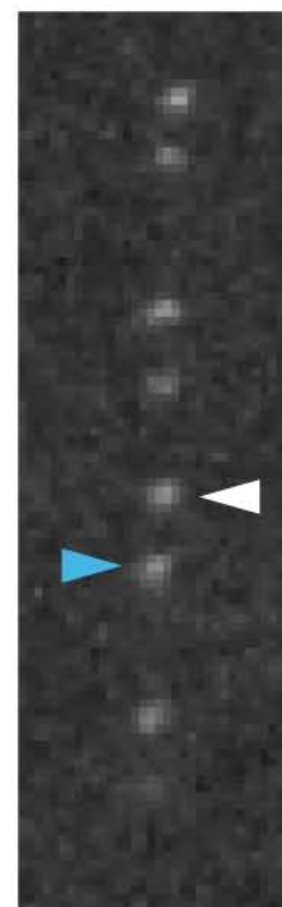
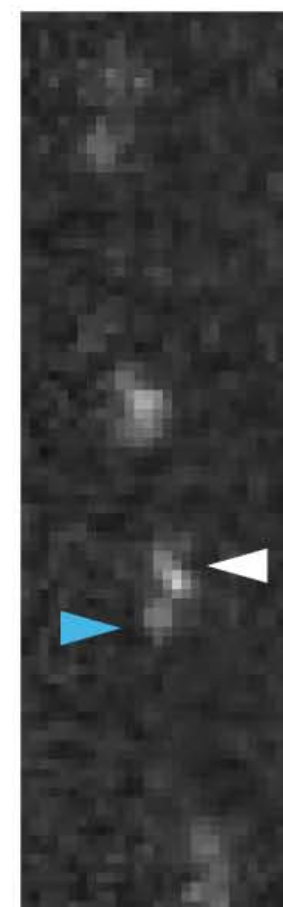


A

Release 2.5h

GFP-Cen1
WTGFP-Cen1
4th EF hand
mutant proteinGFP-Cen1
CTD double
EF hand
mutant
protein**B**

Release 7h

GFP-Cen1
WTGFP-Cen1
4th EF hand
mutant proteinGFP-Cen1
CTD double
EF hand
mutant
protein