

1 **Supplementary Information for**

2 **Biomimetic Magnetite Formation: From Biocombinatorial Approaches to Mineralization Effects**

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6 **Table S1** List of oligonucleotides for gene amplification.

Primer	Sequence
mamJ_forward	5'-GACGACGACAAGATGGCAAAAACCGGCGTGAT-3'
mamJ_His-Tag_reverse	5'-GAGGAGAAGCCCGGTTTATTCTTATCTTCAGCA-3'
mtxA_forward	5'-GACGACGACAAGATGAGCAGAATACTCGCAGT-3'
mtxA <sub>Δ1-24</sub> _forward	5'-GACGACGACAAGTCGGAGCCCCCGGTTTCCATGC-3'
mtxA_His-Tag_reverse	5'-GAGGAGAAGCCCGGTTGCCTTCCAAGTCT-3'

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1 **Table S2** Summary of magnetite-adhering sequences and sequence alignment with magnetotactic  
 2 bacteria-specific proteins. Sequences marked (\*, #) originate from earlier reports by Brown et al. <sup>17a</sup> and  
 3 Barbas et al. <sup>17b</sup>, respectively. GRAVY is the grand average of hydropathy <sup>22</sup>.

selected in this paper			reported in literature		
Sequence	pI	GRAVY	Sequence	pI	GRAVY
AHRHPISFLSTL	9.81	0.158	RFKRVDR <sup>#</sup>	12.00	-2.300
ATTHRDVQNAFR	9.65	-1.125	RRSRHH <sup>#</sup>	12.30	-3.450
DLKLETALSNT	4.37	-0.350	RRTVKHHN <sup>*</sup>	12.01	-2.413
EHLQFSTHGPLR	7.02	-0.917	RSKKMR <sup>#</sup>	12.02	-2.617
GTPPMSPLVSRV	9.75	0.175	RSKRGR <sup>#</sup>	12.30	-3.100
GTPRSHYPAPQV	8.75	-1.100			
IPLPPSRPFFK	11.00	-0.275			
ITHPTGFLTSRP	9.76	-0.258			
KPLDIHGNNYSW	6.74	-1.192			
NDNTYANHGKIH	6.92	-1.700			
NLTSLTQGSAML	5.52	0.392			
NMTKHPLAYTEP	6.75	-1.042			
NPFNQHLHAQHP	7.02	-1.533			
QAYRSSAFLPPM	8.75	-0.167			
QFSLPVAKLVNR	11.00	0.233			
SGHQLLLKMPN	8.49	-0.592			
SILSTMSPHGAT	6.46	0.250			
SPLPSHKSQHTW	8.51	-1.433			
SPTLSNDEHLRM	5.30	-1.050			
TLNKPNRALHFN	11.00	-1.017			
TSASTRPELHYP	6.41	-1.092			
TTHPSTVQTPNW	6.40	-1.142			
VPSLTPSAQSRP	9.72	-0.508			
YHEADPQAYQRT	5.32	-1.917			
YPAPQPLVTKTS	8.59	-0.492			
YSIEQEHPSPFP	4.51	-1.175			
YSPDRPWSSRY	8.59	-1.933			

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2 **Table S3** Sequence alignment of *M. gryphiswaldense* MSR-1 MamJ and phage display selected peptide

3 QFSLPVAKLVNR.

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MamJ	MAKNRRDRGTDLPGDGDQKISTGPEIVSVTVHPSPNLAAAAKPVQGDIWASLLESSPWSA
QFSLPVAKLVNR	-----

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MamJ	NQGGLVETAQPPSAPIRSQDPV <b>PVADLVNR</b> WSQPIWRTAPLAGNAESSEEGVVAPSLTQS
QFSLPVAKLVNR	----- <b>QFSLPVAKLVNR</b> -----

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MamJ	DSVLAVSDLVIDVQPETDAEVEVSIEPEPALVEPVIEIEAEAAEVEPEPA <b>PVADLVNR</b> WA
QFSLPVAKLVNR	----- <b>QFSLPVAKLVNR</b> -----

MamJ	QPIWRTAPLAGNAESSEEGVVAPSLTQSDSVLAVSDLVIDVQPEANAEEVVSIEPEPALV
QFSLPVAKLVNR	-----

MamJ	EPVIEIEAEAAEVEPEPAPVEPAIEIEAIRVELEPVLIDEVVELVTEFEYSQAESVASAD
QFSLPVAKLVNR	-----

MamJ	LIANPAPAESSRLAELLDEAAAIAAPAVAVAVEATRQPNKITASVKKRAPVQEVVEDLL
QFSLPVAKLVNR	-----

MamJ	GGIFGVAGSAVRGVFTIGGGFVDGVVKGGRLVGNSNVVAGTRRLAQTIEVSCGSCSSPKCD
QFSLPVAKLVNR	-----

MamJ	AEDKNK
QFSLPVAKLVNR	-----

**Table S4** Sequence alignment of *M. gryphiswaldense* MSR-1 MtxA and phage display selected peptide

VPSLTPSAQSRLP. Truncated N-terminal signal peptide is marked by italics.

MtxA VPSLTPSAQSRLP	<i>MSRILAV</i> <b>LAAGLMMM</b> <i>GW</i> TQAVQASEPPVSMLMQVAGAVETSKGGEKWAPVTRNKFLFVG -----
MtxA VPSLTPSAQSRLP	TQVRTGADGGGKLIDQNSGMAQTIGANSVVEITAAGPKAVSGSLSAPEAASGDLVAGLSN -----
MtxA VPSLTPSAQSRLP	RFAEAQRYTTVRRSVKKEAADLKLRLVASDITLSPTYPDLVWENMGAQYGYTLVIDGTSHA -----
MtxA VPSLTPSAQSRLP	VPATSGEMVRFRR <b>VPSLT</b> <b>PGAHS</b> FGVTVTEGGQAVGQTEKGGTIVWLSATEDKALVDGVAR ----- <b>VPSLT</b> <b>PGAHS</b> FGVTVTEGGQAVGQTEKGGTIVWLSATEDKALVDGVAR-----
MtxA VPSLTPSAQSRLP	VKAASTGDEFALGNYLDSKGVTVAAAMDAYRKHFASHKDDNDMRPLLIKTYNDLKLRLDLRQ -----
MtxA VPSLTPSAQSRLP	KEALVYNEQLEGN -----

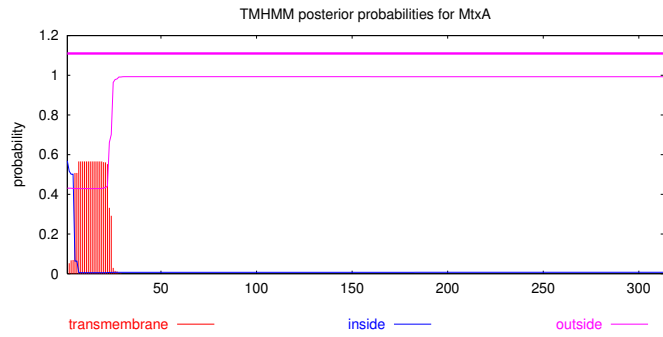


- 1 **Table S5** Fitted kinetic data assuming linear relation reaction-limited growth. Data was obtained from
- 2 three independent experiments except for data marked (\*) that refer to single experiments. (#) refers to
- 3 only two data points.

Additive	Critical Size $D_0$	Kinetic rate $k$ ( $10^{-2}$ nm min $^{-1}$ )	$R^2$
none	$23.0 \pm 1.5$	$3.4 \pm 0.5$	0.896
MtxA $_{\Delta 1-24}$ 0.01 mg mL $^{-1}$	$30.9 \pm 0.5$	$1.3 \pm 0.2$	0.917
MtxA $_{\Delta 1-24}$ 0.1 mg mL $^{-1}$	$4.9 \pm 1.5(*)$	$3.7 \pm 0.4(*)$	0.981
PolyR 0.01 mg mL $^{-1}$	$12.9 \pm 0.8$	$3.8 \pm 0.3$	0.975
PolyR 0.1 mg mL $^{-1}$	$10.5 \pm 1.4$	$2.2 \pm 0.1$	0.997
MamJ 0.01 mg mL $^{-1}$	$13.8 \pm 2.0$	$3.6 \pm 0.7$	0.926
PolyE 0.01 mg mL $^{-1}$	$15.3 \pm 1.3$	$2.4 \pm 0.5$	0.926
PolyE 0.1 mg mL $^{-1}$	4.3(#)	1.8(#)	1

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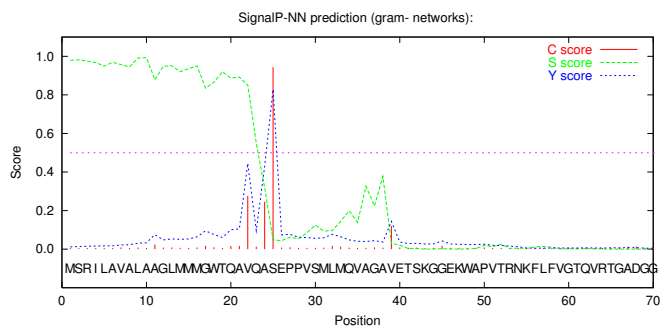
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2 **Figure S1** TMHMM output from MtxA sequence. The program predicts an N-terminal transmembrane  
 3 stretch of 24 amino acids with a probability of  $\sim 0.5$  and a protein location outside the cytosol.

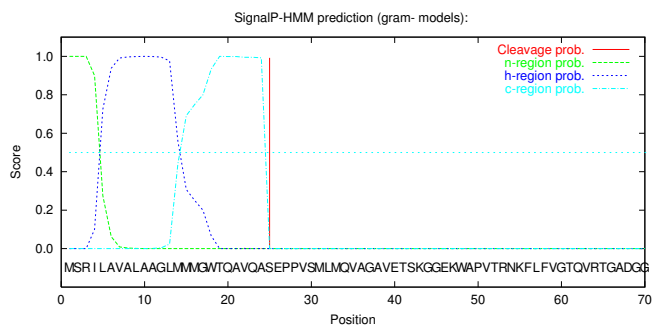
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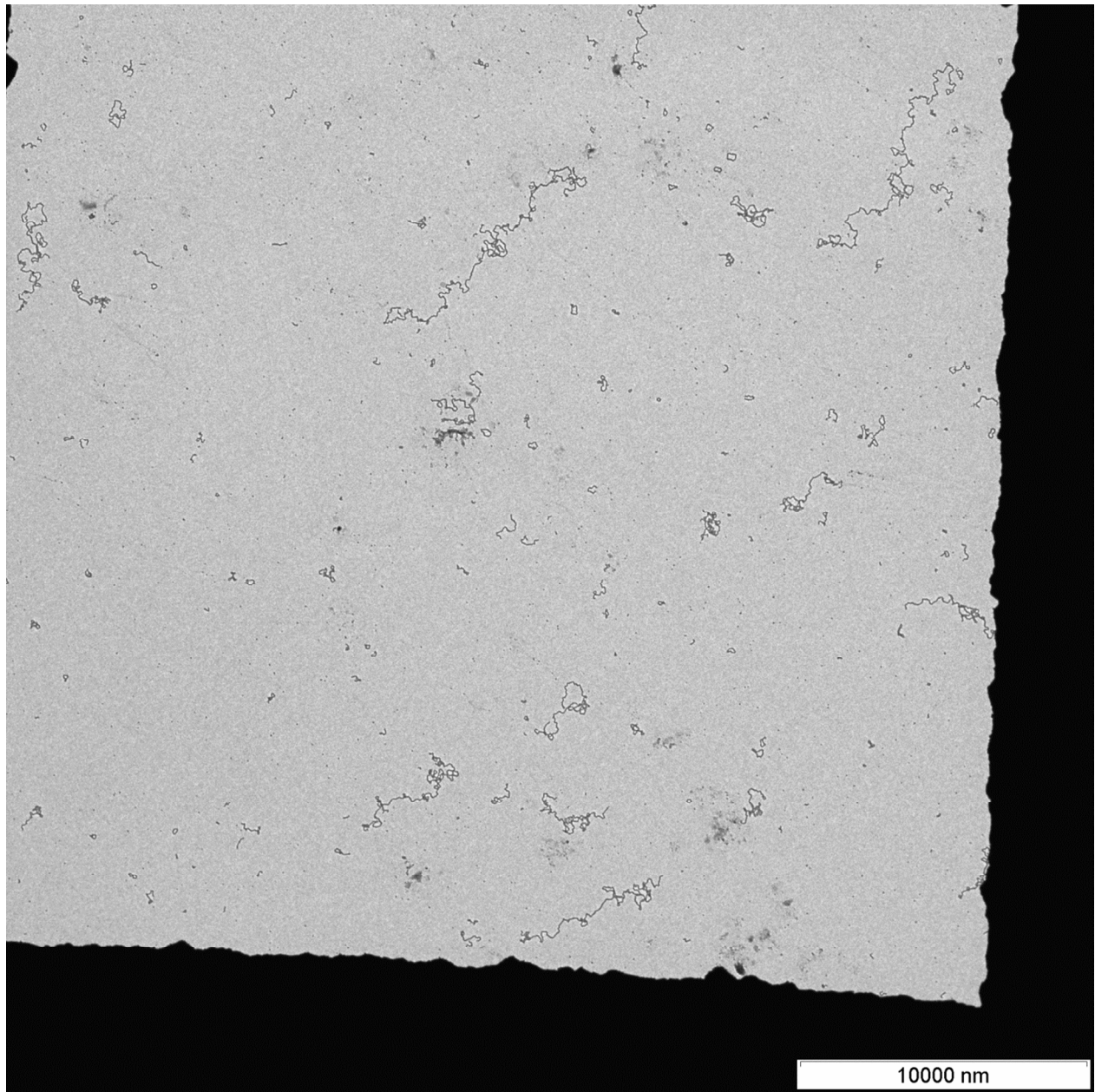
6 **Figure S2** SignalP-NN output for MtxA sequence. C score indicates cleavage probability.

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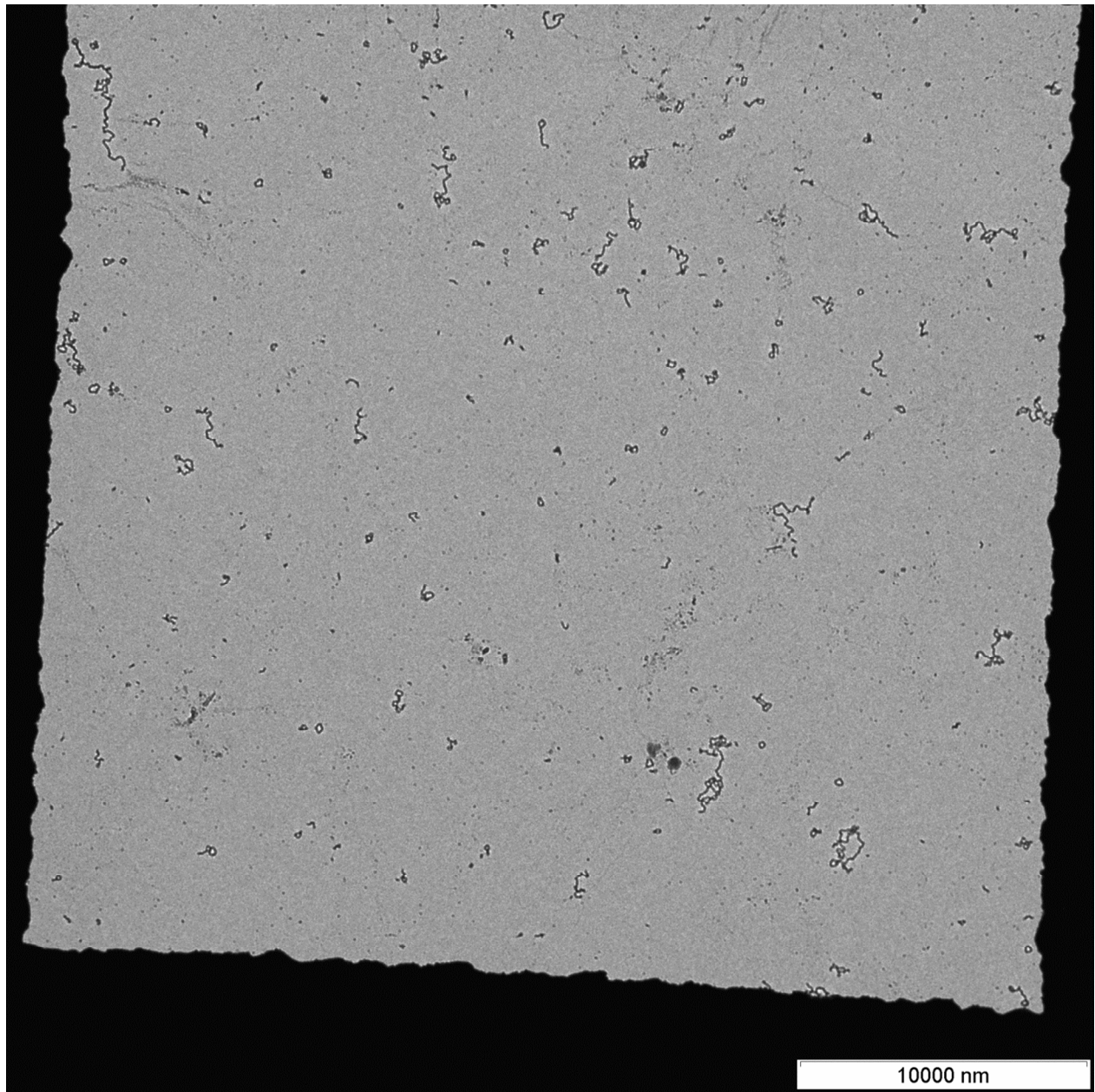
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9 **Figure S3** SignalP-HMM output for MtxA sequence. Cleavage site is indicated by red line.



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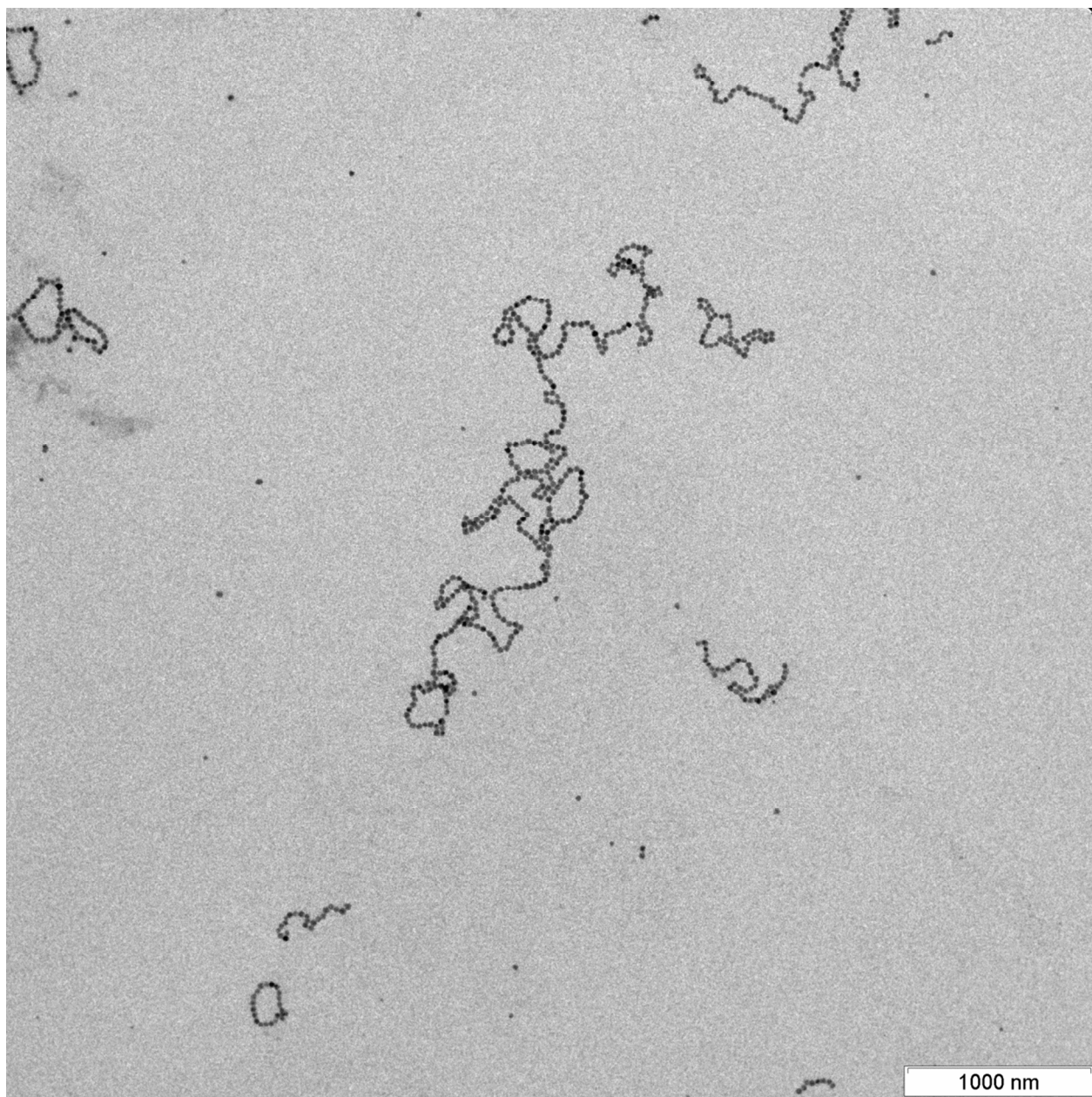
2 **Figure S4** Large field of view transmission electron micrograph of magnetite particles formed in the  
3 presence of poly-L-arginine.



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2 **Figure S5** Large field of view transmission electron micrograph of magnetite particles formed in the  
3 presence of poly-L-arginine.

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2 **Figure S6** Medium field of view transmission electron micrograph of magnetite particles formed in the  
3 presence of poly-L-arginine.

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