

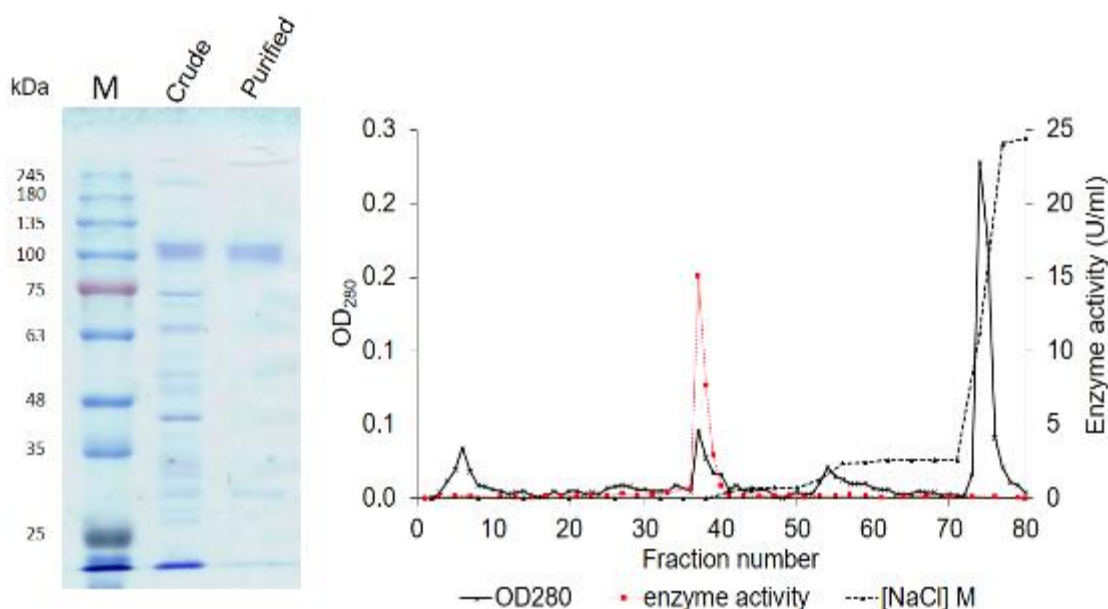
## Supplementary Information

### Highly porous core-shell chitosan beads with superb immobilization efficiency for *Lactobacillus reuteri* 121 inulosucrase and production of inulin-type fructooligosaccharides

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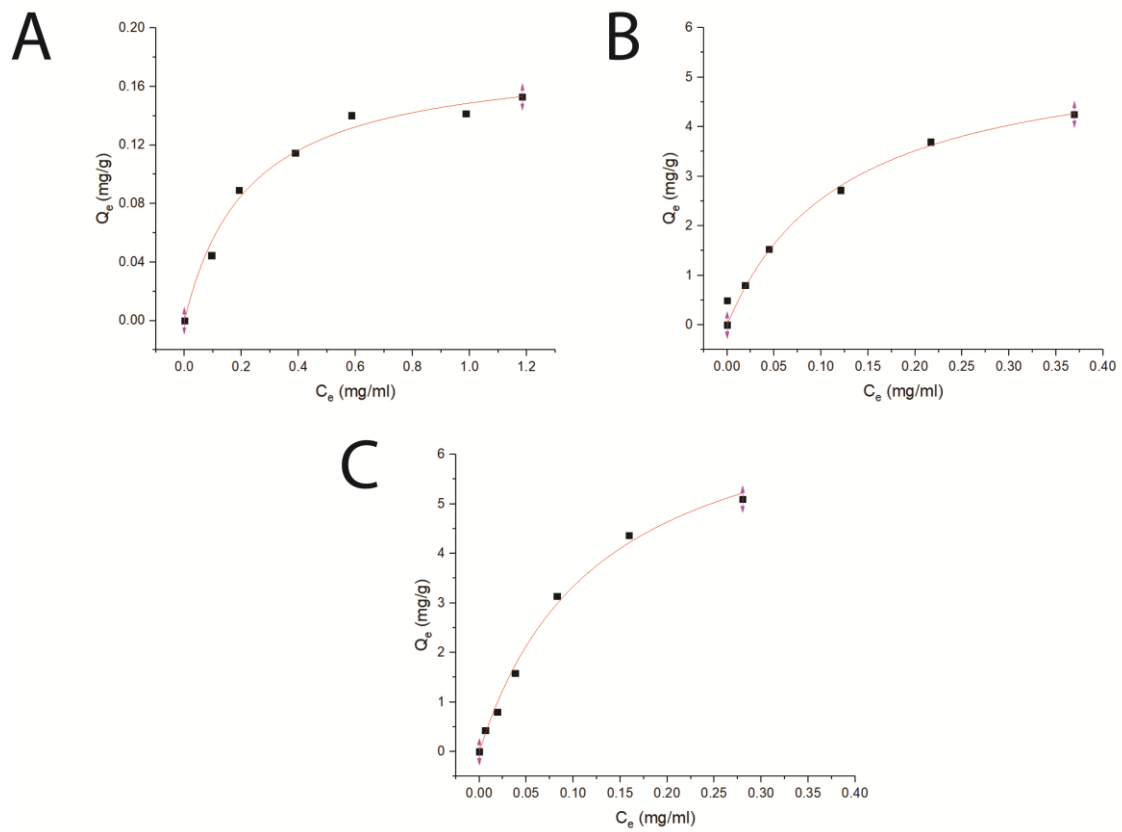
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**Fig. S1** Inulosucrase purification profile by DEAE toyopearl chromatography.

**Table S1** Inulosucrase purification data.

step	Volume (ml)	Protein (mg)	Activity (U)	Specific activity (U/mg)	Purification (fold)	Yield (%)
Crude	20	18.3	$1.23 \times 10^3$	67.0	1	100
DEAE-toyopearl	23	2.22	587	264	3.94	49

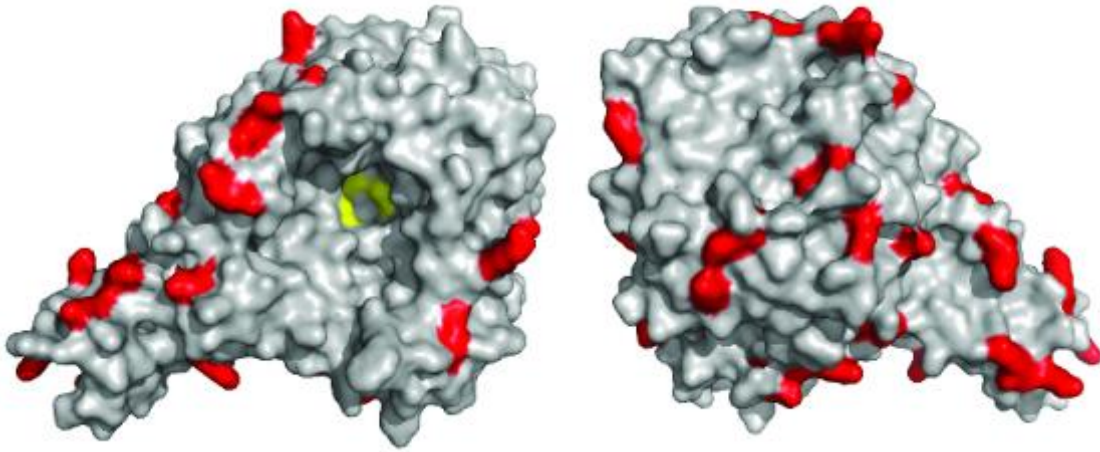


**Fig. S2** BSA isotherm on DBs (A), HGBs (B) and CSBs (C) of the Langmuir model.

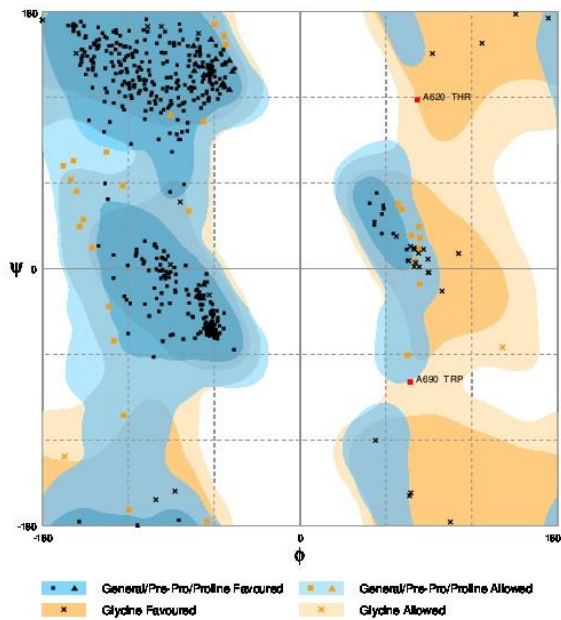
**Table S2** Diameter of CSBs and DBs.

CSBs diameter (mm)				Shell/Core ratio	DBs diameter (mm)	
No.	Total	Core	Shell		No.	Total
1	1.19	1.08	0.11	0.10	1	1.43
2	1.30	1.21	0.09	0.07	2	1.23
3	1.27	1.14	0.13	0.11	3	1.30
4	1.43	1.31	0.13	0.10	4	1.17
5	1.12	1.01	0.11	0.11	5	1.35
6	1.34	1.21	0.13	0.11	6	1.25
7	1.16	1.09	0.07	0.06	7	0.01
8	1.15	1.06	0.09	0.09	8	1.12
9	1.36	1.26	0.10	0.08	9	1.38
10	1.35	1.25	0.10	0.08	10	1.32
11	1.19	1.12	0.07	0.06	11	1.23
12	1.17	1.07	0.11	0.10	12	1.42
13	1.24	1.14	0.10	0.09	13	1.21
14	1.31	1.19	0.12	0.10	14	1.37
15	1.29	1.18	0.11	0.09	15	1.19
16	1.40	1.30	0.10	0.08	16	1.50
17	1.20	1.09	0.12	0.11	17	1.35
18	1.15	1.10	0.05	0.05	18	1.20
19	1.29	1.20	0.09	0.08	19	1.24
20	1.17	1.10	0.08	0.07	20	1.07
21	1.26	1.17	0.08	0.07	21	1.21
22	1.27	1.17	0.10	0.08	22	1.36
23	1.11	1.04	0.07	0.07	23	1.41
24	1.21	1.13	0.09	0.08	24	0.97
25	1.12	1.02	0.10	0.10	25	1.33
26	1.47	1.34	0.13	0.10	26	1.39
27	1.30	1.18	0.12	0.10	27	1.40
28	1.40	1.27	0.13	0.10	28	1.28
29	1.07	0.99	0.08	0.08	29	1.39
30	1.32	1.22	0.11	0.09	30	1.28
31	1.14	1.05	0.09	0.08	31	1.17
32	1.54	1.35	0.19	0.14	32	1.17
33	1.19	1.09	0.10	0.09	33	1.34
34	1.36	1.20	0.16	0.14	34	1.30
35	1.24	1.08	0.16	0.15	35	1.35
Mean	1.26	1.15	0.11	0.09	Mean	1.25
SD	0.11	0.10	0.03	0.02	SD	0.24

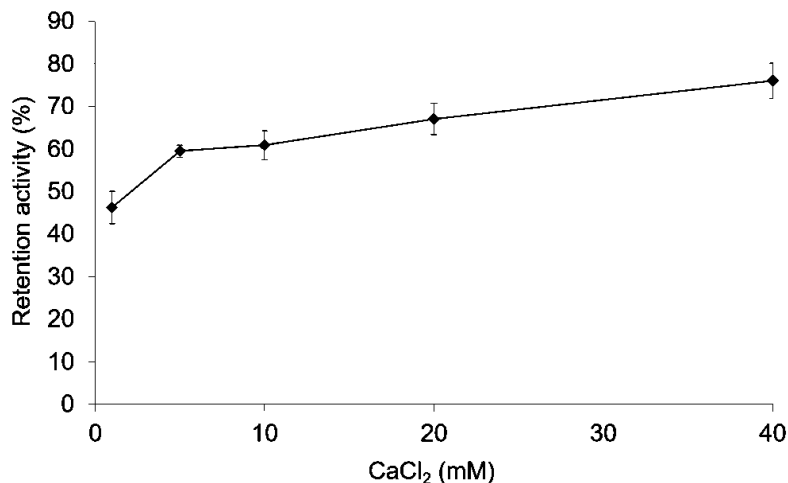
A



B



**Fig. S3** (A) Homology modeling of inulosucrase of *Lactobacillus reuteri* 121 by means of Swissmodel [1-5], using the 3D structure of inulosucrase from *Lactobacillus johnsonii* NCC 533 (Protein Data Bank [PDB] ID: 2YFR, 73% identity) as a template. On the left is a frontal view, and on the right is the posterior view of protein; Lys residues are red, and three catalytic residues are yellow. (B) Ramachandran Plot for homology modeling of Inu calculated by RAMPAGE server (<http://mordred.bioc.cam.ac.uk/~rapper/rampage.php>) [6].



**Fig. S4** Effect of CaCl<sub>2</sub> concentration on INU-CSBs stability.

## Reference

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