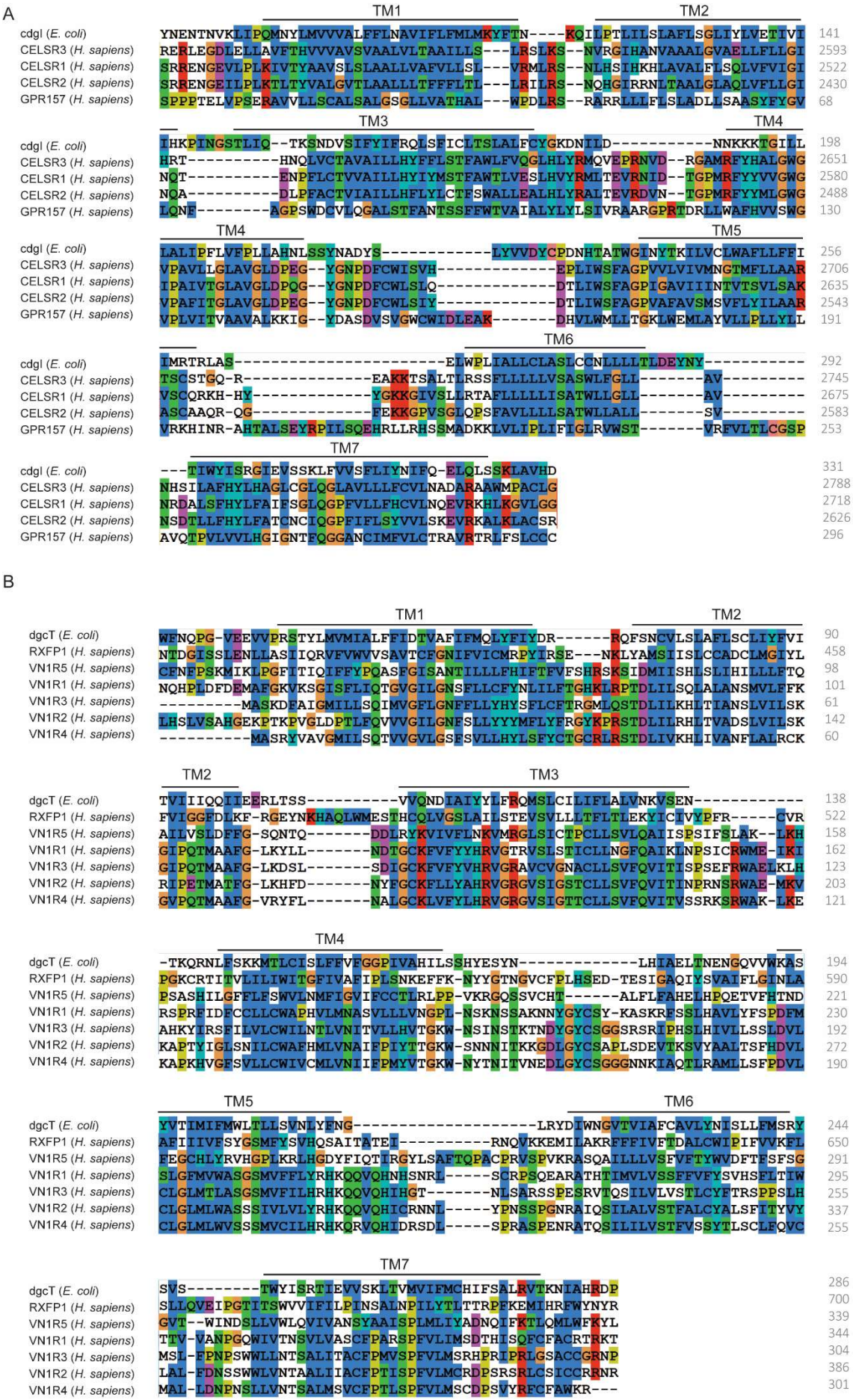
A
TM1
TM2
cdgI (E. coli)
CELSR3 (H. sapiens)
CELSR1 (H. sapiens)
CELSR2 (H. sapiens)
GPR157 (H. sapiens)
141
2593
2522
2430
68
TM3
TM4
198
2651
2580
2488
130
TM4
TM5
256
2706
2635
2543
191
TM6
292
2745
2675
2583
253
TM7
331
2788
2718
2626
296
B
TM1
TM2
dgcT (E. coli)
RXFP1 (H. sapiens)
VN1R5 (H. sapiens)
VN1R1 (H. sapiens)
VN1R3 (H. sapiens)
VN1R2 (H. sapiens)
VN1R4 (H. sapiens)
90
458
98
101
61
142
60
TM2
TM3
138
522
158
162
123
203
121
TM4
194
590
221
230
192
272
190
TM5
TM6
244
650
291
295
255
337
255
TM7
286
700
339
344
304
386
301

Supplemental Figure S4. Sequence alignment between *E. coli* cdgI and dgcT with human GPCR proteins

The 7TM domains of cdgI (A) and dgcT (B) of *E. coli* were aligned with a collection of human GPCRs. The sequence alignment was performed by incorporating the cdgI and dgcT sequences to the existing alignment result of 846 human GPCR proteins using ClustalX2. (PLoS Comput. Biol. **2016**, *12(3)*, e1004805) The established alignment of human GPCR proteins was generated using a structure-guided sequence alignment method. The figure displays the human GPCR proteins that align best to cdgI and dgcT within the multiple sequence alignment file. The color indicates residue groups (blue, hydrophobic; red, positive charge; magenta, negative charge; green, polar).