

**Table S3. Cryo-EM data collection, refinement and validation statistics, related to Figure 4.**

	Echovirus 6 full particle (pH7.4) (EMDB-9690) (PDB 6ILP)	Echovirus 6 empty particle (pH7.4) (EMDB-9689) (PDB 6ILO)	Echovirus 6 full particle (pH5.5) (EMDB-9688) (PDB 6ILN)
<b>Data collection and processing</b>			
Magnification	37037	37037	37037
Voltage (kV)	300	300	300
Electron exposure (e <sup>-</sup> /Å <sup>2</sup> )	40	40	40
Defocus range (µm)	-1.0 to -3.0	-1.0 to -3.0	-1.0 to -3.0
Pixel size (Å)	1.35	1.35	1.35
Symmetry imposed	Icosahedral	Icosahedral	Icosahedral
Initial particle images (no.)	156000	156000	24169
Final particle images (no.)	45346	15077	4321
Map resolution (Å)	2.9	3.2	3.4
FSC threshold	0.143	0.143	0.143
Map resolution range (Å)	2.9-5.0	3.0-5.0	3.0-5.0
<b>Refinement</b>			
Initial model used (PDB code)	1EV1	Echovirus 6	Echovirus 6
Model resolution (Å)	2.9	3.2	3.4
Model resolution range (Å)	540.0-2.9	540.0-3.2	540.0-3.4
Map sharpening <i>B</i> factor (Å <sup>2</sup> )	-127	-129	-114
Model map FSC (masked)	0.81	0.84	0.84
Model composition			
Non-hydrogen atoms	6503	5469	6503
Protein residues	823	693	823
Ligands	1	0	1
<i>B</i> factors (Å <sup>2</sup> )			
Protein	30	56	50
Ligand	22	-	25
R.m.s. deviations			
Bond lengths (Å)	0.006	0.008	0.007
Bond angles (°)	1.24	1.29	1.23
Validation			
MolProbity score	1.53	1.67	1.56
Clashscore	2.9	4.0	3.0
Poor rotamers (%)	0.83	0	0.83
Ramachandran plot			
Favored (%)	93	92.2	93
Allowed (%)	6.75	7.8	6.75
Disallowed (%)	0.25	0	0.25

**Table S3. Cryo-EM data collection, refinement and validation statistics, related to Figure 4.**

	Echovirus 6 bound to CD55 pH 7.4 (EMDB-9685) (PDB 6ILK)	Echovirus 6 bound to CD55 pH 5.5 (EMDB-9684) (PDB 6ILJ)
<b>Data collection and processing</b>		
Magnification	37037	37037
Voltage (kV)	300	300
Electron exposure (e <sup>-</sup> /Å <sup>2</sup> )	40	40
Defocus range (µm)	-1.0 to -3.0	-1.0 to -3.0
Pixel size (Å)	1.35	1.35
Symmetry imposed	Icosahedral	Icosahedral
Initial particle images (no.)	137281	34927
Final particle images (no.)	28528	11494
Map resolution (Å)	3.0	3.6
FSC threshold	0.143	0.143
Map resolution range (Å)	3.0-5.0	3.0-5.0
<b>Refinement</b>		
Initial model used (PDB code)	Echovirus 6	Echovirus 6
Model resolution (Å)	3.0	3.6
Model resolution range (Å)	540.0-3.0	540.0-3.6
Map sharpening <i>B</i> factor (Å <sup>2</sup> )	-125	-131
Model map FSC (masked)	0.80	0.85
Model composition		
Non-hydrogen atoms	8025	8025
Protein residues	1019	1019
Ligands	1	1
<i>B</i> factors (Å <sup>2</sup> )		
Protein	34	61
Ligand	23	47
R.m.s. deviations		
Bond lengths (Å)	0.008	0.008
Bond angles (°)	1.38	1.38
Validation		
MolProbity score	1.84	1.55
Clashscore	6.4	3.2
Poor rotamers (%)	0.89	0.7
Ramachandran plot		
Favored (%)	92.1	93.4
Allowed (%)	7.7	6.4
Disallowed (%)	0.2	0.2

**Table S3. Cryo-EM data collection, refinement and validation statistics, related to Figure 4.**

	Echovirus 6 bound to FcRn pH 7.4 (EMDB-9687) (PDB 6ILM)	Echovirus 6 bound to FcRn pH 5.5 (EMDB-9686) (PDB 6ILL)
<b>Data collection and processing</b>		
Magnification	37037	37037
Voltage (kV)	300	300
Electron exposure (e <sup>-</sup> /Å <sup>2</sup> )	40	40
Defocus range (µm)	-1.0 to -3.0	-1.0 to -3.0
Pixel size (Å)	1.35	1.35
Symmetry imposed	Icosahedral	Icosahedral
Initial particle images (no.)	233531	42367
Final particle images (no.)	26153	937
Map resolution (Å)	3.4	3.8
FSC threshold	0.143	0.143
Map resolution range (Å)	3.0-6.5	3.0-8.0
<b>Refinement</b>		
Initial model used (PDB code)	Echovirus 6	Echovirus 6
Model resolution (Å)	3.4	3.8
Model resolution range (Å)	540.0-3.4	540.0-3.8
Map sharpening <i>B</i> factor (Å <sup>2</sup> )	-151	-78
Model map FSC (masked)	0.77	0.81
Model composition		
Non-hydrogen atoms	9535	6473
Protein residues	1202	821
Ligands	1	0
<i>B</i> factors (Å <sup>2</sup> )		
Protein	54	72
Ligand	41	-
R.m.s. deviations		
Bond lengths (Å)	0.004	0.006
Bond angles (°)	1.11	1.19
Validation		
MolProbity score	1.65	1.98
Clashscore	4.6	6.1
Poor rotamers (%)	0.29	1.24
Ramachandran plot		
Favored (%)	93.9	89.2
Allowed (%)	5.9	10.7
Disallowed (%)	0.2	0.1