Supplementary Table S1. Data collection and refinement statistics

PDB code	7XXU	7XXV	7XXW	7XXX	7XXY	7XXZ	human Gal-10 5XRH
Resolution (Å)	19.99-1.80 (1.84-1.80)	19.97-1.60 (1.63-1.60)	19.96-1.63 (1.66-1.63)	19.99-1.94 (1.99-1.94)	19.47-1.92 (1.97-1.92å)	19.54-1.83 (1.87-1.83)	19.50-1.55 (1.58-1.55)
Space group	$P6_522$	$P6_522$	$P6_522$	$P6_522$	$P6_522$	$P6_522$	$P6_522$
Unit cell parameters (a, b, c) (Å), (α, β, γ) (°)	(48.53, 48.53, 258.91), (90.00, 90.00, 120.00)	(48.53, 48.53, 258.57), (90.00, 90.00, 120.00)	(48.86, 48.86, 259.47), (90.00, 90.00, 120.00)	(48.59, 48.59, 258.91), (90.00, 90.00, 120.00)	(48.60, 48.62, 256.27), (90.00, 90.00, 119.99)	(48.72, 48.72, 259.20), (90.00, 90.00, 120.00)	(48.56, 48.56, 260.33), (90.00, 90.00, 120.00)
No. of measured reflections	289574 (17117)	4266594 (7893)	429428 (18387)	261243 (18307)	264291 (17271)	157494 (9846)	489727 (17756)
No. of unique reflections	17996 (1029)	24980 (1152)	24277 (1145)	14536 (962)	14830 (941)	17232 (1034)	27731 (1288)
Completeness (%)	99.9 (100.0)	99.7 (95.7)	99.9 (100.0)	99.9 (100.0)	99.9 (100.0)	99.6 (99.8)	99.7 (96.9)
Multiplicity	16.1 (16.6)	17.1 (6.9)	17.7 (16.1)	18.0 (19.0)	17.8 (18.4)	9.1 (9.5)	17.7 (13.8)
R_{merge} (%)	9.3 (37.9)	6.8 (76.8)	6.5 (46.9)	9.5 (57.8)	10.3 (74.1)	10.0 (65.0)	8.0 (45.3)
$\langle I/\delta(I)\rangle$	20.1 (6.1)	26.5 (2.6)	26.5 (5.0)	22.6 (5.5)	21.1 (4.6)	14.0 (3.0)	24.3 (6.7)
R_{model} (%)	18.43	17.57	17.71	17.60	17.39	17.70	17.15

R_{free} (%)	21.72	19.29	20.54	21.21	20.90	20.77	19.57
Rmsd bond lengths (Å)	0.006	0.006	0.005	0.006	0.006	0.006	0.006
Rmsd bond angles (°)	0.853	0.92	0.853	0.886	0.934	0.908	0.905
Number of atoms							
Protein	1129	1129	1129	1132	1132	1132	1123
Ligand	-	45	6	-	23	6	-
Water	189	171	166	190	31	204	188
Average B factors (Å^2) (protein/ligand/solvent)	18.97/-/30.45	16.85/24.16/29.42	19.57/32.55/30.80	21.632/-/33.06	24.47/33.92/34.18	19.08/30.38/31.03	16.71/-/29/64
Ramachandran plot[f] residues in favored regions (%)	97.78	97.78	97.78	97.06	97.79	97.79	97.90
Ramachandran plot[f] residues in allowed regions (%)	1.48	1.48	1.48	2.21	1.47	1.47	1.4
Ramachandran plot[f] residues in outliers regions (%)	0.74	0.74	0.74	0.74	0.74	0.74	0.7
Substrate/Ligand	-	Lactose	Glycerol	-	Lactose	Glycerol	-