Supporting Information

Substituted polyfluoroaryl interactions with an arginine side chain in galectin-3 are governed by steric-, desolvation and electronic conjugation effects

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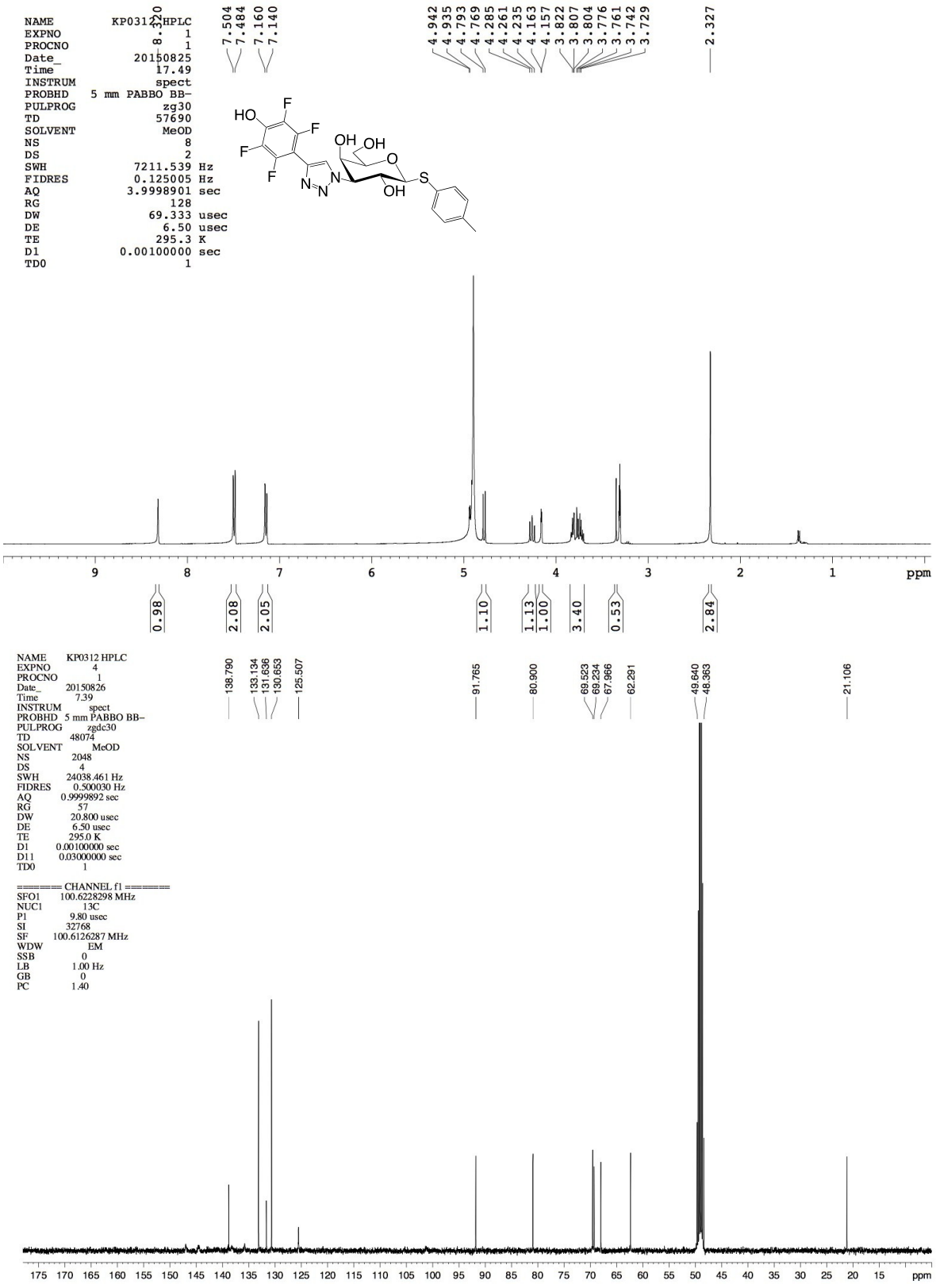
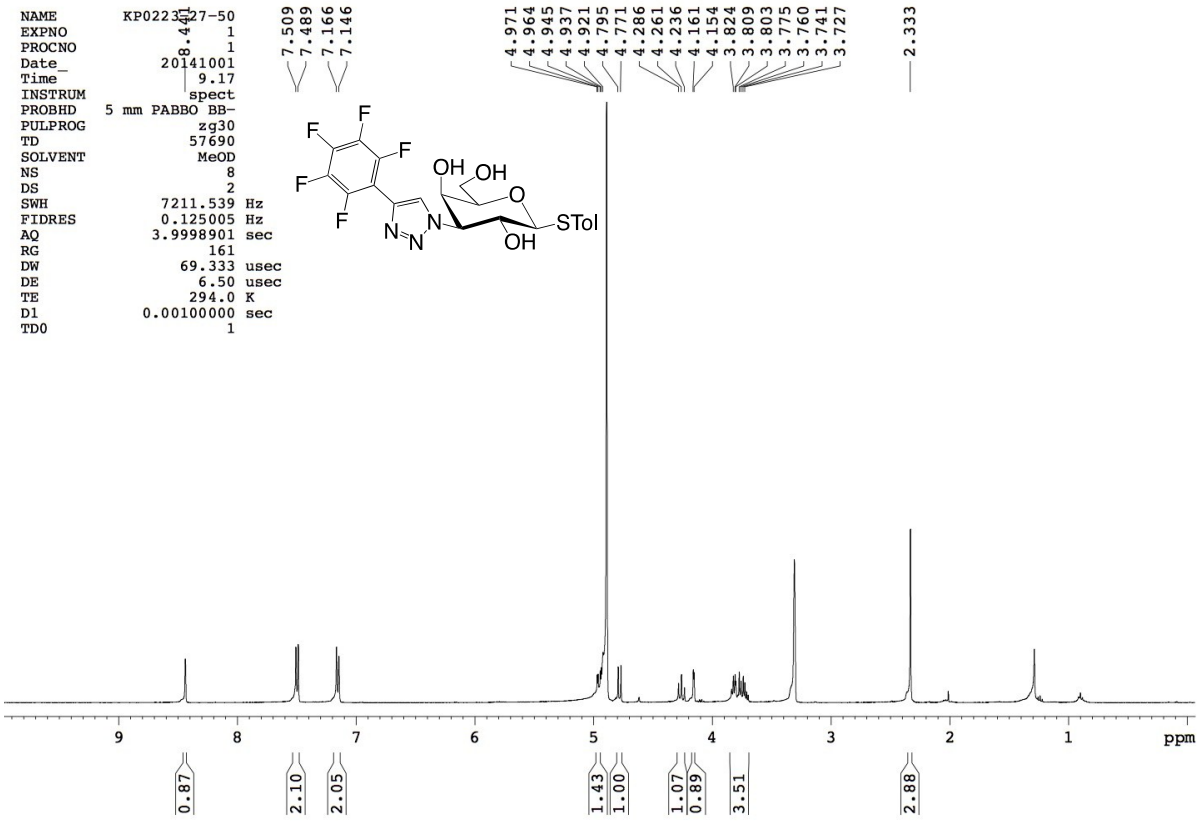
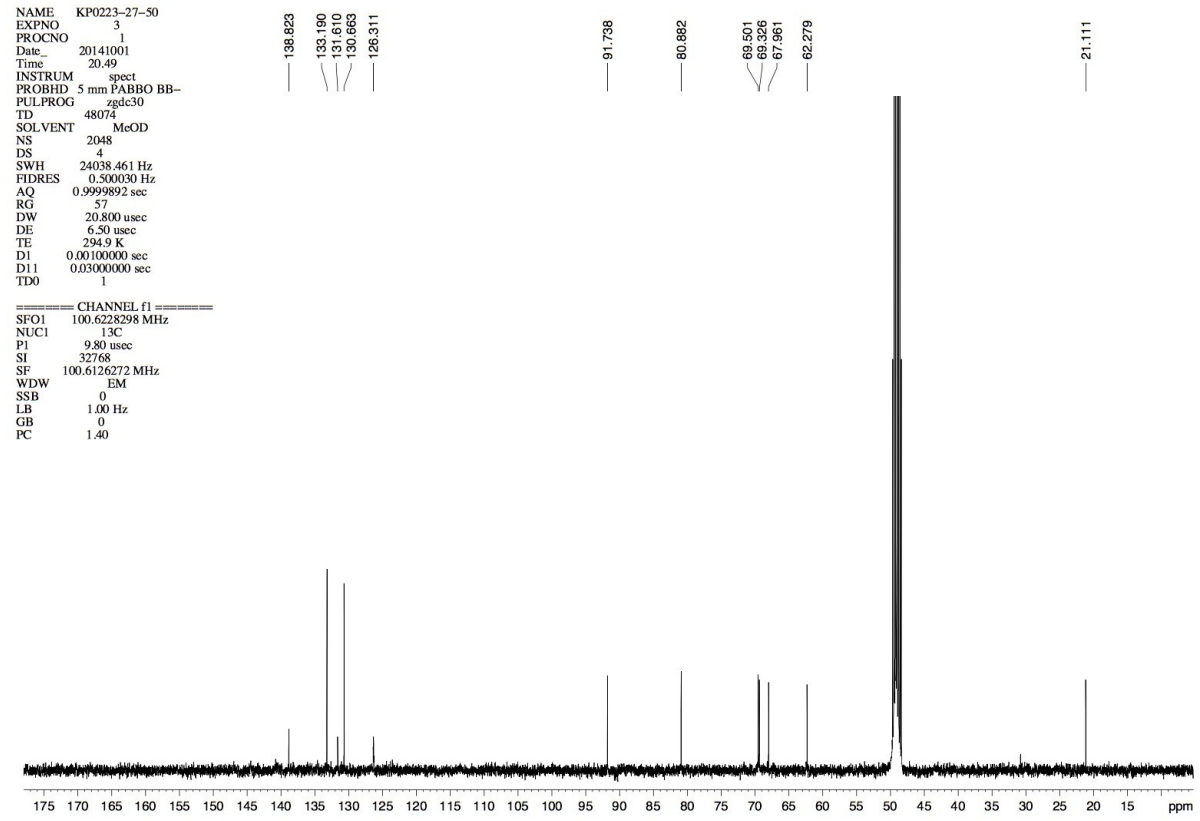
NMR spectra of synthesized compounds

***p*-Methylphenyl 3-deoxy-3-[4-(2,3,5,6-tetrafluoro-4-hydroxyphenyl)-1*H*-1,2,3-triazol-1-yl]-1-thio-β-D-galactopyranoside (2)**

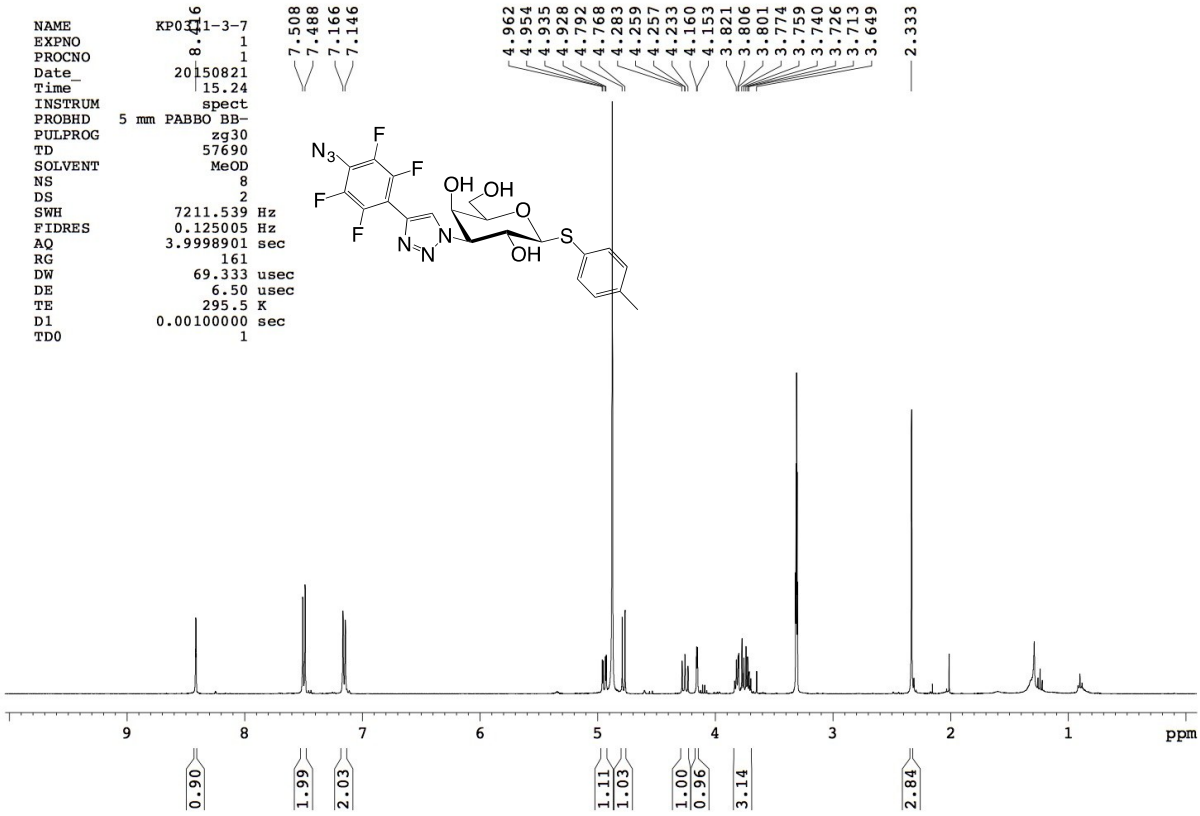


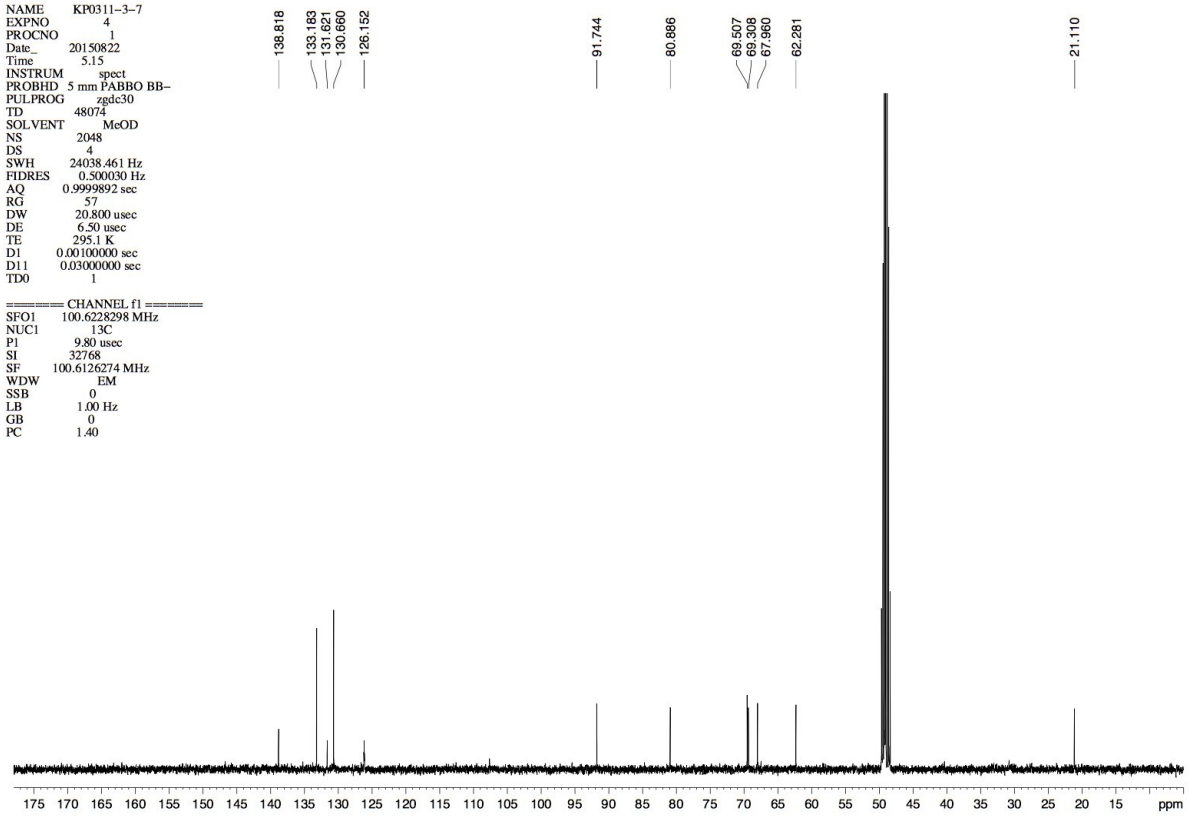
***p*-Methylphenyl 3-deoxy-3-[4-(2,3,4,5,6-pentafluorophenyl)-1*H*-1,2,3-triazol-1-yl]-1-thio-β-D-galactopyranoside (3)**



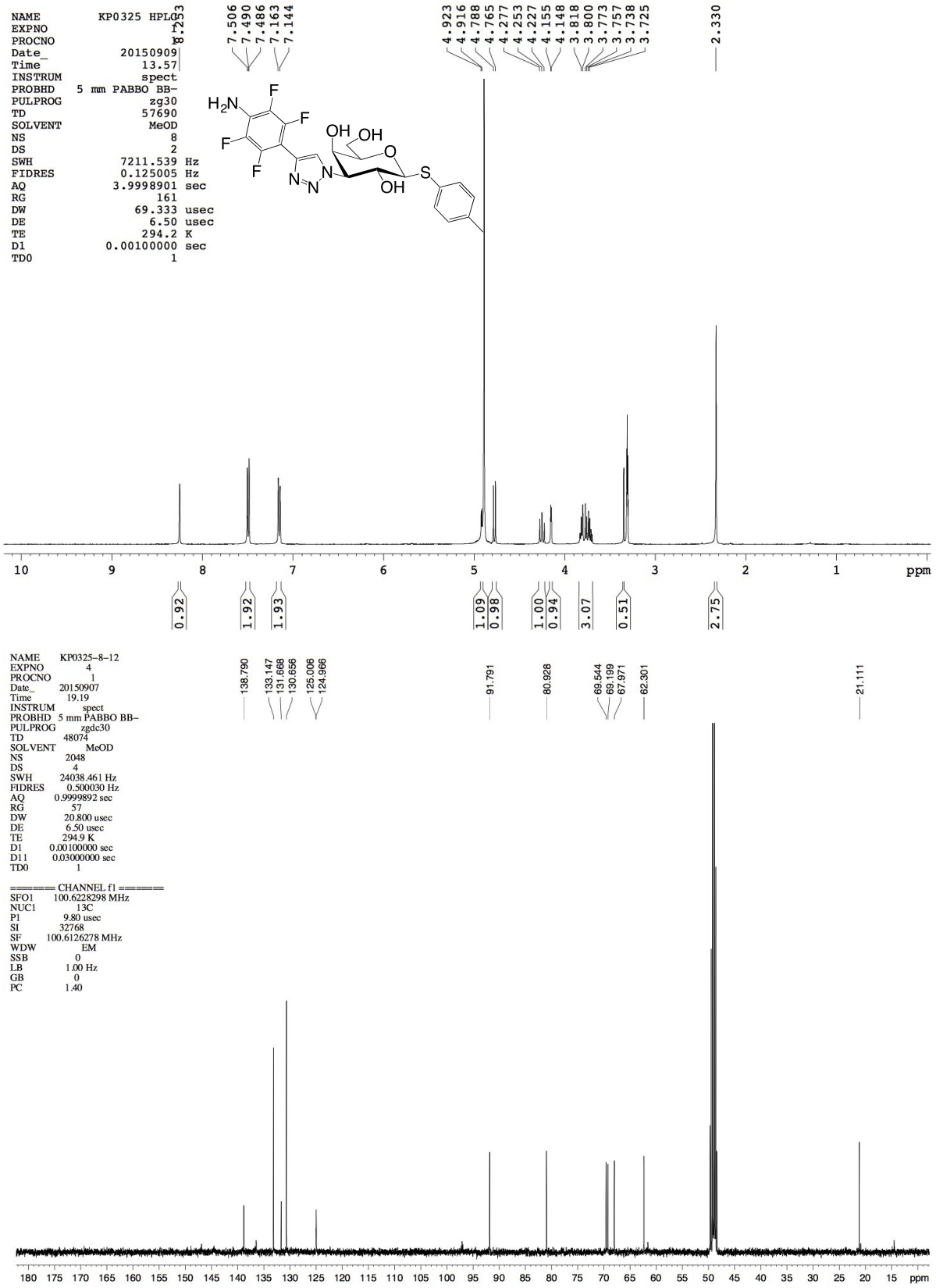


***p*-Methylphenyl 3-deoxy-3-[4-(4-azido-2,3,5,6-tetrafluorophenyl)-1*H*-1,2,3-triazol-1-yl]-1-thio-β-D-galactopyranoside (4)**

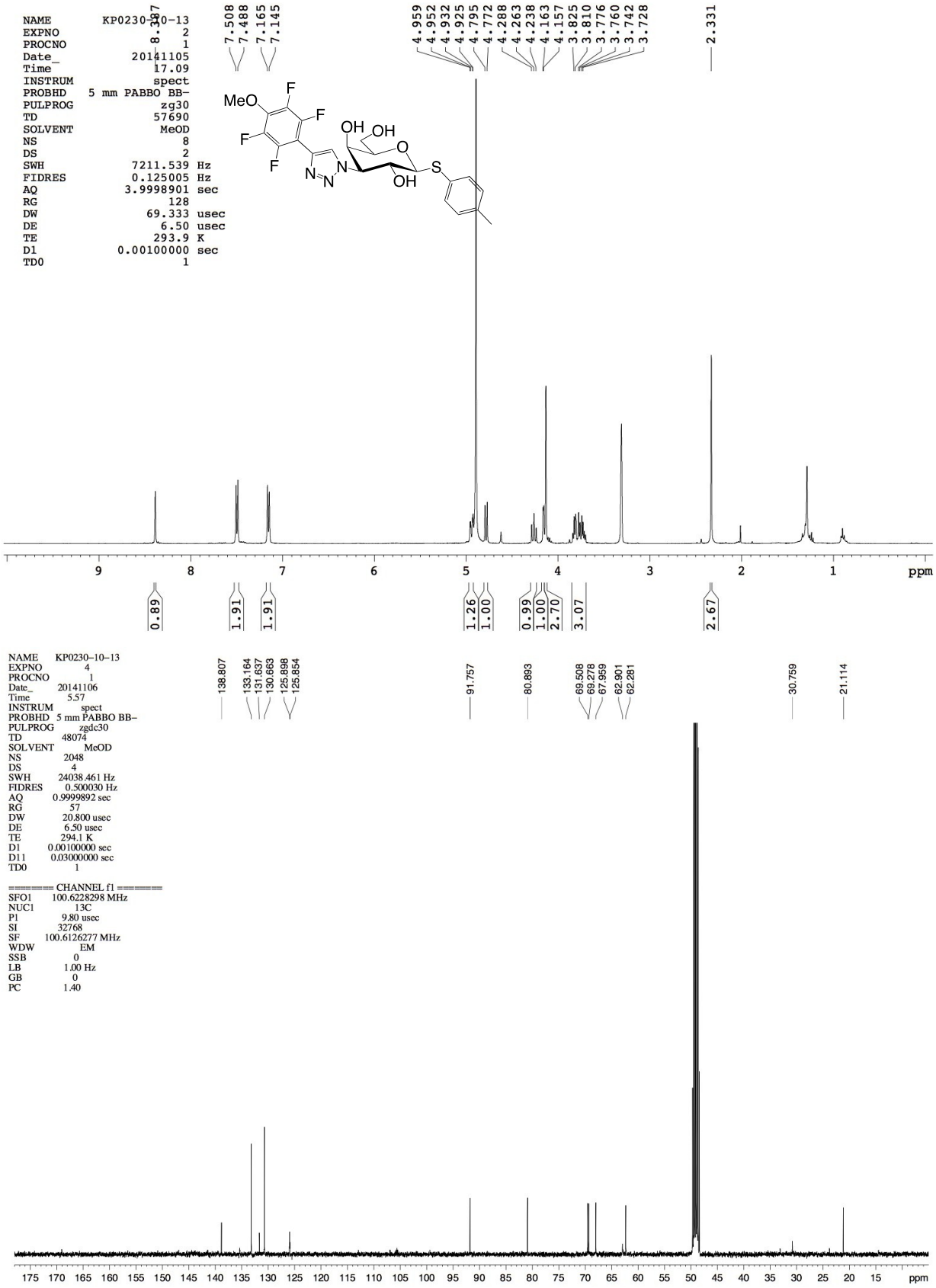




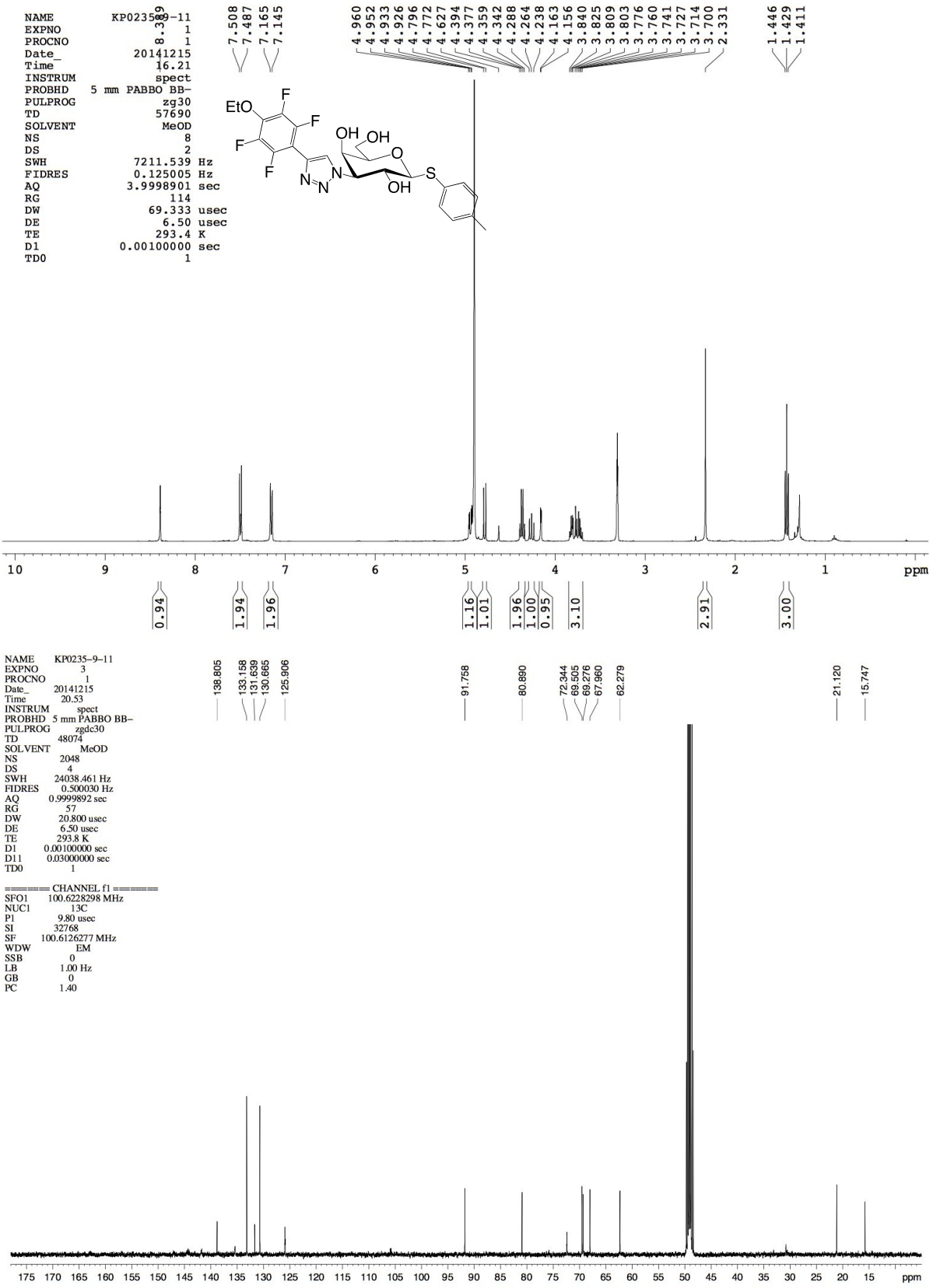
***p*-Methylphenyl 3-deoxy-3-[4-(4-amino-2,3,5,6-tetrafluorophenyl)-1*H*-1,2,3-triazol-1-yl]-1-thio-β-D-galactopyranoside (5)**



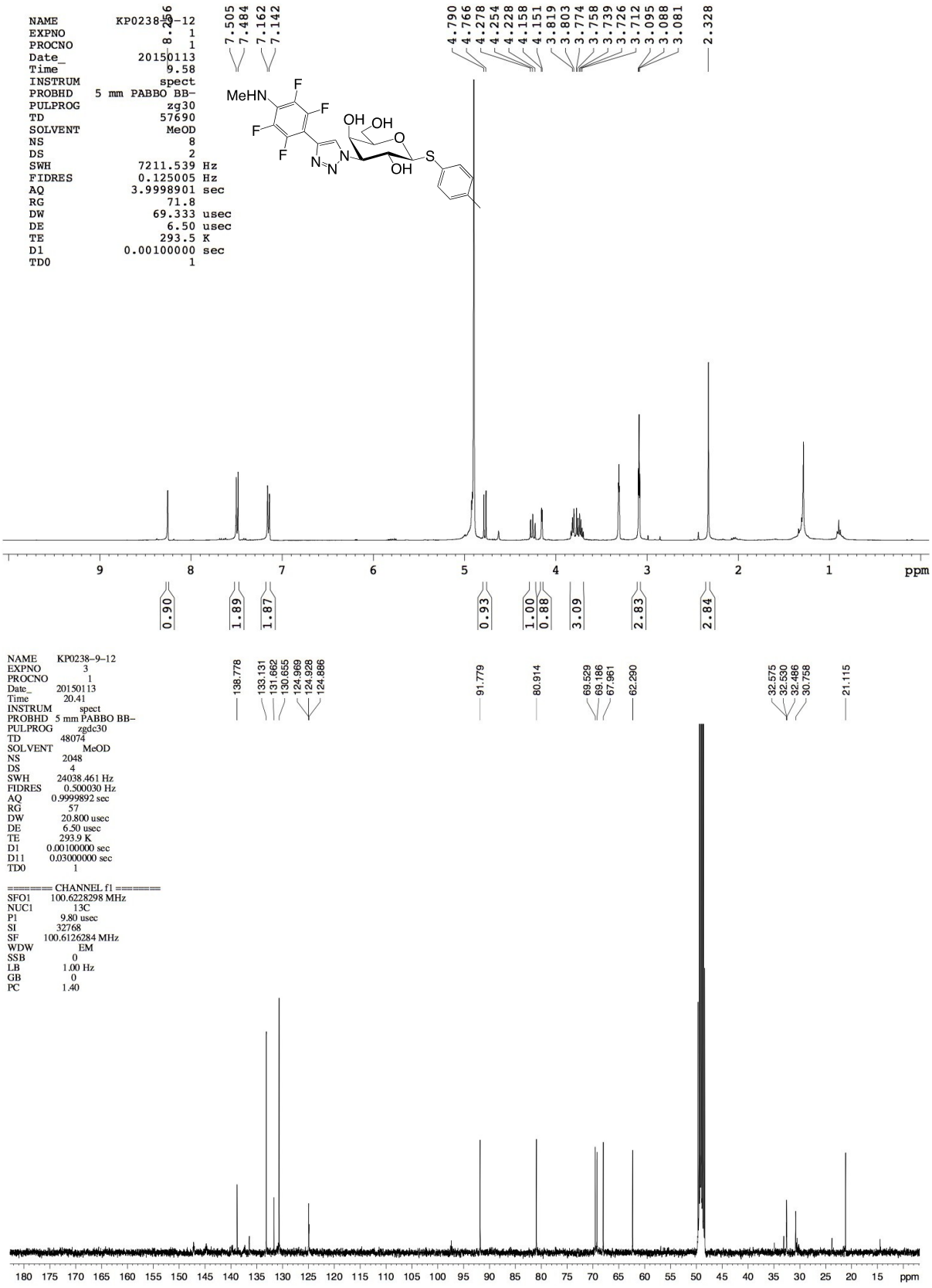
***p*-Methylphenyl 3-deoxy-3-[4-(2,3,5,6-tetrafluoro-4-methoxyphenyl)-1*H*-1,2,3-triazol-1-yl]-1-thio-β-D-galactopyranoside (6)**



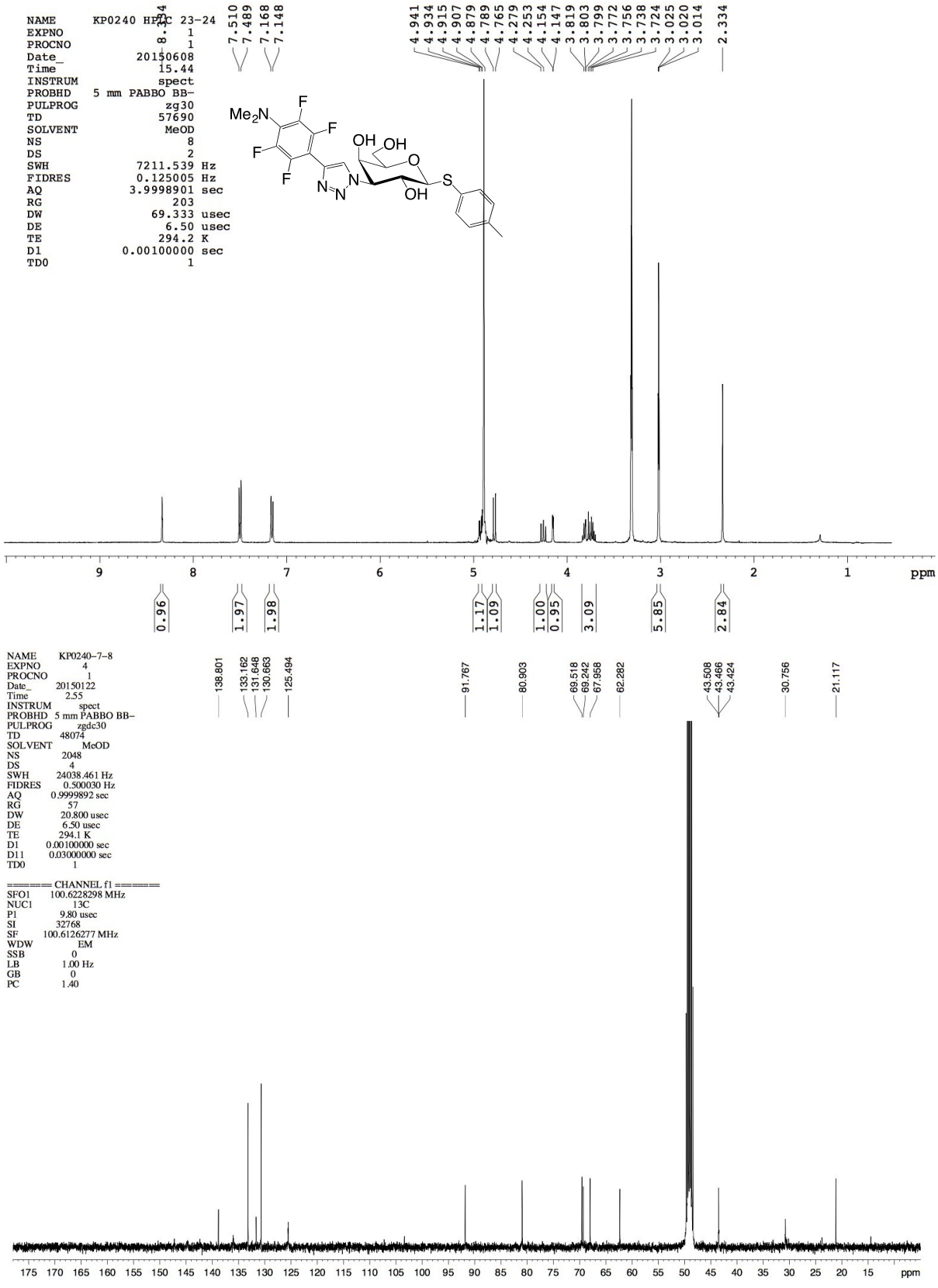
***p*-Methylphenyl 3-deoxy-3-[4-(4-ethoxy-2,3,5,6-tetrafluorophenyl)-1*H*-1,2,3-triazol-1-yl]-1-thio-β-D-galactopyranoside (7)**



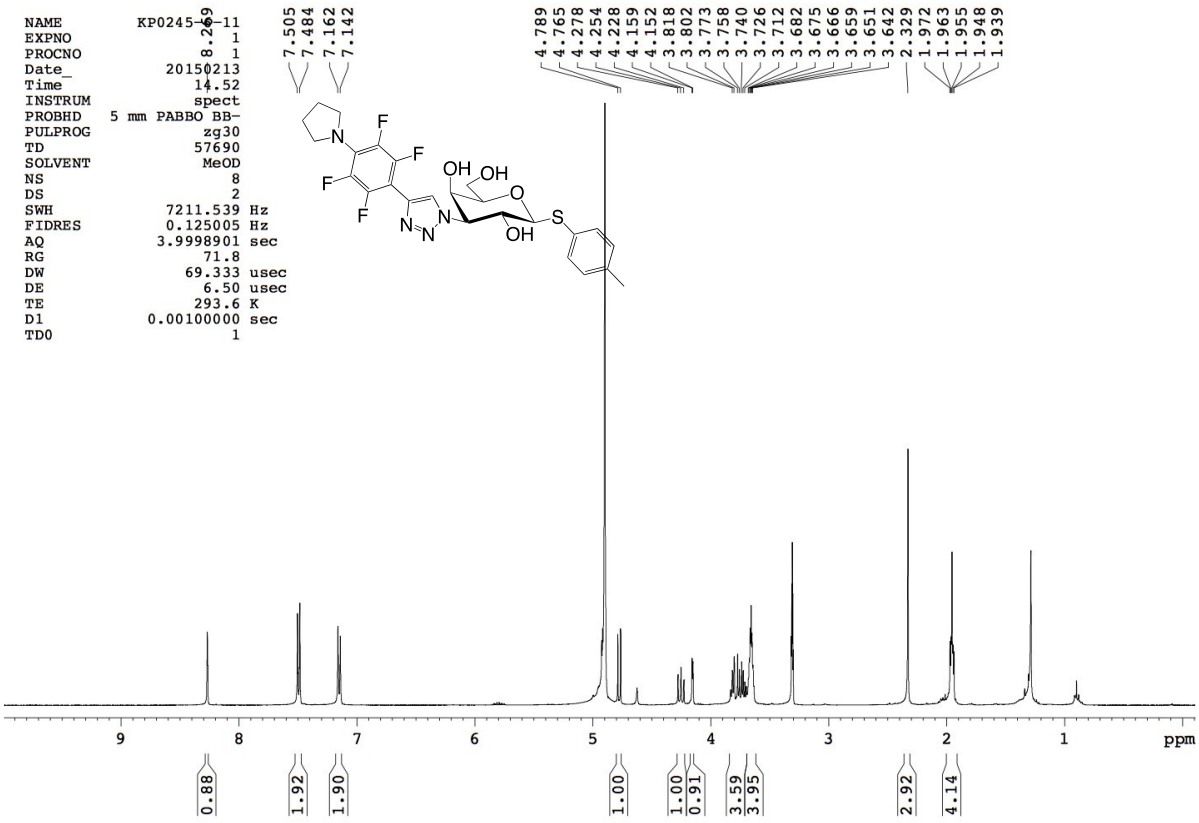
***p*-Methylphenyl 3-deoxy-3-{4-[2,3,5,6-tetrafluoro-4-(methylamino)phenyl]-1*H*-1,2,3-triazol-1-yl}-1-thio-β-D-galactopyranoside (8)**



***p*-Methylphenyl 3-deoxy-3-{4-[2,3,5,6-tetrafluoro-4-(dimethylamino)phenyl]-1*H*-1,2,3-triazol-1-yl}-1-thio-β-D-galactopyranoside (9)**



***p*-Methylphenyl 3-deoxy-3-{4-[2,3,5,6-tetrafluoro-4-(pyrrolidin-1-yl)phenyl]-1*H*-1,2,3-triazol-1-yl}-1-thio-β-D-galactopyranoside (10)**



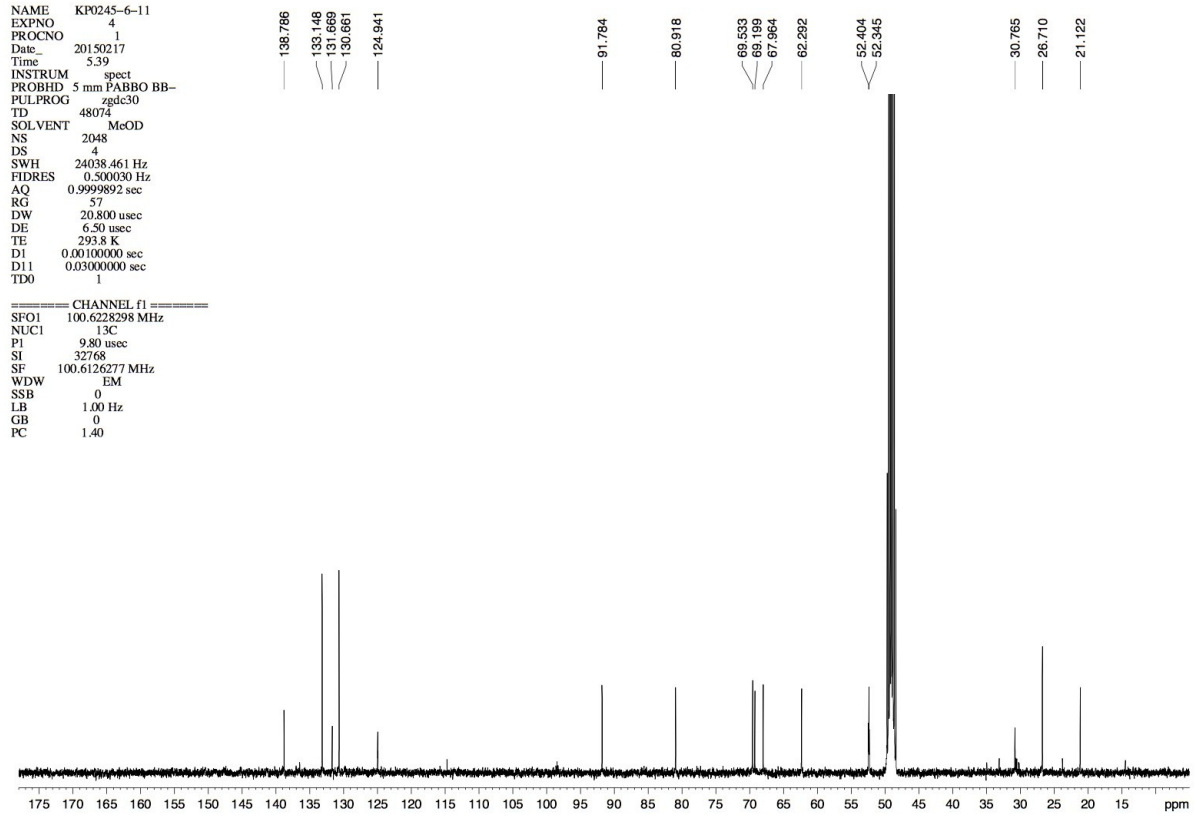


Table S1. Data processing and refinement statistics for the X-ray crystal structures.

Values in parentheses are for the highest resolution shell, unless noted otherwise.

compound	**2**	**3**	**4**	**5**	**8**
PDB code	**6l75**	**6l74**	**6l76**	**6l77**	**6l78**
station	ID23-2	I911-3	I911-3	I911-3	I911-3
wavelength [Å]	0.8760	1.000	1.000	1.000	1.000
unit cell (Å)	a = 34.38 b = 57.59 c = 60.88	a =36.65 b = 57.78 c = 62.75	a = 35.83 b = 57.62 c = 62.97	a = 35.89 b = 57.41 c = 62.84	a = 36.31 b= 57.63 c= 62.91
space group	$P2_12_12_1$	$P2_12_12_1$	$P2_12_12_1$	$P2_12_12_1$	$P2_12_12_1$
resolution range [Å]	41.86 – 1.17 (1.21 – 1.17)	26.24 – 0.95 (0.99 – 0.95)	28.81 – 1.22 (1.24 – 1.2)	31.42 – 1.21 (1.26 – 1.21)	27.61 – 1.15 (1.19 – 1.15)
completeness [%]	99.7 (97.7)	94.4 (78.5)	95.1 (90.7)	99.0 (96.7)	95.8 (89.2)
Total reflections **unique reflections**	435982 (43612) 41460 (4090)	448003 (22191) 77623 (6409)	244694 (23484) 39599 (3765)	252226 (23700) 39442 (3764)	120862 (8581) 45668 (4211)
CC1/2	0.999 (0.421)	1.000 (0.409)	0.999 (0.141)	0.999 (0.207)	0.999 (0.706)
multiplicity	10.5 (10.7)	5.8 (3.5)	6.2 (6.2)	6.4 (6.1)	2.6 (2.0)
R_{merge} [%]	0.149 (2.26)	0.043 (1.207)	0.138 (3.476)	0.113 (1.624)	0.042 (0.545)
mean I/σ(I)	10.10 (1.1)	24.15 (0.93)	12.41 (0.49)	10.85 (1.00)	13.20 (1.50)
Wilson B-factor [Å^2]	9.8	7.4	12.3	10.7	10.8
R_{model} (F) [%]	0.143 (0.245)	0.131 (0.338)	0.162 (0.347)	0.161 (0.317)	0.138 (0.277)
R_{free} (F) [%]	0.170 (0.262)	0.147 (0.371)	0.193 (0.370)	0.200 (0.336)	0.168 (0.277)
reflections used in refinement (for R_{free})	41363 (3995) 2076 (197)	77550 (6369) 3898 (295)	39495 (3692) 1973 (217)	39078 (3763) 1971 (183)	45664 (4206) 2309 (212)
average B-factors [Å^2]	protein: 12.8 ligand: 22.1 solvent: 26.4	protein: 9.3 ligand: 13.6 solvent: 23.0	protein: 15.9 ligand: 28.8 solvent: 33.4	protein: 13.7 ligand: 25.2 solvent: 27.9	protein: 12.3 ligand: 24.9 solvent: 25.9
Ramachandran outliers [%]	0.0	0.0	0.74	0.0	0.0
rotamer outliers [%] **MolProbity clash score**	1.52 0.86	0.0 3.29	0.0 1.70	0.0 1.26	0.0 2.48
bond length rmsd from ideal [Å] **bond angle rmsd from ideal [°]**	0.022 1.62	0.010 1.17	0.007 1.02	0.009 1.04	0.016 1.36