

Supplementary information

Enhanced inhibitory activity of compounds containing purine scaffolds compared to protein kinase CK2 α considering crystalline water

Keiji Nishiwaki,^{*a} Shiori Nakatani,^a Shinya Nakamura,^a Kenji Yoshioka,^a Eri Nakagawa,^a Masato Tsuyuguchi,^{b‡} Takayoshi Kinoshita,^b Isao Nakanishi ^{*ac}

^a Department of Pharmaceutical Sciences, Faculty of Pharmacy, Kindai University, 3-4-1 Kowakae, Higashiosaka, Osaka 577-8502, Japan

^b Graduate School of Science, Osaka Metropolitan University, 1-1 Gakuen-cho, Naka-ku, Sakai, Osaka 599-8531, Japan

^c Antiaging Center, Kindai University, 3-4-1 Kowakae, Higashiosaka, Osaka 577-8502, Japan.

[‡] Present address: High Energy Accelerator Research Organization (KEK), Institute of Materials Structure Science, Structural Biology Research Center, 1-1 Oho, Tsukuba, Ibaraki 305-0801, Japan

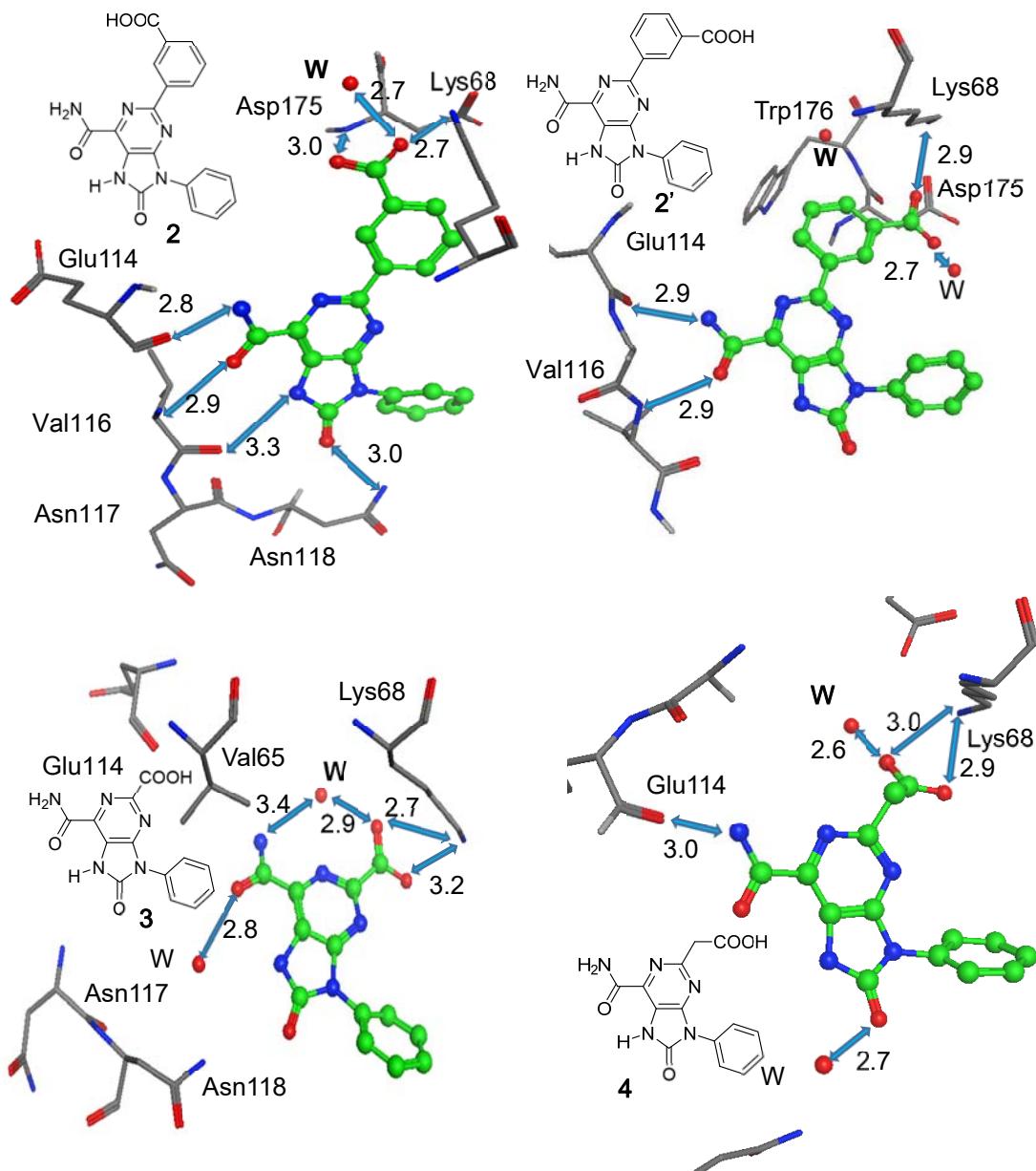
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Trajectory files (zip) of the MD simulation of compounds 2–7 can be downloaded from
<https://doi.org/10.7910/DVN/MMVYEC>

1. Molecular dynamics simulations

1.1 Complex structures of compounds and CK2 α after MD simulation



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Figure S1-1. Complex structures of design compounds and CK2 α after MD simulation

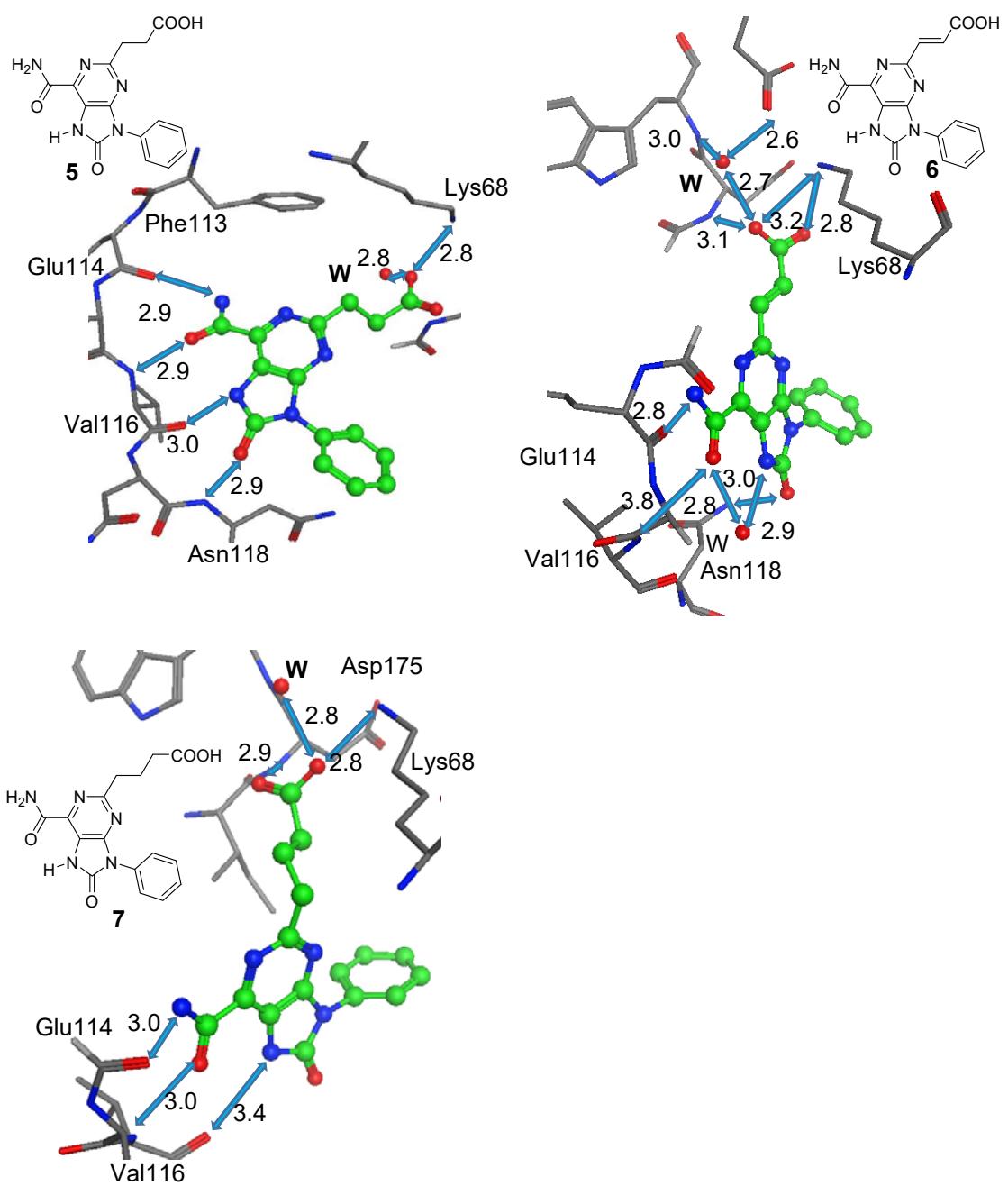


Figure S1-2. Complex structures of design compounds and CK2 α after MD simulation

1.2 Detailed data of calculation results

Table S1-1. RMSD, ΔG_{PBSA} and ΔG_{bind} of compound 1

Run	RMSD (Å)	ΔG_{PBSA} (kcal/mol)	ΔG_{bind} (kcal/mol)
1	2.12	-27.8	-2.67
2	3.10	-40.9	-6.73
3	2.92	-40.7	0.0
4	2.31	-35.8	-7.50
5	2.32	-35.3	-7.9
Average	2.55	-36.1	-5.0
$\pm \text{MAE}$	0.36	3.8	2.9

(MAE : Mean Absolute Error)

Table S1-2. Component analysis of ΔG_{PBSA} of compound 1

Run	E_{vdw}	E_{ele}	E_{PB}	E_{SA}	$E_{\text{interaction}}$	$E_{\text{desolvation}}$	E_{NonPolar}	E_{Polar}	ΔG_{PBSA}
1	-42.4	-163.9	181.9	-3.4	-206.3	178.5	-45.8	18.1	-27.8
2	-40.1	-146.3	148.9	-3.4	-186.5	145.5	-43.5	2.6	-40.9
3	-40.6	-171.0	174.3	-3.4	-211.7	171.0	-44.0	3.3	-40.7
4	-40.1	-151.4	158.9	-3.3	-191.4	155.6	-43.4	7.6	-35.8
5	-40.7	-133.7	142.5	-3.4	-174.4	139.1	-44.0	8.8	-35.3
Average	-40.8	-153.3	161.3	-3.4	-194.0	157.9	-44.2	8.1	-36.1

Table S2-1. RMSD, ΔG_{PBSA} and ΔG_{bind} of compound 2

Run	RMSD (Å)	ΔG_{PBSA} (kcal/mol)	ΔG_{bind} (kcal/mol)
1	3.39	-35.5	-14.0
2	3.71	-367	-13.6
3	3.30	-37.1	-3.2
4	3.68	-36.4	-2.3
5	3.21	-36.4	-1.2
Average	3.46	-36.4	-6.9
$\pm \text{MAE}$	0.19	0.4	5.6

Table S2-2. Component analysis of ΔG_{PBSA} of compound 2

Run	E_{vdw}	E_{ele}	E_{PB}	E_{SA}	$E_{\text{interaction}}$	$E_{\text{desolvation}}$	E_{NonPolar}	E_{Polar}	ΔG_{PBSA}
1	-38.6	-143.1	149.4	-3.2	-181.7	146.2	-41.8	6.3	-35.5

2	-39.3	-156.1	162.0	-3.3	-195.4	158.8	-42.6	5.9	-36.7
3	-39.7	-162.1	168.0	-3.3	-201.9	164.7	-43.0	5.9	-37.1
4	-40.2	-152.5	159.5	-3.3	-192.6	156.2	-43.4	7.0	-36.4
5	-38.8	-142.8	148.4	-3.2	-181.6	145.3	-42.0	5.6	-36.4
Average	-39.3	-151.3	157.5	-3.2	-190.7	154.2	-42.6	6.1	-36.4

Table S3-1. RMSD, ΔG_{PBSA} and ΔG_{bind} of compound 2'

Run	RMSD (\AA)	ΔG_{PBSA} (kcal/mol)	ΔG_{bind} (kcal/mol)
1	3.05	-39.6	16.2
2	2.51	-40.2	6.3
3	1.26	-34.6	1.5
4	1.48	-34.5	-4.5
5	2.22	-37.7	10.6
Average	2.10	-37.3	6.0
$\pm \text{MAE}$	0.59	2.2	6.0

Table S3-2. Component analysis of ΔG_{PBSA} of compound 2'

Run	E_{vdw}	E_{ele}	E_{PB}	E_{SA}	$E_{\text{interaction}}$	$E_{\text{desolvation}}$	E_{NonPolar}	E_{Polar}	ΔG_{PBSA}
1	-44.6	-128.8	137.1	-3.4	-173.4	133.8	-48.0	8.4	-39.6
2	-45.1	-165.0	173.5	-3.6	-210.1	169.9	-48.7	8.5	-40.2
3	-43.0	-133.1	144.9	-3.3	-176.1	141.6	-46.4	11.8	-34.6
4	-43.9	-133.4	146.2	-3.3	-177.3	142.9	-47.3	12.8	-34.5
5	-44.1	-144.1	153.9	-3.4	-188.2	150.5	-47.4	9.8	-37.7
Average	-44.2	-140.9	151.1	-3.4	-185.0	147.7	-47.5	10.2	-37.3

Table S4-1. RMSD, ΔG_{PBSA} and ΔG_{bind} of compound 3

Run	RMSD (\AA)	ΔG_{PBSA} (kcal/mol)	ΔG_{bind} (kcal/mol)
1	3.08	-16.0	21.7
2	2.47	-18.4	14.0
3	2.79	-23.3	15.3
4	4.65	-18.2	18.4
5	2.12	-23.4	9.3
Average	3.02	-19.9	15.7
$\pm \text{MAE}$	0.67	2.8	3.4

Table S4-2. Component analysis of ΔG_{PBSA} of compound 3

Run	E_{vdw}	E_{ele}	E_{PB}	E_{SA}	$E_{\text{interaction}}$	$E_{\text{desolvation}}$	E_{NonPolar}	E_{Polar}	ΔG_{PBSA}
1	-33.0	-119.3	138.8	-2.6	-152.3	136.2	-35.6	19.5	-16.0
2	-32.7	-143.4	160.4	-2.6	-176.1	157.7	-35.3	17.0	-18.4
3	-32.6	-148.0	159.8	-2.5	-180.6	157.3	-35.1	11.8	-23.3
4	-34.0	-170.0	188.5	-2.7	-203.9	185.8	-36.7	18.5	-18.2
5	-33.9	-138.7	151.9	-2.7	-172.6	149.2	-36.6	13.2	-23.4
Average	-33.2	-143.9	159.9	-2.6	-177.1	157.3	-35.8	16.0	-19.9

Table S5-1. RMSD, ΔG_{PBSA} and ΔG_{bind} of compound 4

Run	RMSD (\AA)	ΔG_{PBSA} (kcal/mol)	ΔG_{bind} (kcal/mol)
1	2.02	-31.8	-6.33
2	1.98	-29.6	5.1
3	2.86	-21.3	10.6
4	2.05	-32.6	4.7
5	2.00	-29.3	3.1
Average	2.18	-28.9	3.5
$\pm \text{MAE}$	0.27	3.0	4.1

Table S5-2. Component analysis of ΔG_{PBSA} of compound 4

Run	E_{vdw}	E_{ele}	E_{PB}	E_{SA}	$E_{\text{interaction}}$	$E_{\text{desolvation}}$	E_{NonPolar}	E_{Polar}	ΔG_{PBSA}
1	-37.3	-134.4	142.8	-2.9	-171.7	140.0	-40.2	8.4	-31.8
2	-35.6	-136.8	145.7	-2.9	-172.4	142.8	-38.5	8.9	-29.6
3	-34.1	-139.0	154.5	-2.8	-173.0	151.7	-36.9	15.5	-21.3
4	-35.1	-151.0	156.3	-2.8	-186.1	153.5	-37.8	5.2	-32.6
5	-36.3	-146.9	156.8	-2.9	-183.2	153.9	-39.2	9.9	-29.3
Average	-35.7	-141.6	151.2	-2.8	-177.3	148.4	-38.5	9.6	-28.9

Table S6-1. RMSD, ΔG_{PBSA} and ΔG_{bind} of compound 5

Run	RMSD (\AA)	ΔG_{PBSA} (kcal/mol)	ΔG_{bind} (kcal/mol)
1	2.53	-37.8	-3.4
2	2.40	-39.0	10.3
3	1.89	-32.6	2.1
4	2.11	-35.2	-5.5

5	1.94	-37.9	-6.0
Average	2.17	-36.5	-0.5
± MAE	0.23	2.1	5.4

Table S6-2. Component analysis of ΔG_{PBSA} of compound 5

Run	E_{vdw}	E_{ele}	E_{PB}	E_{SA}	$E_{\text{interaction}}$	$E_{\text{desolvation}}$	E_{NonPolar}	E_{Polar}	ΔG_{PBSA}
1	-36.7	-160.9	162.7	-2.9	-197.6	159.8	-39.6	1.8	-37.8
2	-35.8	-173.8	173.5	-2.8	-209.6	170.6	-38.6	-0.3	-39.0
3	-33.3	-151.4	155.0	-2.9	-184.7	152.1	-36.2	3.6	-32.6
4	-35.1	-163.4	166.2	-3.0	-198.5	163.2	-38.1	2.8	-35.2
5	-35.5	-169.1	169.6	-2.9	-204.5	166.7	-38.4	0.5	-37.9
Average	-35.3	-163.7	165.4	-2.9	-199.0	162.5	-38.2	1.7	-36.5

Table S7-1. RMSD, ΔG_{PBSA} and ΔG_{bind} of compound 6

Run	RMSD (Å)	ΔG_{PBSA} (kcal/mol)	ΔG_{bind} (kcal/mol)
1	2.02	-36.1	-7.2
2	1.46	-36.3	-10.3
3	1.66	-34.4	4.1
4	1.96	-39.2	-21.1
5	2.51	-41.9	-16.2
Average	1.92	-37.6	-10.1
± MAE	0.29	2.4	6.87

Table S7-2. Component analysis of ΔG_{PBSA} of compound 6

Run	E_{vdw}	E_{ele}	E_{PB}	E_{SA}	$E_{\text{interaction}}$	$E_{\text{desolvation}}$	E_{NonPolar}	E_{Polar}	ΔG_{PBSA}
1	-36.2	-161.2	164.2	-2.9	-197.4	161.3	-39.1	3.0	-36.1
2	-36.6	-157.3	160.5	-2.9	-193.8	157.6	-39.5	3.2	-36.3
3	-36.6	-166.8	172.1	-3.0	-203.5	169.1	-39.6	5.2	-34.4
4	-36.0	-141.2	141.1	-3.0	-177.3	138.1	-39.1	-0.1	-39.2
5	-36.8	-157.7	155.5	-2.9	-194.5	152.6	-39.7	-2.2	-41.9
Average	-36.4	-156.8	158.7	-2.9	-193.3	155.7	-39.4	1.8	-37.6

Table S8-1. RMSD, ΔG_{PBSA} and ΔG_{bind} of compound 7

Run	RMSD (Å)	ΔG_{PBSA} (kcal/mol)	ΔG_{bind} (kcal/mol)
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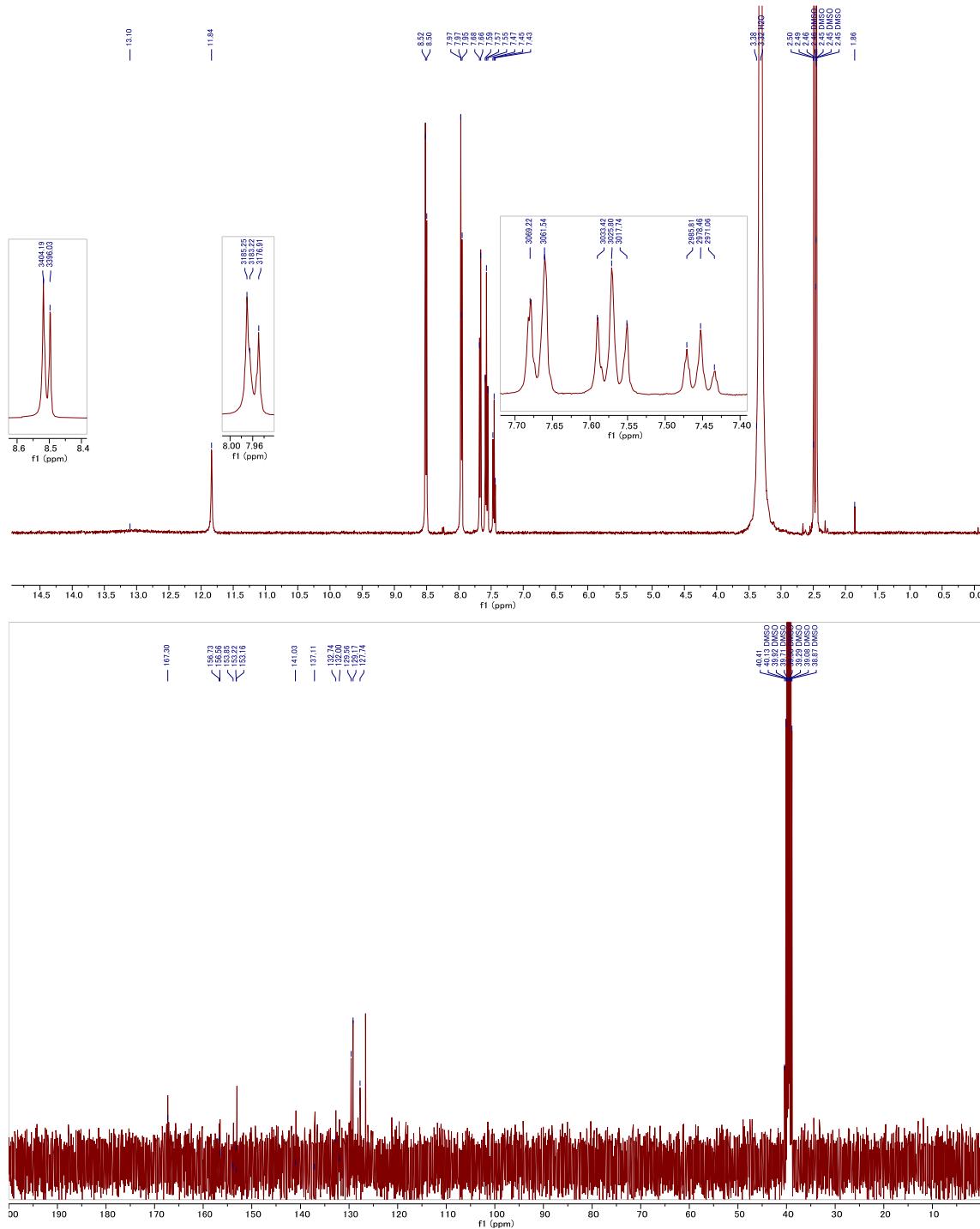
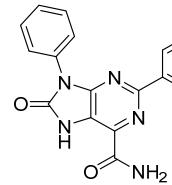
1	2.69	-35.4	6.8
2	2.10	-30.7	16.3
3	2.71	-27.8	38.8
4	1.80	-26.5	1.7
5	2.17	-32.7	4.3
Average	2.29	-30.6	13.6
±MAE	0.32	2.8	11.2

Table S8-2. Component analysis of ΔG_{PBSA} of compound 7

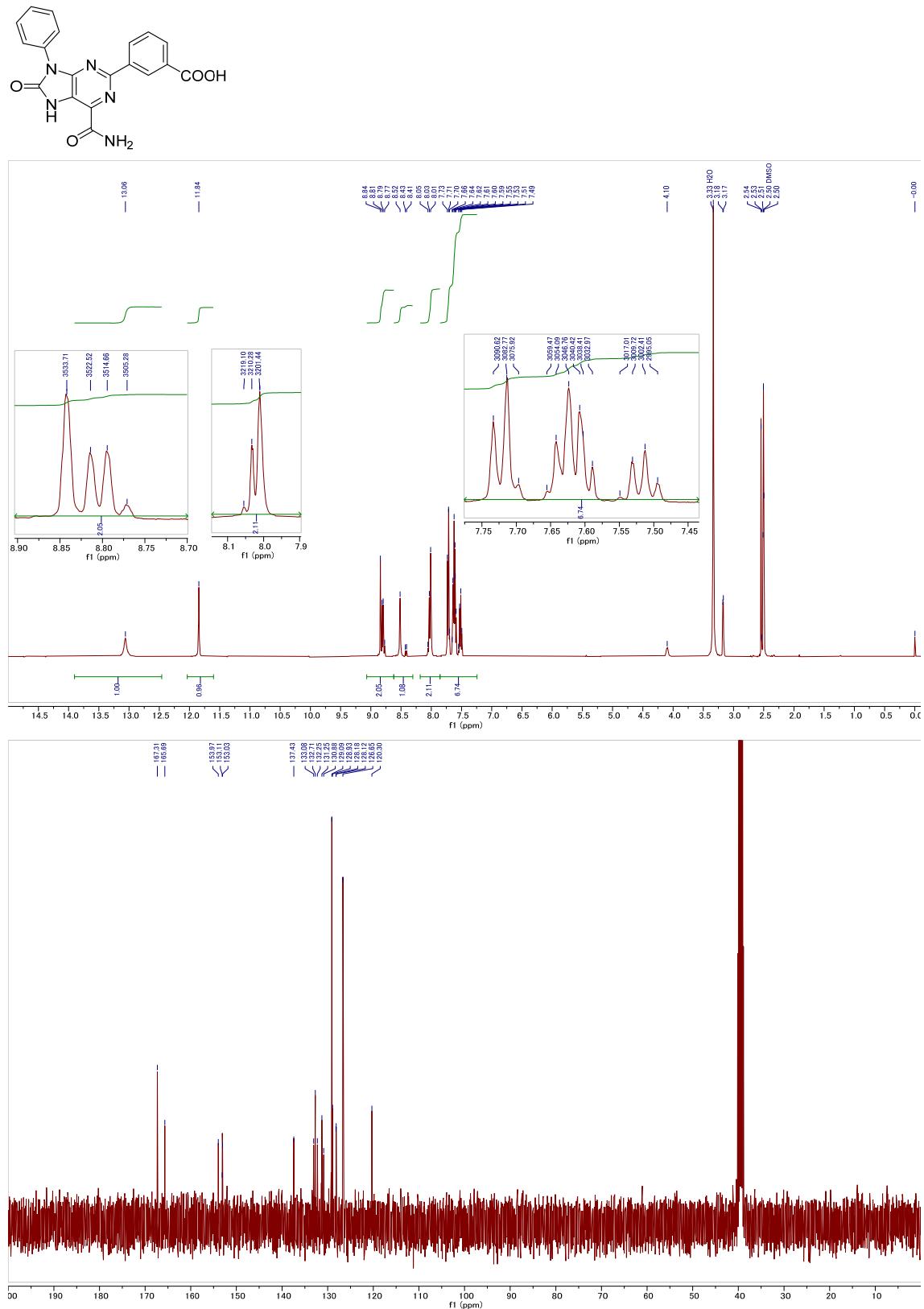
Run	E_{vdw}	E_{ele}	E_{PB}	E_{SA}	$E_{\text{interaction}}$	$E_{\text{desolvation}}$	E_{NonPolar}	E_{Polar}	ΔG_{PBSA}
1	-38.4	-130.5	136.6	-3.1	-168.9	133.5	-41.5	6.1	-35.4
2	-36.3	-151.7	160.4	-3.1	-187.9	157.3	-39.4	8.8	-30.7
3	-35.8	-145.1	156.3	-3.2	-180.9	153.1	-39.0	11.2	-27.8
4	-39.4	-152.1	168.1	-3.1	-191.5	165.0	-42.5	16.0	-26.5
5	-40.8	-148.7	159.9	-3.1	-189.5	156.7	-43.9	11.2	-32.7
Average	-38.1	-145.6	156.3	-3.1	-183.7	153.1	-41.3	10.7	-30.6

2. Spectral data

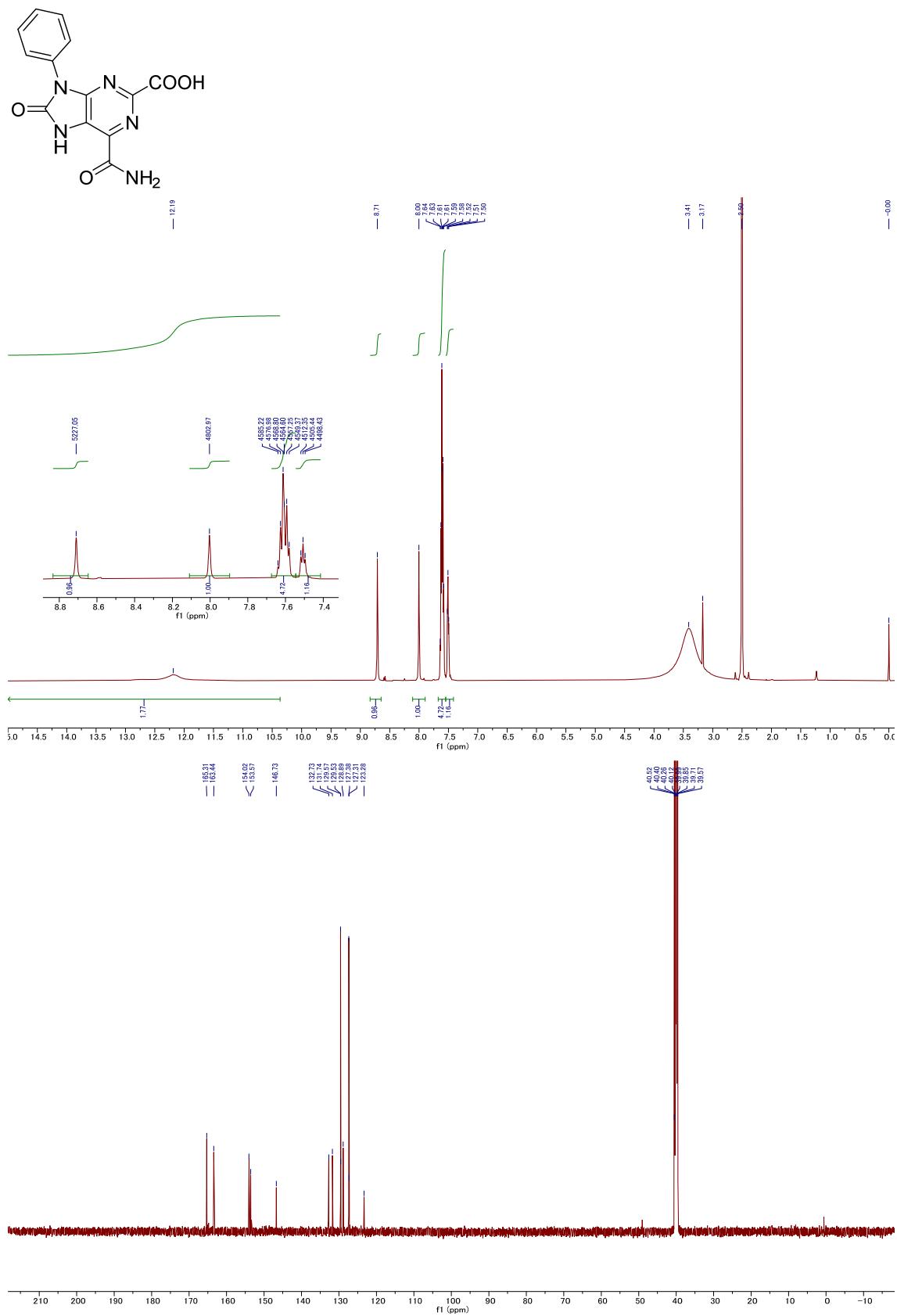
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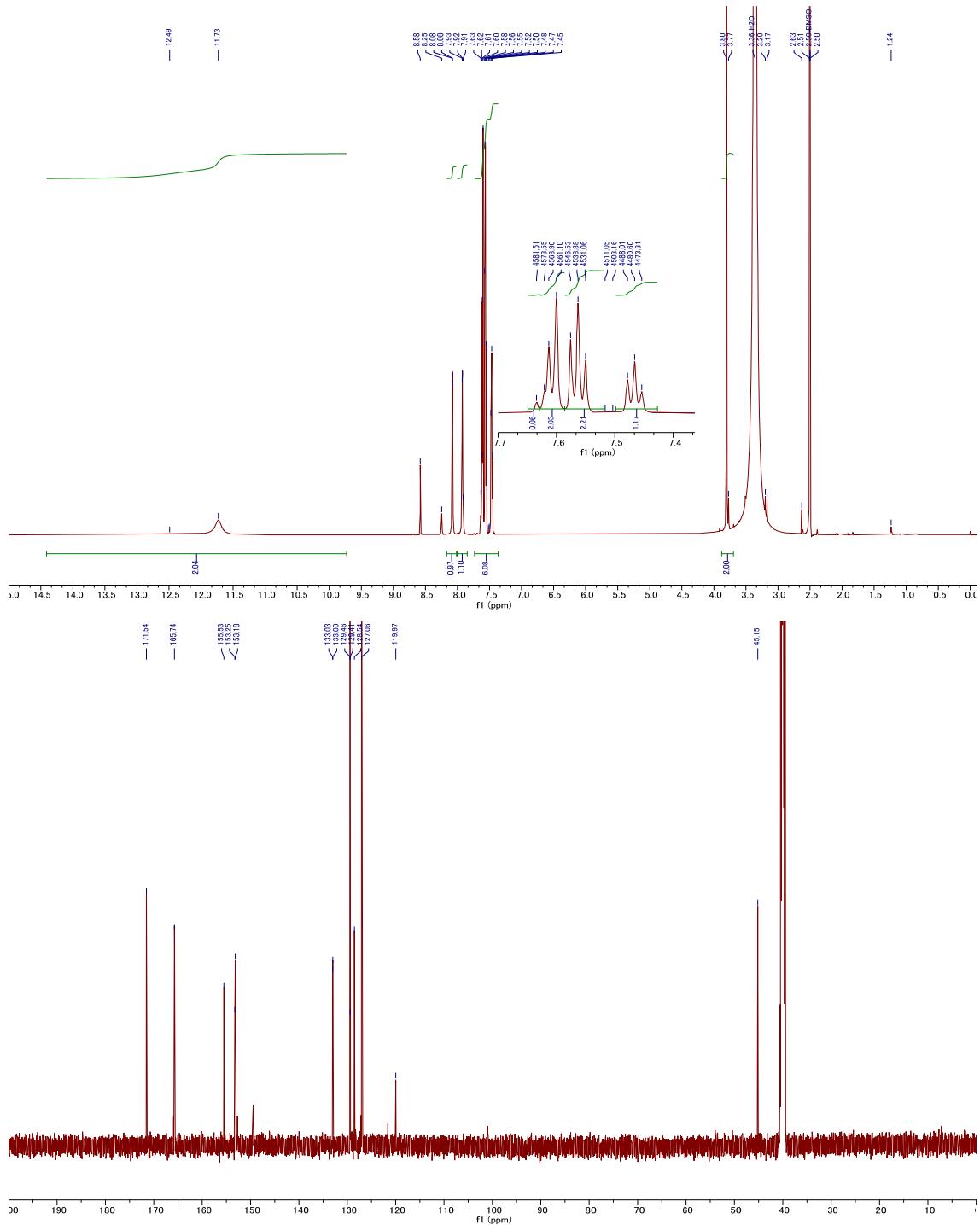
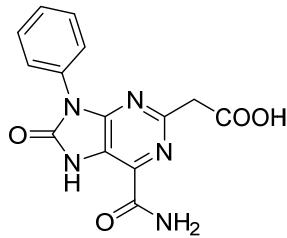
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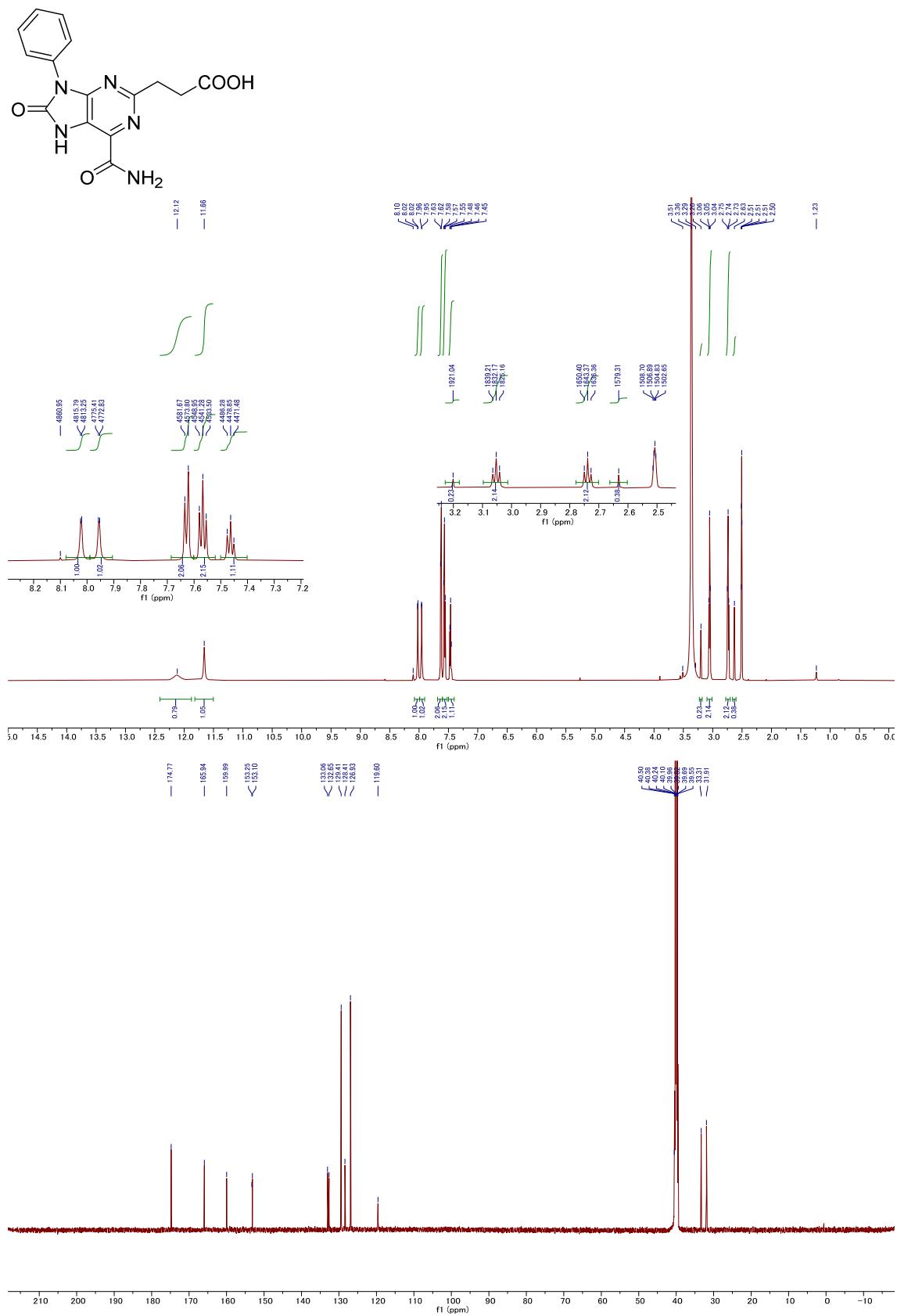
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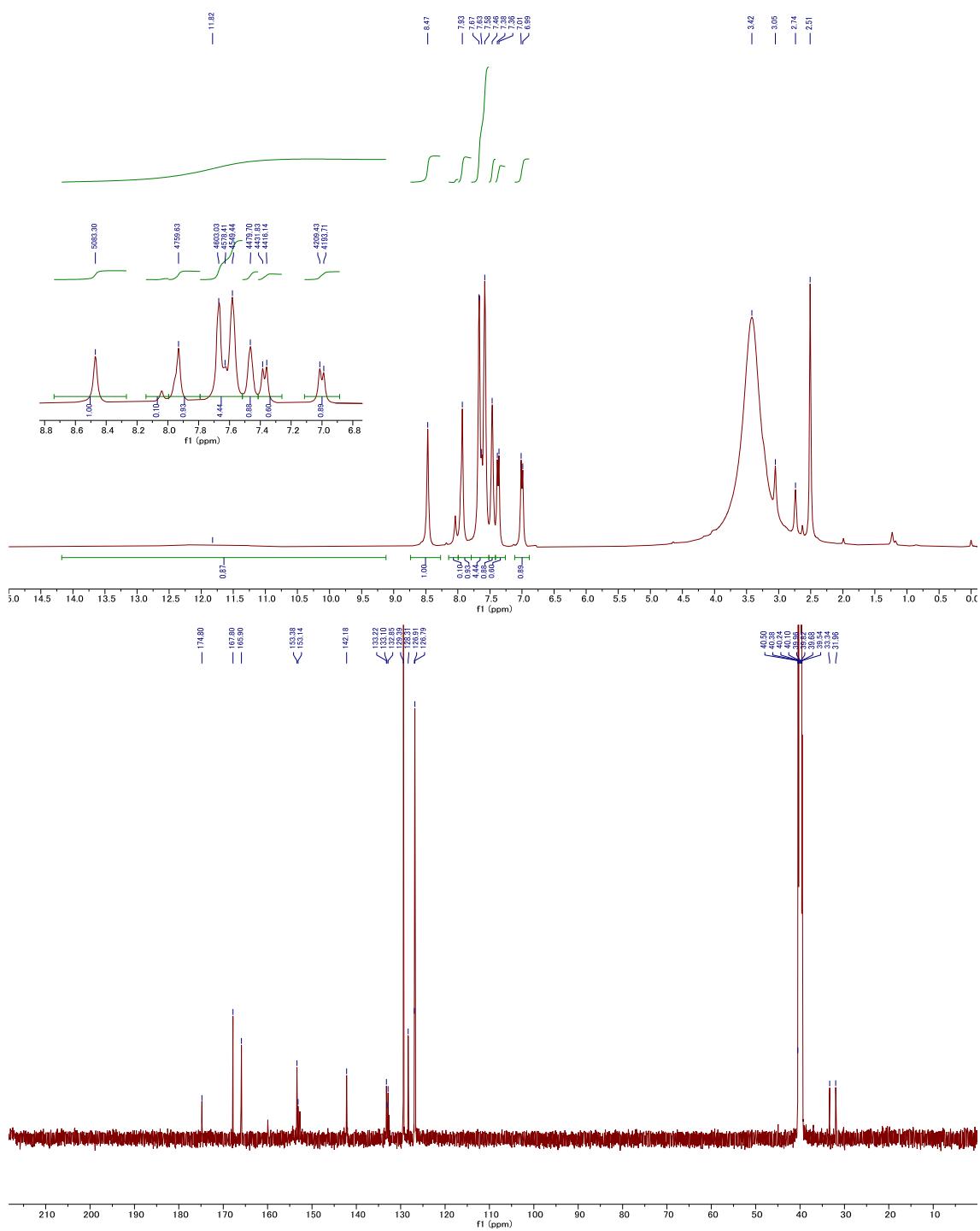
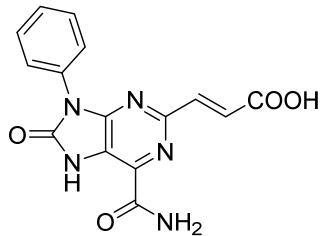
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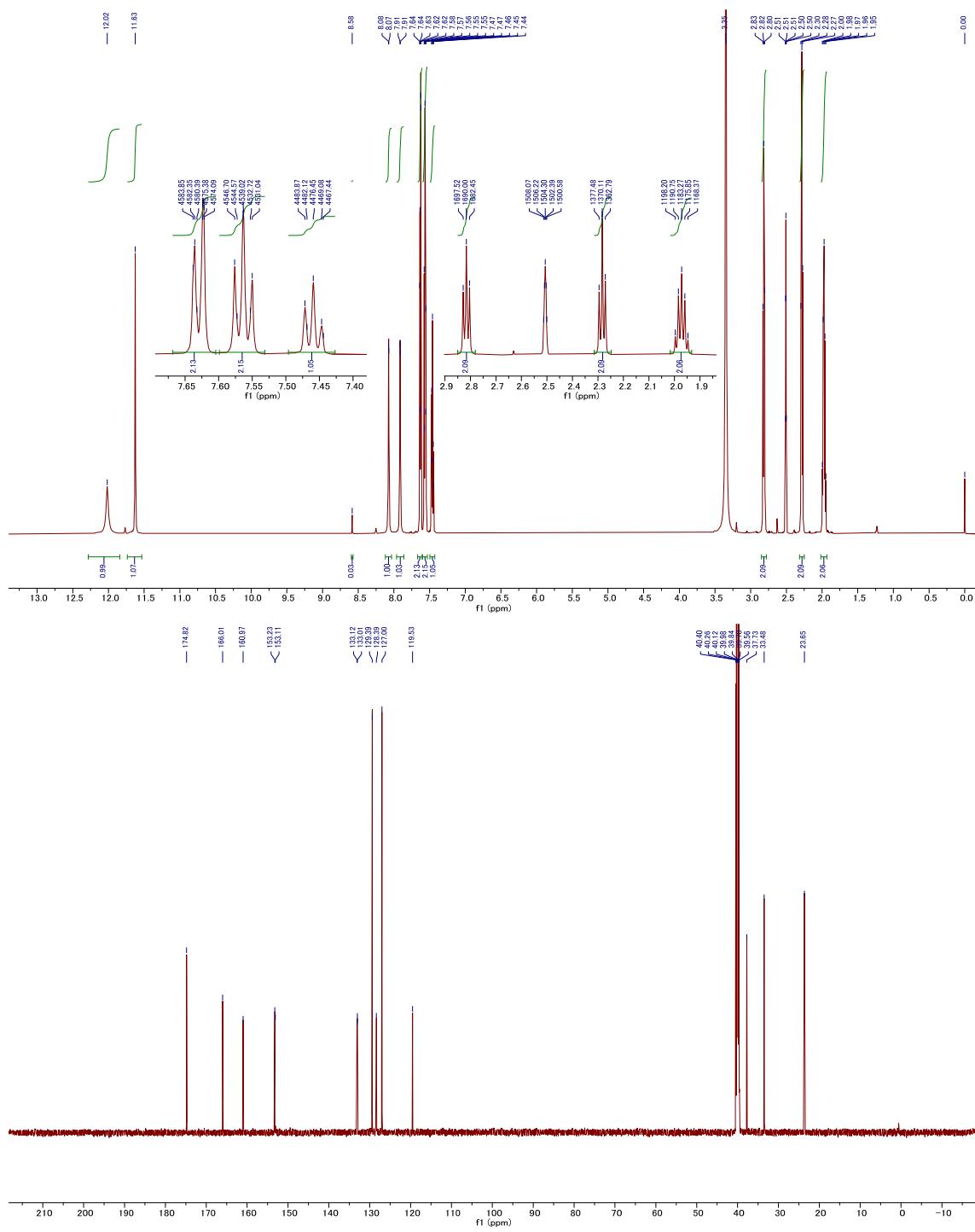
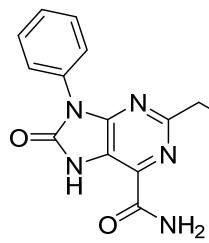
3-(6-carbamoyl-8-oxo-9-phenyl-8,9-dihydro-7H-purin-2-yl)propanoic acid (5)



(E)-3-(6-carbamoyl-8-oxo-9-phenyl-8,9-dihydro-7H-purin-2-yl)acrylic acid (6)

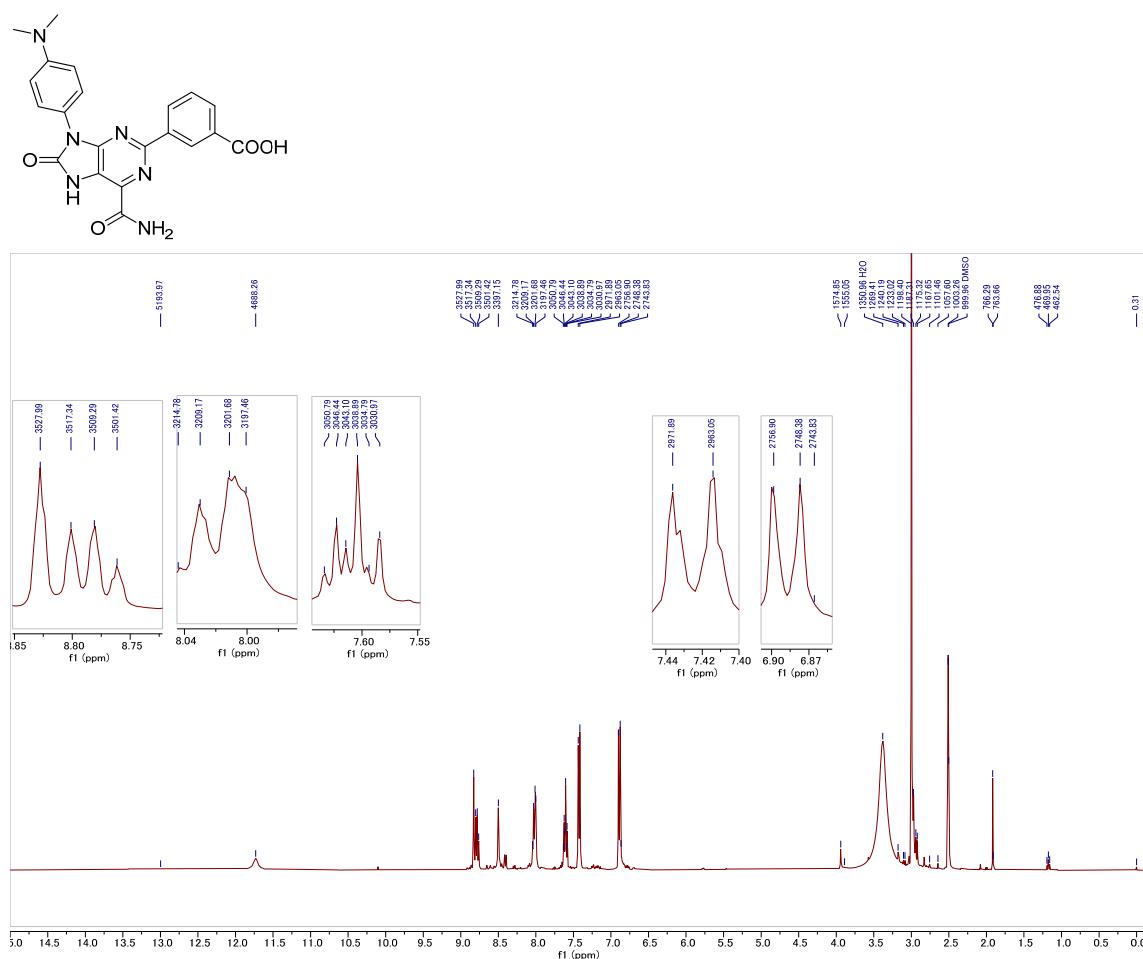


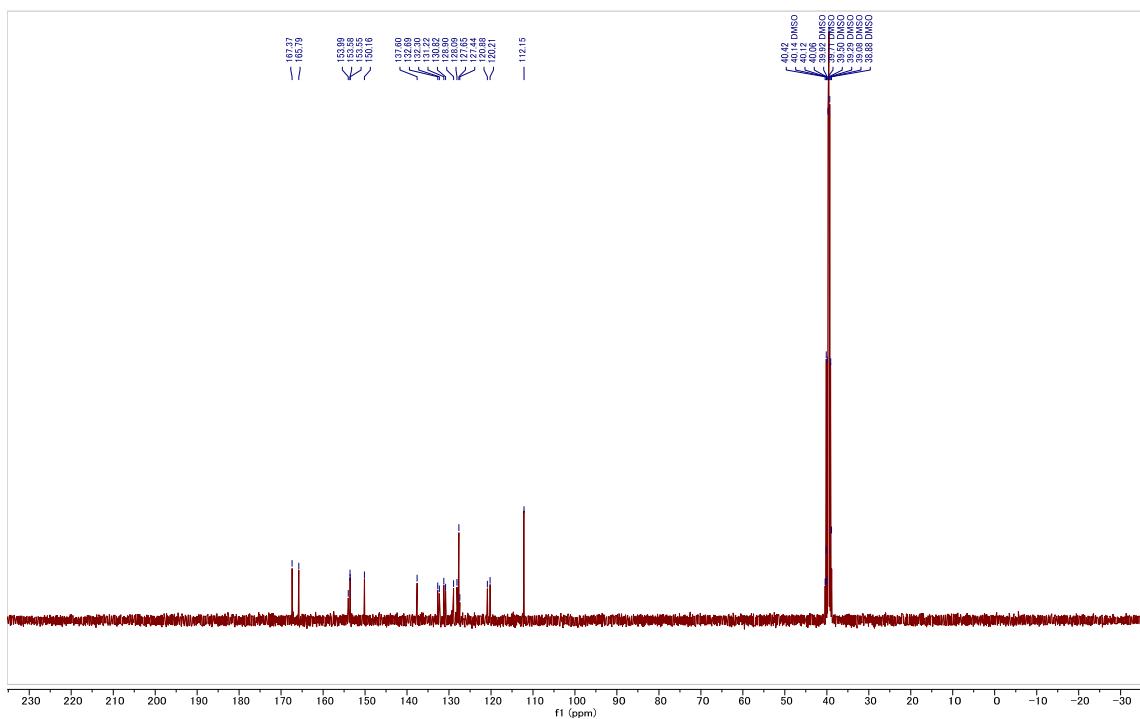
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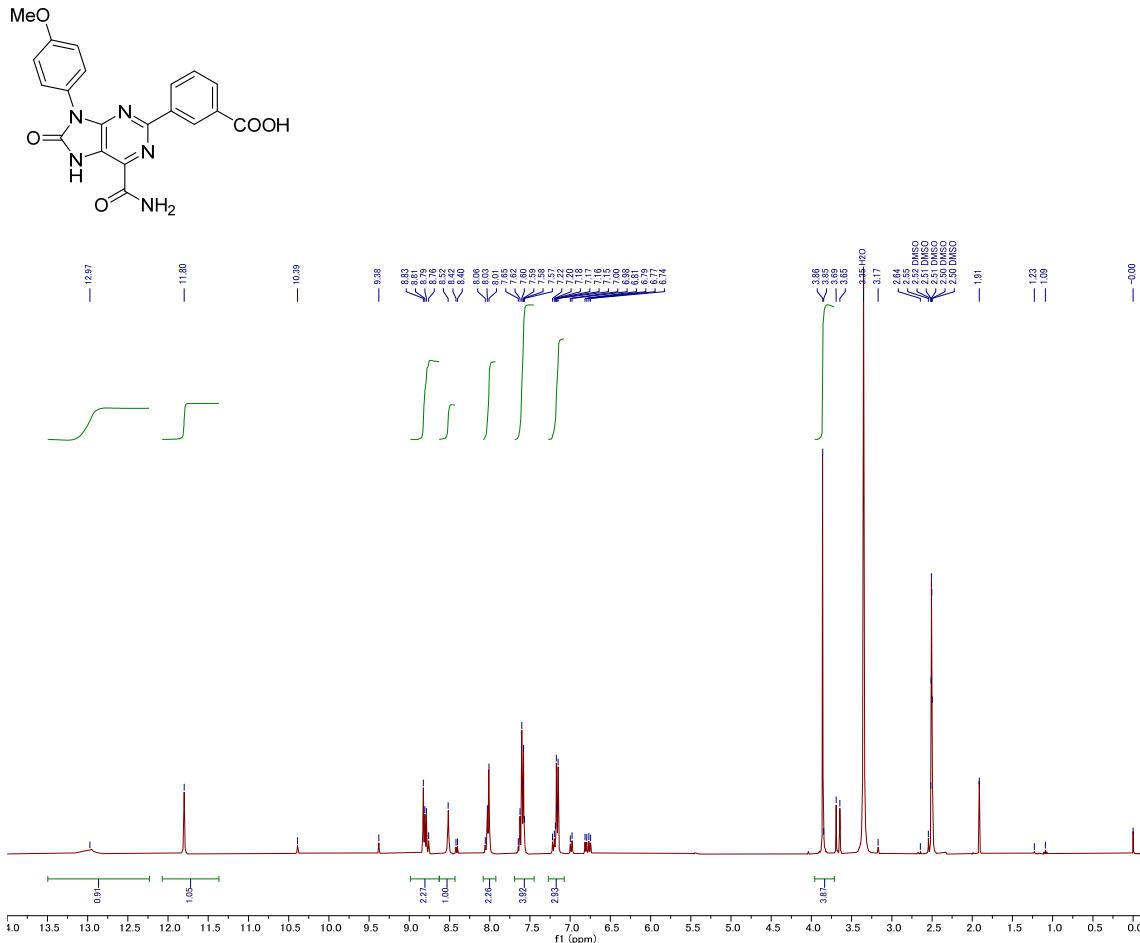
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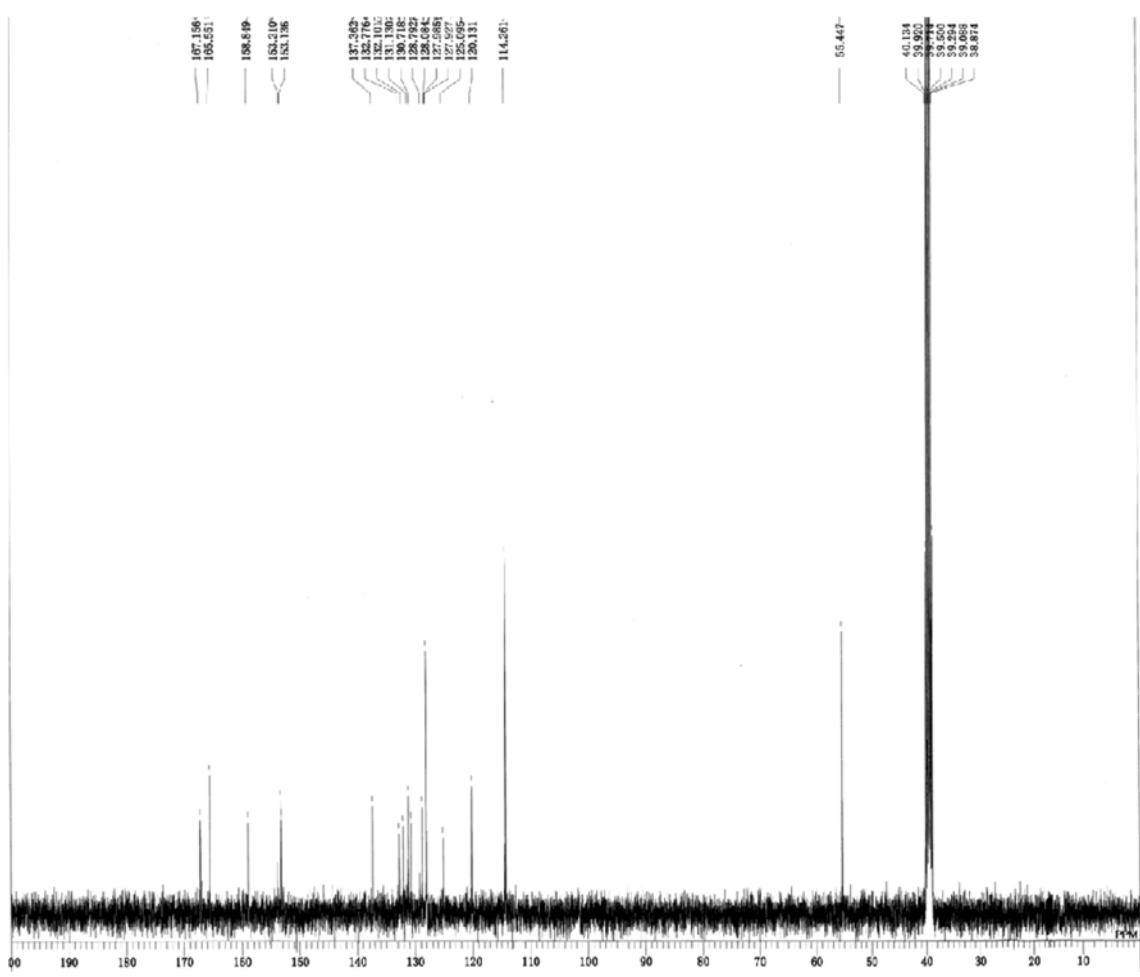
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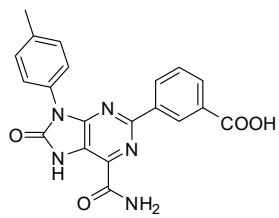


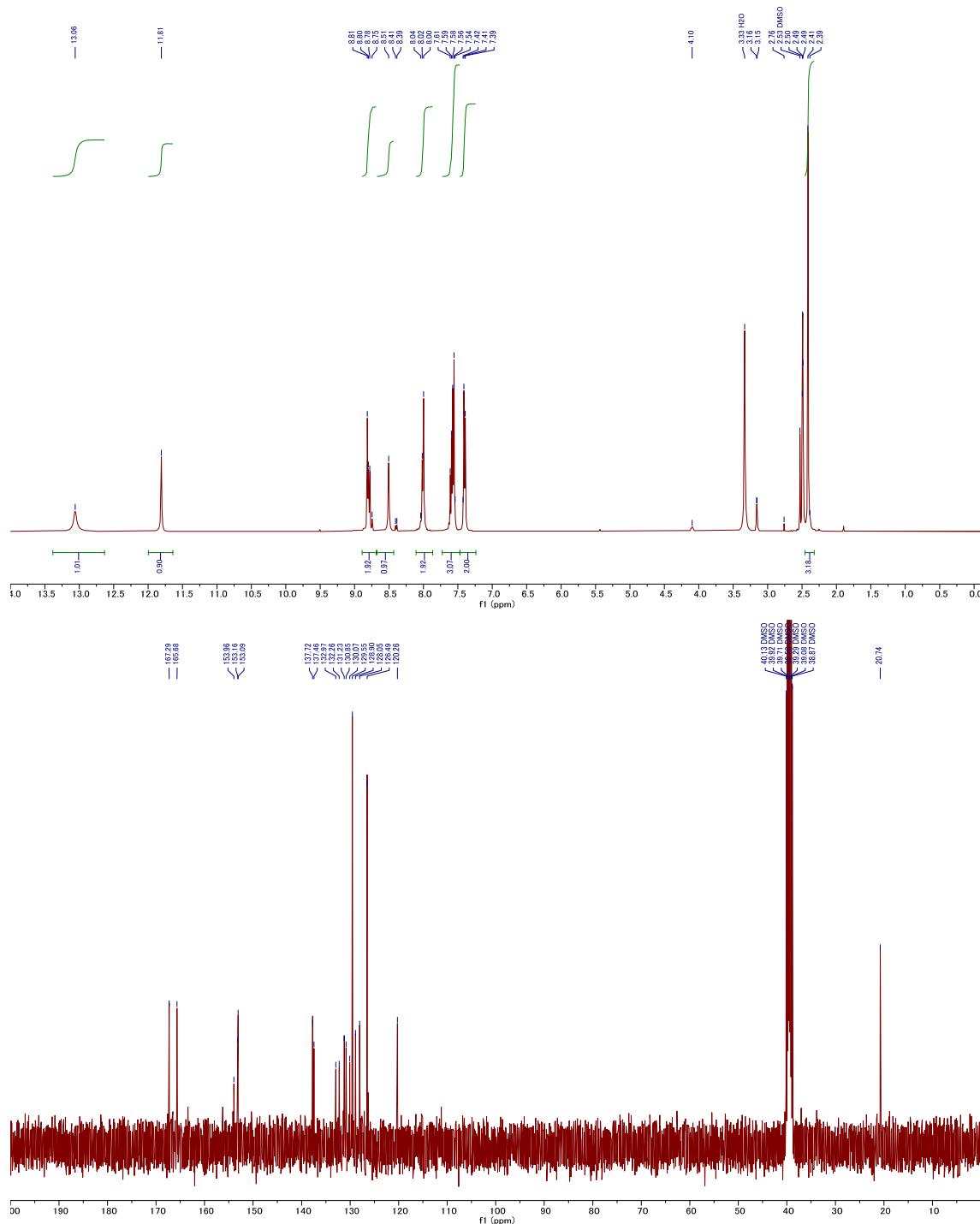
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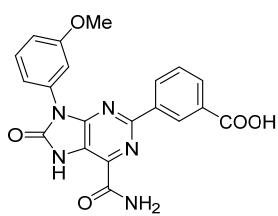


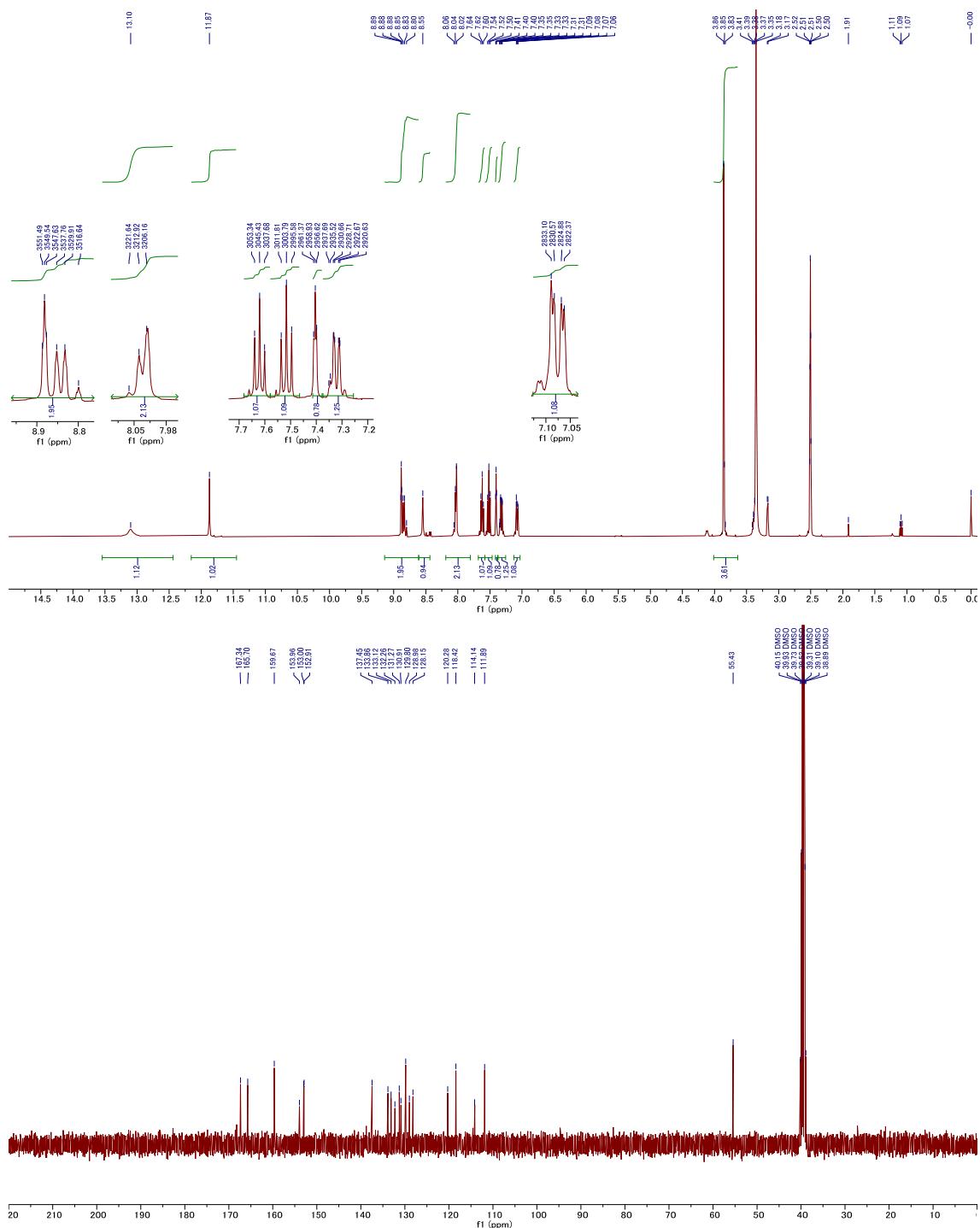
3-(6-Carbamoyl-8-oxo-9-(p-tolyl)-8,9-dihydro-7H-purin-2-yl)benzoic acid (10)



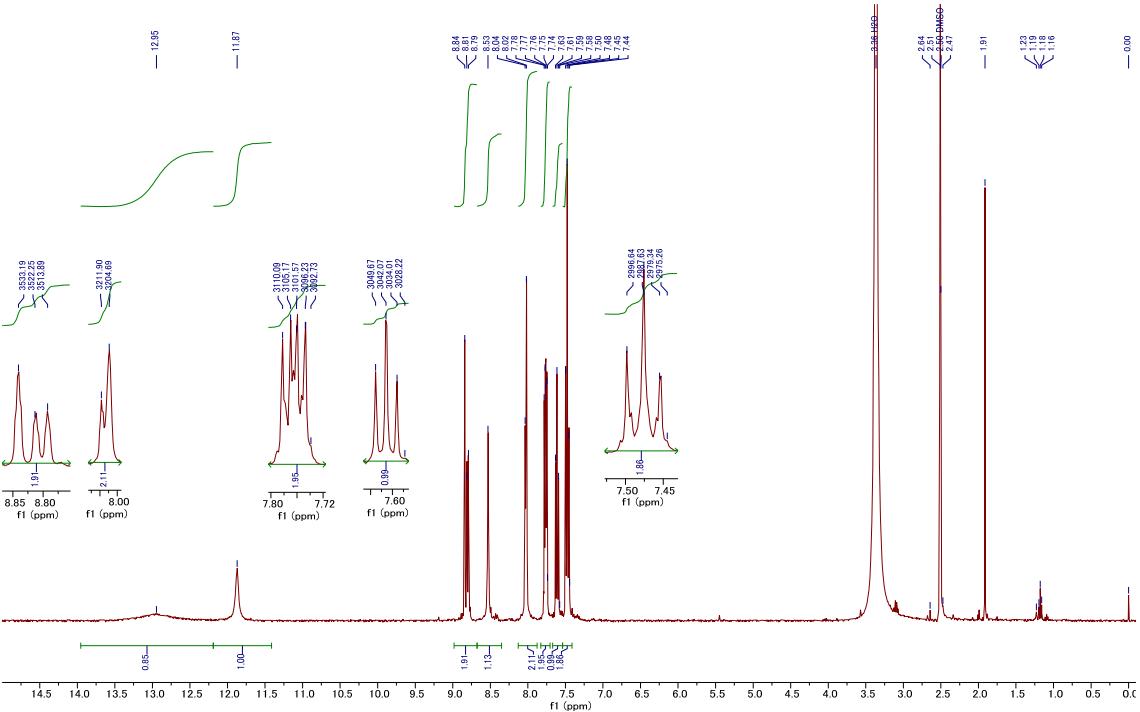
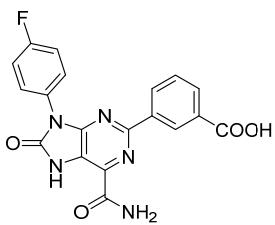


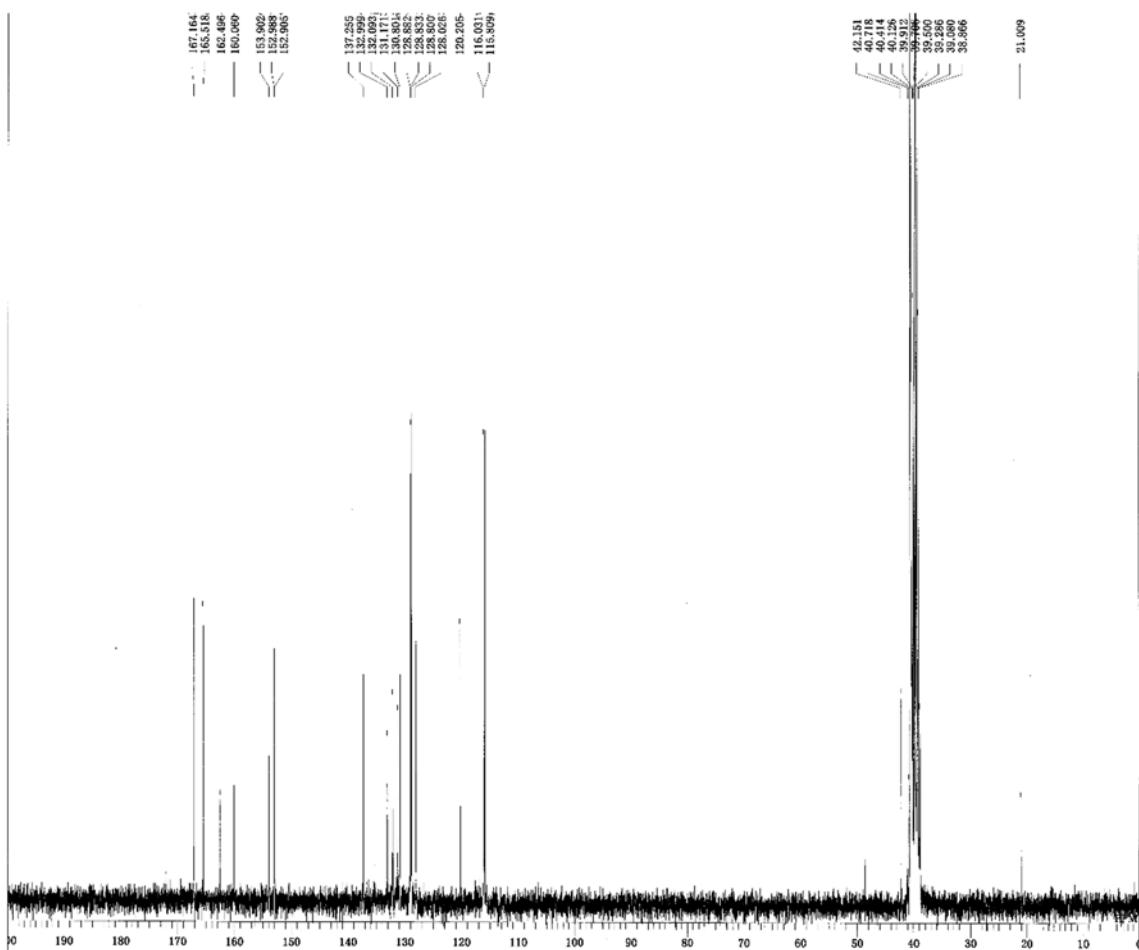
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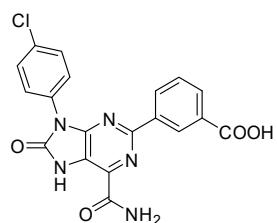


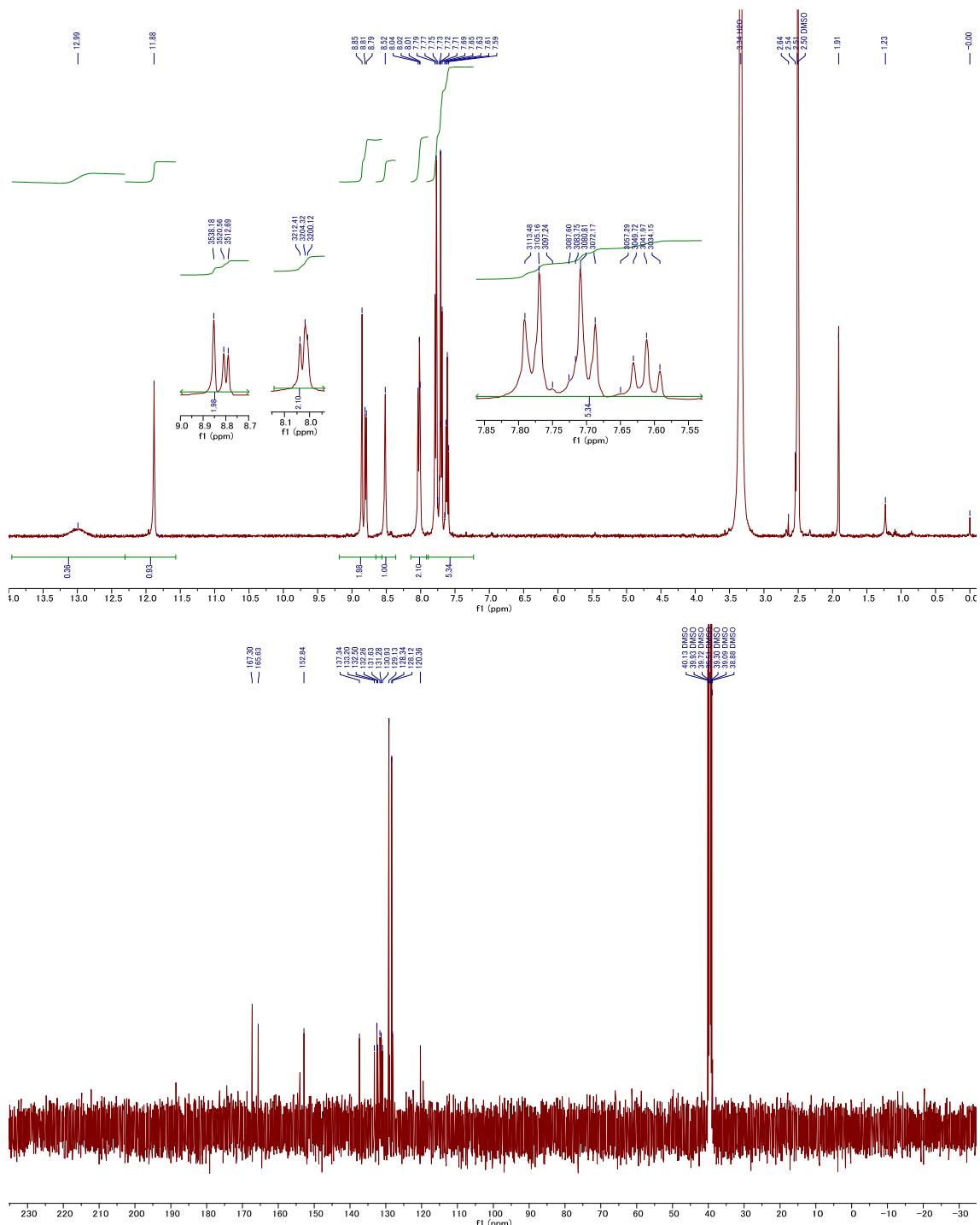
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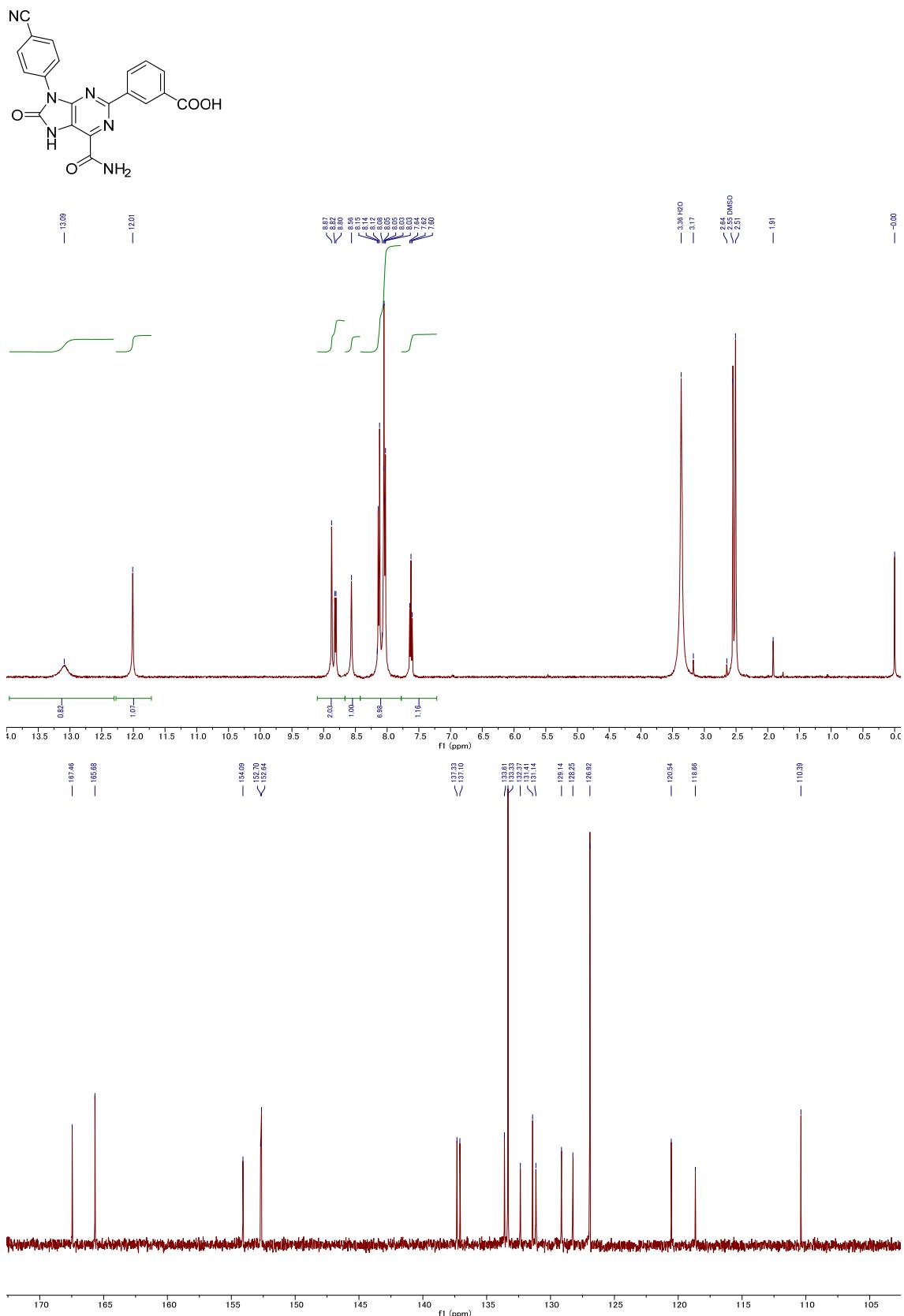


3-(6-Carbamoyl-9-(4-chlorophenyl)-8-oxo-8,9-dihydro-7H-purin-2-yl)benzoic acid (13)





3-(6-Carbamoyl-9-(4-cyanophenyl)-8-oxo-8,9-dihydro-7*H*-purin-2-yl)benzoic acid (14)



3-(6-carbamoyl-9-(4-nitrophenyl)-8-oxo-8,9-dihydro-7*H*-purin-2-yl)benzoic acid (15)

