Full wwPDB X-ray Structure Validation Report (i)

Sep 11, 2023 – 10:27 PM EDT

PDB ID	:	4LY1
Title	:	Structure of Human HDAC2 in complex with inhibitor 4-(acetylamino)-N-[2-amino-5-(thiophen-2-yl)phenyl]benzamide
Authors	:	Fong, R.; Lupardus, P.J.
Deposited on	:	2013-07-30
Resolution	:	1.57 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (i)) were used in the production of this report:

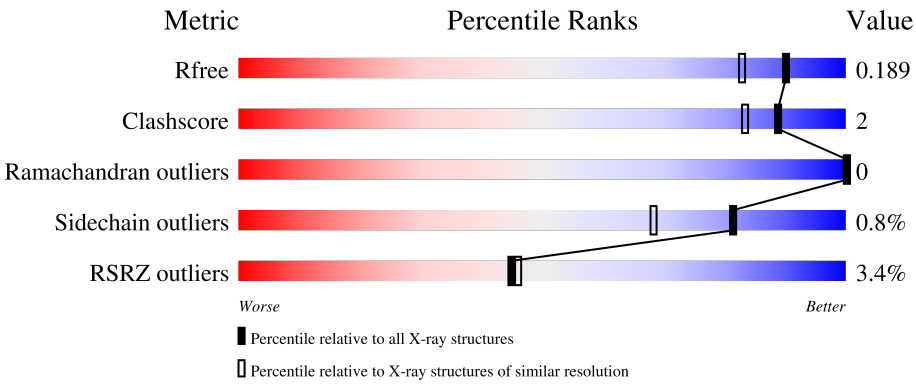
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35.1

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.57 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	5534 (1.60-1.56)
Clashscore	141614	5861 (1.60-1.56)
Ramachandran outliers	138981	5708 (1.60-1.56)
Sidechain outliers	138945	5703 (1.60-1.56)
RSRZ outliers	127900	5431 (1.60-1.56)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	369	2% 98% •
1	B	369	% 94% 6% •
1	C	369	7% 95% 5% •

2 Entry composition (i)

There are 8 unique types of molecules in this entry. The entry contains 10080 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Histone deacetylase 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	368	2996	1916	506	549	25	0	13	0
1	B	367	2982	1908	500	548	26	0	9	0
1	C	366	2980	1904	504	546	26	0	9	0

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Zn		
2	A	1	1	1	0	0
2	B	1	1	1	0	0
2	C	1	1	1	0	0

- Molecule 3 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Ca		
3	A	1	1	1	0	0
3	B	1	1	1	0	0
3	C	1	1	1	0	0

- Molecule 4 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Na		
4	A	1	1	1	0	0

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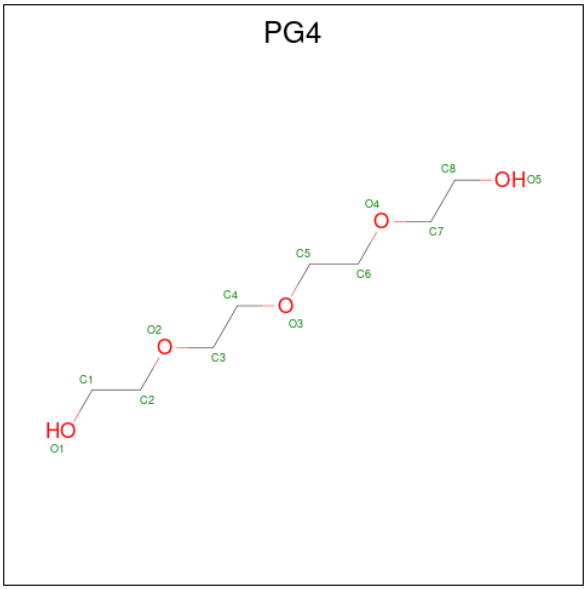
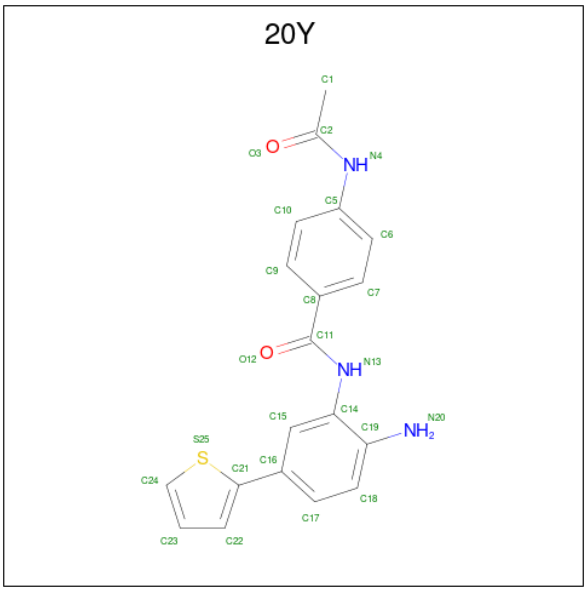
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	1	Total Na 1 1	0	0
4	C	1	Total Na 1 1	0	0

- Molecule 5 is TETRAETHYLENE GLYCOL (three-letter code: PG4) (formula: $C_8H_{18}O_5$).



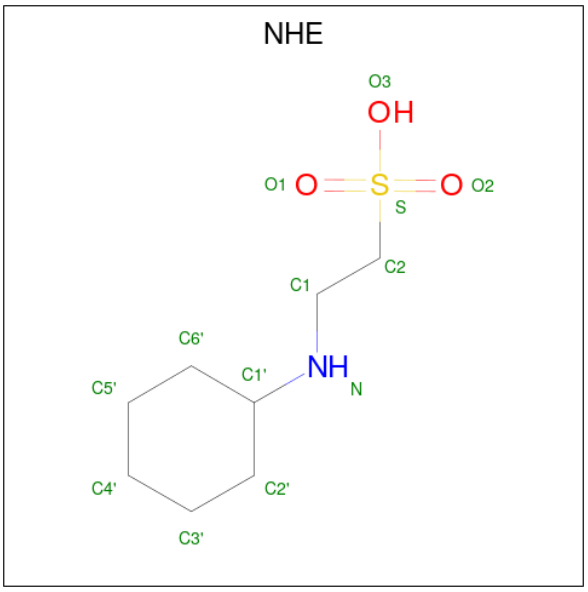
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C O 13 8 5	0	0
5	A	1	Total C O 13 8 5	0	0
5	A	1	Total C O 13 8 5	0	0
5	B	1	Total C O 13 8 5	0	0
5	B	1	Total C O 13 8 5	0	0
5	B	1	Total C O 13 8 5	0	0
5	C	1	Total C O 13 8 5	0	0
5	C	1	Total C O 13 8 5	0	0

- Molecule 6 is 4-(acetylamino)-N-[2-amino-5-(thiophen-2-yl)phenyl]benzamide (three-letter code: 20Y) (formula: $C_{19}H_{17}N_3O_2S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	S		
6	A	1	50	38	6	4	2	0	1
			Total	C	N	O	S		
6	B	1	50	38	6	4	2	0	1
			Total	C	N	O	S		
6	C	1	50	38	6	4	2	0	1

- Molecule 7 is 2-[N-CYCLOHEXYLAMINO]ETHANE SULFONIC ACID (three-letter code: NHE) (formula: $C_8H_{17}NO_3S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	S		
7	B	1	13	8	1	3	1	0	0

- Molecule 8 is water.

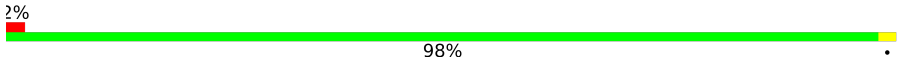
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
8	A	299	299	299	0	0
			Total	O		
8	B	322	322	322	0	0
			Total	O		
8	C	225	225	225	0	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

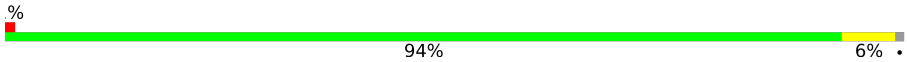
• Molecule 1: Histone deacetylase 2

Chain A:



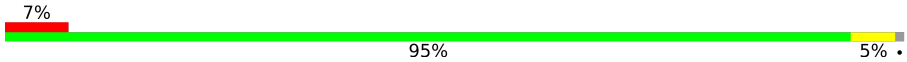
• Molecule 1: Histone deacetylase 2

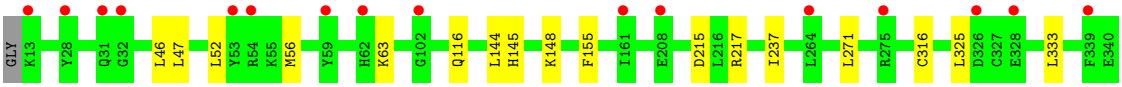
Chain B:

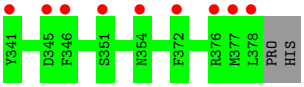


• Molecule 1: Histone deacetylase 2

Chain C:







4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	92.03Å 97.49Å 138.92Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	33.57 – 1.57 33.57 – 1.57	Depositor EDS
% Data completeness (in resolution range)	99.9 (33.57-1.57) 99.7 (33.57-1.57)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.93 (at 1.57Å)	Xtriage
Refinement program	BUSTER 2.11.2	Depositor
R, R_{free}	0.169 , 0.187 0.169 , 0.189	Depositor DCC
R_{free} test set	8703 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å^2)	15.9	Xtriage
Anisotropy	0.585	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 50.2	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.97	EDS
Total number of atoms	10080	wwPDB-VP
Average B, all atoms (Å^2)	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.92% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: PG4, ZN, CA, 20Y, NHE, NA

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\| >5$	RMSZ	$\#\|Z\| >5$
1	A	0.52	0/3096	0.62	0/4179
1	B	0.54	0/3087	0.65	0/4169
1	C	0.49	0/3079	0.61	0/4156
All	All	0.52	0/9262	0.63	0/12504

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2996	0	2906	3	0
1	B	2982	0	2881	20	0
1	C	2980	0	2877	8	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
4	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	1	0	0	0	0
4	C	1	0	0	0	0
5	A	39	0	54	1	0
5	B	39	0	54	2	0
5	C	26	0	36	0	0
6	A	50	0	34	1	0
6	B	50	0	34	0	0
6	C	50	0	34	0	0
7	B	13	0	17	5	0
8	A	299	0	0	1	0
8	B	322	0	0	4	0
8	C	225	0	0	1	0
All	All	10080	0	8927	34	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 2.

All (34) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:205:LYS:HD2	1:B:278[B]:CYS:SG	2.23	0.78
1:B:341:TYR:HA	5:B:405:PG4:H51	1.66	0.77
1:B:63:LYS:HZ1	7:B:404:NHE:H2'1	1.55	0.69
1:B:17[A]:CYS:SG	8:B:799:HOH:O	2.46	0.65
1:B:56:MET:HB3	1:B:325:LEU:HD21	1.81	0.63
1:C:56:MET:HB3	1:C:325:LEU:HD21	1.84	0.60
1:A:56:MET:HB3	1:A:325:LEU:HD21	1.87	0.57
1:B:205:LYS:HD2	1:B:278[B]:CYS:HG	1.69	0.56
1:B:205:LYS:CD	1:B:278[B]:CYS:SG	2.92	0.55
1:B:245:ILE:HG12	1:B:364:MET:CE	2.40	0.52
1:B:245:ILE:HG22	1:B:368:LYS:HE2	1.94	0.48
1:C:46:LEU:HD11	1:C:333:LEU:HD22	1.96	0.48
1:C:148:LYS:HE3	8:C:702:HOH:O	2.14	0.48
1:B:23:ASP:OD1	7:B:404:NHE:HC22	2.13	0.47
1:C:47:LEU:HB2	1:C:52:LEU:HD12	1.94	0.47
1:B:15:LYS:HG2	8:B:799:HOH:O	2.15	0.47
1:B:148:LYS:HE3	8:B:644:HOH:O	2.14	0.47
1:C:271:LEU:HD11	1:C:316:CYS:HB2	1.96	0.47
1:C:215:ASP:OD1	1:C:217[A]:ARG:HG2	2.15	0.47
1:B:17[B]:CYS:HB2	1:B:59:TYR:HE2	1.81	0.46
1:A:243:GLY:O	8:A:795:HOH:O	2.21	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:66:ALA:HB2	1:B:82:ARG:HH11	1.83	0.43
5:A:404:PG4:H32	5:A:404:PG4:H51	1.79	0.43
1:B:63:LYS:NZ	7:B:404:NHE:H2'1	2.28	0.43
7:B:404:NHE:H4'1	5:B:407:PG4:H71	2.00	0.43
1:B:94:LYS:HA	1:B:94:LYS:HD2	1.91	0.42
1:B:40[B]:ILE:HD11	8:B:546:HOH:O	2.20	0.42
1:B:63:LYS:HZ1	7:B:404:NHE:C2'	2.28	0.42
1:C:144:LEU:HD12	1:C:144:LEU:N	2.34	0.42
1:A:245:ILE:HG12	1:A:364:MET:HE3	2.01	0.41
1:B:245:ILE:HG22	1:B:368:LYS:CE	2.51	0.41
6:A:407[B]:20Y:H4	6:A:407[B]:20Y:O3	2.20	0.41
1:C:63:LYS:HB3	1:C:116:GLN:HB3	2.03	0.40
1:B:17[B]:CYS:HB2	1:B:59:TYR:CE2	2.57	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	373/369 (101%)	367 (98%)	6 (2%)	0	100	100
1	B	372/369 (101%)	366 (98%)	6 (2%)	0	100	100
1	C	370/369 (100%)	365 (99%)	5 (1%)	0	100	100
All	All	1115/1107 (101%)	1098 (98%)	17 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	324/318 (102%)	322 (99%)	2 (1%)	86	76
1	B	323/318 (102%)	320 (99%)	3 (1%)	78	64
1	C	321/318 (101%)	318 (99%)	3 (1%)	78	64
All	All	968/954 (102%)	960 (99%)	8 (1%)	81	68

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	145	HIS
1	A	155	PHE
1	B	145	HIS
1	B	155	PHE
1	B	288	LYS
1	C	145	HIS
1	C	155	PHE
1	C	237	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA (i)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains (i)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 24 ligands modelled in this entry, 9 are monoatomic - leaving 15 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
5	PG4	C	404	-	12,12,12	0.48	0	11,11,11	0.35	0
5	PG4	C	405	-	12,12,12	0.45	0	11,11,11	0.28	0
5	PG4	B	407	-	12,12,12	0.42	0	11,11,11	0.40	0
5	PG4	A	404	-	12,12,12	0.53	0	11,11,11	0.51	0
6	20Y	A	407[A]	2	26,27,27	0.95	1 (3%)	32,37,37	1.34	2 (6%)
5	PG4	A	405	-	12,12,12	0.48	0	11,11,11	0.38	0
6	20Y	A	407[B]	2	26,27,27	0.82	1 (3%)	32,37,37	1.11	3 (9%)
6	20Y	C	406[A]	2	26,27,27	0.90	1 (3%)	32,37,37	1.25	2 (6%)
5	PG4	B	405	-	12,12,12	0.48	0	11,11,11	0.42	0
6	20Y	C	406[B]	2	26,27,27	1.05	1 (3%)	32,37,37	1.51	5 (15%)
5	PG4	A	406	-	12,12,12	0.50	0	11,11,11	0.38	0
7	NHE	B	404	-	13,13,13	0.92	1 (7%)	16,17,17	2.34	5 (31%)
5	PG4	B	406	-	12,12,12	0.47	0	11,11,11	0.30	0
6	20Y	B	408[B]	2	26,27,27	0.96	1 (3%)	32,37,37	0.96	1 (3%)
6	20Y	B	408[A]	2	26,27,27	0.79	1 (3%)	32,37,37	1.43	1 (3%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	PG4	C	404	-	-	2/10/10/10	-
5	PG4	C	405	-	-	2/10/10/10	-
5	PG4	B	407	-	-	1/10/10/10	-
5	PG4	A	404	-	-	7/10/10/10	-
6	20Y	A	407[A]	2	-	0/16/16/16	0/3/3/3
5	PG4	A	405	-	-	2/10/10/10	-
6	20Y	A	407[B]	2	-	0/16/16/16	0/3/3/3
6	20Y	C	406[A]	2	-	0/16/16/16	0/3/3/3
5	PG4	B	405	-	-	5/10/10/10	-
6	20Y	C	406[B]	2	-	0/16/16/16	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	PG4	A	406	-	-	3/10/10/10	-
7	NHE	B	404	-	-	2/7/15/15	0/1/1/1
5	PG4	B	406	-	-	1/10/10/10	-
6	20Y	B	408[B]	2	-	2/16/16/16	0/3/3/3
6	20Y	B	408[A]	2	-	0/16/16/16	0/3/3/3

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	C	406[B]	20Y	C21-S25	3.71	1.76	1.72
6	B	408[B]	20Y	C21-S25	3.66	1.76	1.72
6	A	407[A]	20Y	C21-S25	3.38	1.76	1.72
6	C	406[A]	20Y	C21-S25	2.78	1.75	1.72
6	A	407[B]	20Y	C21-S25	2.45	1.75	1.72
7	B	404	NHE	C1'-N	-2.45	1.42	1.48
6	B	408[A]	20Y	C21-S25	2.26	1.75	1.72

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
6	B	408[A]	20Y	C23-C24-S25	-6.19	107.95	112.98
7	B	404	NHE	O2-S-C2	6.07	114.22	106.92
6	A	407[A]	20Y	C23-C24-S25	-5.23	108.73	112.98
6	C	406[A]	20Y	C23-C24-S25	-4.87	109.03	112.98
7	B	404	NHE	C1-N-C1'	3.87	121.73	114.14
6	C	406[B]	20Y	C23-C24-S25	-3.76	109.93	112.98
7	B	404	NHE	O2-S-O1	-3.46	101.99	113.95
6	A	407[B]	20Y	C23-C24-S25	-3.00	110.55	112.98
6	C	406[B]	20Y	C19-C14-N13	2.45	123.75	119.23
6	C	406[B]	20Y	O12-C11-N13	-2.39	118.25	123.71
6	C	406[B]	20Y	C1-C2-N4	2.28	118.33	114.98
6	A	407[A]	20Y	C1-C2-N4	2.26	118.30	114.98
6	A	407[B]	20Y	C1-C2-N4	2.26	118.30	114.98
7	B	404	NHE	C5'-C6'-C1'	2.22	115.30	111.11
6	C	406[A]	20Y	C1-C2-N4	2.20	118.21	114.98
7	B	404	NHE	C6'-C1'-C2'	2.20	114.63	110.82
6	C	406[B]	20Y	C18-C17-C16	-2.10	118.12	121.13
6	A	407[B]	20Y	O3-C2-C1	-2.07	118.21	122.06
6	B	408[B]	20Y	C1-C2-N4	2.06	118.01	114.98

There are no chirality outliers.

All (27) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	B	405	PG4	O3-C5-C6-O4
5	A	406	PG4	O4-C7-C8-O5
5	A	404	PG4	C3-C4-O3-C5
5	A	404	PG4	O2-C3-C4-O3
5	B	405	PG4	O4-C7-C8-O5
5	C	405	PG4	O3-C5-C6-O4
5	A	406	PG4	O3-C5-C6-O4
5	A	404	PG4	O1-C1-C2-O2
5	B	406	PG4	C1-C2-O2-C3
5	C	404	PG4	C1-C2-O2-C3
5	A	404	PG4	C1-C2-O2-C3
5	A	405	PG4	C6-C5-O3-C4
7	B	404	NHE	C1-C2-S-O2
5	C	405	PG4	C1-C2-O2-C3
5	A	404	PG4	C8-C7-O4-C6
5	A	404	PG4	C5-C6-O4-C7
5	B	405	PG4	C5-C6-O4-C7
5	C	404	PG4	O1-C1-C2-O2
5	B	407	PG4	C5-C6-O4-C7
5	B	405	PG4	C4-C3-O2-C2
5	A	405	PG4	O3-C5-C6-O4
5	B	405	PG4	C3-C4-O3-C5
7	B	404	NHE	C1-C2-S-O3
6	B	408[B]	20Y	C6-C5-N4-C2
6	B	408[B]	20Y	C10-C5-N4-C2
5	A	406	PG4	C6-C5-O3-C4
5	A	404	PG4	O3-C5-C6-O4

There are no ring outliers.

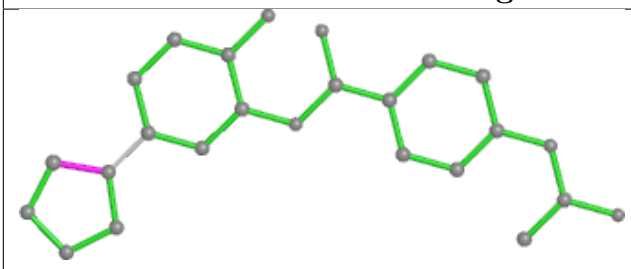
5 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	407	PG4	1	0
5	A	404	PG4	1	0
6	A	407[B]	20Y	1	0
5	B	405	PG4	1	0
7	B	404	NHE	5	0

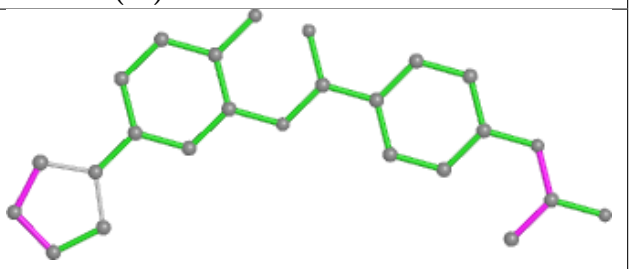
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will

also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

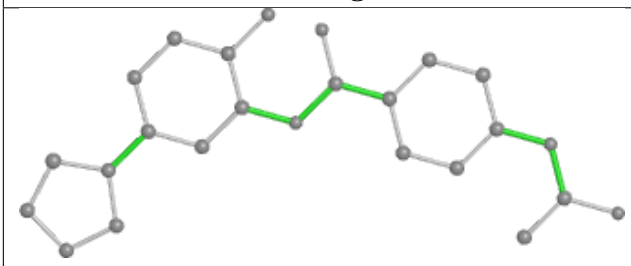
Ligand 20Y A 407 (A)



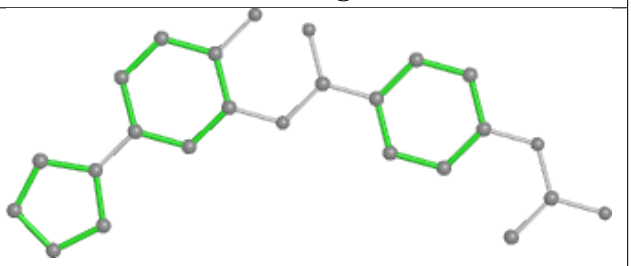
Bond lengths



Bond angles

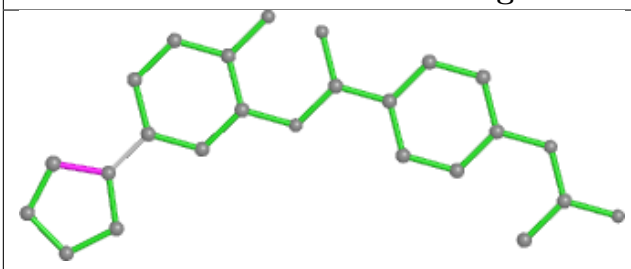


Torsions

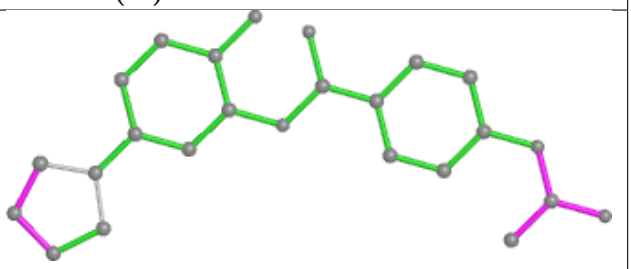


Rings

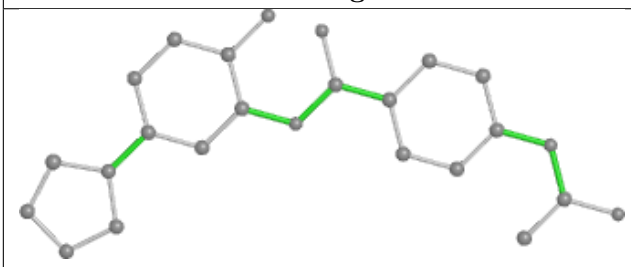
Ligand 20Y A 407 (B)



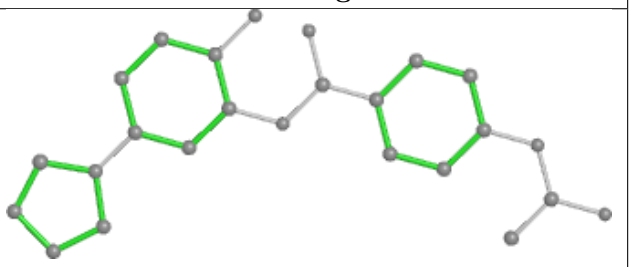
Bond lengths



Bond angles

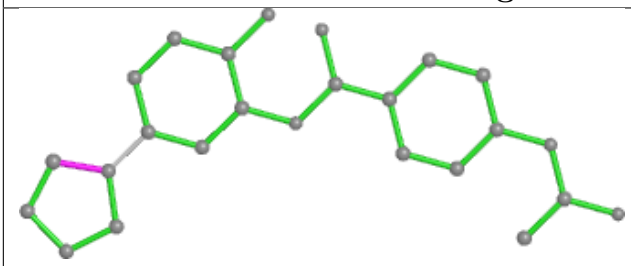


Torsions

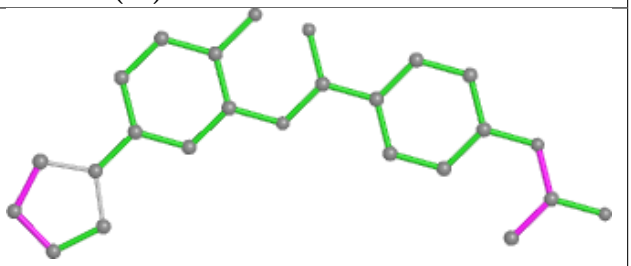


Rings

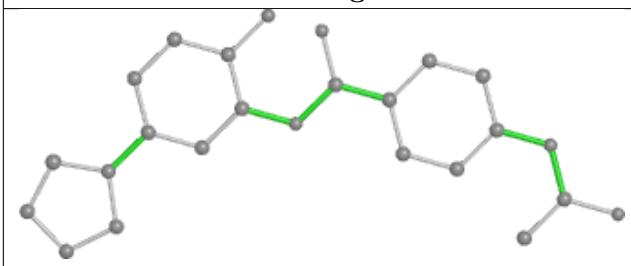
Ligand 20Y C 406 (A)



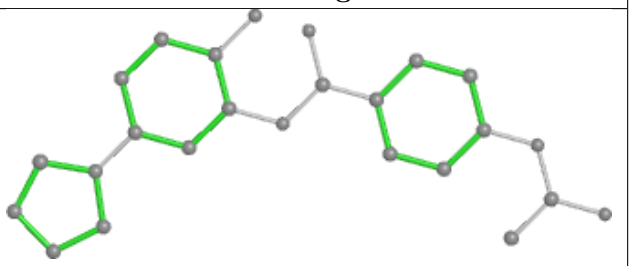
Bond lengths



Bond angles

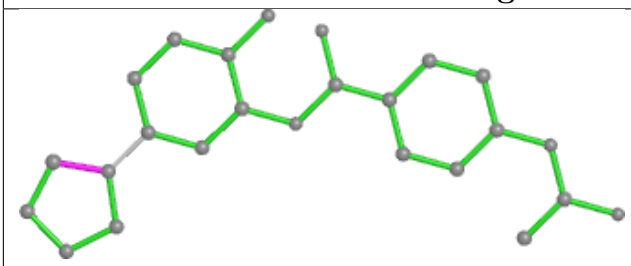


Torsions

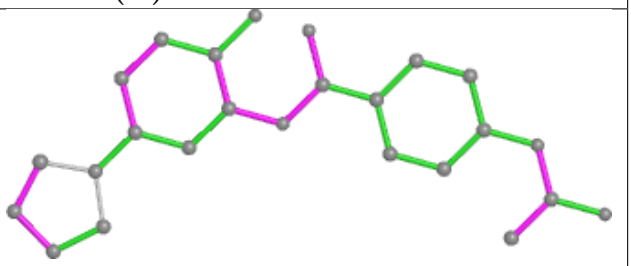


Rings

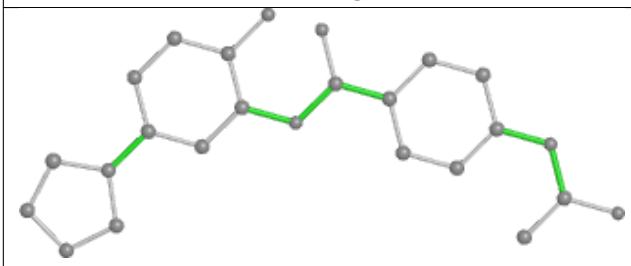
Ligand 20Y C 406 (B)



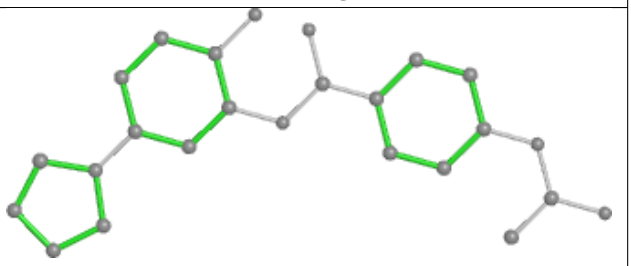
Bond lengths



Bond angles

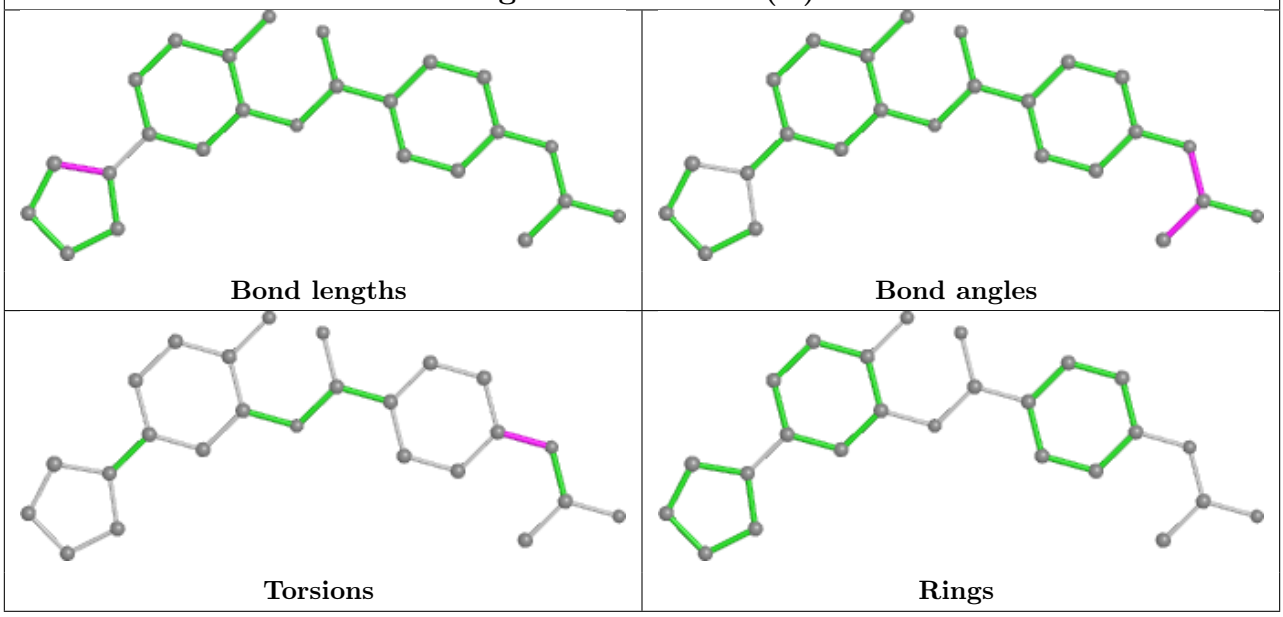


Torsions

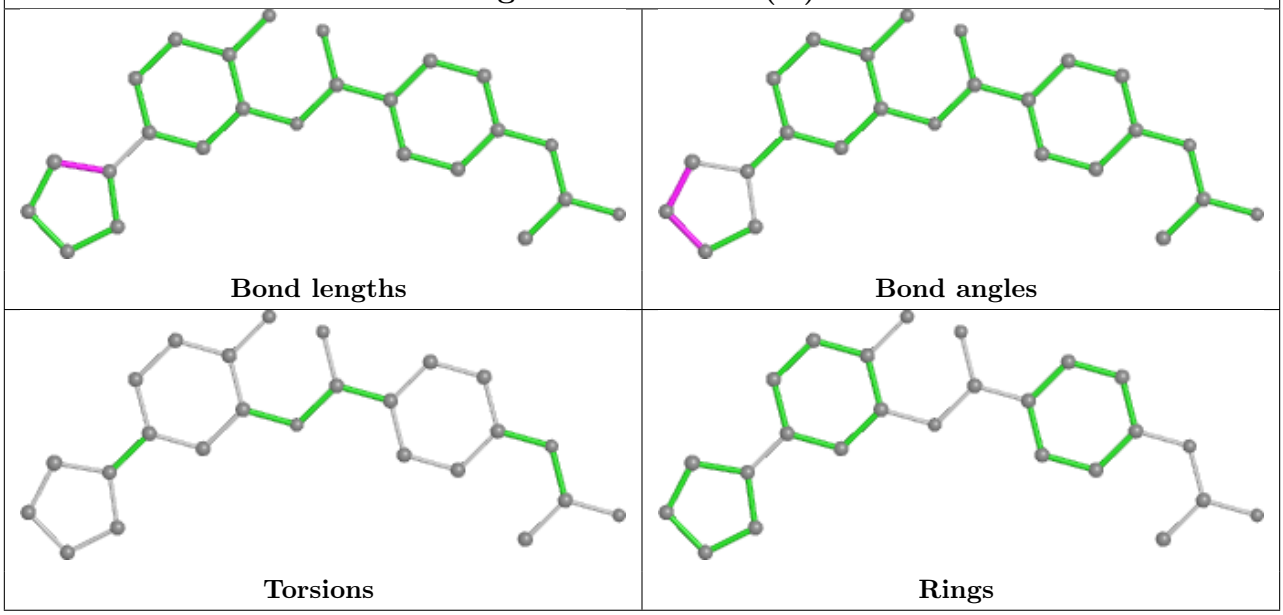


Rings

Ligand 20Y B 408 (B)



Ligand 20Y B 408 (A)



5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data (i)

6.1 Protein, DNA and RNA chains (i)

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å^2)	Q<0.9
1	A	368/369 (99%)	-0.05	9 (2%)	59	60	12, 18, 37, 53	6 (1%)
1	B	367/369 (99%)	-0.16	3 (0%)	86	87	9, 16, 34, 56	1 (0%)
1	C	366/369 (99%)	0.36	25 (6%)	17	17	14, 23, 41, 63	2 (0%)
All	All	1101/1107 (99%)	0.05	37 (3%)	45	46	9, 19, 38, 63	9 (0%)

All (37) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	32	GLY	4.7
1	C	13	LYS	4.7
1	B	379	PRO	4.2
1	C	341	TYR	4.2
1	C	62[A]	HIS	3.9
1	C	31	GLN	3.3
1	C	328	GLU	3.3
1	C	354	ASN	3.1
1	A	102	GLY	3.1
1	A	303	LEU	3.0
1	C	28	TYR	2.8
1	C	59	TYR	2.8
1	C	54	ARG	2.7
1	C	264	LEU	2.7
1	C	326	ASP	2.7
1	B	14	LYS	2.6
1	C	378	LEU	2.6
1	C	208	GLU	2.5
1	A	12	GLY	2.5
1	A	354	ASN	2.5
1	C	275	ARG	2.4
1	C	372	PHE	2.3
1	C	345	ASP	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	171	TYR	2.3
1	A	379	PRO	2.3
1	C	161	ILE	2.3
1	C	102	GLY	2.3
1	C	376[A]	ARG	2.3
1	A	161	ILE	2.3
1	C	53	TYR	2.2
1	C	339	PHE	2.1
1	A	92	TYR	2.1
1	C	351	SER	2.1
1	B	13	LYS	2.1
1	C	346	PHE	2.1
1	A	208[A]	GLU	2.0
1	C	377	MET	2.0

6.2 Non-standard residues in protein, DNA, RNA chains (i)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
5	PG4	A	404	13/13	0.72	0.22	61,62,66,67	0
7	NHE	B	404	13/13	0.72	0.26	39,40,44,47	0
5	PG4	A	405	13/13	0.79	0.17	46,51,54,56	0
5	PG4	B	405	13/13	0.81	0.15	43,47,54,56	0
5	PG4	C	404	13/13	0.82	0.14	26,30,50,51	0
5	PG4	C	405	13/13	0.83	0.13	38,42,47,47	0
5	PG4	A	406	13/13	0.83	0.18	36,43,58,61	0
5	PG4	B	406	13/13	0.85	0.14	32,36,43,43	0
5	PG4	B	407	13/13	0.86	0.17	29,38,48,49	0

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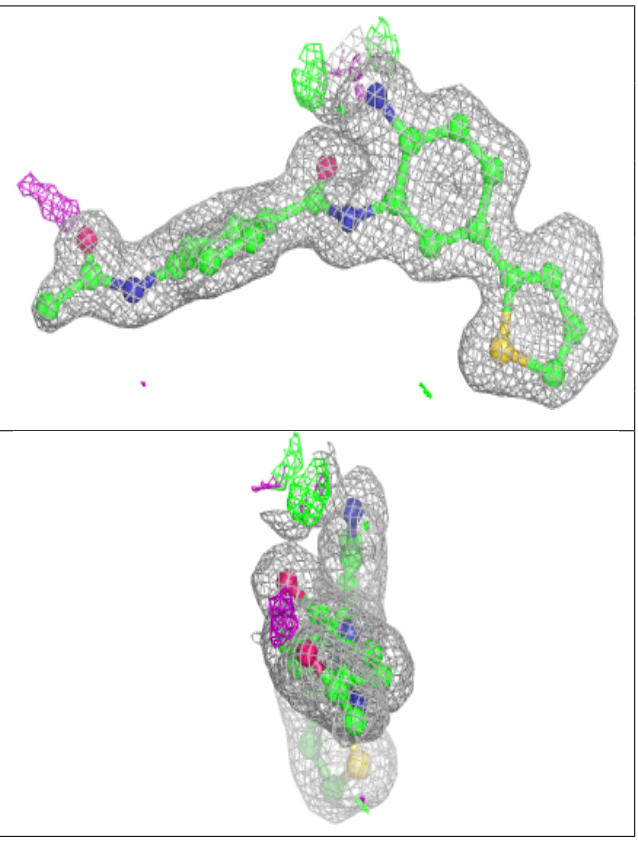
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
6	20Y	C	406[B]	25/25	0.94	0.11	6,12,26,29	25
6	20Y	C	406[A]	25/25	0.94	0.11	15,20,40,43	25
6	20Y	B	408[B]	25/25	0.96	0.11	9,12,23,26	25
6	20Y	A	407[A]	25/25	0.96	0.10	9,14,20,22	25
6	20Y	A	407[B]	25/25	0.96	0.10	10,13,24,27	25
6	20Y	B	408[A]	25/25	0.96	0.11	9,11,19,19	25
2	ZN	C	401	1/1	0.99	0.05	16,16,16,16	0
4	NA	A	403	1/1	0.99	0.10	13,13,13,13	0
4	NA	C	403	1/1	0.99	0.11	11,11,11,11	0
2	ZN	B	401	1/1	1.00	0.06	11,11,11,11	0
4	NA	B	403	1/1	1.00	0.16	12,12,12,12	0
2	ZN	A	401	1/1	1.00	0.07	13,13,13,13	0
3	CA	A	402	1/1	1.00	0.05	14,14,14,14	0
3	CA	B	402	1/1	1.00	0.05	13,13,13,13	0
3	CA	C	402	1/1	1.00	0.03	17,17,17,17	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

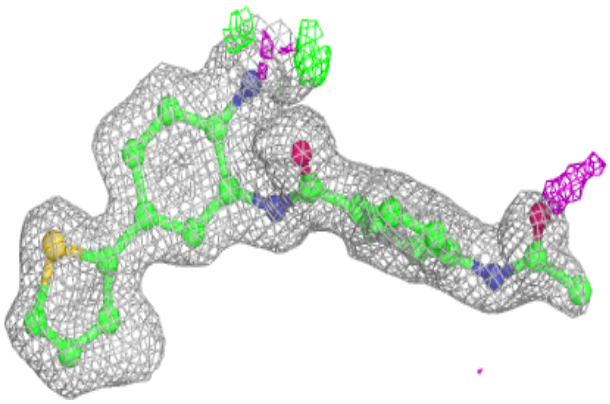
Electron density around 20Y C 406 (B):

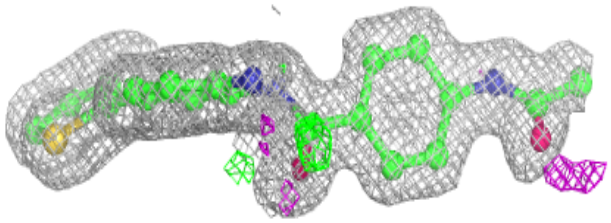
2mF$_o$-DF$_c$ (at 0.7 rmsd) in gray
mF$_o$-DF$_c$ (at 3 rmsd) in purple (negative)
and green (positive)

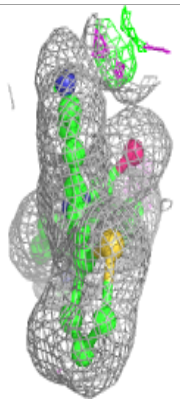


Electron density around 20Y C 406 (A):

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

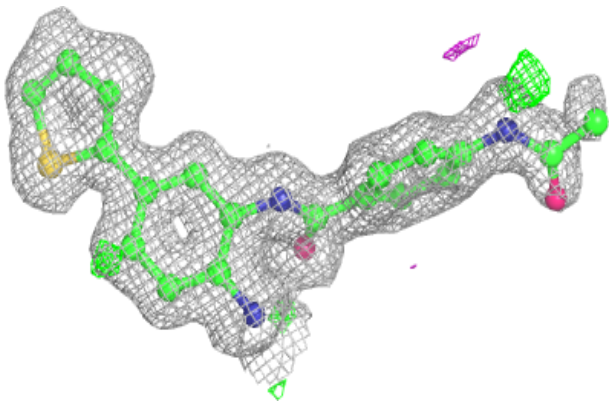


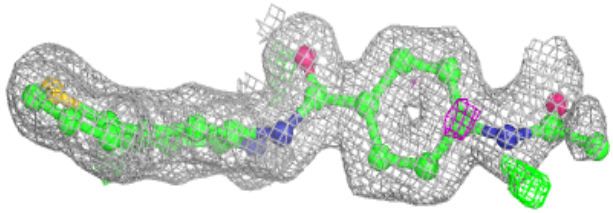


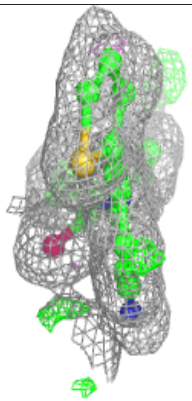


Electron density around 20Y B 408 (B):

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

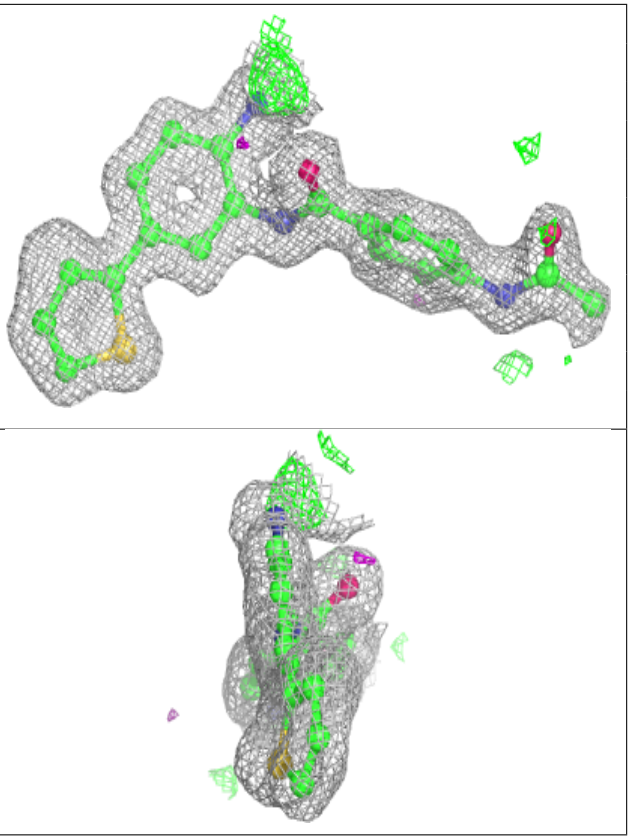






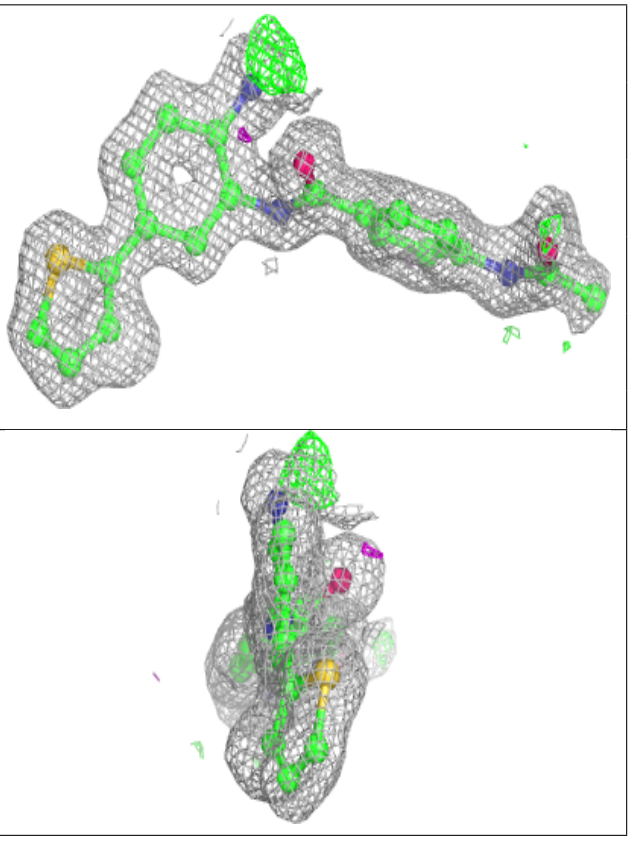
Electron density around 20Y A 407 (A):

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



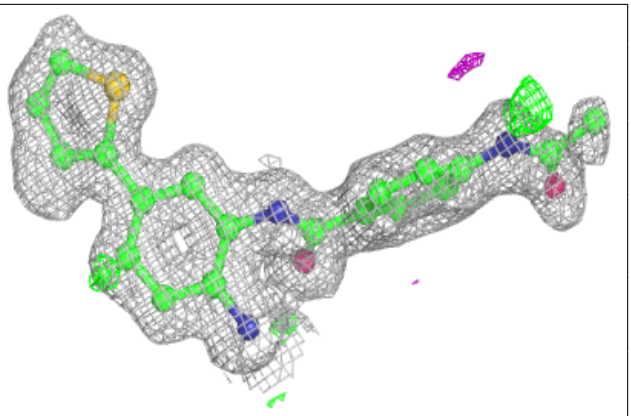
Electron density around 20Y A 407 (B):

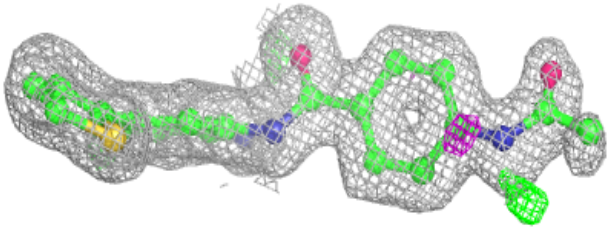
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

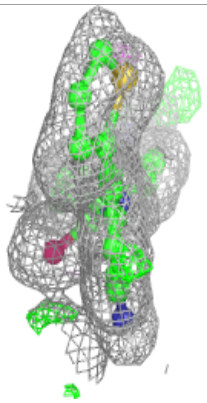


Electron density around 20Y B 408 (A):

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)







6.5 Other polymers (i)

There are no such residues in this entry.