Full wwPDB X-ray Structure Validation Report ⓘ

Nov 4, 2020 – 09:19 PM GMT

PDB ID	:	6ZE8
Title	:	Crystal structure of human chitotriosidase-1 (hCHIT) catalytic domain in complex with compound OATD-01
Authors	:	Nowotny, M.; Bartlomiejczak, A.; Napiorkowska-Gromadzka, A.
Deposited on	:	2020-06-16
Resolution	:	1.50 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 ⓘ symbol.

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

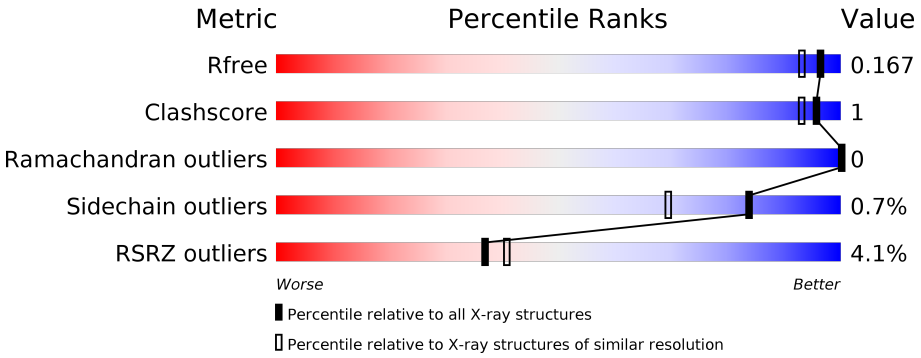
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.14.6
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.14.6

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 1.50 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	2936 (1.50-1.50)
Clashscore	141614	3144 (1.50-1.50)
Ramachandran outliers	138981	3066 (1.50-1.50)
Sidechain outliers	138945	3064 (1.50-1.50)
RSRZ outliers	127900	2884 (1.50-1.50)

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 on 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	365	5% 95% 5%
1	B	365	4% 97% .
1	C	365	4% 98% .
1	D	365	4% 98% .
1	E	365	2% 98% .
1	F	365	6% 95% 5%

2 Entry composition

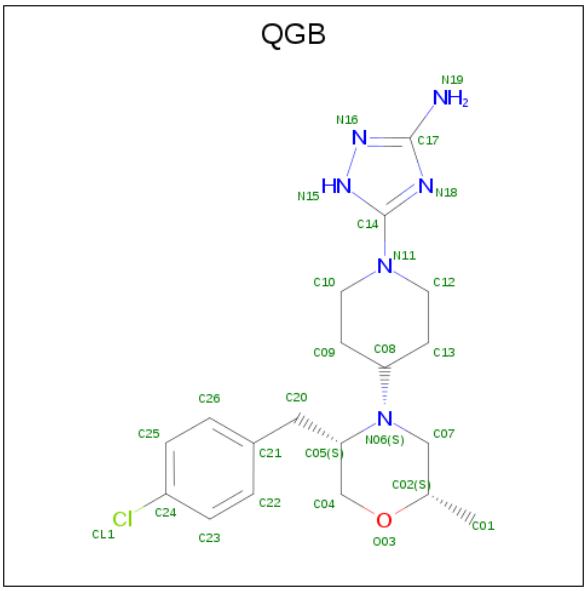
There are 5 unique types of molecules in this entry. The entry contains 20052 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Chitotriosidase-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	365	Total	C	N	O	S	0	14	0
			2922	1862	489	556	15			
1	B	365	Total	C	N	O	S	0	12	0
			2915	1858	494	552	11			
1	C	365	Total	C	N	O	S	0	9	0
			2881	1838	481	550	12			
1	D	365	Total	C	N	O	S	0	9	0
			2915	1857	494	552	12			
1	E	365	Total	C	N	O	S	0	14	0
			2947	1875	497	562	13			
1	F	365	Total	C	N	O	S	0	13	0
			2928	1868	493	554	13			

- Molecule 2 is 5-(4-((2S,5S)-5-(4-chlorobenzyl)-2-methylmorpholino)piperidin-1-yl)-4H-1,2,4-triazol-3-amine (three-letter code: QGB) (formula: $C_{19}H_{27}ClN_6O$) (labeled as "Ligand of Interest" by author).

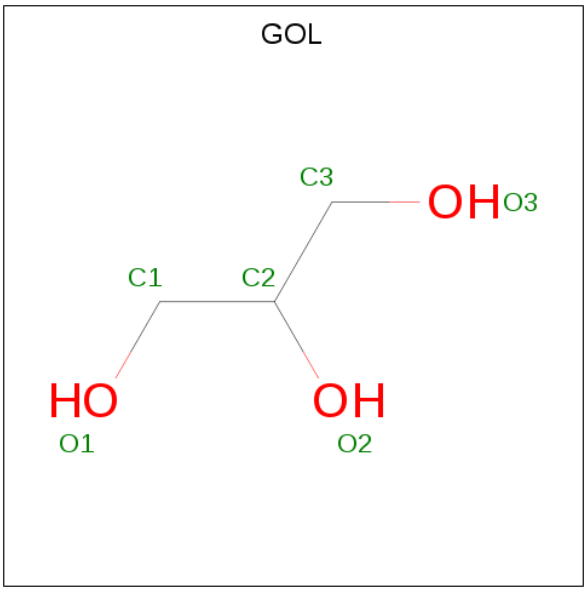


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	Cl	N	O	0	0
			27	19	1	6	1		
2	B	1	Total	C	Cl	N	O	0	0
			27	19	1	6	1		
2	C	1	Total	C	Cl	N	O	0	0
			27	19	1	6	1		
2	D	1	Total	C	Cl	N	O	0	0
			27	19	1	6	1		
2	E	1	Total	C	Cl	N	O	0	0
			27	19	1	6	1		
2	F	1	Total	C	Cl	N	O	0	0
			27	19	1	6	1		

- Molecule 3 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	D	1	Total	Na	0	0
			1	1		
3	E	1	Total	Na	0	0
			1	1		
3	B	1	Total	Na	0	0
			1	1		
3	C	1	Total	Na	0	0
			1	1		
3	A	1	Total	Na	0	0
			1	1		
3	F	1	Total	Na	0	0
			1	1		

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	D	1	Total C O 6 3 3	0	0

- Molecule 5 is water.

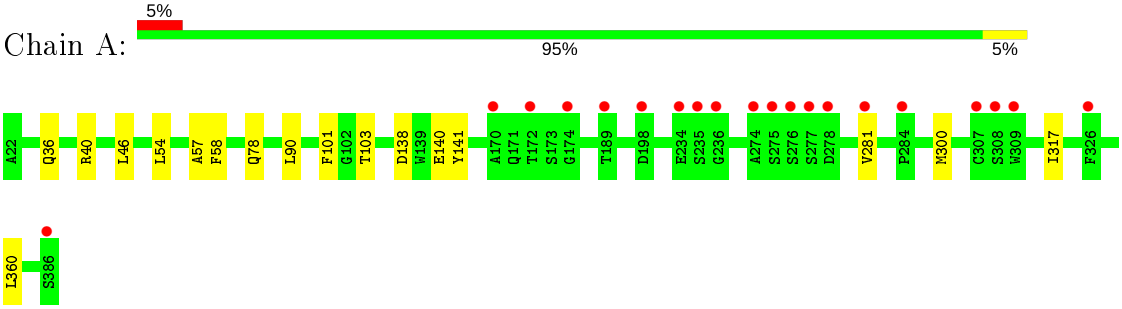
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	338	Total O 338 338	0	0
5	B	396	Total O 396 396	0	0
5	C	413	Total O 413 413	0	0
5	D	429	Total O 429 429	0	0
5	E	420	Total O 420 420	0	0
5	F	374	Total O 374 374	0	0

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.

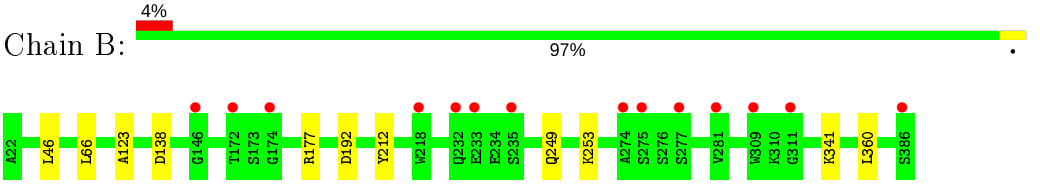
- Molecule 1: Chitotriosidase-1

Chain A:



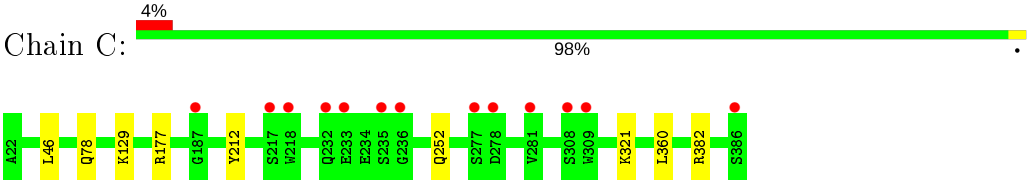
- Molecule 1: Chitotriosidase-1

Chain B:



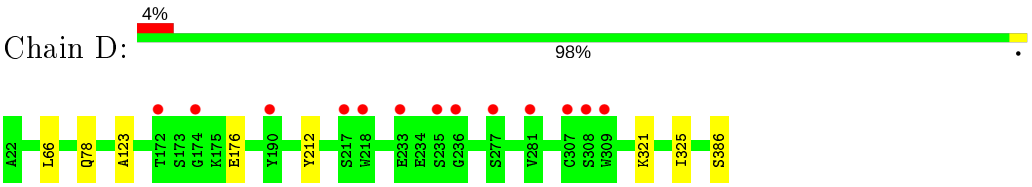
- Molecule 1: Chitotriosidase-1

Chain C:



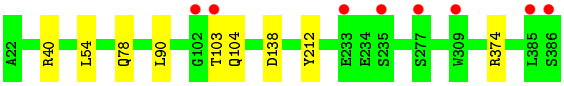
- Molecule 1: Chitotriosidase-1

Chain D:



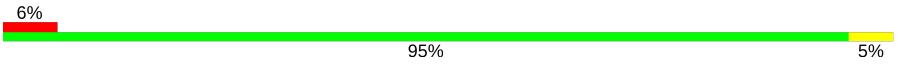
- Molecule 1: Chitotriosidase-1

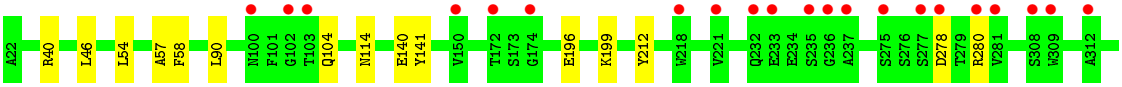
Chain E:



- Molecule 1: Chitotriosidase-1

Chain F:





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	87.33Å 93.74Å 281.64Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.34 – 1.50 47.34 – 1.50	Depositor EDS
% Data completeness (in resolution range)	99.6 (47.34-1.50) 99.6 (47.34-1.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.13 (at 1.50Å)	Xtriage
Refinement program	PHENIX 1.16	Depositor
R, R_{free}	0.123 , 0.168 0.121 , 0.167	Depositor DCC
R_{free} test set	3871 reflections (1.05%)	wwPDB-VP
Wilson B-factor (Å^2)	17.8	Xtriage
Anisotropy	0.029	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.38 , 66.0	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.98	EDS
Total number of atoms	20052	wwPDB-VP
Average B, all atoms (Å^2)	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 12.87% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, QGB, 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	0.62	0/3010	0.69	0/4085
1	B	0.62	0/3002	0.68	0/4075
1	C	0.68	0/2966	0.71	2/4028 (0.0%)
1	D	0.71	0/3002	0.70	0/4073
1	E	0.68	0/3027	0.69	1/4105 (0.0%)
1	F	0.62	0/3016	0.70	1/4094 (0.0%)
All	All	0.66	0/18023	0.70	4/24460 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C	177	ARG	NE-CZ-NH1	6.06	123.33	120.30
1	F	40	ARG	NE-CZ-NH1	-5.68	117.46	120.30
1	E	40	ARG	NE-CZ-NH1	-5.61	117.50	120.30
1	C	177	ARG	NE-CZ-NH2	-5.44	117.58	120.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	2922	0	2780	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	2915	0	2776	6	0
1	C	2881	0	2731	6	0
1	D	2915	0	2786	6	0
1	E	2947	0	2804	3	0
1	F	2928	0	2785	8	0
2	A	27	0	0	0	0
2	B	27	0	0	0	0
2	C	27	0	0	0	0
2	D	27	0	0	0	0
2	E	27	0	0	0	0
2	F	27	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
3	D	1	0	0	0	0
3	E	1	0	0	0	0
3	F	1	0	0	0	0
4	D	6	0	8	1	0
5	A	338	0	0	3	1
5	B	396	0	0	2	1
5	C	413	0	0	5	6
5	D	429	0	0	3	1
5	E	420	0	0	2	5
5	F	374	0	0	2	4
All	All	20052	0	16670	38	10

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 1.

All (38) 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:A:46:LEU:HD21	1:A:360:LEU:HD13	1.63	0.79
1:D:176:GLU:OE1	5:D:501:HOH:O	2.06	0.73
1:F:46:LEU:HD21	1:F:360:LEU:HD13	1.71	0.72
1:D:321[B]:LYS:HE3	4:D:402:GOL:H31	1.75	0.67
1:E:374[B]:ARG:NH1	5:E:504:HOH:O	2.31	0.63
1:A:101:PHE:O	5:A:501:HOH:O	2.15	0.63
1:F:278:ASP:OD2	1:F:280:ARG:NH1	2.34	0.61
1:C:382:ARG:NH1	5:C:503:HOH:O	2.34	0.56
1:C:252[A]:GLN:NE2	5:C:502:HOH:O	2.33	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:321:LYS:NZ	5:C:505:HOH:O	2.39	0.55
1:B:177[B]:ARG:NH1	5:B:501:HOH:O	2.30	0.54
1:B:66:LEU:HD12	1:B:123:ALA:HA	1.91	0.52
1:F:54:LEU:HG	1:F:90:LEU:HD11	1.93	0.51
1:D:321[B]:LYS:NZ	5:D:507:HOH:O	2.43	0.51
1:A:54:LEU:HG	1:A:90:LEU:HD11	1.94	0.48
1:F:196:GLU:HB3	1:F:199:LYS:HD3	1.96	0.48
1:A:103:THR:HG21	1:B:341:LYS:NZ	2.28	0.48
1:D:386:SER:OG	5:D:502:HOH:O	2.16	0.47
1:A:281[A]:VAL:HG21	1:A:317:ILE:HG12	1.97	0.46
1:D:66:LEU:HD12	1:D:123:ALA:HA	1.97	0.46
1:A:57:ALA:HA	1:A:58:PHE:HA	1.78	0.45
1:C:78:GLN:HG2	5:C:653:HOH:O	2.17	0.44
1:A:36:GLN:HG3	5:B:645:HOH:O	2.18	0.44
1:B:192:ASP:OD1	1:B:253:LYS:NZ	2.50	0.44
1:B:46:LEU:CD2	1:B:360:LEU:HD13	2.48	0.44
1:F:140:GLU:HA	1:F:141:TYR:CG	2.54	0.43
1:C:46:LEU:CD2	1:C:360:LEU:HD13	2.49	0.42
1:F:57:ALA:HA	1:F:58:PHE:HA	1.87	0.42
1:B:249:GLN:HG3	1:B:253:LYS:HE3	2.03	0.41
1:C:129:LYS:NZ	5:C:510:HOH:O	2.49	0.41
1:A:140:GLU:HA	1:A:141:TYR:CD1	2.56	0.41
1:E:104[A]:GLN:OE1	5:E:501:HOH:O	2.21	0.41
1:F:386:SER:O	5:F:501:HOH:O	2.22	0.41
1:A:78[A]:GLN:HG2	5:A:677:HOH:O	2.20	0.41
1:D:325:ILE:HD13	1:D:325:ILE:HG21	1.78	0.40
1:E:54:LEU:HG	1:E:90:LEU:HD11	2.03	0.40
1:F:114:ASN:ND2	5:F:512:HOH:O	2.55	0.40
1:A:40[B]:ARG:NH2	5:A:512:HOH:O	2.53	0.40

All (10) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:844:HOH:O	5:E:866:HOH:O[3_655]	2.04	0.16
5:C:664:HOH:O	5:F:872:HOH:O[1_565]	2.06	0.14
5:D:861:HOH:O	5:E:872:HOH:O[3_545]	2.06	0.14
5:C:869:HOH:O	5:E:909:HOH:O[3_655]	2.09	0.11
5:C:831:HOH:O	5:F:818:HOH:O[1_565]	2.12	0.08
5:E:798:HOH:O	5:E:829:HOH:O[3_655]	2.12	0.08

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:900:HOH:O	5:F:818:HOH:O[1_565]	2.15	0.05
5:C:833:HOH:O	5:F:506:HOH:O[1_565]	2.15	0.05
5:C:832:HOH:O	5:E:919:HOH:O[3_655]	2.16	0.04
5:A:781:HOH:O	5:B:858:HOH:O[4_545]	2.18	0.02

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	377/365 (103%)	372 (99%)	5 (1%)	0	100	100
1	B	375/365 (103%)	370 (99%)	5 (1%)	0	100	100
1	C	372/365 (102%)	367 (99%)	5 (1%)	0	100	100
1	D	372/365 (102%)	364 (98%)	8 (2%)	0	100	100
1	E	377/365 (103%)	367 (97%)	10 (3%)	0	100	100
1	F	376/365 (103%)	368 (98%)	8 (2%)	0	100	100
All	All	2249/2190 (103%)	2208 (98%)	41 (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	302/301 (100%)	299 (99%)	3 (1%)	76	57

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	B	298/301 (99%)	296 (99%)	2 (1%)	84 69
1	C	295/301 (98%)	294 (100%)	1 (0%)	92 85
1	D	302/301 (100%)	300 (99%)	2 (1%)	84 69
1	E	305/301 (101%)	300 (98%)	5 (2%)	62 36
1	F	301/301 (100%)	298 (99%)	3 (1%)	76 57
All	All	1803/1806 (100%)	1787 (99%)	16 (1%)	84 61

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	138	ASP
1	A	300[A]	MET
1	A	300[B]	MET
1	B	138	ASP
1	B	212	TYR
1	C	212	TYR
1	D	78	GLN
1	D	212	TYR
1	E	78	GLN
1	E	103[A]	THR
1	E	103[B]	THR
1	E	138	ASP
1	E	212	TYR
1	F	104[A]	GLN
1	F	104[B]	GLN
1	F	212	TYR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	D	188	GLN
1	D	315	GLN
1	E	315	GLN
1	E	383	GLN
1	F	202	GLN

5.3.3 RNA

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 13 ligands modelled in this entry, 6 are monoatomic - leaving 7 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	$\#\|Z\| > 2$
2	QGB	F	401	-	27,30,30	2.58	10 (37%)	28,42,42	1.69	4 (14%)
2	QGB	B	401	-	27,30,30	2.42	9 (33%)	28,42,42	1.43	4 (14%)
2	QGB	D	401	-	27,30,30	2.40	8 (29%)	28,42,42	1.57	4 (14%)
4	GOL	D	402	-	5,5,5	1.10	0	5,5,5	1.14	1 (20%)
2	QGB	E	401	-	27,30,30	2.39	8 (29%)	28,42,42	1.56	3 (10%)
2	QGB	A	401	-	27,30,30	2.62	10 (37%)	28,42,42	1.43	4 (14%)
2	QGB	C	401	-	27,30,30	2.57	9 (33%)	28,42,42	1.59	6 (21%)

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
2	QGB	F	401	-	-	0/8/35/35	0/4/4/4
2	QGB	B	401	-	-	0/8/35/35	0/4/4/4
2	QGB	D	401	-	-	0/8/35/35	0/4/4/4
4	GOL	D	402	-	-	4/4/4/4	-
2	QGB	E	401	-	-	0/8/35/35	0/4/4/4
2	QGB	A	401	-	-	0/8/35/35	0/4/4/4

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	QGB	C	401	-	-	0/8/35/35	0/4/4/4

All (54) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	401	QGB	C08-N06	-8.66	1.35	1.47
2	F	401	QGB	C08-N06	-8.34	1.35	1.47
2	E	401	QGB	C08-N06	-8.10	1.36	1.47
2	D	401	QGB	C08-N06	-7.80	1.36	1.47
2	B	401	QGB	C08-N06	-7.50	1.37	1.47
2	C	401	QGB	C08-N06	-7.28	1.37	1.47
2	C	401	QGB	C07-N06	-4.78	1.41	1.47
2	D	401	QGB	C20-C05	4.71	1.60	1.53
2	C	401	QGB	C20-C05	4.67	1.60	1.53
2	F	401	QGB	C07-N06	-4.60	1.41	1.47
2	A	401	QGB	C20-C05	4.32	1.59	1.53
2	E	401	QGB	C07-N06	-4.01	1.42	1.47
2	B	401	QGB	C14-N11	3.93	1.43	1.35
2	A	401	QGB	C07-N06	-3.87	1.42	1.47
2	A	401	QGB	C14-N11	3.84	1.42	1.35
2	B	401	QGB	C07-N06	-3.79	1.42	1.47
2	D	401	QGB	O03-C04	-3.72	1.37	1.43
2	D	401	QGB	C14-N11	3.72	1.42	1.35
2	E	401	QGB	C20-C05	3.66	1.58	1.53
2	C	401	QGB	C14-N11	3.66	1.42	1.35
2	F	401	QGB	O03-C02	-3.62	1.40	1.43
2	B	401	QGB	C20-C05	3.61	1.58	1.53
2	F	401	QGB	C14-N11	3.40	1.42	1.35
2	C	401	QGB	C05-N06	-3.37	1.42	1.48
2	F	401	QGB	C20-C05	3.36	1.58	1.53
2	C	401	QGB	C17-N19	3.23	1.40	1.33
2	E	401	QGB	C14-N11	3.18	1.41	1.35
2	F	401	QGB	C05-N06	-3.16	1.43	1.48
2	A	401	QGB	C17-N19	3.12	1.40	1.33
2	C	401	QGB	O03-C02	-3.11	1.40	1.43
2	B	401	QGB	C20-C21	3.10	1.58	1.51
2	E	401	QGB	O03-C04	-3.01	1.38	1.43
2	A	401	QGB	C20-C21	2.98	1.58	1.51
2	A	401	QGB	C05-N06	-2.96	1.43	1.48
2	E	401	QGB	C20-C21	2.94	1.58	1.51
2	A	401	QGB	O03-C02	-2.90	1.41	1.43
2	F	401	QGB	C20-C21	2.90	1.58	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	401	QGB	O03-C04	-2.88	1.39	1.43
2	B	401	QGB	C17-N19	2.86	1.39	1.33
2	C	401	QGB	C20-C21	2.83	1.58	1.51
2	B	401	QGB	O03-C02	-2.79	1.41	1.43
2	E	401	QGB	C12-N11	2.75	1.51	1.46
2	D	401	QGB	C05-N06	-2.65	1.44	1.48
2	A	401	QGB	O03-C04	-2.65	1.39	1.43
2	D	401	QGB	C17-N19	2.61	1.39	1.33
2	B	401	QGB	C05-N06	-2.59	1.44	1.48
2	D	401	QGB	C07-N06	-2.56	1.44	1.47
2	D	401	QGB	C20-C21	2.54	1.57	1.51
2	E	401	QGB	C17-N19	2.44	1.38	1.33
2	F	401	QGB	C12-N11	2.39	1.50	1.46
2	F	401	QGB	C17-N19	2.30	1.38	1.33
2	C	401	QGB	C25-C24	2.23	1.42	1.38
2	A	401	QGB	C22-C21	2.04	1.43	1.38
2	B	401	QGB	C04-C05	2.03	1.55	1.51

All (26) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	E	401	QGB	C10-N11-C14	-5.60	112.40	121.69
2	F	401	QGB	C10-N11-C14	-5.24	113.00	121.69
2	B	401	QGB	C10-N11-C14	-5.22	113.03	121.69
2	C	401	QGB	C10-N11-C14	-5.16	113.14	121.69
2	D	401	QGB	C10-N11-C14	-4.71	113.88	121.69
2	F	401	QGB	C20-C05-C04	-4.67	105.16	112.57
2	A	401	QGB	C10-N11-C14	-4.10	114.88	121.69
2	D	401	QGB	C12-N11-C14	-3.70	115.56	121.69
2	A	401	QGB	C12-N11-C14	-3.35	116.13	121.69
2	F	401	QGB	C12-N11-C14	-3.04	116.64	121.69
2	C	401	QGB	C20-C05-C04	-2.91	107.95	112.57
2	C	401	QGB	C12-N11-C14	-2.86	116.94	121.69
2	C	401	QGB	O03-C02-C01	2.81	111.57	107.64
2	B	401	QGB	C20-C05-C04	-2.75	108.21	112.57
2	D	401	QGB	C10-C09-C08	2.58	115.72	110.81
2	E	401	QGB	C12-N11-C14	-2.52	117.52	121.69
2	B	401	QGB	C12-N11-C14	-2.47	117.60	121.69
2	C	401	QGB	C10-C09-C08	2.46	115.49	110.81
2	B	401	QGB	C13-C08-C09	-2.33	105.83	111.19
2	F	401	QGB	O03-C02-C01	2.22	110.75	107.64
2	E	401	QGB	C22-C23-C24	2.16	121.53	119.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	401	QGB	C20-C05-C04	-2.13	109.19	112.57
2	D	401	QGB	C13-C08-C09	-2.09	106.38	111.19
2	A	401	QGB	C13-C08-C09	-2.06	106.45	111.19
4	D	402	GOL	C3-C2-C1	-2.04	103.76	111.70
2	C	401	QGB	C12-N11-C10	2.01	115.96	111.52

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	D	402	GOL	O1-C1-C2-C3
4	D	402	GOL	C1-C2-C3-O3
4	D	402	GOL	O1-C1-C2-O2
4	D	402	GOL	O2-C2-C3-O3

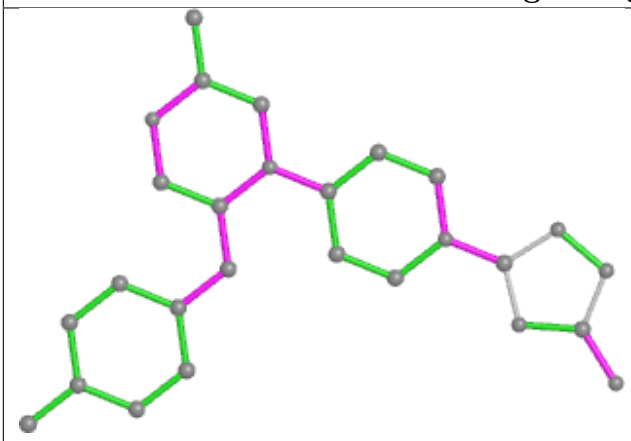
There are no ring outliers.

1 monomer is involved in 1 short contact:

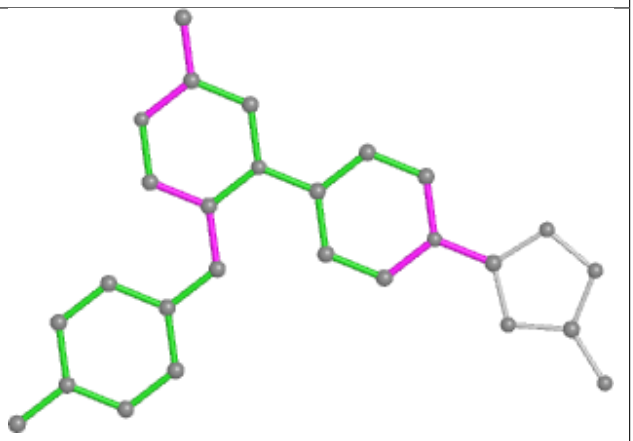
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	D	402	GOL	1	0

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.

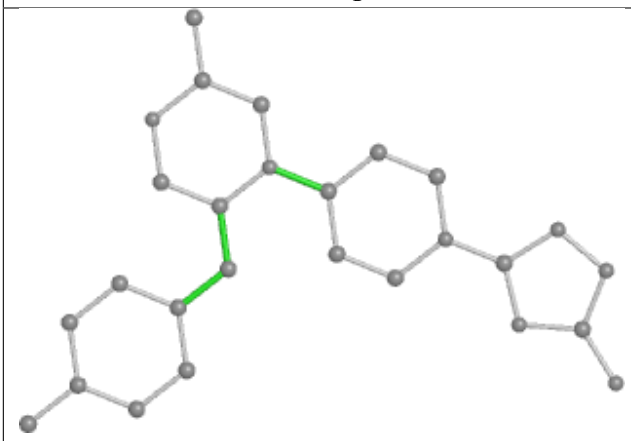
Ligand QGB F 401



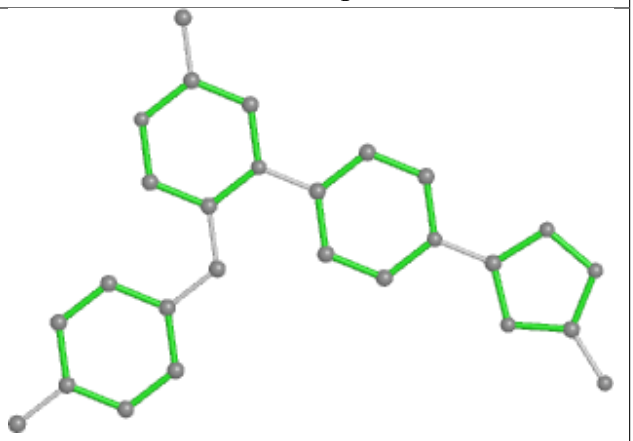
Bond lengths



Bond angles

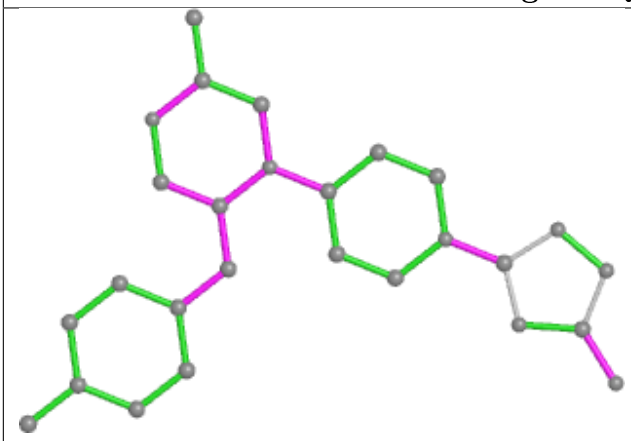


Torsions

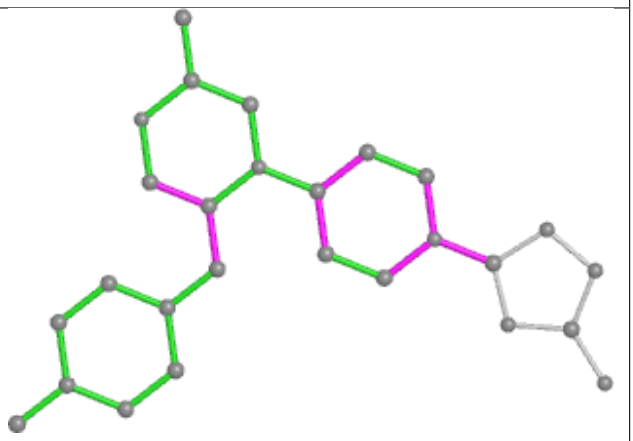


Rings

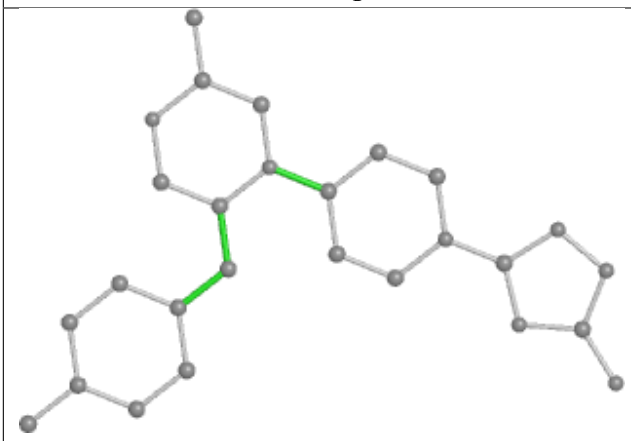
Ligand QGB B 401



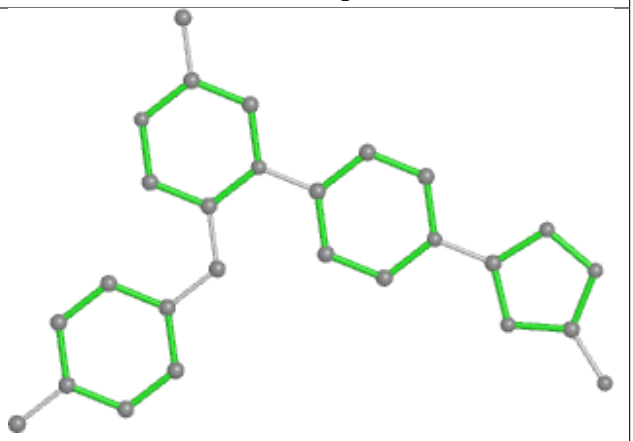
Bond lengths



Bond angles

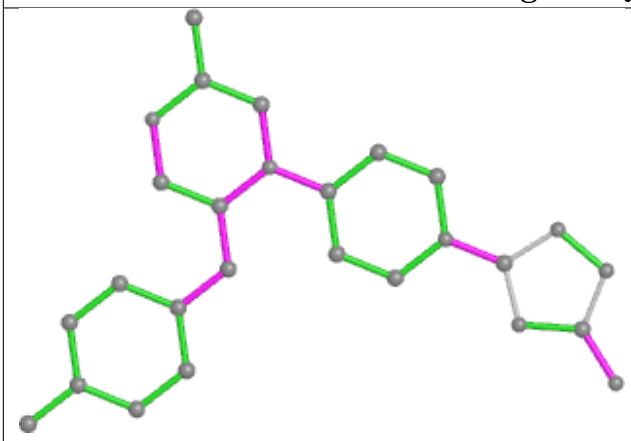


Torsions

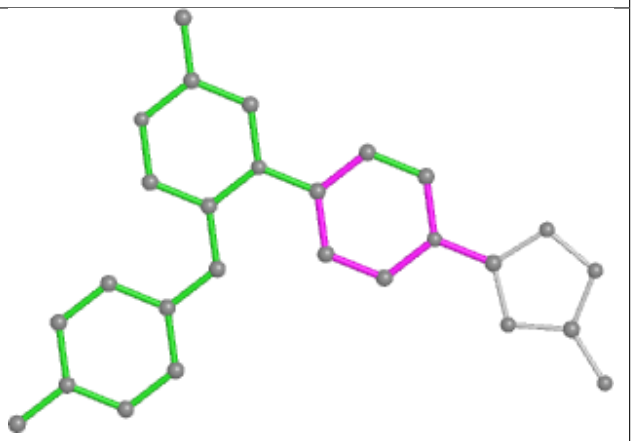


Rings

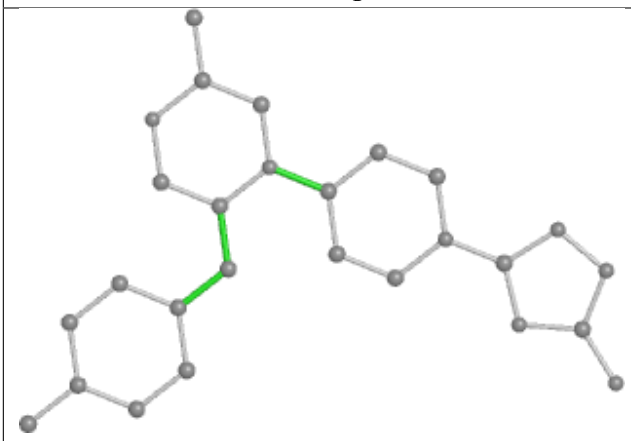
Ligand QGB D 401



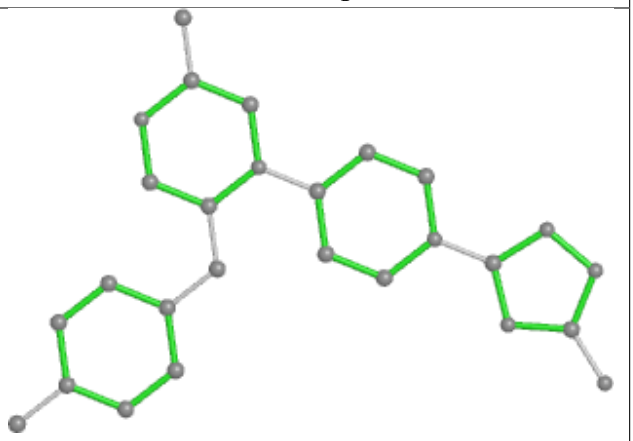
Bond lengths



Bond angles

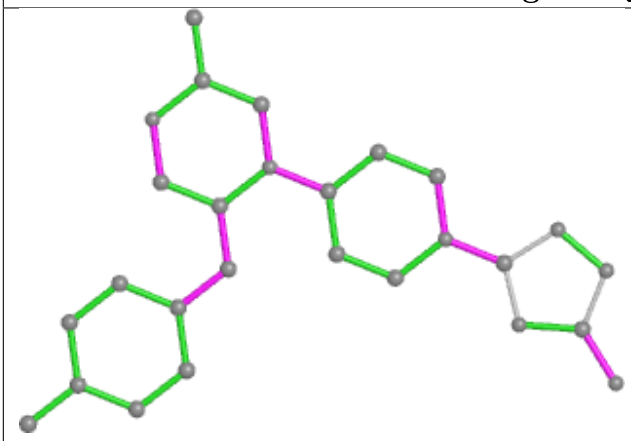


Torsions

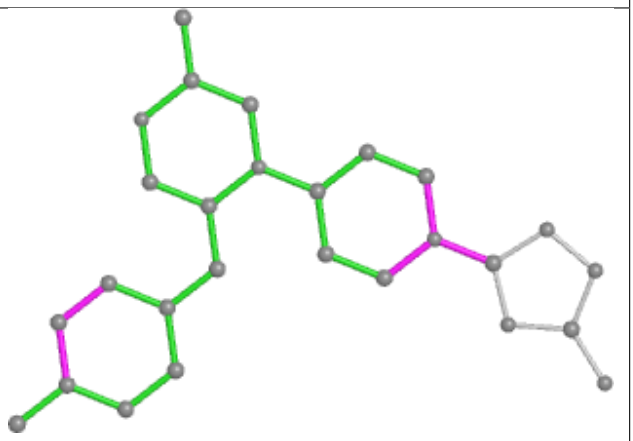


Rings

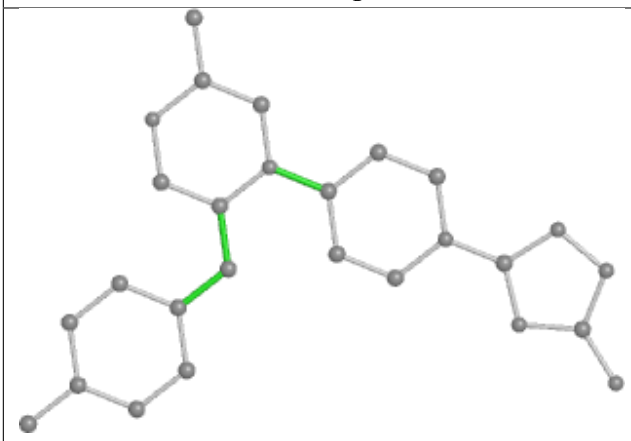
Ligand QGB E 401



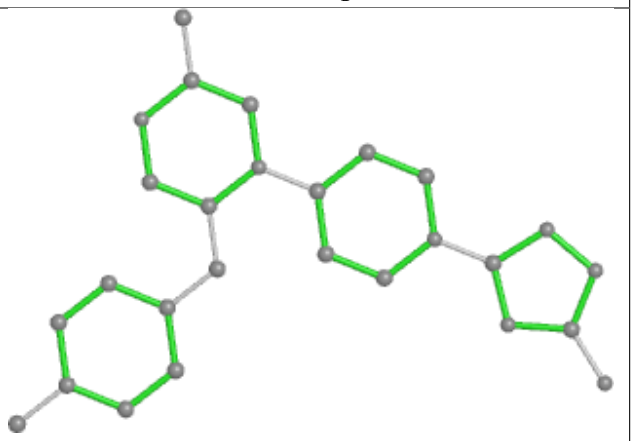
Bond lengths



Bond angles

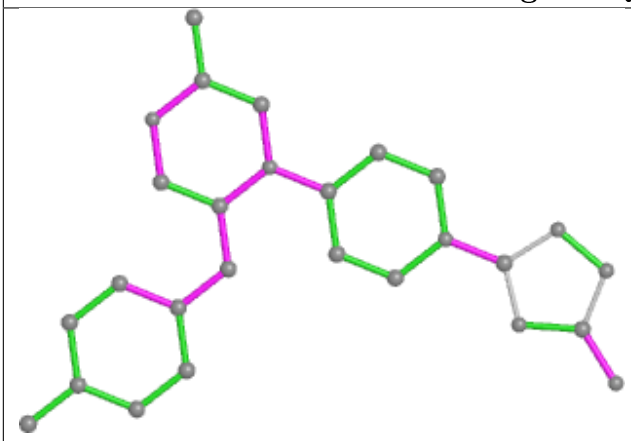


Torsions

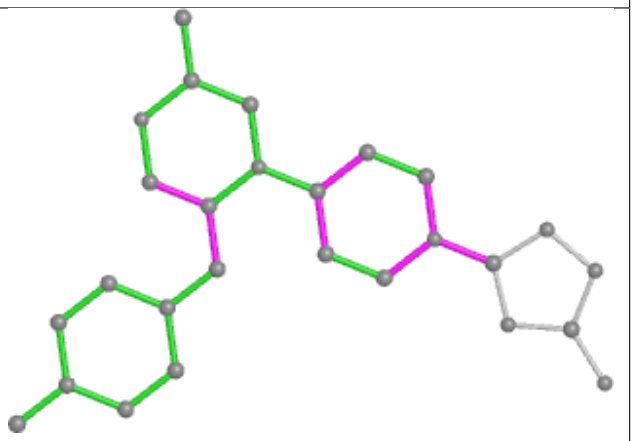


Rings

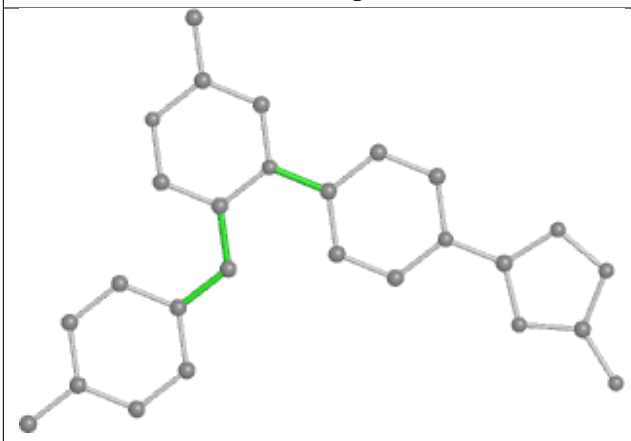
Ligand QGB A 401



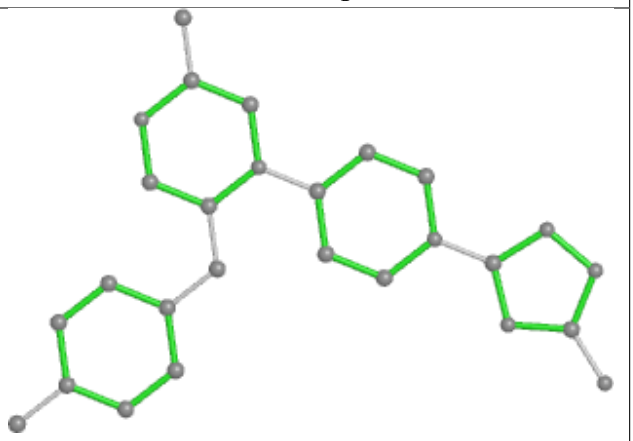
Bond lengths



Bond angles

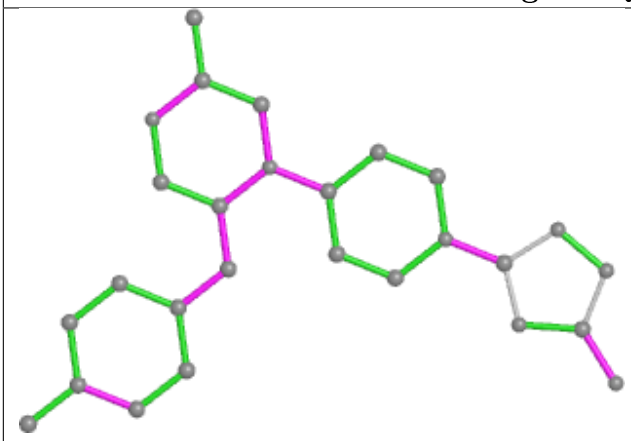


Torsions

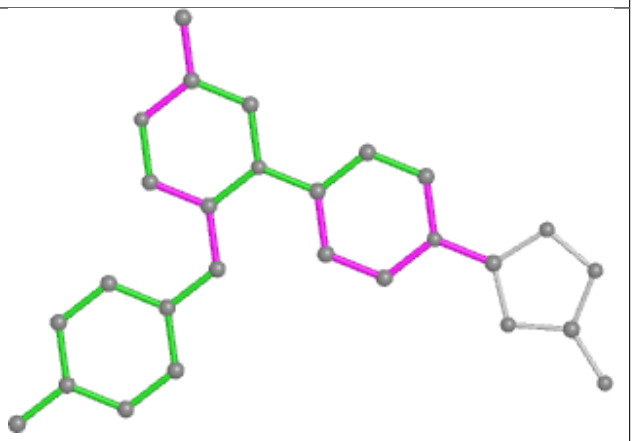


Rings

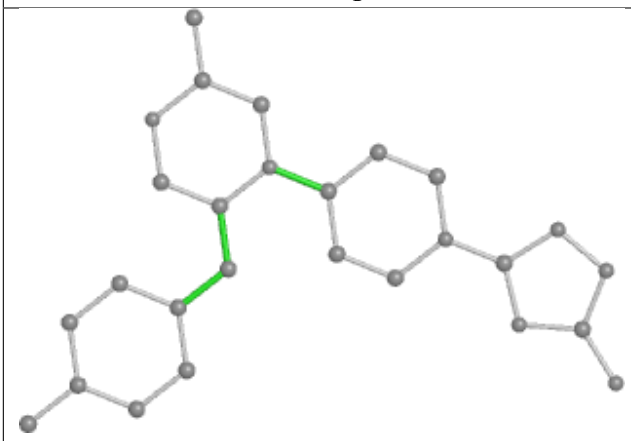
Ligand QGB C 401



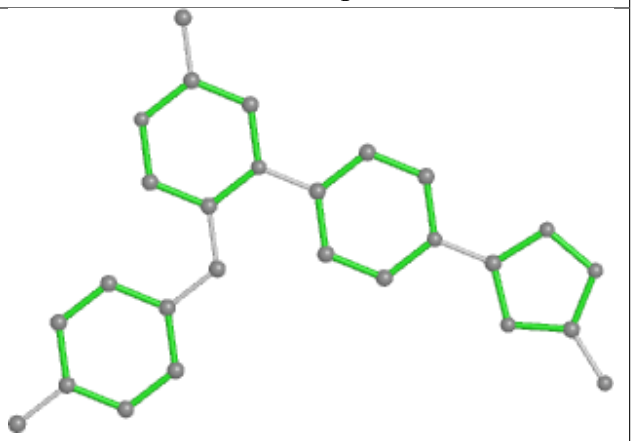
Bond lengths



Bond angles



Torsions



Rings

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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, 95^{th} 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	365/365 (100%)	0.16	20 (5%)	25	27	13, 21, 40, 55	8 (2%)
1	B	365/365 (100%)	0.13	14 (3%)	40	44	13, 20, 35, 65	5 (1%)
1	C	365/365 (100%)	0.10	13 (3%)	42	47	12, 18, 33, 67	5 (1%)
1	D	365/365 (100%)	0.11	13 (3%)	42	47	12, 18, 33, 58	11 (3%)
1	E	365/365 (100%)	0.08	8 (2%)	62	67	12, 18, 33, 58	5 (1%)
1	F	365/365 (100%)	0.22	22 (6%)	21	23	13, 21, 38, 69	7 (1%)
All	All	2190/2190 (100%)	0.13	90 (4%)	37	41	12, 19, 36, 69	41 (1%)

All (90) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	103[A]	THR	5.9
1	F	102[A]	GLY	5.2
1	F	235	SER	4.7
1	A	277	SER	4.4
1	B	172	THR	4.3
1	F	174	GLY	4.2
1	D	277	SER	4.1
1	B	281	VAL	4.1
1	B	235	SER	4.0
1	A	172	THR	3.9
1	D	172	THR	3.9
1	F	103[A]	THR	3.8
1	F	277	SER	3.7
1	D	309[A]	TRP	3.7
1	E	309	TRP	3.6
1	A	235	SER	3.5
1	E	235	SER	3.5
1	A	284	PRO	3.5
1	A	189	THR	3.5

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Mol	Chain	Res	Type	RSRZ
1	A	236	GLY	3.5
1	F	281[A]	VAL	3.4
1	C	386	SER	3.3
1	D	217	SER	3.3
1	B	218	TRP	3.2
1	A	308	SER	3.2
1	E	102[A]	GLY	3.2
1	F	309	TRP	3.2
1	C	217	SER	3.2
1	C	308	SER	3.1
1	C	236	GLY	3.0
1	C	218	TRP	3.0
1	B	277	SER	3.0
1	F	150	VAL	3.0
1	B	146	GLY	3.0
1	F	232	GLN	2.9
1	E	233	GLU	2.9
1	F	172	THR	2.9
1	D	235	SER	2.9
1	B	275	SER	2.8
1	F	280	ARG	2.8
1	B	233	GLU	2.8
1	D	236	GLY	2.8
1	A	326	PHE	2.8
1	E	277	SER	2.7
1	F	218	TRP	2.7
1	F	233	GLU	2.7
1	C	233	GLU	2.7
1	A	174	GLY	2.7
1	A	281[A]	VAL	2.6
1	A	170	ALA	2.6
1	A	278	ASP	2.6
1	F	236[A]	GLY	2.6
1	F	100[A]	ASN	2.5
1	D	233	GLU	2.5
1	C	309	TRP	2.5
1	D	218	TRP	2.5
1	C	281	VAL	2.5
1	A	234	GLU	2.4
1	B	274	ALA	2.4
1	F	312	ALA	2.4
1	F	221	VAL	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	174	GLY	2.4
1	F	308	SER	2.3
1	F	278	ASP	2.3
1	D	174	GLY	2.3
1	D	281	VAL	2.3
1	C	235	SER	2.3
1	B	309	TRP	2.3
1	A	274	ALA	2.3
1	C	232	GLN	2.3
1	F	275	SER	2.3
1	A	275	SER	2.2
1	B	232	GLN	2.2
1	A	309	TRP	2.2
1	D	308[A]	SER	2.2
1	F	237	ALA	2.2
1	D	307[A]	CYS	2.2
1	C	187	GLY	2.2
1	C	277[A]	SER	2.2
1	E	385	LEU	2.2
1	E	386	SER	2.1
1	A	198	ASP	2.1
1	C	278	ASP	2.1
1	B	386	SER	2.1
1	B	311	GLY	2.1
1	A	307	CYS	2.1
1	A	386	SER	2.0
1	D	190	TYR	2.0
1	A	276	SER	2.0
1	F	386	SER	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)

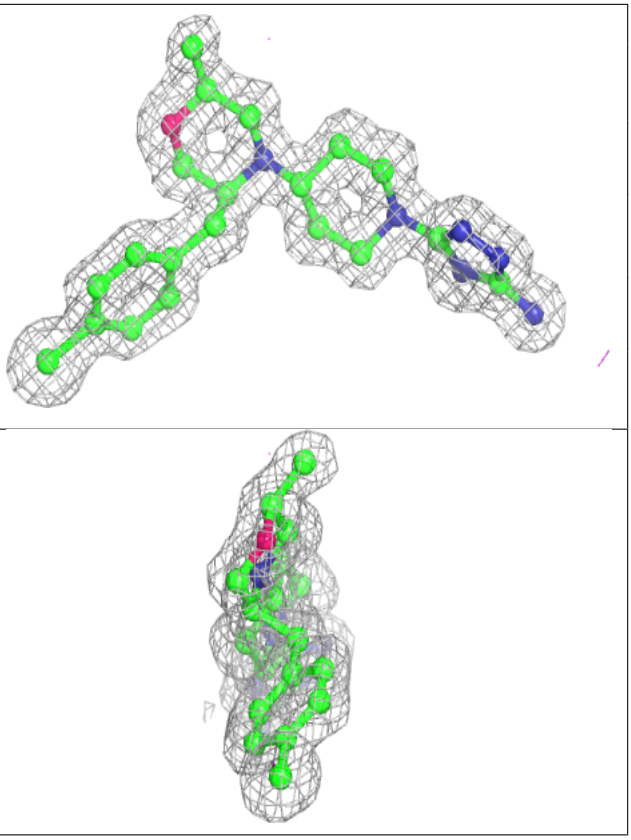
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' 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
3	NA	B	402	1/1	0.84	0.18	55,55,55,55	0
3	NA	E	402	1/1	0.85	0.09	48,48,48,48	0
4	GOL	D	402	6/6	0.85	0.16	40,43,49,94	0
3	NA	A	402	1/1	0.86	0.11	47,47,47,47	0
3	NA	D	403	1/1	0.92	0.09	39,39,39,39	0
3	NA	F	402	1/1	0.95	0.14	42,42,42,42	0
2	QGB	B	401	27/27	0.96	0.08	12,15,18,21	0
2	QGB	A	401	27/27	0.96	0.08	14,15,20,24	0
2	QGB	D	401	27/27	0.97	0.07	11,13,17,20	0
2	QGB	C	401	27/27	0.97	0.08	11,13,19,21	0
2	QGB	E	401	27/27	0.97	0.08	12,15,18,21	0
2	QGB	F	401	27/27	0.97	0.07	14,17,21,22	0
3	NA	C	402	1/1	0.98	0.11	43,43,43,43	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.

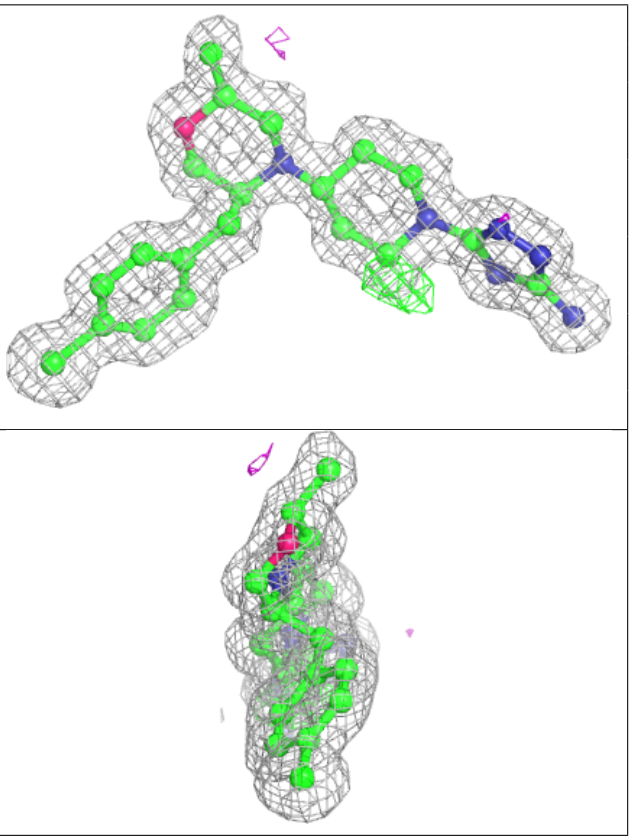
Electron density around QGB B 401:

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



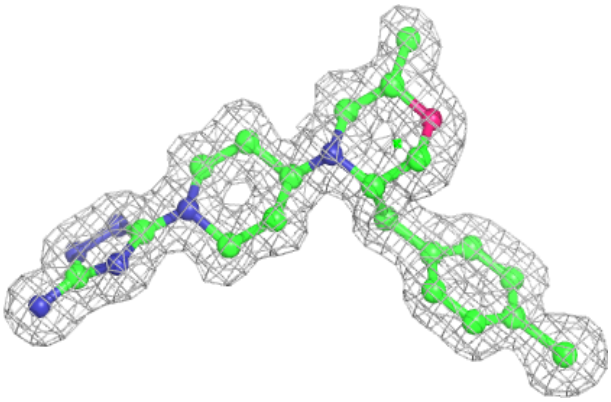
Electron density around QGB A 401:

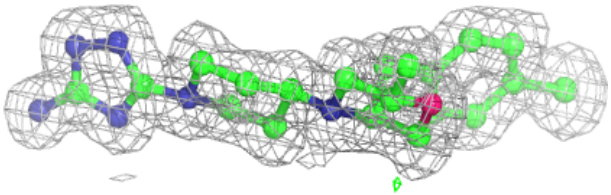
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

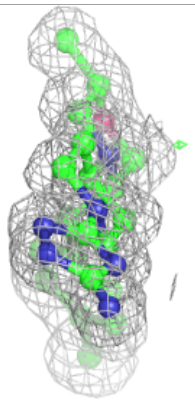


Electron density around QGB D 401:

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

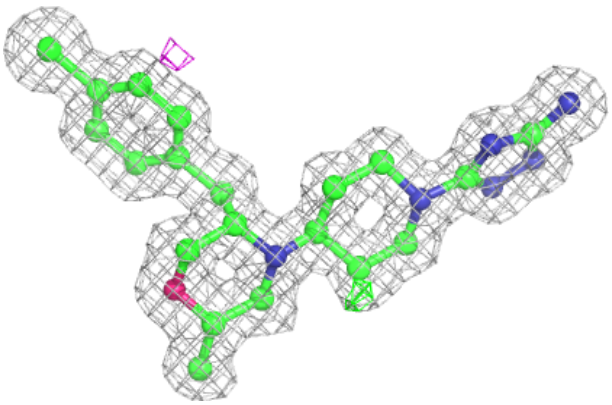


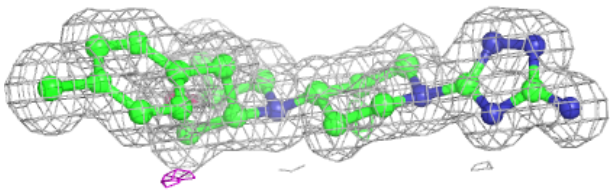


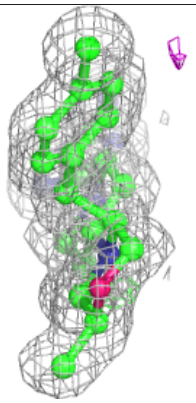


Electron density around QGB C 401:

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

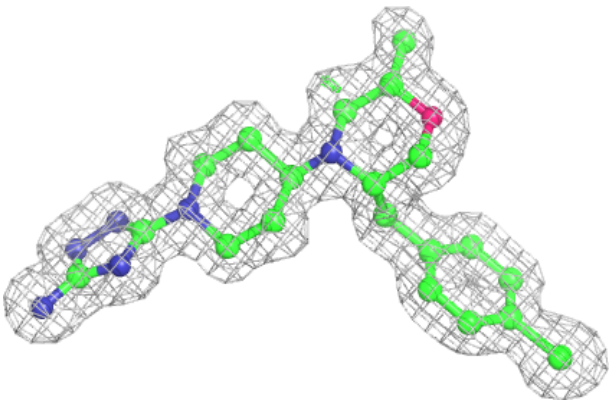


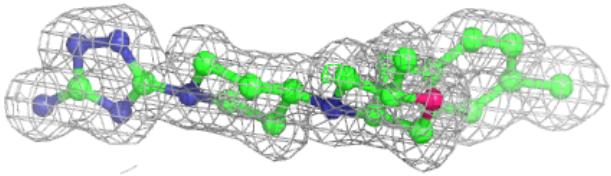


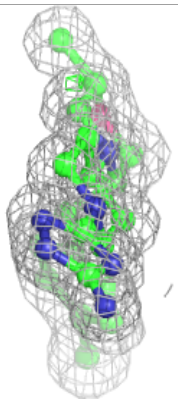


Electron density around QGB E 401:

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

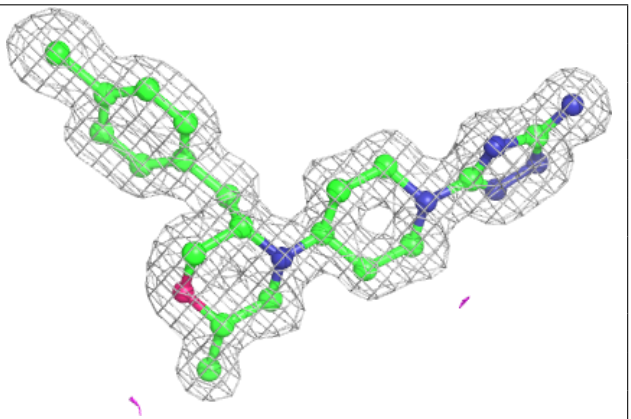


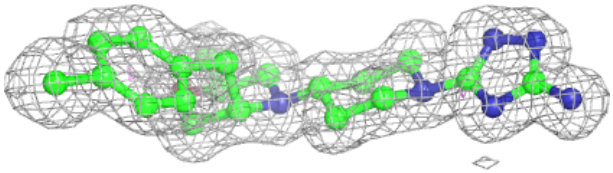


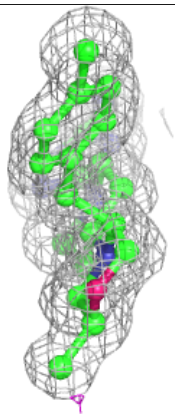


Electron density around QGB F 401:

$2mF_o$-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.