Full wwPDB X-ray Structure Validation Report (i)

Nov 11, 2024 – 04:15 AM EST

PDB ID	:	3K1W
Title	:	New Classes of Potent and Bioavailable Human Renin Inhibitors
Authors	:	Prade, L.
Deposited on	:	2009-09-29
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 (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:

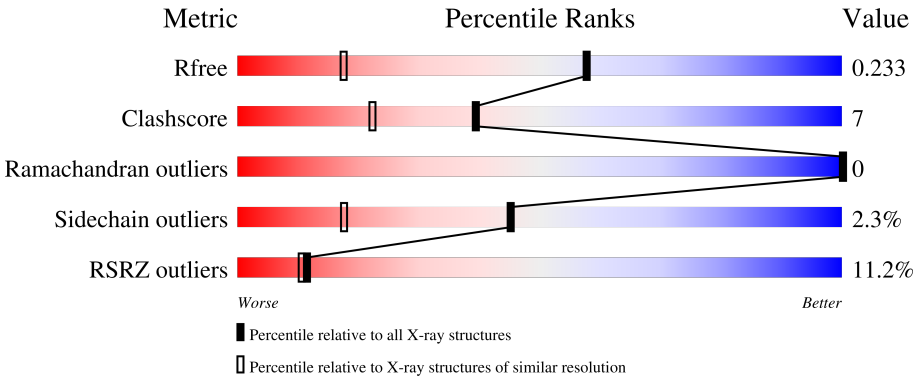
MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	3.0
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.003 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.39

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}	164625	3717 (1.50-1.50)
Clashscore	180529	4048 (1.50-1.50)
Ramachandran outliers	177936	3970 (1.50-1.50)
Sidechain outliers	177891	3967 (1.50-1.50)
RSRZ outliers	164620	3718 (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 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	341	9% 87% 9%
1	B	341	13% 87% 10%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	FMT	A	343	-	-	X	-
3	FMT	B	344	-	-	X	-
4	NAG	A	344	X	-	-	-

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 5990 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.

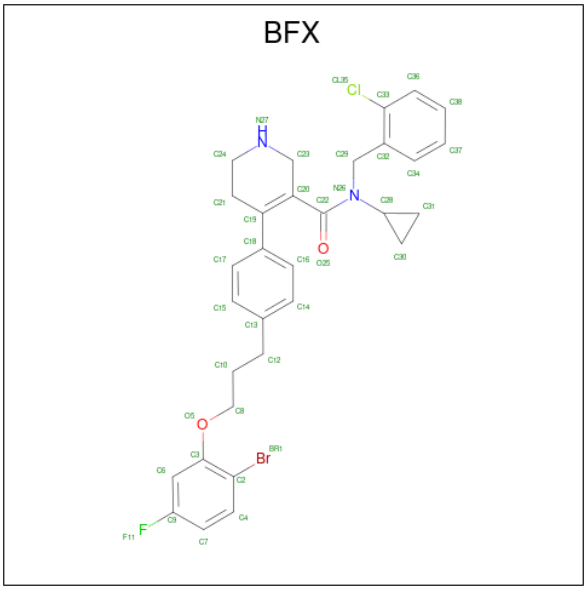
- Molecule 1 is a protein called Renin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	333	Total	C	N	O	S	0	4	0
			2606	1666	423	503	14			
1	B	337	Total	C	N	O	S	0	7	0
			2646	1691	430	511	14			

There are 2 discrepancies between the modelled and reference sequences:

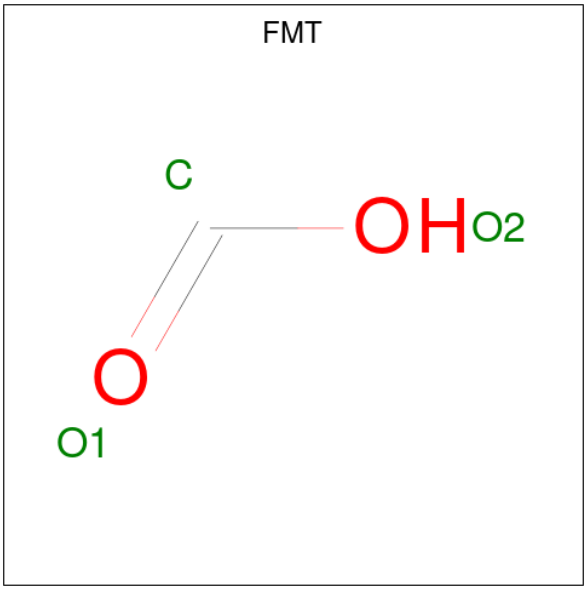
Chain	Residue	Modelled	Actual	Comment	Reference
A	341	HIS	-	expression tag	UNP P00797
B	341	HIS	-	expression tag	UNP P00797

- Molecule 2 is 4-{4-[3-(2-bromo-5-fluorophenoxy)propyl]phenyl}-N-(2-chlorobenzyl)-N-cyclopropyl-1,2,5,6-tetrahydropyridine-3-carboxamide (three-letter code: BFX) (formula: $C_{31}H_{31}BrClFN_2O_2$).



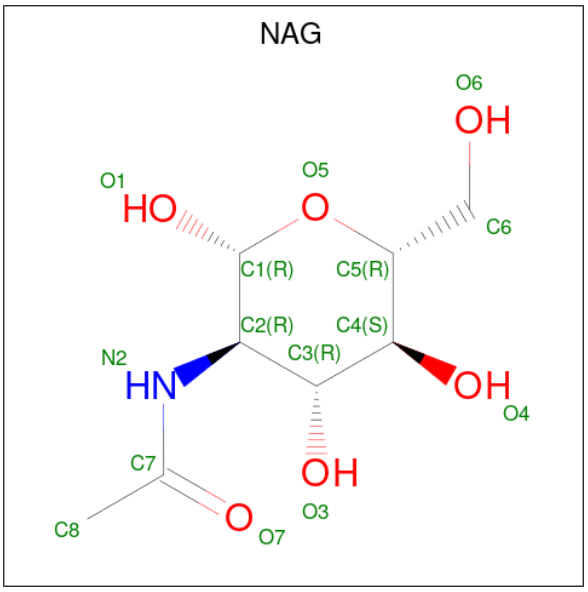
Mol	Chain	Residues	Atoms							ZeroOcc	AltConf
2	A	1	Total	Br	C	Cl	F	N	O	0	0
			38	1	31	1	1	2	2		
2	B	1	Total	Br	C	Cl	F	N	O	0	0
			38	1	31	1	1	2	2		

- Molecule 3 is FORMIC ACID (three-letter code: FMT) (formula: CH_2O_2).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	O		0	0
			3	1	2			
3	B	1	Total	C	O		0	0
			3	1	2			

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).

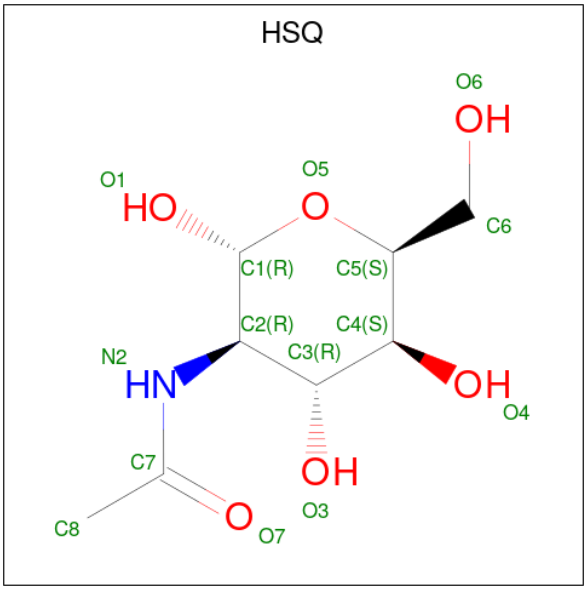


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C N O 14 8 1 5	0	0

- Molecule 5 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	B	1	Total Cl 1 1	0	0

- Molecule 6 is 2-acetylamino-2-deoxy-alpha-L-idopyranose (three-letter code: HSQ) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	B	1	Total C N O 14 8 1 5	0	0

- Molecule 7 is water.

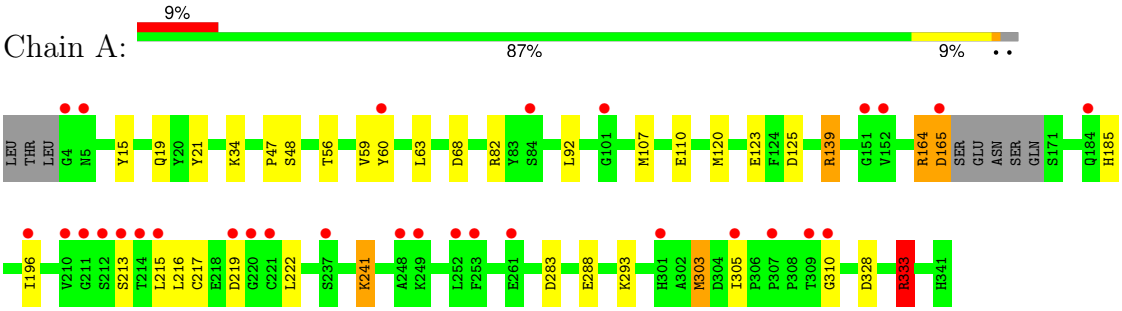
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	336	Total O 336 336	0	0
7	B	291	Total O 291 291	0	0

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.

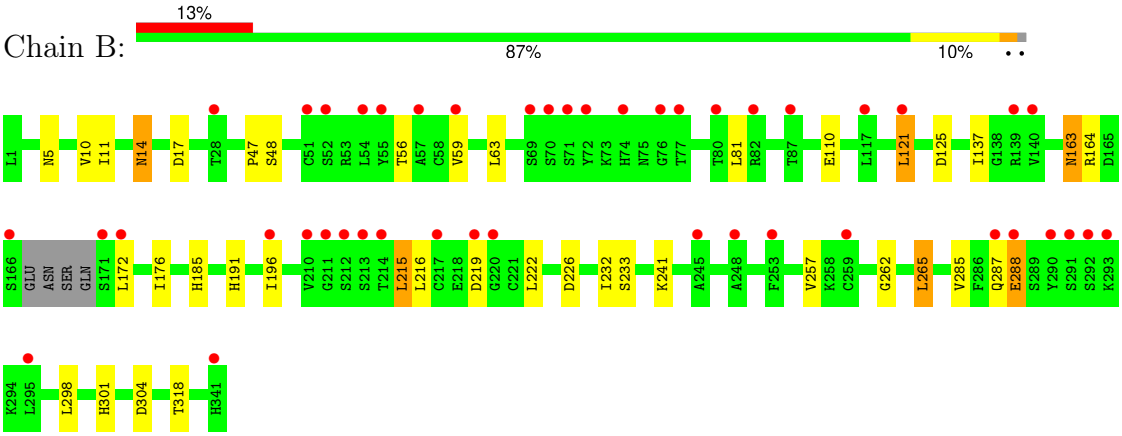
- Molecule 1: Renin

Chain A:



- Molecule 1: Renin

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	66.03Å 88.70Å 118.31Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	31.80 – 1.50 31.80 – 1.50	Depositor EDS
% Data completeness (in resolution range)	88.2 (31.80-1.50) 88.2 (31.80-1.50)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.35 (at 1.50Å)	Xtriage
Refinement program	REFMAC 5.2.0003	Depositor
R, R_{free}	0.199 , 0.233 0.198 , 0.233	Depositor DCC
R_{free} test set	4930 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å^2)	20.9	Xtriage
Anisotropy	0.030	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.39 , 51.1	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	5990	wwPDB-VP
Average B, all atoms (Å^2)	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.46% 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: BFX, NAG, CL, FMT, HSQ

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	0.56	0/2668	0.78	6/3617 (0.2%)
1	B	0.54	0/2707	0.76	4/3670 (0.1%)
All	All	0.55	0/5375	0.77	10/7287 (0.1%)

There are no bond length outliers.

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	333	ARG	NE-CZ-NH1	6.54	123.57	120.30
1	A	165	ASP	CB-CG-OD2	6.42	124.08	118.30
1	B	226	ASP	CB-CG-OD2	5.84	123.56	118.30
1	A	333	ARG	NE-CZ-NH2	-5.29	117.65	120.30
1	A	283	ASP	CB-CG-OD2	5.21	122.99	118.30
1	A	68	ASP	CB-CG-OD2	5.15	122.93	118.30
1	B	219	ASP	CB-CG-OD2	5.12	122.91	118.30
1	B	121	LEU	CA-CB-CG	5.11	127.05	115.30
1	B	304	ASP	CB-CG-OD2	5.08	122.87	118.30
1	A	219	ASP	CB-CG-OD2	5.07	122.86	118.30

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	2606	0	2527	31	0
1	B	2646	0	2579	36	0
2	A	38	0	31	2	0
2	B	38	0	31	0	0
3	A	3	0	1	5	0
3	B	3	0	1	2	0
4	A	14	0	13	0	0
5	B	1	0	0	0	0
6	B	14	0	13	0	0
7	A	336	0	0	9	0
7	B	291	0	0	9	0
All	All	5990	0	5196	70	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 7.

All (70) 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:191[B]:HIS:HD2	7:B:647:HOH:O	1.07	1.30
1:A:164:ARG:HH11	1:A:164:ARG:HG3	1.01	1.16
1:A:82:ARG:HH21	1:B:288:GLU:HB3	1.26	1.00
1:A:164:ARG:HG3	1:A:164:ARG:NH1	1.77	0.92
1:A:288:GLU:HG2	7:A:640:HOH:O	1.73	0.89
1:A:164:ARG:HH11	1:A:164:ARG:CG	1.92	0.74
1:B:215:LEU:HD23	1:B:216:LEU:HG	1.70	0.74
1:A:120:MET:HB2	7:A:572:HOH:O	1.89	0.72
1:B:11:ILE:HD12	1:B:172:LEU:HD11	1.76	0.67
1:B:185:HIS:HD2	7:B:517:HOH:O	1.78	0.66
1:B:285:VAL:HG22	1:B:298:LEU:HD22	1.77	0.65
1:B:14:ASN:HD21	1:B:17:ASP:H	1.44	0.64
1:B:10:VAL:HB	1:B:176[B]:ILE:CG2	2.28	0.64
1:A:164:ARG:O	1:A:165:ASP:HB2	2.00	0.62
1:A:185:HIS:HD2	7:A:551:HOH:O	1.83	0.61
1:B:285:VAL:HG22	1:B:298:LEU:CD2	2.31	0.61
1:B:121:LEU:HD23	7:B:658:HOH:O	2.00	0.60
1:B:191[B]:HIS:CD2	7:B:647:HOH:O	1.99	0.59
1:B:196:ILE:HD13	1:B:222:LEU:HD22	1.84	0.59
1:B:14:ASN:C	1:B:14:ASN:HD22	2.06	0.59
1:A:82:ARG:NH2	1:B:288:GLU:HB3	2.09	0.59
3:A:343:FMT:H	7:A:348:HOH:O	2.03	0.58
1:B:163:ASN:HD22	1:B:164:ARG:H	1.51	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:48:SER:HB2	1:B:110:GLU:HB3	1.87	0.57
1:B:301:HIS:HE1	7:B:354:HOH:O	1.87	0.56
3:A:343:FMT:C	7:A:348:HOH:O	2.54	0.55
1:A:21[B]:TYR:CE2	1:A:34:LYS:HD2	2.41	0.55
1:B:56:THR:HA	1:B:59:VAL:HG22	1.89	0.55
1:A:216:LEU:HD21	1:A:241:LYS:HG2	1.89	0.54
1:A:164:ARG:NH1	1:A:164:ARG:CG	2.58	0.54
1:A:56:THR:HA	1:A:59:VAL:HG12	1.91	0.53
1:B:5:ASN:ND2	7:B:639:HOH:O	2.23	0.52
1:A:185:HIS:HE1	7:A:621:HOH:O	1.92	0.52
3:B:344:FMT:H	7:B:373:HOH:O	2.09	0.52
1:A:82:ARG:HH21	1:B:288:GLU:CB	2.12	0.51
1:A:48:SER:HB2	1:A:110:GLU:HB3	1.92	0.51
1:A:328:ASP:OD2	1:A:333:ARG:HD2	2.12	0.49
1:A:196:ILE:CD1	1:A:222:LEU:HD22	2.43	0.49
1:A:216:LEU:HD21	1:A:241:LYS:HB3	1.95	0.49
1:B:14:ASN:HD21	1:B:17:ASP:N	2.12	0.48
1:A:60:TYR:HD1	7:A:572:HOH:O	1.96	0.48
2:A:342:BFX:C37	3:A:343:FMT:O2	2.62	0.47
1:A:139:ARG:HG3	7:A:652:HOH:O	2.15	0.47
1:B:14:ASN:ND2	1:B:17:ASP:H	2.09	0.47
2:A:342:BFX:H37	3:A:343:FMT:O2	2.15	0.47
1:B:14:ASN:C	1:B:14:ASN:ND2	2.69	0.46
1:B:191[A]:HIS:CD2	7:B:590:HOH:O	2.69	0.46
1:B:257:VAL:HG11	1:B:265:LEU:HD21	1.97	0.46
1:B:232:ILE:HG13	1:B:318:THR:HB	1.97	0.46
1:A:305:ILE:O	1:A:310:GLY:HA3	2.15	0.45
1:A:15:TYR:CD1	1:A:123:GLU:HG3	2.52	0.45
1:B:47:PRO:HB2	1:B:63:LEU:HD23	1.98	0.45
1:A:47:PRO:HD3	1:A:125:ASP:O	2.16	0.45
3:B:344:FMT:C	7:B:373:HOH:O	2.65	0.45
1:A:47:PRO:HB2	1:A:63:LEU:HD23	1.99	0.45
1:B:10:VAL:HB	1:B:176[B]:ILE:HG23	1.99	0.45
1:B:163:ASN:ND2	1:B:164:ARG:H	2.15	0.44
1:B:262:GLY:HA3	1:B:287:GLN:HE22	1.82	0.43
1:B:10:VAL:HB	1:B:176[B]:ILE:HG22	1.99	0.43
1:A:196:ILE:HD13	1:A:222:LEU:HD22	2.00	0.43
1:B:196:ILE:CD1	1:B:222:LEU:HD22	2.48	0.43
1:A:303:MET:HG2	1:A:305:ILE:HG13	2.01	0.42
1:A:19:GLN:HA	3:A:343:FMT:C	2.49	0.42
1:A:92:LEU:HD22	1:A:107:MET:HG3	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:81:LEU:HD13	1:B:137[A]:ILE:HD11	2.02	0.41
1:B:47:PRO:HD3	1:B:125:ASP:O	2.21	0.41
1:A:213:SER:HB3	7:A:629:HOH:O	2.20	0.41
1:A:217:CYS:SG	1:A:217:CYS:O	2.80	0.40
1:B:163:ASN:HD22	1:B:164:ARG:N	2.18	0.40
1:B:233:SER:HA	1:B:301:HIS:O	2.22	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	333/341 (98%)	330 (99%)	3 (1%)	0	100	100
1	B	340/341 (100%)	336 (99%)	4 (1%)	0	100	100
All	All	673/682 (99%)	666 (99%)	7 (1%)	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	287/291 (99%)	280 (98%)	7 (2%)	44	16
1	B	292/291 (100%)	286 (98%)	6 (2%)	48	20

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	579/582 (100%)	566 (98%)	13 (2%)	45 18

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	139	ARG
1	A	164	ARG
1	A	215	LEU
1	A	241	LYS
1	A	293	LYS
1	A	303	MET
1	A	333	ARG
1	B	14	ASN
1	B	163	ASN
1	B	215	LEU
1	B	241	LYS
1	B	265	LEU
1	B	288	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	94	GLN
1	A	150	GLN
1	A	185	HIS
1	A	194	ASN
1	A	331	ASN
1	A	341	HIS
1	B	14	ASN
1	B	74	HIS
1	B	135	GLN
1	B	150	GLN
1	B	163	ASN
1	B	185	HIS
1	B	189	ASN
1	B	194	ASN
1	B	202	GLN
1	B	204	GLN
1	B	287	GLN
1	B	341	HIS

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 oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 7 ligands modelled in this entry, 1 is monoatomic - leaving 6 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	BFX	A	342	-	40,42,42	0.89	2 (5%)	54,58,58	1.55	10 (18%)
3	FMT	A	343	-	2,2,2	0.80	0	1,1,1	0.09	0
3	FMT	B	344	-	2,2,2	0.73	0	1,1,1	0.09	0
4	NAG	A	344	1	14,14,15	0.58	0	17,19,21	1.45	2 (11%)
2	BFX	B	342	-	40,42,42	0.90	3 (7%)	54,58,58	1.82	8 (14%)
6	HSQ	B	345	1	14,14,15	0.79	1 (7%)	17,19,21	1.82	5 (29%)

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	BFX	A	342	-	-	0/27/40/40	0/5/5/5
4	NAG	A	344	1	1/1/5/7	2/6/23/26	0/1/1/1
2	BFX	B	342	-	-	2/27/40/40	0/5/5/5

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	HSQ	B	345	1	-	3/6/23/26	0/1/1/1

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	342	BFX	C31-C28	2.34	1.54	1.48
2	B	342	BFX	C30-C28	2.24	1.53	1.48
2	A	342	BFX	C30-C28	2.24	1.53	1.48
2	B	342	BFX	C33-CL35	2.21	1.78	1.73
6	B	345	HSQ	C1-C2	2.19	1.55	1.52
2	B	342	BFX	C31-C28	2.10	1.53	1.48

All (25) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	342	BFX	C29-N26-C28	-6.22	112.19	118.34
2	B	342	BFX	C30-C28-N26	-5.69	111.38	118.46
2	A	342	BFX	C31-C28-N26	-5.66	111.43	118.46
2	B	342	BFX	C31-C28-N26	-5.25	111.93	118.46
4	A	344	NAG	C1-O5-C5	4.64	118.41	112.19
6	B	345	HSQ	C2-N2-C7	4.29	128.66	122.90
6	B	345	HSQ	C4-C3-C2	3.73	116.49	111.02
2	B	342	BFX	C24-C21-C19	3.68	113.86	108.78
2	A	342	BFX	C29-N26-C28	-3.01	115.36	118.34
2	A	342	BFX	BR1-C2-C3	-2.97	115.95	119.62
2	A	342	BFX	C24-C21-C19	2.89	112.77	108.78
2	A	342	BFX	C14-C16-C18	-2.81	117.79	120.80
2	A	342	BFX	C17-C18-C19	-2.74	117.47	121.00
2	A	342	BFX	C30-C28-N26	-2.73	115.06	118.46
2	B	342	BFX	C14-C16-C18	-2.63	117.99	120.80
2	B	342	BFX	C17-C15-C13	-2.62	117.55	121.00
2	A	342	BFX	C23-N27-C24	2.55	115.63	112.06
6	B	345	HSQ	O5-C5-C6	2.52	112.57	107.66
2	A	342	BFX	O5-C3-C2	2.41	119.83	116.89
2	B	342	BFX	C7-C9-C6	-2.34	120.14	123.23
4	A	344	NAG	C2-N2-C7	2.24	125.90	122.90
2	A	342	BFX	BR1-C2-C4	2.24	122.08	117.82
6	B	345	HSQ	C1-C2-N2	2.13	113.78	110.43
6	B	345	HSQ	C8-C7-N2	2.10	119.60	116.12
2	B	342	BFX	BR1-C2-C4	2.06	121.75	117.82

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
4	A	344	NAG	C1

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	B	345	HSQ	C1-C2-N2-C7
6	B	345	HSQ	C8-C7-N2-C2
6	B	345	HSQ	O7-C7-N2-C2
4	A	344	NAG	C4-C5-C6-O6
4	A	344	NAG	O5-C5-C6-O6
2	B	342	BFX	C8-C10-C12-C13
2	B	342	BFX	C31-C28-N26-C22

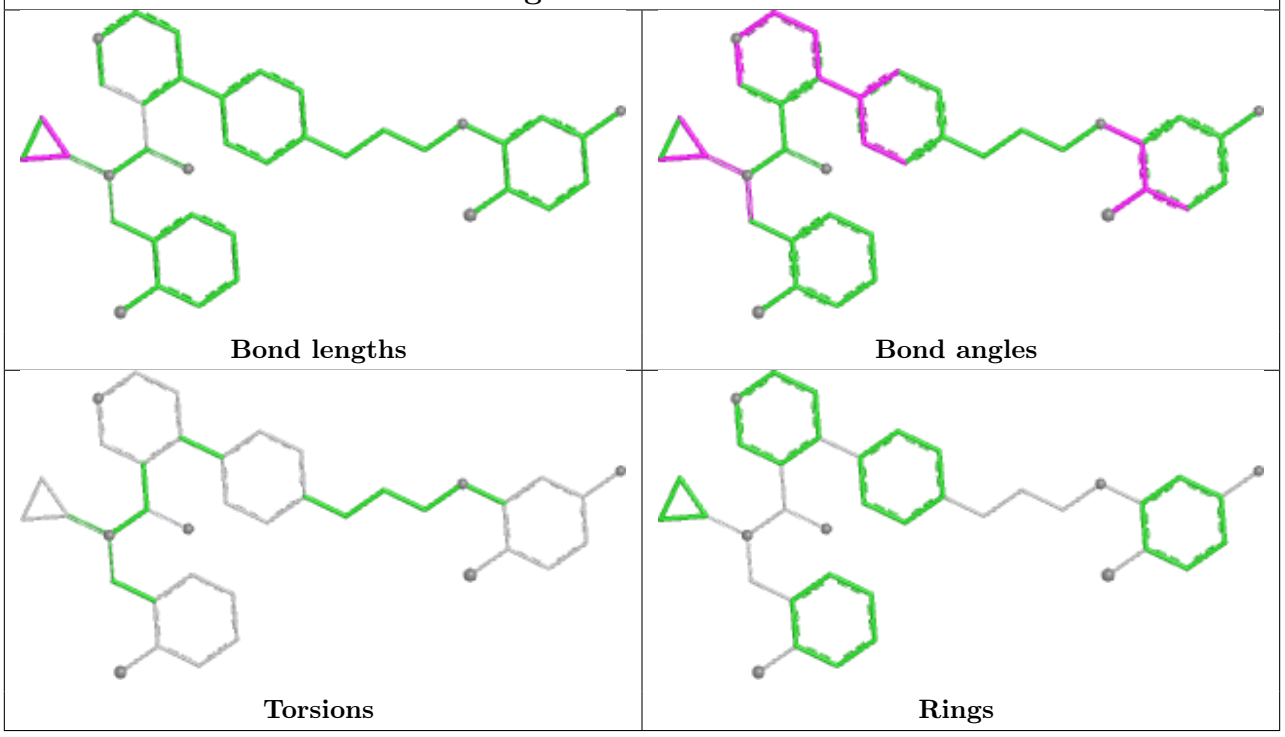
There are no ring outliers.

3 monomers are involved in 7 short contacts:

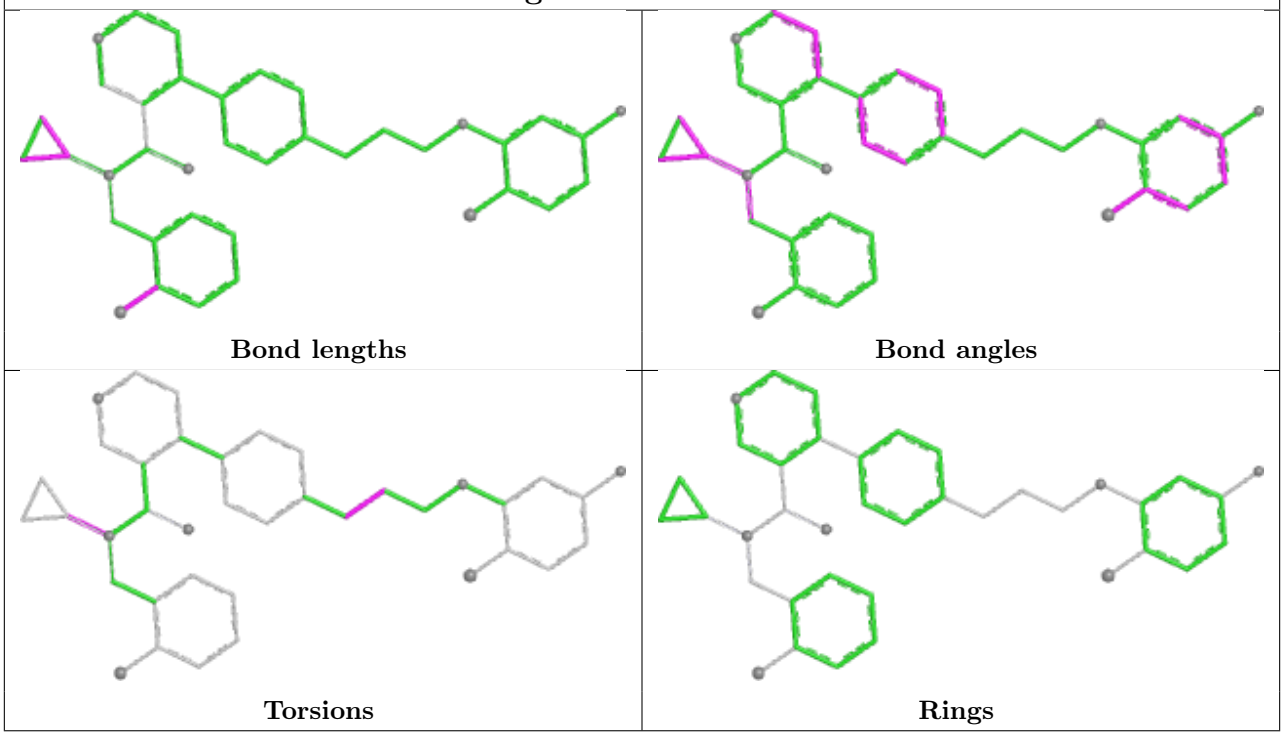
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	342	BFX	2	0
3	A	343	FMT	5	0
3	B	344	FMT	2	0

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 BFX A 342



Ligand BFX B 342



5.7 Other polymers (i)

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	333/341 (97%)	0.60	30 (9%)	17	16	7, 23, 43, 56	4 (1%)
1	B	337/341 (98%)	0.79	45 (13%)	8	8	7, 25, 44, 54	7 (2%)
All	All	670/682 (98%)	0.70	75 (11%)	11	10	7, 24, 43, 56	11 (1%)

All (75) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	54	LEU	6.1
1	A	253	PHE	5.8
1	B	217	CYS	4.3
1	B	59	VAL	4.2
1	A	310	GLY	4.1
1	A	4	GLY	3.7
1	B	121	LEU	3.7
1	B	57	ALA	3.6
1	B	76	GLY	3.6
1	A	212	SER	3.6
1	B	171	SER	3.5
1	B	259	CYS	3.4
1	B	290	TYR	3.2
1	A	211	GLY	3.2
1	A	215	LEU	3.2
1	B	219	ASP	3.1
1	A	151	GLY	3.0
1	B	139	ARG	3.0
1	B	291	SER	3.0
1	A	248	ALA	3.0
1	A	214	THR	2.9
1	B	80	THR	2.9
1	B	214	THR	2.9
1	B	213	SER	2.8

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Mol	Chain	Res	Type	RSRZ
1	B	253	PHE	2.8
1	A	252	LEU	2.8
1	B	77	THR	2.6
1	B	74	HIS	2.6
1	B	341	HIS	2.6
1	A	210	VAL	2.5
1	B	295	LEU	2.5
1	A	307	PRO	2.5
1	B	72	TYR	2.5
1	B	172	LEU	2.5
1	B	210	VAL	2.5
1	A	213	SER	2.5
1	B	55	TYR	2.5
1	B	52	SER	2.5
1	B	293	LYS	2.4
1	A	84	SER	2.4
1	A	261	GLU	2.4
1	B	245	ALA	2.4
1	A	165	ASP	2.4
1	A	237	SER	2.4
1	A	101	GLY	2.4
1	A	5	ASN	2.3
1	B	71	SER	2.3
1	A	184	GLN	2.3
1	B	28	THR	2.3
1	B	69	SER	2.3
1	B	117	LEU	2.2
1	A	152	VAL	2.2
1	B	166	SER	2.2
1	B	292	SER	2.2
1	B	51	CYS	2.2
1	B	196	ILE	2.2
1	B	211	GLY	2.2
1	B	220	GLY	2.2
1	A	196	ILE	2.2
1	B	87	THR	2.1
1	A	220	GLY	2.1
1	B	70	SER	2.1
1	A	221	CYS	2.1
1	A	249	LYS	2.1
1	A	305	ILE	2.1
1	B	140	VAL	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	212	SER	2.1
1	B	248	ALA	2.1
1	B	82	ARG	2.1
1	A	219	ASP	2.1
1	A	309	THR	2.1
1	A	301	HIS	2.1
1	B	288	GLU	2.1
1	B	287	GLN	2.0
1	A	60	TYR	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)

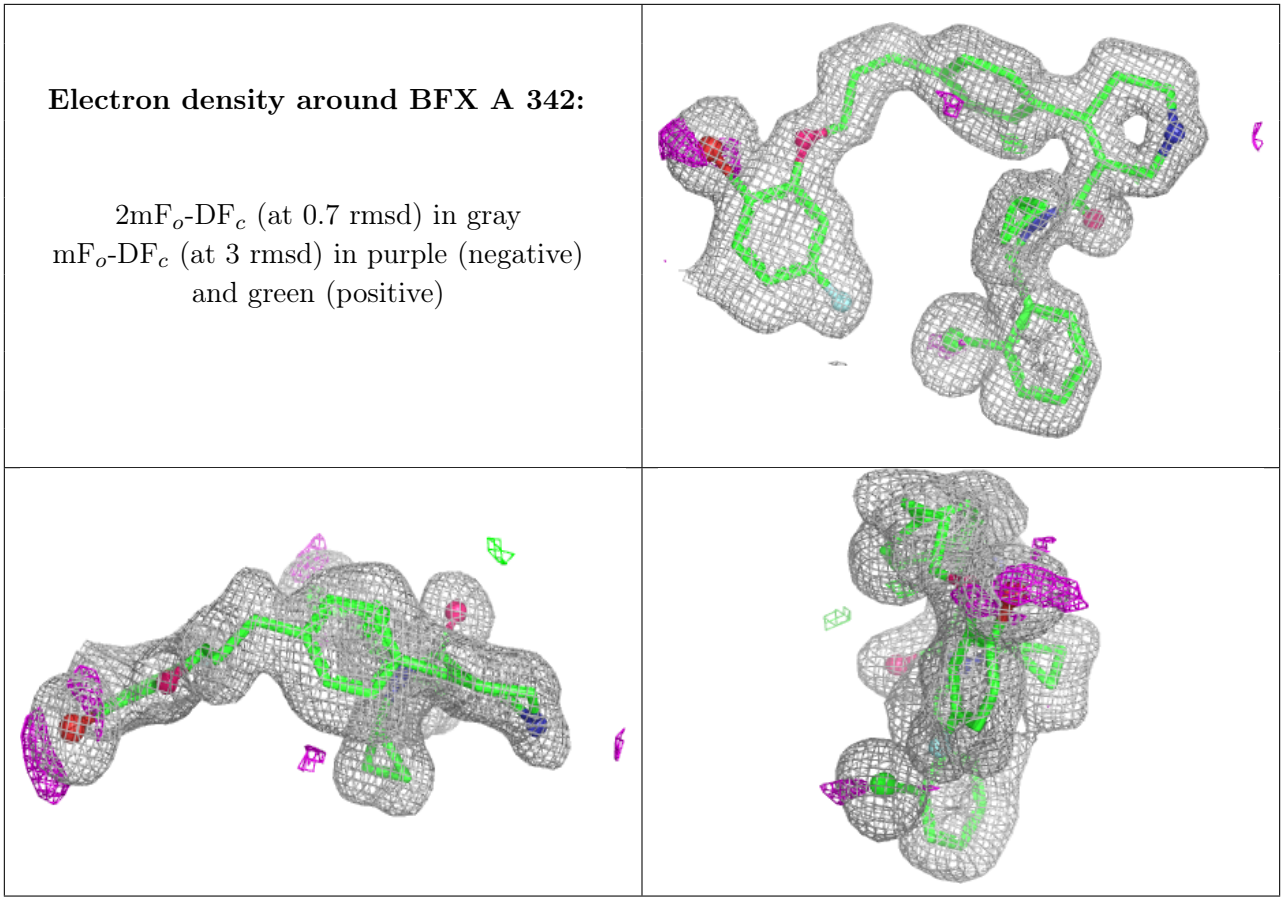
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' 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
4	NAG	A	344	14/15	0.55	0.20	43,50,55,56	0
6	HSQ	B	345	14/15	0.56	0.21	58,63,64,64	0
3	FMT	B	344	3/3	0.89	0.12	37,37,40,42	0
3	FMT	A	343	3/3	0.92	0.13	29,29,35,37	0
2	BFX	A	342	38/38	0.98	0.07	18,21,25,27	0
5	CL	B	343	1/1	0.98	0.04	31,31,31,31	0
2	BFX	B	342	38/38	0.98	0.07	17,22,27,28	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.

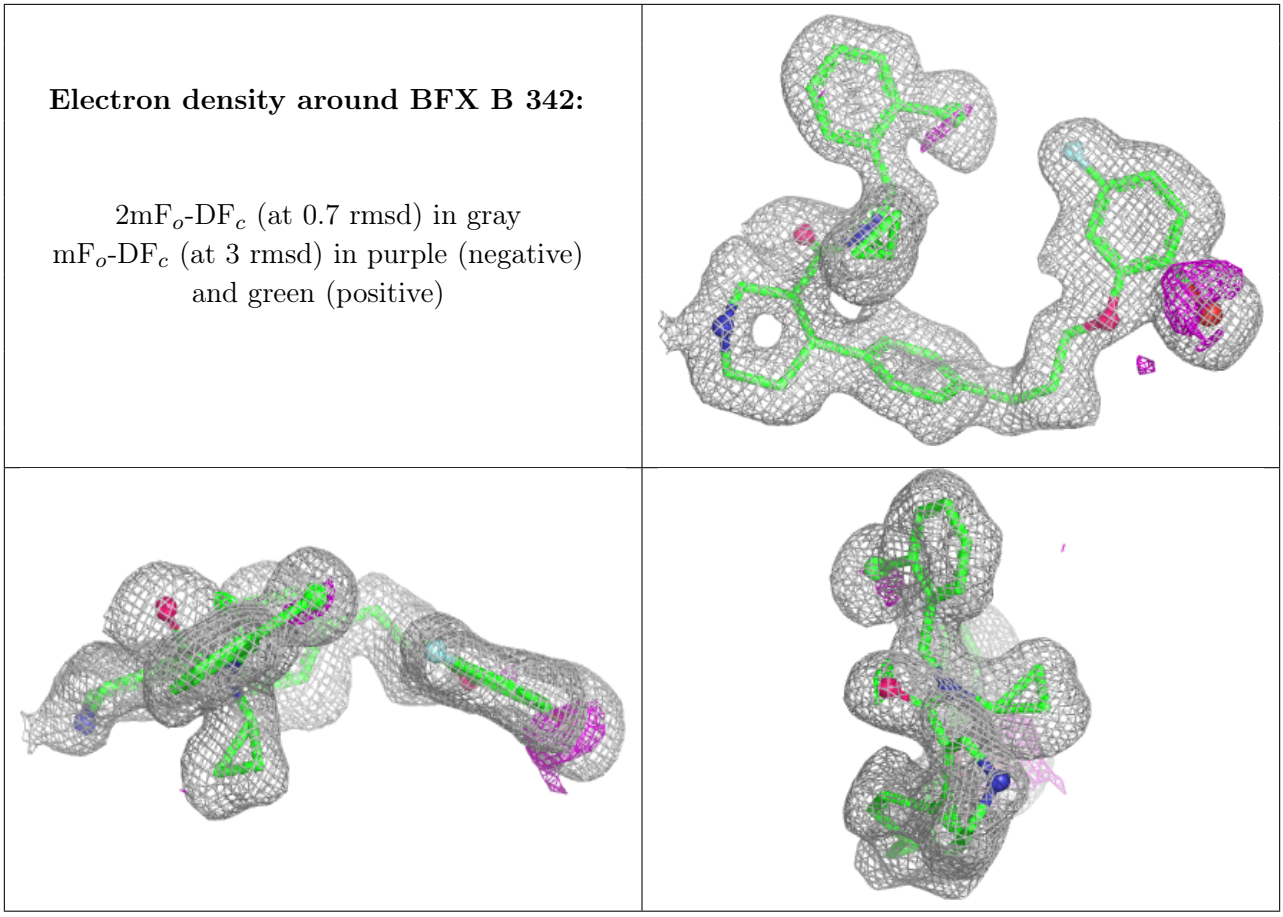
Electron density around BFX A 342:

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



Electron density around BFX B 342:

$2mF_o$-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

There are no such residues in this entry.