Full wwPDB X-ray Structure Validation Report (i)

Aug 23, 2023 – 06:05 AM EDT

PDB ID	:	3BC3
Title	:	Exploring inhibitor binding at the S subsites of cathepsin L
Authors	:	Chowdhury, S.F.; Joseph, L.; Kumar, S.; Tulsidas, S.R.; Bhat, S.; Ziomek, E.; Nard, R.M.; Sivaraman, J.; Purisima, E.O.
Deposited on	:	2007-11-12
Resolution	:	2.20 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:

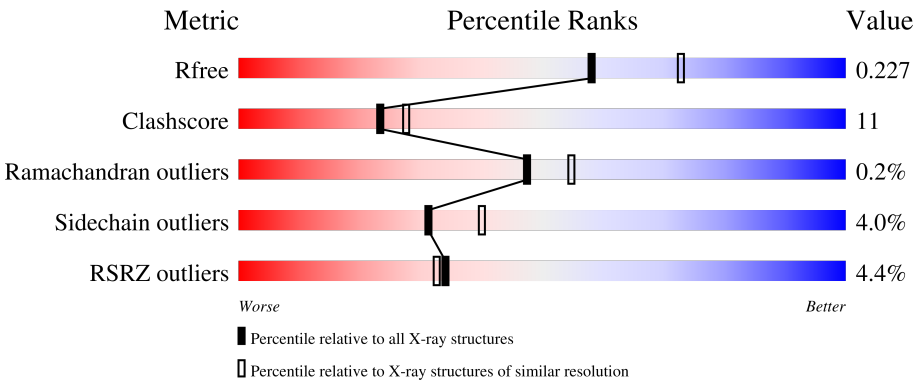
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35

1 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 2.20 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	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

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	220	5% 74% 23% • •
1	B	220	4% 74% 23% • •

2 Entry composition (i)

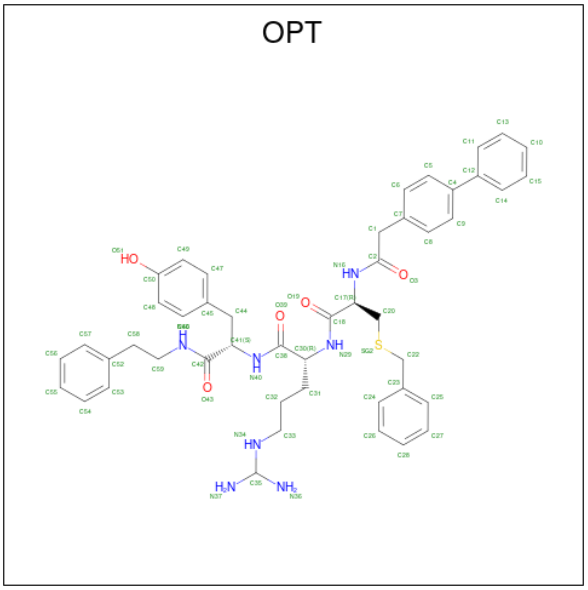
There are 3 unique types of molecules in this entry. The entry contains 3865 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Cathepsin L heavy and light chains.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	215	1661	1041	275	332	13	0	0	0
1	B	215	1661	1041	275	332	13	0	0	0

- Molecule 2 is S-benzyl-N-(biphenyl-4-ylacetyl)-L-cysteinyl-N 5 -(diaminomethyl)-D-ornithyl -N-(2-phenylethyl)-L-tyrosinamide (three-letter code: OPT) (formula: $C_{47}H_{55}N_7O_5S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	S		
2	A	1	60	47	7	5	1	0	0
2	B	1	60	47	7	5	1	0	0

- Molecule 3 is water.

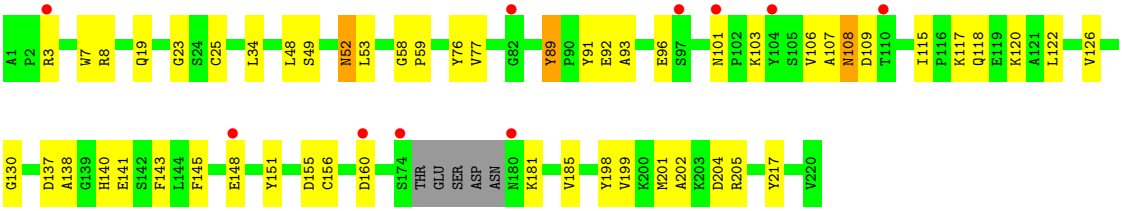
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	A	206	206	206	0	0
			Total	O		
3	B	217	217	217	0	0

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.

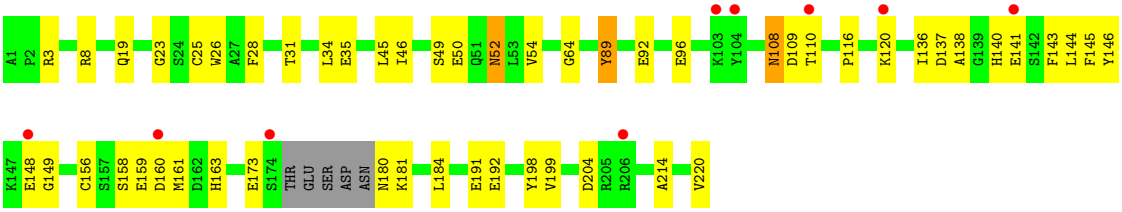
• Molecule 1: Cathepsin L heavy and light chains

Chain A:



• Molecule 1: Cathepsin L heavy and light chains

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α, β, γ	74.77Å 90.93Å 126.03Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 2.20 45.46 – 2.20	Depositor EDS
% Data completeness (in resolution range)	89.7 (30.00-2.20) 93.0 (45.46-2.20)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	0.05	Depositor
$< I/\sigma(I) >$ [1]	5.43 (at 2.20Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.183 , 0.234 0.180 , 0.227	Depositor DCC
R_{free} test set	1639 reflections (7.81%)	wwPDB-VP
Wilson B-factor (Å^2)	29.0	Xtriage
Anisotropy	0.391	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.41 , 49.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	3865	wwPDB-VP
Average B, all atoms (Å^2)	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.54% 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: CSD, OPT

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	0.37	0/1694	0.54	0/2288
1	B	0.36	0/1694	0.53	0/2288
All	All	0.37	0/3388	0.54	0/4576

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	1661	0	1541	36	0
1	B	1661	0	1541	39	0
2	A	60	0	53	0	0
2	B	60	0	53	2	0
3	A	206	0	0	10	0
3	B	217	0	0	17	0
All	All	3865	0	3188	75	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 11.

All (75) 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:23:GLY:HA2	3:A:302:HOH:O	1.53	1.08
1:B:23:GLY:HA2	3:B:406:HOH:O	1.67	0.94
1:B:64:GLY:HA2	3:B:599:HOH:O	1.70	0.90
1:B:54:VAL:HA	3:B:599:HOH:O	1.73	0.87
1:A:77:VAL:HG23	3:A:330:HOH:O	1.87	0.74
1:B:160:ASP:HB3	3:B:503:HOH:O	1.88	0.73
1:B:31:THR:O	1:B:35:GLU:HG3	1.90	0.72
1:A:48:LEU:HD21	3:A:503:HOH:O	1.89	0.71
1:A:76:TYR:HD2	3:A:330:HOH:O	1.73	0.70
1:A:108:ASN:HD22	1:A:109:ASP:H	1.42	0.67
1:B:19:GLN:NE2	3:B:406:HOH:O	2.28	0.66
1:B:92:GLU:OE1	1:B:96:GLU:HG3	1.98	0.64
1:A:3:ARG:HH11	1:A:3:ARG:HG3	1.66	0.61
1:A:106:VAL:HG23	3:A:503:HOH:O	2.01	0.60
1:A:107:ALA:HB2	3:A:503:HOH:O	2.01	0.59
1:A:137:ASP:OD2	1:A:140:HIS:HE1	1.86	0.59
1:B:159:GLU:HG3	3:B:503:HOH:O	2.03	0.58
1:B:25:CSD:OD2	1:B:163:HIS:HA	2.04	0.58
1:B:173:GLU:HG2	3:B:522:HOH:O	2.02	0.57
1:A:115:ILE:HD11	1:A:217:TYR:HE1	1.71	0.56
1:A:19:GLN:NE2	3:A:302:HOH:O	2.38	0.55
1:A:8:ARG:HD3	1:A:198:TYR:CZ	2.42	0.54
1:B:141:GLU:HG3	1:B:145:PHE:CD2	2.44	0.53
1:B:3:ARG:HH11	1:B:3:ARG:HG3	1.75	0.52
1:B:137:ASP:OD2	1:B:140:HIS:HE1	1.92	0.52
1:A:202:ALA:HB1	1:A:205:ARG:HG3	1.91	0.51
1:B:144:LEU:HD11	2:B:400:OPT:H9	1.93	0.51
1:A:138:ALA:HB1	1:A:143:PHE:CD2	2.46	0.51
1:A:108:ASN:HD22	1:A:109:ASP:N	2.08	0.50
1:A:205:ARG:NH1	3:A:368:HOH:O	2.46	0.49
1:A:141:GLU:HB2	1:A:145:PHE:CE2	2.48	0.49
1:A:53:LEU:CD2	3:A:330:HOH:O	2.61	0.49
1:B:26:TRP:HZ2	3:B:599:HOH:O	1.96	0.49
1:A:101:ASN:OD1	1:A:103:LYS:HB3	2.13	0.48
1:B:138:ALA:HB1	1:B:143:PHE:CD2	2.49	0.48
1:B:158:SER:HB3	3:B:448:HOH:O	2.14	0.48
1:B:52:ASN:HD22	1:B:52:ASN:C	2.18	0.47
1:B:108:ASN:ND2	1:B:109:ASP:H	2.12	0.47
1:A:185:VAL:HB	1:A:199:VAL:HG13	1.96	0.47
1:B:140:HIS:HD2	3:B:560:HOH:O	1.98	0.47
1:B:110:THR:HG22	1:B:110:THR:O	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:49:SER:OG	1:B:89:TYR:HB3	2.15	0.46
1:B:181:LYS:HD2	1:B:204:ASP:OD2	2.14	0.46
1:A:160:ASP:OD1	1:A:160:ASP:O	2.33	0.46
1:A:181:LYS:NZ	1:A:204:ASP:HB2	2.31	0.46
1:A:91:TYR:CZ	1:A:93:ALA:HA	2.51	0.46
1:A:49:SER:OG	1:A:89:TYR:HB3	2.17	0.45
1:A:52:ASN:HD22	1:A:52:ASN:C	2.19	0.45
1:A:117:LYS:NZ	3:A:412:HOH:O	2.49	0.45
1:B:180:ASN:N	3:B:441:HOH:O	2.50	0.44
1:B:120:LYS:HG3	3:B:546:HOH:O	2.17	0.44
1:B:214:ALA:HB1	2:B:400:OPT:O51	2.17	0.44
1:A:7:TRP:CE2	1:A:130:GLY:HA2	2.52	0.44
1:A:199:VAL:HG22	1:A:201:MET:HG3	1.98	0.44
1:B:192:GLU:HB2	3:B:443:HOH:O	2.17	0.44
1:A:108:ASN:ND2	1:A:109:ASP:H	2.13	0.44
1:B:25:CSD:OD1	3:B:406:HOH:O	2.16	0.44
1:B:116:PRO:HD3	3:B:605:HOH:O	2.16	0.44
1:B:46:ILE:N	1:B:46:ILE:HD12	2.33	0.43
1:B:8:ARG:HD3	1:B:198:TYR:CZ	2.53	0.43
1:A:58:GLY:N	1:A:59:PRO:CD	2.81	0.43
1:A:120:LYS:C	1:A:120:LYS:HD2	2.39	0.43
1:A:92:GLU:OE2	1:A:96:GLU:HG3	2.19	0.43
1:B:28:PHE:CD2	1:B:50:GLU:HG2	2.53	0.42
1:B:28:PHE:CG	1:B:50:GLU:HG2	2.54	0.42
1:B:136:ILE:CD1	1:B:138:ALA:HB2	2.50	0.42
1:A:122:LEU:O	1:A:126:VAL:HG23	2.20	0.42
1:B:191:GLU:HG3	1:B:192:GLU:OE1	2.20	0.42
1:B:45:LEU:HA	3:B:455:HOH:O	2.20	0.41
1:A:151:TYR:HB3	1:A:201:MET:HG2	2.02	0.41
1:A:34:LEU:HD23	1:A:34:LEU:HA	1.88	0.41
1:B:220:VAL:O	1:B:220:VAL:HG23	2.21	0.40
1:A:3:ARG:HG3	1:A:3:ARG:NH1	2.32	0.40
1:B:146:TYR:CE2	1:B:199:VAL:HG23	2.55	0.40
1:B:149:GLY:HA2	3:B:551:HOH:O	2.21	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	210/220 (96%)	202 (96%)	8 (4%)	0	100	100
1	B	210/220 (96%)	201 (96%)	8 (4%)	1 (0%)	29	31
All	All	420/440 (96%)	403 (96%)	16 (4%)	1 (0%)	47	55

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	161	MET

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	173/178 (97%)	166 (96%)	7 (4%)	31	40
1	B	173/178 (97%)	166 (96%)	7 (4%)	31	40
All	All	346/356 (97%)	332 (96%)	14 (4%)	31	40

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	52	ASN
1	A	89	TYR
1	A	108	ASN
1	A	118	GLN
1	A	148	GLU

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Mol	Chain	Res	Type
1	A	155	ASP
1	A	156	CYS
1	B	34	LEU
1	B	52	ASN
1	B	89	TYR
1	B	108	ASN
1	B	148	GLU
1	B	156	CYS
1	B	184	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	108	ASN
1	A	140	HIS
1	B	108	ASN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

2 non-standard protein/DNA/RNA residues are modelled in this entry.

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	$\#\|Z\| > 2$
1	CSD	A	25	1	3,7,8	0.87	0	1,8,10	2.15	1 (100%)
1	CSD	B	25	1	3,7,8	0.79	0	1,8,10	1.98	0

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
1	CSD	A	25	1	-	1/2/6/8	-
1	CSD	B	25	1	-	0/2/6/8	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	25	CSD	OD1-SG-CB	-2.15	101.44	105.54

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	25	CSD	N-CA-CB-SG

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	B	25	CSD	2	0

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

2 ligands are modelled in this entry.

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	OPT	A	300	-	62,64,64	4.03	44 (70%)	76,83,83	2.19	22 (28%)
2	OPT	B	400	-	62,64,64	4.03	43 (69%)	76,83,83	2.14	19 (25%)

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	OPT	A	300	-	-	7/49/55/55	0/5/5/5
2	OPT	B	400	-	-	9/49/55/55	0/5/5/5

All (87) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	300	OPT	C2-N16	10.02	1.55	1.34
2	B	400	OPT	C2-N16	9.69	1.54	1.34
2	B	400	OPT	C18-N29	9.21	1.54	1.34
2	A	300	OPT	C18-N29	8.77	1.53	1.34
2	B	400	OPT	C42-N60	7.49	1.49	1.33
2	A	300	OPT	C42-N60	7.46	1.49	1.33
2	B	400	OPT	C6-C7	7.43	1.54	1.38
2	A	300	OPT	C6-C7	7.25	1.54	1.38
2	B	400	OPT	C53-C52	6.87	1.53	1.38
2	A	300	OPT	C53-C52	6.83	1.53	1.38
2	B	400	OPT	C15-C14	6.44	1.51	1.36
2	A	300	OPT	C15-C14	6.28	1.51	1.36
2	A	300	OPT	C13-C10	6.25	1.54	1.38
2	B	400	OPT	C13-C10	6.20	1.54	1.38
2	A	300	OPT	C47-C45	5.66	1.51	1.38
2	B	400	OPT	C5-C6	5.63	1.48	1.36
2	B	400	OPT	C47-C45	5.63	1.51	1.38
2	A	300	OPT	C5-C6	5.52	1.48	1.36
2	B	400	OPT	C5-C4	5.34	1.54	1.41
2	B	400	OPT	C13-C11	5.29	1.48	1.36
2	A	300	OPT	C13-C11	5.25	1.48	1.36
2	A	300	OPT	C14-C12	5.17	1.54	1.41
2	B	400	OPT	C14-C12	5.14	1.54	1.41
2	B	400	OPT	C15-C10	5.12	1.51	1.38
2	A	300	OPT	C15-C10	5.05	1.51	1.38
2	B	400	OPT	C57-C52	5.00	1.49	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	300	OPT	C5-C4	4.98	1.54	1.41
2	B	400	OPT	C11-C12	4.90	1.53	1.41
2	A	300	OPT	C11-C12	4.83	1.53	1.41
2	A	300	OPT	C57-C52	4.80	1.49	1.38
2	B	400	OPT	C48-C50	4.74	1.48	1.38
2	A	300	OPT	C48-C50	4.71	1.47	1.38
2	B	400	OPT	C22-SG2	-4.62	1.74	1.82
2	A	300	OPT	C8-C7	4.59	1.48	1.38
2	A	300	OPT	C59-N60	4.55	1.56	1.46
2	B	400	OPT	C8-C7	4.49	1.48	1.38
2	B	400	OPT	C59-N60	4.48	1.56	1.46
2	A	300	OPT	C22-SG2	-4.48	1.74	1.82
2	A	300	OPT	C9-C4	4.31	1.52	1.41
2	A	300	OPT	C54-C53	4.30	1.48	1.38
2	A	300	OPT	C46-C45	4.22	1.47	1.38
2	A	300	OPT	C55-C54	4.18	1.49	1.38
2	B	400	OPT	C56-C57	4.17	1.47	1.38
2	B	400	OPT	C54-C53	4.15	1.47	1.38
2	B	400	OPT	C56-C55	4.15	1.49	1.38
2	A	300	OPT	C56-C57	4.11	1.47	1.38
2	B	400	OPT	C55-C54	4.09	1.48	1.38
2	B	400	OPT	C9-C4	4.08	1.51	1.41
2	A	300	OPT	C9-C8	4.06	1.45	1.36
2	B	400	OPT	C25-C23	3.97	1.47	1.38
2	B	400	OPT	C46-C45	3.94	1.47	1.38
2	B	400	OPT	C31-C30	3.89	1.62	1.53
2	A	300	OPT	C56-C55	3.89	1.48	1.38
2	A	300	OPT	C31-C30	3.88	1.62	1.53
2	A	300	OPT	C49-C50	3.85	1.46	1.38
2	A	300	OPT	C25-C23	3.84	1.47	1.38
2	B	400	OPT	C48-C46	3.82	1.45	1.38
2	A	300	OPT	C33-N34	-3.81	1.38	1.47
2	B	400	OPT	C33-N34	-3.80	1.38	1.47
2	B	400	OPT	C49-C50	3.76	1.46	1.38
2	B	400	OPT	C9-C8	3.72	1.44	1.36
2	A	300	OPT	C41-N40	-3.69	1.38	1.45
2	A	300	OPT	C48-C46	3.69	1.45	1.38
2	B	400	OPT	C41-N40	-3.44	1.38	1.45
2	B	400	OPT	C49-C47	3.13	1.44	1.38
2	A	300	OPT	C49-C47	3.05	1.44	1.38
2	A	300	OPT	C1-C2	-2.73	1.45	1.51
2	A	300	OPT	C44-C41	2.70	1.60	1.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	300	OPT	C30-C38	-2.69	1.45	1.52
2	B	400	OPT	C1-C2	-2.54	1.46	1.51
2	B	400	OPT	C44-C41	2.51	1.60	1.54
2	B	400	OPT	C26-C24	2.40	1.44	1.38
2	A	300	OPT	C30-N29	-2.40	1.40	1.45
2	B	400	OPT	C22-C23	2.39	1.56	1.51
2	A	300	OPT	C28-C27	2.38	1.44	1.38
2	A	300	OPT	C26-C24	2.34	1.43	1.38
2	B	400	OPT	C28-C26	2.28	1.44	1.38
2	A	300	OPT	C22-C23	2.26	1.56	1.51
2	B	400	OPT	C28-C27	2.25	1.44	1.38
2	B	400	OPT	C44-C45	2.24	1.56	1.51
2	B	400	OPT	C30-C38	-2.22	1.47	1.52
2	B	400	OPT	O19-C18	2.21	1.27	1.23
2	A	300	OPT	C28-C26	2.21	1.43	1.38
2	A	300	OPT	C44-C45	2.18	1.56	1.51
2	A	300	OPT	O19-C18	2.10	1.27	1.23
2	B	400	OPT	C27-C25	2.09	1.43	1.38
2	A	300	OPT	C27-C25	2.05	1.43	1.38

All (41) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	300	OPT	C33-N34-C35	6.94	137.25	114.64
2	B	400	OPT	C33-N34-C35	6.31	135.20	114.64
2	A	300	OPT	C23-C22-SG2	6.05	127.65	114.06
2	B	400	OPT	C23-C22-SG2	5.61	126.66	114.06
2	B	400	OPT	C59-C58-C52	5.35	125.26	112.87
2	A	300	OPT	C59-C58-C52	5.13	124.76	112.87
2	A	300	OPT	C31-C30-C38	-4.94	98.66	110.20
2	B	400	OPT	C31-C30-C38	-4.84	98.90	110.20
2	A	300	OPT	C20-SG2-C22	4.72	111.26	101.25
2	B	400	OPT	C18-C17-N16	-4.28	99.52	111.16
2	B	400	OPT	C20-SG2-C22	4.27	110.31	101.25
2	B	400	OPT	C1-C7-C8	-4.25	114.80	120.89
2	A	300	OPT	C7-C1-C2	4.14	124.83	112.57
2	B	400	OPT	O43-C42-N60	4.10	131.81	122.99
2	A	300	OPT	O43-C42-N60	4.04	131.67	122.99
2	A	300	OPT	C59-N60-C42	-3.92	115.60	122.59
2	A	300	OPT	C18-C17-N16	-3.78	100.87	111.16
2	B	400	OPT	C59-N60-C42	-3.73	115.94	122.59
2	A	300	OPT	C1-C7-C8	-3.67	115.64	120.89

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	400	OPT	C7-C1-C2	3.62	123.30	112.57
2	B	400	OPT	C32-C33-N34	3.49	125.02	112.02
2	A	300	OPT	C32-C33-N34	3.32	124.39	112.02
2	B	400	OPT	C20-C17-C18	3.30	116.90	109.73
2	A	300	OPT	C20-C17-C18	3.20	116.67	109.73
2	B	400	OPT	C41-C42-N60	-3.12	110.26	116.54
2	B	400	OPT	C58-C59-N60	-2.97	103.03	111.99
2	A	300	OPT	C41-C42-N60	-2.94	110.62	116.54
2	A	300	OPT	O19-C18-C17	2.91	126.57	120.45
2	B	400	OPT	C20-C17-N16	-2.90	103.15	111.00
2	A	300	OPT	C58-C59-N60	-2.80	103.52	111.99
2	A	300	OPT	C17-C18-N29	-2.57	111.07	116.70
2	A	300	OPT	C20-C17-N16	-2.55	104.12	111.00
2	A	300	OPT	O39-C38-C30	-2.44	115.32	120.45
2	B	400	OPT	O19-C18-C17	2.40	125.51	120.45
2	B	400	OPT	C6-C7-C8	2.23	121.67	118.17
2	A	300	OPT	C32-C31-C30	2.16	120.59	113.92
2	A	300	OPT	O3-C2-N16	2.10	126.50	122.95
2	B	400	OPT	O39-C38-C30	-2.10	116.04	120.45
2	A	300	OPT	C11-C12-C14	2.09	120.50	118.65
2	B	400	OPT	C11-C12-C14	2.08	120.50	118.65
2	A	300	OPT	C6-C7-C8	2.03	121.35	118.17

There are no chirality outliers.

All (16) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	400	OPT	C38-C30-N29-C18
2	A	300	OPT	C38-C30-N29-C18
2	B	400	OPT	C17-C20-SG2-C22
2	A	300	OPT	C30-C31-C32-C33
2	A	300	OPT	C32-C33-N34-C35
2	B	400	OPT	C32-C33-N34-C35
2	A	300	OPT	N29-C30-C31-C32
2	A	300	OPT	C38-C30-C31-C32
2	B	400	OPT	N16-C17-C18-O19
2	A	300	OPT	C53-C52-C58-C59
2	B	400	OPT	C30-C31-C32-C33
2	B	400	OPT	N29-C30-C31-C32
2	B	400	OPT	C53-C52-C58-C59
2	A	300	OPT	C57-C52-C58-C59
2	B	400	OPT	N16-C17-C18-N29

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Mol	Chain	Res	Type	Atoms
2	B	400	OPT	C57-C52-C58-C59

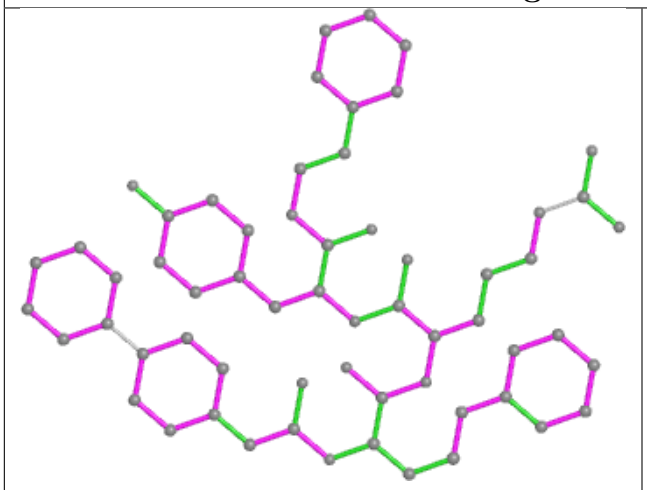
There are no ring outliers.

1 monomer is involved in 2 short contacts:

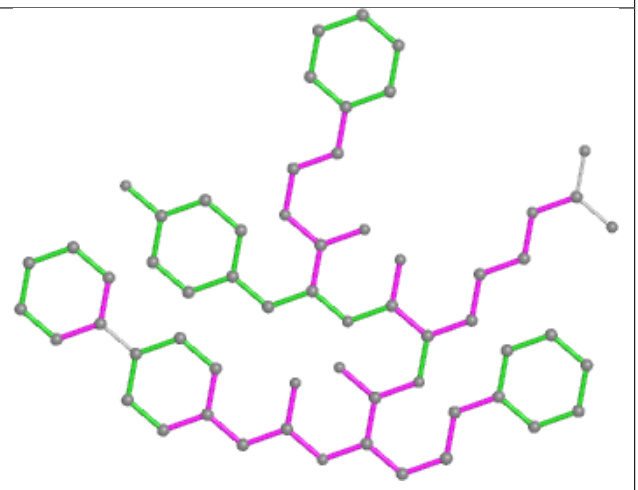
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	400	OPT	2	0

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.

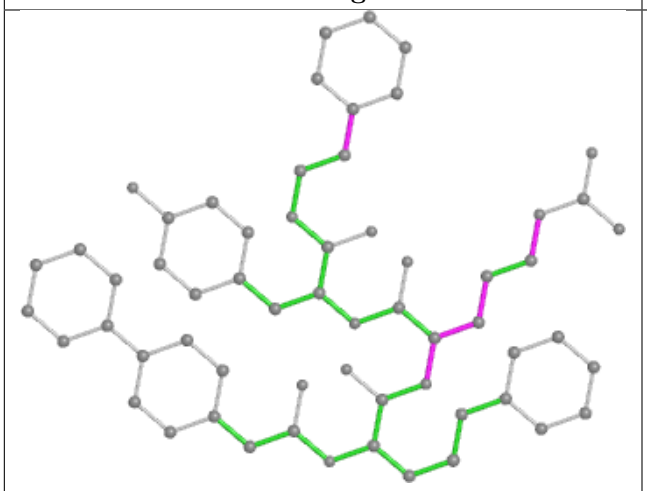
Ligand OPT A 300



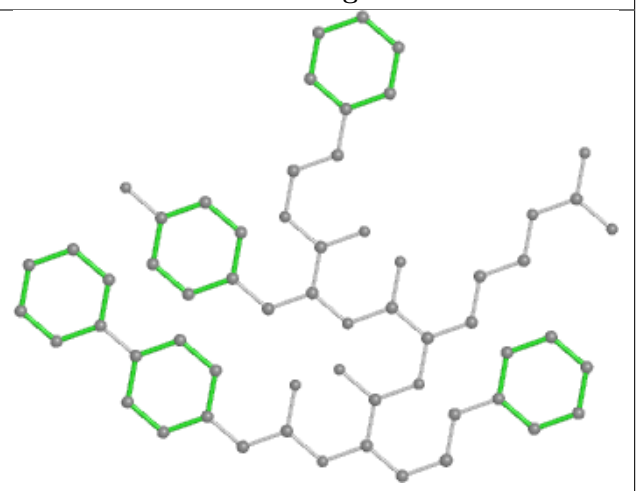
Bond lengths



Bond angles

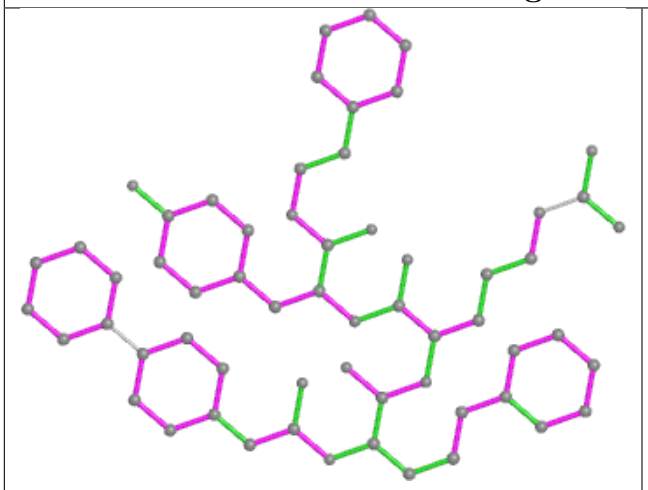


Torsions

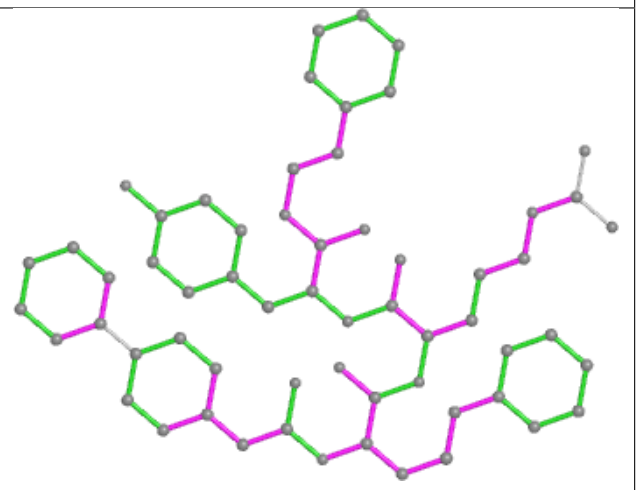


Rings

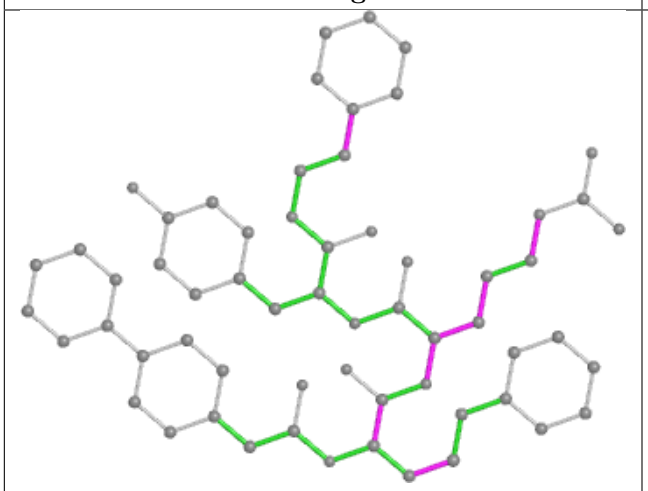
Ligand OPT B 400



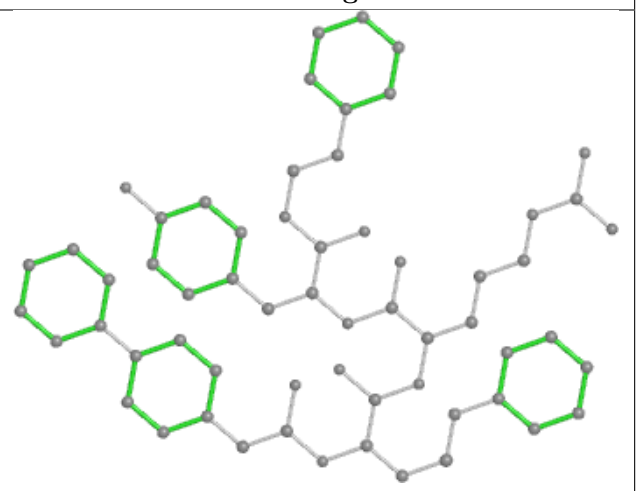
Bond lengths



Bond angles



Torsions



Rings

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	214/220 (97%)	0.09	10 (4%)	31	30	18, 27, 40, 57	0
1	B	214/220 (97%)	0.02	9 (4%)	36	34	18, 28, 42, 56	0
All	All	428/440 (97%)	0.06	19 (4%)	34	32	18, 28, 41, 57	0

All (19) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	104	TYR	5.8
1	A	3	ARG	5.2
1	A	101	ASN	4.4
1	A	104	TYR	4.2
1	B	103	LYS	3.7
1	B	148	GLU	3.6
1	B	110	THR	3.5
1	A	180	ASN	3.5
1	A	174	SER	3.2
1	B	174	SER	3.1
1	A	110	THR	3.1
1	A	160	ASP	3.0
1	B	206	ARG	2.7
1	B	120	LYS	2.7
1	B	160	ASP	2.6
1	A	148	GLU	2.2
1	A	82	GLY	2.1
1	B	141	GLU	2.0
1	A	97	SER	2.0

6.2 Non-standard residues in protein, DNA, RNA chains (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
1	CSD	A	25	8/9	0.98	0.09	17,21,24,24	0
1	CSD	B	25	8/9	0.98	0.11	23,25,28,29	0

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

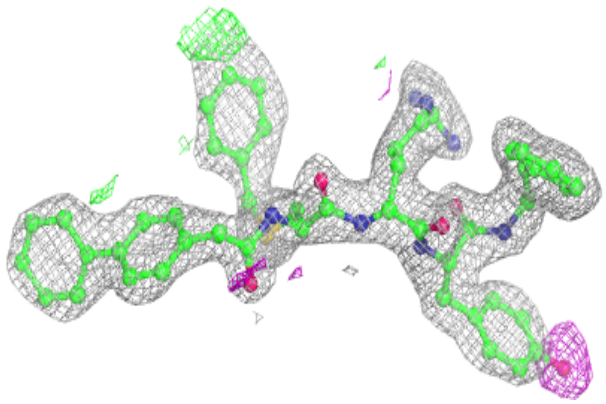
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

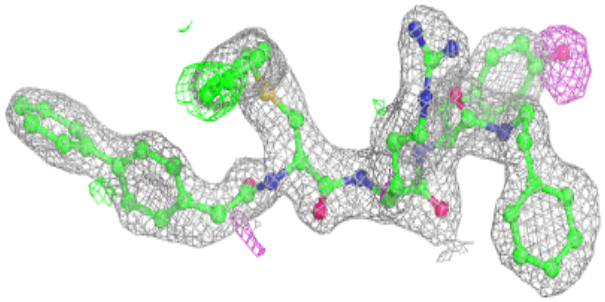
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	OPT	B	400	60/60	0.88	0.20	20,29,40,42	0
2	OPT	A	300	60/60	0.90	0.20	19,26,32,35	0

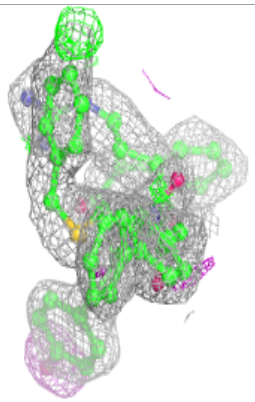
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around OPT B 400:

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

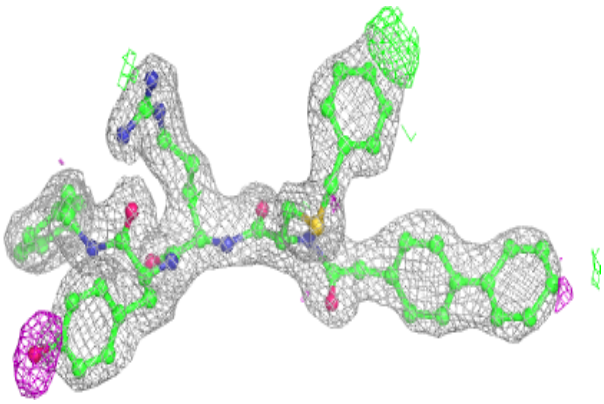


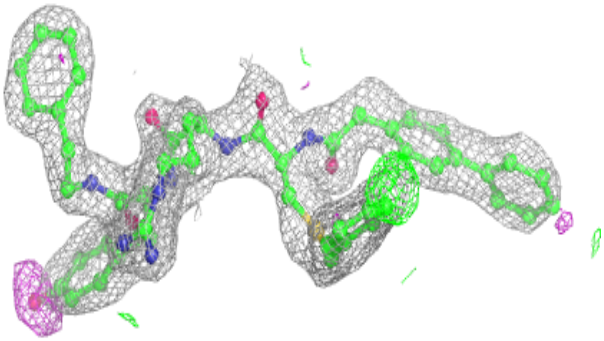


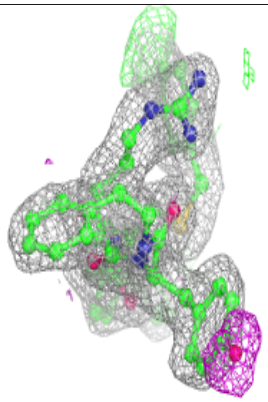


Electron density around OPT A 300:

$2mF_o$-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.