wwPDB X-ray Structure Validation Summary Report (i)

Mar 9, 2024 – 11:32 PM EST

PDB ID	:	3VZC
Title	:	Crystal structure of Sphingosine Kinase 1 with inhibitor
Authors	:	Min, X.; Walker, N.P.; Wang, Z.
Deposited on	:	2012-10-11
Resolution	:	2.30 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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:

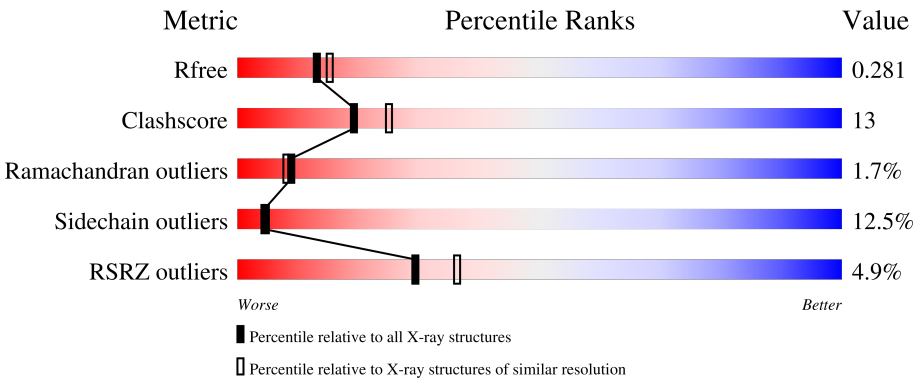
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 2.30 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	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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	361	2%, 70%, 22%, • •
1	B	361	4%, 65%, 23%, 6%, 6%
1	C	361	4%, 62%, 25%, 6%, • 5%
1	D	361	2%, 72%, 19%, • • •
1	E	361	6%, 66%, 24%, • • 5%

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Mol	Chain	Length	Quality of chain
1	F	361	10% 63% 27% 5%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 16468 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 Sphingosine kinase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	347	2694	1726	475	472	21	0	0	0
1	B	340	2653	1702	467	464	20	0	0	0
1	C	342	2664	1707	469	467	21	0	0	0
1	D	348	2701	1731	476	473	21	0	0	0
1	E	342	2663	1707	469	467	20	0	0	0
1	F	344	2673	1712	471	469	21	0	0	0

There are 30 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	4	GLY	-	expression tag	UNP Q9NYA1
A	5	ALA	-	expression tag	UNP Q9NYA1
A	6	MET	-	expression tag	UNP Q9NYA1
A	7	GLY	-	expression tag	UNP Q9NYA1
A	8	SER	-	expression tag	UNP Q9NYA1
B	4	GLY	-	expression tag	UNP Q9NYA1
B	5	ALA	-	expression tag	UNP Q9NYA1
B	6	MET	-	expression tag	UNP Q9NYA1
B	7	GLY	-	expression tag	UNP Q9NYA1
B	8	SER	-	expression tag	UNP Q9NYA1
C	4	GLY	-	expression tag	UNP Q9NYA1
C	5	ALA	-	expression tag	UNP Q9NYA1
C	6	MET	-	expression tag	UNP Q9NYA1
C	7	GLY	-	expression tag	UNP Q9NYA1
C	8	SER	-	expression tag	UNP Q9NYA1
D	4	GLY	-	expression tag	UNP Q9NYA1
D	5	ALA	-	expression tag	UNP Q9NYA1

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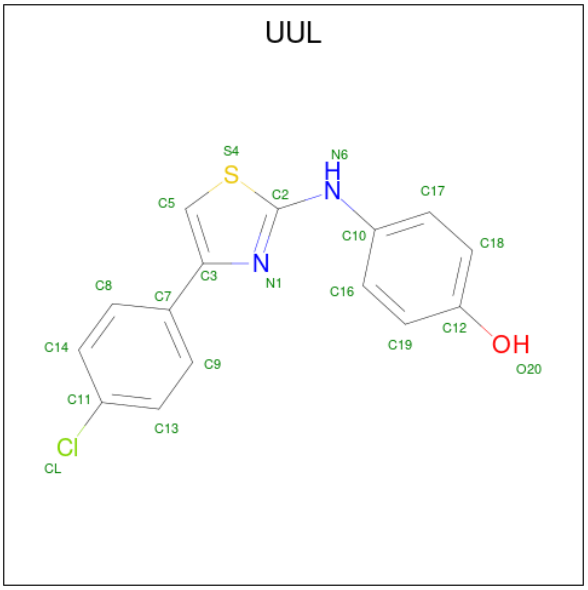
Chain	Residue	Modelled	Actual	Comment	Reference
D	6	MET	-	expression tag	UNP Q9NYA1
D	7	GLY	-	expression tag	UNP Q9NYA1
D	8	SER	-	expression tag	UNP Q9NYA1
E	4	GLY	-	expression tag	UNP Q9NYA1
E	5	ALA	-	expression tag	UNP Q9NYA1
E	6	MET	-	expression tag	UNP Q9NYA1
E	7	GLY	-	expression tag	UNP Q9NYA1
E	8	SER	-	expression tag	UNP Q9NYA1
F	4	GLY	-	expression tag	UNP Q9NYA1
F	5	ALA	-	expression tag	UNP Q9NYA1
F	6	MET	-	expression tag	UNP Q9NYA1
F	7	GLY	-	expression tag	UNP Q9NYA1
F	8	SER	-	expression tag	UNP Q9NYA1

- Molecule 2 is 4-{[4-(4-chlorophenyl)-1,3-thiazol-2-yl]amino}phenol (three-letter code: UUL) (formula: $C_{15}H_{11}ClN_2OS$).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
			Total	C	Cl	N	O	S		
2	A	1	20	15	1	2	1	1	0	0
			Total	C	Cl	N	O	S		
2	B	1	20	15	1	2	1	1	0	0
			Total	C	Cl	N	O	S		
2	C	1	20	15	1	2	1	1	0	0
			Total	C	Cl	N	O	S		
2	D	1	20	15	1	2	1	1	0	0

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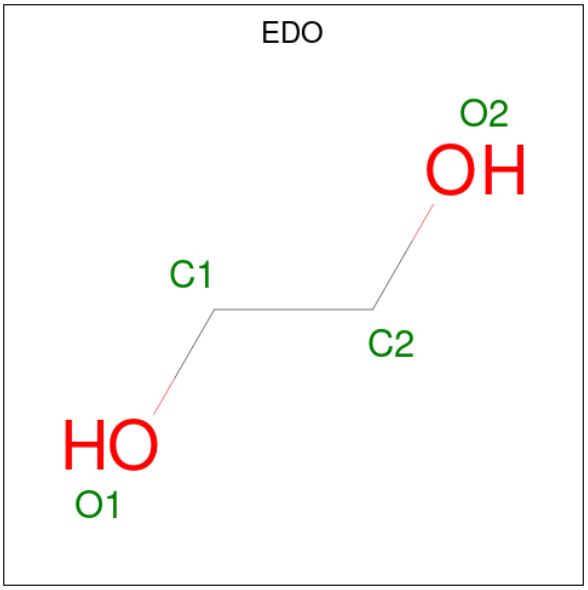
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
			Total	C	Cl	N	O	S		
2	E	1	20	15	1	2	1	1	0	0
2	F	1	20	15	1	2	1	1	0	0

- Molecule 3 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
3	D	1	4	2	2	0	0
3	F	1	4	2	2	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
4	A	60	60	60	0	0
4	B	53	53	53	0	0
4	C	62	62	62	0	0
4	D	35	35	35	0	0
4	E	46	46	46	0	0

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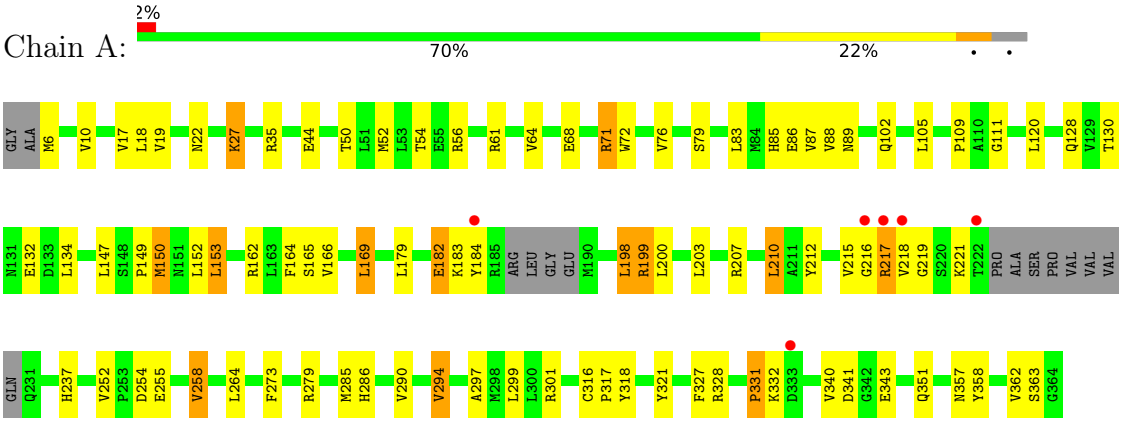
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
4	F	36	36	36	0	0

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.

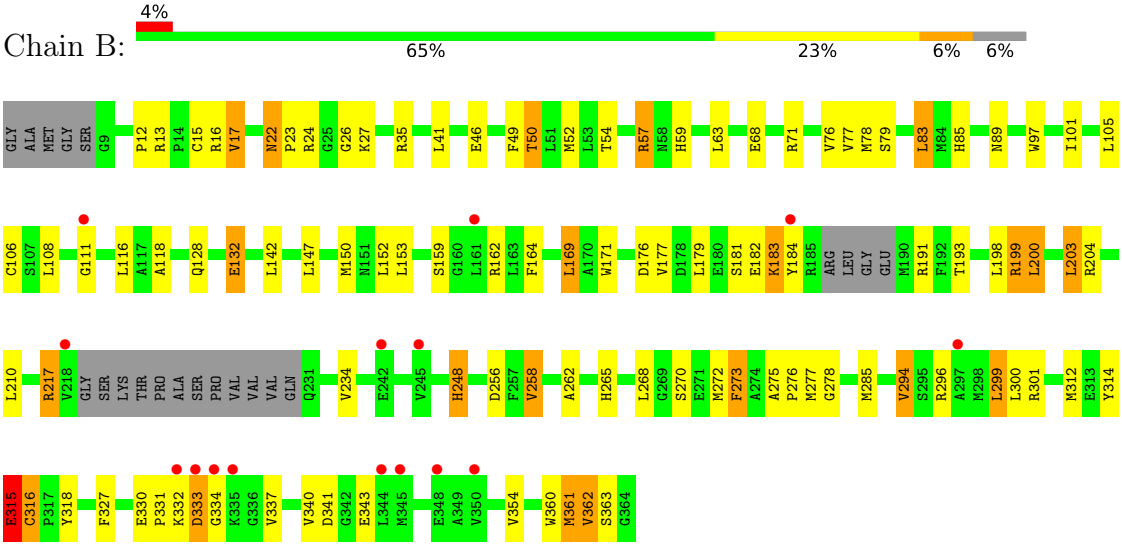
• Molecule 1: Sphingosine kinase 1

Chain A:



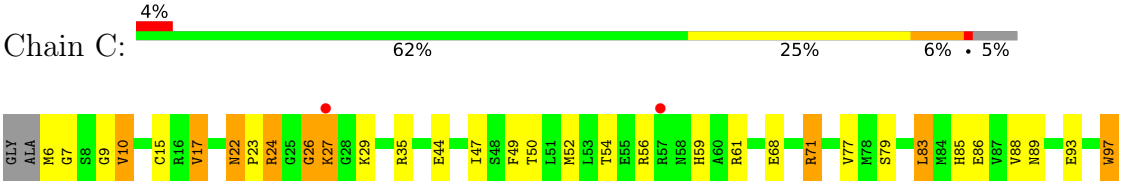
• Molecule 1: Sphingosine kinase 1

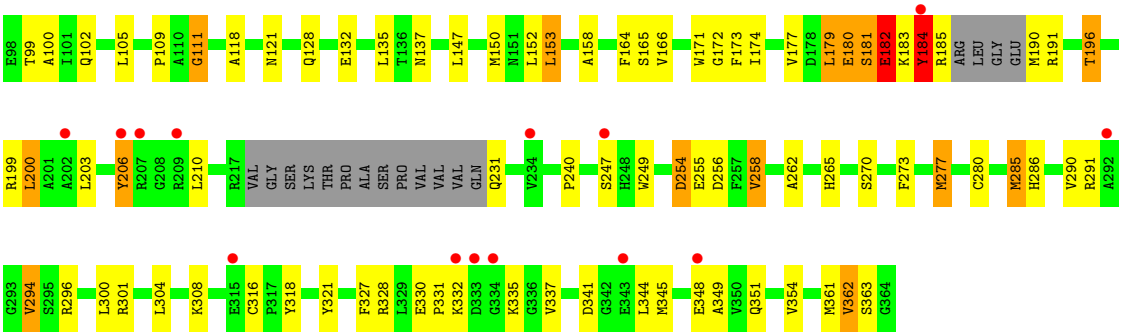
Chain B:



• Molecule 1: Sphingosine kinase 1

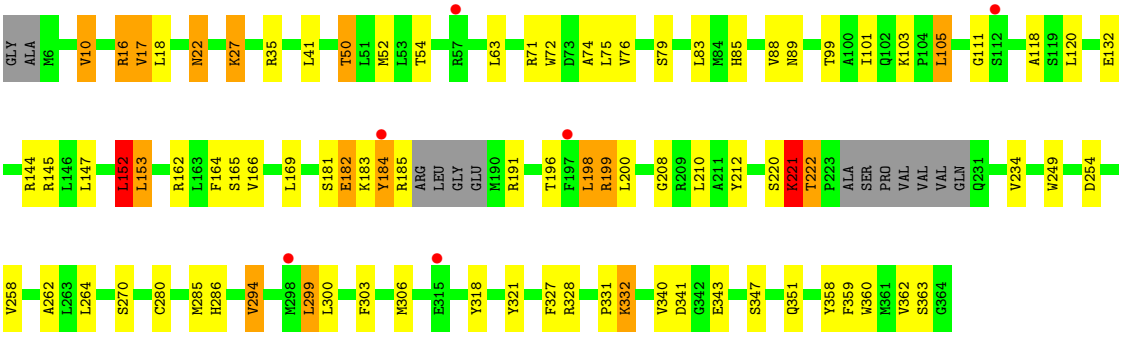
Chain C:





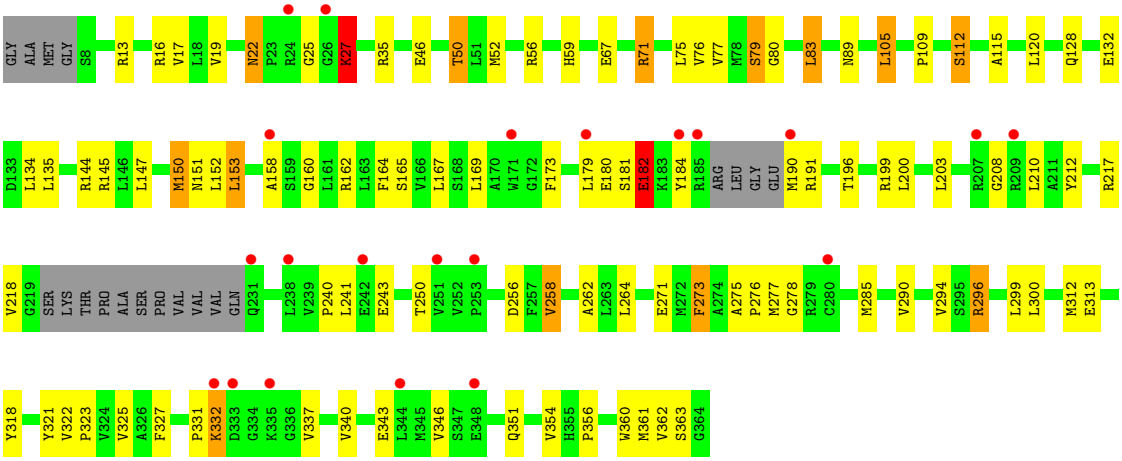
- Molecule 1: Sphingosine kinase 1

Chain D:



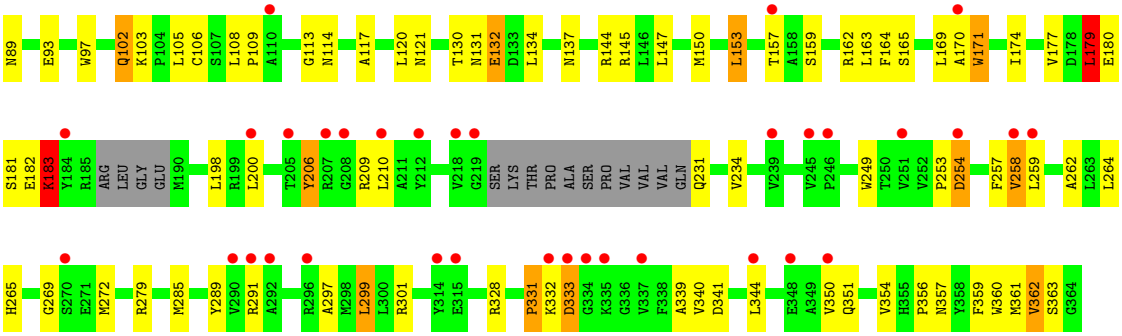
- Molecule 1: Sphingosine kinase 1

Chain E:



- Molecule 1: Sphingosine kinase 1

Chain F:


N89 E93 W97 Q102 K103 P104 L105 C106 S107 L108 P109 A110 G113 N114 A117 L120 N121 T130 N131 E132 D133 L134 N137 R144 R145 L146 L147 M150 L153 T157 A158 S159 R162 L163 F164 S165 L169 A170 W171 I174 V177 D178 L179 E180
S181 E182 K183 Y184 R185 ARG LEU GLY GLU M190 L198 R199 L200 T205 Y206 R207 G208 R209 L210 A211 Y212 V218 G219 SER LYS THR PRO ALA SER PRO VAL VAL VAL GLN Q231 V234 V239 V245 P246 W249 T250 V251 V252 P253 D254 F257 V258 L259 A262 L263 L264
H265 G269 S270 E271 M272 R279 M285 Y289 V290 R291 A292 R296 A297 M298 L299 L300 R301 Y314 E315 R328 P331 K332 D333 G334 K335 G336 V337 F338 A339 V340 D341 L344 E348 A349 V350 Q351 V354 H355 P356 N357 Y358 F359 W360 M361 V362 S363 G364

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	102.22Å 106.61Å 226.18Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.30 49.95 – 2.30	Depositor EDS
% Data completeness (in resolution range)	92.0 (50.00-2.30) 92.0 (49.95-2.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
$< I/\sigma(I) >$ [1]	2.70 (at 2.29Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.229 , 0.285 0.227 , 0.281	Depositor DCC
R_{free} test set	5084 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å^2)	40.2	Xtriage
Anisotropy	0.272	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 34.2	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.000 for k,h,-l	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	16468	wwPDB-VP
Average B, all atoms (Å^2)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 60.74 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.4545e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[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: UUL, EDO

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	0.55	0/2755	0.74	1/3735 (0.0%)
1	B	0.56	3/2714 (0.1%)	0.72	1/3682 (0.0%)
1	C	0.56	3/2725 (0.1%)	0.72	0/3695
1	D	0.54	2/2763 (0.1%)	0.72	3/3747 (0.1%)
1	E	0.54	1/2724 (0.0%)	0.69	0/3695
1	F	0.55	5/2734 (0.2%)	0.68	1/3707 (0.0%)
All	All	0.55	14/16415 (0.1%)	0.71	6/22261 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	B	0	1
1	C	0	1
All	All	0	3

The worst 5 of 14 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	360	TRP	CD2-CE2	5.66	1.48	1.41
1	C	171	TRP	CD2-CE2	5.44	1.47	1.41
1	F	171	TRP	CD2-CE2	5.35	1.47	1.41
1	B	360	TRP	CD2-CE2	5.28	1.47	1.41
1	B	171	TRP	CD2-CE2	5.27	1.47	1.41

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	D	198	LEU	CA-CB-CG	7.69	132.99	115.30
1	B	316	CYS	N-CA-C	-6.90	92.36	111.00
1	A	198	LEU	CA-CB-CG	5.85	128.76	115.30
1	D	152	LEU	CA-CB-CG	5.71	128.43	115.30
1	F	179	LEU	CA-CB-CG	5.22	127.30	115.30

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	331	PRO	Peptide
1	B	315	GLU	Peptide
1	C	26	GLY	Peptide

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	2694	0	2716	59	0
1	B	2653	0	2679	84	0
1	C	2664	0	2687	75	0
1	D	2701	0	2723	66	0
1	E	2663	0	2687	79	0
1	F	2673	0	2692	79	0
2	A	20	0	10	0	0
2	B	20	0	11	1	0
2	C	20	0	10	1	0
2	D	20	0	10	0	0
2	E	20	0	10	0	0
2	F	20	0	11	0	0
3	D	4	0	6	0	0
3	F	4	0	6	2	0
4	A	60	0	0	7	0
4	B	53	0	0	6	0
4	C	62	0	0	5	0
4	D	35	0	0	1	0
4	E	46	0	0	2	0
4	F	36	0	0	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	16468	0	16258	417	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 13.

The worst 5 of 417 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:D:331:PRO:HA	1:D:332:LYS:HB2	1.17	1.15
1:B:262:ALA:HB1	1:B:285:MET:CE	1.91	1.00
1:F:150:MET:HE2	1:F:265:HIS:HE1	1.23	0.98
1:B:315:GLU:HB2	1:D:10:VAL:HG23	1.43	0.97
1:F:17:VAL:HG11	1:F:76:VAL:HG12	1.46	0.96

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	341/361 (94%)	319 (94%)	19 (6%)	3 (1%)	17 20
1	B	334/361 (92%)	311 (93%)	18 (5%)	5 (2%)	10 10
1	C	336/361 (93%)	308 (92%)	18 (5%)	10 (3%)	4 2
1	D	342/361 (95%)	322 (94%)	15 (4%)	5 (2%)	10 10
1	E	336/361 (93%)	317 (94%)	14 (4%)	5 (2%)	10 10
1	F	338/361 (94%)	308 (91%)	24 (7%)	6 (2%)	8 7
All	All	2027/2166 (94%)	1885 (93%)	108 (5%)	34 (2%)	9 8

5 of 34 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	315	GLU
1	C	182	GLU
1	C	183	LYS
1	C	277	MET
1	D	79	SER

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	286/299 (96%)	250 (87%)	36 (13%)	4 4
1	B	283/299 (95%)	244 (86%)	39 (14%)	3 3
1	C	284/299 (95%)	240 (84%)	44 (16%)	2 2
1	D	287/299 (96%)	257 (90%)	30 (10%)	7 8
1	E	284/299 (95%)	251 (88%)	33 (12%)	5 6
1	F	284/299 (95%)	253 (89%)	31 (11%)	6 7
All	All	1708/1794 (95%)	1495 (88%)	213 (12%)	4 5

5 of 213 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	337	VAL
1	D	254	ASP
1	F	183	LYS
1	D	10	VAL
1	D	105	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 55 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	351	GLN
1	D	237	HIS
1	F	351	GLN
1	F	102	GLN

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Mol	Chain	Res	Type
1	D	22	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)

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)

8 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	UUL	F	1001	-	19,22,22	1.56	2 (10%)	24,30,30	1.07	2 (8%)
3	EDO	F	1002	-	3,3,3	0.35	0	2,2,2	0.80	0
3	EDO	D	1002	-	3,3,3	0.48	0	2,2,2	0.21	0
2	UUL	B	1001	-	19,22,22	1.55	2 (10%)	24,30,30	1.33	3 (12%)
2	UUL	E	1001	-	19,22,22	1.56	2 (10%)	24,30,30	1.16	2 (8%)
2	UUL	A	1001	-	19,22,22	1.48	2 (10%)	24,30,30	1.28	2 (8%)
2	UUL	C	1001	-	19,22,22	1.56	2 (10%)	24,30,30	1.27	2 (8%)
2	UUL	D	1001	-	19,22,22	1.50	2 (10%)	24,30,30	1.19	2 (8%)

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	UUL	F	1001	-	-	4/6/8/8	0/3/3/3
3	EDO	F	1002	-	-	0/1/1/1	-
3	EDO	D	1002	-	-	0/1/1/1	-
2	UUL	B	1001	-	-	0/6/8/8	0/3/3/3
2	UUL	E	1001	-	-	0/6/8/8	0/3/3/3
2	UUL	A	1001	-	-	0/6/8/8	0/3/3/3
2	UUL	C	1001	-	-	0/6/8/8	0/3/3/3
2	UUL	D	1001	-	-	0/6/8/8	0/3/3/3

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	1001	UUL	C7-C3	-5.58	1.40	1.48
2	B	1001	UUL	C7-C3	-5.49	1.40	1.48
2	E	1001	UUL	C7-C3	-5.44	1.40	1.48
2	A	1001	UUL	C7-C3	-5.44	1.40	1.48
2	D	1001	UUL	C7-C3	-5.30	1.40	1.48

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	D	1001	UUL	C5-C3-C7	-4.09	123.76	129.44
2	C	1001	UUL	C5-C3-C7	-3.90	124.01	129.44
2	B	1001	UUL	C5-C3-C7	-3.81	124.14	129.44
2	A	1001	UUL	C5-C3-C7	-3.76	124.22	129.44
2	C	1001	UUL	C3-C5-S4	-3.37	107.65	111.79

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	F	1001	UUL	N1-C3-C7-C9
2	F	1001	UUL	N1-C3-C7-C8
2	F	1001	UUL	C5-C3-C7-C9
2	F	1001	UUL	C5-C3-C7-C8

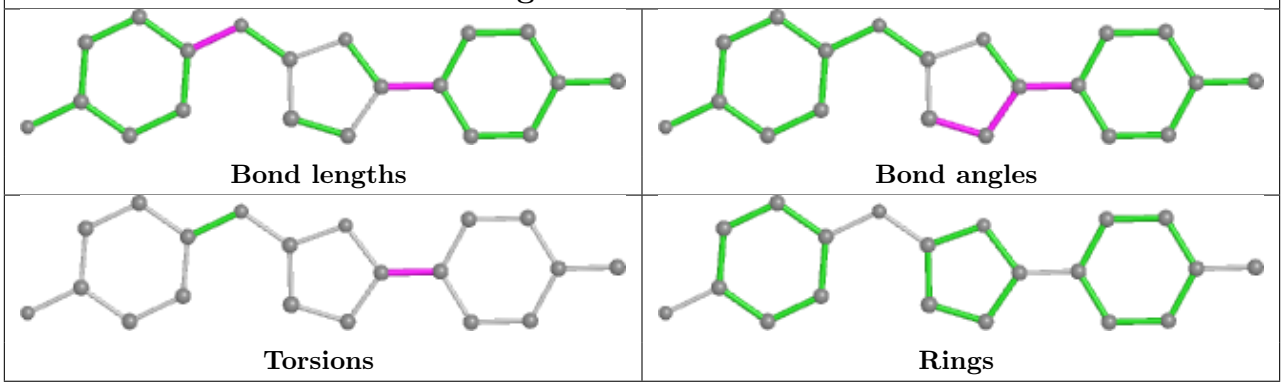
There are no ring outliers.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	F	1002	EDO	2	0
2	B	1001	UUL	1	0
2	C	1001	UUL	1	0

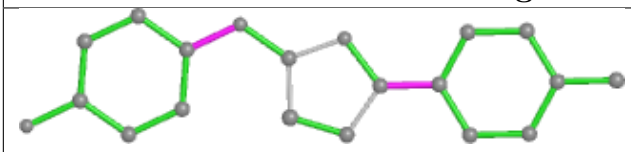
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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 UUL F 1001

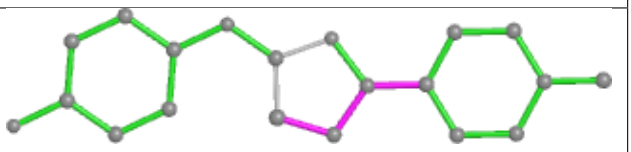


Ligand UUL B 1001

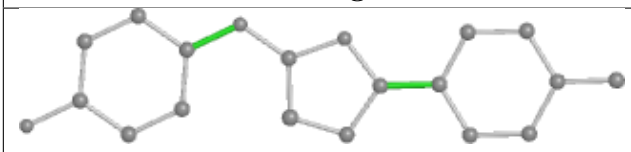
Ligand UUL E 1001



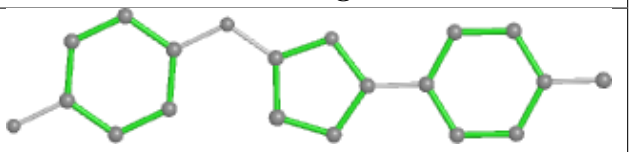
Bond lengths



Bond angles

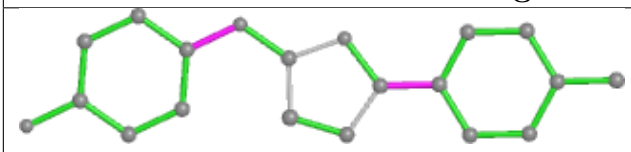


Torsions

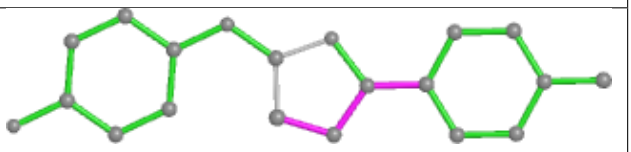


Rings

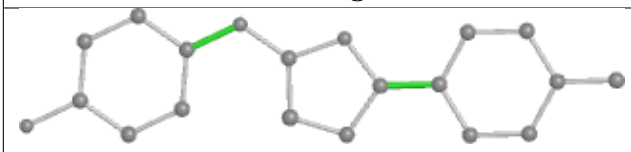
Ligand UUL A 1001



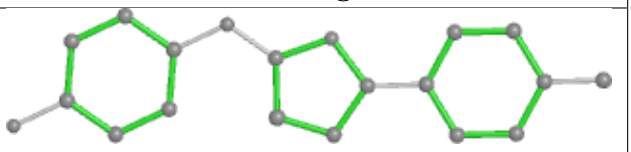
Bond lengths



Bond angles

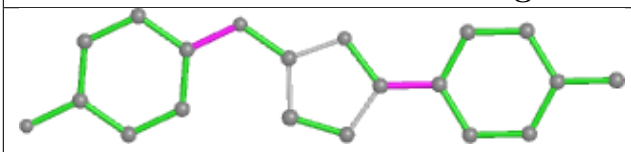


Torsions

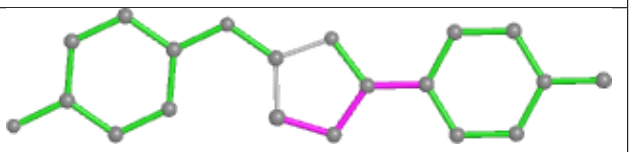


Rings

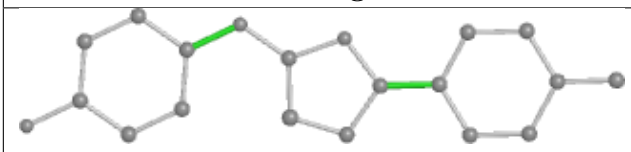
Ligand UUL C 1001



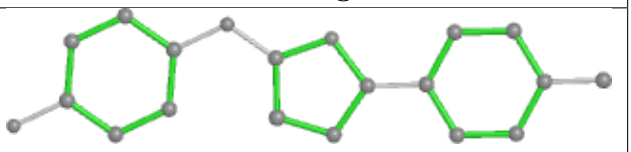
Bond lengths



Bond angles

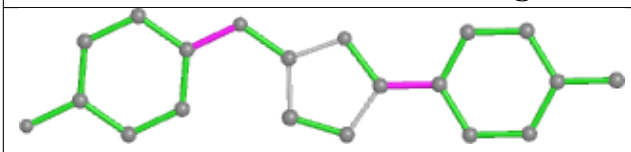


Torsions

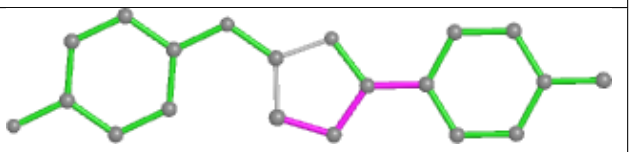


Rings

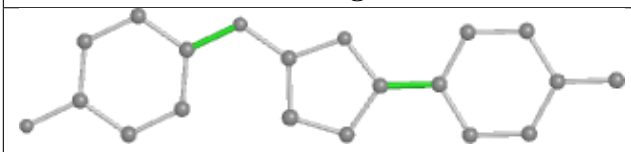
Ligand UUL D 1001



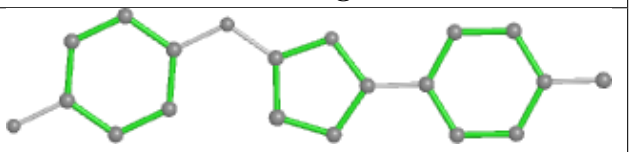
Bond lengths



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	347/361 (96%)	-0.09	6 (1%)	70	76	22, 34, 63, 87	1 (0%)
1	B	340/361 (94%)	0.41	15 (4%)	34	41	22, 39, 75, 116	1 (0%)
1	C	342/361 (94%)	0.20	16 (4%)	31	38	24, 41, 71, 97	1 (0%)
1	D	348/361 (96%)	0.01	6 (1%)	70	76	24, 37, 66, 104	1 (0%)
1	E	342/361 (94%)	0.41	21 (6%)	21	27	25, 41, 73, 110	1 (0%)
1	F	344/361 (95%)	0.61	37 (10%)	5	8	27, 49, 80, 114	1 (0%)
All	All	2063/2166 (95%)	0.26	101 (4%)	29	36	22, 40, 74, 116	6 (0%)

The worst 5 of 101 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	333	ASP	5.5
1	F	332	LYS	5.1
1	B	218	VAL	5.0
1	E	184	TYR	4.7
1	D	184	TYR	4.6

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

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

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

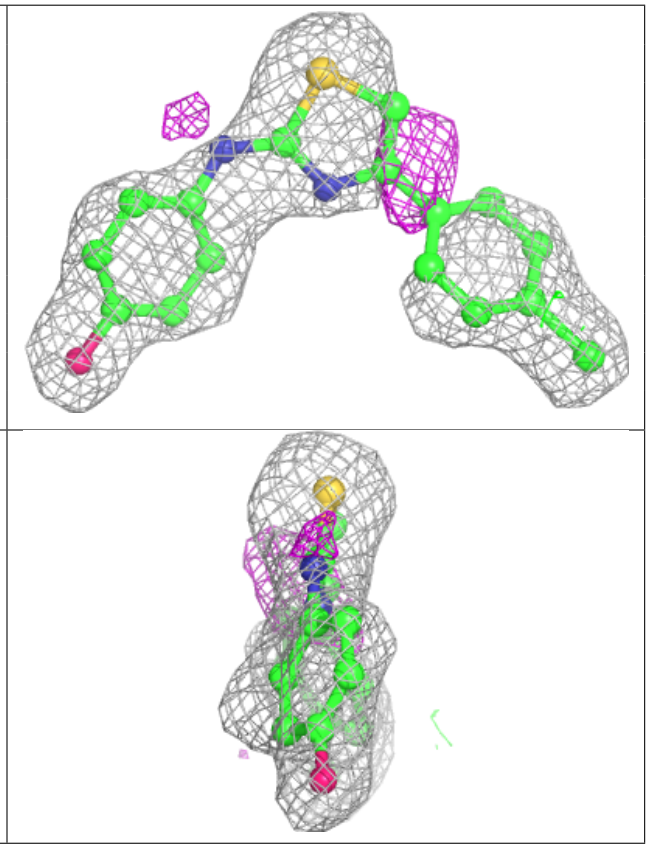
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	UUL	F	1001	20/20	0.85	0.21	43,62,77,77	0
2	UUL	C	1001	20/20	0.86	0.28	51,66,73,75	0
3	EDO	F	1002	4/4	0.90	0.19	35,38,42,44	0
3	EDO	D	1002	4/4	0.91	0.16	36,39,43,47	0
2	UUL	B	1001	20/20	0.92	0.17	52,57,63,64	0
2	UUL	E	1001	20/20	0.96	0.12	41,46,51,52	0
2	UUL	D	1001	20/20	0.96	0.14	35,41,45,46	0
2	UUL	A	1001	20/20	0.97	0.12	28,31,38,40	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.

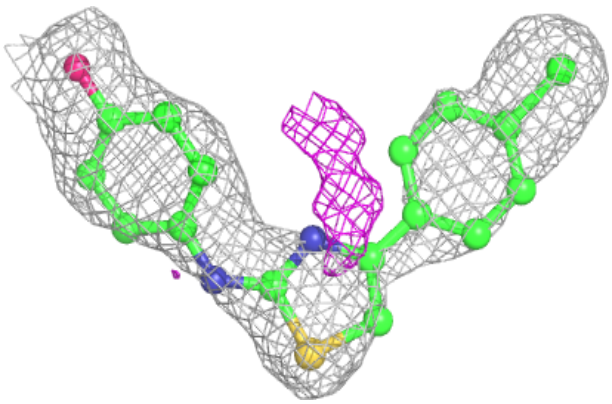
Electron density around UUL F 1001:

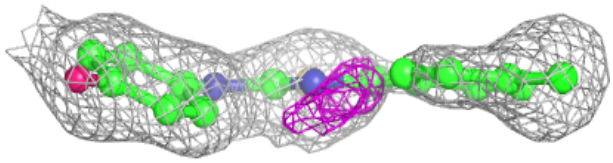
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

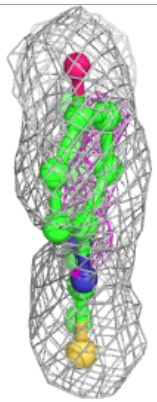


Electron density around UUL C 1001:

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

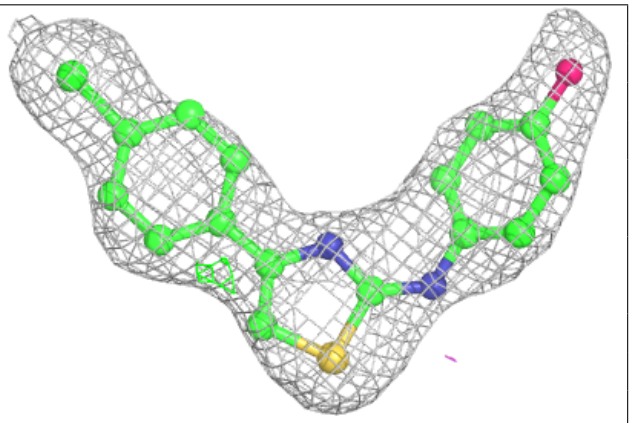


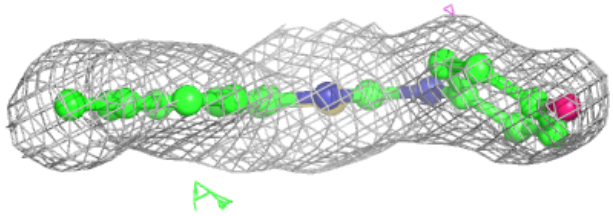


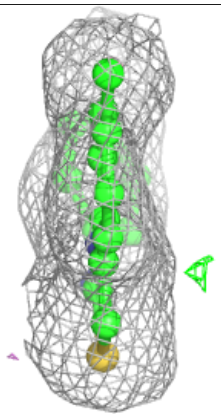


Electron density around UUL B 1001:

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

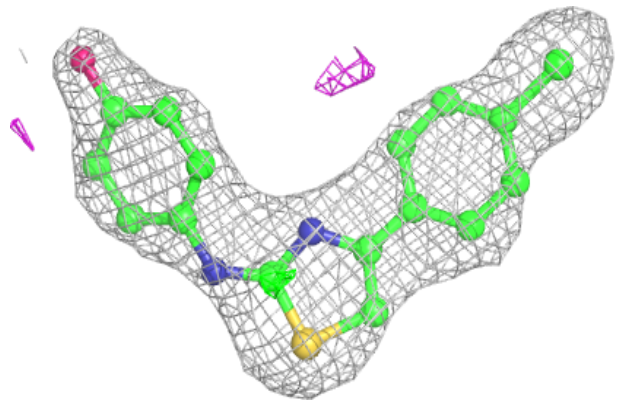


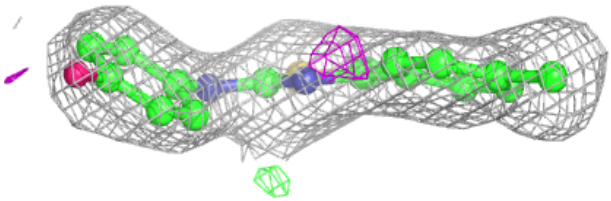


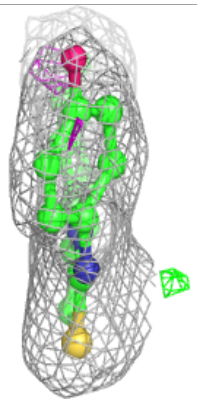


Electron density around UUL E 1001:

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







Electron density around UUL D 1001:

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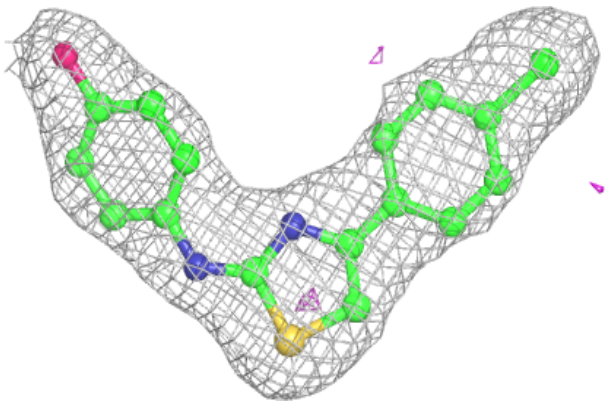
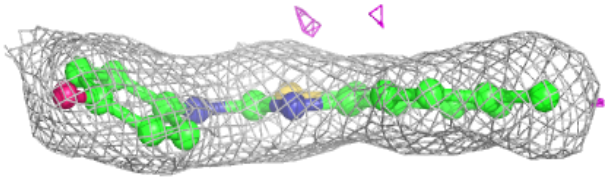
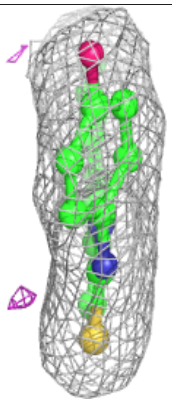
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

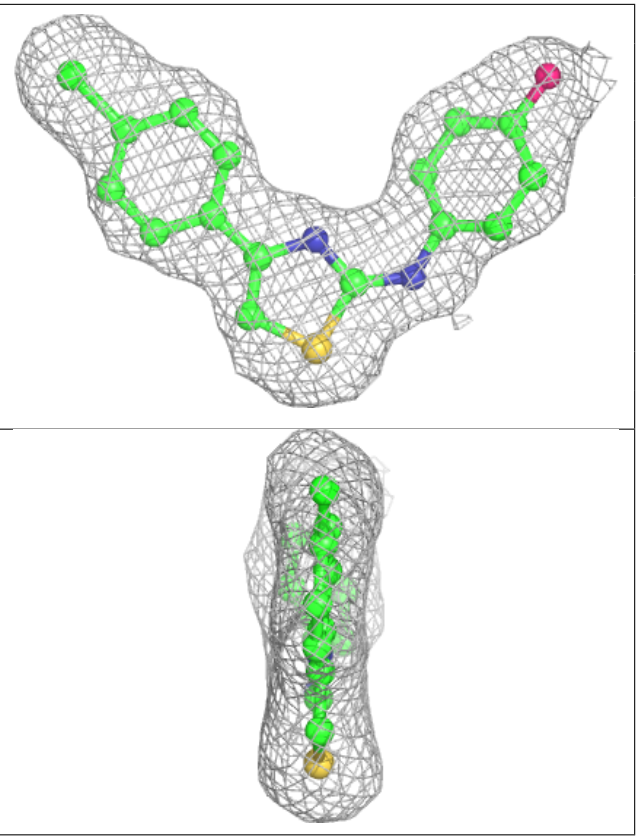






Electron density around UUL A 1001:

$2mF_o$-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.