



wwPDB X-ray Structure Validation Summary Report ⓘ

Sep 20, 2023 – 10:33 am BST

PDB ID : 8B4F
Title : Crystal structure of human cathepsin L forming a thiohemiacetal with N-Boc-2-aminoacetaldehyde
Authors : Falke, S.; Lieske, J.; Guenther, S.; Reinke, P.Y.A.; Ewert, W.; Loboda, J.; Karnicar, K.; Usenik, A.; Lindic, N.; Sekirnik, A.; Chapman, H.N.; Hinrichs, W.; Turk, D.; Meents, A.
Deposited on : 2022-09-20
Resolution : 1.90 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 ⓘ 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](#) ①) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.4, CSD as541be (2020)
Xtrriage (Phenix) : 1.13
EDS : 2.35.1
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.35.1

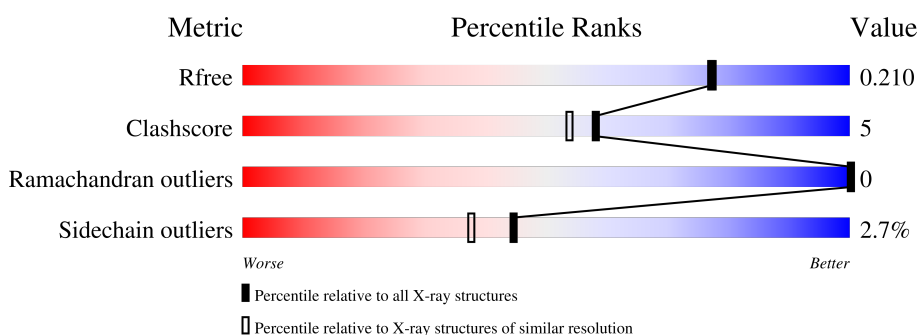
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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	6207 (1.90-1.90)
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)

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 $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	220	88% 12%
1	B	220	87% 13%
1	C	220	89% 9% .
1	D	220	88% 12%

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
4	DMS	D	304	-	-	X	-

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 13779 atoms, of which 6506 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.

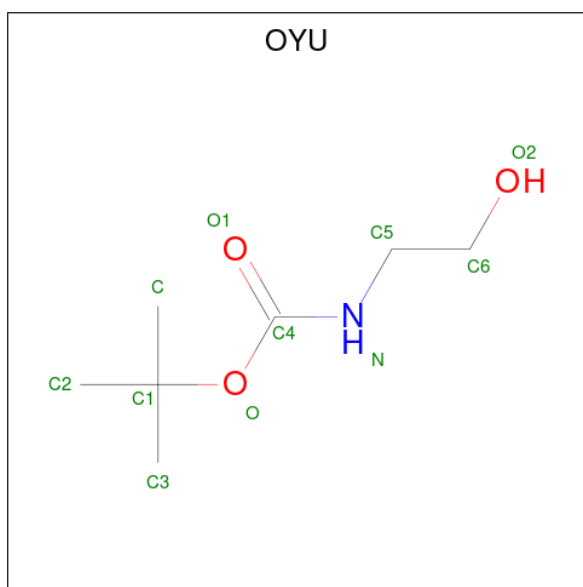
- Molecule 1 is a protein called Cathepsin L.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
1	A	220	3280	1065	1577	282	342	14	0	1	0
1	B	220	3273	1063	1572	282	342	14	0	1	0
1	C	216	3228	1049	1555	278	332	14	0	1	0
1	D	220	3321	1080	1591	286	348	16	0	5	0

There are 4 discrepancies between the modelled and reference sequences:

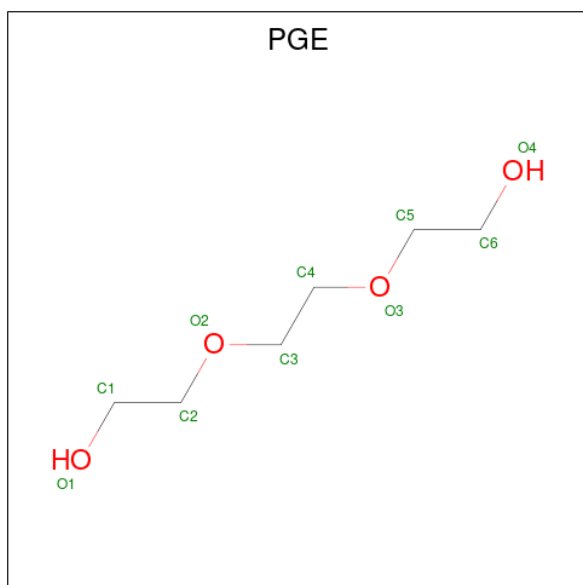
Chain	Residue	Modelled	Actual	Comment	Reference
A	110	ALA	THR	engineered mutation	UNP P07711
B	110	ALA	THR	engineered mutation	UNP P07711
C	110	ALA	THR	engineered mutation	UNP P07711
D	110	ALA	THR	engineered mutation	UNP P07711

- Molecule 2 is {tert}-butyl {N}-(2-hydroxyethyl)carbamate (three-letter code: OYU) (formula: C₇H₁₅NO₃) (labeled as "Ligand of Interest" by depositor).



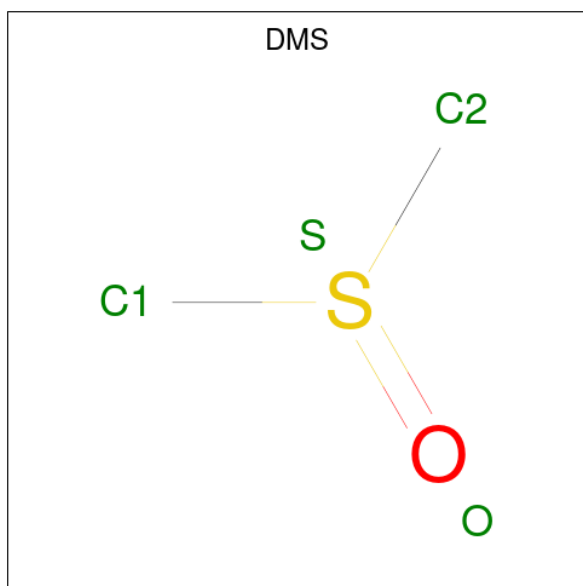
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
2	A	1	11	7	1	3	0	0
2	B	1	24	7	13	1	3	0
2	C	1	25	7	14	1	3	0
2	D	1	25	7	14	1	3	0

- Molecule 3 is TRIETHYLENE GLYCOL (three-letter code: PGE) (formula: C₆H₁₄O₄).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	H	O		
3	A	1	24	6	14	4	0	0

- Molecule 4 is DIMETHYL SULFOXIDE (three-letter code: DMS) (formula: C₂H₆OS).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	H	O	S		
4	A	1	10	2	6	1	1	0	0
4	D	1	10	2	6	1	1	0	0
4	D	1	10	2	6	1	1	0	0

- Molecule 5 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C₂H₆O₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	H	O		
5	A	1	10	2	6	2	0	0
5	A	1	10	2	6	2	0	0
5	B	1	10	2	6	2	0	0
5	B	1	10	2	6	2	0	0
5	C	1	10	2	6	2	0	0
5	C	1	10	2	6	2	0	0
5	D	1	10	2	6	2	0	0
5	D	1	10	2	6	2	0	0

- Molecule 6 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: C₄H₁₀O₃).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	A	1	Total	C	H	O	0	0
			17	4	10	3		
6	B	1	Total	C	H	O	0	0
			17	4	10	3		
6	C	1	Total	C	H	O	0	0
			17	4	10	3		
6	C	1	Total	C	H	O	0	0
			17	4	10	3		
6	D	1	Total	C	H	O	0	0
			17	4	10	3		
6	D	1	Total	C	H	O	0	0
			17	4	10	3		
6	D	1	Total	C	H	O	0	0
			17	4	10	3		
6	D	1	Total	C	H	O	0	0
			17	4	10	3		

- Molecule 7 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	2	Total	Na	0	0
			2	2		
7	C	1	Total	Na	0	0
			1	1		

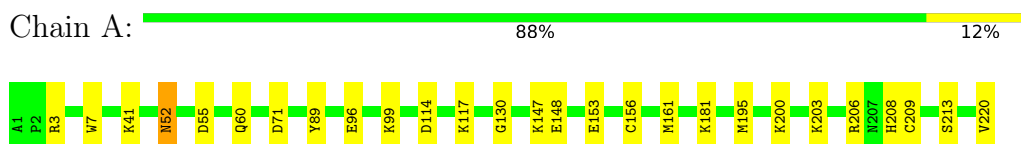
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	75	Total 75	O 75	0	0
8	B	78	Total 78	O 78	0	0
8	C	54	Total 54	O 54	0	0
8	D	95	Total 95	O 95	0	0

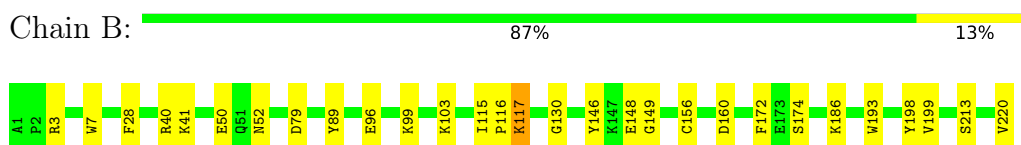
3 Residue-property plots [i](#)

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. 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. 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.

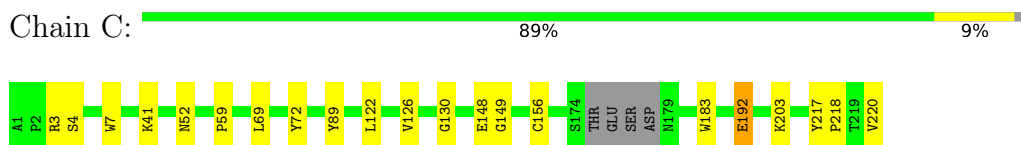
- Molecule 1: Cathepsin L



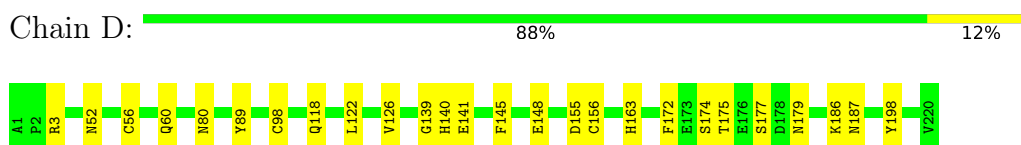
- Molecule 1: Cathepsin L



- Molecule 1: Cathepsin L



- Molecule 1: Cathepsin L



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	57.21Å 62.26Å 67.63Å 105.44° 93.41° 115.90°	Depositor
Resolution (Å)	49.42 – 1.90 49.42 – 1.48	Depositor EDS
% Data completeness (in resolution range)	93.9 (49.42-1.90) 70.3 (49.42-1.48)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.03 (at 1.48Å)	Xtrriage
Refinement program	PHENIX 1.13-2998_9999	Depositor
R, R_{free}	0.177 , 0.210 0.178 , 0.210	Depositor DCC
R_{free} test set	1966 reflections (1.61%)	wwPDB-VP
Wilson B-factor (Å ²)	11.7	Xtrriage
Anisotropy	0.210	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.42 , 43.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.52$, $\langle L^2 \rangle = 0.35$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	13779	wwPDB-VP
Average B, all atoms (Å ²)	31.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.48% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ 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: PGE, NA, DMS, PEG, OYU, 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	0.59	1/1745 (0.1%)	0.66	1/2358 (0.0%)
1	B	0.58	0/1743	0.68	1/2356 (0.0%)
1	C	0.54	1/1714 (0.1%)	0.64	0/2314
1	D	0.58	0/1772	0.70	0/2394
All	All	0.57	2/6974 (0.0%)	0.67	2/9422 (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

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	192	GLU	CD-OE2	-6.52	1.18	1.25
1	A	209	CYS	CB-SG	-6.45	1.71	1.82

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	3	ARG	NE-CZ-NH1	-6.83	116.89	120.30
1	B	79	ASP	CB-CG-OD1	5.13	122.91	118.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	206	ARG	Sidechain

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	1703	1577	1576	17	0
1	B	1701	1572	1572	16	0
1	C	1673	1555	1553	12	0
1	D	1730	1591	1598	18	0
2	A	11	0	0	0	0
2	B	11	13	0	0	0
2	C	11	14	0	0	0
2	D	11	14	0	0	0
3	A	10	14	14	0	0
4	A	4	6	6	0	0
4	D	8	12	12	4	0
5	A	8	12	12	3	0
5	B	8	12	12	0	0
5	C	8	12	12	1	0
5	D	8	12	12	2	0
6	A	7	10	10	0	0
6	B	7	10	10	2	0
6	C	14	20	20	0	0
6	D	35	50	50	2	0
7	A	2	0	0	0	0
7	C	1	0	0	0	0
8	A	75	0	0	0	0
8	B	78	0	0	1	0
8	C	54	0	0	0	0
8	D	95	0	0	2	0
All	All	7273	6506	6469	64	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 5.

The worst 5 of 64 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:C:41:LYS:HD2	1:C:220:VAL:HG12	1.30	1.09
1:C:41:LYS:CD	1:C:220:VAL:HG12	2.17	0.67
1:A:7:TRP:CE2	1:A:130:GLY:HA2	2.32	0.64
1:A:195:MET:HE1	1:A:200:LYS:HE2	1.80	0.63
1:C:41:LYS:HE2	1:C:220:VAL:O	2.00	0.62

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	219/220 (100%)	214 (98%)	5 (2%)	0	100	100
1	B	219/220 (100%)	213 (97%)	6 (3%)	0	100	100
1	C	213/220 (97%)	203 (95%)	10 (5%)	0	100	100
1	D	223/220 (101%)	217 (97%)	6 (3%)	0	100	100
All	All	874/880 (99%)	847 (97%)	27 (3%)	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	179/178 (101%)	176 (98%)	3 (2%)	60	57
1	B	179/178 (101%)	172 (96%)	7 (4%)	32	23

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	175/178 (98%)	171 (98%)	4 (2%)	50	45
1	D	183/178 (103%)	178 (97%)	5 (3%)	44	38
All	All	716/712 (101%)	697 (97%)	19 (3%)	44	38

5 of 19 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	52	ASN
1	D	156	CYS
1	D	174	SER
1	D	118	GLN
1	B	160	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	163	HIS
1	D	140	HIS
1	C	118	GLN
1	C	80	ASN
1	D	80	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](#)

Of 28 ligands modelled in this entry, 3 are monoatomic - leaving 25 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	OYU	A	301	1	10,10,10	1.98	2 (20%)	13,13,13	1.60	3 (23%)
6	PEG	D	306	-	6,6,6	0.41	0	5,5,5	0.32	0
5	EDO	B	302	-	3,3,3	0.42	0	2,2,2	0.44	0
2	OYU	D	301	1	10,10,10	2.38	5 (50%)	13,13,13	1.63	2 (15%)
4	DMS	D	310	-	3,3,3	0.62	0	3,3,3	0.50	0
4	DMS	D	304	-	3,3,3	0.42	0	3,3,3	0.15	0
5	EDO	A	306	-	3,3,3	0.44	0	2,2,2	0.58	0
5	EDO	A	304	-	3,3,3	0.41	0	2,2,2	0.65	0
5	EDO	C	304	-	3,3,3	0.48	0	2,2,2	0.74	0
6	PEG	C	303	-	6,6,6	0.19	0	5,5,5	0.32	0
5	EDO	D	309	-	3,3,3	0.35	0	2,2,2	0.56	0
6	PEG	D	308	-	6,6,6	0.31	0	5,5,5	0.25	0
4	DMS	A	303	-	3,3,3	0.65	0	3,3,3	0.78	0
6	PEG	D	303	-	6,6,6	0.27	0	5,5,5	0.24	0
3	PGE	A	302	-	9,9,9	0.29	0	8,8,8	0.33	0
6	PEG	A	305	7	6,6,6	0.22	0	5,5,5	0.10	0
6	PEG	C	302	-	6,6,6	0.32	0	5,5,5	0.31	0
2	OYU	C	301	1	10,10,10	1.85	2 (20%)	13,13,13	1.36	3 (23%)
5	EDO	C	305	-	3,3,3	0.50	0	2,2,2	0.47	0
5	EDO	D	305	-	3,3,3	0.42	0	2,2,2	0.48	0
6	PEG	D	302	-	6,6,6	0.32	0	5,5,5	0.30	0
6	PEG	B	304	-	6,6,6	0.29	0	5,5,5	0.29	0
2	OYU	B	301	1	10,10,10	2.13	3 (30%)	13,13,13	2.26	4 (30%)
6	PEG	D	307	-	6,6,6	0.33	0	5,5,5	0.57	0
5	EDO	B	303	-	3,3,3	0.55	0	2,2,2	0.28	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
2	OYU	A	301	1	-	0/9/9/9	-
6	PEG	D	306	-	-	4/4/4/4	-

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	EDO	B	302	-	-	0/1/1/1	-
2	OYU	D	301	1	-	2/9/9/9	-
5	EDO	A	306	-	-	0/1/1/1	-
5	EDO	A	304	-	-	1/1/1/1	-
5	EDO	C	304	-	-	0/1/1/1	-
6	PEG	C	303	-	-	1/4/4/4	-
5	EDO	D	309	-	-	0/1/1/1	-
6	PEG	D	308	-	-	3/4/4/4	-
6	PEG	D	303	-	-	1/4/4/4	-
3	PGE	A	302	-	-	4/7/7/7	-
6	PEG	A	305	7	-	3/4/4/4	-
6	PEG	C	302	-	-	3/4/4/4	-
2	OYU	C	301	1	-	0/9/9/9	-
5	EDO	C	305	-	-	0/1/1/1	-
5	EDO	D	305	-	-	1/1/1/1	-
6	PEG	D	302	-	-	2/4/4/4	-
6	PEG	B	304	-	-	0/4/4/4	-
2	OYU	B	301	1	-	0/9/9/9	-
6	PEG	D	307	-	-	4/4/4/4	-
5	EDO	B	303	-	-	0/1/1/1	-

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	301	OYU	O-C4	5.27	1.45	1.34
2	B	301	OYU	O-C4	4.59	1.44	1.34
2	D	301	OYU	O-C1	-4.40	1.40	1.48
2	C	301	OYU	O-C1	-4.06	1.41	1.48
2	D	301	OYU	O1-C4	-3.83	1.14	1.21

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	301	OYU	C1-O-C4	5.55	129.53	120.99
2	B	301	OYU	O-C4-N	3.80	115.63	109.99
2	D	301	OYU	O-C4-N	3.35	114.96	109.99
2	C	301	OYU	O-C4-O1	-3.20	119.78	125.62
2	A	301	OYU	C1-O-C4	3.17	125.86	120.99

There are no chirality outliers.

5 of 29 torsion outliers are listed below:

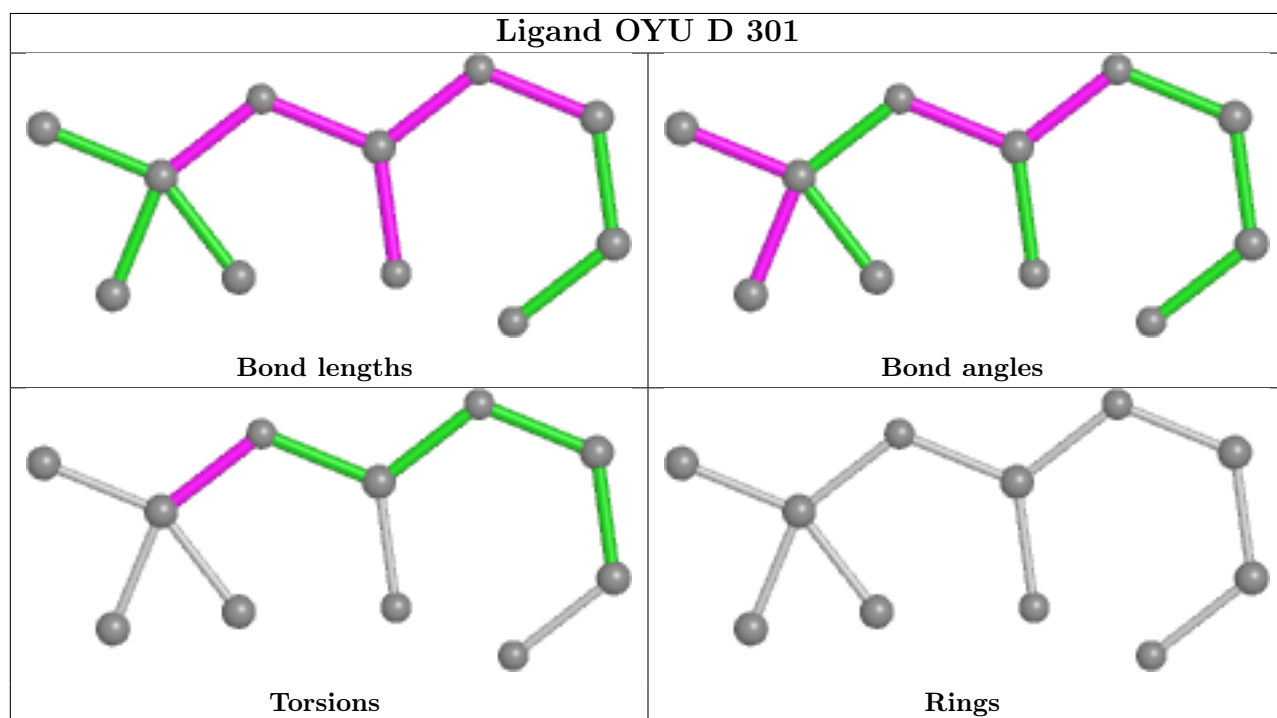
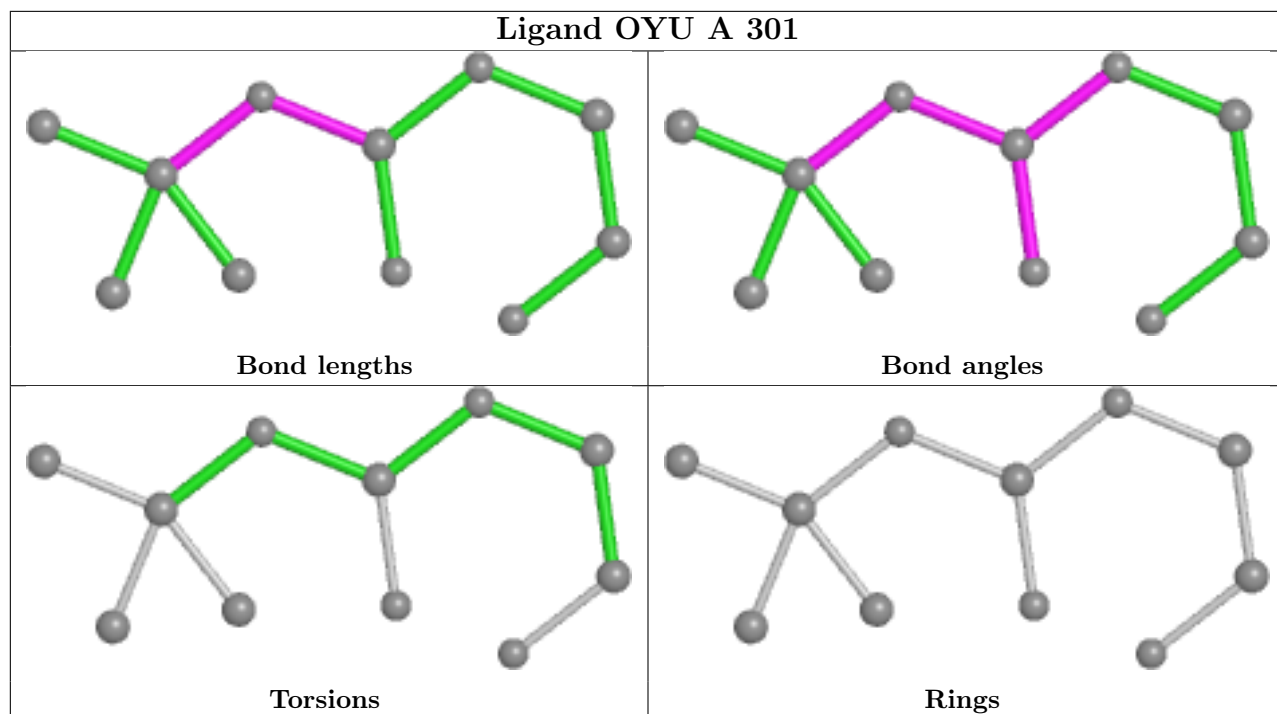
Mol	Chain	Res	Type	Atoms
6	D	307	PEG	C4-C3-O2-C2
6	D	307	PEG	O1-C1-C2-O2
6	D	308	PEG	O2-C3-C4-O4
2	D	301	OYU	C-C1-O-C4
6	C	302	PEG	O2-C3-C4-O4

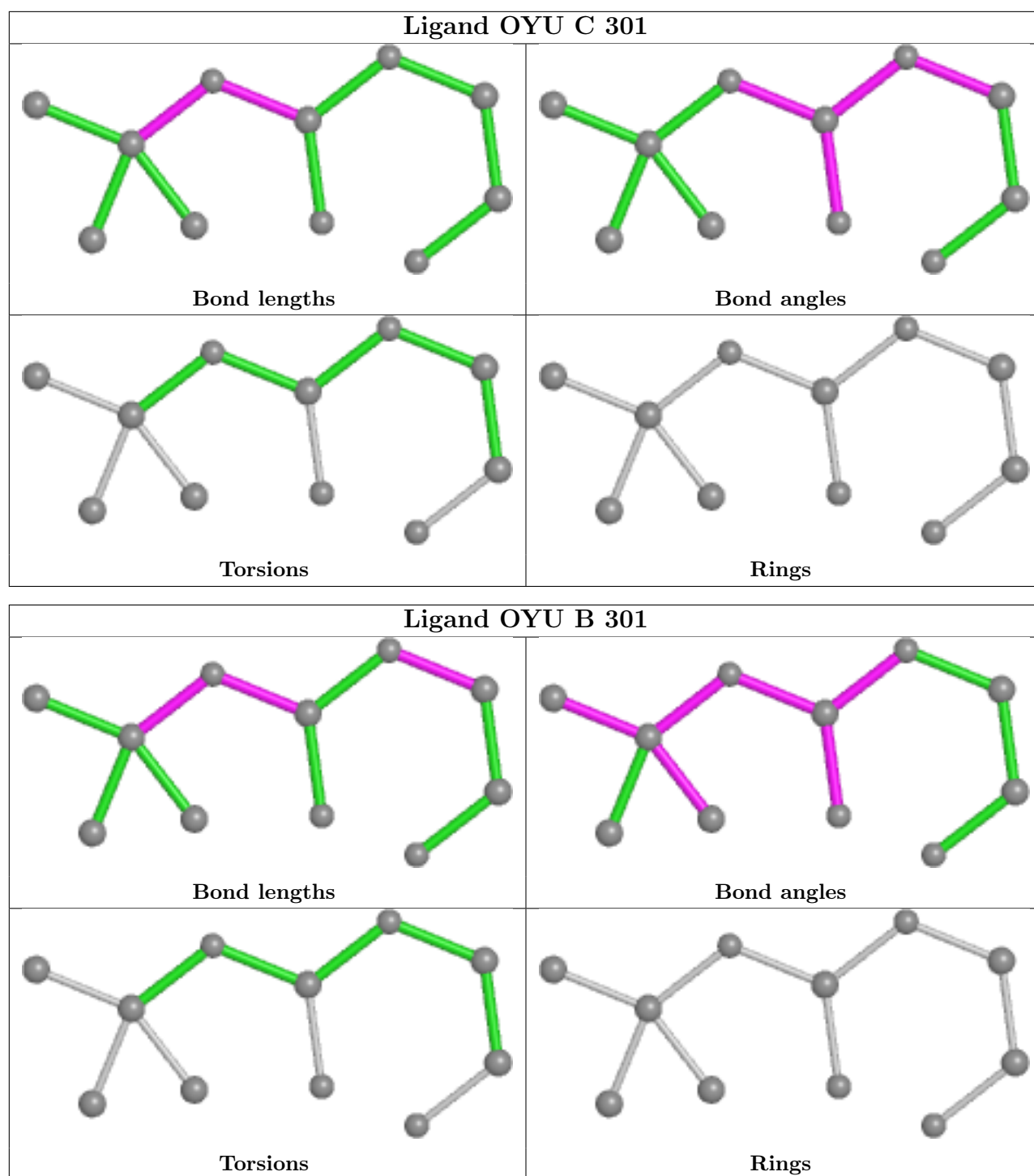
There are no ring outliers.

8 monomers are involved in 14 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	D	306	PEG	1	0
4	D	304	DMS	4	0
5	A	306	EDO	1	0
5	A	304	EDO	2	0
5	C	304	EDO	1	0
5	D	309	EDO	2	0
6	D	302	PEG	1	0
6	B	304	PEG	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 than 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.





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](#)

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

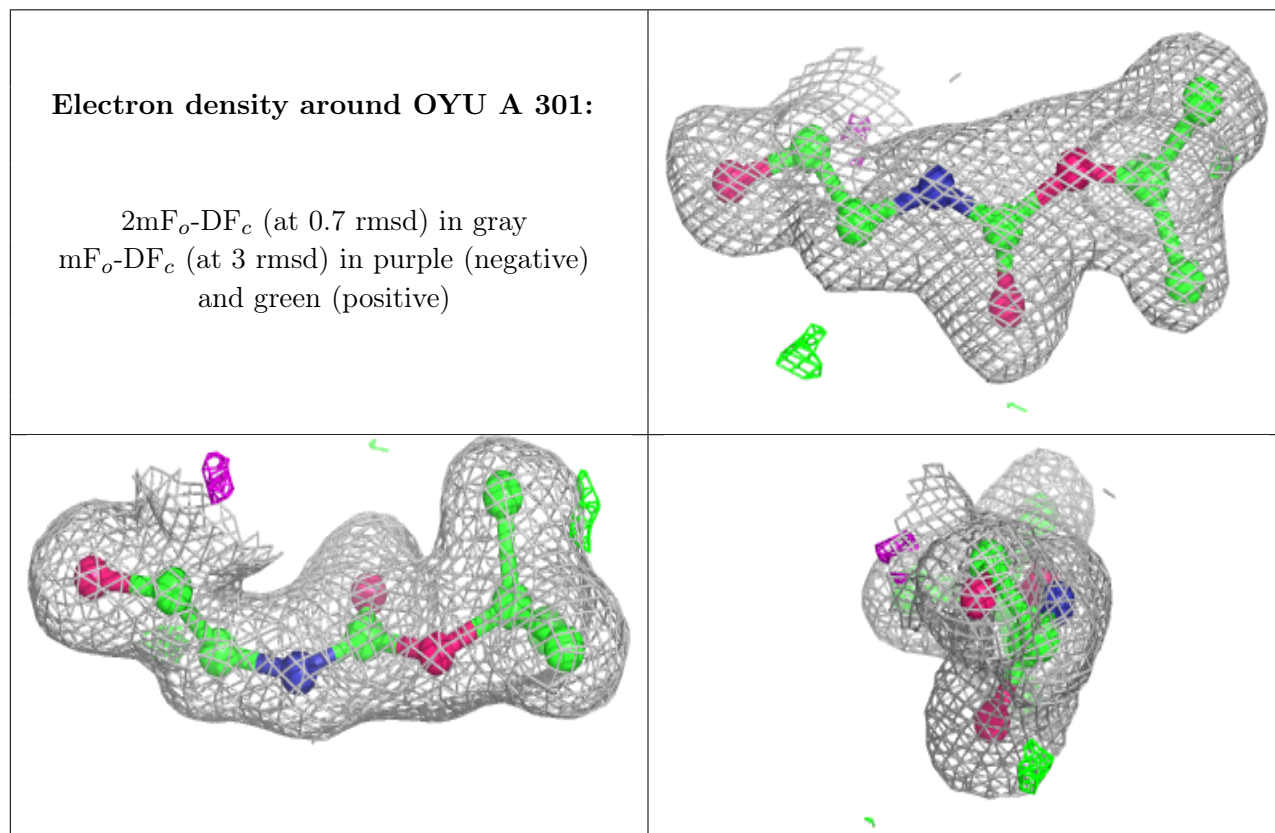
6.3 Carbohydrates [i](#)

Unable to reproduce the depositors R factor - this section is therefore empty.

6.4 Ligands [i](#)

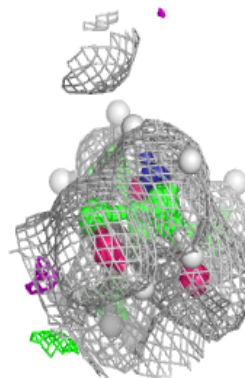
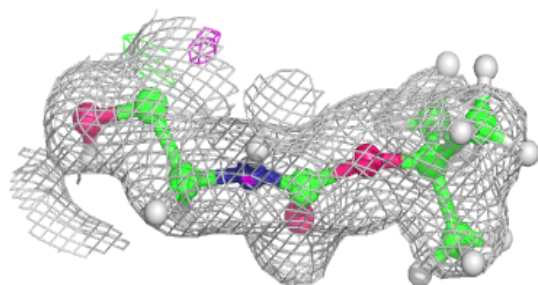
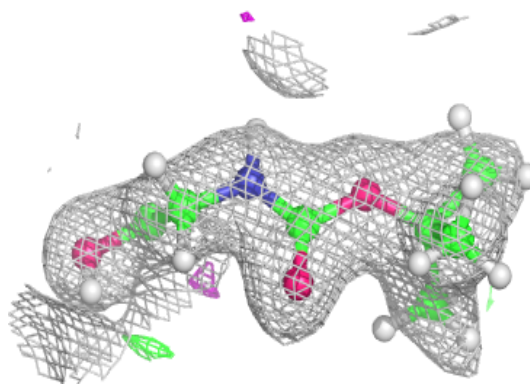
Unable to reproduce the depositors R factor - this section is therefore empty.

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.

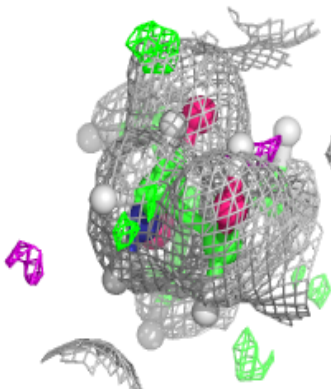
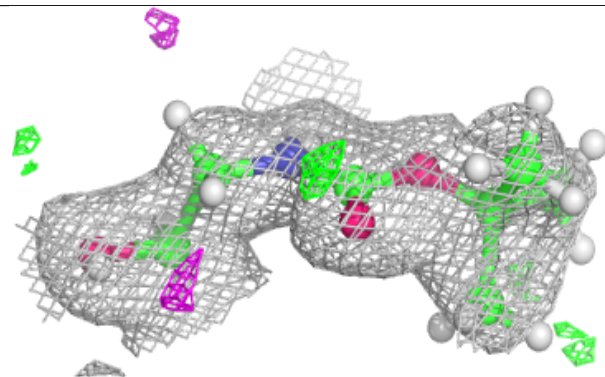
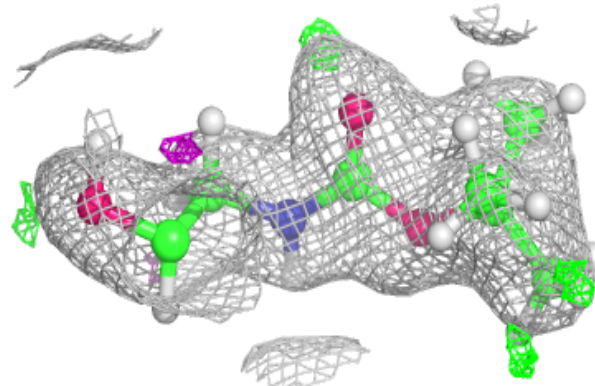


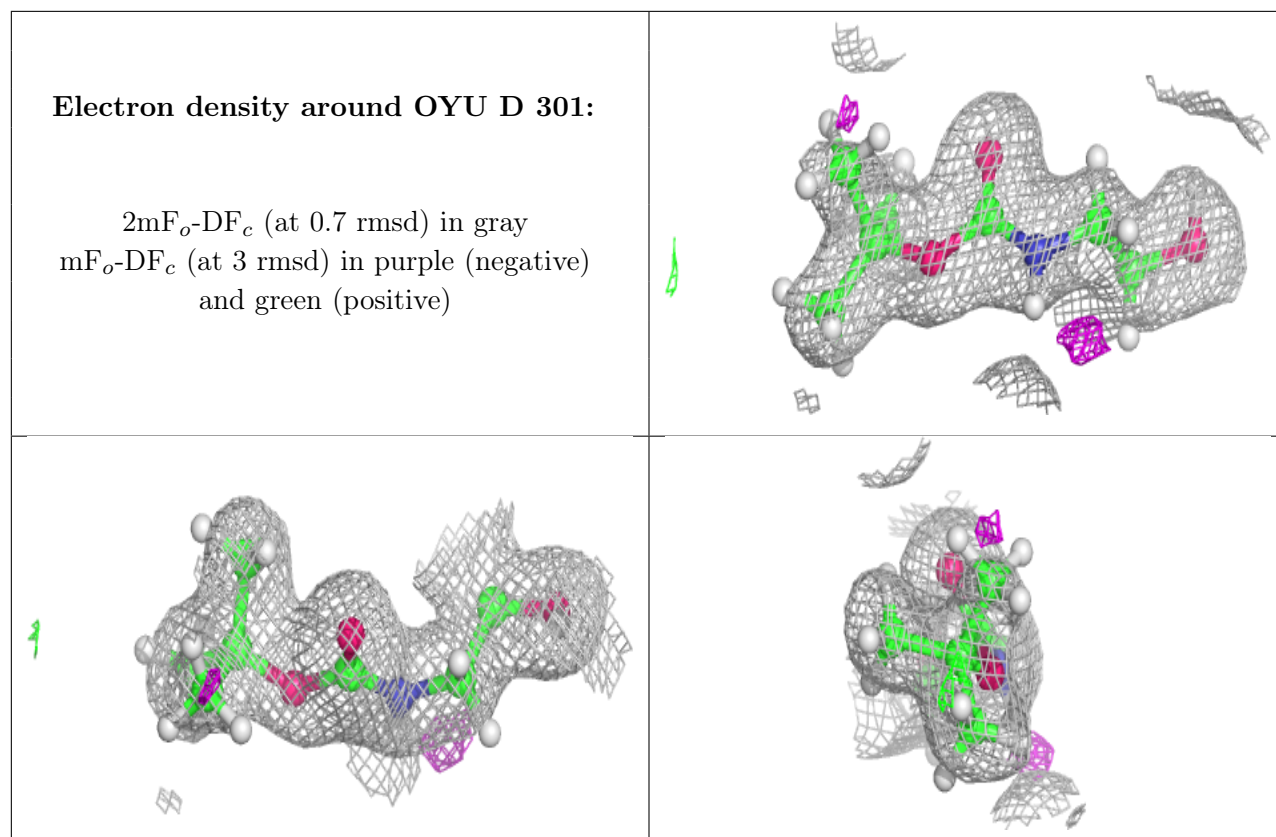
Electron density around OYU B 301:

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

**Electron density around OYU C 301:**

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





6.5 Other polymers [i](#)

Unable to reproduce the depositors R factor - this section is therefore empty.