



# Full wwPDB X-ray Structure Validation Report ⓘ

Sep 25, 2023 – 05:23 PM EDT

PDB ID : 6BW5  
Title : Human GPT (DPAGT1) in complex with tunicamycin  
Authors : Yoo, J.; Kuk, A.C.Y.; Mashalidis, E.H.; Lee, S.-Y.  
Deposited on : 2017-12-14  
Resolution : 3.10 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](mailto: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>.

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

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.35.1  
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

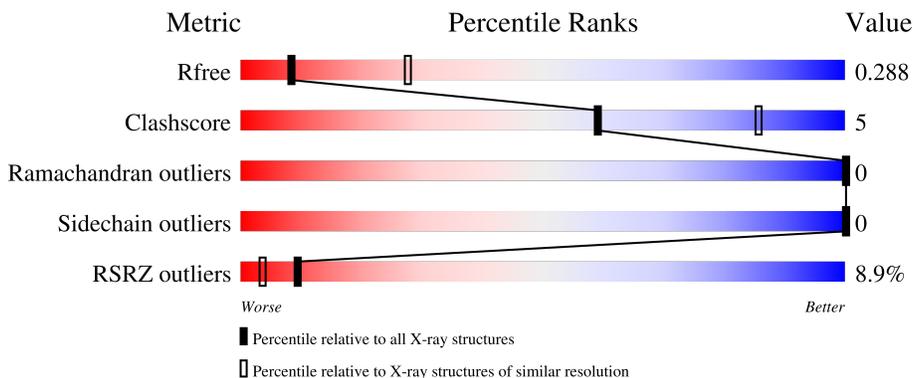
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.10 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	1094 (3.10-3.10)
Clashscore	141614	1184 (3.10-3.10)
Ramachandran outliers	138981	1141 (3.10-3.10)
Sidechain outliers	138945	1141 (3.10-3.10)
RSRZ outliers	127900	1067 (3.10-3.10)

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  $\geq 3$ , 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  $\leq 5\%$ . 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	417	 7% 81% 10% 9%
1	B	417	 7% 80% 9% 12%
1	C	417	 11% 77% 13% 10%
1	D	417	 6% 77% 10% 13%

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 22942 atoms, of which 11412 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 UDP-N-acetylglucosamine--dolichyl-phosphate N-acetylglucosaminephosphotransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
			Total	C	H	N	O				S
1	A	378	5749	1921	2874	454	480	20	0	0	0
1	B	369	5367	1822	2636	429	463	17	0	0	0
1	C	375	5662	1899	2820	449	475	19	0	0	0
1	D	362	5390	1825	2668	417	461	19	0	0	0

There are 36 discrepancies between the modelled and reference sequences:

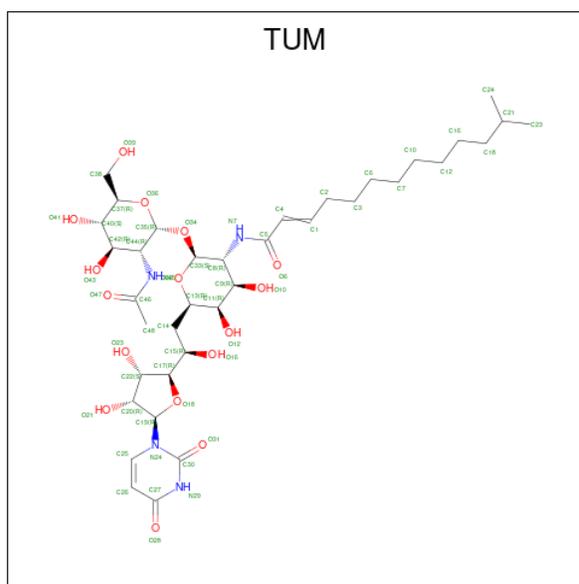
Chain	Residue	Modelled	Actual	Comment	Reference
A	409	THR	-	expression tag	UNP Q9H3H5
A	410	ASN	-	expression tag	UNP Q9H3H5
A	411	SER	-	expression tag	UNP Q9H3H5
A	412	LEU	-	expression tag	UNP Q9H3H5
A	413	GLU	-	expression tag	UNP Q9H3H5
A	414	VAL	-	expression tag	UNP Q9H3H5
A	415	LEU	-	expression tag	UNP Q9H3H5
A	416	PHE	-	expression tag	UNP Q9H3H5
A	417	GLN	-	expression tag	UNP Q9H3H5
B	409	THR	-	expression tag	UNP Q9H3H5
B	410	ASN	-	expression tag	UNP Q9H3H5
B	411	SER	-	expression tag	UNP Q9H3H5
B	412	LEU	-	expression tag	UNP Q9H3H5
B	413	GLU	-	expression tag	UNP Q9H3H5
B	414	VAL	-	expression tag	UNP Q9H3H5
B	415	LEU	-	expression tag	UNP Q9H3H5
B	416	PHE	-	expression tag	UNP Q9H3H5
B	417	GLN	-	expression tag	UNP Q9H3H5
C	409	THR	-	expression tag	UNP Q9H3H5
C	410	ASN	-	expression tag	UNP Q9H3H5

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Chain	Residue	Modelled	Actual	Comment	Reference
C	411	SER	-	expression tag	UNP Q9H3H5
C	412	LEU	-	expression tag	UNP Q9H3H5
C	413	GLU	-	expression tag	UNP Q9H3H5
C	414	VAL	-	expression tag	UNP Q9H3H5
C	415	LEU	-	expression tag	UNP Q9H3H5
C	416	PHE	-	expression tag	UNP Q9H3H5
C	417	GLN	-	expression tag	UNP Q9H3H5
D	409	THR	-	expression tag	UNP Q9H3H5
D	410	ASN	-	expression tag	UNP Q9H3H5
D	411	SER	-	expression tag	UNP Q9H3H5
D	412	LEU	-	expression tag	UNP Q9H3H5
D	413	GLU	-	expression tag	UNP Q9H3H5
D	414	VAL	-	expression tag	UNP Q9H3H5
D	415	LEU	-	expression tag	UNP Q9H3H5
D	416	PHE	-	expression tag	UNP Q9H3H5
D	417	GLN	-	expression tag	UNP Q9H3H5

- Molecule 2 is Tunicamycin (three-letter code: TUM) (formula: C<sub>37</sub>H<sub>60</sub>N<sub>4</sub>O<sub>16</sub>) (labeled as "Ligand of Interest" by depositor).



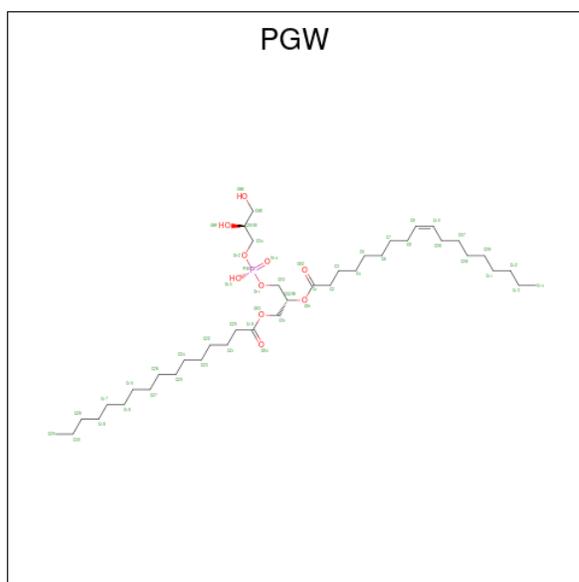
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
2	A	1	Total	C	H	N	O	0	0
				117	37	60	4		
2	B	1	Total	C	H	N	O	0	0
				117	37	60	4		
2	C	1	Total	C	H	N	O	0	0
				117	37	60	4		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	H	N	O		
2	D	1	117	37	60	4	16	0	0

- Molecule 3 is (1R)-2-{[(S)-{[(2S)-2,3-dihydroxypropyl]oxy}(hydroxy)phosphoryl]oxy}-1-[(hexadecanoyloxy)methyl]ethyl (9Z)-octadec-9-enoate (three-letter code: PGW) (formula: C<sub>40</sub>H<sub>77</sub>O<sub>10</sub>P).

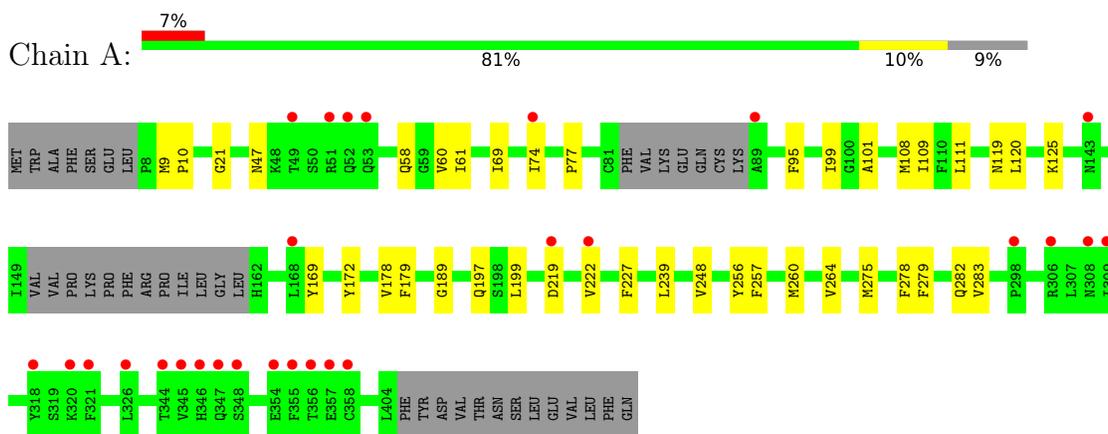


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	H	O	P		
3	A	1	69	22	39	7	1	0	0
3	B	1	79	24	45	9	1	0	0
3	C	1	79	24	45	9	1	0	0
3	D	1	79	24	45	9	1	0	0

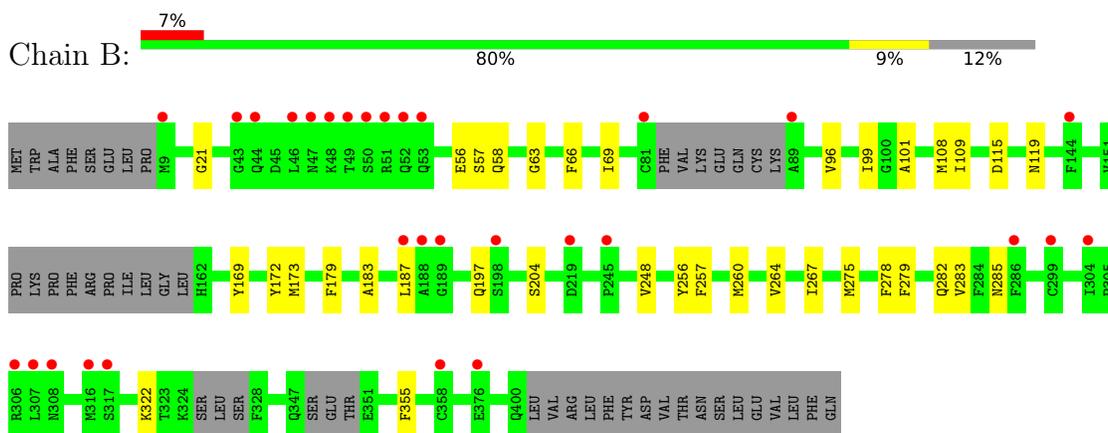
### 3 Residue-property plots [i](#)

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.

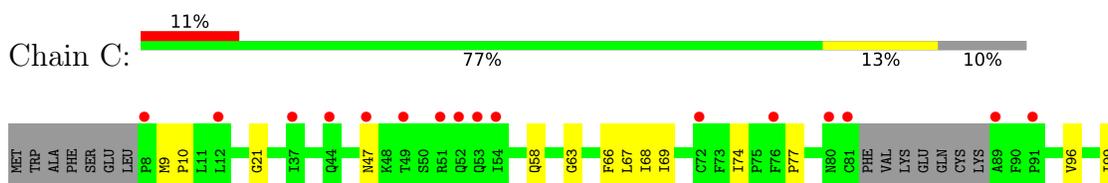
- Molecule 1: UDP-N-acetylglucosamine--dolichyl-phosphate N-acetylglucosaminophosphotransferase

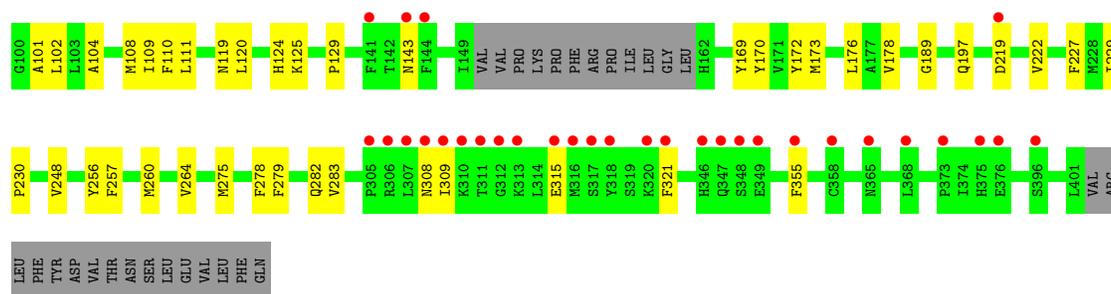


- Molecule 1: UDP-N-acetylglucosamine--dolichyl-phosphate N-acetylglucosaminophosphotransferase

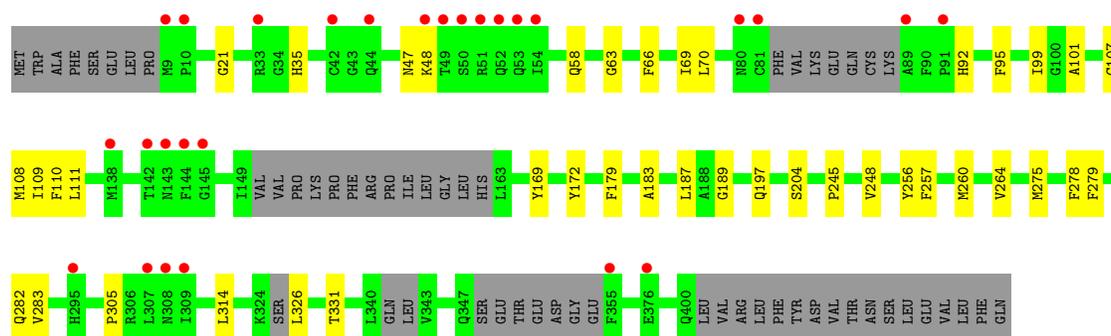
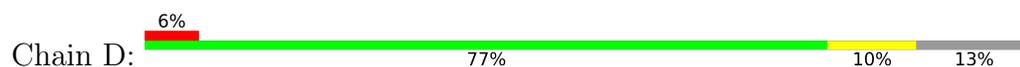


- Molecule 1: UDP-N-acetylglucosamine--dolichyl-phosphate N-acetylglucosaminophosphotransferase





- Molecule 1: UDP-N-acetylglucosamine--dolichyl-phosphate N-acetylglucosaminophosphotransferase



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	212.27Å 105.51Å 149.39Å 90.00° 103.53° 90.00°	Depositor
Resolution (Å)	83.05 – 3.10 95.30 – 3.10	Depositor EDS
% Data completeness (in resolution range)	60.1 (83.05-3.10) 56.2 (95.30-3.10)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.44 (at 3.13Å)	Xtrriage
Refinement program	PHENIX (1.12_2829: ???)	Depositor
R, $R_{free}$	0.256 , 0.288 0.257 , 0.288	Depositor DCC
$R_{free}$ test set	1763 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	45.3	Xtrriage
Anisotropy	0.453	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.27 , 40.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.74	EDS
Total number of atoms	22942	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	48.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.96% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: TUM, PGW

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	0.27	0/2949	0.46	0/4025
1	B	0.27	0/2799	0.43	0/3830
1	C	0.29	0/2916	0.45	0/3982
1	D	0.28	0/2791	0.44	0/3814
All	All	0.28	0/11455	0.45	0/15651

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	2875	2874	2873	25	0
1	B	2731	2636	2633	23	0
1	C	2842	2820	2820	37	0
1	D	2722	2668	2666	27	0
2	A	57	60	0	1	0
2	B	57	60	0	2	0
2	C	57	60	0	1	0
2	D	57	60	0	0	0
3	A	30	39	38	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	34	45	45	0	0
3	C	34	45	45	5	0
3	D	34	45	45	2	0
All	All	11530	11412	11165	107	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.

All (107) 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:197:GLN:OE1	1:B:282:GLN:NE2	2.23	0.71
1:A:119:ASN:OD1	2:A:501:TUM:O10	2.12	0.67
1:D:197:GLN:OE1	1:D:282:GLN:NE2	2.27	0.65
1:C:108:MET:HG2	1:C:260:MET:HB2	1.78	0.65
1:A:108:MET:HG2	1:A:260:MET:HB2	1.79	0.64
1:D:47:ASN:ND2	1:D:189:GLY:O	2.31	0.64
1:B:108:MET:HG3	1:B:256:TYR:HB3	1.80	0.64
1:B:108:MET:HG2	1:B:260:MET:HB2	1.82	0.62
1:A:108:MET:HG3	1:A:256:TYR:HB3	1.82	0.61
1:C:74:ILE:HD11	1:C:102:LEU:HD12	1.83	0.61
1:C:108:MET:HG3	1:C:256:TYR:HB3	1.83	0.59
1:A:47:ASN:ND2	1:A:189:GLY:O	2.35	0.58
1:C:101:ALA:HB1	1:C:264:VAL:HG11	1.85	0.58
1:C:197:GLN:OE1	1:C:282:GLN:NE2	2.31	0.57
1:D:108:MET:HG3	1:D:256:TYR:HB3	1.87	0.57
1:D:58:GLN:HG3	1:D:248:VAL:HB	1.87	0.56
1:A:58:GLN:HG3	1:A:248:VAL:HB	1.86	0.56
1:D:107:CYS:SG	3:D:502:PGW:H12	2.45	0.56
1:A:101:ALA:HB1	1:A:264:VAL:HG11	1.90	0.54
1:C:58:GLN:HG3	1:C:248:VAL:HB	1.91	0.53
1:C:47:ASN:ND2	1:C:189:GLY:O	2.40	0.52
1:B:179:PHE:O	1:B:183:ALA:N	2.38	0.52
1:D:108:MET:HG2	1:D:260:MET:HB2	1.93	0.51
1:A:197:GLN:OE1	1:A:282:GLN:NE2	2.39	0.50
1:C:109:ILE:HG12	1:C:257:PHE:HB2	1.92	0.50
1:A:120:LEU:O	1:A:125:LYS:NZ	2.42	0.50
1:B:58:GLN:HG3	1:B:248:VAL:HB	1.93	0.49
1:D:101:ALA:HB1	1:D:264:VAL:HG11	1.94	0.49
1:C:124:HIS:CE1	3:C:502:PGW:H03	2.48	0.49
1:C:21:GLY:HA3	1:C:69:ILE:HD11	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:101:ALA:HB1	1:B:264:VAL:HG11	1.95	0.48
1:C:74:ILE:HD11	1:C:102:LEU:CD1	2.44	0.47
1:A:109:ILE:HG12	1:A:257:PHE:HB2	1.95	0.47
1:C:110:PHE:HB2	1:D:110:PHE:HB2	1.96	0.47
1:B:187:LEU:HD23	1:B:197:GLN:OE1	2.13	0.47
1:C:229:ILE:HB	1:C:230:PRO:HD3	1.96	0.47
1:B:21:GLY:HA3	1:B:69:ILE:HD11	1.97	0.47
3:C:502:PGW:OAF	1:D:35:HIS:NE2	2.48	0.46
1:B:119:ASN:OD1	2:B:501:TUM:O10	2.33	0.46
1:B:322:LYS:HA	1:B:355:PHE:CD1	2.51	0.46
1:A:111:LEU:HA	3:A:502:PGW:H08A	1.98	0.45
1:C:308:ASN:ND2	1:C:315:GLU:OE2	2.49	0.45
1:D:109:ILE:HG12	1:D:257:PHE:HB2	1.98	0.45
1:B:204:SER:HB3	1:B:278:PHE:CE1	2.51	0.45
1:C:124:HIS:NE2	3:C:502:PGW:H05	2.32	0.45
1:D:111:LEU:HA	3:D:502:PGW:H08A	1.97	0.45
1:C:74:ILE:O	1:C:77:PRO:HD2	2.16	0.45
1:D:204:SER:HB3	1:D:278:PHE:CE1	2.50	0.45
1:C:99:ILE:HG22	1:D:99:ILE:HG22	1.98	0.45
1:A:111:LEU:HB2	3:A:502:PGW:H08A	1.99	0.44
1:C:170:TYR:HA	1:C:173:MET:HE2	1.99	0.44
1:C:111:LEU:HA	3:C:502:PGW:H08A	2.00	0.44
1:A:101:ALA:HB3	1:A:227:PHE:CZ	2.53	0.44
1:D:279:PHE:O	1:D:283:VAL:HG23	2.18	0.43
1:B:109:ILE:HG12	1:B:257:PHE:HB2	2.00	0.43
1:A:99:ILE:HG22	1:B:99:ILE:HG22	1.99	0.43
1:B:275:MET:HA	1:B:278:PHE:HD2	1.83	0.43
1:D:169:TYR:O	1:D:172:TYR:HB3	2.18	0.43
1:A:21:GLY:HA3	1:A:69:ILE:HD11	2.01	0.43
1:B:173:MET:SD	1:B:267:ILE:HG23	2.58	0.43
1:B:279:PHE:O	1:B:283:VAL:HG23	2.17	0.43
1:C:101:ALA:HB3	1:C:227:PHE:CZ	2.54	0.43
1:B:63:GLY:O	1:B:66:PHE:HB3	2.19	0.43
1:B:115:ASP:O	1:B:119:ASN:N	2.43	0.43
1:D:21:GLY:HA3	1:D:69:ILE:HD11	2.01	0.43
1:D:275:MET:O	1:D:278:PHE:N	2.52	0.43
1:A:169:TYR:O	1:A:172:TYR:HB3	2.19	0.43
1:C:143:ASN:OD1	1:D:92:HIS:NE2	2.52	0.43
1:C:275:MET:HA	1:C:278:PHE:HD2	1.83	0.43
1:B:187:LEU:HB2	1:B:285:ASN:HD22	1.84	0.42
1:C:119:ASN:OD1	2:C:501:TUM:O10	2.37	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:199:LEU:HD12	1:A:239:LEU:HD22	2.01	0.42
1:C:309:ILE:N	1:C:309:ILE:HD12	2.34	0.42
1:C:321:PHE:O	1:C:355:PHE:HB2	2.19	0.42
1:A:279:PHE:O	1:A:283:VAL:HG23	2.19	0.42
1:C:96:VAL:HG21	1:D:95:PHE:CD2	2.54	0.42
1:C:169:TYR:O	1:C:172:TYR:HB3	2.20	0.42
1:D:63:GLY:O	1:D:66:PHE:HB3	2.19	0.42
1:A:60:VAL:HG13	1:A:61:ILE:N	2.35	0.42
1:A:219:ASP:O	1:A:222:VAL:HG12	2.20	0.41
1:C:63:GLY:O	1:C:66:PHE:HB3	2.20	0.41
1:B:56:GLU:HG3	1:B:57:SER:N	2.35	0.41
1:C:129:PRO:HB2	1:C:178:VAL:HG22	2.02	0.41
1:A:95:PHE:CD2	1:B:96:VAL:HG21	2.55	0.41
1:D:275:MET:HA	1:D:278:PHE:HD2	1.85	0.41
1:C:67:LEU:O	1:C:68:ILE:C	2.59	0.41
1:C:120:LEU:O	1:C:125:LYS:NZ	2.51	0.41
1:C:219:ASP:O	1:C:222:VAL:HG12	2.20	0.41
1:D:66:PHE:CZ	1:D:70:LEU:HD11	2.56	0.41
1:A:74:ILE:O	1:A:77:PRO:HD2	2.20	0.41
1:B:275:MET:O	1:B:278:PHE:N	2.53	0.41
1:D:179:PHE:O	1:D:183:ALA:N	2.41	0.41
1:A:275:MET:HA	1:A:278:PHE:HD2	1.85	0.41
1:B:169:TYR:O	1:B:172:TYR:HB3	2.20	0.41
1:D:305:PRO:HB2	1:D:314:LEU:HB3	2.03	0.41
1:A:178:VAL:O	1:A:179:PHE:C	2.60	0.41
2:B:501:TUM:O41	2:B:501:TUM:O39	2.38	0.41
1:C:104:ALA:HB1	1:C:260:MET:CE	2.51	0.41
1:C:111:LEU:HB2	3:C:502:PGW:H08A	2.03	0.41
1:D:48:LYS:NZ	1:D:245:PRO:HB3	2.36	0.41
1:D:326:LEU:HD23	1:D:331:THR:HG22	2.02	0.41
1:C:9:MET:N	1:C:10:PRO:CD	2.84	0.41
1:C:279:PHE:O	1:C:283:VAL:HG23	2.20	0.41
1:D:187:LEU:HD23	1:D:197:GLN:OE1	2.21	0.40
1:A:9:MET:N	1:A:10:PRO:CD	2.84	0.40
1:C:173:MET:O	1:C:176:LEU:HB3	2.21	0.40
1:A:60:VAL:CG1	1:A:61:ILE:N	2.84	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	372/417 (89%)	361 (97%)	11 (3%)	0	100	100
1	B	359/417 (86%)	343 (96%)	16 (4%)	0	100	100
1	C	369/417 (88%)	357 (97%)	12 (3%)	0	100	100
1	D	350/417 (84%)	338 (97%)	12 (3%)	0	100	100
All	All	1450/1668 (87%)	1399 (96%)	51 (4%)	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	303/370 (82%)	303 (100%)	0	100	100
1	B	273/370 (74%)	273 (100%)	0	100	100
1	C	296/370 (80%)	296 (100%)	0	100	100
1	D	282/370 (76%)	282 (100%)	0	100	100
All	All	1154/1480 (78%)	1154 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	119	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$
3	PGW	B	502	-	33,33,50	0.88	2 (6%)	35,38,56	0.89	1 (2%)
2	TUM	C	501	-	60,60,60	1.70	13 (21%)	82,84,84	1.50	12 (14%)
2	TUM	B	501	-	60,60,60	1.71	13 (21%)	82,84,84	1.57	17 (20%)
3	PGW	C	502	-	33,33,50	0.91	2 (6%)	35,38,56	0.87	1 (2%)
3	PGW	D	502	-	33,33,50	0.87	2 (6%)	35,38,56	0.91	1 (2%)
3	PGW	A	502	-	29,29,50	0.89	2 (6%)	31,33,56	0.97	1 (3%)
2	TUM	D	501	-	60,60,60	1.69	14 (23%)	82,84,84	1.50	13 (15%)
2	TUM	A	501	-	60,60,60	1.71	13 (21%)	82,84,84	1.54	17 (20%)

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
3	PGW	B	502	-	-	15/37/37/55	-
2	TUM	C	501	-	-	10/39/95/95	0/4/4/4
2	TUM	B	501	-	-	13/39/95/95	0/4/4/4
3	PGW	C	502	-	-	15/37/37/55	-
3	PGW	D	502	-	-	8/37/37/55	-
3	PGW	A	502	-	-	11/32/32/55	-
2	TUM	D	501	-	-	12/39/95/95	0/4/4/4
2	TUM	A	501	-	-	12/39/95/95	0/4/4/4

All (61) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	501	TUM	C5-N7	5.78	1.48	1.34
2	A	501	TUM	C5-N7	5.69	1.48	1.34
2	C	501	TUM	C5-N7	5.67	1.47	1.34
2	D	501	TUM	C5-N7	5.59	1.47	1.34
2	B	501	TUM	O18-C17	3.91	1.50	1.44
2	A	501	TUM	O18-C17	3.80	1.49	1.44
2	A	501	TUM	C26-C27	-3.77	1.35	1.43
2	C	501	TUM	C26-C27	-3.76	1.35	1.43
2	D	501	TUM	C26-C27	-3.75	1.35	1.43
2	B	501	TUM	C26-C27	-3.68	1.35	1.43
2	C	501	TUM	O18-C17	3.66	1.49	1.44
2	D	501	TUM	O18-C17	3.65	1.49	1.44
2	B	501	TUM	O18-C19	3.63	1.50	1.42
2	A	501	TUM	O18-C19	3.60	1.50	1.42
2	D	501	TUM	O18-C19	3.55	1.50	1.42
2	C	501	TUM	O18-C19	3.51	1.50	1.42
2	B	501	TUM	C27-N29	-3.44	1.32	1.38
2	C	501	TUM	C27-N29	-3.38	1.32	1.38
2	A	501	TUM	C27-N29	-3.38	1.32	1.38
2	D	501	TUM	C27-N29	-3.35	1.32	1.38
2	A	501	TUM	C4-C5	3.15	1.54	1.48
2	B	501	TUM	C46-N45	3.11	1.45	1.34
2	D	501	TUM	C46-N45	3.10	1.45	1.34
2	C	501	TUM	C4-C5	3.06	1.54	1.48
2	A	501	TUM	C46-N45	3.06	1.44	1.34
2	C	501	TUM	C46-N45	3.00	1.44	1.34
2	B	501	TUM	C4-C5	2.98	1.54	1.48
2	A	501	TUM	O6-C5	-2.95	1.18	1.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	501	TUM	O6-C5	-2.93	1.18	1.24
2	C	501	TUM	O6-C5	-2.92	1.18	1.24
2	B	501	TUM	O6-C5	-2.86	1.18	1.24
2	D	501	TUM	C4-C5	2.81	1.54	1.48
2	C	501	TUM	O28-C27	-2.79	1.19	1.24
2	B	501	TUM	O28-C27	-2.77	1.19	1.24
2	D	501	TUM	O28-C27	-2.76	1.19	1.24
2	A	501	TUM	O28-C27	-2.72	1.19	1.24
2	A	501	TUM	C22-C20	-2.58	1.46	1.53
2	D	501	TUM	C22-C20	-2.50	1.46	1.53
2	C	501	TUM	C22-C20	-2.47	1.46	1.53
3	A	502	PGW	O01-C02	-2.47	1.40	1.46
2	A	501	TUM	C25-N24	-2.44	1.32	1.38
2	C	501	TUM	C25-N24	-2.43	1.32	1.38
2	B	501	TUM	C22-C20	-2.41	1.46	1.53
3	C	502	PGW	O01-C1	2.39	1.41	1.34
3	D	502	PGW	O01-C02	-2.36	1.40	1.46
2	D	501	TUM	C25-N24	-2.33	1.32	1.38
3	C	502	PGW	O01-C02	-2.32	1.40	1.46
3	B	502	PGW	O01-C02	-2.31	1.40	1.46
3	B	502	PGW	O01-C1	2.24	1.40	1.34
2	B	501	TUM	C25-N24	-2.23	1.32	1.38
2	C	501	TUM	O47-C46	-2.22	1.18	1.23
2	D	501	TUM	O47-C46	-2.22	1.18	1.23
3	D	502	PGW	O01-C1	2.21	1.40	1.34
2	A	501	TUM	O47-C46	-2.21	1.18	1.23
2	B	501	TUM	O47-C46	-2.20	1.18	1.23
2	D	501	TUM	O31-C30	-2.17	1.19	1.23
2	B	501	TUM	O31-C30	-2.16	1.19	1.23
3	A	502	PGW	O01-C1	2.11	1.40	1.34
2	C	501	TUM	O31-C30	-2.07	1.19	1.23
2	A	501	TUM	O31-C30	-2.06	1.19	1.23
2	D	501	TUM	C22-C17	-2.02	1.48	1.52

All (63) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	501	TUM	C27-N29-C30	-4.99	120.00	126.58
2	C	501	TUM	C27-N29-C30	-4.92	120.08	126.58
2	D	501	TUM	C27-N29-C30	-4.88	120.14	126.58
2	A	501	TUM	C27-N29-C30	-4.78	120.28	126.58
2	B	501	TUM	N29-C30-N24	4.20	120.47	114.89

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	501	TUM	C15-C17-C22	-4.19	110.25	115.86
3	B	502	PGW	O01-C1-C2	4.06	120.25	111.50
2	B	501	TUM	C2-C1-C4	-3.93	117.41	125.85
3	D	502	PGW	O01-C1-C2	3.90	119.92	111.50
3	A	502	PGW	O01-C1-C2	3.87	119.83	111.50
2	D	501	TUM	N29-C30-N24	3.84	119.98	114.89
2	C	501	TUM	N29-C30-N24	3.80	119.93	114.89
2	A	501	TUM	N29-C30-N24	3.79	119.92	114.89
3	C	502	PGW	O01-C1-C2	3.79	119.67	111.50
2	A	501	TUM	C15-C17-C22	-3.69	110.93	115.86
2	C	501	TUM	C15-C17-C22	-3.67	110.95	115.86
2	D	501	TUM	C2-C1-C4	-3.40	118.56	125.85
2	C	501	TUM	C26-C27-N29	3.38	119.89	114.84
2	D	501	TUM	C26-C27-N29	3.35	119.86	114.84
2	C	501	TUM	C14-C13-C11	-3.30	108.04	113.47
2	B	501	TUM	C26-C27-N29	3.28	119.75	114.84
2	A	501	TUM	C26-C27-N29	3.26	119.71	114.84
2	B	501	TUM	C40-C42-C44	-3.20	105.66	110.34
2	C	501	TUM	C2-C1-C4	-3.14	119.11	125.85
2	B	501	TUM	C22-C20-C19	3.04	107.20	101.43
2	C	501	TUM	O28-C27-C26	-3.03	119.83	125.16
2	C	501	TUM	C22-C20-C19	2.97	107.07	101.43
2	D	501	TUM	O28-C27-C26	-2.96	119.95	125.16
2	A	501	TUM	O28-C27-C26	-2.94	119.99	125.16
2	B	501	TUM	C48-C46-N45	2.91	121.02	116.10
2	A	501	TUM	C2-C1-C4	-2.89	119.64	125.85
2	D	501	TUM	C22-C20-C19	2.84	106.83	101.43
2	B	501	TUM	O28-C27-C26	-2.81	120.22	125.16
2	C	501	TUM	C20-C22-C17	2.79	106.48	102.45
2	A	501	TUM	C22-C20-C19	2.75	106.65	101.43
2	B	501	TUM	C15-C17-C22	-2.68	112.28	115.86
2	A	501	TUM	C35-O36-C37	2.64	118.87	113.69
2	D	501	TUM	C20-C22-C17	2.58	106.18	102.45
2	A	501	TUM	C48-C46-N45	2.56	120.44	116.10
2	A	501	TUM	C14-C13-C11	-2.52	109.33	113.47
2	B	501	TUM	O31-C30-N24	-2.50	119.47	122.79
2	A	501	TUM	C19-N24-C30	2.48	122.06	117.57
2	B	501	TUM	C17-O18-C19	-2.45	102.82	108.32
2	A	501	TUM	C4-C5-N7	2.40	119.18	114.56
2	A	501	TUM	C38-C37-C40	-2.39	107.41	113.00
2	B	501	TUM	C20-C22-C17	2.37	105.87	102.45
2	D	501	TUM	C48-C46-N45	2.32	120.03	116.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	501	TUM	C40-C42-C44	-2.23	107.07	110.34
2	B	501	TUM	O18-C19-N24	2.22	113.45	108.36
2	C	501	TUM	C11-C9-C8	-2.22	107.09	110.34
2	D	501	TUM	C38-C37-C40	-2.22	107.81	113.00
2	A	501	TUM	C11-C9-C8	-2.15	107.20	110.34
2	D	501	TUM	O32-C33-C8	-2.15	106.39	110.58
2	A	501	TUM	C44-N45-C46	-2.13	117.99	123.18
2	B	501	TUM	O32-C33-C8	-2.11	106.45	110.58
2	B	501	TUM	C42-C40-C37	-2.09	106.52	110.24
2	D	501	TUM	O31-C30-N24	-2.09	120.01	122.79
2	B	501	TUM	C35-O34-C33	-2.08	110.71	114.42
2	C	501	TUM	O31-C30-N24	-2.06	120.04	122.79
2	A	501	TUM	O31-C30-N24	-2.04	120.07	122.79
2	D	501	TUM	C19-N24-C30	2.02	121.23	117.57
2	C	501	TUM	C40-C42-C44	-2.02	107.39	110.34
2	B	501	TUM	C44-N45-C46	-2.01	118.29	123.18

There are no chirality outliers.

All (96) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	501	TUM	C33-C8-N7-C5
2	A	501	TUM	C35-C44-N45-C46
2	B	501	TUM	C33-C8-N7-C5
2	C	501	TUM	C33-C8-N7-C5
2	D	501	TUM	C33-C8-N7-C5
3	A	502	PGW	C03-O11-P-O13
3	A	502	PGW	C03-O11-P-O14
3	B	502	PGW	C04-O12-P-O11
3	B	502	PGW	C04-O12-P-O13
3	B	502	PGW	C04-O12-P-O14
3	B	502	PGW	O03-C01-C02-O01
3	B	502	PGW	O03-C01-C02-C03
3	C	502	PGW	C03-O11-P-O12
3	C	502	PGW	C03-O11-P-O13
3	C	502	PGW	C03-O11-P-O14
3	C	502	PGW	O03-C01-C02-O01
3	C	502	PGW	O03-C01-C02-C03
3	D	502	PGW	C04-O12-P-O11
2	B	501	TUM	C40-C37-C38-O39
2	B	501	TUM	O36-C37-C38-O39
2	A	501	TUM	C1-C4-C5-N7

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Mol	Chain	Res	Type	Atoms
3	B	502	PGW	C1-C2-C3-C4
3	C	502	PGW	C1-C2-C3-C4
2	A	501	TUM	C1-C4-C5-O6
3	B	502	PGW	O12-C04-C05-OAF
3	C	502	PGW	O12-C04-C05-OAF
3	A	502	PGW	C03-O11-P-O12
3	C	502	PGW	O12-C04-C05-CAD
2	D	501	TUM	C16-C18-C21-C24
2	C	501	TUM	C16-C18-C21-C23
2	C	501	TUM	C16-C18-C21-C24
2	D	501	TUM	C16-C18-C21-C23
2	B	501	TUM	C2-C3-C6-C7
3	B	502	PGW	O12-C04-C05-CAD
2	B	501	TUM	C35-C44-N45-C46
2	D	501	TUM	C2-C3-C6-C7
3	A	502	PGW	C07-C08-C09-C11
3	A	502	PGW	C1-C2-C3-C4
3	B	502	PGW	C06-C07-C08-C09
3	B	502	PGW	C07-C08-C09-C11
3	B	502	PGW	C2-C1-O01-C02
3	D	502	PGW	C1-C2-C3-C4
2	B	501	TUM	C16-C18-C21-C23
3	B	502	PGW	C2-C3-C4-C5
3	B	502	PGW	C4-C5-C6-C7
2	B	501	TUM	C16-C18-C21-C24
2	D	501	TUM	C1-C2-C3-C6
3	B	502	PGW	O02-C1-O01-C02
3	A	502	PGW	C01-C02-C03-O11
2	A	501	TUM	C2-C3-C6-C7
3	A	502	PGW	O01-C02-C03-O11
2	D	501	TUM	C13-C14-C15-O16
3	D	502	PGW	C4-C5-C6-C7
2	B	501	TUM	C1-C4-C5-O6
3	C	502	PGW	C5-C6-C7-C8
2	D	501	TUM	C13-C14-C15-C17
3	C	502	PGW	C4-C5-C6-C7
3	D	502	PGW	C09-C11-C12-C13
2	B	501	TUM	C1-C4-C5-N7
3	C	502	PGW	C2-C3-C4-C5
3	C	502	PGW	C7-C8-C9-C10
3	C	502	PGW	C04-O12-P-O11
2	A	501	TUM	C3-C6-C7-C10

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Mol	Chain	Res	Type	Atoms
2	D	501	TUM	C4-C1-C2-C3
2	A	501	TUM	C7-C10-C12-C16
3	A	502	PGW	C02-C03-O11-P
3	C	502	PGW	C6-C7-C8-C9
2	C	501	TUM	C4-C1-C2-C3
3	D	502	PGW	C07-C08-C09-C11
2	C	501	TUM	C1-C4-C5-O6
2	D	501	TUM	C7-C10-C12-C16
3	A	502	PGW	C06-C07-C08-C09
2	D	501	TUM	C12-C10-C7-C6
2	C	501	TUM	C14-C15-C17-C22
2	A	501	TUM	C4-C1-C2-C3
2	C	501	TUM	O36-C37-C38-O39
2	D	501	TUM	C9-C8-N7-C5
2	A	501	TUM	C16-C18-C21-C23
3	C	502	PGW	C06-C07-C08-C09
2	C	501	TUM	C1-C4-C5-N7
3	D	502	PGW	C2-C3-C4-C5
3	A	502	PGW	C10-C06-C07-C08
3	D	502	PGW	C6-C7-C8-C9
2	A	501	TUM	C9-C8-N7-C5
3	B	502	PGW	O01-C02-C03-O11
3	A	502	PGW	C7-C8-C9-C10
2	A	501	TUM	C16-C18-C21-C24
2	B	501	TUM	C4-C1-C2-C3
2	A	501	TUM	C42-C44-N45-C46
2	C	501	TUM	C14-C15-C17-O18
2	B	501	TUM	C3-C6-C7-C10
2	B	501	TUM	C9-C8-N7-C5
2	B	501	TUM	C42-C44-N45-C46
2	C	501	TUM	C9-C8-N7-C5
3	D	502	PGW	O01-C02-C03-O11
2	D	501	TUM	O36-C37-C38-O39

There are no ring outliers.

6 monomers are involved in 13 short contacts:

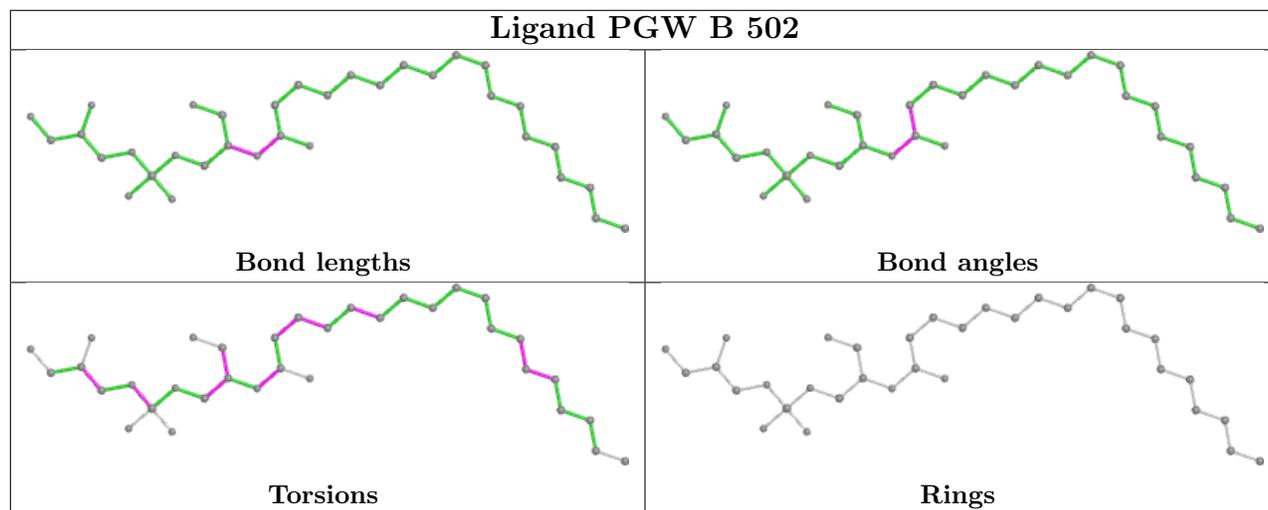
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	501	TUM	1	0
2	B	501	TUM	2	0
3	C	502	PGW	5	0
3	D	502	PGW	2	0

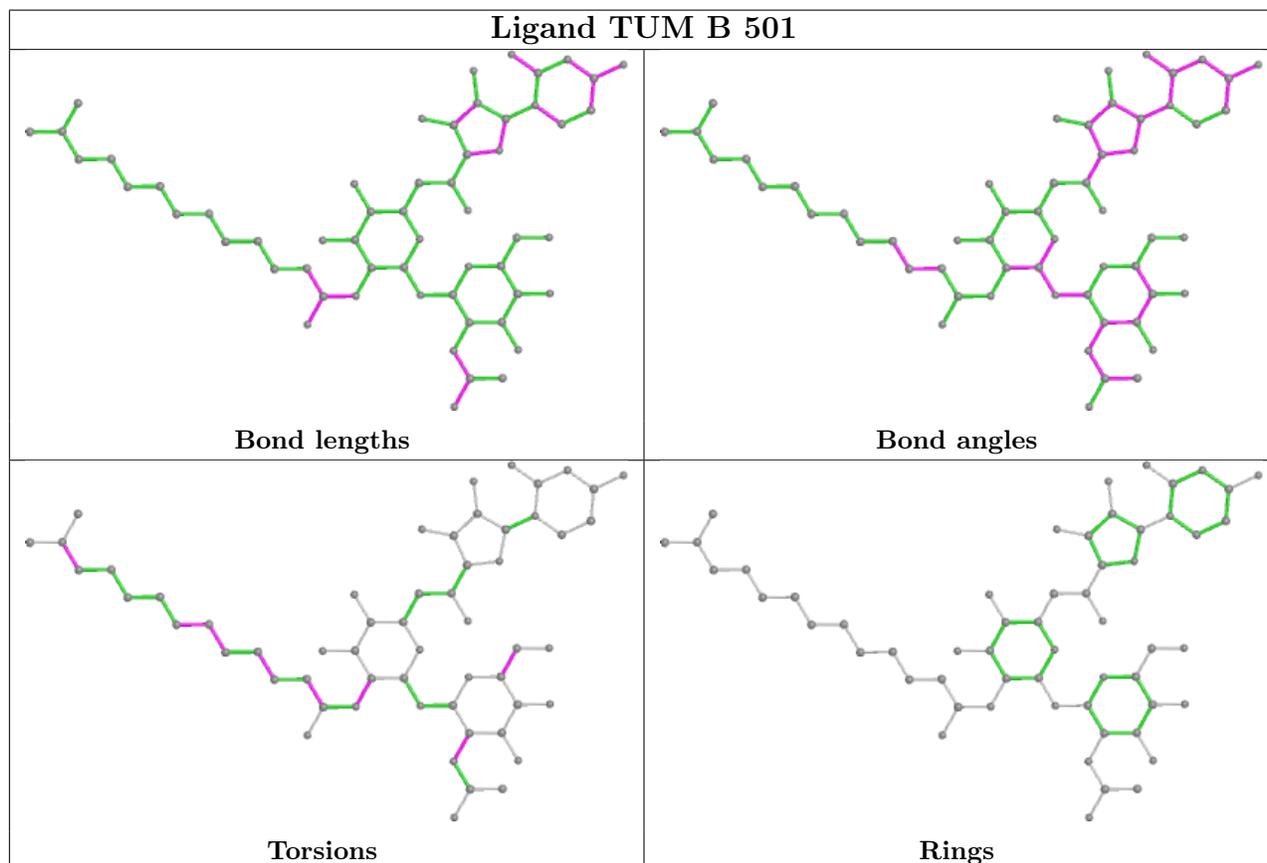
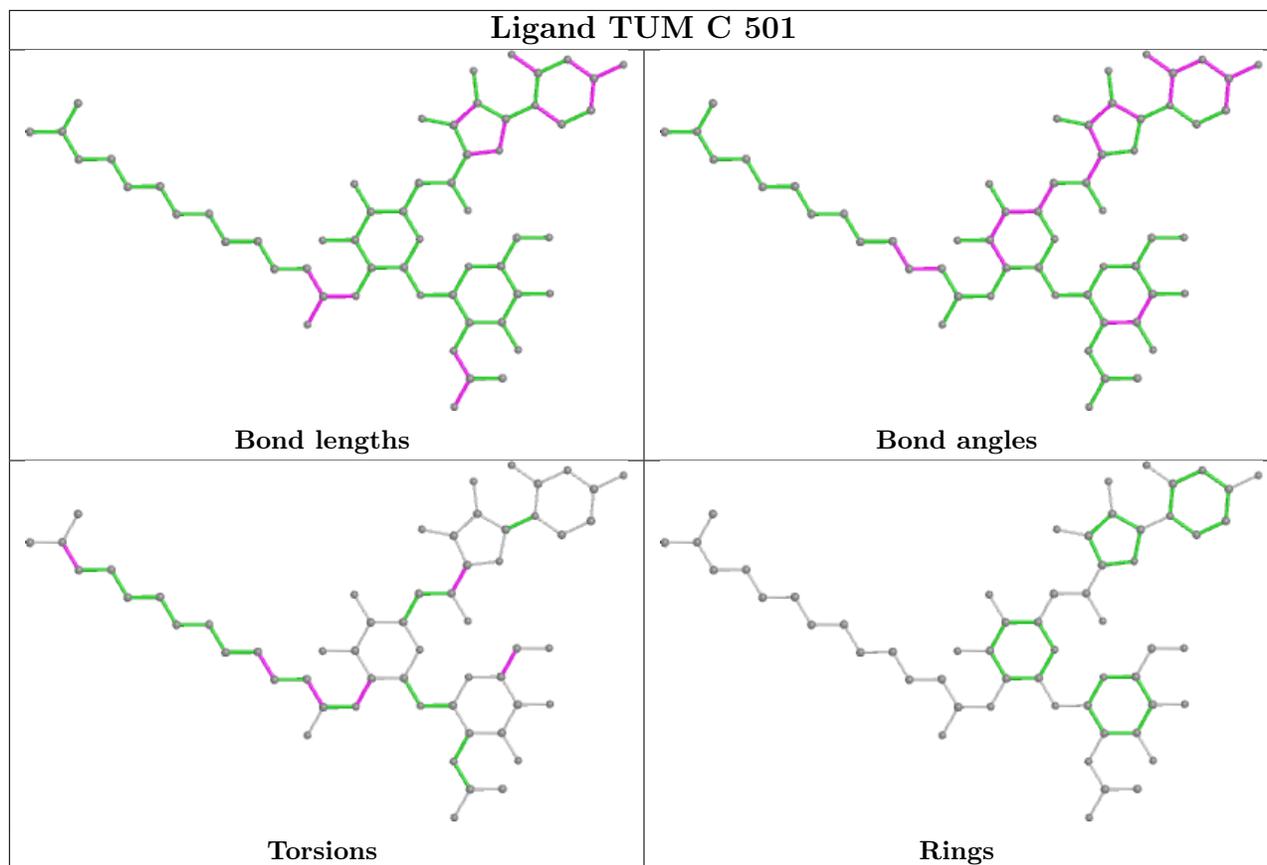
*Continued on next page...*

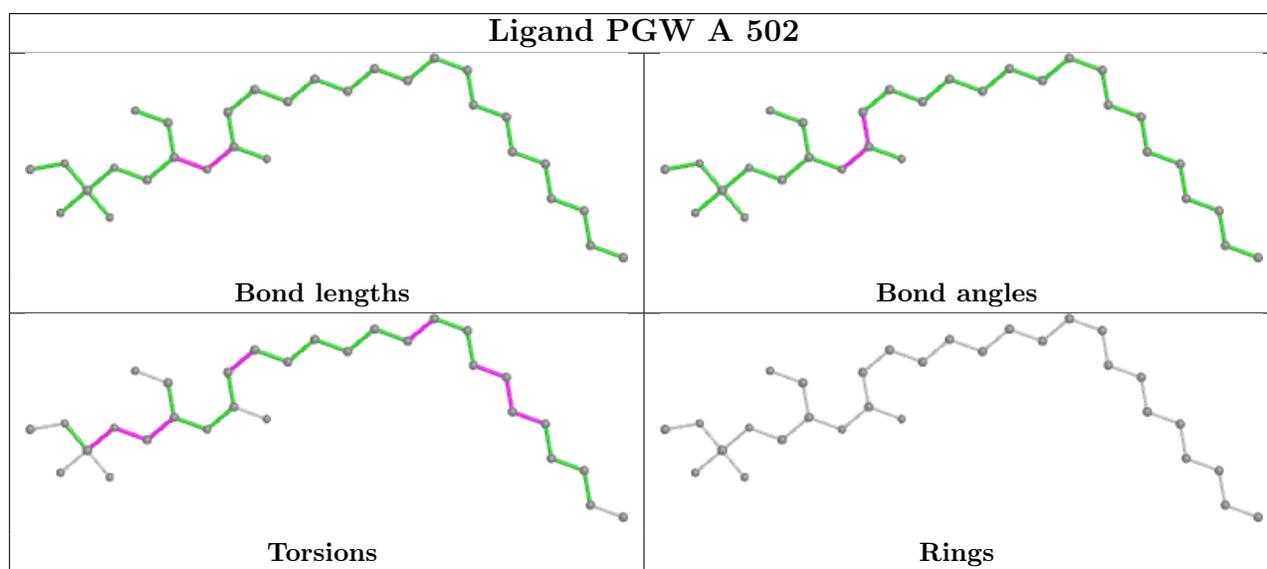
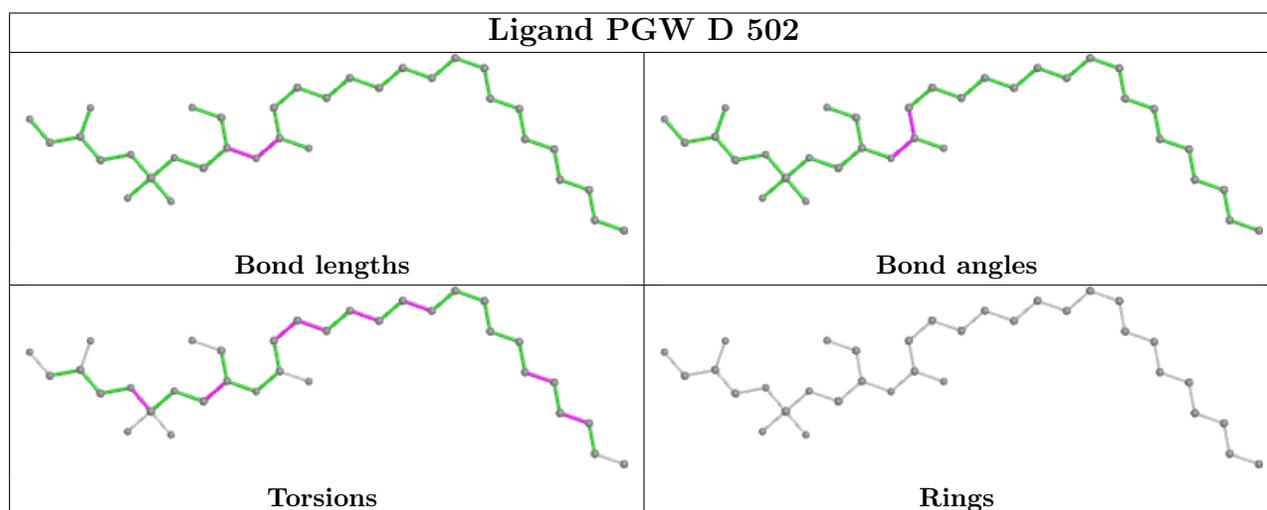
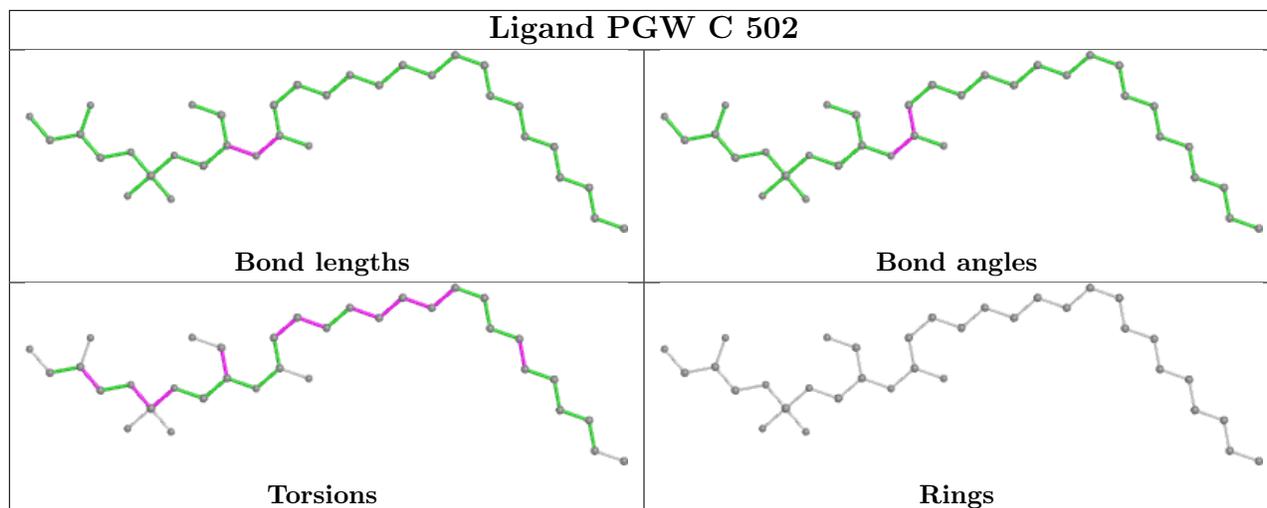
*Continued from previous page...*

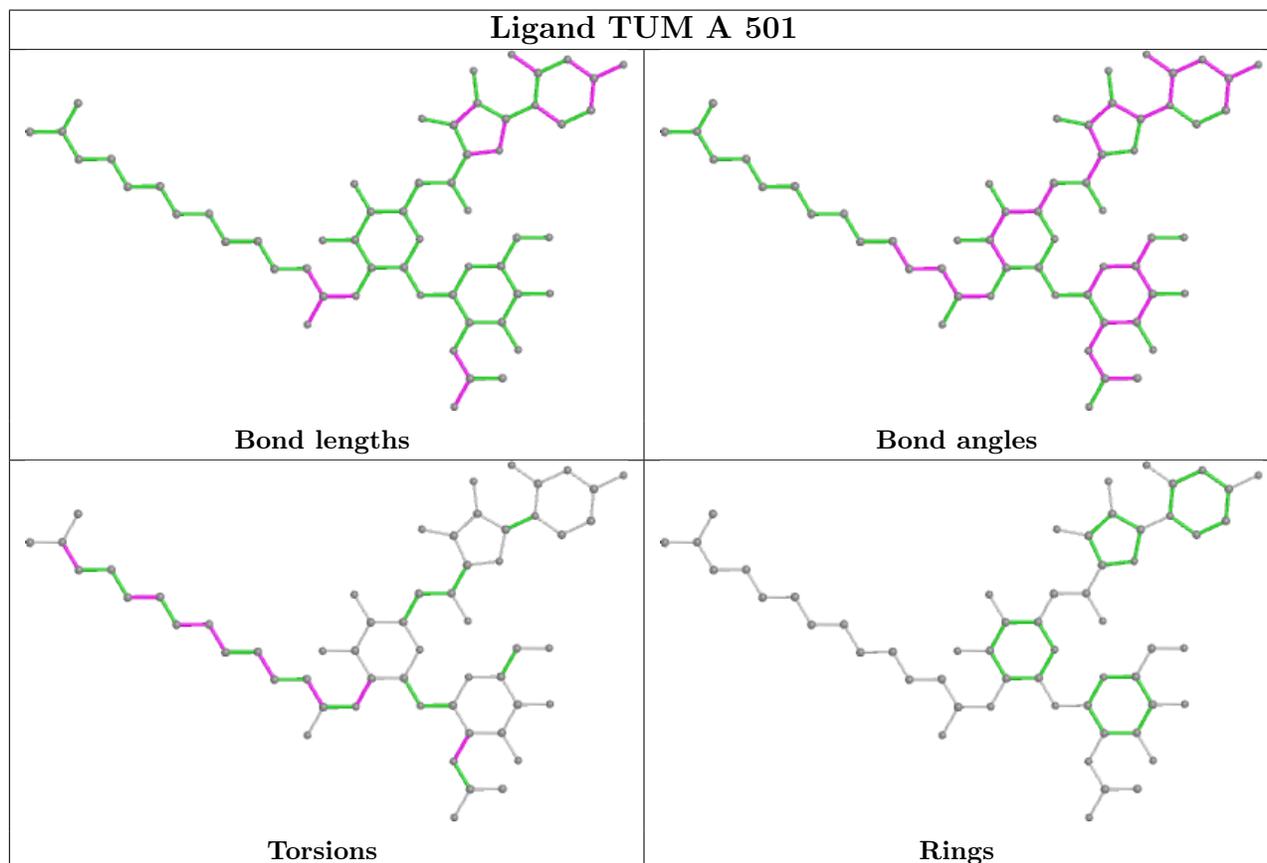
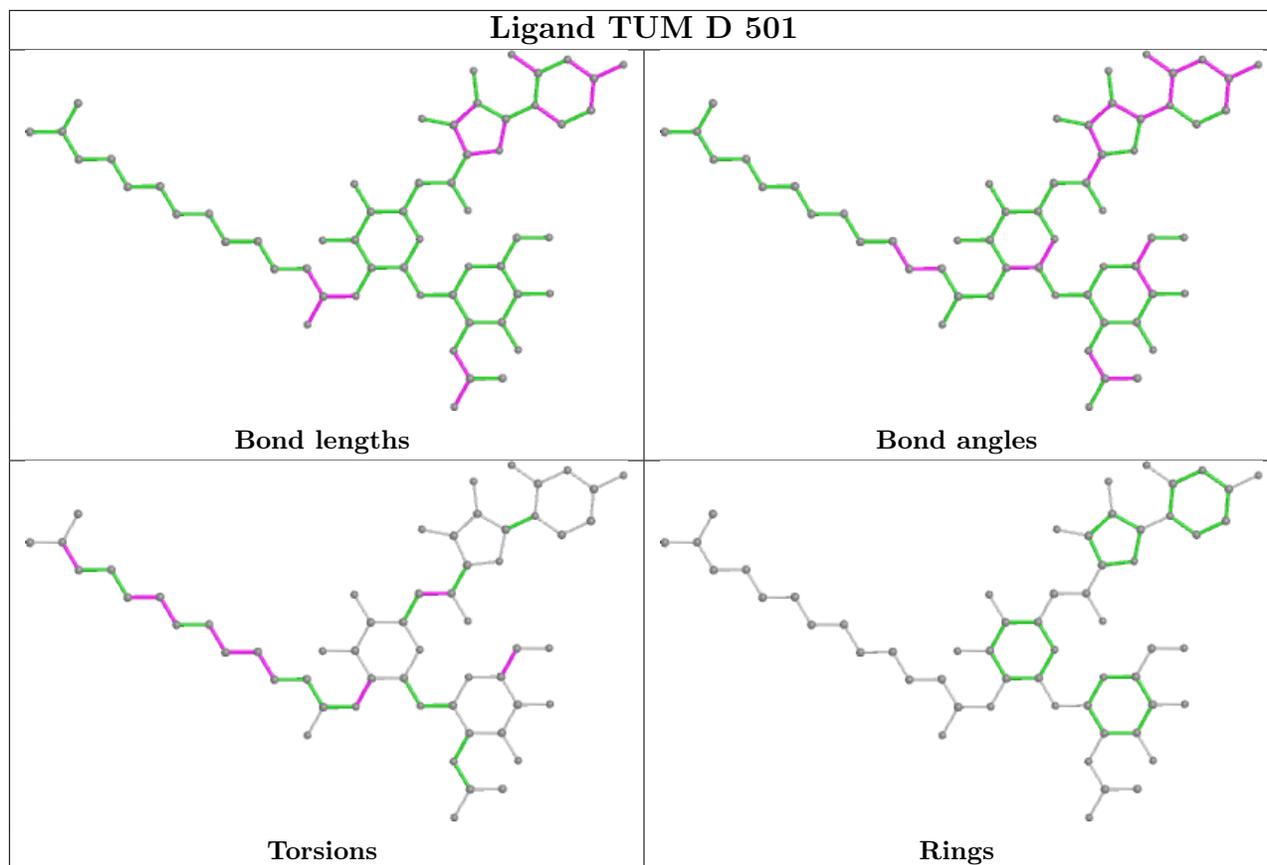
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	502	PGW	2	0
2	A	501	TUM	1	0

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 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](#)

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<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	378/417 (90%)	0.35	28 (7%) 14 5	4, 31, 79, 121	0
1	B	369/417 (88%)	0.46	30 (8%) 12 5	10, 51, 103, 127	0
1	C	375/417 (89%)	0.55	47 (12%) 3 1	6, 38, 109, 127	0
1	D	362/417 (86%)	0.31	27 (7%) 14 5	7, 44, 89, 123	0
All	All	1484/1668 (88%)	0.42	132 (8%) 9 3	4, 40, 97, 127	0

All (132) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	52	GLN	6.9
1	C	308	ASN	6.6
1	A	348	SER	6.5
1	B	188	ALA	6.2
1	D	49	THR	6.1
1	A	358	CYS	6.1
1	B	307	LEU	5.9
1	C	311	THR	5.8
1	C	53	GLN	5.7
1	B	52	GLN	5.6
1	B	44	GLN	5.6
1	C	348	SER	5.6
1	D	51	ARG	5.4
1	C	309	ILE	5.4
1	D	309	ILE	5.2
1	A	357	GLU	5.1
1	A	355	PHE	5.0
1	B	358	CYS	5.0
1	A	52	GLN	4.9
1	B	189	GLY	4.8
1	A	53	GLN	4.7

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	D	9	MET	4.6
1	D	89	ALA	4.6
1	C	313	LYS	4.6
1	D	52	GLN	4.5
1	C	358	CYS	4.4
1	C	44	GLN	4.3
1	D	10	PRO	4.2
1	C	310	LYS	4.1
1	B	316	MET	4.1
1	D	307	LEU	4.1
1	B	51	ARG	4.0
1	C	305	PRO	3.9
1	C	346	HIS	3.9
1	C	355	PHE	3.8
1	C	315	GLU	3.8
1	C	312	GLY	3.8
1	B	47	ASN	3.8
1	C	49	THR	3.8
1	C	368	LEU	3.8
1	C	347	GLN	3.7
1	D	143	ASN	3.7
1	B	50	SER	3.7
1	A	306	ARG	3.6
1	C	307	LEU	3.6
1	D	53	GLN	3.5
1	C	306	ARG	3.5
1	C	373	PRO	3.4
1	B	304	ILE	3.4
1	C	316	MET	3.4
1	C	80	ASN	3.4
1	A	345	VAL	3.3
1	B	46	LEU	3.3
1	A	321	PHE	3.2
1	B	219	ASP	3.2
1	D	44	GLN	3.2
1	A	354	GLU	3.2
1	C	318	TYR	3.1
1	C	365	ASN	3.1
1	C	72	CYS	3.1
1	D	144	PHE	3.0
1	C	37	ILE	3.0
1	B	43	GLY	3.0

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	D	308	ASN	3.0
1	B	308	ASN	3.0
1	C	321	PHE	3.0
1	C	143	ASN	2.9
1	C	144	PHE	2.9
1	B	81	CYS	2.9
1	A	298	PRO	2.8
1	D	42	CYS	2.8
1	A	168	LEU	2.8
1	D	138	MET	2.8
1	A	49	THR	2.8
1	B	53	GLN	2.7
1	D	376	GLU	2.7
1	A	74	ILE	2.7
1	C	89	ALA	2.7
1	D	33	ARG	2.6
1	C	396	SER	2.6
1	B	49	THR	2.6
1	A	309	ILE	2.6
1	A	347	GLN	2.6
1	B	306	ARG	2.6
1	C	317	SER	2.6
1	A	346	HIS	2.6
1	D	142	THR	2.6
1	D	50	SER	2.5
1	A	308	ASN	2.5
1	C	12	LEU	2.5
1	C	51	ARG	2.5
1	B	89	ALA	2.5
1	B	286	PHE	2.4
1	A	326	LEU	2.4
1	C	81	CYS	2.4
1	C	54	ILE	2.4
1	A	51	ARG	2.4
1	D	91	PRO	2.4
1	D	295	HIS	2.4
1	B	376	GLU	2.3
1	A	222	VAL	2.3
1	C	375	HIS	2.3
1	C	320	LYS	2.3
1	A	219	ASP	2.3
1	A	344	THR	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	356	THR	2.3
1	D	81	CYS	2.2
1	C	8	PRO	2.2
1	B	198	SER	2.2
1	B	245	PRO	2.2
1	A	143	ASN	2.2
1	D	145	GLY	2.2
1	B	317	SER	2.2
1	C	376	GLU	2.2
1	D	80	ASN	2.2
1	D	54	ILE	2.2
1	B	48	LYS	2.1
1	C	47	ASN	2.1
1	A	320	LYS	2.1
1	B	187	LEU	2.1
1	A	318	TYR	2.1
1	B	9	MET	2.1
1	C	91	PRO	2.1
1	D	355	PHE	2.1
1	D	48	LYS	2.1
1	A	89	ALA	2.1
1	B	299	CYS	2.1
1	C	141	PHE	2.0
1	B	144	PHE	2.0
1	C	76	PHE	2.0
1	C	349	GLU	2.0
1	C	219	ASP	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.

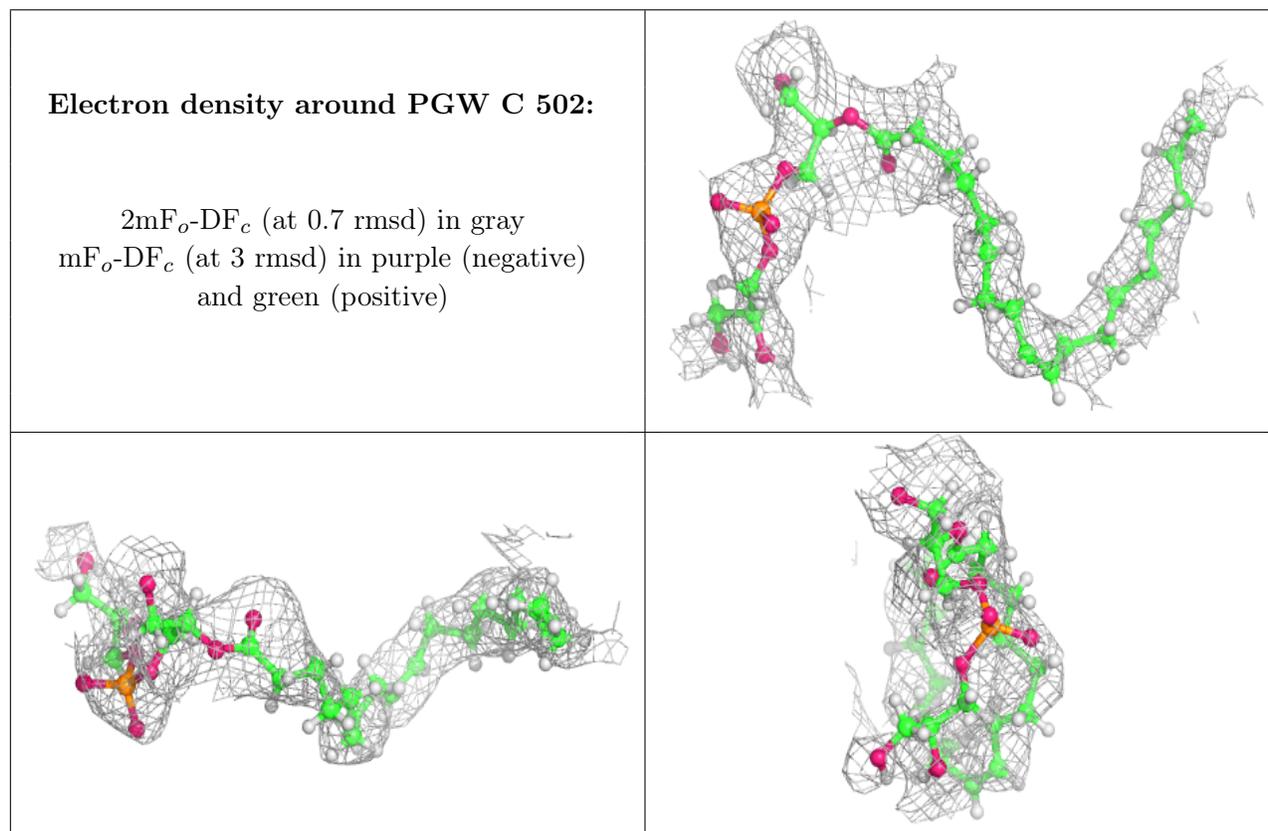
## 6.4 Ligands [i](#)

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<sup>th</sup> 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.

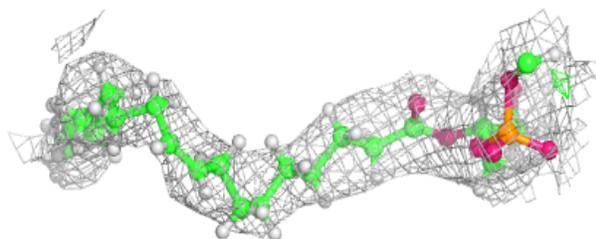
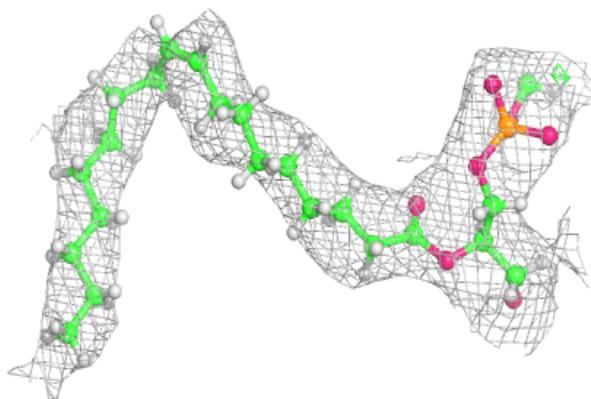
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
3	PGW	C	502	34/51	0.84	0.34	19,63,122,128	0
3	PGW	A	502	30/51	0.86	0.27	23,49,139,159	0
3	PGW	B	502	34/51	0.87	0.30	19,48,118,128	0
3	PGW	D	502	34/51	0.88	0.35	14,42,106,118	0
2	TUM	B	501	57/57	0.90	0.28	25,59,82,92	0
2	TUM	D	501	57/57	0.92	0.29	25,58,89,116	0
2	TUM	C	501	57/57	0.93	0.25	16,40,65,78	0
2	TUM	A	501	57/57	0.93	0.21	8,29,47,53	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.

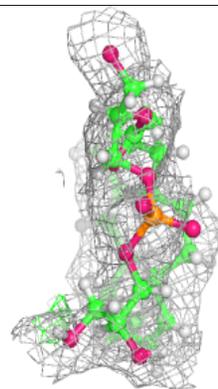
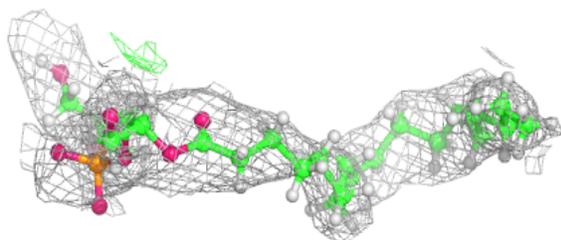
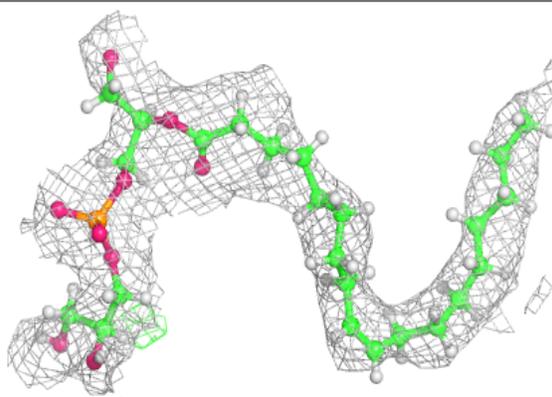


**Electron density around PGW A 502:**

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

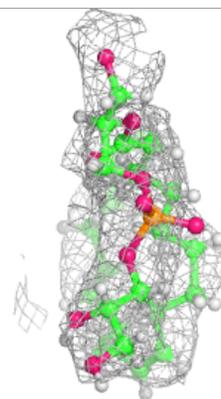
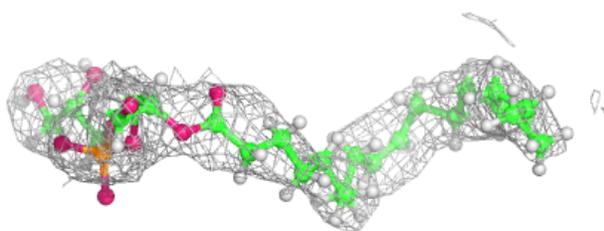
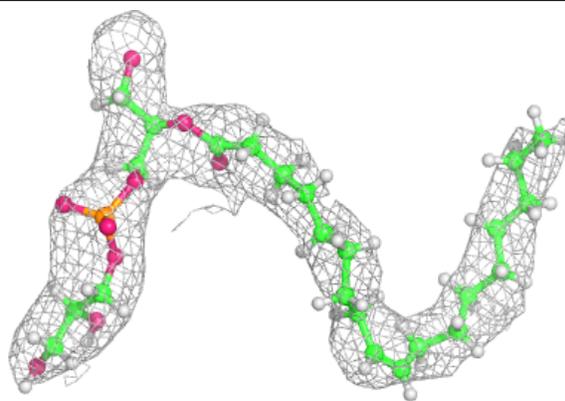
**Electron density around PGW B 502:**

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

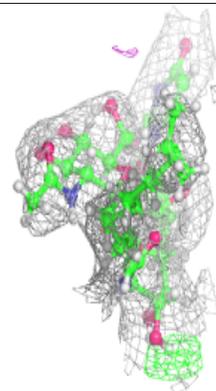
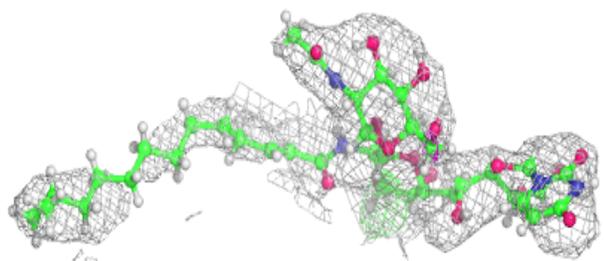
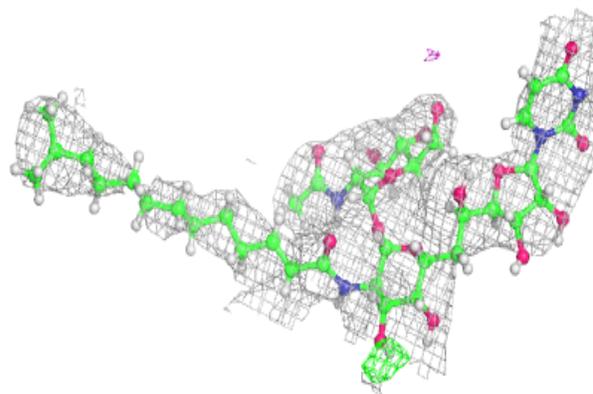


**Electron density around PGW D 502:**

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

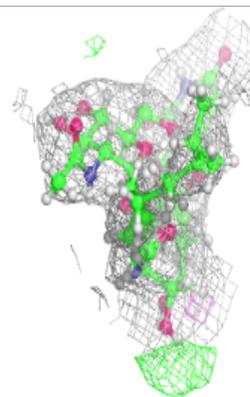
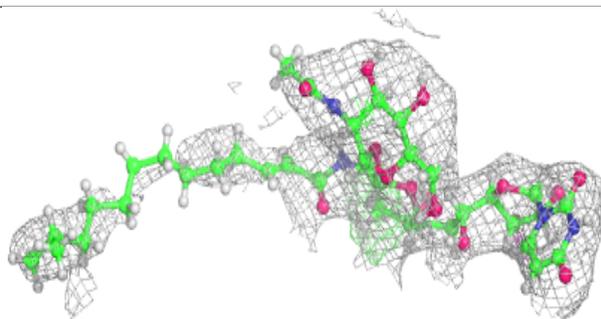
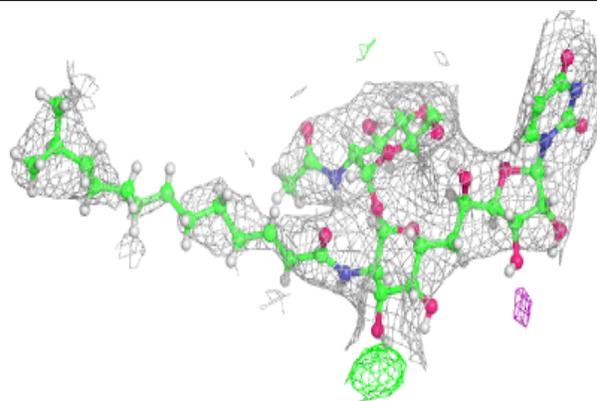
**Electron density around TUM B 501:**

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

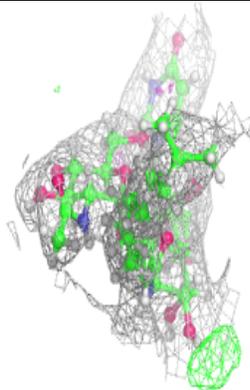
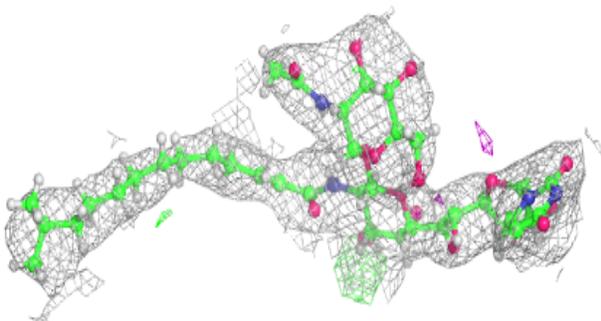
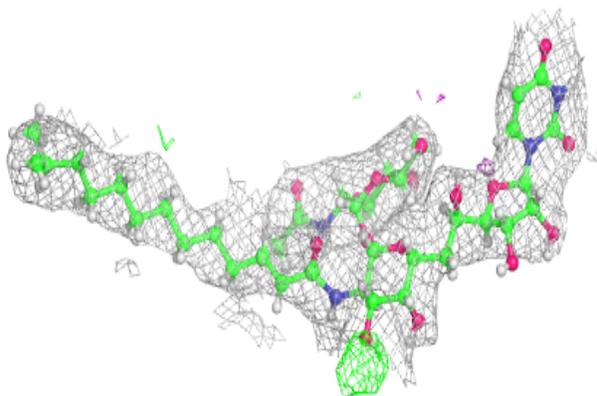


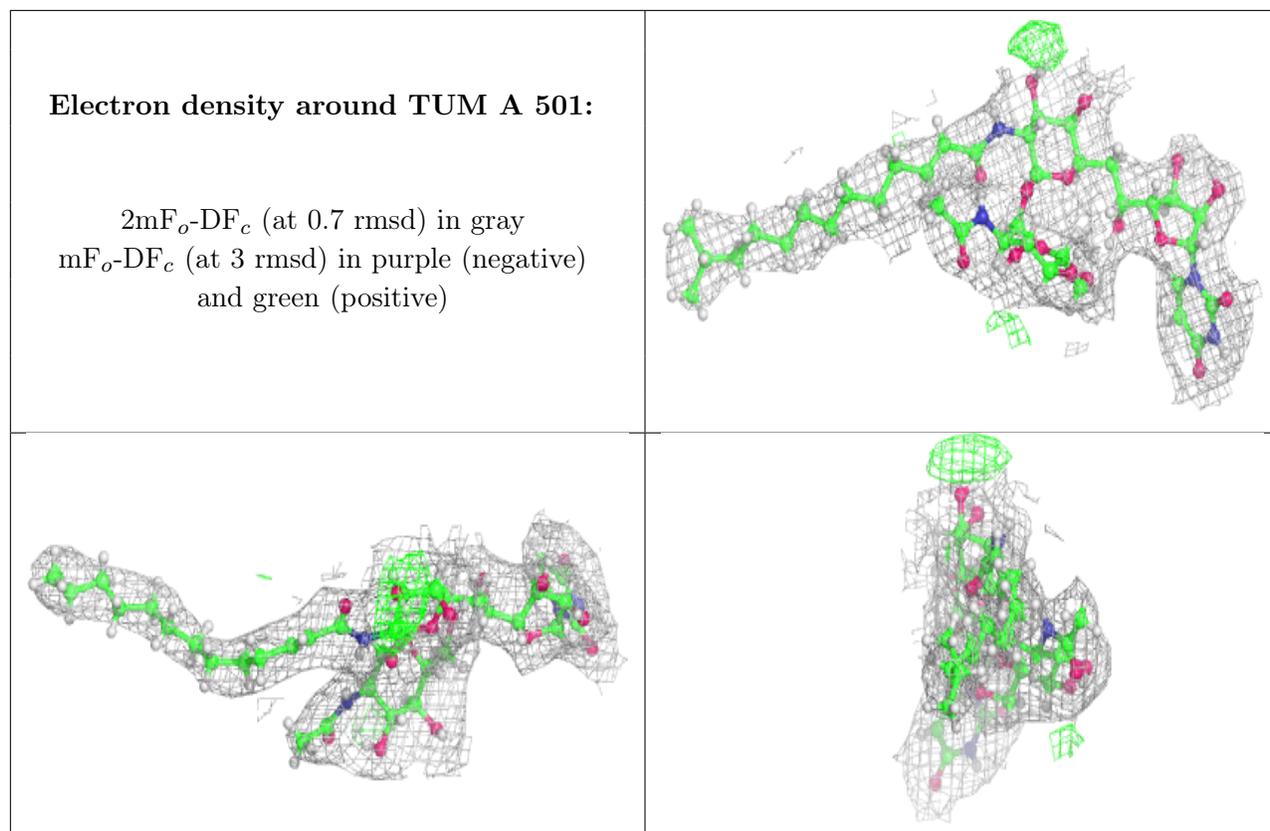
**Electron density around TUM D 501:**

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

**Electron density around TUM C 501:**

$2mF_o-DF_c$  (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.