



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 02:50 AM UTC

PDB ID : 3DR7 / pdb\_00003dr7  
Title : GDP-perosamine synthase from *Caulobacter crescentus* with bound GDP-3-deoxyperosamine  
Authors : Holden, H.M.; Cook, P.D.; Carney, A.E.  
Deposited on : 2008-07-10  
Resolution : 1.70 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](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 : 4-5-2 with Phenix2.0  
Mogul : 2022.3.0, CSD as543be (2022)  
Xtrriage (Phenix) : 2.0  
EDS : 3.0  
Buster-report : wwPDB partial adaption of 1.1.7 (2018)  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
CCP4 : 9.0.010 (Gargrove)  
Density-Fitness : 1.0.12  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

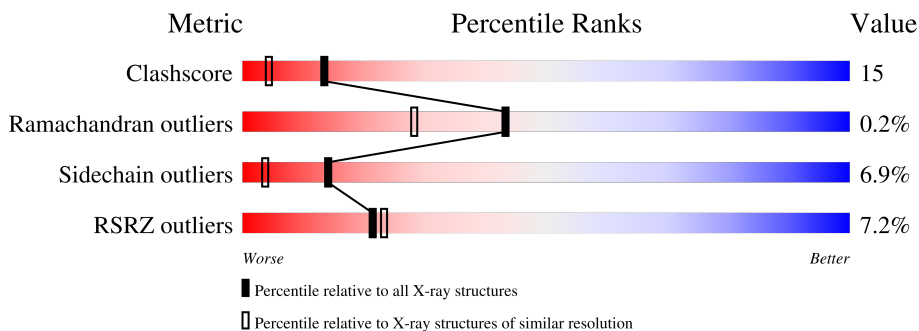
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.70 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))
Clashscore	190562	5924 (1.70-1.70)
Ramachandran outliers	187476	5846 (1.70-1.70)
Sidechain outliers	187428	5846 (1.70-1.70)
RSRZ outliers	180081	5554 (1.70-1.70)

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	391	
1	B	391	
1	C	391	
1	D	391	

## 2 Entry composition i

There are 4 unique types of molecules in this entry. The entry contains 12605 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 Putative perosamine synthetase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	P	S			
1	A	368	2855	1803	501	532	1	18	0	2	0
1	B	367	2881	1820	507	535	1	18	0	6	0
1	C	367	2837	1790	499	529	1	18	0	0	0
1	D	367	2837	1790	499	529	1	18	0	0	0

There are 180 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	expression tag	UNP O85354
A	-18	GLY	-	expression tag	UNP O85354
A	-17	SER	-	expression tag	UNP O85354
A	-16	SER	-	expression tag	UNP O85354
A	-15	HIS	-	expression tag	UNP O85354
A	-14	HIS	-	expression tag	UNP O85354
A	-13	HIS	-	expression tag	UNP O85354
A	-12	HIS	-	expression tag	UNP O85354
A	-11	HIS	-	expression tag	UNP O85354
A	-10	HIS	-	expression tag	UNP O85354
A	-9	SER	-	expression tag	UNP O85354
A	-8	SER	-	expression tag	UNP O85354
A	-7	GLU	-	expression tag	UNP O85354
A	-6	ASN	-	expression tag	UNP O85354
A	-5	LEU	-	expression tag	UNP O85354
A	-4	TYR	-	expression tag	UNP O85354
A	-3	PHE	-	expression tag	UNP O85354
A	-2	GLN	-	expression tag	UNP O85354
A	-1	GLY	-	expression tag	UNP O85354
A	0	HIS	-	expression tag	UNP O85354
A	1	MET	-	expression tag	UNP O85354

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Chain	Residue	Modelled	Actual	Comment	Reference
A	2	SER	-	expression tag	UNP O85354
A	3	ASP	-	expression tag	UNP O85354
A	4	LEU	-	expression tag	UNP O85354
A	5	PRO	-	expression tag	UNP O85354
A	6	ARG	-	expression tag	UNP O85354
A	7	ILE	-	expression tag	UNP O85354
A	8	SER	-	expression tag	UNP O85354
A	9	VAL	-	expression tag	UNP O85354
A	10	ALA	-	expression tag	UNP O85354
A	11	ALA	-	expression tag	UNP O85354
A	12	PRO	-	expression tag	UNP O85354
A	13	ARG	-	expression tag	UNP O85354
A	14	LEU	-	expression tag	UNP O85354
A	15	ASP	-	expression tag	UNP O85354
A	16	GLY	-	expression tag	UNP O85354
A	17	ASN	-	expression tag	UNP O85354
A	18	GLU	-	expression tag	UNP O85354
A	19	ARG	-	expression tag	UNP O85354
A	20	ASP	-	expression tag	UNP O85354
A	21	TYR	-	expression tag	UNP O85354
A	22	VAL	-	expression tag	UNP O85354
A	23	LEU	-	expression tag	UNP O85354
A	24	GLU	-	expression tag	UNP O85354
A	25	CYS	-	expression tag	UNP O85354
B	-19	MET	-	expression tag	UNP O85354
B	-18	GLY	-	expression tag	UNP O85354
B	-17	SER	-	expression tag	UNP O85354
B	-16	SER	-	expression tag	UNP O85354
B	-15	HIS	-	expression tag	UNP O85354
B	-14	HIS	-	expression tag	UNP O85354
B	-13	HIS	-	expression tag	UNP O85354
B	-12	HIS	-	expression tag	UNP O85354
B	-11	HIS	-	expression tag	UNP O85354
B	-10	HIS	-	expression tag	UNP O85354
B	-9	SER	-	expression tag	UNP O85354
B	-8	SER	-	expression tag	UNP O85354
B	-7	GLU	-	expression tag	UNP O85354
B	-6	ASN	-	expression tag	UNP O85354
B	-5	LEU	-	expression tag	UNP O85354
B	-4	TYR	-	expression tag	UNP O85354
B	-3	PHE	-	expression tag	UNP O85354
B	-2	GLN	-	expression tag	UNP O85354

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-1	GLY	-	expression tag	UNP O85354
B	0	HIS	-	expression tag	UNP O85354
B	1	MET	-	expression tag	UNP O85354
B	2	SER	-	expression tag	UNP O85354
B	3	ASP	-	expression tag	UNP O85354
B	4	LEU	-	expression tag	UNP O85354
B	5	PRO	-	expression tag	UNP O85354
B	6	ARG	-	expression tag	UNP O85354
B	7	ILE	-	expression tag	UNP O85354
B	8	SER	-	expression tag	UNP O85354
B	9	VAL	-	expression tag	UNP O85354
B	10	ALA	-	expression tag	UNP O85354
B	11	ALA	-	expression tag	UNP O85354
B	12	PRO	-	expression tag	UNP O85354
B	13	ARG	-	expression tag	UNP O85354
B	14	LEU	-	expression tag	UNP O85354
B	15	ASP	-	expression tag	UNP O85354
B	16	GLY	-	expression tag	UNP O85354
B	17	ASN	-	expression tag	UNP O85354
B	18	GLU	-	expression tag	UNP O85354
B	19	ARG	-	expression tag	UNP O85354
B	20	ASP	-	expression tag	UNP O85354
B	21	TYR	-	expression tag	UNP O85354
B	22	VAL	-	expression tag	UNP O85354
B	23	LEU	-	expression tag	UNP O85354
B	24	GLU	-	expression tag	UNP O85354
B	25	CYS	-	expression tag	UNP O85354
C	-19	MET	-	expression tag	UNP O85354
C	-18	GLY	-	expression tag	UNP O85354
C	-17	SER	-	expression tag	UNP O85354
C	-16	SER	-	expression tag	UNP O85354
C	-15	HIS	-	expression tag	UNP O85354
C	-14	HIS	-	expression tag	UNP O85354
C	-13	HIS	-	expression tag	UNP O85354
C	-12	HIS	-	expression tag	UNP O85354
C	-11	HIS	-	expression tag	UNP O85354
C	-10	HIS	-	expression tag	UNP O85354
C	-9	SER	-	expression tag	UNP O85354
C	-8	SER	-	expression tag	UNP O85354
C	-7	GLU	-	expression tag	UNP O85354
C	-6	ASN	-	expression tag	UNP O85354
C	-5	LEU	-	expression tag	UNP O85354

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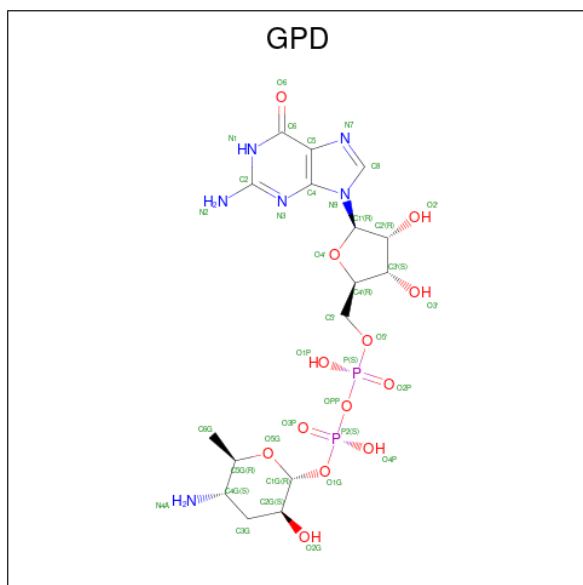
Chain	Residue	Modelled	Actual	Comment	Reference
C	-4	TYR	-	expression tag	UNP O85354
C	-3	PHE	-	expression tag	UNP O85354
C	-2	GLN	-	expression tag	UNP O85354
C	-1	GLY	-	expression tag	UNP O85354
C	0	HIS	-	expression tag	UNP O85354
C	1	MET	-	expression tag	UNP O85354
C	2	SER	-	expression tag	UNP O85354
C	3	ASP	-	expression tag	UNP O85354
C	4	LEU	-	expression tag	UNP O85354
C	5	PRO	-	expression tag	UNP O85354
C	6	ARG	-	expression tag	UNP O85354
C	7	ILE	-	expression tag	UNP O85354
C	8	SER	-	expression tag	UNP O85354
C	9	VAL	-	expression tag	UNP O85354
C	10	ALA	-	expression tag	UNP O85354
C	11	ALA	-	expression tag	UNP O85354
C	12	PRO	-	expression tag	UNP O85354
C	13	ARG	-	expression tag	UNP O85354
C	14	LEU	-	expression tag	UNP O85354
C	15	ASP	-	expression tag	UNP O85354
C	16	GLY	-	expression tag	UNP O85354
C	17	ASN	-	expression tag	UNP O85354
C	18	GLU	-	expression tag	UNP O85354
C	19	ARG	-	expression tag	UNP O85354
C	20	ASP	-	expression tag	UNP O85354
C	21	TYR	-	expression tag	UNP O85354
C	22	VAL	-	expression tag	UNP O85354
C	23	LEU	-	expression tag	UNP O85354
C	24	GLU	-	expression tag	UNP O85354
C	25	CYS	-	expression tag	UNP O85354
D	-19	MET	-	expression tag	UNP O85354
D	-18	GLY	-	expression tag	UNP O85354
D	-17	SER	-	expression tag	UNP O85354
D	-16	SER	-	expression tag	UNP O85354
D	-15	HIS	-	expression tag	UNP O85354
D	-14	HIS	-	expression tag	UNP O85354
D	-13	HIS	-	expression tag	UNP O85354
D	-12	HIS	-	expression tag	UNP O85354
D	-11	HIS	-	expression tag	UNP O85354
D	-10	HIS	-	expression tag	UNP O85354
D	-9	SER	-	expression tag	UNP O85354
D	-8	SER	-	expression tag	UNP O85354

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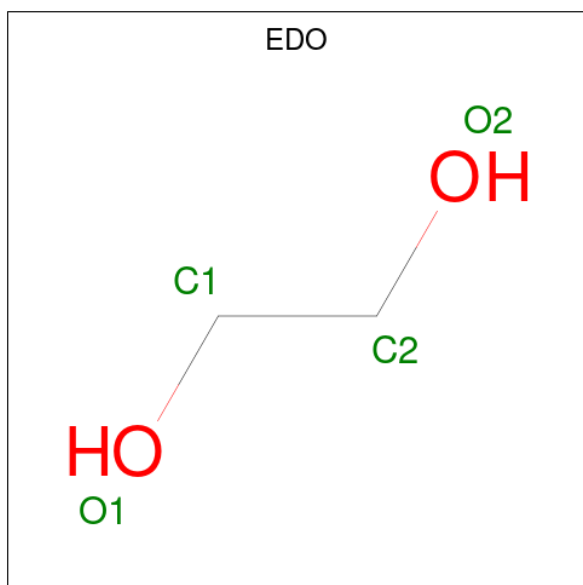
Chain	Residue	Modelled	Actual	Comment	Reference
D	-7	GLU	-	expression tag	UNP O85354
D	-6	ASN	-	expression tag	UNP O85354
D	-5	LEU	-	expression tag	UNP O85354
D	-4	TYR	-	expression tag	UNP O85354
D	-3	PHE	-	expression tag	UNP O85354
D	-2	GLN	-	expression tag	UNP O85354
D	-1	GLY	-	expression tag	UNP O85354
D	0	HIS	-	expression tag	UNP O85354
D	1	MET	-	expression tag	UNP O85354
D	2	SER	-	expression tag	UNP O85354
D	3	ASP	-	expression tag	UNP O85354
D	4	LEU	-	expression tag	UNP O85354
D	5	PRO	-	expression tag	UNP O85354
D	6	ARG	-	expression tag	UNP O85354
D	7	ILE	-	expression tag	UNP O85354
D	8	SER	-	expression tag	UNP O85354
D	9	VAL	-	expression tag	UNP O85354
D	10	ALA	-	expression tag	UNP O85354
D	11	ALA	-	expression tag	UNP O85354
D	12	PRO	-	expression tag	UNP O85354
D	13	ARG	-	expression tag	UNP O85354
D	14	LEU	-	expression tag	UNP O85354
D	15	ASP	-	expression tag	UNP O85354
D	16	GLY	-	expression tag	UNP O85354
D	17	ASN	-	expression tag	UNP O85354
D	18	GLU	-	expression tag	UNP O85354
D	19	ARG	-	expression tag	UNP O85354
D	20	ASP	-	expression tag	UNP O85354
D	21	TYR	-	expression tag	UNP O85354
D	22	VAL	-	expression tag	UNP O85354
D	23	LEU	-	expression tag	UNP O85354
D	24	GLU	-	expression tag	UNP O85354
D	25	CYS	-	expression tag	UNP O85354

- Molecule 2 is (2R,3S,5S,6R)-5-amino-3-hydroxy-6-methyl-oxan-2-yl (CCD ID: GPD) (formula: C<sub>16</sub>H<sub>26</sub>N<sub>6</sub>O<sub>13</sub>P<sub>2</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
			Total	C	N	O			P
2	A	1	Total	C	N	O	P	0	0
			37	16	6	13	2		
2	A	1	Total	C	N	O	P	0	0
			37	16	6	13	2		
2	D	1	Total	C	N	O	P	0	0
			37	16	6	13	2		
2	D	1	Total	C	N	O	P	0	0
			37	16	6	13	2		

- Molecule 3 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C<sub>2</sub>H<sub>6</sub>O<sub>2</sub>).

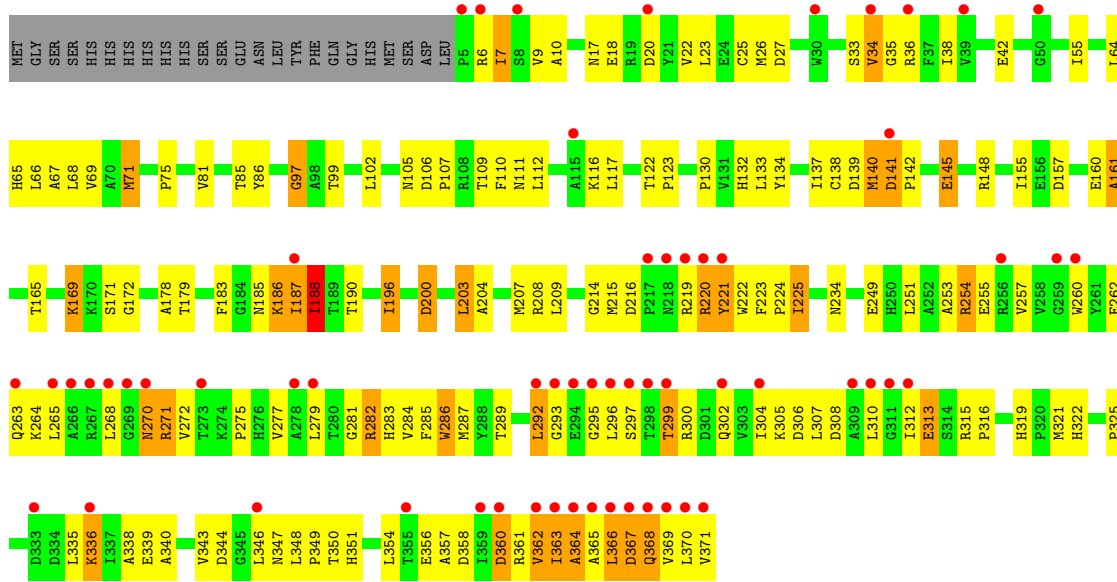


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	B	1	Total	C	O	0	0
			4	2	2		
3	D	1	Total	C	O	0	0
			4	2	2		

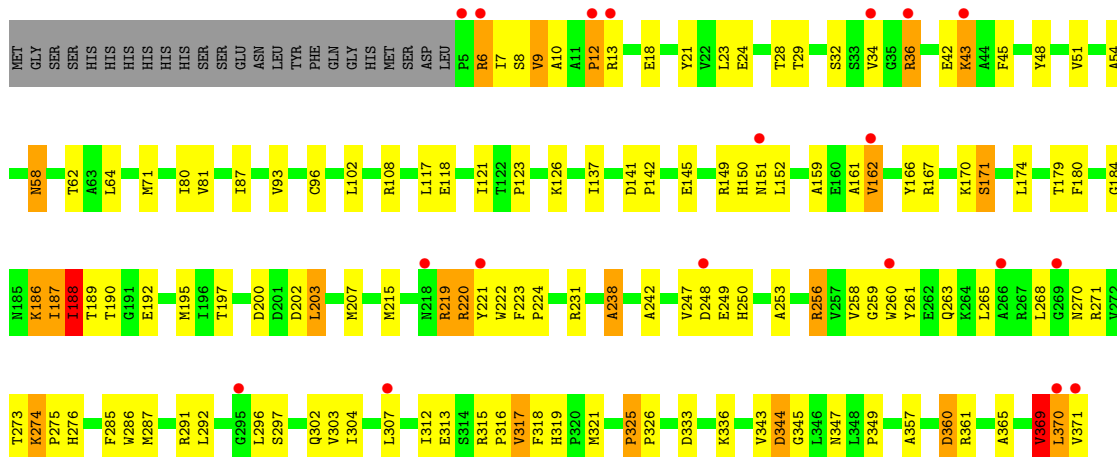
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	318	Total	O	0	0
			318	318		
4	B	287	Total	O	0	0
			287	287		
4	C	195	Total	O	0	0
			195	195		
4	D	239	Total	O	0	0
			239	239		





● Molecule 1: Putative perosamine synthetase



## 4 Data and refinement statistics i

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	50.41Å 152.23Å 105.75Å 90.00° 101.83° 90.00°	Depositor
Resolution (Å)	30.00 – 1.70 30.00 – 1.70	Depositor EDS
% Data completeness (in resolution range)	94.6 (30.00-1.70) 94.6 (30.00-1.70)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.09	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	0.69 (at 1.70Å)	Xtrriage
Refinement program	TNT	Depositor
R, $R_{free}$	0.197 , 0.263 0.196 , (Not available)	Depositor DCC
$R_{free}$ test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	9.0	Xtrriage
Anisotropy	0.406	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 75.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	0.033 for h,-k,-h-l	Xtrriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	12605	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	22.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.21% 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: GPD, LLP, 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	0.98	4/2890 (0.1%)	1.52	34/3928 (0.9%)
1	B	0.92	1/2916 (0.0%)	1.51	29/3962 (0.7%)
1	C	0.87	6/2869 (0.2%)	1.48	32/3898 (0.8%)
1	D	0.90	2/2869 (0.1%)	1.46	29/3898 (0.7%)
All	All	0.92	13/11544 (0.1%)	1.50	124/15686 (0.8%)

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	71	MET	SD-CE	-10.70	1.52	1.79
1	C	71	MET	SD-CE	-9.94	1.54	1.79
1	C	140	MET	SD-CE	-8.94	1.57	1.79
1	D	71	MET	SD-CE	-7.97	1.59	1.79
1	A	287	MET	SD-CE	6.96	1.97	1.79

The worst 5 of 124 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	6	ARG	N-CA-C	10.81	125.48	110.24
1	C	117	LEU	N-CA-C	10.17	122.32	111.03
1	B	265	LEU	N-CA-C	9.79	123.18	111.33
1	A	140	MET	N-CA-C	9.61	122.76	111.71
1	D	36	ARG	N-CA-C	8.81	121.84	111.71

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	2855	0	2845	60	0
1	B	2881	0	2875	66	0
1	C	2837	0	2823	135	0
1	D	2837	0	2822	78	0
2	A	74	0	46	10	0
2	D	74	0	48	12	0
3	B	4	0	6	0	0
3	D	4	0	6	3	0
4	A	318	0	0	3	0
4	B	287	0	0	7	0
4	C	195	0	0	5	0
4	D	239	0	0	3	0
All	All	12605	0	11471	338	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 15.

The worst 5 of 338 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:186:LLP:C4'	2:D:501:GPD:HN4B	1.44	1.31
1:D:276:HIS:HB2	3:D:1041:EDO:H12	1.36	1.05
1:D:186:LLP:C4'	2:D:501:GPD:N4A	2.23	1.01
1:A:186:LLP:C4'	2:A:500:GPD:HN4B	1.72	1.01
1:C:264:LYS:HB2	1:C:363:ILE:HD12	1.48	0.95

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	367/391 (94%)	358 (98%)	9 (2%)	0	100	100
1	B	370/391 (95%)	358 (97%)	12 (3%)	0	100	100
1	C	364/391 (93%)	341 (94%)	21 (6%)	2 (0%)	24	12
1	D	364/391 (93%)	350 (96%)	13 (4%)	1 (0%)	36	22
All	All	1465/1564 (94%)	1407 (96%)	55 (4%)	3 (0%)	43	28

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	292	LEU
1	C	364	ALA
1	D	184	GLY

### 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	299/318 (94%)	286 (96%)	13 (4%)	26	10
1	B	302/318 (95%)	284 (94%)	18 (6%)	17	5
1	C	296/318 (93%)	268 (90%)	28 (10%)	8	1
1	D	296/318 (93%)	271 (92%)	25 (8%)	10	2
All	All	1193/1272 (94%)	1109 (93%)	84 (7%)	14	3

5 of 84 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	367	ASP
1	D	174	LEU
1	D	6	ARG
1	D	58	ASN
1	D	203	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 11 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	347	ASN
1	D	58	ASN
1	D	347	ASN
1	D	263	GLN
1	C	91	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](#)

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

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
1	LLP	B	186	1	23,24,25	1.22	3 (13%)	25,32,34	1.74	7 (28%)
1	LLP	C	186	1	23,24,25	1.24	1 (4%)	25,32,34	1.30	4 (16%)
1	LLP	A	186	1	23,24,25	1.30	1 (4%)	25,32,34	1.50	5 (20%)
1	LLP	D	186	1	23,24,25	1.30	3 (13%)	25,32,34	1.31	4 (16%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	LLP	B	186	1	-	5/16/17/19	0/1/1/1
1	LLP	C	186	1	-	2/16/17/19	0/1/1/1
1	LLP	A	186	1	-	1/16/17/19	0/1/1/1
1	LLP	D	186	1	-	3/16/17/19	0/1/1/1

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	186	LLP	P-OP1	3.86	1.62	1.50
1	C	186	LLP	P-OP1	3.48	1.61	1.50
1	D	186	LLP	P-OP1	3.37	1.60	1.50
1	B	186	LLP	P-OP1	2.95	1.59	1.50
1	B	186	LLP	C2-N1	-2.29	1.29	1.33

The worst 5 of 20 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	186	LLP	OP4-C5'-C5	4.72	118.20	109.36
1	A	186	LLP	CD-CG-CB	3.42	126.53	113.62
1	B	186	LLP	C4-C3-C2	3.28	121.99	120.14
1	C	186	LLP	OP4-C5'-C5	3.07	115.11	109.36
1	B	186	LLP	OP2-P-OP4	-2.97	98.93	106.67

There are no chirality outliers.

5 of 11 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	186	LLP	CG-CD-CE-NZ
1	B	186	LLP	CG-CD-CE-NZ
1	D	186	LLP	CG-CD-CE-NZ
1	C	186	LLP	CA-CB-CG-CD
1	B	186	LLP	CA-CB-CG-CD

There are no ring outliers.

4 monomers are involved in 17 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	B	186	LLP	5	0
1	C	186	LLP	3	0
1	A	186	LLP	4	0
1	D	186	LLP	5	0

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry

6 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	GPD	D	500	-	39,40,40	1.00	2 (5%)	57,62,62	1.61	9 (15%)
2	GPD	A	501	-	39,40,40	2.20	13 (33%)	57,62,62	2.74	18 (31%)
3	EDO	D	1041	-	3,3,3	0.47	0	2,2,2	0.11	0
2	GPD	D	501	-	39,40,40	0.91	2 (5%)	57,62,62	1.76	10 (17%)
2	GPD	A	500	-	39,40,40	0.99	2 (5%)	57,62,62	1.69	12 (21%)
3	EDO	B	1040	-	3,3,3	0.41	0	2,2,2	0.40	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	GPD	D	500	-	-	5/21/53/53	0/4/4/4
2	GPD	A	501	-	-	3/21/53/53	1/4/4/4
3	EDO	D	1041	-	-	1/1/1/1	-
2	GPD	D	501	-	-	2/21/53/53	0/4/4/4
2	GPD	A	500	-	-	3/21/53/53	0/4/4/4
3	EDO	B	1040	-	-	1/1/1/1	-

The worst 5 of 19 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	501	GPD	P2-O1G	-5.92	1.41	1.59
2	A	501	GPD	P-O1P	-4.57	1.34	1.55
2	A	501	GPD	C2-N1	-3.76	1.28	1.37
2	A	501	GPD	C5-N7	-3.66	1.31	1.39
2	A	501	GPD	C4-N9	-3.53	1.29	1.38

The worst 5 of 49 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	501	GPD	O4'-C1'-N9	7.82	126.08	108.36
2	A	501	GPD	C5-C4-N3	-7.65	116.22	128.39
2	A	501	GPD	N9-C4-N3	5.90	137.74	125.95
2	A	501	GPD	O5G-C1G-O1G	5.83	118.99	111.36
2	A	500	GPD	C5-C4-N3	-5.77	119.21	128.39

There are no chirality outliers.

5 of 15 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	500	GPD	C1G-O1G-P2-OPP
2	A	501	GPD	P2-OPP-P-O1P
3	D	1041	EDO	O1-C1-C2-O2
2	D	500	GPD	C1G-O1G-P2-OPP
2	D	501	GPD	P2-OPP-P-O1P

All (1) ring outliers are listed below:

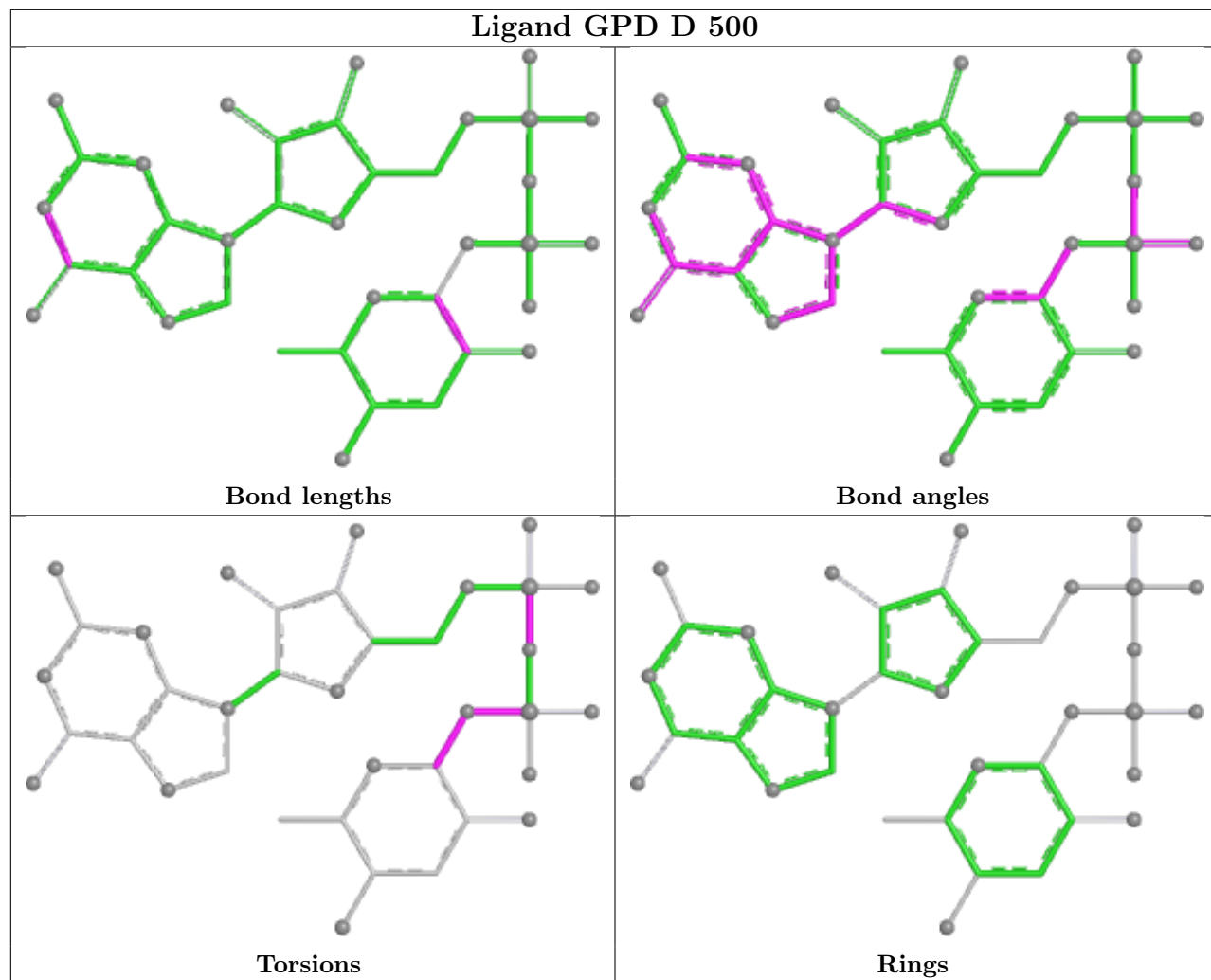
Mol	Chain	Res	Type	Atoms
2	A	501	GPD	C1G-C2G-C3G-C4G-C5G-O5G

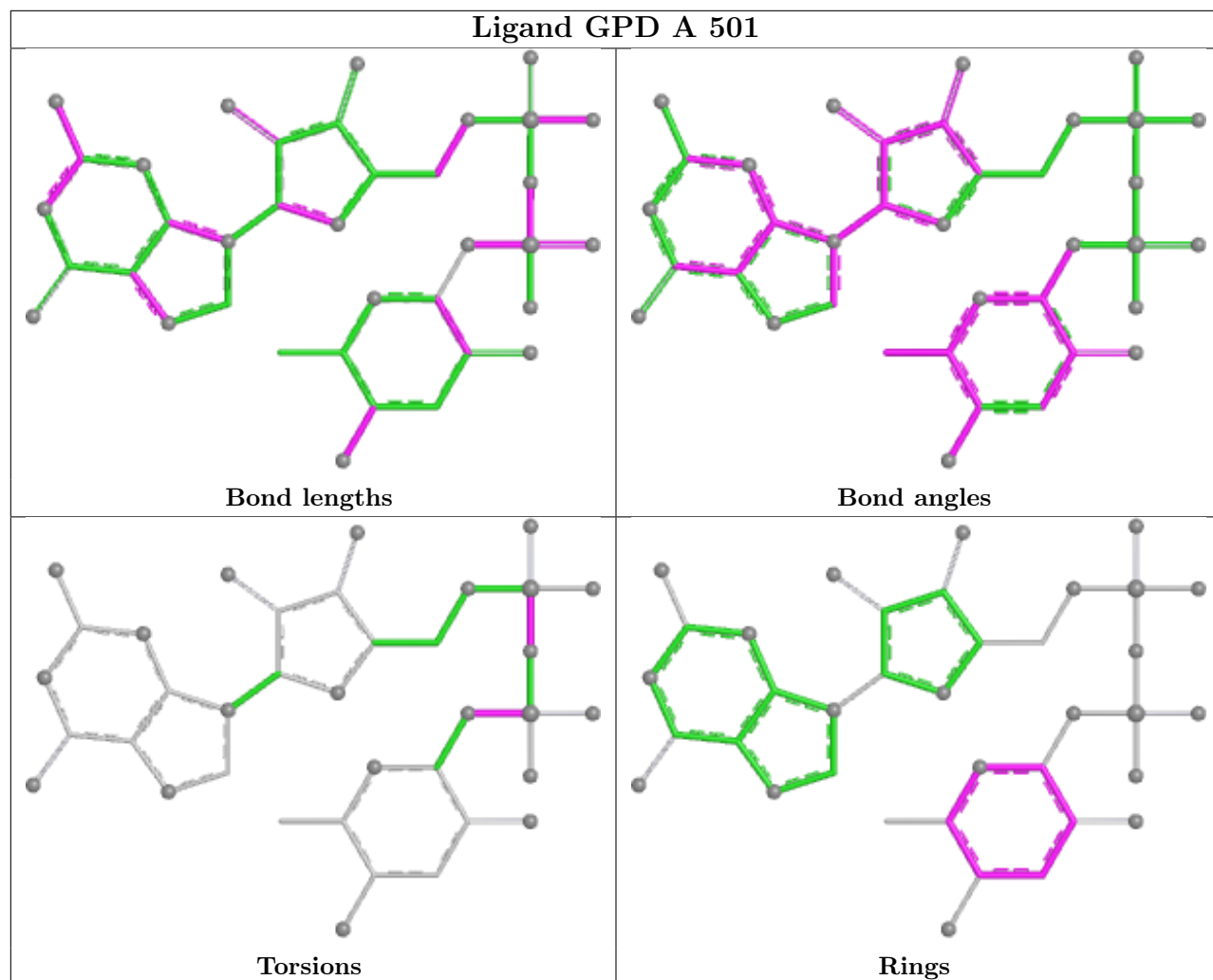
5 monomers are involved in 25 short contacts:

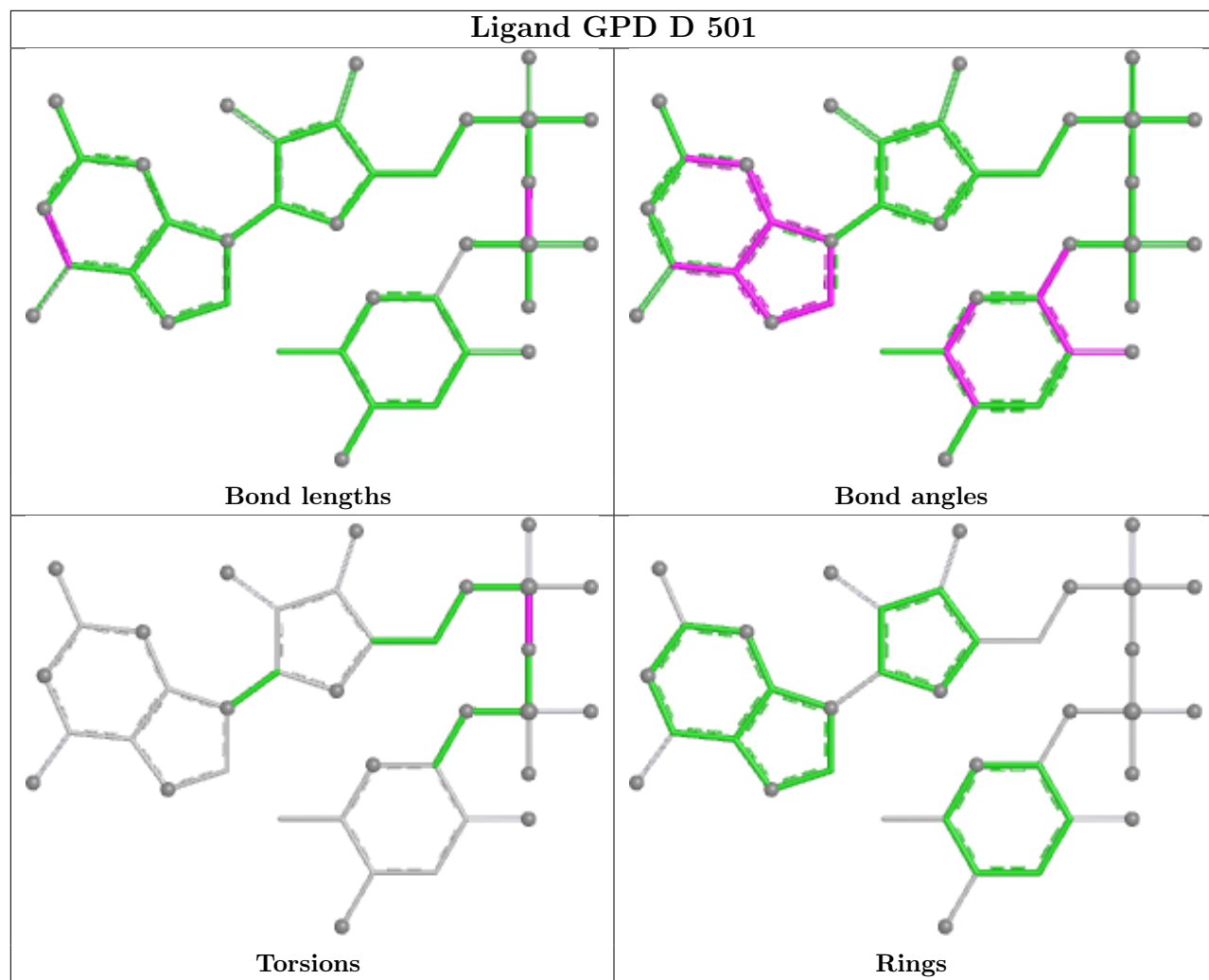
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	500	GPD	3	0
2	A	501	GPD	5	0
3	D	1041	EDO	3	0
2	D	501	GPD	9	0
2	A	500	GPD	5	0

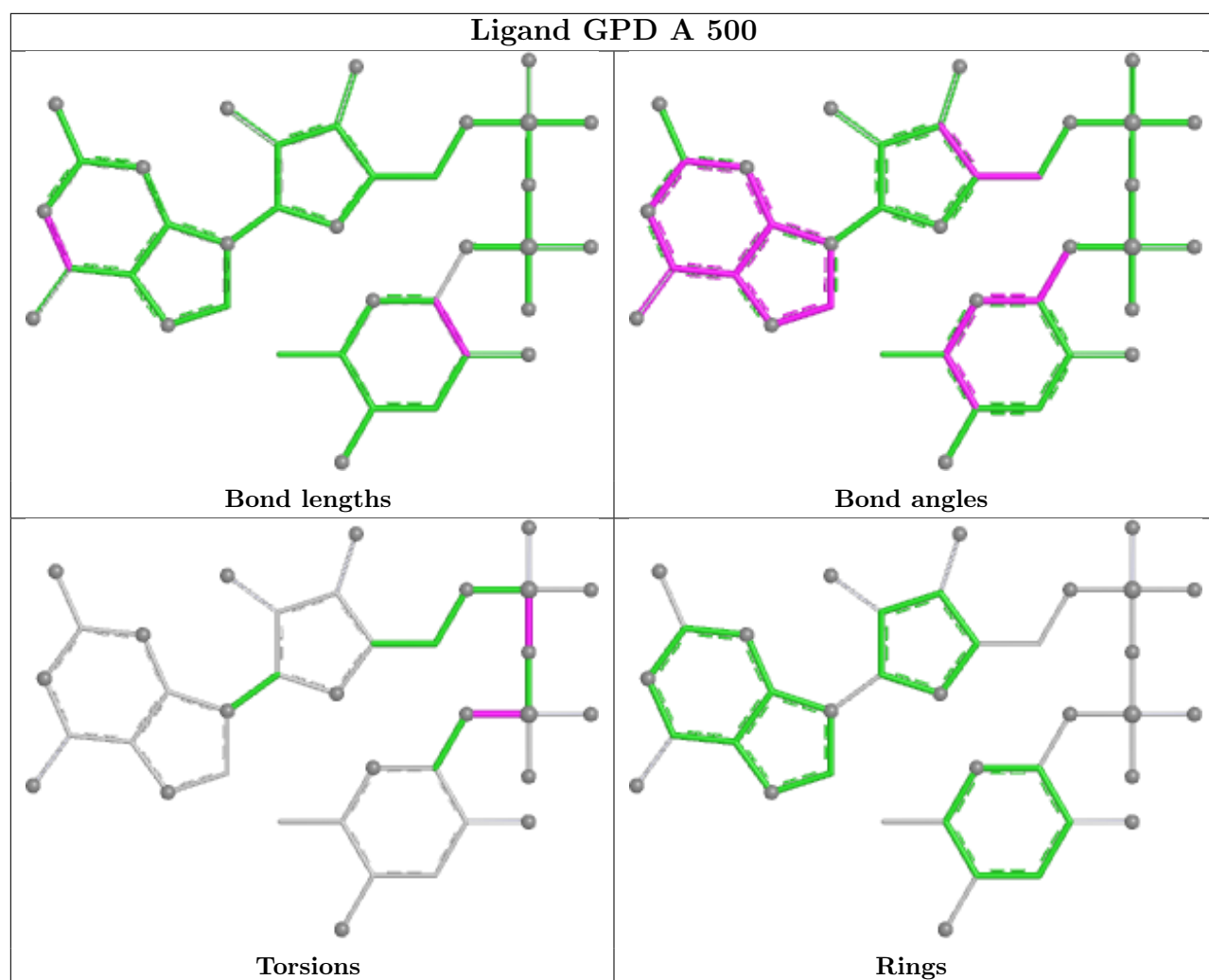
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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	367/391 (93%)	-0.09	11 (2%) 52 56	5, 13, 37, 75	2 (0%)
1	B	366/391 (93%)	0.01	15 (4%) 41 45	5, 14, 39, 80	6 (1%)
1	C	366/391 (93%)	0.71	60 (16%) 4 4	5, 21, 64, 90	0
1	D	366/391 (93%)	0.26	19 (5%) 33 36	4, 19, 46, 74	0
All	All	1465/1564 (93%)	0.22	105 (7%) 21 23	4, 16, 51, 90	8 (0%)

The worst 5 of 105 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	371	VAL	8.3
1	C	369	VAL	5.6
1	C	5	PRO	5.6
1	C	296	LEU	5.0
1	C	311	GLY	4.9

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

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 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
1	LLP	C	186	24/25	0.96	0.07	1,13,18,26	0
1	LLP	B	186	24/25	0.97	0.06	2,8,17,22	0
1	LLP	A	186	24/25	0.97	0.06	2,9,16,24	0
1	LLP	D	186	24/25	0.97	0.07	1,14,21,28	0

### 6.3 Carbohydrates [i](#)

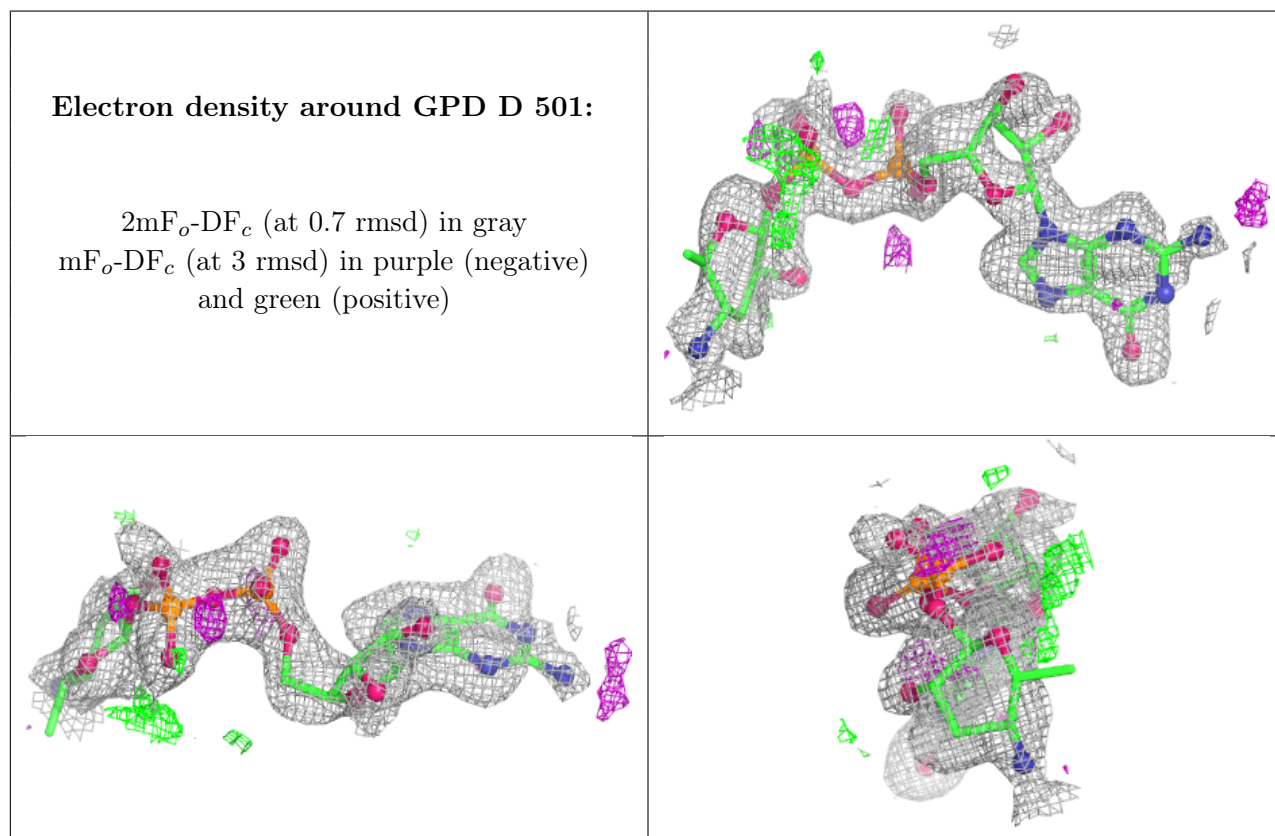
There are no oligosaccharides in this entry.

### 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.

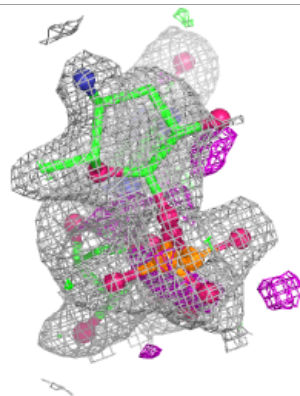
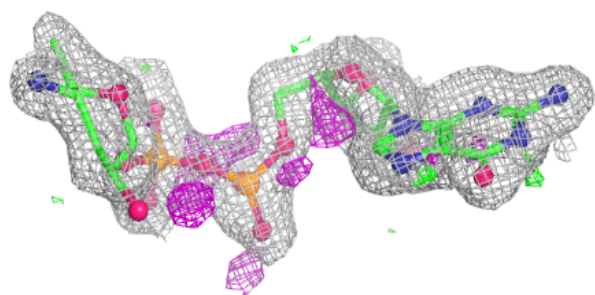
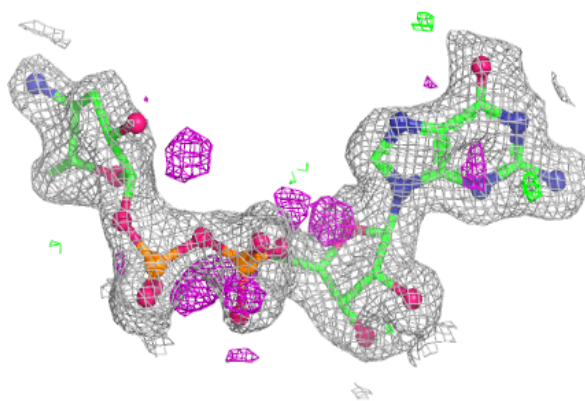
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	GPD	D	501	37/37	0.84	0.18	25,61,99,99	0
3	EDO	B	1040	4/4	0.85	0.11	17,32,32,36	0
3	EDO	D	1041	4/4	0.91	0.13	23,23,31,50	0
2	GPD	A	500	37/37	0.92	0.12	16,31,99,99	0
2	GPD	D	500	37/37	0.93	0.11	20,30,82,99	0
2	GPD	A	501	37/37	0.96	0.07	6,18,35,69	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.

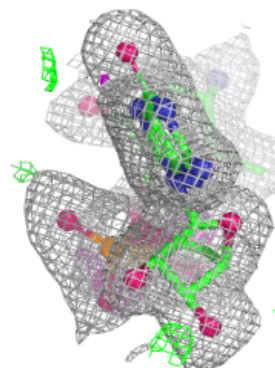
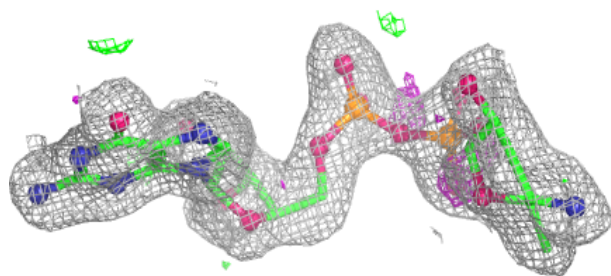
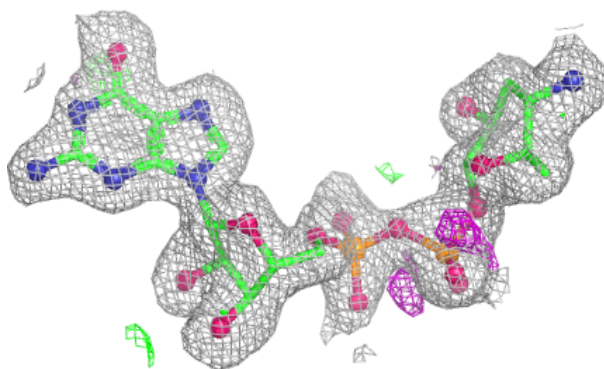


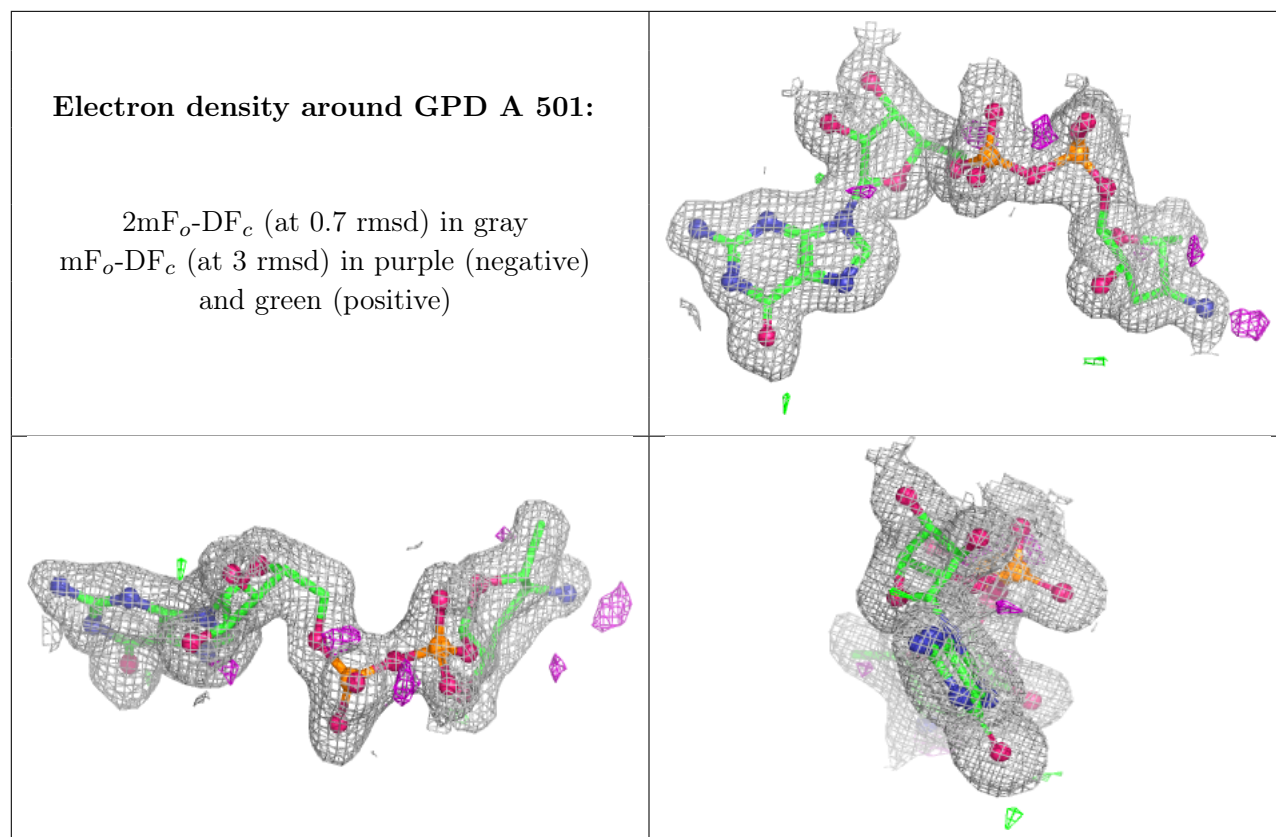
**Electron density around GPD A 500:**

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

**Electron density around GPD D 500:**

$2mF_o-DF_c$  (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.