



# Full wwPDB X-ray Structure Validation Report ⓘ

May 16, 2020 – 09:17 pm BST

PDB ID : 3DR7  
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 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.

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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 : 2.11  
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) : 2.11

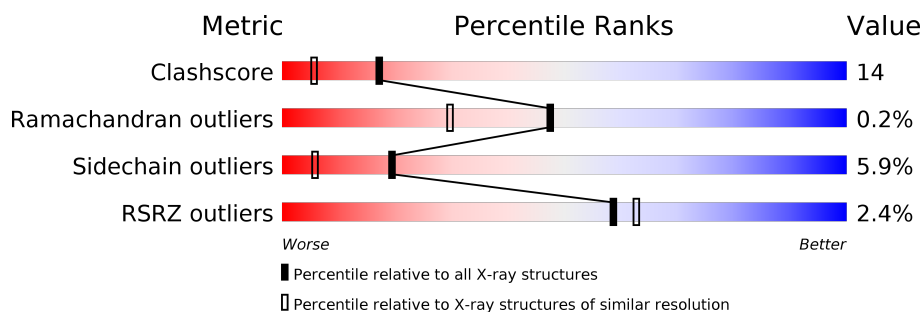
# 1 Overall quality at a glance

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	141614	4695 (1.70-1.70)
Ramachandran outliers	138981	4610 (1.70-1.70)
Sidechain outliers	138945	4610 (1.70-1.70)
RSRZ outliers	127900	4222 (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 on 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	<div> <div></div> <div>72%19%6%</div> </div>
1	B	391	<div> <div></div> <div>72%19%6%</div> </div>
1	C	391	<div> <div>8%</div> <div>58%31%5%6%</div> </div>
1	D	391	<div> <div>%</div> <div>66%24%6%</div> </div>

## 2 Entry composition

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

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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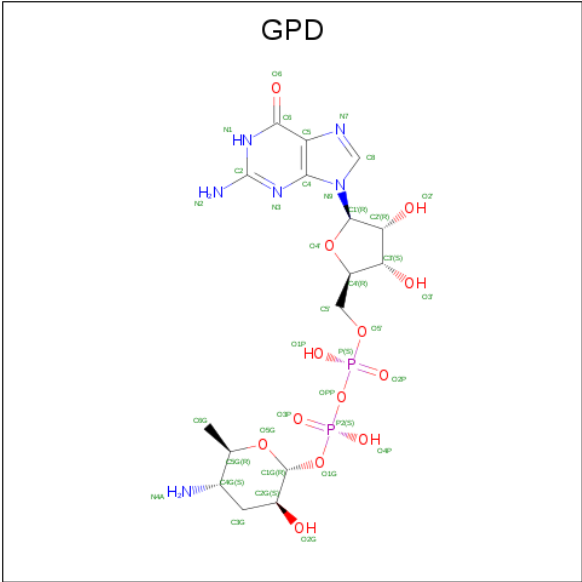
Chain	Residue	Modelled	Actual	Comment	Reference
C	-4	TYR	-	EXPRESSION TAG	UNP O85354
C	-3	PHE	-	EXPRESSION TAG	UNP O85354
C	-2	GLN	-	EXPRESSION TAG	UNP O85354
C	-1	GLY	-	EXPRESSION TAG	UNP O85354
C	0	HIS	-	EXPRESSION TAG	UNP O85354
C	1	MET	-	EXPRESSION TAG	UNP O85354
C	2	SER	-	EXPRESSION TAG	UNP O85354
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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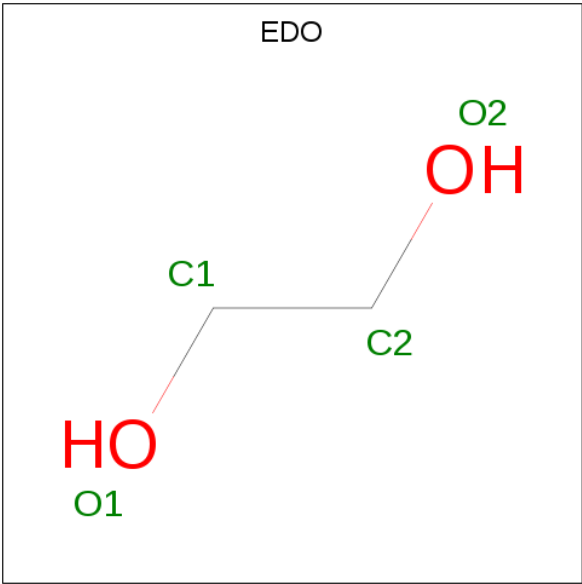
Chain	Residue	Modelled	Actual	Comment	Reference
D	-7	GLU	-	EXPRESSION TAG	UNP O85354
D	-6	ASN	-	EXPRESSION TAG	UNP O85354
D	-5	LEU	-	EXPRESSION TAG	UNP O85354
D	-4	TYR	-	EXPRESSION TAG	UNP O85354
D	-3	PHE	-	EXPRESSION TAG	UNP O85354
D	-2	GLN	-	EXPRESSION TAG	UNP O85354
D	-1	GLY	-	EXPRESSION TAG	UNP O85354
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 (three-letter code: 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
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 (three-letter code: 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		

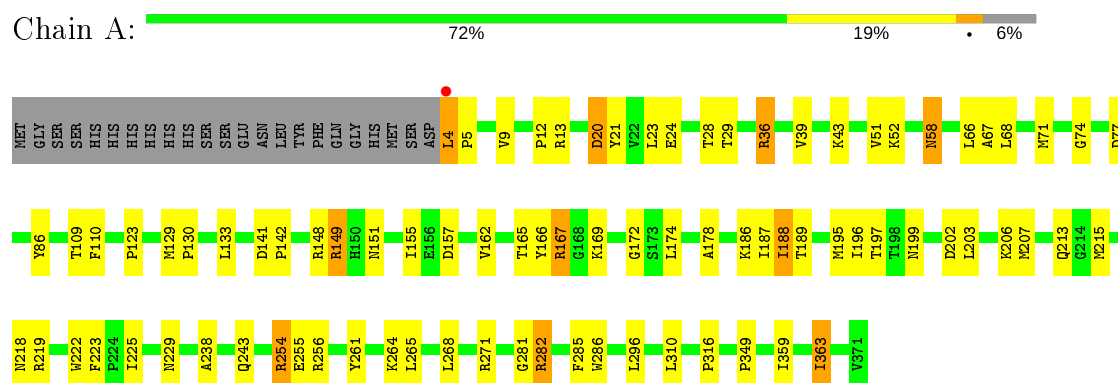
- Molecule 4 is water.

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		

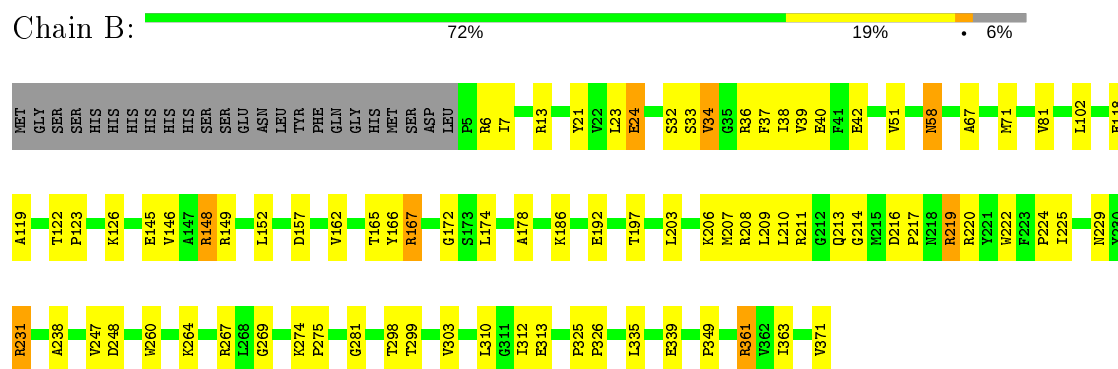
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA 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.

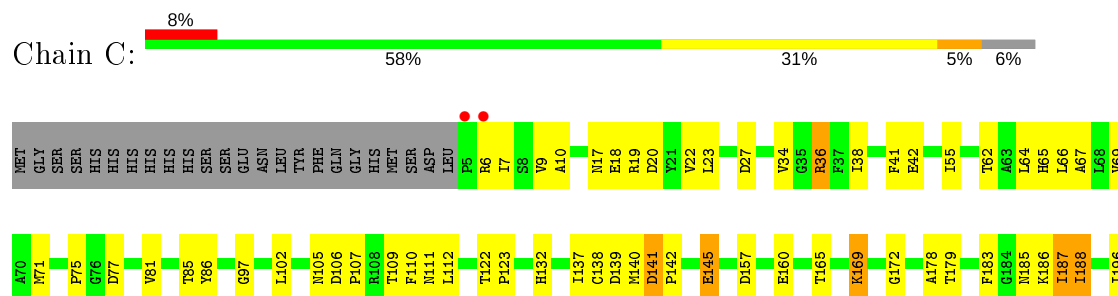
- Molecule 1: Putative perosamine synthetase

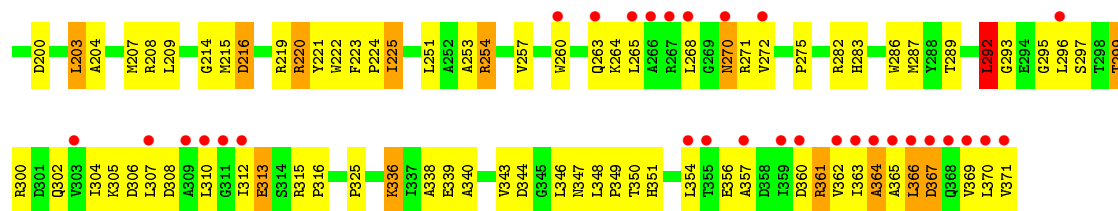


- Molecule 1: Putative perosamine synthetase

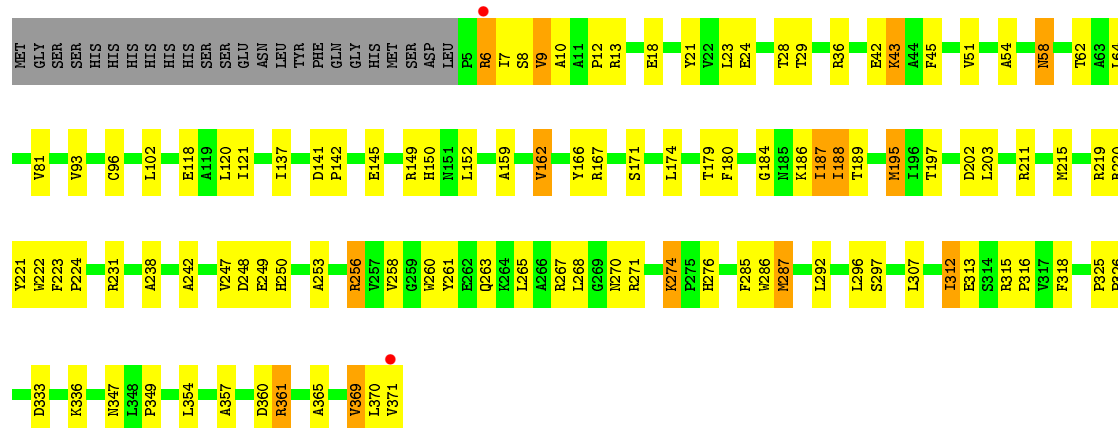


- Molecule 1: Putative perosamine synthetase





● Molecule 1: Putative perosamine synthetase



## 4 Data and refinement statistics

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 42.80 – 1.70	Depositor EDS
% Data completeness (in resolution range)	94.6 (30.00-1.70) 94.6 (42.80-1.70)	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)	Xtriage
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	Xtriage
Anisotropy	0.406	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 73.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.033 for h,-k,-h-l	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	12605	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	22.0	wwPDB-VP

Xtriage'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

### 5.1 Standard geometry

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	0.75	0/2890	1.23	13/3928 (0.3%)
1	B	0.73	0/2916	1.19	9/3962 (0.2%)
1	C	0.67	0/2869	1.15	8/3898 (0.2%)
1	D	0.71	2/2869 (0.1%)	1.14	7/3898 (0.2%)
All	All	0.72	2/11544 (0.0%)	1.18	37/15686 (0.2%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	371	VAL	CB-CG1	-6.52	1.39	1.52
1	D	371	VAL	C-OXT	-5.79	1.12	1.23

All (37) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	361	ARG	NE-CZ-NH1	8.81	124.71	120.30
1	A	271	ARG	NE-CZ-NH2	8.63	124.62	120.30
1	D	120	LEU	CB-CG-CD2	-8.18	97.09	111.00
1	B	361	ARG	NE-CZ-NH2	-8.08	116.26	120.30
1	A	149	ARG	NE-CZ-NH2	-7.94	116.33	120.30
1	C	19	ARG	NE-CZ-NH2	-7.44	116.58	120.30
1	A	271	ARG	NE-CZ-NH1	-7.29	116.66	120.30
1	D	287	MET	CG-SD-CE	7.10	111.56	100.20
1	B	231[A]	ARG	NE-CZ-NH2	-6.95	116.83	120.30
1	B	231[B]	ARG	NE-CZ-NH2	-6.95	116.83	120.30
1	C	62	THR	CA-CB-CG2	-6.61	103.14	112.40
1	C	77	ASP	CB-CG-OD1	-6.42	112.52	118.30
1	C	292	LEU	CA-CB-CG	-6.29	100.84	115.30
1	C	157	ASP	N-CA-C	-5.91	95.04	111.00
1	A	225	ILE	CB-CA-C	-5.91	99.78	111.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	256	ARG	NE-CZ-NH1	-5.82	117.39	120.30
1	A	68	LEU	CB-CG-CD2	5.82	120.89	111.00
1	D	195	MET	CG-SD-CE	5.80	109.47	100.20
1	A	157	ASP	CB-CG-OD1	-5.73	113.15	118.30
1	B	174	LEU	CB-CG-CD2	-5.70	101.31	111.00
1	C	216	ASP	CB-CG-OD1	5.68	123.41	118.30
1	A	133	LEU	CB-CG-CD2	5.60	120.52	111.00
1	C	41	PHE	CB-CG-CD2	-5.55	116.92	120.80
1	D	354	LEU	CB-CG-CD1	-5.50	101.65	111.00
1	A	296	LEU	CB-CG-CD1	-5.47	101.70	111.00
1	A	167	ARG	NE-CZ-NH2	5.44	123.02	120.30
1	B	192	GLU	N-CA-C	-5.41	96.40	111.00
1	A	157	ASP	CB-CG-OD2	5.37	123.13	118.30
1	D	6	ARG	N-CA-C	5.36	125.48	111.00
1	B	152	LEU	CB-CG-CD2	-5.34	101.92	111.00
1	B	208	ARG	NE-CZ-NH2	-5.28	117.66	120.30
1	A	195	MET	CG-SD-CE	5.28	108.64	100.20
1	C	17	ASN	N-CA-CB	-5.21	101.23	110.60
1	D	211	ARG	NE-CZ-NH1	5.17	122.88	120.30
1	B	157	ASP	N-CA-C	-5.13	97.14	111.00
1	A	282	ARG	NE-CZ-NH1	-5.11	117.75	120.30
1	D	312	ILE	CG1-CB-CG2	5.04	122.48	111.40

There are no chirality outliers.

There are no planarity outliers.

## 5.2 Too-close contacts ⓘ

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	2844	59	0
1	B	2881	0	2875	62	0
1	C	2837	0	2823	130	0
1	D	2837	0	2821	71	0
2	A	74	0	46	10	0
2	D	74	0	48	12	0
3	B	4	0	6	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	D	4	0	6	3	0
4	A	318	0	0	3	0
4	B	287	0	0	6	0
4	C	195	0	0	5	0
4	D	239	0	0	3	0
All	All	12605	0	11469	321	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 14.

All (321) 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
1:D:219:ARG:HG2	1:D:222:TRP:CB	2.00	0.92
1:A:219:ARG:HG2	1:A:222:TRP:HB2	1.58	0.85
1:A:186:LLP:C4'	2:A:500:GPD:N4A	2.42	0.82
1:B:67:ALA:O	1:B:71:MET:HG3	1.79	0.82
1:C:216:ASP:HB3	1:C:219:ARG:HB3	1.61	0.81
1:B:224:PRO:O	1:B:225[A]:ILE:HD13	1.81	0.81
1:C:264:LYS:CB	1:C:363:ILE:HD12	2.12	0.79
1:C:36:ARG:HH21	1:C:36:ARG:HG2	1.47	0.79
1:A:219:ARG:HG2	1:A:222:TRP:CB	2.12	0.79
1:A:186:LLP:C4	2:A:500:GPD:HN4B	1.95	0.79
1:C:219:ARG:HG2	1:C:222:TRP:HB3	1.65	0.78
1:B:264:LYS:O	1:B:267:ARG:HG3	1.84	0.78
1:D:219:ARG:HG2	1:D:222:TRP:HB2	1.64	0.77
1:C:265:LEU:HD12	1:C:268:LEU:HD12	1.67	0.76
1:C:293:GLY:O	1:C:296:LEU:HD12	1.86	0.76
1:A:36:ARG:HH11	1:A:36:ARG:HG3	1.51	0.75
1:C:253:ALA:O	1:C:257:VAL:HG23	1.86	0.75
1:D:261:TYR:O	1:D:265:LEU:HB2	1.87	0.74
1:C:293:GLY:H	1:C:296:LEU:CD1	2.02	0.73
1:D:249:GLU:N	1:D:249:GLU:OE1	2.22	0.73
1:D:118:GLU:OE1	1:D:149:ARG:NH1	2.23	0.72
1:A:52:LYS:HE2	1:A:199:ASN:O	1.89	0.72
1:C:216:ASP:CB	1:C:219:ARG:HB3	2.20	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:264:LYS:HB2	1:C:363:ILE:CD1	2.20	0.71
1:A:21:TYR:HB3	1:A:238:ALA:HB1	1.72	0.71
1:C:268:LEU:O	1:C:271:ARG:HB2	1.91	0.69
1:C:186:LLP:C4'	2:D:500:GPD:HN4B	2.06	0.69
1:C:36:ARG:NH2	1:C:36:ARG:HG2	2.09	0.68
1:D:219:ARG:HG2	1:D:222:TRP:HB3	1.75	0.68
1:C:260:TRP:O	1:C:264:LYS:HG3	1.94	0.67
1:C:225:ILE:HG22	4:C:419:HOH:O	1.94	0.66
1:D:296:LEU:HD11	1:D:370:LEU:HD13	1.77	0.66
1:D:145:GLU:OE2	1:D:149:ARG:NH2	2.28	0.66
1:C:141:ASP:N	1:C:142:PRO:HD2	2.09	0.66
1:C:366:LEU:O	1:C:370:LEU:HG	1.96	0.66
1:A:265:LEU:HD22	1:A:268:LEU:HD12	1.77	0.65
1:C:265:LEU:HD12	1:C:268:LEU:CD1	2.26	0.65
1:C:251:LEU:HB3	1:C:282:ARG:NH2	2.10	0.65
1:D:21:TYR:HB3	1:D:238:ALA:HB1	1.78	0.65
1:A:316:PRO:HG3	4:A:634:HOH:O	1.97	0.65
1:A:4:LEU:HD12	1:A:5:PRO:CD	2.27	0.65
1:A:36:ARG:HG3	1:A:36:ARG:NH1	2.09	0.64
1:C:306:ASP:HB2	1:C:369:VAL:CG1	2.28	0.64
1:C:260:TRP:CE2	1:C:356:GLU:HG3	2.33	0.63
1:A:58:ASN:H	1:A:58:ASN:HD22	1.46	0.63
1:A:255:GLU:OE1	1:A:282:ARG:NH2	2.32	0.63
1:D:286:TRP:HH2	2:D:501:GPD:H6GA	1.64	0.63
1:C:264:LYS:NZ	1:C:360:ASP:OD1	2.20	0.63
1:A:58:ASN:N	1:A:58:ASN:HD22	1.97	0.62
1:B:118:GLU:OE1	1:B:149:ARG:NH1	2.33	0.62
1:C:344:ASP:OD1	1:C:344:ASP:C	2.39	0.61
1:C:365:ALA:O	1:C:369:VAL:N	2.29	0.61
1:B:260:TRP:O	1:B:264:LYS:HD2	2.00	0.61
1:D:315:ARG:HB2	1:D:316:PRO:CD	2.31	0.61
1:B:122:THR:HB	1:B:123:PRO:CD	2.30	0.61
1:A:203:LEU:HG	1:A:207:MET:CE	2.30	0.61
1:C:81:VAL:O	1:C:102:LEU:HA	2.00	0.60
1:C:38:ILE:O	1:C:42:GLU:HG3	2.02	0.60
1:B:224:PRO:C	1:B:225[A]:ILE:HD13	2.21	0.60
1:C:293:GLY:H	1:C:296:LEU:HD12	1.67	0.60
1:C:187:ILE:HG22	1:C:188:ILE:N	2.16	0.59
1:B:335:LEU:O	1:B:339:GLU:HG3	2.03	0.59
1:D:231:ARG:HH11	1:D:231:ARG:HG2	1.67	0.59
1:B:166:TYR:CD1	1:B:167:ARG:HG3	2.36	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:215:MET:HB2	1:C:223:PHE:CE2	2.38	0.59
1:C:219:ARG:HG2	1:C:222:TRP:CB	2.32	0.59
1:D:187:ILE:HG22	1:D:188:ILE:HG23	1.85	0.59
1:C:9:VAL:HB	1:C:313:GLU:HG2	1.83	0.58
1:C:293:GLY:N	1:C:296:LEU:HD12	2.18	0.58
1:C:312:ILE:HD13	1:C:362:VAL:HA	1.86	0.58
4:C:469:HOH:O	2:D:500:GPD:H3G	2.03	0.58
1:C:138:CYS:O	1:C:140:MET:HG2	2.04	0.58
2:A:500:GPD:O4P	1:B:220:ARG:NH1	2.37	0.57
1:C:220:ARG:HD2	1:C:221:TYR:CZ	2.40	0.57
1:C:254:ARG:NH2	1:C:286:TRP:O	2.36	0.57
1:C:304:ILE:CG1	1:C:346:LEU:HD11	2.35	0.57
1:C:304:ILE:HG12	1:C:346:LEU:HD11	1.87	0.57
1:C:325:PRO:HG2	1:D:224:PRO:HA	1.87	0.57
1:C:271:ARG:O	1:C:296:LEU:HD11	2.04	0.57
1:C:186:LLP:C4'	2:D:500:GPD:N4A	2.68	0.57
1:A:58:ASN:H	1:A:58:ASN:ND2	2.03	0.56
1:C:216:ASP:HB3	1:C:219:ARG:O	2.05	0.56
1:C:7:ILE:HD11	1:C:361:ARG:HG2	1.87	0.56
1:D:365:ALA:O	1:D:369:VAL:HG13	2.05	0.56
1:B:267:ARG:HD2	1:B:363:ILE:HG21	1.86	0.56
1:B:7:ILE:HD12	1:B:312[A]:ILE:CD1	2.35	0.56
1:C:306:ASP:HB2	1:C:369:VAL:HG13	1.86	0.56
1:A:172:GLY:HA2	1:A:178:ALA:CB	2.35	0.56
1:A:13:ARG:HH11	1:A:13:ARG:HG3	1.71	0.56
1:C:220:ARG:NH2	1:C:220:ARG:HG3	2.21	0.56
1:D:186:LLP:H4'1	2:D:501:GPD:HN4B	1.55	0.56
1:D:357:ALA:O	1:D:360:ASP:HB2	2.07	0.55
1:C:122:THR:HB	1:C:123:PRO:CD	2.37	0.55
1:C:302:GLN:NE2	1:C:306:ASP:OD1	2.40	0.55
1:C:339:GLU:O	1:C:343:VAL:HG23	2.07	0.55
1:D:42:GLU:HG2	1:D:54:ALA:O	2.07	0.55
1:A:264:LYS:HB2	1:A:363:ILE:HD13	1.88	0.55
1:A:4:LEU:HD12	1:A:5:PRO:HD2	1.89	0.54
1:C:306:ASP:CB	1:C:369:VAL:HG13	2.36	0.54
1:D:247:VAL:HG13	1:D:248:ASP:N	2.22	0.54
1:B:172:GLY:HA2	1:B:178:ALA:CB	2.36	0.54
1:C:220:ARG:HD2	1:C:221:TYR:CE2	2.42	0.54
1:A:28:THR:C	1:A:29:THR:HG23	2.28	0.54
1:B:166:TYR:CE1	1:B:167:ARG:HG3	2.43	0.54
1:A:188:ILE:HD12	1:A:243:GLN:HB3	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:172:GLY:HA2	1:C:178:ALA:CB	2.38	0.54
1:A:141:ASP:N	1:A:142:PRO:HD2	2.22	0.53
1:A:24:GLU:O	1:A:28:THR:HG23	2.09	0.53
1:C:295:GLY:O	1:C:296:LEU:C	2.46	0.53
1:A:67:ALA:O	1:A:71:MET:HG3	2.09	0.52
1:D:18:GLU:HG3	1:D:242:ALA:HB3	1.91	0.52
1:B:7:ILE:HD12	1:B:312[A]:ILE:HD13	1.92	0.52
1:D:274:LYS:O	1:D:274:LYS:HG2	1.99	0.52
1:C:293:GLY:H	1:C:296:LEU:HD11	1.75	0.52
1:A:265:LEU:CD2	1:A:268:LEU:HD12	2.40	0.52
1:C:18:GLU:O	1:C:22:VAL:HG23	2.10	0.52
1:C:336:LYS:HB2	4:C:463:HOH:O	2.10	0.52
1:D:186:LLP:NZ	2:D:501:GPD:N4A	2.56	0.52
1:C:209:LEU:HD21	1:C:225:ILE:HD11	1.92	0.51
1:A:86:TYR:OH	1:B:213:GLN:HG3	2.11	0.51
1:C:287:MET:HE3	1:C:287:MET:HA	1.92	0.51
1:A:186:LLP:C4	2:A:500:GPD:N4A	2.70	0.51
1:A:203:LEU:HG	1:A:207:MET:HE1	1.93	0.51
1:D:286:TRP:CH2	2:D:501:GPD:H6GA	2.45	0.51
2:A:501:GPD:H4G	1:B:186:LLP:C4'	2.41	0.51
1:B:298:THR:HG22	1:B:371:VAL:O	2.12	0.50
1:C:299:THR:O	1:C:302:GLN:HB3	2.11	0.50
1:D:250:HIS:O	1:D:253:ALA:HB3	2.10	0.50
1:D:12:PRO:HB3	1:D:189:THR:HG21	1.93	0.50
1:B:219:ARG:HB2	1:B:222:TRP:CB	2.42	0.50
1:C:271:ARG:HH22	1:C:367:ASP:HA	1.76	0.50
1:C:287:MET:HE3	1:C:350:THR:OG1	2.11	0.50
1:B:126:LYS:HE2	4:B:1107:HOH:O	2.10	0.50
1:C:306:ASP:HB2	1:C:369:VAL:HG11	1.93	0.50
1:B:21:TYR:HB3	1:B:238:ALA:HB1	1.93	0.49
1:C:287:MET:HE2	1:C:347:ASN:HB3	1.93	0.49
1:A:213:GLN:NE2	1:A:229:ASN:HB2	2.27	0.49
1:B:81:VAL:O	1:B:102:LEU:HA	2.12	0.49
1:B:210:LEU:CD2	1:B:225[B]:ILE:HD12	2.43	0.49
1:D:325:PRO:HB2	1:D:326:PRO:HD3	1.94	0.49
1:A:359:ILE:HG22	1:A:363:ILE:HD12	1.95	0.49
1:C:66:LEU:HD23	1:C:196:ILE:HD11	1.93	0.49
1:C:351:HIS:H	1:C:354:LEU:HD12	1.78	0.49
1:B:13:ARG:HG3	4:B:1285:HOH:O	2.13	0.48
4:C:506:HOH:O	1:D:219:ARG:HD2	2.12	0.48
1:C:183:PHE:HD2	1:C:185:ASN:OD1	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:203:LEU:HG	1:B:207:MET:CE	2.43	0.48
1:B:219:ARG:HB2	1:B:222:TRP:HB3	1.95	0.48
1:C:109:THR:O	1:C:110:PHE:HB2	2.12	0.48
1:D:7:ILE:HD11	1:D:361:ARG:HD3	1.96	0.48
1:C:306:ASP:HB3	1:C:369:VAL:HG22	1.96	0.48
1:D:220:ARG:O	1:D:221:TYR:HB2	2.14	0.48
1:A:310:LEU:HD23	1:A:310:LEU:HA	1.73	0.48
1:C:141:ASP:N	1:C:142:PRO:CD	2.77	0.48
1:D:186:LLP:C4	2:D:501:GPD:N4A	2.75	0.48
1:B:269:GLY:HA2	4:B:1155:HOH:O	2.14	0.47
1:B:33:SER:HB2	1:B:231[A]:ARG:HD2	1.95	0.47
1:C:220:ARG:HD3	1:C:221:TYR:N	2.28	0.47
1:D:141:ASP:N	1:D:142:PRO:HD2	2.29	0.47
1:C:132:HIS:CE1	1:C:137:ILE:HG23	2.48	0.47
1:C:287:MET:HE1	1:C:348:LEU:O	2.15	0.47
1:C:55:ILE:HD12	1:C:55:ILE:N	2.29	0.47
1:D:307:LEU:HB3	1:D:312:ILE:HG22	1.95	0.47
1:D:9:VAL:CG1	1:D:10:ALA:N	2.76	0.47
1:A:51:VAL:HG21	1:A:197:THR:HB	1.96	0.47
1:B:162[B]:VAL:HG23	4:B:1163:HOH:O	2.13	0.47
1:B:38:ILE:O	1:B:42:GLU:HG3	2.14	0.47
1:D:318:PHE:CE1	2:D:501:GPD:H6G	2.50	0.47
1:B:165:THR:O	1:B:281:GLY:HA3	2.14	0.47
1:D:271:ARG:HB3	1:D:370:LEU:HD12	1.96	0.47
2:A:501:GPD:N4A	1:B:186:LLP:C4'	2.78	0.47
1:A:149:ARG:HH21	1:A:149:ARG:HG2	1.80	0.47
1:C:106:ASP:CG	1:C:107:PRO:HD2	2.35	0.47
1:C:220:ARG:HD3	1:C:221:TYR:H	1.80	0.47
1:A:172:GLY:HA2	1:A:178:ALA:HB3	1.97	0.46
1:B:58:ASN:HB3	4:B:1216:HOH:O	2.15	0.46
1:C:371:VAL:O	1:C:371:VAL:HG12	2.14	0.46
1:D:81:VAL:O	1:D:102:LEU:HA	2.15	0.46
1:A:162:VAL:HG12	1:A:187:ILE:HB	1.97	0.46
1:A:23:LEU:HD23	1:A:23:LEU:HA	1.76	0.46
1:C:348:LEU:O	1:C:350:THR:OG1	2.29	0.46
1:C:139:ASP:O	1:C:142:PRO:HG2	2.15	0.46
1:D:215:MET:HB2	1:D:223:PHE:CE2	2.50	0.46
1:C:23:LEU:HD23	1:C:23:LEU:HA	1.58	0.46
1:C:67:ALA:O	1:C:71:MET:HG3	2.16	0.46
1:D:286:TRP:O	1:D:287:MET:HE2	2.16	0.46
1:A:203:LEU:HG	1:A:207:MET:HE3	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:261:TYR:O	1:A:265:LEU:HG	2.16	0.46
1:C:302:GLN:OE1	1:C:302:GLN:HA	2.16	0.46
1:D:276:HIS:CB	3:D:1041:EDO:H12	2.27	0.46
1:A:12:PRO:HB3	1:A:189:THR:HG21	1.96	0.46
1:A:165:THR:O	1:A:281:GLY:HA3	2.15	0.45
1:C:220:ARG:O	1:C:221:TYR:HB2	2.14	0.45
1:B:231[A]:ARG:HD3	1:B:231[A]:ARG:HH21	1.62	0.45
1:B:148:ARG:NH2	4:B:1159:HOH:O	2.49	0.45
1:B:210:LEU:HD21	1:B:225[B]:ILE:HD12	1.98	0.45
1:C:299:THR:OG1	1:C:302:GLN:HB2	2.16	0.45
1:C:315:ARG:O	1:C:346:LEU:HD12	2.17	0.45
1:D:219:ARG:CG	1:D:222:TRP:HB2	2.40	0.45
1:B:209:LEU:O	1:B:214:GLY:HA2	2.16	0.45
1:C:275:PRO:HD3	1:C:289:THR:O	2.17	0.45
1:D:231:ARG:HG2	1:D:231:ARG:NH1	2.30	0.45
1:D:28:THR:C	1:D:29:THR:HG23	2.37	0.45
1:C:36:ARG:NH2	1:C:36:ARG:CG	2.77	0.45
1:C:300:ARG:CZ	1:C:316:PRO:CB	2.95	0.45
1:C:75:PRO:HA	1:C:97:GLY:O	2.17	0.45
1:C:67:ALA:HA	1:C:207:MET:HE2	1.99	0.44
1:C:220:ARG:HG3	1:C:220:ARG:HH21	1.81	0.44
1:C:302:GLN:HA	1:C:305:LYS:HE3	1.99	0.44
1:A:141:ASP:N	1:A:142:PRO:CD	2.79	0.44
1:B:216:ASP:HA	1:B:217:PRO:HD2	1.82	0.44
1:A:129:MET:O	1:A:129:MET:HG2	2.18	0.44
1:B:51:VAL:HG21	1:B:197:THR:HB	1.99	0.44
1:C:66:LEU:HD23	1:C:196:ILE:CD1	2.48	0.44
1:D:166:TYR:O	1:D:167:ARG:C	2.55	0.44
1:C:216:ASP:HB3	1:C:219:ARG:CB	2.40	0.44
1:C:310:LEU:HA	1:C:310:LEU:HD23	1.70	0.44
2:A:501:GPD:C4G	1:B:186:LLP:H4'1	2.48	0.44
1:B:36:ARG:O	1:B:39[A]:VAL:HG12	2.16	0.44
1:C:169:LYS:HB3	1:C:169:LYS:HE3	1.44	0.44
1:C:220:ARG:HD2	1:C:221:TYR:CD2	2.53	0.44
1:C:312:ILE:HD11	1:C:361:ARG:O	2.18	0.44
1:D:315:ARG:HE	1:D:316:PRO:HD2	1.83	0.44
1:C:111:ASN:O	1:C:112:LEU:C	2.55	0.43
1:D:64:LEU:HA	1:D:179:THR:HG21	2.00	0.43
1:C:64:LEU:HA	1:C:179:THR:HG21	2.00	0.43
1:C:265:LEU:HA	1:C:265:LEU:HD12	1.81	0.43
1:C:306:ASP:OD2	1:C:369:VAL:HG13	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:122:THR:HB	1:B:123:PRO:HD3	1.99	0.43
1:B:23:LEU:HD23	1:B:23:LEU:HA	1.75	0.43
1:B:24:GLU:HG2	1:B:37:PHE:HE2	1.84	0.43
1:B:39[A]:VAL:HG13	1:B:40:GLU:N	2.32	0.43
1:D:258:VAL:HG21	1:D:285:PHE:CG	2.54	0.43
1:D:51:VAL:HG21	1:D:197:THR:HB	2.00	0.43
1:A:66:LEU:HD23	1:A:196:ILE:CD1	2.48	0.43
1:D:24:GLU:O	1:D:28:THR:HG23	2.18	0.43
1:C:105:ASN:HD21	1:C:338:ALA:HA	1.83	0.43
1:C:307:LEU:O	1:C:308:ASP:C	2.55	0.43
1:A:166:TYR:O	1:A:167:ARG:C	2.56	0.43
1:B:146:VAL:HG22	1:B:149:ARG:NH1	2.34	0.43
1:C:304:ILE:CG1	1:C:346:LEU:CD1	2.97	0.43
1:D:93:VAL:O	1:D:96:CYS:HB2	2.19	0.43
1:C:271:ARG:NH2	1:C:367:ASP:O	2.52	0.43
1:A:130:PRO:HD2	1:A:155:ILE:O	2.19	0.43
1:B:34:VAL:O	1:B:34:VAL:HG12	2.18	0.43
1:C:200:ASP:OD2	1:C:203:LEU:HB2	2.19	0.43
1:B:172:GLY:HA2	1:B:178:ALA:HB3	2.00	0.42
1:C:292:LEU:HD23	1:C:292:LEU:HA	1.77	0.42
1:D:270:ASN:OD1	1:D:270:ASN:N	2.52	0.42
1:D:43:LYS:HD2	4:D:1228:HOH:O	2.19	0.42
1:B:325:PRO:HB2	1:B:326:PRO:HD3	2.01	0.42
1:C:145:GLU:OE2	1:C:145:GLU:HA	2.19	0.42
1:C:270:ASN:C	1:C:272:VAL:N	2.72	0.42
1:C:340:ALA:O	1:C:343:VAL:HB	2.19	0.42
1:C:10:ALA:CB	1:C:185:ASN:HB2	2.49	0.42
1:C:315:ARG:HB2	1:C:347:ASN:HD22	1.84	0.42
1:D:318:PHE:HE1	2:D:501:GPD:H6G	1.85	0.42
1:A:39[A]:VAL:HG12	4:A:690:HOH:O	2.19	0.42
1:C:204:ALA:O	1:C:208:ARG:HG3	2.20	0.42
1:C:27:ASP:HB2	4:C:562:HOH:O	2.20	0.42
1:D:152:LEU:HA	1:D:152:LEU:HD23	1.82	0.42
1:A:20:ASP:OD1	1:A:21:TYR:CD1	2.72	0.42
1:B:247:VAL:HG13	1:B:248:ASP:N	2.34	0.42
1:C:300:ARG:CZ	1:C:316:PRO:HB2	2.49	0.42
1:D:333:ASP:O	1:D:336:LYS:NZ	2.52	0.42
1:A:71:MET:HG2	1:A:203:LEU:HD11	2.02	0.42
1:A:9:VAL:HA	1:A:349:PRO:HA	2.01	0.42
1:B:274:LYS:HB2	1:B:275:PRO:HD2	2.02	0.42
1:B:313:GLU:O	1:B:349:PRO:HG3	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:160:GLU:HG2	1:C:286:TRP:CE3	2.55	0.42
1:C:287:MET:CE	1:C:348:LEU:O	2.68	0.42
1:D:220:ARG:HA	4:D:1187:HOH:O	2.19	0.42
1:C:356:GLU:O	1:C:357:ALA:C	2.58	0.42
1:C:200:ASP:HB3	1:C:203:LEU:HB2	2.02	0.41
1:D:159:ALA:HA	1:D:180:PHE:HA	2.01	0.41
1:D:118:GLU:OE2	1:D:150:HIS:NE2	2.49	0.41
1:B:216:ASP:OD2	1:B:219:ARG:HG3	2.20	0.41
1:D:256:ARG:HG3	1:D:260:TRP:CH2	2.56	0.41
1:A:109:THR:O	1:A:110:PHE:HB2	2.19	0.41
2:A:501:GPD:N4A	1:B:186:LLP:H4'	2.35	0.41
1:C:312:ILE:CD1	1:C:362:VAL:HA	2.49	0.41
1:D:315:ARG:HB2	1:D:316:PRO:HD2	2.02	0.41
1:D:315:ARG:HG3	1:D:347:ASN:HD22	1.85	0.41
1:A:148:ARG:HD2	4:A:729:HOH:O	2.19	0.41
1:A:254:ARG:NH2	1:A:286:TRP:O	2.53	0.41
1:A:74:GLY:O	1:A:77:ASP:HB2	2.20	0.41
2:A:501:GPD:HN4B	1:B:186:LLP:C4'	2.34	0.41
1:C:209:LEU:CD2	1:C:225:ILE:HD11	2.50	0.41
1:C:364:ALA:O	1:C:367:ASP:HB3	2.21	0.41
1:D:247:VAL:CG1	1:D:248:ASP:N	2.84	0.41
1:B:299:THR:O	1:B:303:VAL:HG23	2.21	0.41
1:C:165:THR:HA	1:C:169:LYS:O	2.21	0.41
1:D:162:VAL:HG12	1:D:187:ILE:HG21	2.03	0.41
1:B:211:ARG:HG2	1:B:231[A]:ARG:HG2	2.03	0.41
1:B:310:LEU:HD23	1:B:310:LEU:HA	1.92	0.41
1:C:264:LYS:H	1:C:264:LYS:HG3	1.66	0.41
1:D:313:GLU:O	1:D:349:PRO:HG3	2.21	0.41
1:A:36:ARG:CG	1:A:36:ARG:HH11	2.23	0.41
1:C:122:THR:HB	1:C:123:PRO:HD2	2.01	0.41
1:C:348:LEU:O	1:C:349:PRO:C	2.60	0.41
1:B:213:GLN:NE2	1:B:229:ASN:HB2	2.36	0.41
1:C:65:HIS:O	1:C:69:VAL:HG23	2.21	0.40
1:D:268:LEU:O	1:D:271:ARG:HB2	2.21	0.40
1:A:264:LYS:CB	1:A:363:ILE:HD13	2.51	0.40
1:C:214:GLY:O	1:C:224:PRO:HD2	2.21	0.40
1:D:137:ILE:HD11	1:D:171:SER:HB3	2.03	0.40
1:B:32[A]:SER:OG	1:B:33:SER:N	2.54	0.40
1:A:215:MET:HB2	1:A:223:PHE:CE2	2.57	0.40
1:B:118:GLU:O	1:B:119:ALA:C	2.60	0.40
1:C:23:LEU:HD11	1:D:23:LEU:HD21	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:254:ARG:HD3	1:A:285:PHE:O	2.20	0.40
1:B:36:ARG:HG3	1:B:37:PHE:N	2.37	0.40
1:C:85:THR:OG1	1:C:86:TYR:N	2.55	0.40
3:D:1041:EDO:C1	4:D:1160:HOH:O	2.69	0.40
1:D:45:PHE:CD2	1:D:195:MET:HG2	2.56	0.40
1:D:58:ASN:ND2	1:D:62:THR:OG1	2.54	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	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%)	29	13
1	D	364/391 (93%)	350 (96%)	13 (4%)	1 (0%)	41	24
All	All	1465/1564 (94%)	1407 (96%)	55 (4%)	3 (0%)	47	30

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%)	284 (95%)	15 (5%)	24	8
1	B	302/318 (95%)	292 (97%)	10 (3%)	38	19
1	C	296/318 (93%)	273 (92%)	23 (8%)	12	3
1	D	296/318 (93%)	274 (93%)	22 (7%)	13	3
All	All	1193/1272 (94%)	1123 (94%)	70 (6%)	19	6

All (70) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4	LEU
1	A	20	ASP
1	A	36	ARG
1	A	43	LYS
1	A	58	ASN
1	A	123	PRO
1	A	151	ASN
1	A	169	LYS
1	A	174	LEU
1	A	188	ILE
1	A	202	ASP
1	A	206	LYS
1	A	218	ASN
1	A	254	ARG
1	A	363	ILE
1	B	6	ARG
1	B	24	GLU
1	B	34	VAL
1	B	58	ASN
1	B	145	GLU
1	B	148	ARG
1	B	167	ARG
1	B	206	LYS
1	B	219	ARG
1	B	361	ARG
1	C	6	ARG
1	C	20	ASP
1	C	34	VAL
1	C	36	ARG
1	C	141	ASP

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Mol	Chain	Res	Type
1	C	145	GLU
1	C	169	LYS
1	C	187	ILE
1	C	188	ILE
1	C	203	LEU
1	C	220	ARG
1	C	225	ILE
1	C	254	ARG
1	C	263	GLN
1	C	270	ASN
1	C	283	HIS
1	C	297	SER
1	C	299	THR
1	C	313	GLU
1	C	336	LYS
1	C	361	ARG
1	C	366	LEU
1	C	367	ASP
1	D	6	ARG
1	D	8	SER
1	D	9	VAL
1	D	13	ARG
1	D	36	ARG
1	D	43	LYS
1	D	58	ASN
1	D	121	ILE
1	D	162	VAL
1	D	174	LEU
1	D	187	ILE
1	D	188	ILE
1	D	202	ASP
1	D	203	LEU
1	D	256	ARG
1	D	263	GLN
1	D	267	ARG
1	D	274	LYS
1	D	292	LEU
1	D	297	SER
1	D	361	ARG
1	D	369	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	58	ASN
1	A	347	ASN
1	B	58	ASN
1	C	91	ASN
1	C	105	ASN
1	C	250	HIS
1	C	263	GLN
1	C	347	ASN
1	D	58	ASN
1	D	263	GLN
1	D	347	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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	D	186	1	23,24,25	1.29	3 (13%)	25,32,34	1.30	3 (12%)
1	LLP	C	186	1	23,24,25	1.24	1 (4%)	25,32,34	1.28	4 (16%)
1	LLP	B	186	1	23,24,25	1.19	3 (13%)	25,32,34	1.70	7 (28%)
1	LLP	A	186	1	23,24,25	1.31	3 (13%)	25,32,34	1.51	5 (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
1	LLP	D	186	1	-	3/16/17/19	0/1/1/1

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

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	186	LLP	P-OP1	3.70	1.62	1.50
1	C	186	LLP	P-OP1	3.34	1.61	1.50
1	D	186	LLP	P-OP1	3.22	1.60	1.50
1	B	186	LLP	P-OP1	2.82	1.59	1.50
1	D	186	LLP	C4-C4'	2.25	1.50	1.46
1	A	186	LLP	C4-C5	2.16	1.44	1.42
1	B	186	LLP	C2-N1	-2.15	1.29	1.33
1	B	186	LLP	CE-NZ	2.12	1.51	1.46
1	D	186	LLP	C3-C2	-2.10	1.38	1.40
1	A	186	LLP	C4-C4'	2.02	1.50	1.46

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	186	LLP	OP4-C5'-C5	4.64	118.20	109.35
1	A	186	LLP	CD-CG-CB	3.65	126.53	113.62
1	B	186	LLP	C3-C4-C5	-3.05	115.92	118.26
1	C	186	LLP	OP4-C5'-C5	3.02	115.11	109.35
1	B	186	LLP	OP2-P-OP4	-2.93	98.93	106.73
1	B	186	LLP	C4-C3-C2	2.91	121.99	120.19
1	A	186	LLP	OP3-P-OP4	2.85	114.31	106.73
1	A	186	LLP	OP4-P-OP1	2.75	114.18	106.47
1	C	186	LLP	OP2-P-OP4	2.72	113.97	106.73
1	A	186	LLP	C3-C4-C5	-2.67	116.21	118.26
1	A	186	LLP	CE-NZ-C4'	2.54	126.69	118.90
1	B	186	LLP	CE-NZ-C4'	2.34	126.08	118.90
1	D	186	LLP	CG-CD-CE	-2.24	105.77	113.57
1	C	186	LLP	CE-NZ-C4'	2.23	125.74	118.90
1	D	186	LLP	CD-CG-CB	2.18	121.32	113.62
1	C	186	LLP	C6-N1-C2	2.11	123.08	119.17
1	D	186	LLP	OP2-P-OP4	2.08	112.27	106.73
1	B	186	LLP	OP3-P-OP4	2.08	112.26	106.73
1	B	186	LLP	OP4-P-OP1	2.05	112.22	106.47

There are no chirality outliers.

All (11) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	186	LLP	CG-CD-CE-NZ
1	D	186	LLP	CG-CD-CE-NZ
1	B	186	LLP	CG-CD-CE-NZ
1	C	186	LLP	CA-CB-CG-CD
1	B	186	LLP	CA-CB-CG-CD
1	B	186	LLP	N-CA-CB-CG
1	D	186	LLP	CA-CB-CG-CD
1	B	186	LLP	C3-C4-C4'-NZ
1	B	186	LLP	CD-CE-NZ-C4'
1	C	186	LLP	CG-CD-CE-NZ
1	D	186	LLP	CD-CE-NZ-C4'

There are no ring outliers.

4 monomers are involved in 16 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	D	186	LLP	5	0
1	C	186	LLP	2	0
1	B	186	LLP	5	0
1	A	186	LLP	4	0

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

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	$\# Z  > 2$
3	EDO	D	1041	-	3,3,3	0.50	0	2,2,2	0.10	0
2	GPD	D	500	-	31,40,40	0.82	0	38,62,62	1.74	6 (15%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	EDO	B	1040	-	3,3,3	0.44	0	2,2,2	0.44	0
2	GPD	D	501	-	31,40,40	0.56	0	38,62,62	1.99	8 (21%)
2	GPD	A	500	-	31,40,40	0.61	0	38,62,62	1.69	8 (21%)
2	GPD	A	501	-	31,40,40	2.56	12 (38%)	38,62,62	2.79	16 (42%)

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	EDO	D	1041	-	-	1/1/1/1	-
2	GPD	D	500	-	-	2/17/53/53	0/4/4/4
3	EDO	B	1040	-	-	1/1/1/1	-
2	GPD	D	501	-	-	2/17/53/53	0/4/4/4
2	GPD	A	500	-	-	3/17/53/53	0/4/4/4
2	GPD	A	501	-	-	2/17/53/53	1/4/4/4

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	501	GPD	P2-O1G	-7.35	1.41	1.60
2	A	501	GPD	C6-N1	4.60	1.41	1.33
2	A	501	GPD	P-O1P	-4.51	1.34	1.55
2	A	501	GPD	C2-N1	-3.89	1.28	1.35
2	A	501	GPD	O4'-C1'	-3.52	1.36	1.41
2	A	501	GPD	C2-N2	-3.44	1.27	1.33
2	A	501	GPD	O2'-C2'	-3.27	1.35	1.43
2	A	501	GPD	C4G-N4A	-2.67	1.38	1.47
2	A	501	GPD	P2-O4P	-2.53	1.43	1.55
2	A	501	GPD	O5'-C5'	-2.35	1.35	1.44
2	A	501	GPD	C8-N7	-2.34	1.30	1.34
2	A	501	GPD	C3G-C2G	-2.04	1.49	1.52

All (38) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	501	GPD	C5-C6-N1	-8.00	112.49	123.43
2	A	501	GPD	O5G-C1G-O1G	5.83	118.99	111.36
2	A	501	GPD	C2-N3-C4	5.78	121.96	115.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	501	GPD	O1G-C1G-C2G	-5.39	98.50	108.38
2	A	501	GPD	O5G-C5G-C6G	5.17	117.86	106.70
2	D	500	GPD	N3-C2-N1	-4.95	120.62	127.22
2	D	501	GPD	N3-C2-N1	-4.87	120.73	127.22
2	A	501	GPD	O5G-C1G-C2G	-4.68	102.95	111.31
2	A	500	GPD	C2-N3-C4	4.45	120.44	115.36
2	A	500	GPD	N3-C2-N1	-4.39	121.37	127.22
2	D	500	GPD	O5G-C1G-O1G	-4.13	105.97	111.36
2	D	500	GPD	C2-N3-C4	4.00	119.92	115.36
2	A	501	GPD	O2G-C2G-C3G	-3.95	100.14	109.94
2	A	501	GPD	C6-N1-C2	3.93	122.17	115.93
2	D	501	GPD	C6-N1-C2	3.85	122.05	115.93
2	D	501	GPD	C2-N3-C4	3.84	119.75	115.36
2	D	501	GPD	C5-C6-N1	-3.82	118.21	123.43
2	D	500	GPD	C6-N1-C2	3.64	121.71	115.93
2	D	500	GPD	C5-C6-N1	-3.61	118.50	123.43
2	A	501	GPD	C5G-C4G-N4A	3.60	118.83	110.90
2	A	501	GPD	O3'-C3'-C4'	3.45	121.02	111.05
2	A	501	GPD	C1G-O5G-C5G	3.39	119.50	113.67
2	A	500	GPD	O5G-C1G-O1G	-3.34	106.99	111.36
2	A	500	GPD	P-OPP-P2	-2.82	123.15	132.83
2	D	501	GPD	C4-C5-N7	-2.76	106.53	109.40
2	A	501	GPD	C1'-N9-C4	2.72	131.43	126.64
2	A	500	GPD	C5-C6-N1	-2.72	119.72	123.43
2	A	500	GPD	C4-C5-N7	-2.55	106.74	109.40
2	D	501	GPD	P-OPP-P2	-2.55	124.08	132.83
2	A	501	GPD	N3-C2-N1	-2.49	123.90	127.22
2	A	500	GPD	C6-N1-C2	2.48	119.87	115.93
2	A	501	GPD	O2'-C2'-C3'	2.43	119.68	111.82
2	A	501	GPD	C6-C5-C4	2.41	123.10	120.80
2	D	501	GPD	N2-C2-N3	2.26	121.47	117.79
2	A	501	GPD	O2'-C2'-C1'	2.22	119.07	110.85
2	A	501	GPD	C2'-C3'-C4'	2.04	106.61	102.64
2	D	500	GPD	OPP-P2-O1G	-2.03	98.39	102.48
2	A	500	GPD	C5'-C4'-C3'	-2.01	107.65	115.18

There are no chirality outliers.

All (11) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	500	GPD	C1G-O1G-P2-OPP
2	D	500	GPD	C1G-O1G-P2-OPP

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Mol	Chain	Res	Type	Atoms
3	D	1041	EDO	O1-C1-C2-O2
2	A	501	GPD	P2-OPP-P-O1P
2	D	501	GPD	P2-OPP-P-O1P
2	D	501	GPD	P2-OPP-P-O2P
3	B	1040	EDO	O1-C1-C2-O2
2	D	500	GPD	P2-OPP-P-O2P
2	A	500	GPD	P2-OPP-P-O1P
2	A	500	GPD	P2-OPP-P-O2P
2	A	501	GPD	P2-OPP-P-O2P

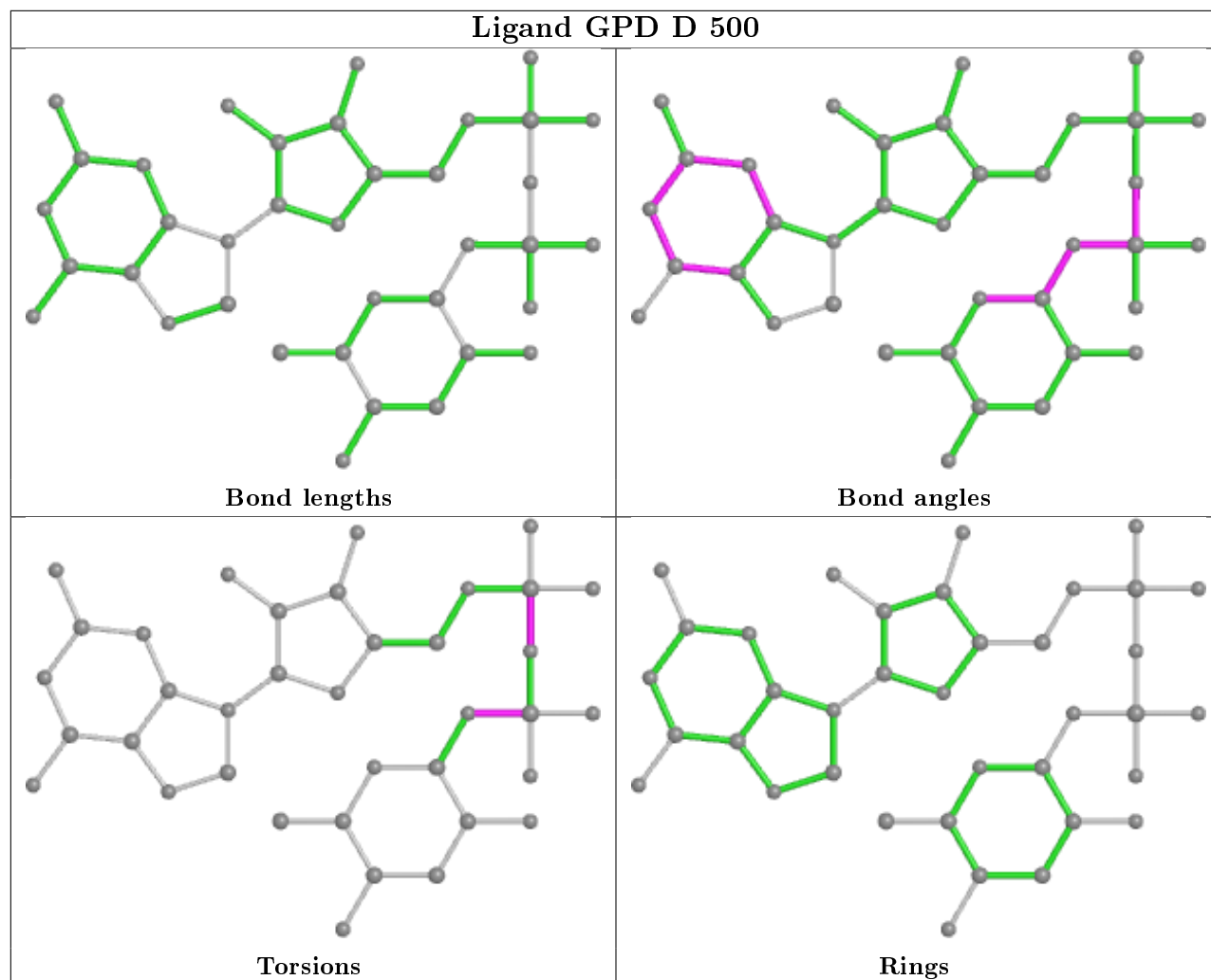
All (1) ring outliers are listed below:

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

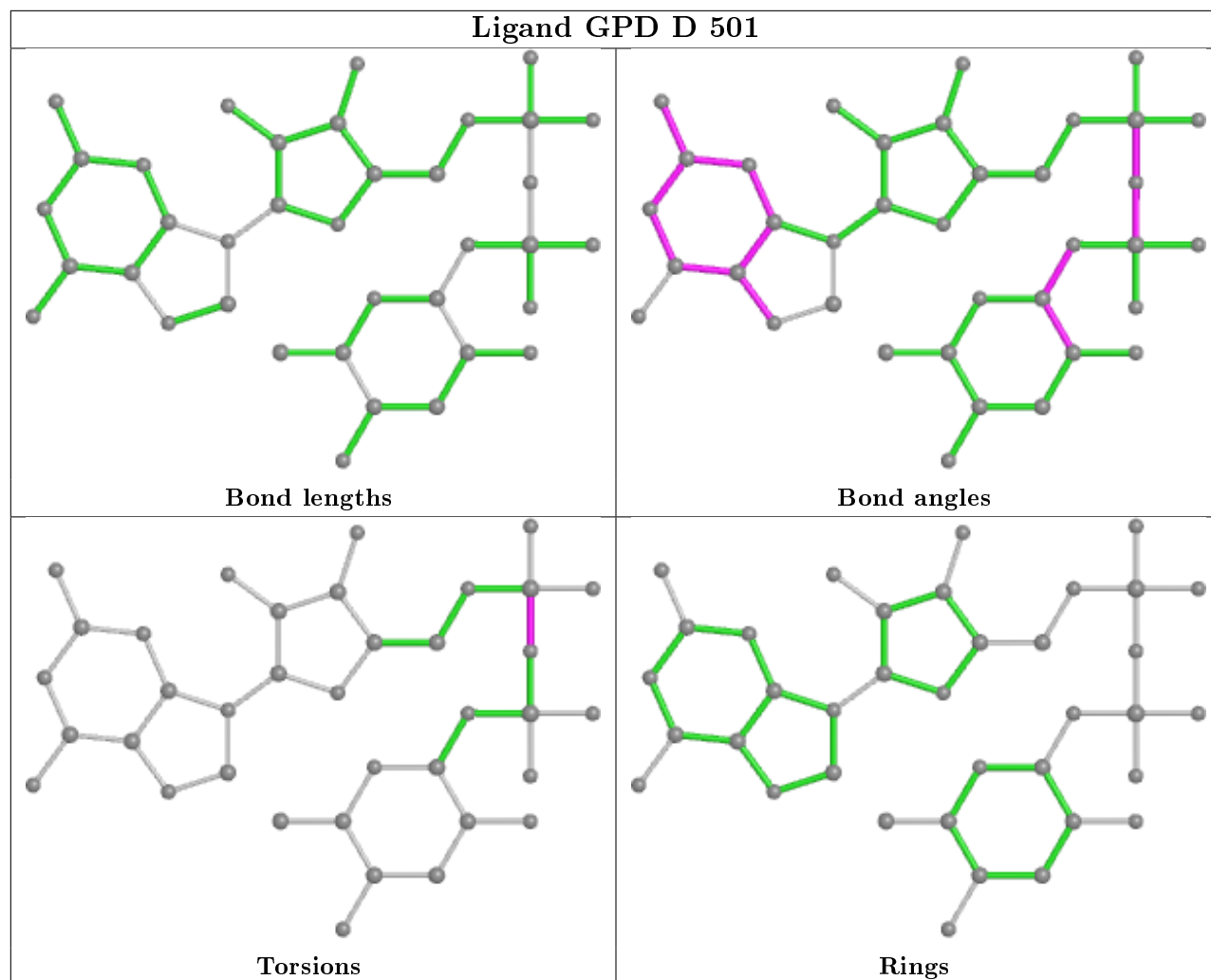
5 monomers are involved in 25 short contacts:

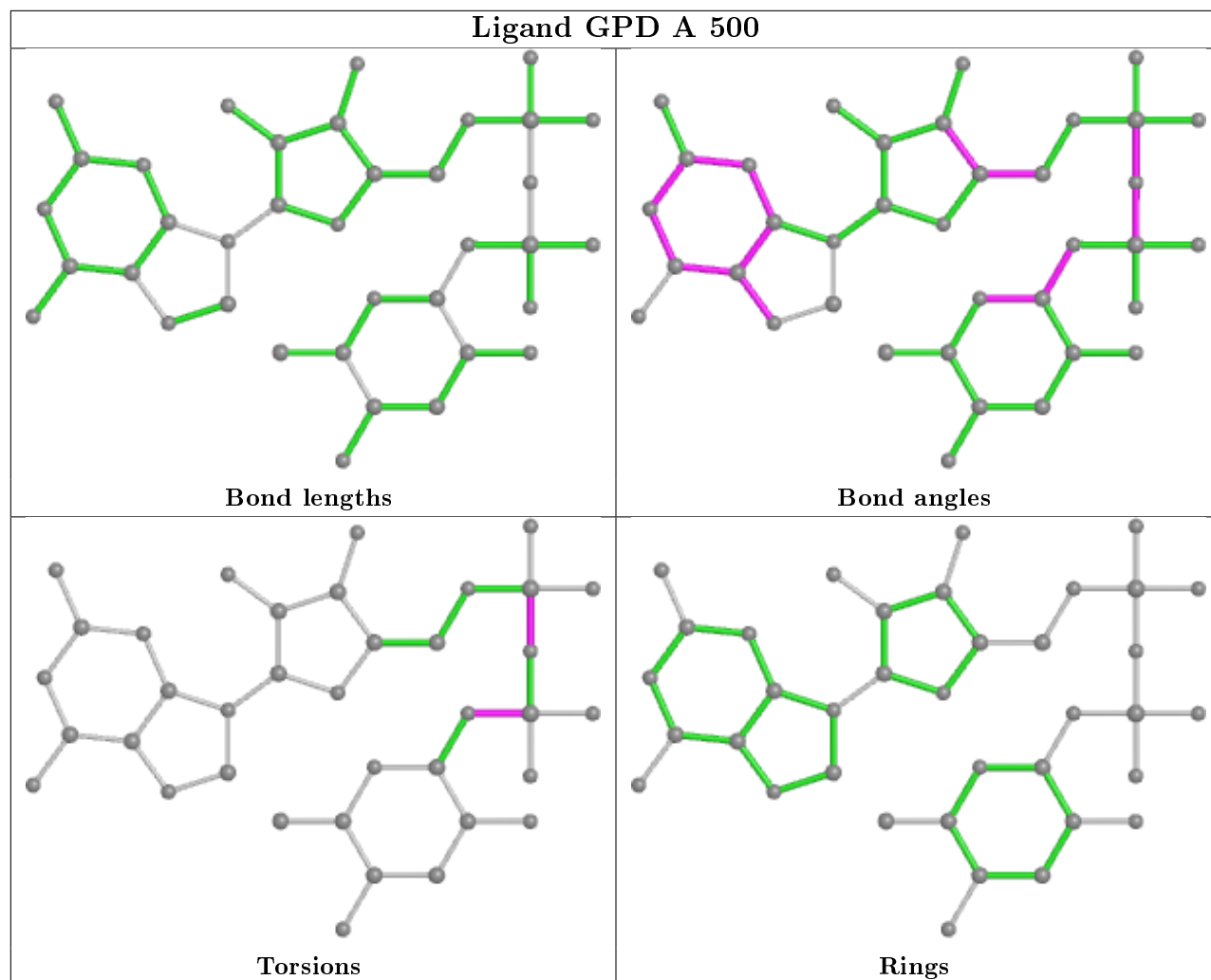
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	1041	EDO	3	0
2	D	500	GPD	3	0
2	D	501	GPD	9	0
2	A	500	GPD	5	0
2	A	501	GPD	5	0

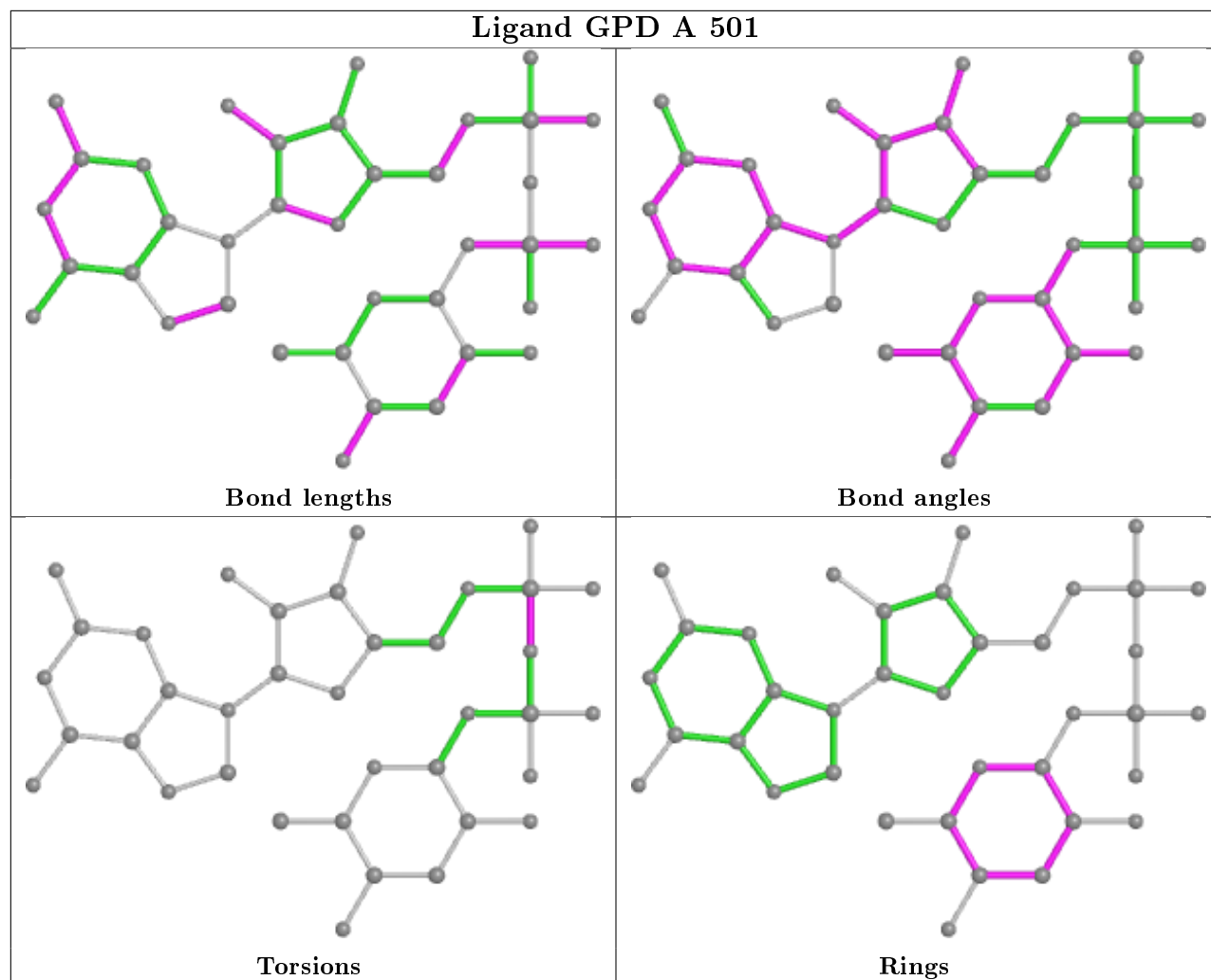
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

### 6.1 Protein, DNA and RNA chains ⓘ

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%)	-0.08	1 (0%) 94 94	5, 13, 37, 75	0
1	B	366/391 (93%)	-0.11	0 100 100	5, 14, 39, 80	0
1	C	366/391 (93%)	0.43	32 (8%) 10 11	5, 21, 64, 90	0
1	D	366/391 (93%)	0.03	2 (0%) 91 92	4, 19, 46, 74	0
All	All	1465/1564 (93%)	0.07	35 (2%) 59 63	4, 16, 51, 90	0

All (35) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	371	VAL	11.3
1	C	363	ILE	5.6
1	C	362	VAL	5.1
1	C	369	VAL	5.0
1	C	366	LEU	4.8
1	C	268	LEU	4.8
1	C	265	LEU	4.5
1	C	364	ALA	4.4
1	C	365	ALA	4.1
1	C	357	ALA	4.0
1	C	296	LEU	3.6
1	A	4	LEU	3.3
1	C	266	ALA	3.3
1	C	263	GLN	3.3
1	C	311	GLY	3.3
1	C	309	ALA	3.2
1	C	6	ARG	3.1
1	C	368	GLN	2.9
1	D	6	ARG	2.8
1	C	355	THR	2.7
1	C	310	LEU	2.7

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Mol	Chain	Res	Type	RSRZ
1	C	260	TRP	2.7
1	C	5	PRO	2.6
1	C	312	ILE	2.6
1	C	370	LEU	2.6
1	C	367	ASP	2.5
1	C	359	ILE	2.5
1	C	267	ARG	2.4
1	C	360	ASP	2.3
1	C	270	ASN	2.2
1	C	272	VAL	2.2
1	C	303	VAL	2.2
1	C	354	LEU	2.1
1	D	371	VAL	2.1
1	C	307	LEU	2.1

## 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( $\text{\AA}^2$ )	Q<0.9
1	LLP	D	186	24/25	0.95	0.10	1,14,21,28	0
1	LLP	C	186	24/25	0.95	0.11	1,13,18,26	0
1	LLP	B	186	24/25	0.95	0.12	2,8,17,22	0
1	LLP	A	186	24/25	0.95	0.10	2,9,16,24	0

## 6.3 Carbohydrates [i](#)

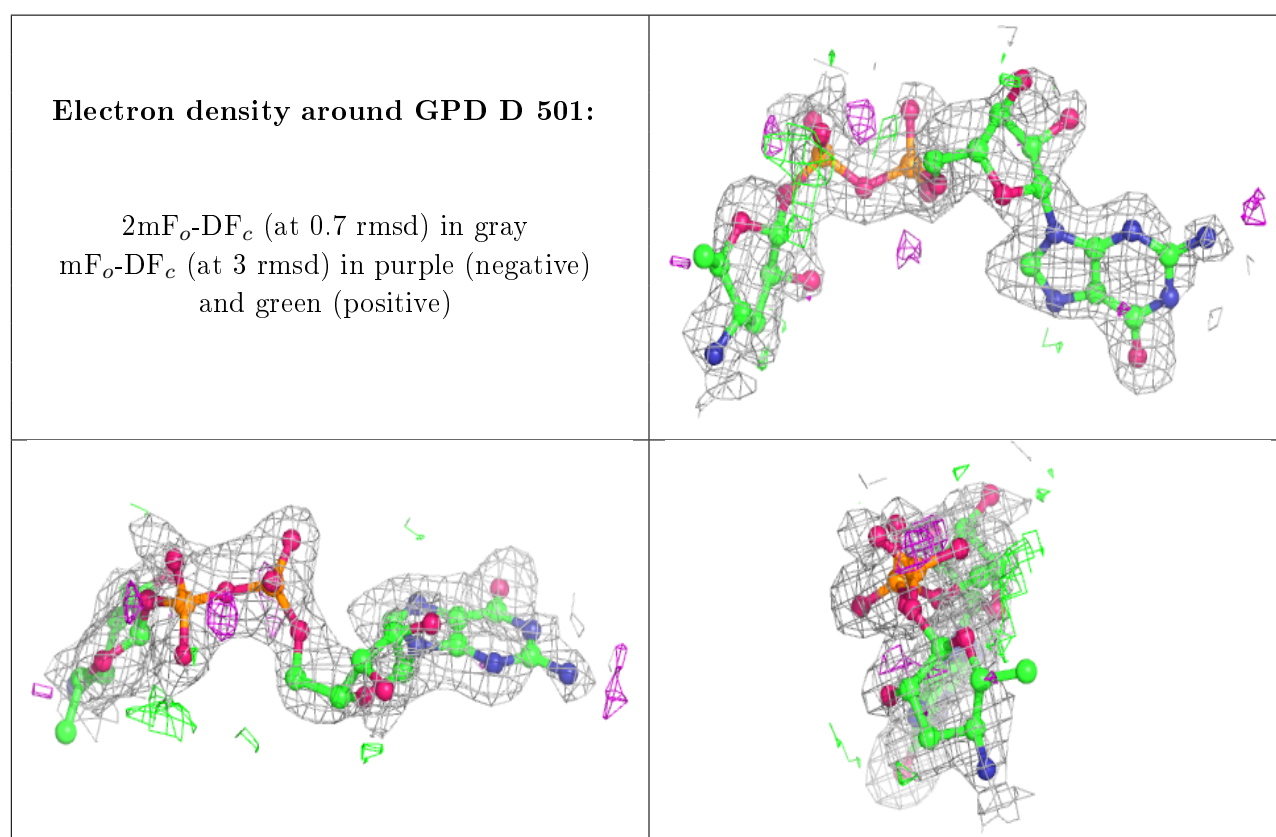
There are no carbohydrates in this entry.

## 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.

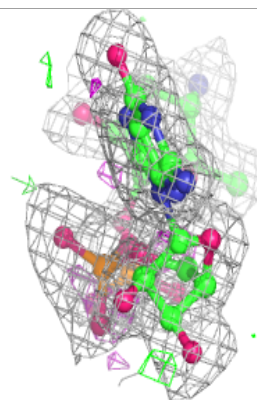
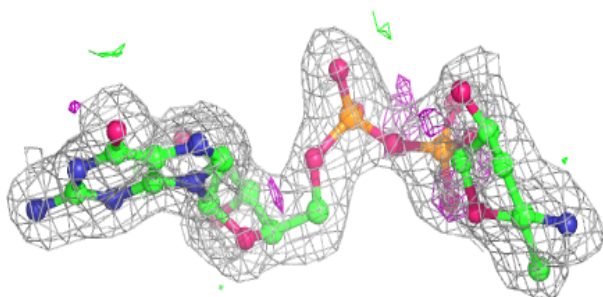
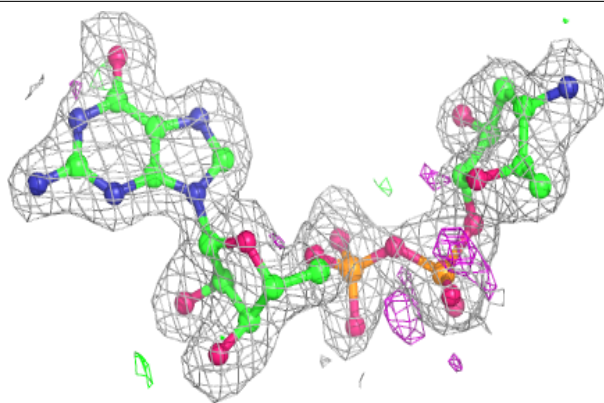
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
3	EDO	B	1040	4/4	0.80	0.15	17,32,32,36	0
2	GPD	D	501	37/37	0.85	0.16	25,61,99,99	0
3	EDO	D	1041	4/4	0.87	0.19	23,23,31,50	0
2	GPD	D	500	37/37	0.92	0.11	20,30,82,99	0
2	GPD	A	500	37/37	0.92	0.12	16,31,99,99	0
2	GPD	A	501	37/37	0.95	0.09	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.

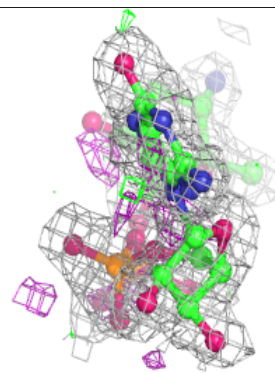
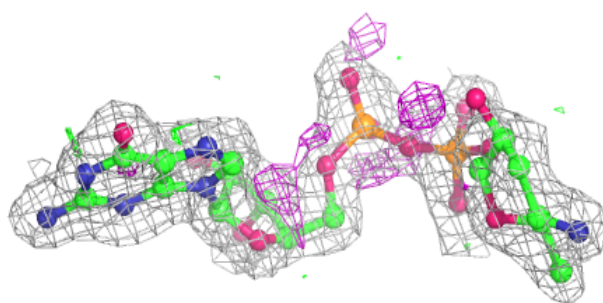
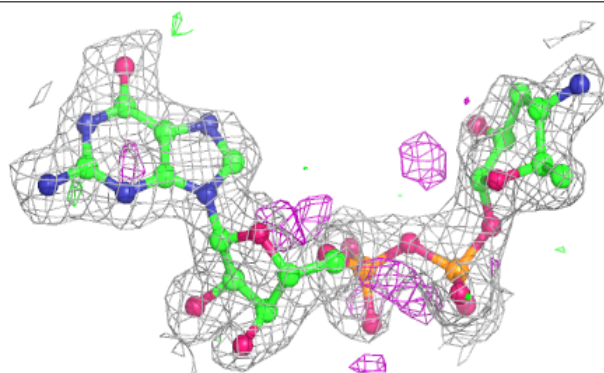


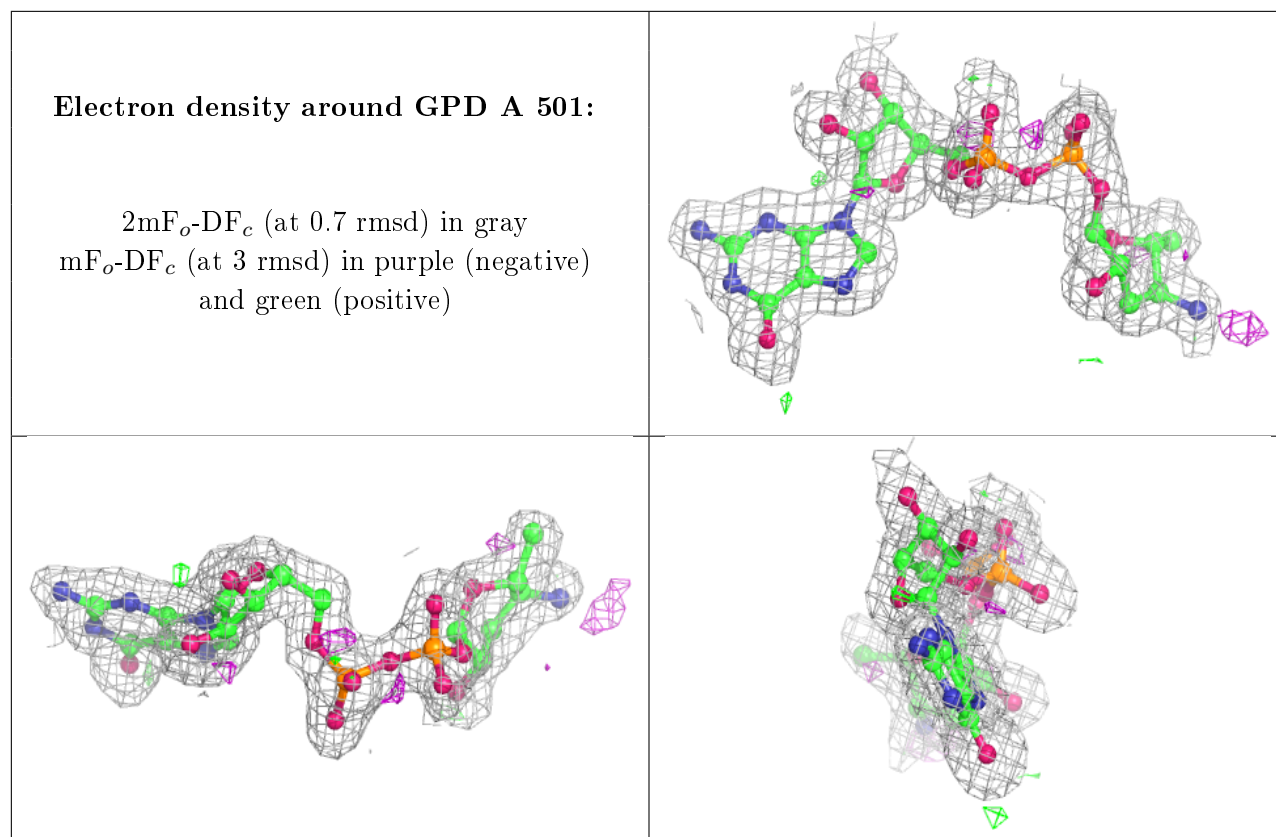
**Electron density around GPD D 500:**

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

**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)





## 6.5 Other polymers [i](#)

There are no such residues in this entry.