



# Full wwPDB X-ray Structure Validation Report ⓘ

Nov 6, 2023 – 04:17 AM EST

PDB ID : 6C3A  
Title : O2-, PLP-dependent L-arginine hydroxylase RohP 4-hydroxy-2-ketoarginine complex  
Authors : Hedges, J.B.; Ryan, K.S.  
Deposited on : 2018-01-09  
Resolution : 1.53 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 : 2.36  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.36

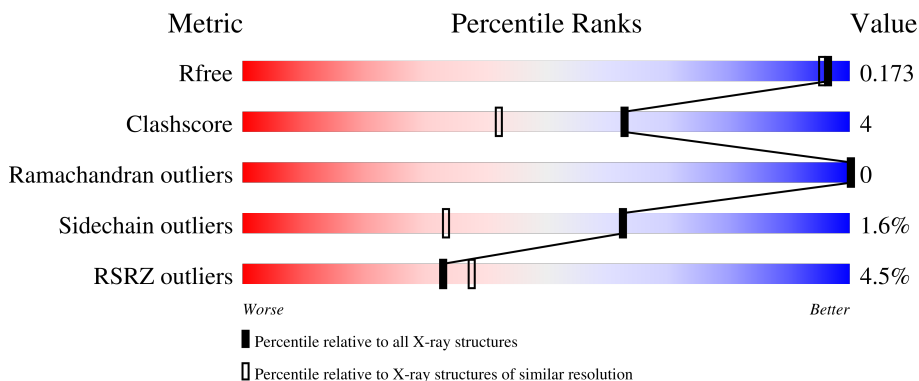
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.53 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	2556 (1.56-1.52)
Clashscore	141614	2634 (1.56-1.52)
Ramachandran outliers	138981	2580 (1.56-1.52)
Sidechain outliers	138945	2577 (1.56-1.52)
RSRZ outliers	127900	2524 (1.56-1.52)

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	413	
1	B	413	

## 2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 7121 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 Uncharacterized protein.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	P	S			
1	A	378	Total 3049	C 1951	N 507	O 572	P 1	S 18	0	4	0
1	B	377	Total 3091	C 1979	N 522	O 570	P 1	S 19	0	7	0

- Molecule 2 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C<sub>2</sub>H<sub>6</sub>O<sub>2</sub>).



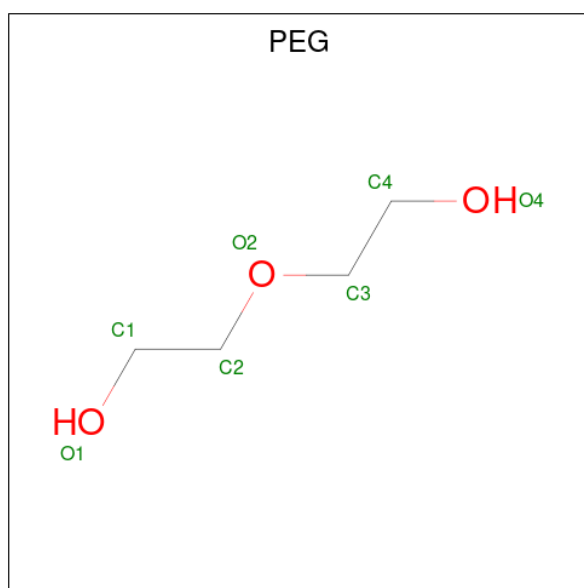
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
2	A	1	Total 4	C 2	O 2	0	0
2	A	1	Total 4	C 2	O 2	0	0
2	A	1	Total 4	C 2	O 2	0	0
2	A	1	Total 4	C 2	O 2	0	0

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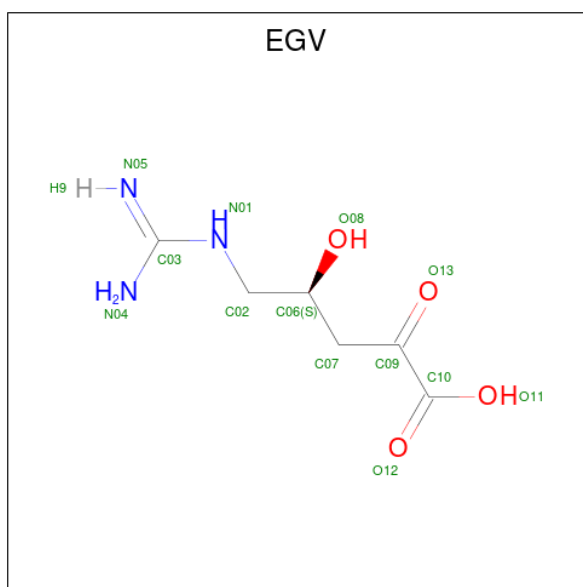
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			4	2	2		
2	B	1	Total	C	O	0	0
			4	2	2		
2	B	1	Total	C	O	0	0
			4	2	2		
2	B	1	Total	C	O	0	0
			4	2	2		
2	B	1	Total	C	O	0	0
			4	2	2		
2	B	1	Total	C	O	0	0
			4	2	2		

- Molecule 3 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: C<sub>4</sub>H<sub>10</sub>O<sub>3</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			7	4	3		

- Molecule 4 is (4S)-5-carbamimidamido-4-hydroxy-2-oxopentanoic acid (three-letter code: EGV) (formula: C<sub>6</sub>H<sub>11</sub>N<sub>3</sub>O<sub>4</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			13	6	3	4		
4	B	1	Total	C	N	O	0	0
			13	6	3	4		

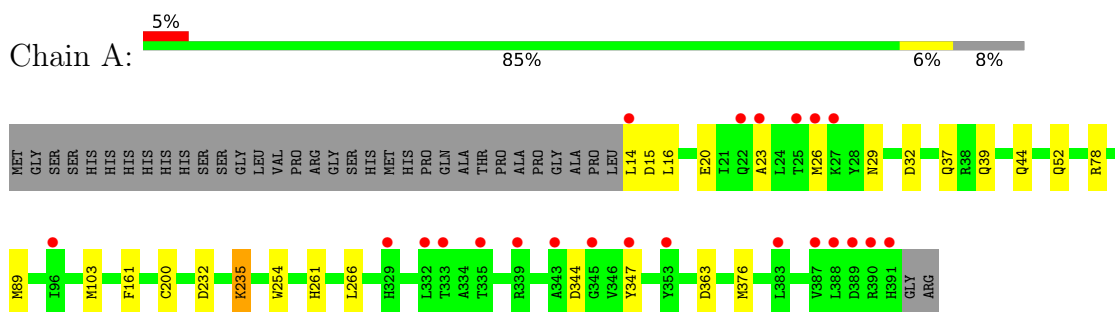
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	434	Total	O	0	0
			434	434		
5	B	470	Total	O	0	0
			470	470		

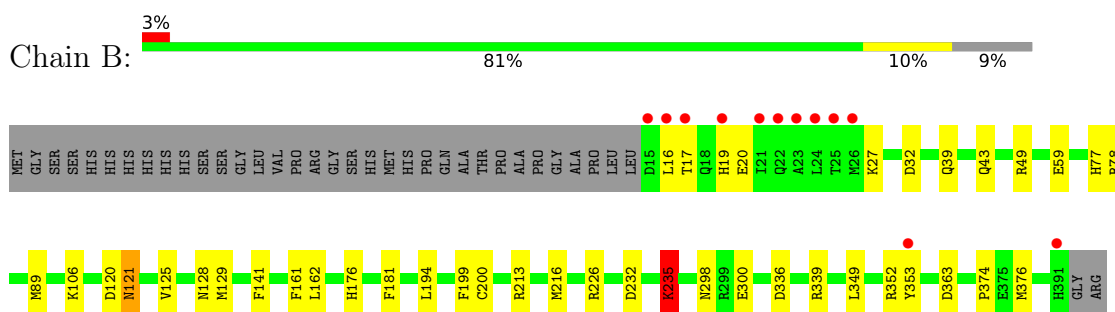
### 3 Residue-property plots [i](#)

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: Uncharacterized protein



- Molecule 1: Uncharacterized protein



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	78.80Å 112.55Å 101.97Å 90.00° 96.39° 90.00°	Depositor
Resolution (Å)	41.69 – 1.53 41.69 – 1.53	Depositor EDS
% Data completeness (in resolution range)	100.0 (41.69-1.53) 100.0 (41.69-1.53)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.05 (at 1.53Å)	Xtrriage
Refinement program	PHENIX 1.11.1_2575	Depositor
R, $R_{free}$	0.153 , 0.173 0.153 , 0.173	Depositor DCC
$R_{free}$ test set	6722 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	15.6	Xtrriage
Anisotropy	0.284	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 54.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	7121	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	23.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.33% 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: PEG, EGV, EDO, LLP

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	0.32	0/3107	0.52	0/4229
1	B	0.35	0/3155	0.56	1/4285 (0.0%)
All	All	0.34	0/6262	0.54	1/8514 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	B	352	ARG	C-N-CA	-5.43	108.12	121.70

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	235	LLP	Mainchain

### 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	3049	0	2946	17	0
1	B	3091	0	3033	37	0
2	A	20	0	30	4	0
2	B	24	0	36	6	0
3	A	7	0	10	0	0
4	A	13	0	0	0	0
4	B	13	0	0	0	0
5	A	434	0	0	2	0
5	B	470	0	0	5	0
All	All	7121	0	6055	53	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 4.

All (53) 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:336:ASP:OD1	1:B:339:ARG:NH2	2.22	0.72
1:B:300:GLU:OE1	5:B:501:HOH:O	2.09	0.70
1:B:16:LEU:HG	1:B:353[B]:TYR:HB3	1.77	0.67
1:A:89[B]:MET:CE	2:A:401:EDO:H11	2.25	0.66
1:B:162:LEU:HB3	2:B:402:EDO:H11	1.79	0.64
1:B:77:HIS:CD2	1:B:213:ARG:HH11	2.17	0.62
1:B:19:HIS:O	5:B:502:HOH:O	2.16	0.62
1:B:49:ARG:NH2	5:B:506:HOH:O	2.33	0.61
1:A:78:ARG:HH12	2:A:406:EDO:H11	1.65	0.61
1:A:37:GLN:NE2	5:A:504:HOH:O	2.34	0.60
1:B:20:GLU:HB3	1:B:32:ASP:HB3	1.84	0.59
1:B:59:GLU:OE1	5:B:503:HOH:O	2.16	0.59
1:B:125:VAL:O	1:B:129[B]:MET:HG2	2.04	0.58
1:B:200[A]:CYS:SG	1:B:232:ASP:HB2	2.44	0.57
1:A:89[B]:MET:HE3	1:A:261:HIS:CD2	2.39	0.57
2:B:406:EDO:O2	5:B:504:HOH:O	2.17	0.56
1:B:199:PHE:CZ	1:B:216[B]:MET:HG2	2.40	0.56
1:B:77:HIS:HD2	1:B:213:ARG:HH11	1.54	0.55
1:A:89[B]:MET:HE2	2:A:401:EDO:H11	1.88	0.55
1:B:16:LEU:HD22	1:B:349:LEU:HD13	1.87	0.55
1:B:120:ASP:HB3	1:B:353[A]:TYR:O	2.07	0.55
1:B:298:ASN:HD21	1:B:374:PRO:HA	1.71	0.55
1:B:78:ARG:HH22	2:B:405:EDO:HO2	1.55	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:78:ARG:NH2	2:B:405:EDO:O2	2.31	0.53
1:B:121:ASN:O	1:B:125:VAL:HG13	2.09	0.53
1:B:199:PHE:HZ	1:B:216[B]:MET:HG2	1.72	0.53
1:A:200[B]:CYS:SG	1:A:232:ASP:HB2	2.50	0.52
1:A:89[B]:MET:HE3	1:A:261:HIS:CG	2.44	0.52
1:B:16:LEU:CD2	1:B:349:LEU:HD13	2.39	0.52
1:B:141:PHE:O	1:B:176:HIS:HE1	1.93	0.51
1:B:39:GLN:HE21	1:B:43:GLN:HB3	1.77	0.50
1:B:200[B]:CYS:HB3	1:B:235:LLP:H2'2	1.95	0.49
1:A:23:ALA:O	1:A:29:ASN:HB2	2.13	0.48
1:B:16:LEU:CG	1:B:353[B]:TYR:HB3	2.43	0.48
1:B:89[B]:MET:HG3	2:B:401:EDO:H22	1.96	0.47
1:B:120:ASP:HB3	1:B:353[B]:TYR:O	2.14	0.47
1:A:200[A]:CYS:HB3	1:A:235:LLP:H2'2	1.97	0.46
5:A:782:HOH:O	1:B:106:LYS:HG2	2.16	0.45
1:B:16:LEU:HD23	1:B:16:LEU:HA	1.72	0.45
1:A:20:GLU:HB3	1:A:32:ASP:HB3	1.99	0.45
1:B:16:LEU:HB2	1:B:120:ASP:OD1	2.16	0.45
1:A:254:TRP:CD1	2:A:401:EDO:H12	2.52	0.45
1:A:14:LEU:HD23	1:A:15:ASP:N	2.33	0.44
1:A:16:LEU:O	1:A:20:GLU:HG3	2.18	0.44
1:B:200[A]:CYS:HB2	1:B:235:LLP:H2'2	2.00	0.44
1:A:39:GLN:HB2	1:A:44:GLN:HG2	2.00	0.43
1:A:26:MET:HG3	1:A:347:TYR:CE2	2.54	0.42
1:B:162:LEU:HD22	2:B:402:EDO:H12	2.01	0.42
1:B:181:PHE:CD2	1:B:216[B]:MET:HE1	2.56	0.41
1:A:266:LEU:HA	1:B:17:THR:HG23	2.03	0.41
1:A:103:MET:SD	1:B:128:ASN:HB3	2.61	0.40
1:B:120:ASP:OD1	1:B:121:ASN:N	2.54	0.40
1:B:194:LEU:HD13	1:B:226[B]:ARG:HG2	2.04	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	379/413 (92%)	376 (99%)	3 (1%)	0	100	100
1	B	381/413 (92%)	373 (98%)	8 (2%)	0	100	100
All	All	760/826 (92%)	749 (99%)	11 (1%)	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	324/360 (90%)	319 (98%)	5 (2%)	65	36
1	B	330/360 (92%)	325 (98%)	5 (2%)	65	36
All	All	654/720 (91%)	644 (98%)	10 (2%)	62	36

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	52	GLN
1	A	161	PHE
1	A	344	ASP
1	A	363	ASP
1	A	376	MET
1	B	27	LYS
1	B	121	ASN
1	B	161	PHE
1	B	363	ASP
1	B	376	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	39	GLN
1	B	77	HIS
1	B	176	HIS
1	B	240	GLN
1	B	298	ASN
1	B	314	GLN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

2 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	235	1	23,24,25	1.13	2 (8%)	25,32,34	1.14	1 (4%)
1	LLP	A	235	1	23,24,25	0.89	1 (4%)	25,32,34	1.36	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	235	1	-	1/16/17/19	0/1/1/1
1	LLP	A	235	1	-	1/16/17/19	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	235	LLP	O-C	3.86	1.35	1.19
1	A	235	LLP	C3-C2	2.64	1.43	1.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	235	LLP	C3-C2	2.03	1.42	1.40

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	235	LLP	OP3-P-OP4	-3.10	98.50	106.73
1	A	235	LLP	OP4-P-OP1	2.76	114.23	106.47
1	A	235	LLP	C5'-C5-C6	-2.73	114.88	119.37
1	B	235	LLP	C5'-C5-C6	-2.38	115.46	119.37
1	A	235	LLP	OP4-C5'-C5	2.03	113.23	109.35

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	B	235	LLP	C4-C4'-NZ-CE
1	A	235	LLP	C4-C4'-NZ-CE

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	B	235	LLP	2	0
1	A	235	LLP	1	0

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

14 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	EDO	B	401	-	3,3,3	0.53	0	2,2,2	0.29	0
2	EDO	B	404	-	3,3,3	0.41	0	2,2,2	0.50	0
2	EDO	A	405	-	3,3,3	0.47	0	2,2,2	0.30	0
3	PEG	A	403	-	6,6,6	0.48	0	5,5,5	0.29	0
2	EDO	A	406	-	3,3,3	0.41	0	2,2,2	0.58	0
2	EDO	B	402	-	3,3,3	0.44	0	2,2,2	0.24	0
2	EDO	A	402	-	3,3,3	0.42	0	2,2,2	0.48	0
2	EDO	A	404	-	3,3,3	0.48	0	2,2,2	0.38	0
2	EDO	A	401	-	3,3,3	0.44	0	2,2,2	0.57	0
2	EDO	B	405	-	3,3,3	0.40	0	2,2,2	0.58	0
4	EGV	B	407	-	12,12,12	2.22	3 (25%)	12,15,15	1.30	3 (25%)
2	EDO	B	403	-	3,3,3	0.45	0	2,2,2	0.36	0
2	EDO	B	406	-	3,3,3	0.22	0	2,2,2	0.59	0
4	EGV	A	407	-	12,12,12	2.34	4 (33%)	12,15,15	1.23	2 (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
2	EDO	B	401	-	-	0/1/1/1	-
2	EDO	B	404	-	-	0/1/1/1	-
2	EDO	A	405	-	-	0/1/1/1	-
3	PEG	A	403	-	-	3/4/4/4	-
2	EDO	A	406	-	-	1/1/1/1	-
2	EDO	B	402	-	-	1/1/1/1	-
2	EDO	A	402	-	-	0/1/1/1	-
2	EDO	A	404	-	-	0/1/1/1	-
2	EDO	A	401	-	-	0/1/1/1	-
2	EDO	B	405	-	-	0/1/1/1	-
4	EGV	B	407	-	-	0/13/13/13	-
2	EDO	B	403	-	-	1/1/1/1	-
2	EDO	B	406	-	-	0/1/1/1	-
4	EGV	A	407	-	-	0/13/13/13	-

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	407	EGV	C03-N01	6.22	1.45	1.33
4	A	407	EGV	C03-N01	6.05	1.45	1.33
4	A	407	EGV	C03-N05	3.48	1.46	1.32

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	407	EGV	C03-N04	2.56	1.45	1.34
4	A	407	EGV	C03-N04	-2.26	1.25	1.34
4	A	407	EGV	O13-C09	-2.15	1.18	1.23
4	B	407	EGV	O13-C09	-2.13	1.18	1.23

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	407	EGV	O12-C10-C09	-3.13	117.54	121.72
4	A	407	EGV	O12-C10-C09	-2.60	118.25	121.72
4	A	407	EGV	O11-C10-C09	2.27	120.18	113.97
4	B	407	EGV	C06-C07-C09	-2.16	108.94	113.46
4	B	407	EGV	O11-C10-C09	2.10	119.71	113.97

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	403	PEG	O1-C1-C2-O2
3	A	403	PEG	O2-C3-C4-O4
3	A	403	PEG	C1-C2-O2-C3
2	A	406	EDO	O1-C1-C2-O2
2	B	402	EDO	O1-C1-C2-O2
2	B	403	EDO	O1-C1-C2-O2

There are no ring outliers.

6 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	401	EDO	1	0
2	A	406	EDO	1	0
2	B	402	EDO	2	0
2	A	401	EDO	3	0
2	B	405	EDO	2	0
2	B	406	EDO	1	0

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues

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	377/413 (91%)	-0.02	22 (5%) 23 26	11, 19, 44, 66	0
1	B	376/413 (91%)	-0.28	12 (3%) 47 54	11, 17, 34, 80	12 (3%)
All	All	753/826 (91%)	-0.15	34 (4%) 33 38	11, 18, 42, 80	12 (1%)

All (34) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	16	LEU	8.6
1	A	14	LEU	5.6
1	B	21	ILE	5.3
1	A	26	MET	5.1
1	A	391	HIS	4.6
1	A	25	THR	4.5
1	B	26	MET	4.5
1	B	25	THR	4.2
1	B	17	THR	3.7
1	A	353	TYR	3.6
1	B	15	ASP	3.4
1	B	353[A]	TYR	3.4
1	B	22	GLN	3.4
1	B	23	ALA	3.1
1	A	383	LEU	3.0
1	A	388	LEU	3.0
1	B	391	HIS	2.9
1	A	343	ALA	2.9
1	A	389	ASP	2.7
1	B	24	LEU	2.7
1	A	332	LEU	2.5
1	A	27	LYS	2.4
1	A	390	ARG	2.3
1	A	339	ARG	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	335	THR	2.3
1	A	329	HIS	2.3
1	A	333	THR	2.2
1	A	96	ILE	2.2
1	A	347	TYR	2.2
1	A	387	VAL	2.2
1	A	23	ALA	2.2
1	B	19	HIS	2.2
1	A	345	GLY	2.1
1	A	22	GLN	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(Å <sup>2</sup> )	Q<0.9
1	LLP	A	235	24/25	0.97	0.09	14,20,25,26	0
1	LLP	B	235	24/25	0.97	0.08	14,18,25,32	0

## 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
2	EDO	A	405	4/4	0.65	0.14	55,57,58,59	0
2	EDO	B	406	4/4	0.79	0.17	21,23,31,38	0
3	PEG	A	403	7/7	0.83	0.16	51,52,58,59	0
2	EDO	B	403	4/4	0.84	0.10	48,48,54,60	0
4	EGV	B	407	13/13	0.87	0.18	23,33,48,56	0
2	EDO	B	405	4/4	0.88	0.14	42,42,53,54	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	EDO	A	401	4/4	0.90	0.11	16,18,20,21	0
4	EGV	A	407	13/13	0.91	0.10	20,26,39,39	0
2	EDO	A	406	4/4	0.92	0.12	39,40,45,49	0
2	EDO	B	401	4/4	0.93	0.12	17,18,19,21	0
2	EDO	B	402	4/4	0.95	0.09	17,20,23,33	0
2	EDO	A	404	4/4	0.97	0.12	16,32,37,38	0
2	EDO	B	404	4/4	0.98	0.13	14,17,31,33	0
2	EDO	A	402	4/4	0.98	0.06	17,19,20,21	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.