



wwPDB X-ray Structure Validation Summary Report ⓘ

May 26, 2020 – 04:06 pm BST

PDB ID : 6N9R
Title : Structure of the Quorum Quenching lactonase from *Parageobacillus caldoyticus* bound to substrate 3-oxo-C12-AHL
Authors : Bergonzi, C.; Schwab, M.; Elias, M.
Deposited on : 2018-12-03
Resolution : 1.75 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The 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

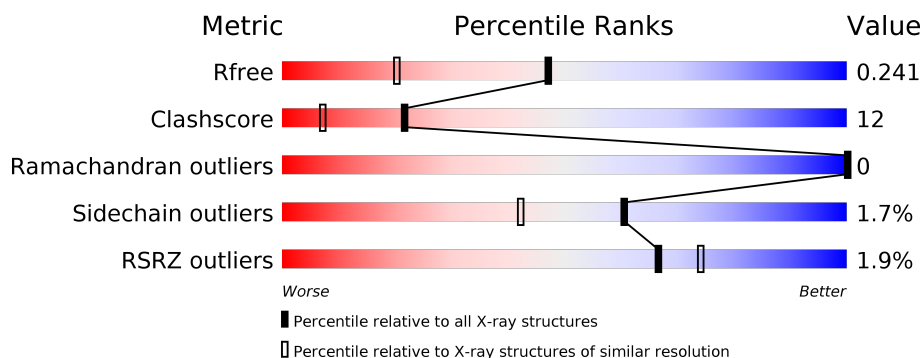
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.75 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	2340 (1.76-1.76)
Clashscore	141614	2466 (1.76-1.76)
Ramachandran outliers	138981	2437 (1.76-1.76)
Sidechain outliers	138945	2437 (1.76-1.76)
RSRZ outliers	127900	2298 (1.76-1.76)

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 ≥ 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	297	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 15%, green 77%, grey 7%);"></div> <div style="display: flex; justify-content: space-between; font-size: 0.8em;"> 1% 77% 15% 7% </div> </div>
1	P	297	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 3%, orange 1%, yellow 14%, green 78%, grey 7%);"></div> <div style="display: flex; justify-content: space-between; font-size: 0.8em;"> 3% 78% 14% 7% </div> </div>
1	X	297	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 2%, orange 1%, yellow 15%, green 77%, grey 7%);"></div> <div style="display: flex; justify-content: space-between; font-size: 0.8em;"> 2% 77% 15% 7% </div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	ACT	A	304	-	-	X	-
5	ACT	X	306	-	-	X	-
6	EDO	A	309	-	-	X	-
6	EDO	A	310	-	-	X	-
6	EDO	P	312	-	-	X	-
6	EDO	X	313	-	-	X	-
7	1PE	A	312	-	-	X	-

2 Entry composition

There are 10 unique types of molecules in this entry. The entry contains 7868 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 hydrolase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	276	Total	C	N	O	S	0	18	0
			2390	1515	416	443	16			
1	P	276	Total	C	N	O	S	0	19	0
			2406	1521	419	451	15			
1	X	276	Total	C	N	O	S	0	15	0
			2371	1501	413	442	15			

There are 45 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-13	TRP	-	expression tag	UNP A0A023DFE8
A	-12	SER	-	expression tag	UNP A0A023DFE8
A	-11	HIS	-	expression tag	UNP A0A023DFE8
A	-10	PRO	-	expression tag	UNP A0A023DFE8
A	-9	GLN	-	expression tag	UNP A0A023DFE8
A	-8	PHE	-	expression tag	UNP A0A023DFE8
A	-7	GLU	-	expression tag	UNP A0A023DFE8
A	-6	LYS	-	expression tag	UNP A0A023DFE8
A	-5	GLU	-	expression tag	UNP A0A023DFE8
A	-4	ASN	-	expression tag	UNP A0A023DFE8
A	-3	LEU	-	expression tag	UNP A0A023DFE8
A	-2	TYR	-	expression tag	UNP A0A023DFE8
A	-1	PHE	-	expression tag	UNP A0A023DFE8
A	0	GLN	-	expression tag	UNP A0A023DFE8
A	1	SER	-	expression tag	UNP A0A023DFE8
P	-13	TRP	-	expression tag	UNP A0A023DFE8
P	-12	SER	-	expression tag	UNP A0A023DFE8
P	-11	HIS	-	expression tag	UNP A0A023DFE8
P	-10	PRO	-	expression tag	UNP A0A023DFE8
P	-9	GLN	-	expression tag	UNP A0A023DFE8
P	-8	PHE	-	expression tag	UNP A0A023DFE8
P	-7	GLU	-	expression tag	UNP A0A023DFE8
P	-6	LYS	-	expression tag	UNP A0A023DFE8

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Chain	Residue	Modelled	Actual	Comment	Reference
P	-5	GLU	-	expression tag	UNP A0A023DFE8
P	-4	ASN	-	expression tag	UNP A0A023DFE8
P	-3	LEU	-	expression tag	UNP A0A023DFE8
P	-2	TYR	-	expression tag	UNP A0A023DFE8
P	-1	PHE	-	expression tag	UNP A0A023DFE8
P	0	GLN	-	expression tag	UNP A0A023DFE8
P	1	SER	-	expression tag	UNP A0A023DFE8
X	-13	TRP	-	expression tag	UNP A0A023DFE8
X	-12	SER	-	expression tag	UNP A0A023DFE8
X	-11	HIS	-	expression tag	UNP A0A023DFE8
X	-10	PRO	-	expression tag	UNP A0A023DFE8
X	-9	GLN	-	expression tag	UNP A0A023DFE8
X	-8	PHE	-	expression tag	UNP A0A023DFE8
X	-7	GLU	-	expression tag	UNP A0A023DFE8
X	-6	LYS	-	expression tag	UNP A0A023DFE8
X	-5	GLU	-	expression tag	UNP A0A023DFE8
X	-4	ASN	-	expression tag	UNP A0A023DFE8
X	-3	LEU	-	expression tag	UNP A0A023DFE8
X	-2	TYR	-	expression tag	UNP A0A023DFE8
X	-1	PHE	-	expression tag	UNP A0A023DFE8
X	0	GLN	-	expression tag	UNP A0A023DFE8
X	1	SER	-	expression tag	UNP A0A023DFE8

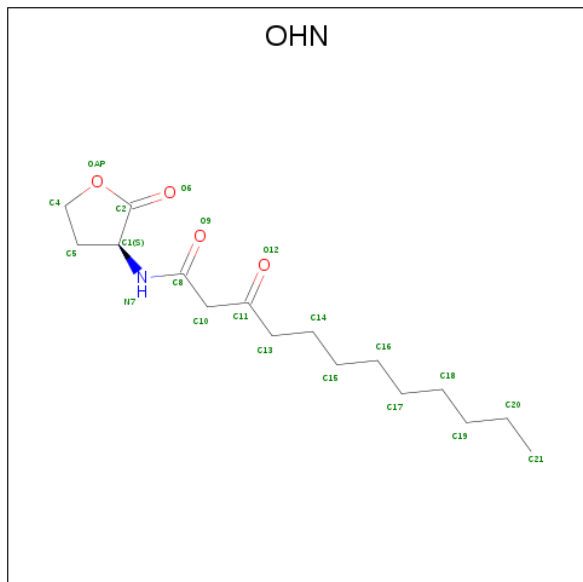
- Molecule 2 is COBALT (II) ION (three-letter code: CO) (formula: Co).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	P	1	Total Co 1 1	0	0
2	X	1	Total Co 1 1	0	0
2	A	1	Total Co 1 1	0	0

- Molecule 3 is FE (III) ION (three-letter code: FE) (formula: Fe).

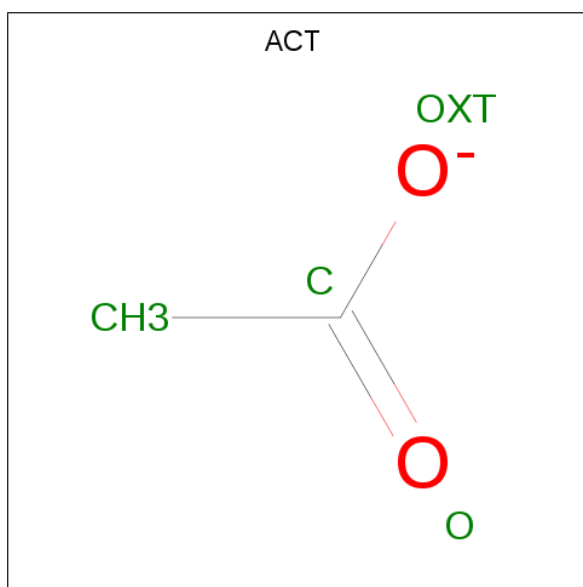
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	P	1	Total Fe 1 1	0	0
3	X	1	Total Fe 1 1	0	0
3	A	1	Total Fe 1 1	0	0

- Molecule 4 is N-3-OXO-DODECANOYL-L-HOMOSERINE LACTONE (three-letter code: OHN) (formula: $C_{16}H_{27}NO_4$).



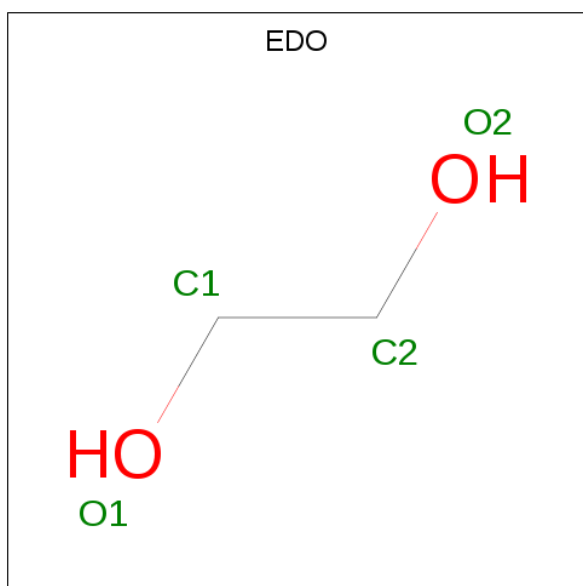
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			21	16	1	4		
4	P	1	Total	C	N	O	0	0
			21	16	1	4		
4	X	1	Total	C	N	O	0	0
			21	16	1	4		

- Molecule 5 is ACETATE ION (three-letter code: ACT) (formula: $C_2H_3O_2$).



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

- Molecule 6 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C₂H₆O₂).



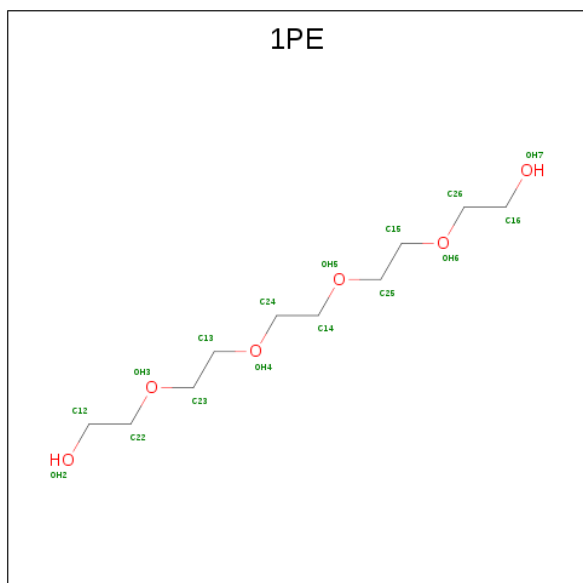
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total C O 4 2 2	0	0
6	A	1	Total C O 4 2 2	0	0
6	A	1	Total C O 4 2 2	0	0
6	A	1	Total C O 4 2 2	0	0
6	A	1	Total C O 4 2 2	0	0
6	P	1	Total C O 4 2 2	0	0
6	P	1	Total C O 4 2 2	0	0

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	P	1	Total	C	O	0	0
			4	2	2		
6	P	1	Total	C	O	0	0
			4	2	2		
6	P	1	Total	C	O	0	0
			4	2	2		
6	X	1	Total	C	O	0	0
			4	2	2		
6	X	1	Total	C	O	0	0
			4	2	2		
6	X	1	Total	C	O	0	0
			4	2	2		
6	X	1	Total	C	O	0	0
			4	2	2		
6	X	1	Total	C	O	0	0
			4	2	2		

- Molecule 7 is PENTAETHYLENE GLYCOL (three-letter code: 1PE) (formula: $C_{10}H_{22}O_6$).



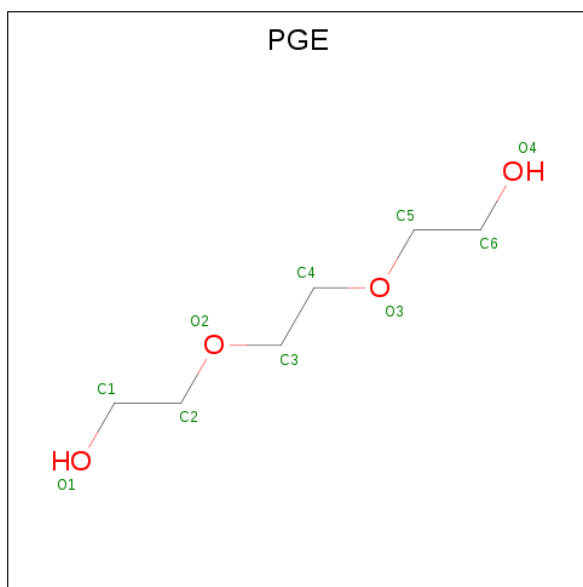
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	C	O	0	0
			16	10	6		

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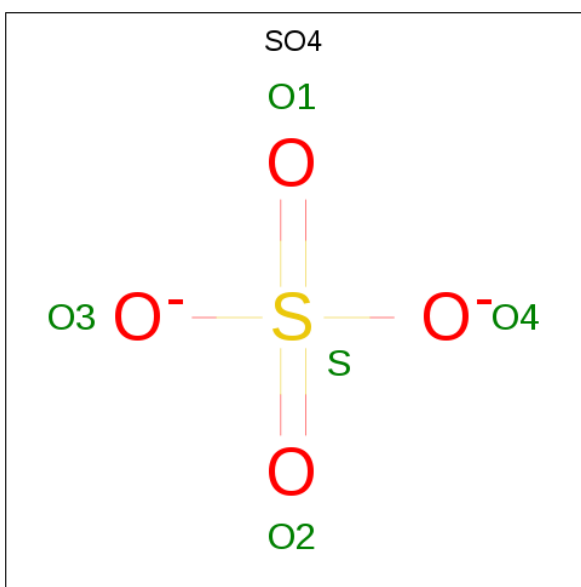
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	P	1	Total	C	O	0	0
			16	10	6		
7	X	1	Total	C	O	0	0
			16	10	6		

- Molecule 8 is TRIETHYLENE GLYCOL (three-letter code: PGE) (formula: $C_6H_{14}O_4$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	A	1	Total	C	O	0	0
			10	6	4		

- Molecule 9 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
9	P	1	Total	O	S	0	0
			5	4	1		
9	P	1	Total	O	S	0	0
			5	4	1		
9	P	1	Total	O	S	0	0
			5	4	1		
9	P	1	Total	O	S	0	0
			5	4	1		
9	P	1	Total	O	S	0	0
			5	4	1		
9	X	1	Total	O	S	0	0
			5	4	1		
9	X	1	Total	O	S	0	0
			5	4	1		

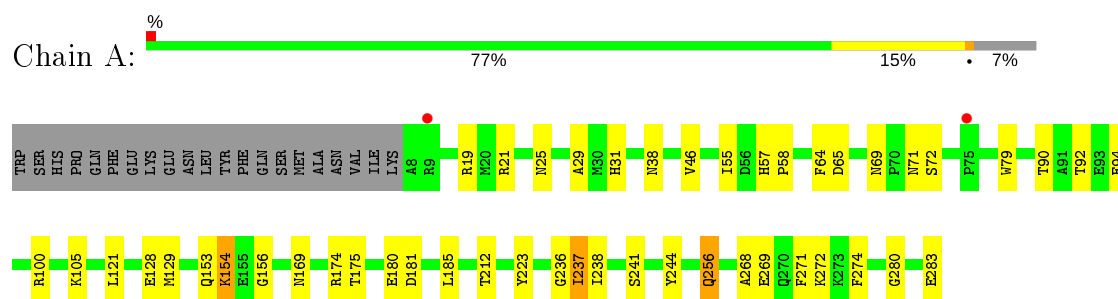
- Molecule 10 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	A	131	Total	O	0	0
			131	131		
10	P	175	Total	O	0	0
			175	175		
10	X	145	Total	O	0	0
			145	145		

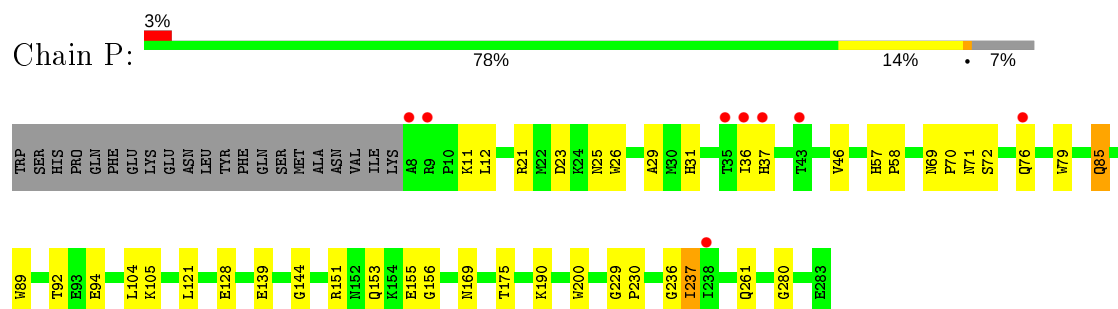
3 Residue-property plots [i](#)

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.

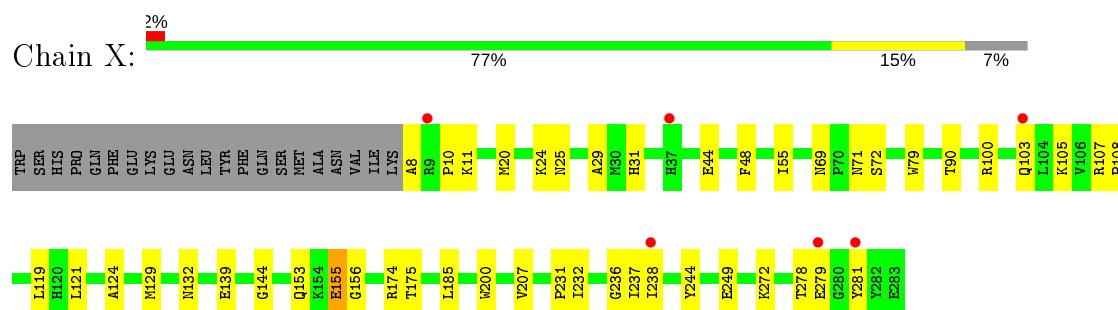
• Molecule 1: Putative hydrolase



• Molecule 1: Putative hydrolase



• Molecule 1: Putative hydrolase



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	145.01Å 108.59Å 78.60Å 90.00° 115.75° 90.00°	Depositor
Resolution (Å)	70.80 – 1.75 70.79 – 1.75	Depositor EDS
% Data completeness (in resolution range)	99.3 (70.80-1.75) 99.3 (70.79-1.75)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.05	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.73 (at 1.75Å)	Xtriage
Refinement program	REFMAC 5.8.0222	Depositor
R, R_{free}	0.176 , 0.235 0.186 , 0.241	Depositor DCC
R_{free} test set	5476 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	15.8	Xtriage
Anisotropy	0.643	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 48.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	7868	wwPDB-VP
Average B, all atoms (Å ²)	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 10.51% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: OHN, PGE, CO, EDO, 1PE, FE, ACT, SO4

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	0.25	0/2452	0.45	0/3318
1	P	0.25	0/2469	0.45	0/3342
1	X	0.25	0/2435	0.44	0/3300
All	All	0.25	0/7356	0.45	0/9960

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2390	0	2293	59	1
1	P	2406	0	2285	57	0
1	X	2371	0	2250	52	0
2	A	1	0	0	0	0
2	P	1	0	0	0	0
2	X	1	0	0	0	0
3	A	1	0	0	0	0
3	P	1	0	0	0	0
3	X	1	0	0	0	0
4	A	21	0	27	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	P	21	0	27	4	0
4	X	21	0	27	1	0
5	A	12	0	9	5	0
5	P	4	0	3	1	0
5	X	4	0	3	7	0
6	A	20	0	30	11	0
6	P	20	0	30	9	0
6	X	28	0	42	10	0
7	A	16	0	22	8	0
7	P	16	0	22	0	0
7	X	16	0	22	3	0
8	A	10	0	14	0	0
9	P	25	0	0	1	0
9	X	10	0	0	0	0
10	A	131	0	0	8	1
10	P	175	0	0	4	0
10	X	145	0	0	6	0
All	All	7868	0	7106	174	1

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 12.

The worst 5 of 174 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:X:100:ARG:HD3	6:X:313:EDO:H22	1.20	1.20
1:X:231:PRO:HD2	10:X:404:HOH:O	1.48	1.11
1:P:139[B]:GLU:OE2	1:P:175:THR:OG1	1.73	1.06
1:P:36:ILE:HG23	1:P:37[A]:HIS:HD2	1.16	1.03
4:A:303:OHN:C2	10:A:401:HOH:O	2.11	0.98

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:269[B]:GLU:OE1	10:A:489:HOH:O[2_655]	2.07	0.13

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	291/297 (98%)	278 (96%)	13 (4%)	0	100	100
1	P	292/297 (98%)	277 (95%)	15 (5%)	0	100	100
1	X	288/297 (97%)	277 (96%)	11 (4%)	0	100	100
All	All	871/891 (98%)	832 (96%)	39 (4%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	254/256 (99%)	249 (98%)	5 (2%)	55	34
1	P	255/256 (100%)	251 (98%)	4 (2%)	62	45
1	X	251/256 (98%)	245 (98%)	6 (2%)	49	26
All	All	760/768 (99%)	745 (98%)	15 (2%)	60	34

5 of 15 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	P	76[B]	GLN
1	P	85	GLN
1	X	155[B]	GLU
1	P	76[A]	GLN
1	X	155[A]	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 24 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	256	GLN
1	P	69	ASN
1	X	179	HIS
1	P	25	ASN
1	P	31	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 42 ligands modelled in this entry, 6 are monoatomic - leaving 36 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
4	OHN	A	303	3,2	21,21,21	1.46	1 (4%)	20,25,25	1.92	2 (10%)
6	EDO	A	309	-	3,3,3	0.45	0	2,2,2	0.31	0
6	EDO	A	310	-	3,3,3	0.31	0	2,2,2	0.53	0
6	EDO	X	307	-	3,3,3	0.44	0	2,2,2	0.33	0
6	EDO	X	309	-	3,3,3	0.46	0	2,2,2	0.29	0
7	1PE	P	315	-	15,15,15	0.50	0	14,14,14	0.19	0
8	PGE	A	313	-	9,9,9	0.45	0	8,8,8	0.24	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
9	SO4	P	304	-	4,4,4	0.32	0	6,6,6	0.06	0
6	EDO	P	312	-	3,3,3	0.47	0	2,2,2	0.28	0
6	EDO	A	311	-	3,3,3	0.45	0	2,2,2	0.31	0
6	EDO	A	307	-	3,3,3	0.45	0	2,2,2	0.32	0
6	EDO	P	310	-	3,3,3	0.45	0	2,2,2	0.33	0
6	EDO	P	311	-	3,3,3	0.46	0	2,2,2	0.29	0
6	EDO	P	314	-	3,3,3	0.44	0	2,2,2	0.28	0
7	1PE	X	314	-	15,15,15	0.45	0	14,14,14	0.26	0
6	EDO	A	308	-	3,3,3	0.43	0	2,2,2	0.34	0
9	SO4	P	306	-	4,4,4	0.32	0	6,6,6	0.05	0
9	SO4	X	303	-	4,4,4	0.32	0	6,6,6	0.04	0
5	ACT	A	306	-	1,3,3	1.34	0	0,3,3	0.00	-
5	ACT	A	305	-	1,3,3	1.31	0	0,3,3	0.00	-
6	EDO	X	308	-	3,3,3	0.46	0	2,2,2	0.28	0
4	OHN	P	308	3,2	21,21,21	1.49	1 (4%)	20,25,25	2.03	2 (10%)
9	SO4	P	303	-	4,4,4	0.32	0	6,6,6	0.06	0
5	ACT	X	306	-	1,3,3	1.01	0	0,3,3	0.00	-
9	SO4	P	307	-	4,4,4	0.33	0	6,6,6	0.05	0
6	EDO	X	313	-	3,3,3	0.43	0	2,2,2	0.32	0
5	ACT	A	304	-	1,3,3	1.06	0	0,3,3	0.00	-
6	EDO	P	313	-	3,3,3	0.47	0	2,2,2	0.30	0
9	SO4	P	305	-	4,4,4	0.33	0	6,6,6	0.04	0
6	EDO	X	311	-	3,3,3	0.46	0	2,2,2	0.28	0
7	1PE	A	312	-	15,15,15	0.46	0	14,14,14	0.22	0
6	EDO	X	312	-	3,3,3	0.47	0	2,2,2	0.28	0
6	EDO	X	310	-	3,3,3	0.46	0	2,2,2	0.29	0
9	SO4	X	304	-	4,4,4	0.21	0	6,6,6	0.25	0
5	ACT	P	309	-	1,3,3	1.47	0	0,3,3	0.00	-
4	OHN	X	305	3,2	21,21,21	1.47	1 (4%)	20,25,25	1.95	4 (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
4	OHN	A	303	3,2	-	9/17/27/27	0/1/1/1
6	EDO	A	309	-	-	1/1/1/1	-
6	EDO	A	310	-	-	1/1/1/1	-
6	EDO	X	307	-	-	0/1/1/1	-
6	EDO	X	309	-	-	0/1/1/1	-
7	1PE	P	315	-	-	6/13/13/13	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
8	PGE	A	313	-	-	4/7/7/7	-
6	EDO	P	312	-	-	1/1/1/1	-
6	EDO	A	311	-	-	0/1/1/1	-
6	EDO	A	307	-	-	0/1/1/1	-
6	EDO	P	310	-	-	0/1/1/1	-
6	EDO	P	311	-	-	1/1/1/1	-
6	EDO	P	314	-	-	0/1/1/1	-
7	1PE	X	314	-	-	8/13/13/13	-
6	EDO	A	308	-	-	1/1/1/1	-
6	EDO	P	313	-	-	1/1/1/1	-
7	1PE	A	312	-	-	10/13/13/13	-
4	OHN	P	308	3,2	-	11/17/27/27	0/1/1/1
6	EDO	X	313	-	-	0/1/1/1	-
6	EDO	X	308	-	-	1/1/1/1	-
6	EDO	X	310	-	-	1/1/1/1	-
6	EDO	X	311	-	-	1/1/1/1	-
6	EDO	X	312	-	-	1/1/1/1	-
4	OHN	X	305	3,2	-	8/17/27/27	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	P	308	OHN	C1-C2	-6.24	1.39	1.52
4	X	305	OHN	C1-C2	-6.16	1.39	1.52
4	A	303	OHN	C1-C2	-6.08	1.39	1.52

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	P	308	OHN	C4-OAP-C2	-7.43	103.52	110.39
4	X	305	OHN	C4-OAP-C2	-7.01	103.91	110.39
4	A	303	OHN	C4-OAP-C2	-6.95	103.96	110.39
4	P	308	OHN	OAP-C2-O6	2.81	124.34	121.42
4	X	305	OHN	OAP-C2-O6	2.78	124.30	121.42

There are no chirality outliers.

5 of 66 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	P	308	OHN	O12-C11-C13-C14

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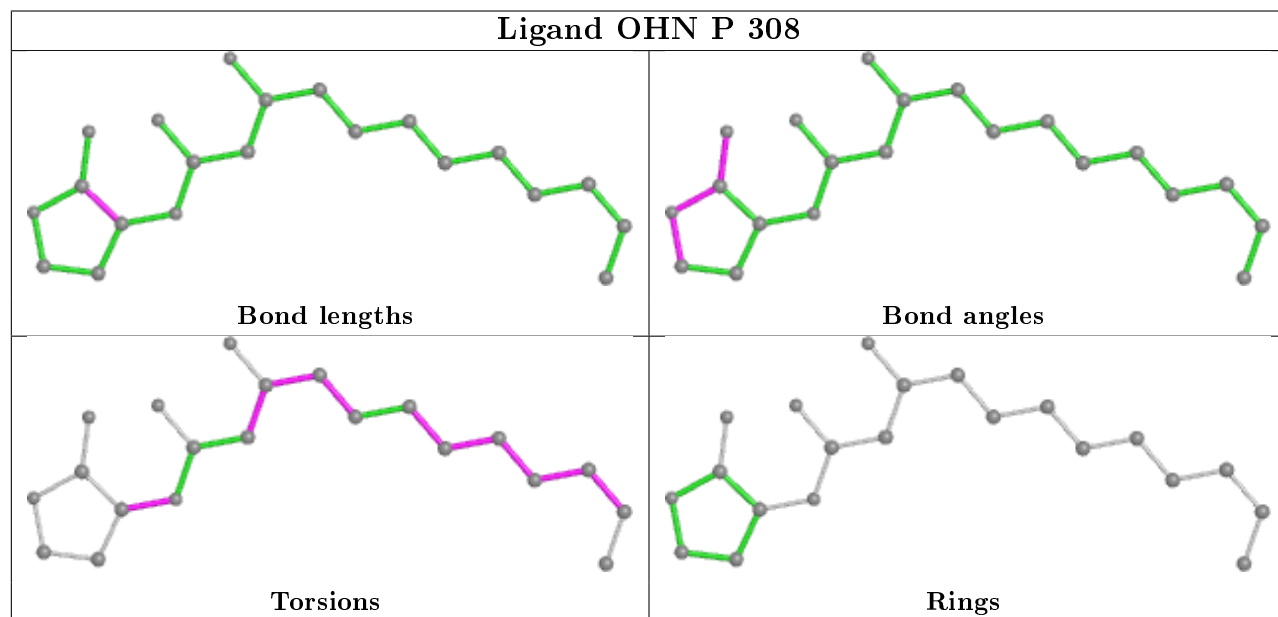
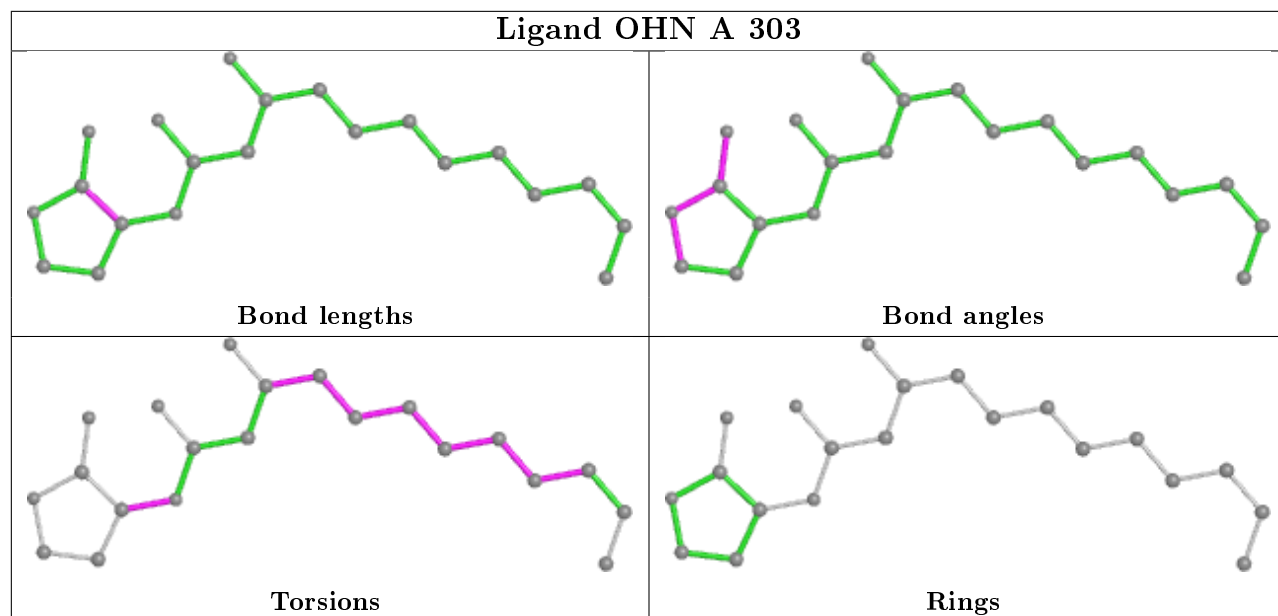
Mol	Chain	Res	Type	Atoms
4	P	308	OHN	C10-C11-C13-C14
4	P	308	OHN	C5-C1-N7-C8
7	A	312	1PE	C16-C26-OH6-C15
7	A	312	1PE	OH4-C13-C23-OH3

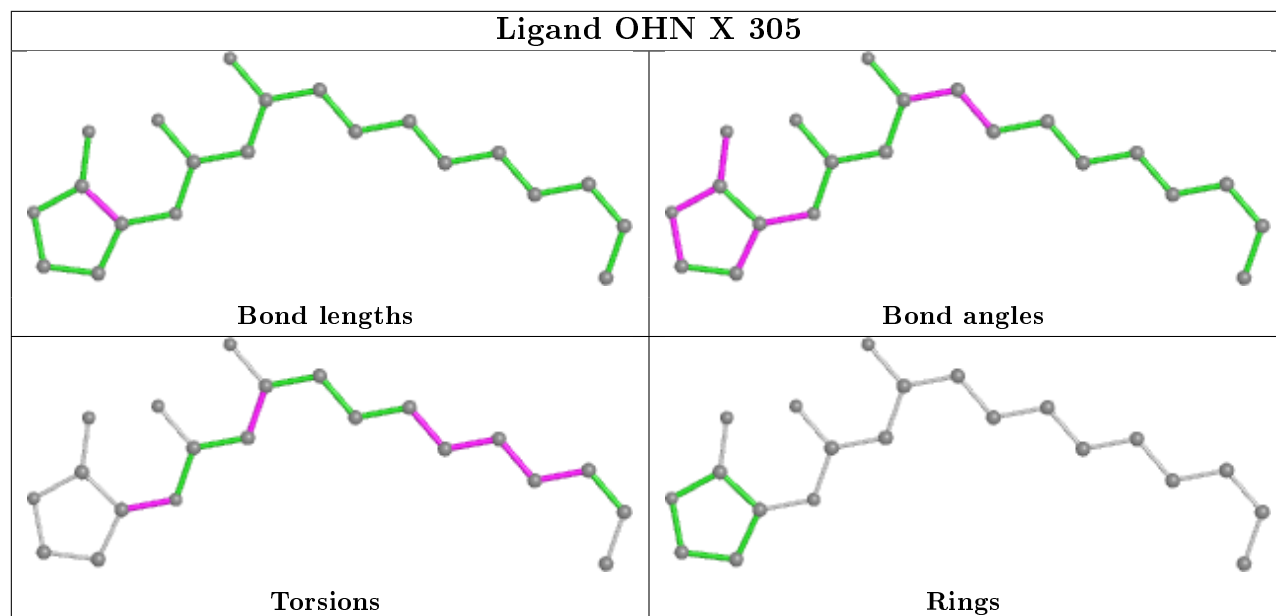
There are no ring outliers.

16 monomers are involved in 65 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	303	OHN	5	0
6	A	309	EDO	4	0
6	A	310	EDO	5	0
6	P	312	EDO	7	0
6	A	311	EDO	2	0
6	P	311	EDO	2	0
7	X	314	1PE	3	0
5	A	305	ACT	1	0
4	P	308	OHN	4	0
5	X	306	ACT	7	0
9	P	307	SO4	1	0
6	X	313	EDO	10	0
5	A	304	ACT	4	0
7	A	312	1PE	8	0
5	P	309	ACT	1	0
4	X	305	OHN	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

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, 95th 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 ²)	Q<0.9
1	A	276/297 (92%)	-0.13	2 (0%) 87 92	11, 19, 33, 61	1 (0%)
1	P	276/297 (92%)	-0.05	8 (2%) 51 57	11, 20, 35, 55	2 (0%)
1	X	276/297 (92%)	-0.05	6 (2%) 62 69	12, 22, 41, 58	4 (1%)
All	All	828/891 (92%)	-0.08	16 (1%) 66 74	11, 20, 37, 61	7 (0%)

The worst 5 of 16 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	X	37[A]	HIS	3.6
1	P	37[A]	HIS	3.4
1	A	9	ARG	3.0
1	P	36	ILE	2.7
1	P	8	ALA	2.7

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

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, 95th 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.

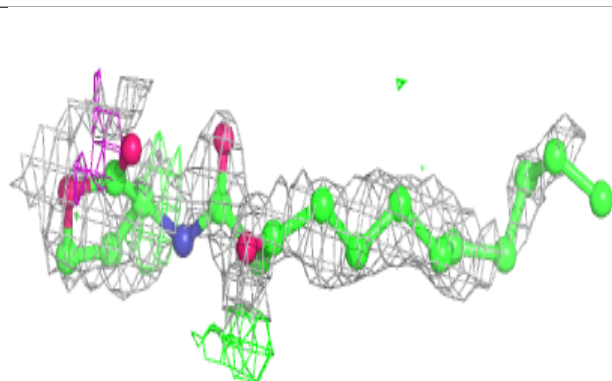
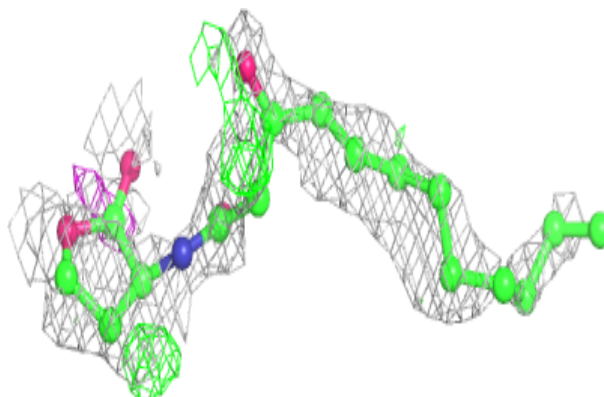
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	OHN	X	305	21/21	0.59	0.33	24,46,59,60	21
6	EDO	A	311	4/4	0.71	0.22	35,39,41,42	0
4	OHN	P	308	21/21	0.72	0.28	24,49,64,65	21
4	OHN	A	303	21/21	0.73	0.26	18,31,45,46	21
6	EDO	X	312	4/4	0.81	0.15	37,38,41,58	0
5	ACT	A	306	4/4	0.82	0.14	28,48,51,72	0
6	EDO	X	308	4/4	0.82	0.11	44,46,47,49	0
6	EDO	P	312	4/4	0.82	0.12	37,40,41,43	0
7	1PE	A	312	16/16	0.82	0.17	33,50,61,70	0
6	EDO	X	309	4/4	0.82	0.16	36,45,60,73	0
6	EDO	P	310	4/4	0.82	0.19	42,43,51,57	0
6	EDO	P	313	4/4	0.84	0.12	37,38,39,40	0
7	1PE	P	315	16/16	0.85	0.17	28,39,56,65	0
6	EDO	A	308	4/4	0.86	0.14	30,34,41,44	0
8	PGE	A	313	10/10	0.86	0.17	46,49,54,56	0
7	1PE	X	314	16/16	0.87	0.17	28,43,57,60	0
5	ACT	X	306	4/4	0.88	0.16	16,22,43,52	0
6	EDO	X	311	4/4	0.88	0.15	41,42,45,53	0
9	SO4	P	307	5/5	0.89	0.22	32,46,53,58	5
9	SO4	X	304	5/5	0.89	0.19	27,33,33,35	0
6	EDO	X	313	4/4	0.90	0.21	30,33,33,37	0
6	EDO	X	307	4/4	0.90	0.16	34,37,37,41	0
6	EDO	P	314	4/4	0.91	0.27	22,30,34,39	0
6	EDO	A	307	4/4	0.91	0.14	28,29,37,42	0
6	EDO	A	310	4/4	0.91	0.15	23,24,29,34	0
5	ACT	A	304	4/4	0.92	0.14	14,18,43,45	0
6	EDO	P	311	4/4	0.93	0.10	31,35,42,52	0
9	SO4	P	306	5/5	0.94	0.12	34,44,58,61	0
6	EDO	A	309	4/4	0.94	0.17	36,41,41,48	0
5	ACT	P	309	4/4	0.95	0.10	38,40,50,58	0
6	EDO	X	310	4/4	0.97	0.09	33,35,36,46	0
5	ACT	A	305	4/4	0.97	0.09	34,38,38,46	0
9	SO4	P	305	5/5	0.98	0.09	23,39,48,64	0
9	SO4	X	303	5/5	0.99	0.08	29,33,37,40	0
9	SO4	P	304	5/5	0.99	0.05	28,30,35,37	0
9	SO4	P	303	5/5	0.99	0.05	31,31,37,37	0
3	FE	X	302	1/1	1.00	0.07	19,19,19,19	0
2	CO	X	301	1/1	1.00	0.09	14,14,14,14	0
2	CO	A	301	1/1	1.00	0.09	13,13,13,13	0
3	FE	A	302	1/1	1.00	0.05	17,17,17,17	0
2	CO	P	301	1/1	1.00	0.09	14,14,14,14	0
3	FE	P	302	1/1	1.00	0.06	18,18,18,18	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.

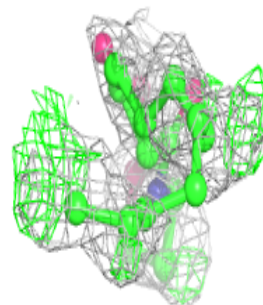
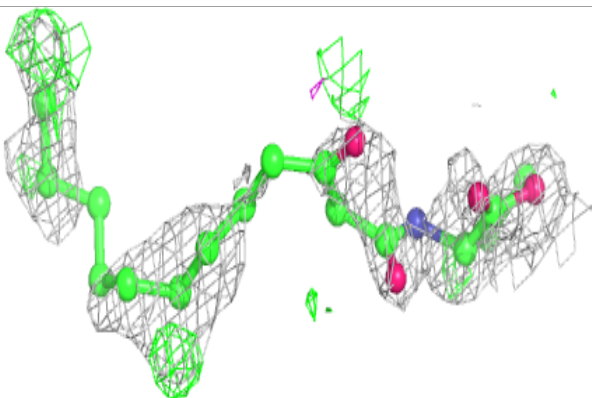
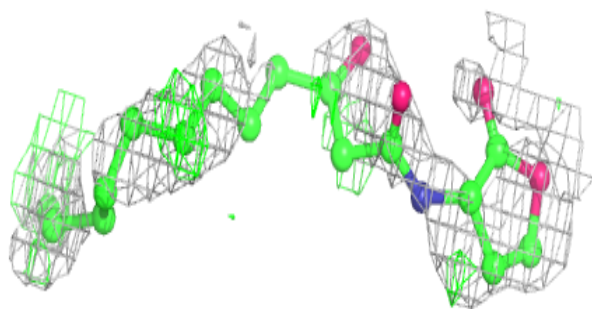
Electron density around OHN X 305:

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

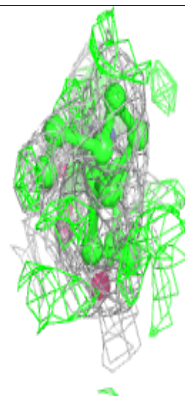
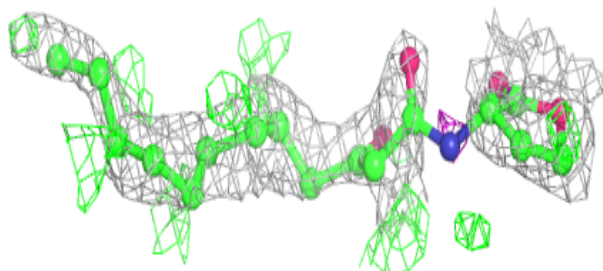
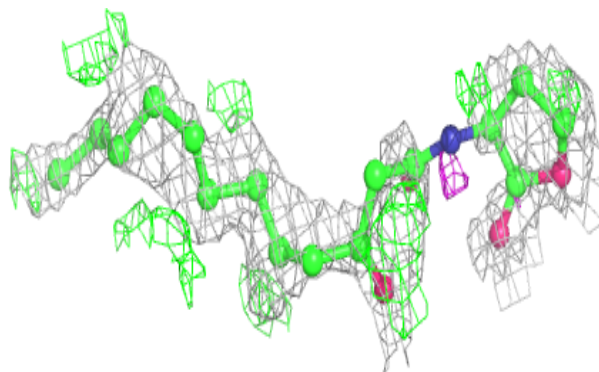


Electron density around OHN P 308:

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

**Electron density around OHN A 303:**

$2mF_o-DF_c$ (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.