



# Full wwPDB X-ray Structure Validation Report ⓘ

May 25, 2020 – 09:46 pm BST

PDB ID : 3OBI  
Title : Crystal structure of a formyltetrahydrofolate deformylase (NP\_949368) from RHODOPSEUDOMONAS PALUSTRIS CGA009 at 1.95 Å resolution  
Authors : Joint Center for Structural Genomics (JCSG)  
Deposited on : 2010-08-06  
Resolution : 1.95 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  
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

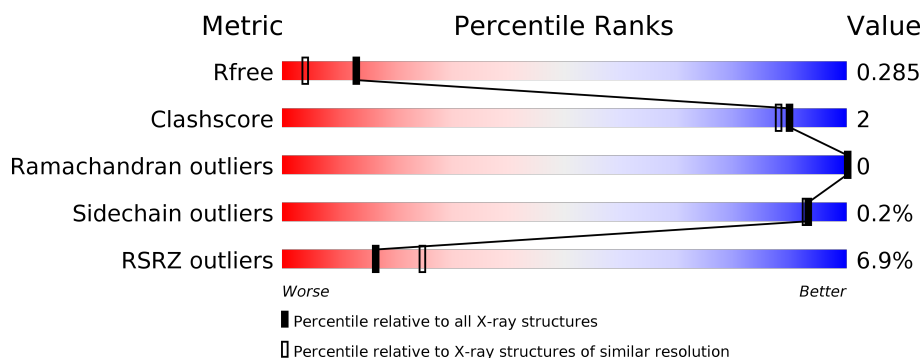
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.95 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	2580 (1.96-1.96)
Clashscore	141614	2705 (1.96-1.96)
Ramachandran outliers	138981	2678 (1.96-1.96)
Sidechain outliers	138945	2678 (1.96-1.96)
RSRZ outliers	127900	2539 (1.96-1.96)

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	288	<div> <div>10%</div> <div> <div></div> <div>91%</div> <div>8%</div> </div> </div>
1	B	288	<div> <div>5%</div> <div> <div></div> <div>91%</div> <div>8%</div> </div> </div>
1	C	288	<div> <div>5%</div> <div> <div></div> <div>93%</div> <div>5%</div> </div> </div>
1	D	288	<div> <div>7%</div> <div> <div></div> <div>95%</div> <div></div> </div> </div>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 10515 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 Formyltetrahydrofolate deformylase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	285	Total	C	N	O	S	Se	0	14	0
			2366	1502	436	417	3	8			
1	B	285	Total	C	N	O	S	Se	0	16	0
			2374	1509	441	413	3	8			
1	C	284	Total	C	N	O	S	Se	0	8	0
			2316	1470	431	405	3	7			
1	D	284	Total	C	N	O	S	Se	0	11	0
			2330	1478	432	409	3	8			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	GLY	-	leader sequence	UNP Q6N2L8
B	0	GLY	-	leader sequence	UNP Q6N2L8
C	0	GLY	-	leader sequence	UNP Q6N2L8
D	0	GLY	-	leader sequence	UNP Q6N2L8

- 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
2	A	1	Total	C	O	0	0
			4	2	2		
2	A	1	Total	C	O	0	0
			4	2	2		
2	A	1	Total	C	O	0	0
			4	2	2		
2	A	1	Total	C	O	0	0
			4	2	2		
2	A	1	Total	C	O	0	0
			4	2	2		
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		

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

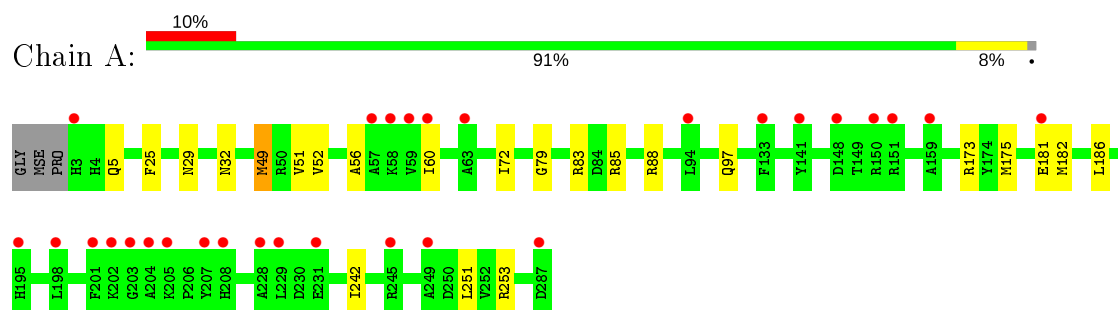
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	259	Total O 261 261	0	2
3	B	266	Total O 272 272	0	6
3	C	263	Total O 264 264	0	1
3	D	213	Total O 216 216	0	3

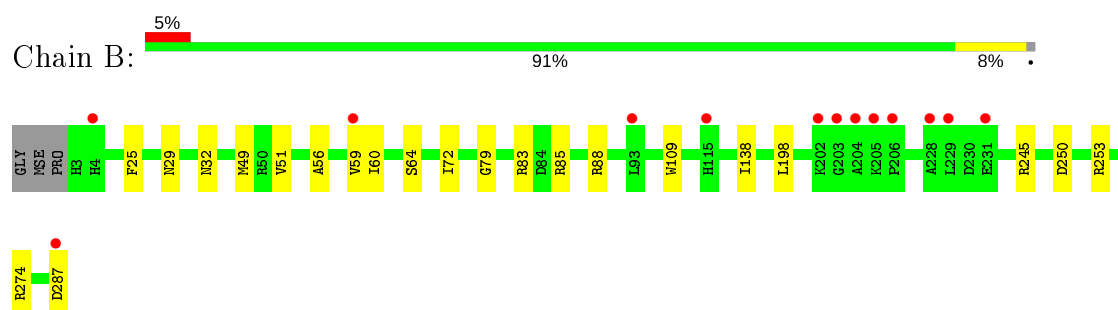
### 3 Residue-property plots [i](#)

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.

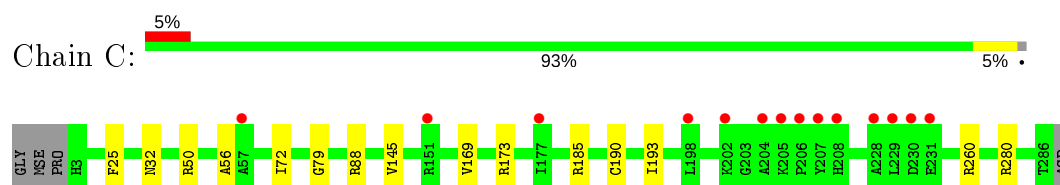
- Molecule 1: Formyltetrahydrofolate deformylase



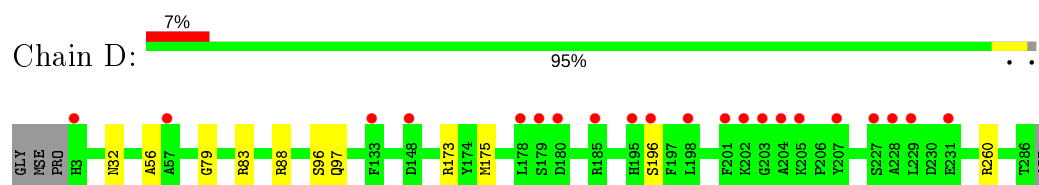
- Molecule 1: Formyltetrahydrofolate deformylase



- Molecule 1: Formyltetrahydrofolate deformylase



- Molecule 1: Formyltetrahydrofolate deformylase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	70.05Å 141.11Å 77.56Å 90.00° 107.83° 90.00°	Depositor
Resolution (Å)	29.67 – 1.95 29.67 – 1.95	Depositor EDS
% Data completeness (in resolution range)	97.1 (29.67-1.95) 97.1 (29.67-1.95)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.11	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.37 (at 1.95Å)	Xtriage
Refinement program	REFMAC 5.5.0110	Depositor
R, $R_{free}$	0.234 , 0.278 0.239 , 0.285	Depositor DCC
$R_{free}$ test set	5035 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	19.9	Xtriage
Anisotropy	0.296	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 47.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.57$ , $\langle L^2 \rangle = 0.41$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	10515	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 60.25 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.5648e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<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: 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	0.72	0/2450	0.88	4/3301 (0.1%)
1	B	0.77	0/2467	0.89	4/3321 (0.1%)
1	C	0.76	0/2385	0.89	6/3215 (0.2%)
1	D	0.68	0/2409	0.86	6/3248 (0.2%)
All	All	0.73	0/9711	0.88	20/13085 (0.2%)

There are no bond length outliers.

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	88	ARG	NE-CZ-NH1	6.50	123.55	120.30
1	B	88	ARG	NE-CZ-NH1	6.32	123.46	120.30
1	C	88	ARG	NE-CZ-NH1	6.02	123.31	120.30
1	B	83	ARG	NE-CZ-NH1	5.85	123.23	120.30
1	B	79	GLY	N-CA-C	-5.81	98.58	113.10
1	A	88	ARG	NE-CZ-NH1	5.76	123.18	120.30
1	C	79	GLY	N-CA-C	-5.75	98.72	113.10
1	D	79	GLY	N-CA-C	-5.51	99.34	113.10
1	C	260	ARG	NE-CZ-NH2	-5.49	117.56	120.30
1	D	260	ARG	NE-CZ-NH1	5.45	123.03	120.30
1	A	79	GLY	N-CA-C	-5.39	99.62	113.10
1	B	274	ARG	NE-CZ-NH1	5.34	122.97	120.30
1	D	173	ARG	NE-CZ-NH1	5.20	122.90	120.30
1	C	280	ARG	NE-CZ-NH1	5.19	122.89	120.30
1	A	173	ARG	NE-CZ-NH1	5.17	122.88	120.30
1	D	260	ARG	NE-CZ-NH2	-5.16	117.72	120.30
1	D	83	ARG	NE-CZ-NH1	5.09	122.85	120.30
1	C	185	ARG	NE-CZ-NH1	5.06	122.83	120.30
1	C	50	ARG	NE-CZ-NH1	5.04	122.82	120.30
1	A	49	MSE	CG-SE-CE	5.00	109.91	98.90



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	2366	0	2364	11	0
1	B	2374	0	2409	13	0
1	C	2316	0	2326	6	0
1	D	2330	0	2330	5	0
2	A	32	0	48	1	0
2	B	36	0	54	0	0
2	C	36	0	54	0	0
2	D	12	0	18	0	0
3	A	261	0	0	1	0
3	B	272	0	0	1	0
3	C	264	0	0	1	0
3	D	216	0	0	0	0
All	All	10515	0	9603	34	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 2.

All (34) 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:245[B]:ARG:HB3	1:B:245[B]:ARG:HH11	1.18	1.03
1:B:245[B]:ARG:HB3	1:B:245[B]:ARG:NH1	1.83	0.94
1:B:59:VAL:HG23	3:B:1063:HOH:O	1.89	0.71
1:B:198:LEU:HD11	1:D:196[B]:SER:OG	1.91	0.71
1:A:242:ILE:HD12	1:A:251:LEU:HD23	1.80	0.64
1:C:32:ASN:HB2	1:C:56:ALA:HB2	1.86	0.58
1:D:96:SER:HB3	1:D:175[B]:MSE:HE2	1.90	0.54
1:D:97:GLN:HE21	1:D:175[B]:MSE:HE1	1.72	0.54
1:D:32:ASN:HB2	1:D:56:ALA:HB2	1.91	0.52
1:B:250:ASP:OD1	1:B:253[A]:ARG:NH2	2.43	0.51
1:A:5:GLN:OE1	1:A:85[B]:ARG:NH2	2.44	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:173[A]:ARG:HD3	1:C:193:ILE:HG23	1.95	0.48
1:B:60[B]:ILE:HG22	1:B:64[B]:SER:HB2	1.96	0.47
1:C:173[A]:ARG:HA	1:C:173[A]:ARG:HD2	1.61	0.47
1:A:49:MSE:HE2	1:A:51[A]:VAL:CG2	2.45	0.46
1:C:145:VAL:HG21	3:C:940:HOH:O	2.16	0.45
1:A:32:ASN:HB2	1:A:56:ALA:HB2	1.98	0.45
1:B:25:PHE:HB2	1:B:72:ILE:CD1	2.46	0.45
1:B:32:ASN:HB2	1:B:56:ALA:HB2	1.99	0.44
1:B:85[B]:ARG:CB	1:B:85[B]:ARG:HH21	2.29	0.44
1:B:49:MSE:HE2	1:B:51[B]:VAL:CG2	2.47	0.44
1:A:83:ARG:NH1	3:A:934:HOH:O	2.49	0.44
1:A:253:ARG:NH1	2:A:305:EDO:O1	2.51	0.43
1:C:25:PHE:HB2	1:C:72:ILE:CD1	2.49	0.43
1:D:97:GLN:NE2	1:D:175[B]:MSE:HE1	2.33	0.43
1:A:97:GLN:H	1:A:175[B]:MSE:HE2	1.84	0.42
1:B:109:TRP:CZ3	1:B:138:ILE:HD11	2.55	0.42
1:A:29:ASN:HB3	1:A:60:ILE:HD12	2.02	0.41
1:A:182:MSE:HE3	1:A:186:LEU:HD11	2.02	0.41
1:A:52:VAL:HG11	1:A:85[B]:ARG:NH1	2.35	0.41
1:B:29:ASN:HB3	1:B:60[B]:ILE:HD12	2.02	0.41
1:B:85[B]:ARG:HB3	1:B:85[B]:ARG:NH2	2.35	0.41
1:C:169:VAL:O	1:C:190:CYS:HA	2.21	0.40
1:A:25:PHE:HB2	1:A:72:ILE:CD1	2.52	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	297/288 (103%)	293 (99%)	4 (1%)	0	100	100
1	B	299/288 (104%)	293 (98%)	6 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	290/288 (101%)	285 (98%)	5 (2%)	0	100	100
1	D	293/288 (102%)	290 (99%)	3 (1%)	0	100	100
All	All	1179/1152 (102%)	1161 (98%)	18 (2%)	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	256/237 (108%)	255 (100%)	1 (0%)	91	90
1	B	258/237 (109%)	257 (100%)	1 (0%)	91	90
1	C	249/237 (105%)	249 (100%)	0	100	100
1	D	251/237 (106%)	251 (100%)	0	100	100
All	All	1014/948 (107%)	1012 (100%)	2 (0%)	93	93

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	181	GLU
1	B	287	ASP

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

Mol	Chain	Res	Type
1	D	97	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](#)

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](#)

29 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	D	318	-	3,3,3	0.44	0	2,2,2	0.29	0
2	EDO	C	302	-	3,3,3	0.53	0	2,2,2	0.12	0
2	EDO	A	311	-	3,3,3	0.55	0	2,2,2	0.08	0
2	EDO	A	309	-	3,3,3	0.39	0	2,2,2	0.42	0
2	EDO	C	314	-	3,3,3	0.31	0	2,2,2	0.33	0
2	EDO	A	327	-	3,3,3	0.48	0	2,2,2	0.16	0
2	EDO	C	316	-	3,3,3	0.48	0	2,2,2	0.15	0
2	EDO	A	305	-	3,3,3	0.42	0	2,2,2	0.37	0
2	EDO	A	308	-	3,3,3	0.49	0	2,2,2	0.15	0
2	EDO	B	319	-	3,3,3	0.57	0	2,2,2	0.19	0
2	EDO	D	315	-	3,3,3	0.49	0	2,2,2	0.19	0
2	EDO	B	304	-	3,3,3	0.48	0	2,2,2	0.45	0
2	EDO	B	301	-	3,3,3	0.56	0	2,2,2	0.23	0
2	EDO	B	313	-	3,3,3	0.54	0	2,2,2	0.27	0
2	EDO	C	317	-	3,3,3	0.37	0	2,2,2	0.57	0
2	EDO	B	328	-	3,3,3	0.47	0	2,2,2	0.16	0
2	EDO	B	322	-	3,3,3	0.52	0	2,2,2	0.15	0
2	EDO	A	310	-	3,3,3	0.59	0	2,2,2	0.05	0
2	EDO	A	300	-	3,3,3	0.44	0	2,2,2	0.31	0
2	EDO	B	326	-	3,3,3	0.46	0	2,2,2	0.31	0
2	EDO	C	324	-	3,3,3	0.58	0	2,2,2	0.11	0
2	EDO	B	307	-	3,3,3	0.47	0	2,2,2	0.39	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	EDO	D	303	-	3,3,3	0.55	0	2,2,2	0.18	0
2	EDO	A	320	-	3,3,3	0.54	0	2,2,2	0.22	0
2	EDO	C	306	-	3,3,3	0.50	0	2,2,2	0.14	0
2	EDO	C	325	-	3,3,3	0.60	0	2,2,2	0.18	0
2	EDO	C	323	-	3,3,3	0.46	0	2,2,2	0.29	0
2	EDO	B	312	-	3,3,3	0.49	0	2,2,2	0.20	0
2	EDO	C	321	-	3,3,3	0.48	0	2,2,2	0.29	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	EDO	D	318	-	-	0/1/1/1	-
2	EDO	C	302	-	-	0/1/1/1	-
2	EDO	A	311	-	-	0/1/1/1	-
2	EDO	A	309	-	-	0/1/1/1	-
2	EDO	C	314	-	-	0/1/1/1	-
2	EDO	A	327	-	-	1/1/1/1	-
2	EDO	C	316	-	-	0/1/1/1	-
2	EDO	A	305	-	-	1/1/1/1	-
2	EDO	A	308	-	-	0/1/1/1	-
2	EDO	B	319	-	-	1/1/1/1	-
2	EDO	D	315	-	-	0/1/1/1	-
2	EDO	B	304	-	-	0/1/1/1	-
2	EDO	B	301	-	-	1/1/1/1	-
2	EDO	B	313	-	-	1/1/1/1	-
2	EDO	C	317	-	-	0/1/1/1	-
2	EDO	B	328	-	-	0/1/1/1	-
2	EDO	B	322	-	-	1/1/1/1	-
2	EDO	A	310	-	-	1/1/1/1	-
2	EDO	A	300	-	-	0/1/1/1	-
2	EDO	B	326	-	-	1/1/1/1	-
2	EDO	C	324	-	-	0/1/1/1	-
2	EDO	B	307	-	-	1/1/1/1	-
2	EDO	D	303	-	-	0/1/1/1	-
2	EDO	A	320	-	-	0/1/1/1	-
2	EDO	C	306	-	-	0/1/1/1	-
2	EDO	C	325	-	-	1/1/1/1	-
2	EDO	C	323	-	-	0/1/1/1	-
2	EDO	B	312	-	-	0/1/1/1	-
2	EDO	C	321	-	-	1/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (11) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	327	EDO	O1-C1-C2-O2
2	A	305	EDO	O1-C1-C2-O2
2	B	319	EDO	O1-C1-C2-O2
2	B	326	EDO	O1-C1-C2-O2
2	C	321	EDO	O1-C1-C2-O2
2	B	307	EDO	O1-C1-C2-O2
2	C	325	EDO	O1-C1-C2-O2
2	B	301	EDO	O1-C1-C2-O2
2	B	313	EDO	O1-C1-C2-O2
2	B	322	EDO	O1-C1-C2-O2
2	A	310	EDO	O1-C1-C2-O2

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	305	EDO	1	0

## 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	278/288 (96%)	0.54	29 (10%) 6 10	17, 30, 52, 63	0
1	B	278/288 (96%)	0.37	13 (4%) 31 41	17, 25, 46, 59	0
1	C	277/288 (96%)	0.26	14 (5%) 28 37	16, 26, 46, 59	0
1	D	277/288 (96%)	0.24	21 (7%) 13 21	16, 30, 51, 60	0
All	All	1110/1152 (96%)	0.35	77 (6%) 16 25	16, 27, 49, 63	0

All (77) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	204	ALA	9.7
1	B	204	ALA	9.3
1	D	204	ALA	7.5
1	C	229	LEU	5.8
1	A	229	LEU	5.6
1	B	229	LEU	5.5
1	B	202	LYS	5.3
1	A	228	ALA	5.3
1	A	287	ASP	5.2
1	C	202	LYS	5.2
1	D	229	LEU	4.3
1	D	3	HIS	4.2
1	C	204	ALA	4.0
1	A	133	PHE	3.9
1	A	202	LYS	3.9
1	B	203	GLY	3.9
1	B	287	ASP	3.8
1	D	178	LEU	3.7
1	C	205	LYS	3.6
1	A	60	ILE	3.6
1	D	205	LYS	3.5

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Mol	Chain	Res	Type	RSRZ
1	D	228	ALA	3.4
1	D	57	ALA	3.3
1	A	3	HIS	3.3
1	A	198	LEU	3.3
1	D	198[A]	LEU	3.3
1	D	133	PHE	3.2
1	B	231	GLU	3.1
1	D	179	SER	3.1
1	B	59	VAL	3.0
1	A	231	GLU	3.0
1	A	205[A]	LYS	2.9
1	A	150	ARG	2.9
1	A	151	ARG	2.9
1	D	185	ARG	2.8
1	D	231	GLU	2.8
1	D	203	GLY	2.7
1	C	206	PRO	2.7
1	D	180	ASP	2.7
1	A	201	PHE	2.7
1	B	4	HIS	2.7
1	B	228	ALA	2.7
1	D	148	ASP	2.6
1	C	207	TYR	2.6
1	A	195[A]	HIS	2.5
1	D	201	PHE	2.5
1	A	159	ALA	2.5
1	A	59	VAL	2.5
1	C	177	ILE	2.4
1	C	198	LEU	2.4
1	C	230	ASP	2.4
1	C	228	ALA	2.4
1	D	202	LYS	2.4
1	A	63	ALA	2.4
1	D	196[A]	SER	2.3
1	B	93	LEU	2.3
1	A	141	TYR	2.3
1	C	208	HIS	2.3
1	A	203	GLY	2.3
1	A	207[A]	TYR	2.2
1	A	181	GLU	2.2
1	C	231	GLU	2.2
1	D	195	HIS	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	206	PRO	2.2
1	A	148	ASP	2.1
1	C	151	ARG	2.1
1	D	207	TYR	2.1
1	B	115[A]	HIS	2.1
1	A	57	ALA	2.1
1	A	58	LYS	2.1
1	C	57	ALA	2.1
1	B	205	LYS	2.1
1	A	249	ALA	2.0
1	A	245	ARG	2.0
1	D	227	SER	2.0
1	A	94	LEU	2.0
1	A	208	HIS	2.0

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

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

## 6.3 Carbohydrates [i](#)

There are no 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(Å <sup>2</sup> )	Q<0.9
2	EDO	C	321	4/4	0.58	0.27	57,57,58,58	0
2	EDO	C	314	4/4	0.62	0.38	58,58,58,58	0
2	EDO	A	327	4/4	0.70	0.24	66,67,67,67	0
2	EDO	A	320	4/4	0.72	0.23	49,49,51,51	0
2	EDO	C	325	4/4	0.74	0.19	54,55,56,56	0
2	EDO	B	326	4/4	0.77	0.18	70,70,70,70	0
2	EDO	C	323	4/4	0.77	0.29	65,66,66,66	0
2	EDO	C	317	4/4	0.77	0.22	44,45,46,48	0
2	EDO	D	303	4/4	0.78	0.18	48,49,49,50	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	EDO	B	307	4/4	0.79	0.23	54,55,56,58	0
2	EDO	C	316	4/4	0.80	0.22	33,37,38,41	0
2	EDO	B	304	4/4	0.80	0.26	41,45,45,48	0
2	EDO	A	310	4/4	0.81	0.30	57,57,57,57	0
2	EDO	B	322	4/4	0.81	0.25	47,47,47,48	0
2	EDO	C	306	4/4	0.82	0.24	48,49,50,50	0
2	EDO	B	319	4/4	0.83	0.20	42,45,46,46	0
2	EDO	A	305	4/4	0.85	0.22	38,40,41,42	0
2	EDO	D	318	4/4	0.85	0.16	44,45,45,45	0
2	EDO	B	312	4/4	0.87	0.20	50,51,52,52	0
2	EDO	C	324	4/4	0.88	0.16	35,38,38,39	0
2	EDO	B	313	4/4	0.89	0.17	37,38,39,40	0
2	EDO	B	301	4/4	0.90	0.12	41,42,43,44	0
2	EDO	A	300	4/4	0.90	0.17	47,48,48,48	0
2	EDO	A	311	4/4	0.90	0.16	49,49,49,50	0
2	EDO	A	308	4/4	0.91	0.13	33,37,37,40	0
2	EDO	B	328	4/4	0.92	0.14	33,38,40,43	0
2	EDO	D	315	4/4	0.92	0.16	31,36,37,40	0
2	EDO	A	309	4/4	0.93	0.28	41,43,44,44	0
2	EDO	C	302	4/4	0.93	0.16	33,37,38,40	0

## 6.5 Other polymers

There are no such residues in this entry.