



# Full wwPDB X-ray Structure Validation Report ⓘ

Jan 10, 2022 – 10:29 AM EST

PDB ID : 7LQM  
Title : Glucosamine-6-phosphate Deaminase from *Pasturella multocida*  
Authors : Subramanian, R.; Srinivasachari, S.  
Deposited on : 2021-02-14  
Resolution : 2.30 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 : 2.25  
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) : 2.25

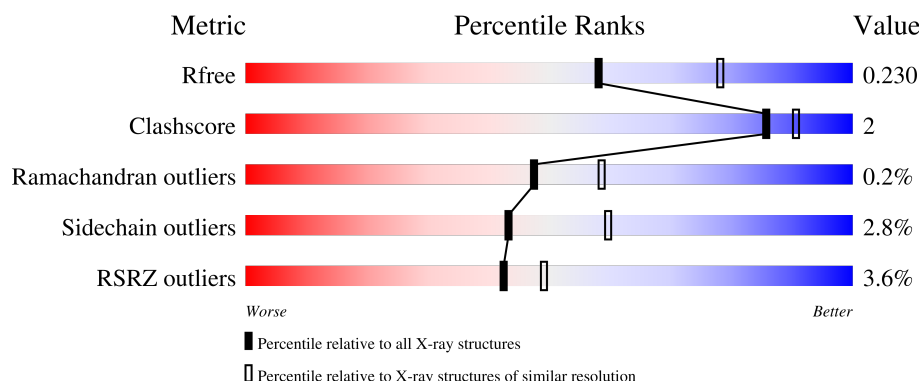
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.30 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	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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	284	<div> <div>4%</div> <div>82%</div> <div>9%</div> <div>9%</div> </div>
1	B	284	<div> <div>2%</div> <div>83%</div> <div>10%</div> <div>7%</div> </div>
1	C	284	<div> <div>8%</div> <div>85%</div> <div>6%</div> <div>10%</div> </div>
1	D	284	<div> <div>87%</div> <div>7%</div> <div>6%</div> </div>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 8464 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 Glucosamine-6-phosphate deaminase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	258	Total	C	N	O	S	0	0	0
			2042	1304	341	389	8			
1	B	265	Total	C	N	O	S	0	0	0
			2111	1346	359	398	8			
1	C	257	Total	C	N	O	S	0	0	0
			2036	1300	347	381	8			
1	D	267	Total	C	N	O	S	0	0	0
			2129	1358	363	400	8			

There are 68 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	MET	-	expression tag	UNP Q9CMF4
A	0	HIS	-	expression tag	UNP Q9CMF4
A	1	HIS	-	expression tag	UNP Q9CMF4
A	2	HIS	-	expression tag	UNP Q9CMF4
A	3	HIS	-	expression tag	UNP Q9CMF4
A	4	HIS	-	expression tag	UNP Q9CMF4
A	5	HIS	-	expression tag	UNP Q9CMF4
A	6	ILE	-	expression tag	UNP Q9CMF4
A	7	THR	-	expression tag	UNP Q9CMF4
A	8	SER	-	expression tag	UNP Q9CMF4
A	9	LEU	-	expression tag	UNP Q9CMF4
A	10	TYR	-	expression tag	UNP Q9CMF4
A	11	LYS	-	expression tag	UNP Q9CMF4
A	12	LYS	-	expression tag	UNP Q9CMF4
A	13	ALA	-	expression tag	UNP Q9CMF4
A	14	GLY	-	expression tag	UNP Q9CMF4
A	15	PHE	-	expression tag	UNP Q9CMF4
B	-1	MET	-	expression tag	UNP Q9CMF4
B	0	HIS	-	expression tag	UNP Q9CMF4
B	1	HIS	-	expression tag	UNP Q9CMF4
B	2	HIS	-	expression tag	UNP Q9CMF4

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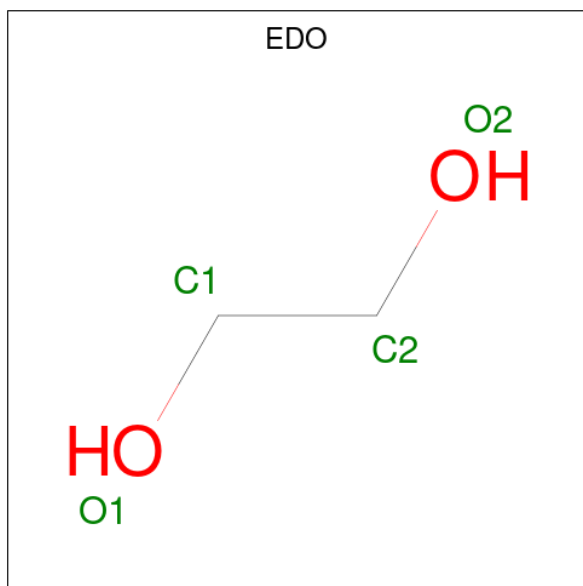
Chain	Residue	Modelled	Actual	Comment	Reference
B	3	HIS	-	expression tag	UNP Q9CMF4
B	4	HIS	-	expression tag	UNP Q9CMF4
B	5	HIS	-	expression tag	UNP Q9CMF4
B	6	ILE	-	expression tag	UNP Q9CMF4
B	7	THR	-	expression tag	UNP Q9CMF4
B	8	SER	-	expression tag	UNP Q9CMF4
B	9	LEU	-	expression tag	UNP Q9CMF4
B	10	TYR	-	expression tag	UNP Q9CMF4
B	11	LYS	-	expression tag	UNP Q9CMF4
B	12	LYS	-	expression tag	UNP Q9CMF4
B	13	ALA	-	expression tag	UNP Q9CMF4
B	14	GLY	-	expression tag	UNP Q9CMF4
B	15	PHE	-	expression tag	UNP Q9CMF4
C	-1	MET	-	expression tag	UNP Q9CMF4
C	0	HIS	-	expression tag	UNP Q9CMF4
C	1	HIS	-	expression tag	UNP Q9CMF4
C	2	HIS	-	expression tag	UNP Q9CMF4
C	3	HIS	-	expression tag	UNP Q9CMF4
C	4	HIS	-	expression tag	UNP Q9CMF4
C	5	HIS	-	expression tag	UNP Q9CMF4
C	6	ILE	-	expression tag	UNP Q9CMF4
C	7	THR	-	expression tag	UNP Q9CMF4
C	8	SER	-	expression tag	UNP Q9CMF4
C	9	LEU	-	expression tag	UNP Q9CMF4
C	10	TYR	-	expression tag	UNP Q9CMF4
C	11	LYS	-	expression tag	UNP Q9CMF4
C	12	LYS	-	expression tag	UNP Q9CMF4
C	13	ALA	-	expression tag	UNP Q9CMF4
C	14	GLY	-	expression tag	UNP Q9CMF4
C	15	PHE	-	expression tag	UNP Q9CMF4
D	-1	MET	-	expression tag	UNP Q9CMF4
D	0	HIS	-	expression tag	UNP Q9CMF4
D	1	HIS	-	expression tag	UNP Q9CMF4
D	2	HIS	-	expression tag	UNP Q9CMF4
D	3	HIS	-	expression tag	UNP Q9CMF4
D	4	HIS	-	expression tag	UNP Q9CMF4
D	5	HIS	-	expression tag	UNP Q9CMF4
D	6	ILE	-	expression tag	UNP Q9CMF4
D	7	THR	-	expression tag	UNP Q9CMF4
D	8	SER	-	expression tag	UNP Q9CMF4
D	9	LEU	-	expression tag	UNP Q9CMF4
D	10	TYR	-	expression tag	UNP Q9CMF4

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Chain	Residue	Modelled	Actual	Comment	Reference
D	11	LYS	-	expression tag	UNP Q9CMF4
D	12	LYS	-	expression tag	UNP Q9CMF4
D	13	ALA	-	expression tag	UNP Q9CMF4
D	14	GLY	-	expression tag	UNP Q9CMF4
D	15	PHE	-	expression tag	UNP Q9CMF4

- Molecule 2 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula:  $C_2H_6O_2$ ).



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

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	18	Total	O	0	0
			18	18		
3	B	44	Total	O	0	0
			44	44		
3	C	7	Total	O	0	0
			7	7		

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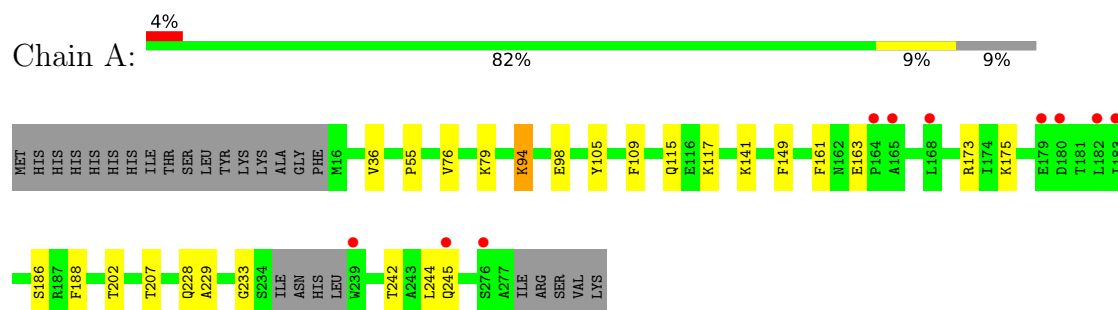
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	D	61	Total	O	0	0
			61	61		

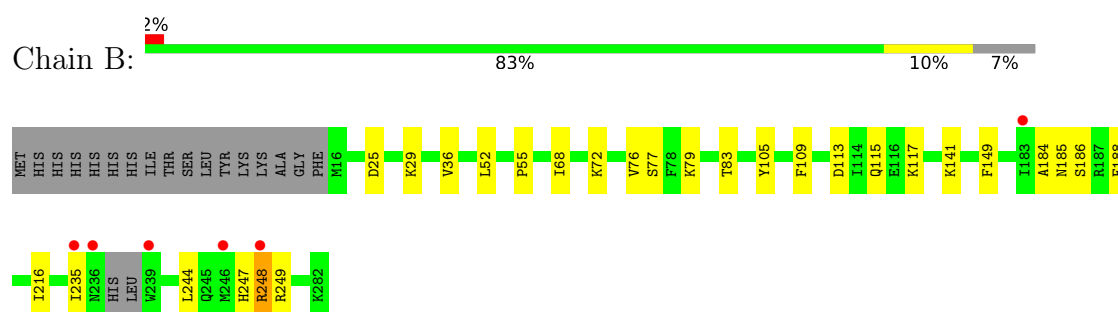
### 3 Residue-property plots [i](#)

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.

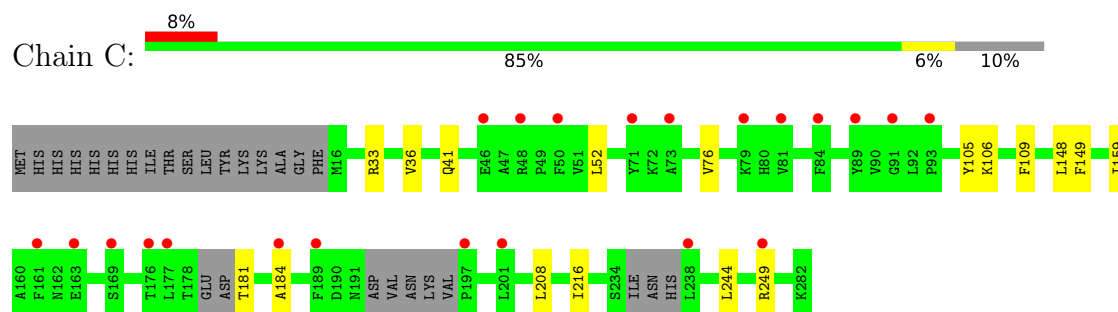
- Molecule 1: Glucosamine-6-phosphate deaminase



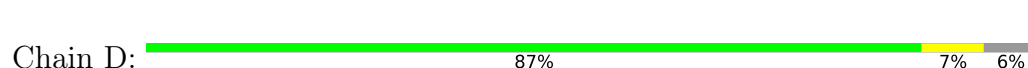
- Molecule 1: Glucosamine-6-phosphate deaminase



- Molecule 1: Glucosamine-6-phosphate deaminase



- Molecule 1: Glucosamine-6-phosphate deaminase



MET	HIS	HIS	HIS	HIS	HIS	HIS	HIS	ILE	THR	SER	LEU	TYR	LYS	LYS	ALA	GLY	PHE	M16	R17	L18	V36	R48	V76	K106	K117	F149	I159	E163	K175	L208	I216	L217	Q228	L244	A250	P287	Q260	E274	K282
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## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	84.80Å 79.57Å 85.30Å 90.00° 109.13° 90.00°	Depositor
Resolution (Å)	37.10 – 2.30 41.91 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.1 (37.10-2.30) 99.2 (41.91-2.30)	Depositor EDS
$R_{merge}$	0.04	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.99 (at 2.29Å)	Xtriage
Refinement program	PHENIX 1.19.1_4122	Depositor
R, $R_{free}$	0.200 , 0.232 0.200 , 0.230	Depositor DCC
$R_{free}$ test set	2279 reflections (4.80%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	42.5	Xtriage
Anisotropy	0.469	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 32.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.016 for l,-k,h	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	8464	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	58.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.62% 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: 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	0.31	0/2086	0.51	0/2828
1	B	0.25	0/2155	0.48	0/2918
1	C	0.29	0/2077	0.52	0/2809
1	D	0.28	0/2175	0.50	0/2947
All	All	0.28	0/8493	0.50	0/11502

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	2042	0	2006	9	0
1	B	2111	0	2096	13	0
1	C	2036	0	2020	6	0
1	D	2129	0	2115	8	0
2	A	4	0	6	0	0
2	C	12	0	18	0	0
3	A	18	0	0	0	0
3	B	44	0	0	0	0
3	C	7	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	D	61	0	0	0	0
All	All	8464	0	8261	36	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 (36) 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:C:216:ILE:HG13	1:C:244:LEU:HD11	1.84	0.60
1:B:79:LYS:HG3	1:B:115:GLN:HE21	1.67	0.59
1:B:216:ILE:HG13	1:B:244:LEU:HD11	1.84	0.58
1:C:159:ILE:HG21	1:C:208:LEU:HD22	1.85	0.57
1:C:36:VAL:HG13	1:C:76:VAL:HB	1.89	0.54
1:D:159:ILE:HG21	1:D:208:LEU:HD22	1.89	0.54
1:A:105:TYR:HA	1:A:109:PHE:HB2	1.90	0.53
1:B:68:ILE:HG22	1:B:72:LYS:HE2	1.92	0.51
1:D:216:ILE:HG13	1:D:244:LEU:HD11	1.93	0.50
1:D:16:MET:HB2	1:D:250:ALA:HB3	1.96	0.48
1:D:36:VAL:HG13	1:D:76:VAL:HB	1.94	0.48
1:B:105:TYR:HA	1:B:109:PHE:HB2	1.96	0.47
1:C:105:TYR:HA	1:C:109:PHE:HB2	1.97	0.47
1:C:181:THR:HG23	1:C:184:ALA:H	1.80	0.46
1:B:235:ILE:HD12	1:B:235:ILE:H	1.80	0.46
1:B:247:HIS:CE1	1:B:248:ARG:HD3	2.51	0.45
1:D:257:PRO:O	1:D:260:GLN:HG2	2.17	0.45
1:A:36:VAL:HG13	1:A:76:VAL:HB	1.99	0.44
1:B:25:ASP:OD2	1:B:29:LYS:HE2	2.18	0.44
1:B:36:VAL:HG13	1:B:76:VAL:HB	2.00	0.43
1:D:18:LEU:O	1:D:274:GLU:HG3	2.18	0.43
1:C:52:LEU:HD12	1:C:148:LEU:O	2.19	0.42
1:B:184:ALA:C	1:B:186:SER:H	2.22	0.42
1:B:185:ASN:HA	1:B:188:PHE:CD2	2.54	0.42
1:D:175:LYS:HD2	1:D:175:LYS:HA	1.79	0.42
1:A:173:ARG:HE	1:A:175:LYS:HE2	1.85	0.42
1:B:77:SER:OG	1:B:113:ASP:OD2	2.31	0.41
1:A:94:LYS:HE3	1:A:94:LYS:HB3	1.79	0.41
1:B:248:ARG:HH21	1:B:249:ARG:HH12	1.68	0.41
1:B:52:LEU:O	1:B:83:THR:HA	2.20	0.41
1:A:233:GLY:O	1:A:245:GLN:NE2	2.49	0.41
1:D:163:GLU:OE1	1:D:175:LYS:HE3	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:161:PHE:HB2	1:A:202:THR:HB	2.02	0.41
1:A:98:GLU:OE1	1:A:188:PHE:HB3	2.20	0.41
1:A:79:LYS:HG2	1:A:115:GLN:HE21	1.86	0.41
1:A:229:ALA:O	1:A:242:THR:HG22	2.21	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	254/284 (89%)	243 (96%)	10 (4%)	1 (0%)	34	42
1	B	261/284 (92%)	251 (96%)	9 (3%)	1 (0%)	34	42
1	C	249/284 (88%)	239 (96%)	10 (4%)	0	100	100
1	D	265/284 (93%)	257 (97%)	8 (3%)	0	100	100
All	All	1029/1136 (91%)	990 (96%)	37 (4%)	2 (0%)	47	58

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	55	PRO
1	A	55	PRO

### 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	221/247 (90%)	212 (96%)	9 (4%)	30	43
1	B	230/247 (93%)	226 (98%)	4 (2%)	60	76
1	C	220/247 (89%)	215 (98%)	5 (2%)	50	67
1	D	232/247 (94%)	225 (97%)	7 (3%)	41	57
All	All	903/988 (91%)	878 (97%)	25 (3%)	43	60

All (25) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	94	LYS
1	A	117	LYS
1	A	141	LYS
1	A	149	PHE
1	A	163	GLU
1	A	186	SER
1	A	207	THR
1	A	228	GLN
1	A	244	LEU
1	B	117	LYS
1	B	141	LYS
1	B	149	PHE
1	B	248	ARG
1	C	33	ARG
1	C	41	GLN
1	C	106	LYS
1	C	149	PHE
1	C	249	ARG
1	D	16	MET
1	D	48	ARG
1	D	106	LYS
1	D	117	LYS
1	D	149	PHE
1	D	217	LEU
1	D	228	GLN

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

Mol	Chain	Res	Type
1	B	115	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

## 5.6 Ligand geometry ⓘ

4 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	C	303	-	3,3,3	0.47	0	2,2,2	0.33	0
2	EDO	C	301	-	3,3,3	0.44	0	2,2,2	0.35	0
2	EDO	C	302	-	3,3,3	0.46	0	2,2,2	0.29	0
2	EDO	A	301	-	3,3,3	0.47	0	2,2,2	0.31	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	C	303	-	-	1/1/1/1	-
2	EDO	C	301	-	-	0/1/1/1	-
2	EDO	C	302	-	-	1/1/1/1	-
2	EDO	A	301	-	-	0/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	C	302	EDO	O1-C1-C2-O2
2	C	303	EDO	O1-C1-C2-O2

There are no ring outliers.

No monomer is involved in short contacts.

## 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	258/284 (90%)	0.18	10 (3%) 39 46	34, 55, 91, 112	0
1	B	265/284 (93%)	-0.10	6 (2%) 60 67	31, 45, 81, 113	0
1	C	257/284 (90%)	0.55	22 (8%) 10 14	37, 78, 117, 135	0
1	D	267/284 (94%)	-0.18	0 100 100	34, 45, 65, 87	0
All	All	1047/1136 (92%)	0.11	38 (3%) 42 49	31, 50, 103, 135	0

All (38) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	48	ARG	5.0
1	A	183	ILE	4.2
1	C	197	PRO	3.7
1	C	81	VAL	3.7
1	B	236	ASN	3.6
1	A	245	GLN	3.4
1	C	73	ALA	3.3
1	C	184	ALA	3.2
1	A	165	ALA	3.1
1	A	276	SER	3.1
1	A	239	TRP	3.1
1	C	91	GLY	3.0
1	B	235	ILE	2.9
1	A	168	LEU	2.8
1	A	180	ASP	2.8
1	C	84	PHE	2.7
1	C	93	PRO	2.7
1	A	182	LEU	2.7
1	C	46	GLU	2.6
1	C	79	LYS	2.6
1	C	176	THR	2.5

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Mol	Chain	Res	Type	RSRZ
1	C	50	PHE	2.5
1	C	71	TYR	2.5
1	C	189	PHE	2.5
1	C	161	PHE	2.4
1	C	238	LEU	2.4
1	A	164	PRO	2.3
1	C	169	SER	2.3
1	C	249	ARG	2.3
1	C	89	TYR	2.2
1	C	163	GLU	2.2
1	B	239	TRP	2.2
1	C	177	LEU	2.2
1	A	179	GLU	2.1
1	B	183	ILE	2.1
1	B	246	MET	2.1
1	B	248	ARG	2.0
1	C	201	LEU	2.0

## 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 monosaccharides 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, 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	303	4/4	0.84	0.34	53,54,54,60	0
2	EDO	A	301	4/4	0.87	0.23	48,58,62,62	0
2	EDO	C	302	4/4	0.90	0.24	55,56,60,67	0
2	EDO	C	301	4/4	0.93	0.25	46,46,48,55	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.