



# Full wwPDB X-ray Structure Validation Report

Feb 27, 2014 – 09:07 PM GMT

PDB ID : 2Q4R  
Title : Ensemble refinement of the protein crystal structure of human phosphomannomutase 2 (PMM2)  
Authors : Levin, E.J.; Kondrashov, D.A.; Wesenberg, G.E.; Phillips Jr., G.N.; Center for Eukaryotic Structural Genomics (CESG)  
Deposited on : 2007-05-31  
Resolution : 2.09 Å(reported)

This is a full wwPDB 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 <http://wwpdb.org/ValidationPDFNotes.html>

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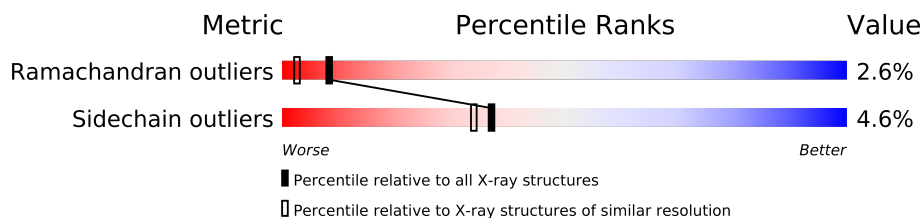
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.15 2013
Xtriage (Phenix)	:	dev-1323
EDS	:	<b>FAILED</b>
Percentile statistics	:	21963
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP)	:	stable22683

# 1 Overall quality at a glance

The reported resolution of this entry is 2.09 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))
Ramachandran outliers	78287	3610 (2.10-2.10)
Sidechain outliers	78261	3611 (2.10-2.10)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Note EDS failed to run properly.

Mol	Chain	Length	Quality of chain
1	1-A	246	<div><div></div><div><div></div><div></div><div></div><div></div></div></div>
1	10-A	246	<div><div></div><div><div></div><div></div><div></div><div></div></div></div>
1	11-A	246	<div><div></div><div><div></div><div></div><div></div><div></div></div></div>
1	12-A	246	<div><div></div><div><div></div><div></div><div></div><div></div></div></div>
1	13-A	246	<div><div></div><div><div></div><div></div><div></div><div></div></div></div>
1	14-A	246	<div><div></div><div><div></div><div></div><div></div><div></div></div></div>
1	15-A	246	<div><div></div><div><div></div><div></div><div></div><div></div></div></div>
1	16-A	246	<div><div></div><div><div></div><div></div><div></div><div></div></div></div>
1	2-A	246	<div><div></div><div><div></div><div></div><div></div><div></div></div></div>
1	3-A	246	<div><div></div><div><div></div><div></div><div></div><div></div></div></div>
1	4-A	246	<div><div></div><div><div></div><div></div><div></div><div></div></div></div>
1	5-A	246	<div><div></div><div><div></div><div></div><div></div><div></div></div></div>
1	6-A	246	<div><div></div><div><div></div><div></div><div></div><div></div></div></div>
1	7-A	246	<div><div></div><div><div></div><div></div><div></div><div></div></div></div>
1	8-A	246	<div><div></div><div><div></div><div></div><div></div><div></div></div></div>
1	9-A	246	<div><div></div><div><div></div><div></div><div></div><div></div></div></div>

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 33616 atoms, of which 0 are hydrogen and 0 are deuterium.

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.

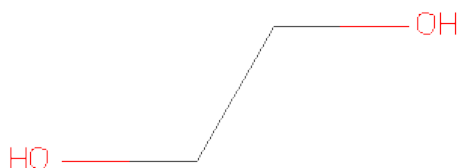
- Molecule 1 is a protein called Phosphomannomutase 2.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	1-A	240	Total 1943	C 1239	N 330	O 364	S 6	Se 4	0	0	0
1	2-A	240	Total 1943	C 1239	N 330	O 364	S 6	Se 4	0	0	0
1	3-A	240	Total 1943	C 1239	N 330	O 364	S 6	Se 4	0	0	0
1	4-A	240	Total 1943	C 1239	N 330	O 364	S 6	Se 4	0	0	0
1	5-A	240	Total 1943	C 1239	N 330	O 364	S 6	Se 4	0	0	0
1	6-A	240	Total 1943	C 1239	N 330	O 364	S 6	Se 4	0	0	0
1	7-A	240	Total 1943	C 1239	N 330	O 364	S 6	Se 4	0	0	0
1	8-A	240	Total 1943	C 1239	N 330	O 364	S 6	Se 4	0	0	0
1	9-A	240	Total 1943	C 1239	N 330	O 364	S 6	Se 4	0	0	0
1	10-A	240	Total 1943	C 1239	N 330	O 364	S 6	Se 4	0	0	0
1	11-A	240	Total 1943	C 1239	N 330	O 364	S 6	Se 4	0	0	0
1	12-A	240	Total 1943	C 1239	N 330	O 364	S 6	Se 4	0	0	0
1	13-A	240	Total 1943	C 1239	N 330	O 364	S 6	Se 4	0	0	0
1	14-A	240	Total 1943	C 1239	N 330	O 364	S 6	Se 4	0	0	0
1	15-A	240	Total 1943	C 1239	N 330	O 364	S 6	Se 4	0	0	0
1	16-A	240	Total 1943	C 1239	N 330	O 364	S 6	Se 4	0	0	0

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	SER	-	EXPRESSION TAG	UNP O15305
A	28	MSE	MET	MODIFIED RESIDUE	UNP O15305
A	126	MSE	MET	MODIFIED RESIDUE	UNP O15305
A	212	MSE	MET	MODIFIED RESIDUE	UNP O15305
A	227	MSE	MET	MODIFIED RESIDUE	UNP O15305

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



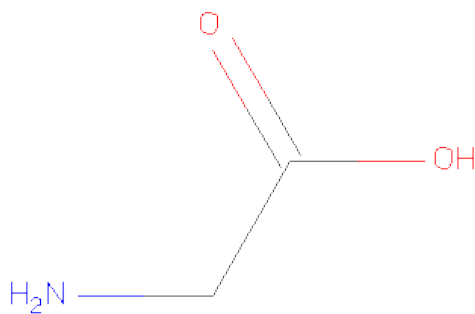
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	1-A	1	Total C O 4 2 2	0	0
2	2-A	1	Total C O 4 2 2	0	0
2	3-A	1	Total C O 4 2 2	0	0
2	4-A	1	Total C O 4 2 2	0	0
2	5-A	1	Total C O 4 2 2	0	0
2	6-A	1	Total C O 4 2 2	0	0
2	7-A	1	Total C O 4 2 2	0	0
2	8-A	1	Total C O 4 2 2	0	0

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	9-A	1	Total	C	O	0	0
			4	2	2		
2	10-A	1	Total	C	O	0	0
			4	2	2		
2	11-A	1	Total	C	O	0	0
			4	2	2		
2	12-A	1	Total	C	O	0	0
			4	2	2		
2	13-A	1	Total	C	O	0	0
			4	2	2		
2	14-A	1	Total	C	O	0	0
			4	2	2		
2	15-A	1	Total	C	O	0	0
			4	2	2		
2	16-A	1	Total	C	O	0	0
			4	2	2		

- Molecule 3 is GLYCINE (three-letter code: GLY) (formula: C<sub>2</sub>H<sub>5</sub>NO<sub>2</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	1-A	3	Total	C	N	O	0	0
			12	6	3	3		
3	2-A	3	Total	C	N	O	0	0
			12	6	3	3		
3	3-A	3	Total	C	N	O	0	0
			12	6	3	3		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	4-A	3	Total	C	N	O	0	0
			12	6	3	3		
3	5-A	3	Total	C	N	O	0	0
			12	6	3	3		
3	6-A	3	Total	C	N	O	0	0
			12	6	3	3		
3	7-A	3	Total	C	N	O	0	0
			12	6	3	3		
3	8-A	3	Total	C	N	O	0	0
			12	6	3	3		
3	9-A	3	Total	C	N	O	0	0
			12	6	3	3		
3	10-A	3	Total	C	N	O	0	0
			12	6	3	3		
3	11-A	3	Total	C	N	O	0	0
			12	6	3	3		
3	12-A	3	Total	C	N	O	0	0
			12	6	3	3		
3	13-A	3	Total	C	N	O	0	0
			12	6	3	3		
3	14-A	3	Total	C	N	O	0	0
			12	6	3	3		
3	15-A	3	Total	C	N	O	0	0
			12	6	3	3		
3	16-A	3	Total	C	N	O	0	0
			12	6	3	3		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	1-A	142	Total	O	0	0
			142	142		
4	2-A	142	Total	O	0	0
			142	142		
4	3-A	142	Total	O	0	0
			142	142		
4	4-A	142	Total	O	0	0
			142	142		
4	5-A	142	Total	O	0	0
			142	142		
4	6-A	142	Total	O	0	0
			142	142		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	7-A	142	Total 142	O 142	0	0
4	8-A	142	Total 142	O 142	0	0
4	9-A	142	Total 142	O 142	0	0
4	10-A	142	Total 142	O 142	0	0
4	11-A	142	Total 142	O 142	0	0
4	12-A	142	Total 142	O 142	0	0
4	13-A	142	Total 142	O 142	0	0
4	14-A	142	Total 142	O 142	0	0
4	15-A	142	Total 142	O 142	0	0
4	16-A	142	Total 142	O 142	0	0

### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

Note EDS failed to run properly.

- Molecule 1: Phosphomannomutase 2

Chain 1-A: 



- Molecule 1: Phosphomannomutase 2

Chain 2-A: 



- Molecule 1: Phosphomannomutase 2

Chain 3-A: 



- Molecule 1: Phosphomannomutase 2

Chain 4-A: 



- Molecule 1: Phosphomannomutase 2

Chain 5-A: 



- Molecule 1: Phosphomannomutase 2

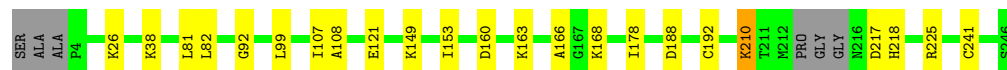
Chain 6-A: 





- Molecule 1: Phosphomannomutase 2

Chain 7-A: 



- Molecule 1: Phosphomannomutase 2

Chain 8-A: 



- Molecule 1: Phosphomannomutase 2

Chain 9-A: 



- Molecule 1: Phosphomannomutase 2

Chain 10-A: 



- Molecule 1: Phosphomannomutase 2

Chain 11-A: 



- Molecule 1: Phosphomannomutase 2

Chain 12-A: 



- Molecule 1: Phosphomannomutase 2

Chain 13-A: 



- Molecule 1: Phosphomannomutase 2

Chain 14-A: 



- Molecule 1: Phosphomannomutase 2

Chain 15-A:



● Molecule 1: Phosphomannomutase 2

Chain 16-A:



## 4 Data and refinement statistics i

EDS failed to run properly - this section will therefore be incomplete.

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	70.62Å 70.62Å 100.15Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	30.58 – 2.09	Depositor
% Data completeness (in resolution range)	99.4 (30.58-2.09)	Depositor
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.57 (at 2.10Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.207 , 0.298	Depositor
Wilson B-factor (Å <sup>2</sup> )	45.5	Xtriage
Anisotropy	0.043	Xtriage
Estimated twinning fraction	0.031 for -h,-k,l	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	1 of 17514 reflections (0.006%)	Xtriage
Total number of atoms	33616	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	42.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.10% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

## 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	1-A	0.36	0/1977	0.58	0/2646
1	2-A	0.35	0/1977	0.59	0/2646
1	3-A	0.36	0/1977	0.58	0/2646
1	4-A	0.38	0/1977	0.60	0/2646
1	5-A	0.36	0/1977	0.59	0/2646
1	6-A	0.35	0/1977	0.59	0/2646
1	7-A	0.37	0/1977	0.61	0/2646
1	8-A	0.39	0/1977	0.61	0/2646
1	9-A	0.36	0/1977	0.58	0/2646
1	10-A	0.37	0/1977	0.58	0/2646
1	11-A	0.36	0/1977	0.60	0/2646
1	12-A	0.37	0/1977	0.60	0/2646
1	13-A	0.40	0/1977	0.66	0/2646
1	14-A	0.39	0/1977	0.65	0/2646
1	15-A	0.41	0/1977	0.66	0/2646
1	16-A	0.41	0/1977	0.65	0/2646
All	All	0.37	0/31632	0.61	0/42336

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the

chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1-A	1943	0	1930	0	0
1	2-A	1943	0	1930	0	0
1	3-A	1943	0	1930	0	0
1	4-A	1943	0	1930	0	0
1	5-A	1943	0	1930	0	0
1	6-A	1943	0	1930	0	0
1	7-A	1943	0	1930	0	0
1	8-A	1943	0	1930	0	0
1	9-A	1943	0	1930	0	0
1	10-A	1943	0	1930	0	0
1	11-A	1943	0	1930	0	0
1	12-A	1943	0	1930	0	0
1	13-A	1943	0	1930	0	0
1	14-A	1943	0	1930	0	0
1	15-A	1943	0	1930	0	0
1	16-A	1943	0	1930	0	0
2	1-A	4	0	6	0	0
2	2-A	4	0	6	0	0
2	3-A	4	0	6	0	0
2	4-A	4	0	6	0	0
2	5-A	4	0	6	0	0
2	6-A	4	0	6	0	0
2	7-A	4	0	6	0	0
2	8-A	4	0	6	0	0
2	9-A	4	0	6	0	0
2	10-A	4	0	6	0	0
2	11-A	4	0	6	0	0
2	12-A	4	0	6	0	0
2	13-A	4	0	6	0	0
2	14-A	4	0	6	0	0
2	15-A	4	0	6	0	0
2	16-A	4	0	6	0	0
3	1-A	12	0	6	0	0
3	2-A	12	0	6	0	0
3	3-A	12	0	6	0	0
3	4-A	12	0	6	0	0
3	5-A	12	0	6	0	0
3	6-A	12	0	6	0	0
3	7-A	12	0	6	0	0
3	8-A	12	0	6	0	0
3	9-A	12	0	6	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	10-A	12	0	6	0	0
3	11-A	12	0	6	0	0
3	12-A	12	0	6	0	0
3	13-A	12	0	6	0	0
3	14-A	12	0	6	0	0
3	15-A	12	0	6	0	0
3	16-A	12	0	6	0	0
4	1-A	142	0	0	0	0
4	2-A	142	0	0	0	0
4	3-A	142	0	0	0	0
4	4-A	142	0	0	0	0
4	5-A	142	0	0	0	0
4	6-A	142	0	0	0	0
4	7-A	142	0	0	0	0
4	8-A	142	0	0	0	0
4	9-A	142	0	0	0	0
4	10-A	142	0	0	0	0
4	11-A	142	0	0	0	0
4	12-A	142	0	0	0	0
4	13-A	142	0	0	0	0
4	14-A	142	0	0	0	0
4	15-A	142	0	0	0	0
4	16-A	142	0	0	0	0
All	All	33616	0	31072	0	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. Clashscore could not be calculated for this entry.

There are no clashes within the asymmetric unit.

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone ⓘ

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	1-A	236/246 (96%)	208 (88%)	24 (10%)	4 (2%)	14 6

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	2-A	236/246 (96%)	210 (89%)	19 (8%)	7 (3%)	7	2
1	3-A	236/246 (96%)	215 (91%)	17 (7%)	4 (2%)	14	6
1	4-A	236/246 (96%)	202 (86%)	30 (13%)	4 (2%)	14	6
1	5-A	236/246 (96%)	200 (85%)	26 (11%)	10 (4%)	4	1
1	6-A	236/246 (96%)	214 (91%)	19 (8%)	3 (1%)	18	10
1	7-A	236/246 (96%)	190 (80%)	37 (16%)	9 (4%)	5	1
1	8-A	236/246 (96%)	193 (82%)	31 (13%)	12 (5%)	3	0
1	9-A	236/246 (96%)	204 (86%)	27 (11%)	5 (2%)	11	4
1	10-A	236/246 (96%)	201 (85%)	28 (12%)	7 (3%)	7	2
1	11-A	236/246 (96%)	204 (86%)	27 (11%)	5 (2%)	11	4
1	12-A	236/246 (96%)	214 (91%)	17 (7%)	5 (2%)	11	4
1	13-A	236/246 (96%)	203 (86%)	24 (10%)	9 (4%)	5	1
1	14-A	236/246 (96%)	205 (87%)	26 (11%)	5 (2%)	11	4
1	15-A	236/246 (96%)	210 (89%)	19 (8%)	7 (3%)	7	2
1	16-A	236/246 (96%)	207 (88%)	26 (11%)	3 (1%)	18	10
All	All	3776/3936 (96%)	3280 (87%)	397 (10%)	99 (3%)	8	2

All (99) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	1-A	130	SER
1	5-A	39	ILE
1	5-A	193	LEU
1	7-A	163	LYS
1	8-A	21	ARG
1	8-A	136	CYS
1	10-A	89	SER
1	13-A	60	VAL
1	13-A	138	GLN
1	14-A	39	ILE
1	14-A	60	VAL
1	15-A	82	LEU
1	15-A	135	SER
1	1-A	134	ARG
1	4-A	6	PRO
1	4-A	193	LEU
1	5-A	13	VAL

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Mol	Chain	Res	Type
1	5-A	169	GLY
1	5-A	192	CYS
1	6-A	79	GLY
1	6-A	210	LYS
1	7-A	92	GLY
1	7-A	107	ILE
1	7-A	166	ALA
1	7-A	217	ASP
1	8-A	13	VAL
1	8-A	89	SER
1	8-A	217	ASP
1	8-A	228	GLY
1	9-A	5	GLY
1	10-A	180	PHE
1	11-A	13	VAL
1	11-A	21	ARG
1	12-A	201	TYR
1	13-A	135	SER
1	13-A	244	LEU
1	14-A	197	GLU
1	16-A	13	VAL
1	16-A	197	GLU
1	2-A	5	GLY
1	2-A	210	LYS
1	3-A	217	ASP
1	4-A	135	SER
1	5-A	21	ARG
1	5-A	200	GLY
1	7-A	82	LEU
1	8-A	6	PRO
1	8-A	180	PHE
1	10-A	217	ASP
1	12-A	217	ASP
1	13-A	136	CYS
1	13-A	243	LEU
1	14-A	210	LYS
1	14-A	217	ASP
1	15-A	210	LYS
1	16-A	217	ASP
1	1-A	13	VAL
1	2-A	93	GLU
1	3-A	13	VAL

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Mol	Chain	Res	Type
1	3-A	36	ARG
1	4-A	197	GLU
1	5-A	58	ASN
1	5-A	83	CYS
1	5-A	217	ASP
1	7-A	210	LYS
1	8-A	36	ARG
1	8-A	174	ILE
1	9-A	217	ASP
1	11-A	79	GLY
1	12-A	21	ARG
1	13-A	6	PRO
1	13-A	199	ASP
1	15-A	58	ASN
1	15-A	136	CYS
1	2-A	13	VAL
1	3-A	192	CYS
1	7-A	108	ALA
1	8-A	20	PRO
1	10-A	58	ASN
1	10-A	82	LEU
1	11-A	20	PRO
1	12-A	20	PRO
1	13-A	13	VAL
1	1-A	129	VAL
1	8-A	165	PHE
1	10-A	13	VAL
1	12-A	13	VAL
1	2-A	153	ILE
1	2-A	169	GLY
1	6-A	13	VAL
1	9-A	72	GLY
1	15-A	13	VAL
1	15-A	60	VAL
1	9-A	13	VAL
1	10-A	174	ILE
1	2-A	224	PRO
1	7-A	153	ILE
1	9-A	79	GLY
1	11-A	233	ALA

### 5.3.2 Protein sidechains ⓘ

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	1-A	212/210 (101%)	207 (98%)	5 (2%)	61	65
1	2-A	212/210 (101%)	203 (96%)	9 (4%)	40	38
1	3-A	212/210 (101%)	203 (96%)	9 (4%)	40	38
1	4-A	212/210 (101%)	204 (96%)	8 (4%)	44	44
1	5-A	212/210 (101%)	206 (97%)	6 (3%)	56	59
1	6-A	212/210 (101%)	204 (96%)	8 (4%)	44	44
1	7-A	212/210 (101%)	197 (93%)	15 (7%)	21	16
1	8-A	212/210 (101%)	200 (94%)	12 (6%)	29	24
1	9-A	212/210 (101%)	207 (98%)	5 (2%)	61	65
1	10-A	212/210 (101%)	202 (95%)	10 (5%)	36	33
1	11-A	212/210 (101%)	201 (95%)	11 (5%)	32	29
1	12-A	212/210 (101%)	205 (97%)	7 (3%)	50	51
1	13-A	212/210 (101%)	196 (92%)	16 (8%)	19	14
1	14-A	212/210 (101%)	201 (95%)	11 (5%)	32	29
1	15-A	212/210 (101%)	200 (94%)	12 (6%)	29	24
1	16-A	212/210 (101%)	200 (94%)	12 (6%)	29	24
All	All	3392/3360 (101%)	3236 (95%)	156 (5%)	37	34

All (156) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	1-A	38	LYS
1	1-A	106	TYR
1	1-A	134	ARG
1	1-A	178	ILE
1	1-A	225	ARG
1	2-A	26	LYS
1	2-A	38	LYS
1	2-A	83	CYS
1	2-A	98	ASP
1	2-A	106	TYR

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Mol	Chain	Res	Type
1	2-A	111	LYS
1	2-A	157	PHE
1	2-A	178	ILE
1	2-A	227	MSE
1	3-A	25	THR
1	3-A	38	LYS
1	3-A	106	TYR
1	3-A	146	GLU
1	3-A	157	PHE
1	3-A	168	LYS
1	3-A	178	ILE
1	3-A	188	ASP
1	3-A	242	GLU
1	4-A	26	LYS
1	4-A	27	GLU
1	4-A	83	CYS
1	4-A	136	CYS
1	4-A	139	GLU
1	4-A	146	GLU
1	4-A	178	ILE
1	4-A	244	LEU
1	5-A	50	GLU
1	5-A	157	PHE
1	5-A	178	ILE
1	5-A	225	ARG
1	5-A	231	VAL
1	5-A	241	CYS
1	6-A	26	LYS
1	6-A	35	LEU
1	6-A	38	LYS
1	6-A	50	GLU
1	6-A	157	PHE
1	6-A	178	ILE
1	6-A	225	ARG
1	6-A	242	GLU
1	7-A	26	LYS
1	7-A	38	LYS
1	7-A	81	LEU
1	7-A	99	LEU
1	7-A	121	GLU
1	7-A	149	LYS
1	7-A	160	ASP

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Mol	Chain	Res	Type
1	7-A	168	LYS
1	7-A	178	ILE
1	7-A	188	ASP
1	7-A	192	CYS
1	7-A	210	LYS
1	7-A	218	HIS
1	7-A	225	ARG
1	7-A	241	CYS
1	8-A	20	PRO
1	8-A	26	LYS
1	8-A	36	ARG
1	8-A	87	ILE
1	8-A	99	LEU
1	8-A	138	GLN
1	8-A	157	PHE
1	8-A	170	LEU
1	8-A	178	ILE
1	8-A	181	ASP
1	8-A	241	CYS
1	8-A	244	LEU
1	9-A	28	MSE
1	9-A	38	LYS
1	9-A	50	GLU
1	9-A	178	ILE
1	9-A	231	VAL
1	10-A	22	GLN
1	10-A	25	THR
1	10-A	26	LYS
1	10-A	38	LYS
1	10-A	87	ILE
1	10-A	157	PHE
1	10-A	178	ILE
1	10-A	181	ASP
1	10-A	231	VAL
1	10-A	244	LEU
1	11-A	38	LYS
1	11-A	51	LYS
1	11-A	81	LEU
1	11-A	84	ARG
1	11-A	111	LYS
1	11-A	138	GLN
1	11-A	157	PHE

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Mol	Chain	Res	Type
1	11-A	164	GLU
1	11-A	178	ILE
1	11-A	219	GLU
1	11-A	231	VAL
1	12-A	25	THR
1	12-A	26	LYS
1	12-A	38	LYS
1	12-A	48	ASP
1	12-A	157	PHE
1	12-A	168	LYS
1	12-A	178	ILE
1	13-A	9	CYS
1	13-A	26	LYS
1	13-A	39	ILE
1	13-A	50	GLU
1	13-A	123	ARG
1	13-A	135	SER
1	13-A	141	ARG
1	13-A	157	PHE
1	13-A	178	ILE
1	13-A	210	LYS
1	13-A	218	HIS
1	13-A	225	ARG
1	13-A	227	MSE
1	13-A	230	SER
1	13-A	231	VAL
1	13-A	244	LEU
1	14-A	26	LYS
1	14-A	29	ASP
1	14-A	38	LYS
1	14-A	59	ASP
1	14-A	83	CYS
1	14-A	157	PHE
1	14-A	178	ILE
1	14-A	188	ASP
1	14-A	227	MSE
1	14-A	231	VAL
1	14-A	242	GLU
1	15-A	27	GLU
1	15-A	81	LEU
1	15-A	99	LEU
1	15-A	135	SER

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Mol	Chain	Res	Type
1	15-A	157	PHE
1	15-A	170	LEU
1	15-A	178	ILE
1	15-A	188	ASP
1	15-A	192	CYS
1	15-A	219	GLU
1	15-A	227	MSE
1	15-A	244	LEU
1	16-A	38	LYS
1	16-A	47	SER
1	16-A	81	LEU
1	16-A	83	CYS
1	16-A	157	PHE
1	16-A	170	LEU
1	16-A	178	ILE
1	16-A	185	ASP
1	16-A	210	LYS
1	16-A	225	ARG
1	16-A	231	VAL
1	16-A	236	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (43) such sidechains are listed below:

Mol	Chain	Res	Type
1	2-A	138	GLN
1	2-A	152	ASN
1	3-A	55	GLN
1	3-A	138	GLN
1	3-A	218	HIS
1	4-A	138	GLN
1	5-A	138	GLN
1	5-A	198	ASN
1	5-A	218	HIS
1	6-A	138	GLN
1	6-A	152	ASN
1	7-A	37	GLN
1	7-A	55	GLN
1	7-A	97	GLN
1	7-A	101	ASN
1	7-A	152	ASN
1	7-A	177	GLN
1	8-A	37	GLN

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Mol	Chain	Res	Type
1	8-A	55	GLN
1	8-A	97	GLN
1	8-A	101	ASN
1	8-A	138	GLN
1	9-A	138	GLN
1	9-A	218	HIS
1	10-A	55	GLN
1	10-A	97	GLN
1	10-A	101	ASN
1	10-A	138	GLN
1	10-A	152	ASN
1	11-A	97	GLN
1	11-A	101	ASN
1	11-A	138	GLN
1	11-A	216	ASN
1	12-A	71	ASN
1	12-A	152	ASN
1	12-A	218	HIS
1	13-A	198	ASN
1	14-A	138	GLN
1	15-A	22	GLN
1	15-A	55	GLN
1	15-A	90	HIS
1	16-A	90	HIS
1	16-A	138	GLN

### 5.3.3 RNA ⓘ

There are no RNA chains 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 carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

64 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	1-A	300	-	3,3,3	0.57	0	2,2,2	0.35	0
3	GLY	1-A	400	-	3,3,4	10.07	2 (66%)	0,2,4	0.00	-
3	GLY	1-A	401	-	3,3,4	10.24	2 (66%)	0,2,4	0.00	-
3	GLY	1-A	402	-	3,3,4	10.39	2 (66%)	0,2,4	0.00	-
2	EDO	10-A	300	-	3,3,3	0.57	0	2,2,2	0.37	0
3	GLY	10-A	400	-	3,3,4	10.06	2 (66%)	0,2,4	0.00	-
3	GLY	10-A	401	-	3,3,4	10.31	2 (66%)	0,2,4	0.00	-
3	GLY	10-A	402	-	3,3,4	10.42	2 (66%)	0,2,4	0.00	-
2	EDO	11-A	300	-	3,3,3	0.57	0	2,2,2	0.36	0
3	GLY	11-A	400	-	3,3,4	10.06	2 (66%)	0,2,4	0.00	-
3	GLY	11-A	401	-	3,3,4	10.23	2 (66%)	0,2,4	0.00	-
3	GLY	11-A	402	-	3,3,4	10.38	2 (66%)	0,2,4	0.00	-
2	EDO	12-A	300	-	3,3,3	0.58	0	2,2,2	0.37	0
3	GLY	12-A	400	-	3,3,4	10.07	2 (66%)	0,2,4	0.00	-
3	GLY	12-A	401	-	3,3,4	10.29	2 (66%)	0,2,4	0.00	-
3	GLY	12-A	402	-	3,3,4	10.44	2 (66%)	0,2,4	0.00	-
2	EDO	13-A	300	-	3,3,3	0.58	0	2,2,2	0.36	0
3	GLY	13-A	400	-	3,3,4	10.03	2 (66%)	0,2,4	0.00	-
3	GLY	13-A	401	-	3,3,4	10.08	2 (66%)	0,2,4	0.00	-
3	GLY	13-A	402	-	3,3,4	10.46	2 (66%)	0,2,4	0.00	-
2	EDO	14-A	300	-	3,3,3	0.58	0	2,2,2	0.36	0
3	GLY	14-A	400	-	3,3,4	10.14	2 (66%)	0,2,4	0.00	-
3	GLY	14-A	401	-	3,3,4	10.26	2 (66%)	0,2,4	0.00	-
3	GLY	14-A	402	-	3,3,4	10.39	2 (66%)	0,2,4	0.00	-
2	EDO	15-A	300	-	3,3,3	0.58	0	2,2,2	0.37	0
3	GLY	15-A	400	-	3,3,4	10.09	2 (66%)	0,2,4	0.00	-
3	GLY	15-A	401	-	3,3,4	10.24	2 (66%)	0,2,4	0.00	-



Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	GLY	15-A	402	-	3,3,4	10.44	2 (66%)	0,2,4	0.00	-
2	EDO	16-A	300	-	3,3,3	0.58	0	2,2,2	0.36	0
3	GLY	16-A	400	-	3,3,4	10.07	2 (66%)	0,2,4	0.00	-
3	GLY	16-A	401	-	3,3,4	10.17	2 (66%)	0,2,4	0.00	-
3	GLY	16-A	402	-	3,3,4	10.45	2 (66%)	0,2,4	0.00	-
2	EDO	2-A	300	-	3,3,3	0.58	0	2,2,2	0.36	0
3	GLY	2-A	400	-	3,3,4	10.08	2 (66%)	0,2,4	0.00	-
3	GLY	2-A	401	-	3,3,4	10.28	2 (66%)	0,2,4	0.00	-
3	GLY	2-A	402	-	3,3,4	10.38	2 (66%)	0,2,4	0.00	-
2	EDO	3-A	300	-	3,3,3	0.57	0	2,2,2	0.36	0
3	GLY	3-A	400	-	3,3,4	10.13	2 (66%)	0,2,4	0.00	-
3	GLY	3-A	401	-	3,3,4	10.34	2 (66%)	0,2,4	0.00	-
3	GLY	3-A	402	-	3,3,4	10.40	2 (66%)	0,2,4	0.00	-
2	EDO	4-A	300	-	3,3,3	0.58	0	2,2,2	0.36	0
3	GLY	4-A	400	-	3,3,4	10.07	2 (66%)	0,2,4	0.00	-
3	GLY	4-A	401	-	3,3,4	10.26	2 (66%)	0,2,4	0.00	-
3	GLY	4-A	402	-	3,3,4	10.46	2 (66%)	0,2,4	0.00	-
2	EDO	5-A	300	-	3,3,3	0.58	0	2,2,2	0.37	0
3	GLY	5-A	400	-	3,3,4	10.05	2 (66%)	0,2,4	0.00	-
3	GLY	5-A	401	-	3,3,4	10.24	2 (66%)	0,2,4	0.00	-
3	GLY	5-A	402	-	3,3,4	10.36	2 (66%)	0,2,4	0.00	-
2	EDO	6-A	300	-	3,3,3	0.57	0	2,2,2	0.36	0
3	GLY	6-A	400	-	3,3,4	10.12	2 (66%)	0,2,4	0.00	-
3	GLY	6-A	401	-	3,3,4	10.26	2 (66%)	0,2,4	0.00	-
3	GLY	6-A	402	-	3,3,4	10.39	2 (66%)	0,2,4	0.00	-
2	EDO	7-A	300	-	3,3,3	0.57	0	2,2,2	0.36	0
3	GLY	7-A	400	-	3,3,4	10.08	2 (66%)	0,2,4	0.00	-
3	GLY	7-A	401	-	3,3,4	10.28	2 (66%)	0,2,4	0.00	-
3	GLY	7-A	402	-	3,3,4	10.41	2 (66%)	0,2,4	0.00	-
2	EDO	8-A	300	-	3,3,3	0.57	0	2,2,2	0.37	0
3	GLY	8-A	400	-	3,3,4	10.08	2 (66%)	0,2,4	0.00	-
3	GLY	8-A	401	-	3,3,4	10.36	2 (66%)	0,2,4	0.00	-
3	GLY	8-A	402	-	3,3,4	10.47	2 (66%)	0,2,4	0.00	-
2	EDO	9-A	300	-	3,3,3	0.58	0	2,2,2	0.37	0
3	GLY	9-A	400	-	3,3,4	10.10	2 (66%)	0,2,4	0.00	-
3	GLY	9-A	401	-	3,3,4	10.24	2 (66%)	0,2,4	0.00	-

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	GLY	9-A	402	-	3,3,4	10.38	2 (66%)	0,2,4	0.00	-

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	1-A	300	-	-	0/1/1/1	0/0/0/0
3	GLY	1-A	400	-	-	0/0/1/2	0/0/0/0
3	GLY	1-A	401	-	-	0/0/1/2	0/0/0/0
3	GLY	1-A	402	-	-	0/0/1/2	0/0/0/0
2	EDO	10-A	300	-	-	0/1/1/1	0/0/0/0
3	GLY	10-A	400	-	-	0/0/1/2	0/0/0/0
3	GLY	10-A	401	-	-	0/0/1/2	0/0/0/0
3	GLY	10-A	402	-	-	0/0/1/2	0/0/0/0
2	EDO	11-A	300	-	-	0/1/1/1	0/0/0/0
3	GLY	11-A	400	-	-	0/0/1/2	0/0/0/0
3	GLY	11-A	401	-	-	0/0/1/2	0/0/0/0
3	GLY	11-A	402	-	-	0/0/1/2	0/0/0/0
2	EDO	12-A	300	-	-	0/1/1/1	0/0/0/0
3	GLY	12-A	400	-	-	0/0/1/2	0/0/0/0
3	GLY	12-A	401	-	-	0/0/1/2	0/0/0/0
3	GLY	12-A	402	-	-	0/0/1/2	0/0/0/0
2	EDO	13-A	300	-	-	0/1/1/1	0/0/0/0
3	GLY	13-A	400	-	-	0/0/1/2	0/0/0/0
3	GLY	13-A	401	-	-	0/0/1/2	0/0/0/0
3	GLY	13-A	402	-	-	0/0/1/2	0/0/0/0
2	EDO	14-A	300	-	-	0/1/1/1	0/0/0/0
3	GLY	14-A	400	-	-	0/0/1/2	0/0/0/0
3	GLY	14-A	401	-	-	0/0/1/2	0/0/0/0
3	GLY	14-A	402	-	-	0/0/1/2	0/0/0/0
2	EDO	15-A	300	-	-	0/1/1/1	0/0/0/0
3	GLY	15-A	400	-	-	0/0/1/2	0/0/0/0
3	GLY	15-A	401	-	-	0/0/1/2	0/0/0/0
3	GLY	15-A	402	-	-	0/0/1/2	0/0/0/0
2	EDO	16-A	300	-	-	0/1/1/1	0/0/0/0
3	GLY	16-A	400	-	-	0/0/1/2	0/0/0/0
3	GLY	16-A	401	-	-	0/0/1/2	0/0/0/0
3	GLY	16-A	402	-	-	0/0/1/2	0/0/0/0
2	EDO	2-A	300	-	-	0/1/1/1	0/0/0/0
3	GLY	2-A	400	-	-	0/0/1/2	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	GLY	2-A	401	-	-	0/0/1/2	0/0/0/0
3	GLY	2-A	402	-	-	0/0/1/2	0/0/0/0
2	EDO	3-A	300	-	-	0/1/1/1	0/0/0/0
3	GLY	3-A	400	-	-	0/0/1/2	0/0/0/0
3	GLY	3-A	401	-	-	0/0/1/2	0/0/0/0
3	GLY	3-A	402	-	-	0/0/1/2	0/0/0/0
2	EDO	4-A	300	-	-	0/1/1/1	0/0/0/0
3	GLY	4-A	400	-	-	0/0/1/2	0/0/0/0
3	GLY	4-A	401	-	-	0/0/1/2	0/0/0/0
3	GLY	4-A	402	-	-	0/0/1/2	0/0/0/0
2	EDO	5-A	300	-	-	0/1/1/1	0/0/0/0
3	GLY	5-A	400	-	-	0/0/1/2	0/0/0/0
3	GLY	5-A	401	-	-	0/0/1/2	0/0/0/0
3	GLY	5-A	402	-	-	0/0/1/2	0/0/0/0
2	EDO	6-A	300	-	-	0/1/1/1	0/0/0/0
3	GLY	6-A	400	-	-	0/0/1/2	0/0/0/0
3	GLY	6-A	401	-	-	0/0/1/2	0/0/0/0
3	GLY	6-A	402	-	-	0/0/1/2	0/0/0/0
2	EDO	7-A	300	-	-	0/1/1/1	0/0/0/0
3	GLY	7-A	400	-	-	0/0/1/2	0/0/0/0
3	GLY	7-A	401	-	-	0/0/1/2	0/0/0/0
3	GLY	7-A	402	-	-	0/0/1/2	0/0/0/0
2	EDO	8-A	300	-	-	0/1/1/1	0/0/0/0
3	GLY	8-A	400	-	-	0/0/1/2	0/0/0/0
3	GLY	8-A	401	-	-	0/0/1/2	0/0/0/0
3	GLY	8-A	402	-	-	0/0/1/2	0/0/0/0
2	EDO	9-A	300	-	-	0/1/1/1	0/0/0/0
3	GLY	9-A	400	-	-	0/0/1/2	0/0/0/0
3	GLY	9-A	401	-	-	0/0/1/2	0/0/0/0
3	GLY	9-A	402	-	-	0/0/1/2	0/0/0/0

All (96) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	8-A	402	GLY	O-C	17.85	1.23	1.11
3	13-A	402	GLY	O-C	17.84	1.23	1.11
3	4-A	402	GLY	O-C	17.82	1.23	1.11
3	16-A	402	GLY	O-C	17.81	1.23	1.11
3	12-A	402	GLY	O-C	17.80	1.23	1.11
3	15-A	402	GLY	O-C	17.80	1.23	1.11
3	10-A	402	GLY	O-C	17.77	1.23	1.11
3	8-A	401	GLY	O-C	17.76	1.23	1.11

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	7-A	402	GLY	O-C	17.74	1.23	1.11
3	3-A	402	GLY	O-C	17.73	1.23	1.11
3	3-A	401	GLY	O-C	17.73	1.23	1.11
3	2-A	402	GLY	O-C	17.71	1.23	1.11
3	14-A	402	GLY	O-C	17.70	1.23	1.11
3	6-A	402	GLY	O-C	17.70	1.23	1.11
3	9-A	402	GLY	O-C	17.70	1.23	1.11
3	1-A	402	GLY	O-C	17.69	1.23	1.11
3	11-A	402	GLY	O-C	17.69	1.23	1.11
3	10-A	401	GLY	O-C	17.68	1.23	1.11
3	12-A	401	GLY	O-C	17.65	1.23	1.11
3	5-A	402	GLY	O-C	17.65	1.23	1.11
3	7-A	401	GLY	O-C	17.64	1.23	1.11
3	2-A	401	GLY	O-C	17.63	1.23	1.11
3	14-A	401	GLY	O-C	17.61	1.23	1.11
3	4-A	401	GLY	O-C	17.60	1.23	1.11
3	6-A	401	GLY	O-C	17.59	1.23	1.11
3	5-A	401	GLY	O-C	17.57	1.23	1.11
3	1-A	401	GLY	O-C	17.56	1.23	1.11
3	15-A	401	GLY	O-C	17.56	1.23	1.11
3	9-A	401	GLY	O-C	17.54	1.23	1.11
3	11-A	401	GLY	O-C	17.53	1.23	1.11
3	16-A	401	GLY	O-C	17.43	1.23	1.11
3	13-A	401	GLY	O-C	17.29	1.23	1.11
3	14-A	400	GLY	O-C	17.24	1.23	1.11
3	3-A	400	GLY	O-C	17.23	1.23	1.11
3	6-A	400	GLY	O-C	17.22	1.23	1.11
3	9-A	400	GLY	O-C	17.18	1.23	1.11
3	2-A	400	GLY	O-C	17.16	1.23	1.11
3	8-A	400	GLY	O-C	17.14	1.23	1.11
3	15-A	400	GLY	O-C	17.14	1.23	1.11
3	4-A	400	GLY	O-C	17.14	1.23	1.11
3	1-A	400	GLY	O-C	17.13	1.23	1.11
3	12-A	400	GLY	O-C	17.12	1.23	1.11
3	16-A	400	GLY	O-C	17.11	1.23	1.11
3	11-A	400	GLY	O-C	17.10	1.23	1.11
3	7-A	400	GLY	O-C	17.10	1.23	1.11
3	5-A	400	GLY	O-C	17.07	1.23	1.11
3	10-A	400	GLY	O-C	17.07	1.23	1.11
3	13-A	400	GLY	O-C	17.04	1.23	1.11
3	7-A	400	GLY	CA-C	3.52	1.53	1.48
3	10-A	400	GLY	CA-C	3.48	1.52	1.48

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	15-A	400	GLY	CA-C	3.39	1.52	1.48
3	5-A	400	GLY	CA-C	3.36	1.52	1.48
3	16-A	400	GLY	CA-C	3.35	1.52	1.48
3	14-A	400	GLY	CA-C	3.33	1.52	1.48
3	13-A	400	GLY	CA-C	3.33	1.52	1.48
3	11-A	400	GLY	CA-C	3.32	1.52	1.48
3	8-A	400	GLY	CA-C	3.32	1.52	1.48
3	12-A	400	GLY	CA-C	3.31	1.52	1.48
3	3-A	400	GLY	CA-C	3.29	1.52	1.48
3	1-A	400	GLY	CA-C	3.28	1.52	1.48
3	9-A	400	GLY	CA-C	3.27	1.52	1.48
3	6-A	400	GLY	CA-C	3.27	1.52	1.48
3	2-A	400	GLY	CA-C	3.27	1.52	1.48
3	7-A	402	GLY	CA-C	3.25	1.52	1.48
3	4-A	400	GLY	CA-C	3.25	1.52	1.48
3	15-A	402	GLY	CA-C	3.25	1.52	1.48
3	1-A	402	GLY	CA-C	3.23	1.52	1.48
3	14-A	402	GLY	CA-C	3.23	1.52	1.48
3	16-A	402	GLY	CA-C	3.21	1.52	1.48
3	4-A	402	GLY	CA-C	3.21	1.52	1.48
3	5-A	402	GLY	CA-C	3.20	1.52	1.48
3	6-A	402	GLY	CA-C	3.19	1.52	1.48
3	8-A	402	GLY	CA-C	3.18	1.52	1.48
3	11-A	402	GLY	CA-C	3.18	1.52	1.48
3	10-A	402	GLY	CA-C	3.17	1.52	1.48
3	2-A	402	GLY	CA-C	3.16	1.52	1.48
3	13-A	402	GLY	CA-C	3.14	1.52	1.48
3	12-A	402	GLY	CA-C	3.14	1.52	1.48
3	9-A	402	GLY	CA-C	3.13	1.52	1.48
3	3-A	402	GLY	CA-C	3.13	1.52	1.48
3	11-A	401	GLY	CA-C	2.59	1.51	1.48
3	9-A	401	GLY	CA-C	2.55	1.51	1.48
3	8-A	401	GLY	CA-C	2.55	1.51	1.48
3	6-A	401	GLY	CA-C	2.53	1.51	1.48
3	4-A	401	GLY	CA-C	2.50	1.51	1.48
3	1-A	401	GLY	CA-C	2.50	1.51	1.48
3	12-A	401	GLY	CA-C	2.50	1.51	1.48
3	16-A	401	GLY	CA-C	2.49	1.51	1.48
3	3-A	401	GLY	CA-C	2.47	1.51	1.48
3	2-A	401	GLY	CA-C	2.46	1.51	1.48
3	10-A	401	GLY	CA-C	2.46	1.51	1.48
3	13-A	401	GLY	CA-C	2.45	1.51	1.48

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	7-A	401	GLY	CA-C	2.44	1.51	1.48
3	15-A	401	GLY	CA-C	2.44	1.51	1.48
3	5-A	401	GLY	CA-C	2.44	1.51	1.48
3	14-A	401	GLY	CA-C	2.40	1.51	1.48

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

## 5.7 Other polymers ⓘ

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 ⓘ

EDS failed to run properly - this section will therefore be empty.

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

EDS failed to run properly - this section will therefore be empty.

### 6.3 Carbohydrates ⓘ

EDS failed to run properly - this section will therefore be empty.

### 6.4 Ligands ⓘ

EDS failed to run properly - this section will therefore be empty.

### 6.5 Other polymers ⓘ

EDS failed to run properly - this section will therefore be empty.