



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 06:09 AM GMT

PDB ID : 2W40  
Title : CRYSTAL STRUCTURE OF PLASMODIUM FALCIPARUM GLYCEROL KINASE WITH BOUND GLYCEROL  
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Deposited on : 2008-11-18  
Resolution : 1.49 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  
<http://wwpdb.org/validation/2016/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 : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

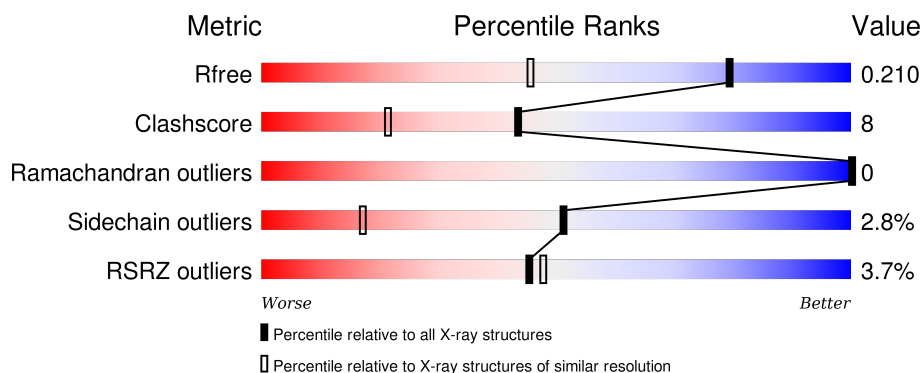
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.49 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))
$R_{free}$	91344	2072 (1.50-1.50)
Clashscore	102246	2274 (1.50-1.50)
Ramachandran outliers	100387	2218 (1.50-1.50)
Sidechain outliers	100360	2216 (1.50-1.50)
RSRZ outliers	91569	2075 (1.50-1.50)

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. 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	503	<div> <div>5%</div> <div>86% 13% .</div> </div>
1	B	503	<div> <div>3%</div> <div>83% 15% .</div> </div>
1	C	503	<div> <div>2%</div> <div>82% 15% .</div> </div>
1	D	503	<div> <div>4%</div> <div>84% 13% .</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
2	EDO	A	1504	-	-	-	X
2	EDO	A	1507	-	-	X	X
2	EDO	A	1508	-	-	-	X
2	EDO	A	1509	-	-	X	-
2	EDO	A	1510	-	-	-	X
2	EDO	B	1502	-	-	-	X
2	EDO	B	1506	-	-	-	X
2	EDO	B	1507	-	-	-	X
2	EDO	B	1509	-	-	-	X
2	EDO	B	1510	-	-	-	X
2	EDO	B	1514	-	-	X	X
2	EDO	B	1518	-	-	X	X
2	EDO	B	1520	-	-	-	X
2	EDO	C	1507	-	-	-	X
2	EDO	C	1509	-	-	-	X
2	EDO	C	1510	-	-	X	X
2	EDO	C	1511	-	-	-	X
2	EDO	C	1512	-	-	-	X
2	EDO	C	1513	-	-	-	X
2	EDO	C	1514	-	X	X	X
2	EDO	C	1515	-	-	-	X
2	EDO	C	1516	-	-	-	X
2	EDO	C	1517	-	-	-	X
2	EDO	C	1519	-	-	-	X
2	EDO	C	1520	-	-	X	-
2	EDO	D	1505	-	-	-	X
2	EDO	D	1506	-	-	-	X
2	EDO	D	1507	-	-	-	X
2	EDO	D	1508	-	-	-	X
2	EDO	D	1510	-	-	X	X
2	EDO	D	1511	-	-	-	X
2	EDO	D	1512	-	-	-	X
2	EDO	D	1515	-	X	X	X
3	GOL	A	1512	-	-	-	X
3	GOL	C	1523	-	-	-	X
3	GOL	C	1524	-	-	-	X
3	GOL	C	1526	-	-	-	X
3	GOL	C	1527	-	-	X	X

## 2 Entry composition [i](#)

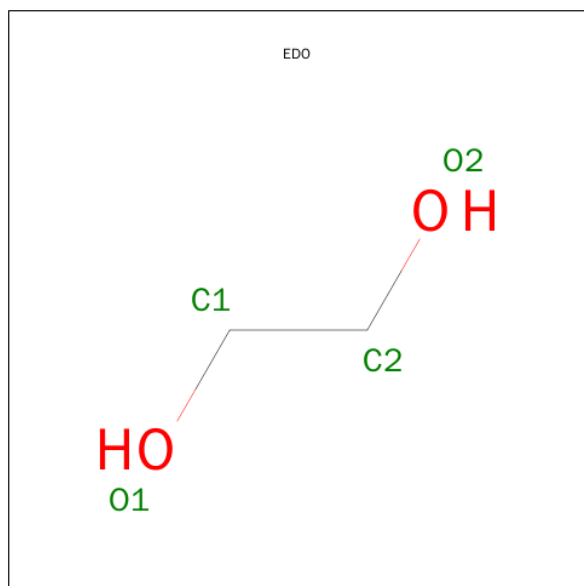
There are 4 unique types of molecules in this entry. The entry contains 18365 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 GLYCEROL KINASE, PUTATIVE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	501	Total	C	N	O	S	11	10	0
			4034	2568	668	771	27			
1	B	503	Total	C	N	O	S	5	7	0
			4030	2565	667	771	27			
1	C	502	Total	C	N	O	S	21	9	0
			4037	2569	669	773	26			
1	D	503	Total	C	N	O	S	3	7	0
			4015	2555	662	772	26			

- 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		

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

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

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

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: C<sub>3</sub>H<sub>8</sub>O<sub>3</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			6	3	3		
3	A	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		
3	C	1	Total	C	O	0	0
			6	3	3		
3	C	1	Total	C	O	0	0
			6	3	3		
3	C	1	Total	C	O	0	0
			6	3	3		
3	C	1	Total	C	O	0	0
			6	3	3		
3	C	1	Total	C	O	0	0
			6	3	3		
3	D	1	Total	C	O	0	0
			6	3	3		

- Molecule 4 is water.

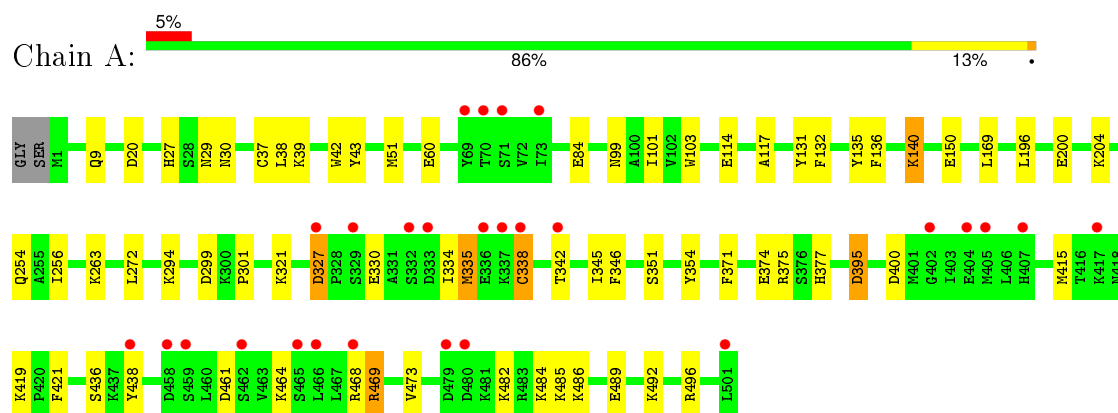


Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	463	Total 463	O 463	0	0
4	B	492	Total 492	O 492	0	0
4	C	499	Total 499	O 499	0	0
4	D	475	Total 475	O 475	0	0

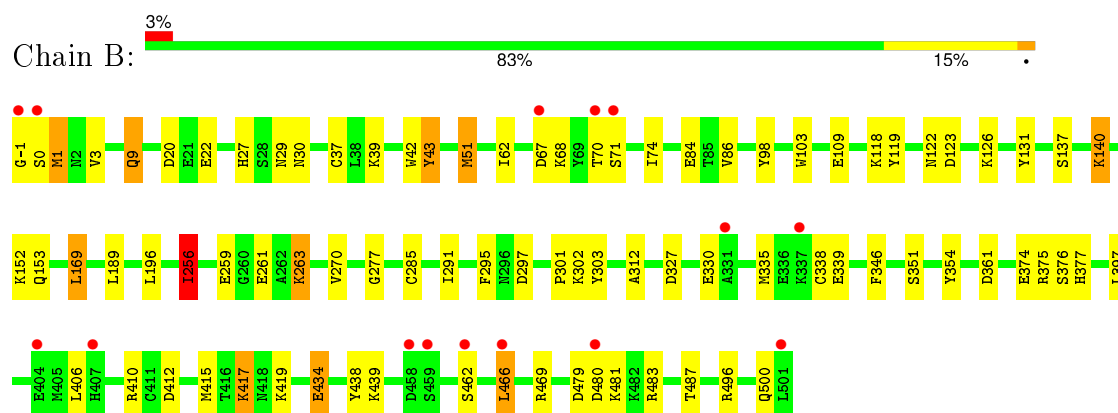
### 3 Residue-property plots

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.

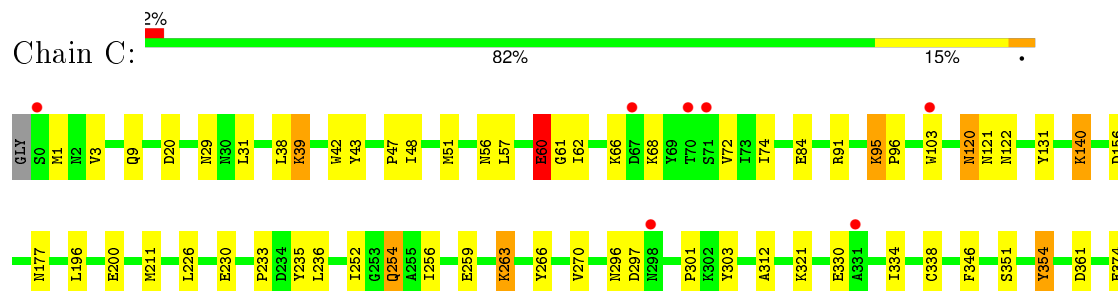
#### • Molecule 1: GLYCEROL KINASE, PUTATIVE



#### • Molecule 1: GLYCEROL KINASE, PUTATIVE

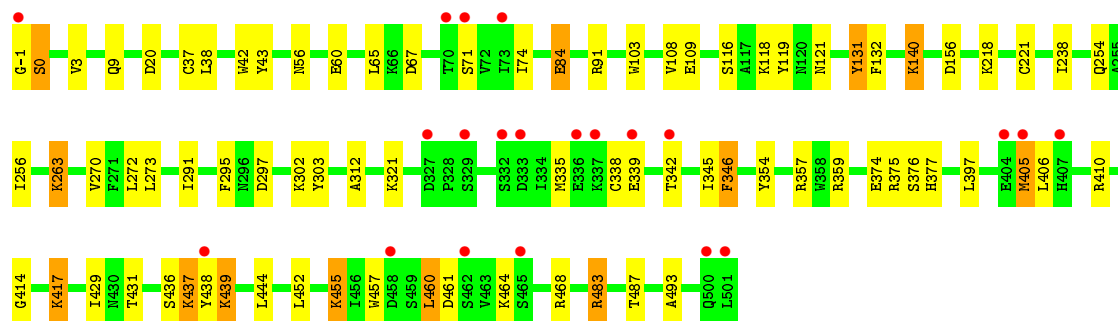
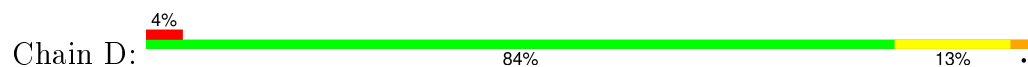


#### • Molecule 1: GLYCEROL KINASE, PUTATIVE





● Molecule 1: GLYCEROL KINASE, PUTATIVE



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	101.92Å 100.72Å 107.81Å 90.00° 92.56° 90.00°	Depositor
Resolution (Å)	107.83 – 1.49 36.78 – 1.49	Depositor EDS
% Data completeness (in resolution range)	73.5 (107.83-1.49) 73.6 (36.78-1.49)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.66 (at 1.49Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, $R_{free}$	0.168 , 0.210 0.161 , 0.210	Depositor DCC
$R_{free}$ test set	13130 reflections (5.31%)	DCC
Wilson B-factor (Å <sup>2</sup> )	13.0	Xtriage
Anisotropy	0.258	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.38 , 55.7	EDS
Estimated twinning fraction	0.000 for k,h,-l 0.000 for -k,-h,-l 0.000 for h,-k,-l	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.51$ , $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	0 of 260539 reflections	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	18365	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	17.0	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 49.76 % 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 7.1291e-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, 0.375 respectively for untwinned datasets, and 0.333, 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: GOL, 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	1.28	10/4133 (0.2%)	1.07	13/5592 (0.2%)
1	B	1.34	16/4113 (0.4%)	1.11	18/5565 (0.3%)
1	C	1.36	22/4132 (0.5%)	1.11	15/5590 (0.3%)
1	D	1.30	11/4111 (0.3%)	1.10	21/5563 (0.4%)
All	All	1.32	59/16489 (0.4%)	1.10	67/22310 (0.3%)

All (59) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	95	LYS	CD-CE	-14.72	1.14	1.51
1	C	434	GLU	CB-CG	-13.96	1.25	1.52
1	C	68	LYS	CG-CD	-10.44	1.17	1.52
1	B	285[A]	CYS	CB-SG	-9.32	1.66	1.82
1	B	285[B]	CYS	CB-SG	-9.32	1.66	1.82
1	C	60	GLU	CD-OE2	8.46	1.34	1.25
1	D	375	ARG	CB-CG	-8.01	1.30	1.52
1	C	439	LYS	CB-CG	7.74	1.73	1.52
1	C	439	LYS	C-O	7.52	1.37	1.23
1	D	295	PHE	CE1-CZ	-7.47	1.23	1.37
1	B	375	ARG	CB-CG	-7.04	1.33	1.52
1	A	375	ARG	CB-CG	-6.95	1.33	1.52
1	B	439	LYS	CA-CB	6.95	1.69	1.53
1	D	67	ASP	CB-CG	6.93	1.66	1.51
1	B	131	TYR	CE1-CZ	-6.92	1.29	1.38
1	B	480	ASP	CB-CG	6.90	1.66	1.51
1	C	351	SER	CB-OG	-6.87	1.33	1.42
1	B	351	SER	CB-OG	-6.86	1.33	1.42
1	C	60	GLU	CG-CD	6.83	1.62	1.51
1	C	230	GLU	CG-CD	6.68	1.61	1.51
1	A	338[A]	CYS	CB-SG	-6.65	1.71	1.82
1	A	338[B]	CYS	CB-SG	-6.65	1.71	1.82

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	439	LYS	N-CA	6.62	1.59	1.46
1	C	321	LYS	CD-CE	6.61	1.67	1.51
1	A	135	TYR	CD2-CE2	-6.59	1.29	1.39
1	D	140	LYS	CE-NZ	-6.51	1.32	1.49
1	C	354	TYR	CG-CD1	-6.43	1.30	1.39
1	D	218	LYS	CD-CE	-6.37	1.35	1.51
1	D	109	GLU	CD-OE2	6.27	1.32	1.25
1	B	98	TYR	CD2-CE2	-5.97	1.30	1.39
1	A	351	SER	CB-OG	-5.89	1.34	1.42
1	C	354	TYR	CD1-CE1	5.86	1.48	1.39
1	C	131	TYR	CE1-CZ	-5.85	1.30	1.38
1	B	354	TYR	CG-CD1	-5.84	1.31	1.39
1	C	60	GLU	CD-OE1	5.78	1.32	1.25
1	C	266	TYR	CE2-CZ	-5.73	1.31	1.38
1	C	375	ARG	CB-CG	-5.69	1.37	1.52
1	D	60	GLU	CD-OE2	5.56	1.31	1.25
1	B	480	ASP	CG-OD1	5.55	1.38	1.25
1	B	434	GLU	CG-CD	5.51	1.60	1.51
1	B	412	ASP	CB-CG	5.48	1.63	1.51
1	A	150	GLU	CD-OE2	-5.47	1.19	1.25
1	D	438	TYR	CB-CG	-5.43	1.43	1.51
1	D	131	TYR	CG-CD2	-5.38	1.32	1.39
1	B	43	TYR	CE2-CZ	5.38	1.45	1.38
1	B	39	LYS	CD-CE	-5.38	1.37	1.51
1	A	140[A]	LYS	CD-CE	5.30	1.64	1.51
1	A	140[B]	LYS	CD-CE	5.30	1.64	1.51
1	C	453	GLU	CD-OE2	5.22	1.31	1.25
1	A	200	GLU	CG-CD	5.21	1.59	1.51
1	A	131	TYR	CE1-CZ	-5.16	1.31	1.38
1	D	84	GLU	CD-OE2	5.13	1.31	1.25
1	B	109	GLU	CD-OE1	5.12	1.31	1.25
1	C	259	GLU	CD-OE1	5.11	1.31	1.25
1	B	295	PHE	CE1-CZ	-5.08	1.27	1.37
1	D	221	CYS	CB-SG	-5.07	1.73	1.81
1	C	303	TYR	CE1-CZ	5.03	1.45	1.38
1	C	480	ASP	CG-OD2	5.02	1.36	1.25
1	C	95	LYS	CE-NZ	5.00	1.61	1.49

All (67) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	439	LYS	N-CA-CB	-9.97	92.65	110.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	91	ARG	NE-CZ-NH2	-9.65	115.47	120.30
1	D	91	ARG	NE-CZ-NH1	8.31	124.45	120.30
1	D	67	ASP	CB-CG-OD1	8.14	125.62	118.30
1	B	406	LEU	CB-CG-CD2	-7.93	97.52	111.00
1	A	335	MET	CG-SD-CE	-7.86	87.62	100.20
1	A	51	MET	CG-SD-CE	7.84	112.75	100.20
1	A	496	ARG	NE-CZ-NH1	7.35	123.98	120.30
1	D	359	ARG	NE-CZ-NH2	-7.20	116.70	120.30
1	B	480	ASP	CB-CG-OD1	7.19	124.77	118.30
1	D	156	ASP	CB-CG-OD1	7.12	124.71	118.30
1	D	359	ARG	NE-CZ-NH1	7.00	123.80	120.30
1	C	156	ASP	CB-CG-OD1	6.90	124.51	118.30
1	D	335	MET	CG-SD-CE	6.85	111.15	100.20
1	A	395	ASP	CB-CG-OD2	-6.74	112.23	118.30
1	C	480	ASP	CB-CG-OD1	-6.70	112.27	118.30
1	D	297	ASP	CB-CG-OD1	-6.59	112.36	118.30
1	A	469	ARG	NE-CZ-NH1	6.58	123.59	120.30
1	B	297	ASP	CB-CG-OD1	-6.55	112.41	118.30
1	D	483	ARG	NE-CZ-NH1	6.50	123.55	120.30
1	D	321	LYS	CD-CE-NZ	6.46	126.57	111.70
1	A	321	LYS	CD-CE-NZ	6.42	126.47	111.70
1	B	20	ASP	CB-CG-OD1	6.36	124.02	118.30
1	C	95	LYS	CG-CD-CE	6.32	130.87	111.90
1	D	20	ASP	CB-CG-OD1	6.29	123.96	118.30
1	B	295	PHE	CB-CG-CD1	6.26	125.18	120.80
1	D	357	ARG	NE-CZ-NH1	6.21	123.41	120.30
1	D	132	PHE	CB-CG-CD1	6.19	125.13	120.80
1	C	410	ARG	NE-CZ-NH1	6.18	123.39	120.30
1	A	132	PHE	CB-CG-CD1	6.13	125.09	120.80
1	D	444	LEU	CB-CG-CD2	-6.13	100.59	111.00
1	A	327	ASP	CB-CG-OD2	-6.08	112.83	118.30
1	B	335	MET	CG-SD-CE	6.00	109.80	100.20
1	B	361	ASP	CB-CG-OD1	5.99	123.69	118.30
1	B	123	ASP	CB-CG-OD2	-5.98	112.92	118.30
1	A	20	ASP	CB-CG-OD1	5.97	123.67	118.30
1	C	20	ASP	CB-CG-OD1	5.96	123.67	118.30
1	C	354	TYR	CZ-CE2-CD2	-5.95	114.44	119.80
1	D	346	PHE	CB-CG-CD2	5.89	124.92	120.80
1	C	20	ASP	CB-CG-OD2	-5.85	113.04	118.30
1	C	361	ASP	CB-CG-OD1	5.77	123.49	118.30
1	A	38	LEU	CA-CB-CG	5.70	128.41	115.30
1	A	400	ASP	CB-CG-OD2	-5.63	113.23	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	39	LYS	CD-CE-NZ	-5.63	98.76	111.70
1	D	437	LYS	CB-CG-CD	-5.63	96.97	111.60
1	B	327	ASP	CB-CG-OD1	5.58	123.32	118.30
1	A	327	ASP	CB-CG-OD1	5.58	123.32	118.30
1	C	297	ASP	CB-CG-OD1	-5.57	113.28	118.30
1	C	480	ASP	CB-CG-OD2	5.56	123.31	118.30
1	B	496	ARG	NE-CZ-NH1	5.52	123.06	120.30
1	C	481	LYS	CA-CB-CG	-5.49	101.32	113.40
1	C	380	ARG	NE-CZ-NH2	-5.46	117.57	120.30
1	B	1	MET	CA-CB-CG	5.44	122.55	113.30
1	A	469	ARG	NE-CZ-NH2	-5.38	117.61	120.30
1	D	132	PHE	CB-CG-CD2	-5.37	117.04	120.80
1	C	438	TYR	CA-C-N	5.34	128.95	117.20
1	C	51	MET	CG-SD-CE	5.29	108.67	100.20
1	D	297	ASP	CB-CG-OD2	5.23	123.00	118.30
1	D	38	LEU	CB-CG-CD1	5.21	119.86	111.00
1	D	218	LYS	CD-CE-NZ	5.17	123.60	111.70
1	B	123	ASP	CB-CG-OD1	5.15	122.94	118.30
1	B	51	MET	CG-SD-CE	5.13	108.41	100.20
1	C	39	LYS	CD-CE-NZ	-5.08	100.00	111.70
1	D	20	ASP	CB-CG-OD2	-5.08	113.72	118.30
1	B	256[A]	ILE	CG1-CB-CG2	-5.06	100.27	111.40
1	B	256[B]	ILE	CG1-CB-CG2	-5.06	100.27	111.40
1	B	412	ASP	CB-CG-OD2	-5.04	113.76	118.30

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	4034	0	4060	46	0
1	B	4030	0	4051	63	0
1	C	4037	0	4064	73	0
1	D	4015	0	4033	59	0
2	A	36	0	53	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	80	0	120	17	0
2	C	76	0	114	27	0
2	D	56	0	81	14	0
3	A	12	0	16	3	0
3	B	12	0	15	1	0
3	C	42	0	56	14	0
3	D	6	0	8	0	0
4	A	463	0	0	10	1
4	B	492	0	0	25	2
4	C	499	0	0	24	0
4	D	475	0	0	14	1
All	All	18365	0	16671	266	2

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 8.

All (266) 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)
2:C:1510:EDO:C1	2:C:1510:EDO:O1	1.64	1.44
1:D:116:SER:O	2:D:1515:EDO:H12	1.31	1.27
1:D:116:SER:O	2:D:1515:EDO:C1	1.98	1.10
1:B:22[B]:GLU:OE1	4:B:2032:HOH:O	1.71	1.09
3:C:1522:GOL:H2	4:C:2429:HOH:O	1.53	1.08
1:D:452:LEU:O	1:D:455:LYS:HE2	1.51	1.07
1:C:226:LEU:H	2:C:1510:EDO:H12	1.19	1.05
1:B:126:LYS:NZ	4:B:2173:HOH:O	1.95	0.99
2:C:1514:EDO:H21	4:C:2356:HOH:O	1.62	0.96
1:B:500:GLN:HG2	4:B:2467:HOH:O	1.64	0.96
1:C:140:LYS:HE2	4:C:2110:HOH:O	1.65	0.95
3:B:1523:GOL:H2	4:B:2432:HOH:O	1.65	0.95
1:B:374:GLU:H	1:B:377:HIS:HD2	1.16	0.93
1:D:374:GLU:H	1:D:377:HIS:HD2	1.17	0.93
1:C:91[B]:ARG:NH1	4:C:2119:HOH:O	1.88	0.91
1:B:22[B]:GLU:CD	4:B:2032:HOH:O	2.05	0.91
1:D:121:ASN:ND2	2:D:1515:EDO:H21	1.84	0.91
1:B:118:LYS:HE3	4:B:2156:HOH:O	1.70	0.91
1:C:374:GLU:H	1:C:377:HIS:HD2	1.21	0.88
1:A:374:GLU:H	1:A:377:HIS:HD2	1.20	0.88
3:C:1527:GOL:O1	4:C:2499:HOH:O	1.86	0.86
1:D:452:LEU:O	1:D:455:LYS:CE	2.26	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:330:GLU:OE2	4:A:2327:HOH:O	1.95	0.84
1:D:118:LYS:NZ	4:D:2162:HOH:O	2.12	0.83
1:D:354[A]:TYR:HD1	4:D:2322:HOH:O	1.63	0.82
1:C:140:LYS:CE	4:C:2110:HOH:O	2.24	0.80
1:C:479:ASP:OD2	1:C:481:LYS:HB2	1.83	0.79
1:C:200:GLU:CG	3:C:1527:GOL:O2	2.31	0.79
1:A:117:ALA:HB3	3:A:1512:GOL:H32	1.64	0.77
1:D:116:SER:C	2:D:1515:EDO:H12	2.03	0.77
1:C:458:ASP:OD2	4:C:2433:HOH:O	2.02	0.77
1:D:338[A]:CYS:SG	1:D:376[A]:SER:HB2	2.26	0.75
1:D:457:TRP:O	4:D:2429:HOH:O	2.04	0.75
2:D:1515:EDO:H22	4:D:2472:HOH:O	1.85	0.75
1:C:226:LEU:N	2:C:1510:EDO:H12	2.00	0.75
1:B:37:CYS:HB3	2:B:1514:EDO:H11	1.67	0.74
1:A:485:LYS:NZ	1:A:489:GLU:OE2	2.21	0.73
1:A:117:ALA:CB	3:A:1512:GOL:H32	2.17	0.73
1:C:200:GLU:HG2	3:C:1527:GOL:O2	1.88	0.73
1:B:-1:GLY:HA2	1:B:1:MET:N	2.03	0.72
1:C:438:TYR:OH	1:C:466:LEU:CD2	2.38	0.71
1:C:236:LEU:HD22	2:C:1520:EDO:H12	1.71	0.71
1:B:22[B]:GLU:OE2	4:B:2032:HOH:O	2.06	0.71
1:C:330:GLU:OE1	4:C:2341:HOH:O	2.08	0.71
1:A:327:ASP:O	1:A:330:GLU:HG2	1.91	0.70
2:A:1507:EDO:H22	4:A:2341:HOH:O	1.92	0.70
2:B:1518:EDO:O2	4:B:2488:HOH:O	1.90	0.69
1:C:200:GLU:HG3	3:C:1527:GOL:O2	1.92	0.69
1:C:57:LEU:O	1:C:60:GLU:HG3	1.94	0.68
1:D:436:SER:O	4:D:2417:HOH:O	2.13	0.66
1:B:410:ARG:NH1	1:B:434:GLU:OE2	2.28	0.66
1:C:177:ASN:HD21	2:C:1510:EDO:H11	1.61	0.66
1:B:417:LYS:HE2	4:B:2442:HOH:O	1.94	0.66
1:C:62:ILE:HG13	1:C:66:LYS:HE2	1.78	0.66
1:B:0:SER:CB	1:B:71:SER:OG	2.44	0.65
1:A:196:LEU:HD11	1:A:301:PRO:HG3	1.78	0.65
1:B:27:HIS:HD2	4:B:2010:HOH:O	1.78	0.65
1:A:114[A]:GLU:HG3	4:A:2139:HOH:O	1.96	0.65
1:C:31:LEU:HD21	3:C:1523:GOL:H32	1.79	0.64
1:B:330:GLU:OE1	4:B:2341:HOH:O	2.14	0.64
1:D:3:VAL:CG2	1:D:74:ILE:HD13	2.27	0.64
1:A:473:VAL:H	1:B:153:GLN:HE22	1.45	0.64
2:C:1514:EDO:C2	4:C:2356:HOH:O	2.33	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:56:ASN:HB3	2:D:1514:EDO:O1	1.97	0.64
1:A:204:LYS:HG2	2:A:1509:EDO:H11	1.78	0.63
1:C:42:TRP:O	2:C:1514:EDO:H12	1.98	0.63
1:C:233:PRO:O	2:C:1520:EDO:H21	1.98	0.63
1:A:464:LYS:HB3	1:A:468:ARG:NH1	2.14	0.62
1:D:439:LYS:H	1:D:439:LYS:CD	2.10	0.62
1:C:392:GLU:O	2:C:1516:EDO:H21	2.00	0.62
1:D:119:TYR:O	2:D:1515:EDO:O1	2.17	0.62
1:D:342:THR:HG23	1:D:377:HIS:CE1	2.34	0.62
1:A:371:PHE:HD2	2:C:1514:EDO:H21	1.65	0.61
1:A:37:CYS:HB3	2:A:1507:EDO:H11	1.82	0.61
1:C:338[B]:CYS:SG	1:C:376:SER:HB2	2.40	0.61
1:C:376:SER:HB3	4:C:2387:HOH:O	1.99	0.61
1:A:204:LYS:HG2	2:A:1509:EDO:C1	2.30	0.60
1:D:121:ASN:HD22	2:D:1515:EDO:H21	1.65	0.60
1:A:99:ASN:HD22	2:A:1508:EDO:H22	1.65	0.60
1:D:338[A]:CYS:SG	1:D:376[A]:SER:CB	2.90	0.60
1:C:121:ASN:HB2	4:C:2166:HOH:O	2.02	0.60
2:C:1510:EDO:C1	2:C:1510:EDO:HO1	2.08	0.60
1:D:397:LEU:C	1:D:397:LEU:HD23	2.22	0.59
1:A:354[A]:TYR:HD2	4:A:2345:HOH:O	1.85	0.59
1:B:118:LYS:CE	4:B:2156:HOH:O	2.40	0.59
1:A:334:ILE:O	1:A:338[B]:CYS:HB2	2.03	0.59
1:C:438:TYR:OH	1:C:466:LEU:HD23	2.03	0.58
1:C:29:ASN:ND2	1:C:60:GLU:OE1	2.27	0.57
2:B:1517:EDO:O2	4:B:2487:HOH:O	2.11	0.57
2:B:1517:EDO:H12	4:B:2070:HOH:O	2.04	0.57
1:C:438:TYR:OH	1:C:466:LEU:HD22	2.04	0.56
1:A:464:LYS:NZ	4:A:2423:HOH:O	2.38	0.56
1:B:119:TYR:HA	2:B:1519:EDO:H12	1.85	0.56
1:D:339:GLU:O	1:D:339:GLU:HG2	2.05	0.56
1:C:296:ASN:HD21	2:C:1507:EDO:H22	1.71	0.56
1:A:335:MET:CE	1:A:421:PHE:HB2	2.36	0.56
1:D:272:LEU:C	1:D:272:LEU:HD23	2.27	0.55
2:D:1510:EDO:H22	4:D:2347:HOH:O	2.06	0.55
1:B:42:TRP:O	2:B:1514:EDO:C2	2.55	0.55
1:C:338[B]:CYS:SG	1:C:376:SER:OG	2.65	0.55
1:A:30:ASN:ND2	4:A:2029:HOH:O	2.39	0.55
1:C:177:ASN:ND2	2:C:1510:EDO:H11	2.20	0.55
1:C:397:LEU:C	1:C:397:LEU:HD23	2.27	0.55
1:A:436:SER:O	4:A:2411:HOH:O	2.18	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:1510:EDO:C2	4:D:2138:HOH:O	2.55	0.55
1:B:277:GLY:HA3	2:B:1518:EDO:H12	1.88	0.54
1:A:204:LYS:NZ	2:A:1509:EDO:H11	2.22	0.54
1:C:121:ASN:ND2	4:C:2157:HOH:O	2.41	0.54
1:D:0:SER:HA	1:D:71:SER:OG	2.06	0.54
1:B:29:ASN:C	2:B:1521:EDO:H22	2.27	0.54
1:B:419:LYS:HE3	4:B:2181:HOH:O	2.07	0.53
1:C:354:TYR:HD2	4:C:2360:HOH:O	1.90	0.53
2:B:1514:EDO:H22	4:B:2356:HOH:O	2.09	0.53
2:C:1516:EDO:H11	4:C:2487:HOH:O	2.08	0.53
1:C:338[B]:CYS:SG	1:C:376:SER:CB	2.96	0.53
1:B:3:VAL:CG2	1:B:74:ILE:HD13	2.39	0.53
1:A:136:PHE:O	1:A:140[B]:LYS:HE2	2.07	0.53
1:D:439:LYS:HD3	1:D:439:LYS:H	1.72	0.52
1:B:137:SER:HA	1:B:140[B]:LYS:HE2	1.92	0.52
1:D:460:LEU:HD13	1:D:464:LYS:CE	2.40	0.52
1:A:42:TRP:O	2:A:1507:EDO:H12	2.10	0.52
1:D:338[A]:CYS:SG	1:D:376[A]:SER:OG	2.68	0.52
1:D:483:ARG:O	1:D:487:THR:HG23	2.10	0.52
1:B:30:ASN:OD1	2:B:1521:EDO:H21	2.10	0.52
1:B:376:SER:HB3	4:B:2384:HOH:O	2.08	0.52
1:A:272:LEU:C	1:A:272:LEU:HD23	2.31	0.52
1:B:256[B]:ILE:HG23	1:B:261:GLU:HB3	1.92	0.51
1:C:452:LEU:HB3	2:C:1507:EDO:H11	1.93	0.51
1:D:256:ILE:O	1:D:256:ILE:HG22	2.09	0.51
1:B:302:LYS:NZ	2:B:1502:EDO:H22	2.27	0.50
1:B:67:ASP:HB2	4:B:2097:HOH:O	2.09	0.50
1:C:96:PRO:HB2	2:C:1511:EDO:H11	1.92	0.50
1:A:374:GLU:H	1:A:377:HIS:CD2	2.12	0.50
1:B:42:TRP:O	2:B:1514:EDO:C1	2.60	0.50
1:C:91[B]:ARG:NE	4:C:2116:HOH:O	2.43	0.50
1:C:31:LEU:HD11	3:C:1523:GOL:H11	1.94	0.50
1:D:460:LEU:HD13	1:D:464:LYS:HE2	1.93	0.50
1:B:338[A]:CYS:SG	1:B:376:SER:OG	2.66	0.50
1:B:438:TYR:HE2	1:B:466:LEU:O	1.95	0.49
1:B:68:LYS:NZ	4:B:2101:HOH:O	2.35	0.49
1:D:342:THR:HG23	1:D:377:HIS:ND1	2.28	0.49
1:A:101:ILE:HG21	1:A:140[A]:LYS:HG2	1.93	0.49
1:D:354[A]:TYR:CD1	4:D:2322:HOH:O	2.49	0.49
1:B:42:TRP:O	2:B:1514:EDO:H12	2.12	0.49
1:C:236:LEU:HD22	2:C:1520:EDO:C1	2.41	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:374:GLU:H	1:B:377:HIS:CD2	2.09	0.49
1:B:0:SER:HA	1:B:71:SER:OG	2.13	0.49
1:D:468:ARG:NH2	4:D:2436:HOH:O	2.46	0.49
1:B:397:LEU:C	1:B:397:LEU:HD23	2.33	0.49
1:B:263:LYS:C	1:B:263:LYS:HD2	2.33	0.49
1:B:27:HIS:HE1	4:B:2096:HOH:O	1.96	0.48
1:D:405:MET:HE2	1:D:406:LEU:O	2.12	0.48
1:D:291:ILE:HD13	1:D:303:TYR:CE1	2.48	0.48
1:D:272:LEU:HD23	1:D:273:LEU:N	2.29	0.48
1:A:342:THR:HG23	1:A:377:HIS:CE1	2.49	0.48
1:D:37:CYS:HB3	2:D:1510:EDO:H11	1.94	0.48
1:C:256:ILE:HG13	1:C:256:ILE:O	2.14	0.48
2:C:1510:EDO:H22	4:C:2481:HOH:O	2.13	0.47
1:D:42:TRP:O	2:D:1510:EDO:H12	2.13	0.47
1:D:464:LYS:HB3	1:D:468:ARG:HH11	1.79	0.47
1:A:415:MET:HG3	4:A:2284:HOH:O	2.13	0.47
1:D:84:GLU:HB2	1:D:103:TRP:HB3	1.96	0.47
1:B:338[A]:CYS:SG	1:B:376:SER:HB2	2.54	0.47
1:C:48:ILE:HD12	2:C:1511:EDO:H22	1.95	0.47
1:A:482:LYS:HE3	1:A:486:LYS:HE2	1.97	0.47
1:A:492:LYS:HD3	4:A:2450:HOH:O	2.15	0.47
1:B:-1:GLY:HA2	1:B:0:SER:C	2.34	0.47
1:A:42:TRP:O	2:A:1507:EDO:C1	2.63	0.47
1:C:120:ASN:HD22	1:C:120:ASN:C	2.19	0.47
1:D:414:GLY:O	1:D:417:LYS:HD3	2.15	0.47
1:B:51:MET:SD	1:B:169[B]:LEU:HD12	2.55	0.47
1:A:374:GLU:N	1:A:377:HIS:HD2	1.99	0.46
3:C:1522:GOL:C2	4:C:2429:HOH:O	2.33	0.46
3:C:1525:GOL:C3	4:C:2495:HOH:O	2.63	0.46
2:D:1510:EDO:H21	4:D:2138:HOH:O	2.14	0.46
1:B:483:ARG:O	1:B:487:THR:HG23	2.16	0.46
1:C:57:LEU:HA	1:C:60:GLU:HG2	1.96	0.46
1:D:-1:GLY:HA3	1:D:71:SER:H	1.81	0.46
1:A:335:MET:HE3	1:A:421:PHE:HB2	1.97	0.45
1:C:296:ASN:ND2	2:C:1507:EDO:H22	2.31	0.45
1:B:270:VAL:HG23	1:B:312:ALA:CB	2.46	0.45
1:D:429:ILE:HG13	1:D:431:THR:HB	1.99	0.45
1:C:334:ILE:O	1:C:338[B]:CYS:HB2	2.16	0.45
1:C:484:LYS:HD2	1:C:484:LYS:N	2.30	0.45
1:B:152:LYS:HE3	4:B:2199:HOH:O	2.17	0.45
1:C:66:LYS:HZ3	1:C:72:VAL:HB	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:302:LYS:HZ3	2:B:1502:EDO:H22	1.81	0.44
1:C:211:MET:HG3	3:C:1527:GOL:H31	2.00	0.44
1:C:122:ASN:H	1:C:122:ASN:HD22	1.66	0.44
1:C:374:GLU:N	1:C:377:HIS:HD2	2.03	0.44
1:D:140:LYS:HD3	4:D:2112:HOH:O	2.17	0.44
1:B:0:SER:CA	1:B:71:SER:OG	2.66	0.44
1:B:0:SER:HB3	1:B:71:SER:OG	2.17	0.44
1:C:270:VAL:HG23	1:C:312:ALA:CB	2.48	0.44
1:C:438:TYR:HH	1:C:466:LEU:CD2	2.30	0.44
1:D:464:LYS:HB3	1:D:468:ARG:NH1	2.33	0.44
1:C:395[B]:ASP:HB3	2:C:1516:EDO:H21	1.99	0.44
1:B:62:ILE:HD13	1:B:74:ILE:HD11	1.99	0.44
1:B:415:MET:HG3	4:B:2295:HOH:O	2.17	0.44
1:A:39:LYS:HD2	1:A:42:TRP:CE2	2.53	0.43
1:B:338[A]:CYS:SG	1:B:376:SER:CB	3.06	0.43
1:C:263:LYS:HA	1:C:410:ARG:O	2.17	0.43
1:D:342:THR:CG2	1:D:377:HIS:CE1	3.00	0.43
1:C:42:TRP:O	2:C:1514:EDO:C1	2.66	0.43
1:B:259:GLU:OE1	2:B:1518:EDO:C1	2.67	0.43
1:A:117:ALA:HB1	3:A:1512:GOL:H32	1.98	0.43
1:C:47:PRO:HD2	2:C:1511:EDO:H12	2.01	0.43
1:D:302:LYS:HE3	4:D:2293:HOH:O	2.19	0.43
1:C:254:GLN:NE2	1:C:410:ARG:HE	2.17	0.43
1:B:86:VAL:HG12	1:B:140[B]:LYS:HE3	2.01	0.43
1:D:270:VAL:HG23	1:D:312:ALA:HB2	1.99	0.43
1:C:60:GLU:HG3	1:C:61:GLY:N	2.34	0.42
1:C:270:VAL:HG23	1:C:312:ALA:HB2	2.01	0.42
3:C:1526:GOL:H32	4:C:2498:HOH:O	2.19	0.42
1:C:62:ILE:HD13	1:C:74:ILE:HD11	2.01	0.42
1:C:74:ILE:HD13	1:C:235:TYR:CE1	2.54	0.42
1:B:259:GLU:OE1	2:B:1518:EDO:H11	2.19	0.42
1:B:291:ILE:HD13	1:B:303:TYR:CE1	2.53	0.42
1:D:345:ILE:HG21	1:D:493:ALA:CB	2.48	0.42
1:D:121:ASN:HB3	1:D:131:TYR:CD1	2.54	0.42
1:C:140:LYS:HE3	4:C:2110:HOH:O	2.05	0.42
1:C:252[A]:ILE:HD13	1:C:449:LEU:HD21	2.01	0.42
1:A:84:GLU:HB2	1:A:103:TRP:HB3	2.02	0.42
1:A:294:LYS:HE3	1:A:299:ASP:O	2.19	0.42
1:D:108:VAL:HG22	4:D:2139:HOH:O	2.19	0.42
1:A:438:TYR:OH	1:A:469:ARG:HD2	2.19	0.42
1:D:374:GLU:H	1:D:377:HIS:CD2	2.10	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:371:PHE:HD2	2:C:1514:EDO:C2	2.32	0.42
1:B:84:GLU:HB2	1:B:103:TRP:HB3	2.01	0.42
1:A:345:ILE:HD11	1:A:489:GLU:HB3	2.02	0.42
1:D:270:VAL:HG23	1:D:312:ALA:CB	2.50	0.42
1:C:196:LEU:HD11	1:C:301:PRO:HG3	2.01	0.42
1:C:56:ASN:HB3	3:C:1523:GOL:O1	2.20	0.41
1:D:74:ILE:O	1:D:238:ILE:HD12	2.20	0.41
2:B:1514:EDO:C2	4:B:2132:HOH:O	2.67	0.41
1:C:233:PRO:O	2:C:1520:EDO:C2	2.68	0.41
1:B:466:LEU:HD12	1:B:469:ARG:NH2	2.35	0.41
1:B:479:ASP:OD2	1:B:481:LYS:HB2	2.20	0.41
1:C:464:LYS:NZ	4:C:2437:HOH:O	2.52	0.41
1:C:84:GLU:HB2	1:C:103:TRP:HB3	2.03	0.41
1:B:196:LEU:HD11	1:B:301:PRO:HG3	2.02	0.41
1:B:339:GLU:HB3	4:B:2350:HOH:O	2.20	0.41
1:C:1:MET:HG3	1:C:3:VAL:HG13	2.02	0.41
1:A:204:LYS:HZ2	2:A:1509:EDO:H11	1.86	0.41
2:C:1510:EDO:H22	4:C:2220:HOH:O	2.20	0.41
3:C:1527:GOL:H12	4:C:2242:HOH:O	2.19	0.41
2:D:1510:EDO:H22	4:D:2138:HOH:O	2.19	0.41
3:C:1525:GOL:H31	4:C:2495:HOH:O	2.19	0.41
1:A:29:ASN:ND2	1:A:60:GLU:OE2	2.47	0.41
1:A:256:ILE:O	1:A:256:ILE:HG22	2.20	0.41
1:D:439:LYS:HD3	1:D:439:LYS:N	2.35	0.41
1:C:38[A]:LEU:HG	1:C:39:LYS:HG3	2.02	0.41
1:C:374:GLU:H	1:C:377:HIS:CD2	2.14	0.41
1:D:263:LYS:HA	1:D:410:ARG:O	2.21	0.41
1:D:405:MET:HG3	1:D:405:MET:O	2.20	0.41
1:D:263:LYS:HD2	1:D:263:LYS:C	2.42	0.41
1:A:27:HIS:HE1	4:A:2081:HOH:O	2.04	0.41
1:B:9:GLN:HB2	1:B:169[A]:LEU:HD21	2.03	0.40
1:B:122:ASN:ND2	4:B:2167:HOH:O	2.53	0.40
1:D:342:THR:HG23	1:D:377:HIS:CG	2.56	0.40
1:A:335:MET:HE1	1:A:421:PHE:HB2	2.02	0.40
1:D:65:LEU:HD23	1:D:65:LEU:HA	1.91	0.40

All (2) 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)
4:A:2181:HOH:O	4:B:2203:HOH:O[1_556]	2.00	0.20

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:2266:HOH:O	4:D:2117:HOH:O[1_565]	2.16	0.04

## 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	509/503 (101%)	496 (97%)	13 (3%)	0	100	100
1	B	508/503 (101%)	495 (97%)	13 (3%)	0	100	100
1	C	509/503 (101%)	497 (98%)	12 (2%)	0	100	100
1	D	508/503 (101%)	496 (98%)	12 (2%)	0	100	100
All	All	2034/2012 (101%)	1984 (98%)	50 (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	459/450 (102%)	449 (98%)	10 (2%)	60	25
1	B	457/450 (102%)	442 (97%)	15 (3%)	45	12
1	C	459/450 (102%)	444 (97%)	15 (3%)	45	12
1	D	457/450 (102%)	444 (97%)	13 (3%)	51	17
All	All	1832/1800 (102%)	1779 (97%)	53 (3%)	51	16



All (53) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	9	GLN
1	A	43	TYR
1	A	169	LEU
1	A	254	GLN
1	A	263	LYS
1	A	346	PHE
1	A	395	ASP
1	A	419	LYS
1	A	461	ASP
1	A	484	LYS
1	B	9	GLN
1	B	43	TYR
1	B	70	THR
1	B	140[A]	LYS
1	B	140[B]	LYS
1	B	169[A]	LEU
1	B	169[B]	LEU
1	B	189	LEU
1	B	256[A]	ILE
1	B	256[B]	ILE
1	B	263	LYS
1	B	346	PHE
1	B	417	LYS
1	B	462	SER
1	B	466	LEU
1	C	9	GLN
1	C	43	TYR
1	C	60	GLU
1	C	95	LYS
1	C	120	ASN
1	C	140	LYS
1	C	254	GLN
1	C	263	LYS
1	C	346	PHE
1	C	404	GLU
1	C	439	LYS
1	C	462	SER
1	C	466	LEU
1	C	484	LYS
1	C	492	LYS
1	D	0	SER
1	D	9	GLN

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Mol	Chain	Res	Type
1	D	43	TYR
1	D	254	GLN
1	D	263	LYS
1	D	346	PHE
1	D	405	MET
1	D	417	LYS
1	D	437	LYS
1	D	439	LYS
1	D	455	LYS
1	D	460	LEU
1	D	461	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (34) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	12	GLN
1	A	27	HIS
1	A	30	ASN
1	A	99	ASN
1	A	125	GLN
1	A	254	GLN
1	A	322	ASN
1	A	377	HIS
1	B	27	HIS
1	B	99	ASN
1	B	122	ASN
1	B	153	GLN
1	B	322	ASN
1	B	377	HIS
1	B	500	GLN
1	C	24	ASN
1	C	27	HIS
1	C	99	ASN
1	C	120	ASN
1	C	122	ASN
1	C	153	GLN
1	C	172	ASN
1	C	177	ASN
1	C	254	GLN
1	C	322	ASN
1	C	377	HIS
1	D	27	HIS

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Mol	Chain	Res	Type
1	D	99	ASN
1	D	122	ASN
1	D	125	GLN
1	D	231	HIS
1	D	254	GLN
1	D	322	ASN
1	D	377	HIS

### 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 carbohydrates in this entry.

### 5.6 Ligand geometry ⓘ

74 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	A	1502	-	3,3,3	0.38	0	2,2,2	1.15	0
2	EDO	A	1503	-	3,3,3	0.44	0	2,2,2	0.67	0
2	EDO	A	1504	-	3,3,3	0.10	0	2,2,2	0.93	0
2	EDO	A	1505	-	3,3,3	0.36	0	2,2,2	0.12	0
2	EDO	A	1506	-	3,3,3	0.73	0	2,2,2	0.61	0
2	EDO	A	1507	-	3,3,3	1.15	0	2,2,2	1.64	0
2	EDO	A	1508	-	3,3,3	0.79	0	2,2,2	1.62	1 (50%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	EDO	A	1509	-	3,3,3	0.65	0	2,2,2	0.43	0
2	EDO	A	1510	-	3,3,3	0.21	0	2,2,2	0.25	0
3	GOL	A	1511	-	5,5,5	1.11	0	5,5,5	0.88	0
3	GOL	A	1512	-	5,5,5	0.43	0	5,5,5	0.58	0
2	EDO	B	1502	-	3,3,3	0.56	0	2,2,2	1.10	0
2	EDO	B	1503	-	3,3,3	0.42	0	2,2,2	0.66	0
2	EDO	B	1504	-	3,3,3	0.67	0	2,2,2	1.09	0
2	EDO	B	1505	-	3,3,3	0.16	0	2,2,2	1.23	0
2	EDO	B	1506	-	3,3,3	1.01	0	2,2,2	0.80	0
2	EDO	B	1507	-	3,3,3	0.49	0	2,2,2	0.39	0
2	EDO	B	1508	-	3,3,3	0.60	0	2,2,2	0.81	0
2	EDO	B	1509	-	3,3,3	0.32	0	2,2,2	1.80	1 (50%)
2	EDO	B	1510	-	3,3,3	0.88	0	2,2,2	0.68	0
2	EDO	B	1511	-	3,3,3	0.43	0	2,2,2	0.27	0
2	EDO	B	1512	-	3,3,3	0.38	0	2,2,2	0.27	0
2	EDO	B	1513	-	3,3,3	0.38	0	2,2,2	0.37	0
2	EDO	B	1514	-	3,3,3	0.83	0	2,2,2	1.12	0
2	EDO	B	1515	-	3,3,3	0.50	0	2,2,2	0.25	0
2	EDO	B	1516	-	3,3,3	1.05	0	2,2,2	0.18	0
2	EDO	B	1517	-	3,3,3	0.53	0	2,2,2	0.59	0
2	EDO	B	1518	-	3,3,3	0.64	0	2,2,2	0.44	0
2	EDO	B	1519	-	3,3,3	0.32	0	2,2,2	0.94	0
2	EDO	B	1520	-	3,3,3	1.13	0	2,2,2	0.29	0
2	EDO	B	1521	-	3,3,3	0.55	0	2,2,2	0.39	0
3	GOL	B	1522	-	5,5,5	0.77	0	5,5,5	0.54	0
3	GOL	B	1523	-	5,5,5	1.54	1 (20%)	5,5,5	1.12	0
2	EDO	C	1502	-	3,3,3	0.67	0	2,2,2	0.80	0
2	EDO	C	1503	-	3,3,3	0.46	0	2,2,2	1.18	0
2	EDO	C	1504	-	3,3,3	0.70	0	2,2,2	1.04	0
2	EDO	C	1505	-	3,3,3	0.42	0	2,2,2	1.17	0
2	EDO	C	1506	-	3,3,3	0.61	0	2,2,2	0.74	0
2	EDO	C	1507	-	3,3,3	0.37	0	2,2,2	0.46	0
2	EDO	C	1508	-	3,3,3	0.69	0	2,2,2	0.20	0
2	EDO	C	1509	-	3,3,3	1.86	1 (33%)	2,2,2	1.94	1 (50%)
2	EDO	C	1510	-	3,3,3	2.50	1 (33%)	2,2,2	1.44	0
2	EDO	C	1511	-	3,3,3	0.60	0	2,2,2	0.46	0
2	EDO	C	1512	-	3,3,3	0.39	0	2,2,2	0.23	0
2	EDO	C	1513	-	3,3,3	0.33	0	2,2,2	0.36	0
2	EDO	C	1514	-	3,3,3	2.16	1 (33%)	2,2,2	2.58	2 (100%)
2	EDO	C	1515	-	3,3,3	0.83	0	2,2,2	0.37	0
2	EDO	C	1516	-	3,3,3	1.05	0	2,2,2	1.32	0
2	EDO	C	1517	-	3,3,3	0.49	0	2,2,2	0.48	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	EDO	C	1518	-	3,3,3	0.26	0	2,2,2	0.78	0
2	EDO	C	1519	-	3,3,3	0.65	0	2,2,2	0.48	0
2	EDO	C	1520	-	3,3,3	0.37	0	2,2,2	0.16	0
3	GOL	C	1521	-	5,5,5	0.99	0	5,5,5	0.49	0
3	GOL	C	1522	-	5,5,5	1.10	1 (20%)	5,5,5	1.21	0
3	GOL	C	1523	-	5,5,5	0.40	0	5,5,5	0.20	0
3	GOL	C	1524	-	5,5,5	0.67	0	5,5,5	1.81	2 (40%)
3	GOL	C	1525	-	5,5,5	0.35	0	5,5,5	1.07	0
3	GOL	C	1526	-	5,5,5	0.61	0	5,5,5	0.47	0
3	GOL	C	1527	-	5,5,5	0.39	0	5,5,5	1.05	0
2	EDO	D	1502	-	3,3,3	0.60	0	2,2,2	1.12	0
2	EDO	D	1503	-	3,3,3	0.51	0	2,2,2	0.77	0
2	EDO	D	1504	-	3,3,3	0.52	0	2,2,2	0.89	0
2	EDO	D	1505	-	3,3,3	0.16	0	2,2,2	1.35	0
2	EDO	D	1506	-	3,3,3	0.20	0	2,2,2	0.93	0
2	EDO	D	1507	-	3,3,3	0.87	0	2,2,2	1.00	0
2	EDO	D	1508	-	3,3,3	0.73	0	2,2,2	0.40	0
2	EDO	D	1509	-	3,3,3	0.42	0	2,2,2	0.05	0
2	EDO	D	1510	-	3,3,3	0.86	0	2,2,2	1.31	0
2	EDO	D	1511	-	3,3,3	0.40	0	2,2,2	0.31	0
2	EDO	D	1512	-	3,3,3	0.74	0	2,2,2	0.06	0
2	EDO	D	1513	-	3,3,3	0.40	0	2,2,2	0.75	0
2	EDO	D	1514	-	3,3,3	0.34	0	2,2,2	0.95	0
2	EDO	D	1515	-	3,3,3	3.71	2 (66%)	2,2,2	2.23	1 (50%)
3	GOL	D	1516	-	5,5,5	0.99	0	5,5,5	0.88	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	A	1502	-	-	0/1/1/1	0/0/0/0
2	EDO	A	1503	-	-	0/1/1/1	0/0/0/0
2	EDO	A	1504	-	-	0/1/1/1	0/0/0/0
2	EDO	A	1505	-	-	0/1/1/1	0/0/0/0
2	EDO	A	1506	-	-	0/1/1/1	0/0/0/0
2	EDO	A	1507	-	-	0/1/1/1	0/0/0/0
2	EDO	A	1508	-	-	0/1/1/1	0/0/0/0
2	EDO	A	1509	-	-	0/1/1/1	0/0/0/0
2	EDO	A	1510	-	-	0/1/1/1	0/0/0/0
3	GOL	A	1511	-	-	0/4/4/4	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	GOL	A	1512	-	-	0/4/4/4	0/0/0/0
2	EDO	B	1502	-	-	0/1/1/1	0/0/0/0
2	EDO	B	1503	-	-	0/1/1/1	0/0/0/0
2	EDO	B	1504	-	-	0/1/1/1	0/0/0/0
2	EDO	B	1505	-	-	0/1/1/1	0/0/0/0
2	EDO	B	1506	-	-	0/1/1/1	0/0/0/0
2	EDO	B	1507	-	-	0/1/1/1	0/0/0/0
2	EDO	B	1508	-	-	0/1/1/1	0/0/0/0
2	EDO	B	1509	-	-	0/1/1/1	0/0/0/0
2	EDO	B	1510	-	-	0/1/1/1	0/0/0/0
2	EDO	B	1511	-	-	0/1/1/1	0/0/0/0
2	EDO	B	1512	-	-	0/1/1/1	0/0/0/0
2	EDO	B	1513	-	-	0/1/1/1	0/0/0/0
2	EDO	B	1514	-	-	0/1/1/1	0/0/0/0
2	EDO	B	1515	-	-	0/1/1/1	0/0/0/0
2	EDO	B	1516	-	-	0/1/1/1	0/0/0/0
2	EDO	B	1517	-	-	0/1/1/1	0/0/0/0
2	EDO	B	1518	-	-	0/1/1/1	0/0/0/0
2	EDO	B	1519	-	-	0/1/1/1	0/0/0/0
2	EDO	B	1520	-	-	0/1/1/1	0/0/0/0
2	EDO	B	1521	-	-	0/1/1/1	0/0/0/0
3	GOL	B	1522	-	-	0/4/4/4	0/0/0/0
3	GOL	B	1523	-	-	0/4/4/4	0/0/0/0
2	EDO	C	1502	-	-	0/1/1/1	0/0/0/0
2	EDO	C	1503	-	-	0/1/1/1	0/0/0/0
2	EDO	C	1504	-	-	0/1/1/1	0/0/0/0
2	EDO	C	1505	-	-	0/1/1/1	0/0/0/0
2	EDO	C	1506	-	-	0/1/1/1	0/0/0/0
2	EDO	C	1507	-	-	0/1/1/1	0/0/0/0
2	EDO	C	1508	-	-	0/1/1/1	0/0/0/0
2	EDO	C	1509	-	-	0/1/1/1	0/0/0/0
2	EDO	C	1510	-	-	0/1/1/1	0/0/0/0
2	EDO	C	1511	-	-	0/1/1/1	0/0/0/0
2	EDO	C	1512	-	-	0/1/1/1	0/0/0/0
2	EDO	C	1513	-	-	0/1/1/1	0/0/0/0
2	EDO	C	1514	-	-	0/1/1/1	0/0/0/0
2	EDO	C	1515	-	-	0/1/1/1	0/0/0/0
2	EDO	C	1516	-	-	0/1/1/1	0/0/0/0
2	EDO	C	1517	-	-	0/1/1/1	0/0/0/0
2	EDO	C	1518	-	-	0/1/1/1	0/0/0/0
2	EDO	C	1519	-	-	0/1/1/1	0/0/0/0
2	EDO	C	1520	-	-	0/1/1/1	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	GOL	C	1521	-	-	0/4/4/4	0/0/0/0
3	GOL	C	1522	-	-	0/4/4/4	0/0/0/0
3	GOL	C	1523	-	-	0/4/4/4	0/0/0/0
3	GOL	C	1524	-	-	0/4/4/4	0/0/0/0
3	GOL	C	1525	-	-	0/4/4/4	0/0/0/0
3	GOL	C	1526	-	-	0/4/4/4	0/0/0/0
3	GOL	C	1527	-	-	0/4/4/4	0/0/0/0
2	EDO	D	1502	-	-	0/1/1/1	0/0/0/0
2	EDO	D	1503	-	-	0/1/1/1	0/0/0/0
2	EDO	D	1504	-	-	0/1/1/1	0/0/0/0
2	EDO	D	1505	-	-	0/1/1/1	0/0/0/0
2	EDO	D	1506	-	-	0/1/1/1	0/0/0/0
2	EDO	D	1507	-	-	0/1/1/1	0/0/0/0
2	EDO	D	1508	-	-	0/1/1/1	0/0/0/0
2	EDO	D	1509	-	-	0/1/1/1	0/0/0/0
2	EDO	D	1510	-	-	0/1/1/1	0/0/0/0
2	EDO	D	1511	-	-	0/1/1/1	0/0/0/0
2	EDO	D	1512	-	-	0/1/1/1	0/0/0/0
2	EDO	D	1513	-	-	0/1/1/1	0/0/0/0
2	EDO	D	1514	-	-	0/1/1/1	0/0/0/0
2	EDO	D	1515	-	-	0/1/1/1	0/0/0/0
3	GOL	D	1516	-	-	0/4/4/4	0/0/0/0

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	1515	EDO	O1-C1	-5.42	1.12	1.42
2	D	1515	EDO	O2-C2	-3.42	1.23	1.42
2	C	1509	EDO	O1-C1	2.10	1.53	1.42
3	C	1522	GOL	O2-C2	2.13	1.49	1.43
3	B	1523	GOL	O2-C2	2.27	1.50	1.43
2	C	1514	EDO	O1-C1	2.92	1.57	1.42
2	C	1510	EDO	O1-C1	4.15	1.64	1.42

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	1515	EDO	O2-C2-C1	-2.83	92.28	112.54
3	C	1524	GOL	O2-C2-C1	-2.64	96.55	108.65
2	A	1508	EDO	O2-C2-C1	-2.28	96.19	112.54
2	B	1509	EDO	O1-C1-C2	-2.18	96.92	112.54
3	C	1524	GOL	O2-C2-C3	2.06	118.09	108.65

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	1514	EDO	O1-C1-C2	2.32	129.18	112.54
2	C	1509	EDO	O1-C1-C2	2.53	130.67	112.54
2	C	1514	EDO	O2-C2-C1	2.82	132.76	112.54

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

25 monomers are involved in 85 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1507	EDO	4	0
2	A	1508	EDO	1	0
2	A	1509	EDO	4	0
3	A	1512	GOL	3	0
2	B	1502	EDO	2	0
2	B	1514	EDO	6	0
2	B	1517	EDO	2	0
2	B	1518	EDO	4	0
2	B	1519	EDO	1	0
2	B	1521	EDO	2	0
3	B	1523	GOL	1	0
2	C	1507	EDO	3	0
2	C	1510	EDO	8	0
2	C	1511	EDO	3	0
2	C	1514	EDO	6	0
2	C	1516	EDO	3	0
2	C	1520	EDO	4	0
3	C	1522	GOL	2	0
3	C	1523	GOL	3	0
3	C	1525	GOL	2	0
3	C	1526	GOL	1	0
3	C	1527	GOL	6	0
2	D	1510	EDO	6	0
2	D	1514	EDO	1	0
2	D	1515	EDO	7	0

## 5.7 Other polymers [i](#)

There are no such residues in this entry.



## 5.8 Polymer linkage issues

There are no chain breaks in this entry.

## 6 Fit of model and data

### 6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2		OWAB(Å <sup>2</sup> )	Q<0.9
1	A	501/503 (99%)	-0.09	27 (5%)	29 30	7, 14, 33, 44	4 (0%)
1	B	503/503 (100%)	-0.21	15 (2%)	54 57	6, 12, 31, 40	3 (0%)
1	C	502/503 (99%)	-0.23	12 (2%)	62 66	6, 12, 28, 40	8 (1%)
1	D	503/503 (100%)	-0.13	21 (4%)	40 42	6, 13, 32, 44	3 (0%)
All	All	2009/2012 (99%)	-0.16	75 (3%)	45 48	6, 13, 32, 44	18 (0%)

All (75) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	70	THR	8.9
1	B	70	THR	7.4
1	D	70	THR	6.7
1	A	70	THR	6.1
1	D	-1	GLY	4.6
1	A	336	GLU	4.3
1	D	501	LEU	4.2
1	D	458	ASP	4.1
1	D	337	LYS	4.0
1	C	71	SER	3.8
1	A	404	GLU	3.7
1	A	458	ASP	3.7
1	A	69	TYR	3.7
1	A	71	SER	3.6
1	D	404	GLU	3.6
1	A	417	LYS	3.5
1	A	333	ASP	3.4
1	C	407	HIS	3.3
1	A	466	LEU	3.3
1	A	465	SER	3.3
1	C	67	ASP	3.2

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Mol	Chain	Res	Type	RSRZ
1	D	407	HIS	3.2
1	D	71	SER	3.2
1	A	405	MET	3.1
1	B	-1	GLY	3.1
1	A	407	HIS	3.1
1	B	0	SER	3.1
1	C	404	GLU	3.0
1	B	67	ASP	2.9
1	B	71	SER	2.9
1	C	298	ASN	2.9
1	D	462	SER	2.9
1	A	480	ASP	2.8
1	C	438	TYR	2.8
1	D	342	THR	2.7
1	B	337	LYS	2.7
1	C	465	SER	2.7
1	A	332	SER	2.6
1	A	438	TYR	2.6
1	B	407	HIS	2.6
1	D	73	ILE	2.6
1	A	338[A]	CYS	2.6
1	A	342	THR	2.5
1	B	404	GLU	2.5
1	D	336	GLU	2.5
1	C	0	SER	2.4
1	A	327	ASP	2.4
1	A	73	ILE	2.4
1	B	501	LEU	2.4
1	D	333	ASP	2.3
1	D	339	GLU	2.3
1	A	329	SER	2.3
1	B	458	ASP	2.3
1	A	501	LEU	2.3
1	A	402	GLY	2.3
1	B	466	LEU	2.2
1	A	479	ASP	2.2
1	A	337	LYS	2.2
1	C	103	TRP	2.2
1	A	459	SER	2.2
1	D	329	SER	2.2
1	A	462	SER	2.1
1	D	500	GLN	2.1

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Mol	Chain	Res	Type	RSRZ
1	C	458	ASP	2.1
1	D	405	MET	2.1
1	B	480	ASP	2.1
1	B	462	SER	2.1
1	A	468	ARG	2.1
1	B	331	ALA	2.1
1	D	327	ASP	2.1
1	D	438	TYR	2.0
1	B	459	SER	2.0
1	C	331	ALA	2.0
1	D	332	SER	2.0
1	D	465	SER	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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
2	EDO	C	1511	4/4	0.90	0.22	26.37	23,31,33,35	0
2	EDO	B	1514	4/4	0.93	0.36	24.17	19,20,26,39	0
2	EDO	D	1510	4/4	0.92	0.31	16.53	22,26,27,41	0
2	EDO	A	1508	4/4	0.84	0.20	13.74	18,31,35,36	0
2	EDO	A	1507	4/4	0.94	0.33	13.58	19,25,27,40	0
3	GOL	C	1526	6/6	0.67	0.32	11.89	32,34,36,41	0
2	EDO	C	1517	4/4	0.62	0.15	11.07	54,54,55,55	0
3	GOL	C	1527	6/6	0.69	0.40	9.05	31,36,39,40	0
2	EDO	D	1511	4/4	0.79	0.37	8.30	40,40,43,50	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
2	EDO	C	1509	4/4	0.81	0.17	8.23	24,31,31,32	0
2	EDO	D	1512	4/4	0.86	0.13	7.49	34,36,36,38	0
2	EDO	B	1507	4/4	0.86	0.09	5.88	29,32,37,40	0
3	GOL	A	1512	6/6	0.76	0.29	5.79	48,49,51,53	0
3	GOL	C	1523	6/6	0.83	0.29	5.34	58,60,61,61	0
2	EDO	C	1514	4/4	0.92	0.20	5.29	18,20,21,28	0
2	EDO	D	1508	4/4	0.84	0.13	5.26	33,34,36,38	0
2	EDO	C	1507	4/4	0.93	0.10	4.74	32,33,37,40	0
2	EDO	C	1510	4/4	0.85	0.14	4.10	11,18,24,28	0
2	EDO	D	1515	4/4	0.97	0.19	3.68	10,16,18,18	0
2	EDO	B	1510	4/4	0.90	0.10	3.26	29,31,31,38	0
2	EDO	B	1506	4/4	0.94	0.11	3.26	15,21,24,34	0
2	EDO	D	1507	4/4	0.94	0.11	3.16	17,18,20,20	0
2	EDO	A	1504	4/4	0.88	0.13	3.02	25,30,30,35	0
2	EDO	B	1518	4/4	0.89	0.25	2.99	35,37,41,43	0
2	EDO	D	1505	4/4	0.95	0.10	2.81	25,28,30,38	0
2	EDO	A	1510	4/4	0.96	0.11	2.81	15,22,23,26	0
3	GOL	C	1524	6/6	0.85	0.17	2.76	20,34,39,43	0
2	EDO	B	1509	4/4	0.96	0.17	2.71	33,34,35,36	0
2	EDO	C	1516	4/4	0.89	0.19	2.68	22,26,27,36	0
2	EDO	B	1520	4/4	0.93	0.12	2.64	17,23,23,32	0
2	EDO	D	1506	4/4	0.94	0.14	2.60	19,22,26,32	0
2	EDO	C	1519	4/4	0.71	0.20	2.56	30,32,37,41	0
2	EDO	C	1512	4/4	0.98	0.11	2.29	12,19,23,28	0
2	EDO	C	1515	4/4	0.92	0.11	2.28	19,25,26,32	0
2	EDO	C	1513	4/4	0.88	0.09	2.22	39,40,40,40	0
2	EDO	B	1502	4/4	0.94	0.12	2.05	18,27,28,33	0
3	GOL	C	1525	6/6	0.82	0.19	2.00	42,46,48,51	0
2	EDO	A	1503	4/4	0.94	0.07	1.90	18,18,20,21	0
2	EDO	B	1515	4/4	0.90	0.10	1.85	36,36,37,39	0
2	EDO	D	1503	4/4	0.97	0.09	1.75	14,16,21,22	0
2	EDO	C	1503	4/4	0.90	0.08	1.61	21,24,24,25	0
2	EDO	A	1506	4/4	0.94	0.08	1.53	15,16,16,18	0
2	EDO	B	1521	4/4	0.82	0.15	1.37	24,27,38,38	0
3	GOL	A	1511	6/6	0.97	0.12	1.33	8,9,15,21	0
2	EDO	B	1504	4/4	0.94	0.09	1.33	20,21,21,23	0
2	EDO	B	1511	4/4	0.95	0.11	1.30	23,32,35,38	0
3	GOL	C	1522	6/6	0.92	0.16	1.27	15,21,23,26	0
3	GOL	B	1523	6/6	0.90	0.12	1.17	15,23,29,29	0
2	EDO	A	1505	4/4	0.91	0.12	1.15	22,28,31,37	0
2	EDO	C	1505	4/4	0.94	0.10	1.13	22,23,28,32	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
2	EDO	B	1505	4/4	0.95	0.08	0.80	21,27,30,35	0
2	EDO	C	1508	4/4	0.96	0.07	0.77	12,15,16,18	0
3	GOL	B	1522	6/6	0.97	0.11	0.74	7,8,14,20	0
3	GOL	C	1521	6/6	0.96	0.11	0.70	7,7,15,18	0
2	EDO	B	1508	4/4	0.95	0.08	0.67	14,19,19,21	0
2	EDO	D	1509	4/4	0.98	0.08	0.09	13,18,19,25	0
2	EDO	B	1503	4/4	0.97	0.06	0.07	14,15,16,16	0
2	EDO	C	1518	4/4	0.97	0.07	-0.04	25,29,30,32	0
2	EDO	C	1504	4/4	0.91	0.10	-0.09	22,27,28,33	0
3	GOL	D	1516	6/6	0.98	0.09	-0.35	6,8,16,22	0
2	EDO	C	1502	4/4	0.98	0.06	-0.38	12,14,15,15	0
2	EDO	A	1502	4/4	0.97	0.06	-0.66	16,16,17,21	0
2	EDO	D	1504	4/4	0.95	0.05	-0.72	17,18,20,21	0
2	EDO	D	1502	4/4	0.98	0.05	-1.15	15,15,15,18	0
2	EDO	A	1509	4/4	0.79	0.29	-	39,45,46,46	0
2	EDO	C	1506	4/4	0.89	0.20	-	38,43,44,44	0
2	EDO	B	1513	4/4	0.97	0.11	-	21,31,35,39	0
2	EDO	C	1520	4/4	0.94	0.30	-	25,26,28,32	0
2	EDO	B	1519	4/4	0.91	0.14	-	25,35,36,38	0
2	EDO	B	1516	4/4	0.76	0.26	-	29,30,33,34	0
2	EDO	D	1513	4/4	0.83	0.16	-	37,38,40,47	0
2	EDO	B	1512	4/4	0.90	0.16	-	43,43,44,44	0
2	EDO	D	1514	4/4	0.80	0.15	-	45,45,45,51	0
2	EDO	B	1517	4/4	0.87	0.15	-	30,31,32,33	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.