



# wwPDB X-ray Structure Validation Summary Report ⓘ

Sep 13, 2020 – 10:44 AM BST

PDB ID : 2JE4  
Title : Atomic-resolution crystal structure of chemically-synthesized HIV-1 protease  
in complex with JG-365  
Authors : Malito, E.; Johnson, E.C.B.; Tang, W.J.  
Deposited on : 2007-01-15  
Resolution : 1.07 Å(reported)

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

We welcome your comments at [validation@mail.wwpdb.org](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 : 2.14.4.dev1  
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) : 2.14.4.dev1

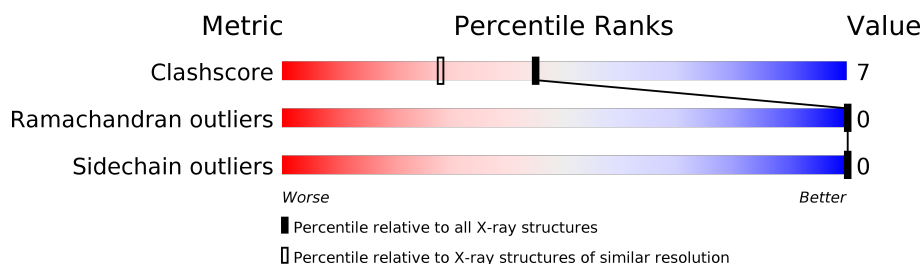
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.07 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))
Clashscore	141614	1021 (1.10-1.06)
Ramachandran outliers	138981	1381 (1.12-1.04)
Sidechain outliers	138945	1379 (1.12-1.04)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ .

Mol	Chain	Length	Quality of chain
1	1-A	99	
1	1-B	99	
1	2-A	99	
1	2-B	99	
2	1-C	7	
2	2-C	7	

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	JG3	1-C	4[A]	X	-	-	-
2	JG3	2-C	4[B]	X	-	-	-
4	GOL	1-A	1104[A]	-	X	-	-
5	SO4	1-A	1112[A]	-	X	-	-
5	SO4	1-B	1102[A]	-	X	X	-
5	SO4	1-B	1103[A]	-	X	X	-
5	SO4	2-B	1102[B]	-	-	X	-
5	SO4	2-B	1103[B]	-	-	X	-

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 4236 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 PROTEASE.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
1	1-A	99	Total	C	N	O	0	99	0
			810	529	140	141			
1	2-A	99	Total	C	N	O	0	99	0
			810	529	140	141			
1	1-B	99	Total	C	N	O	0	99	0
			800	523	138	139			
1	2-B	99	Total	C	N	O	0	99	0
			800	523	138	139			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	7	LYS	GLN	conflict	UNP O38716
A	33	ILE	LEU	conflict	UNP O38716
B	7	LYS	GLN	conflict	UNP O38716
B	33	ILE	LEU	conflict	UNP O38716

- Molecule 2 is a protein called INHIBITOR MOLECULE JG365.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	1-C	6	Total	C	N	O	0	5	0
			58	40	8	10			
2	2-C	5	Total	C	N	O	0	5	0
			52	37	7	8			

- Molecule 3 is ACETATE ION (three-letter code: ACT) (formula: C<sub>2</sub>H<sub>3</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	1-A	1	Total	C	O	0	1
			4	2	2		
3	2-A	1	Total	C	O	0	1
			4	2	2		
3	1-A	1	Total	C	O	0	1
			4	2	2		
3	2-A	1	Total	C	O	0	1
			4	2	2		
3	1-B	1	Total	C	O	0	1
			4	2	2		
3	2-B	1	Total	C	O	0	1
			4	2	2		
3	1-B	1	Total	C	O	0	1
			4	2	2		
3	2-B	1	Total	C	O	0	1
			4	2	2		

- Molecule 4 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
4	1-A	1	Total	C	O	0	1
			6	3	3		
4	2-A	1	Total	C	O	0	1
			6	3	3		
4	1-A	1	Total	C	O	0	1
			6	3	3		
4	2-A	1	Total	C	O	0	1
			6	3	3		
4	1-A	1	Total	C	O	0	1
			6	3	3		
4	2-A	1	Total	C	O	0	1
			6	3	3		

- Molecule 5 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	1-A	1	Total	O	S	0	1
			5	4	1		
5	2-A	1	Total	O	S	0	1
			5	4	1		
5	1-A	1	Total	O	S	0	1
			5	4	1		
5	2-A	1	Total	O	S	0	1
			5	4	1		
5	1-A	1	Total	O	S	0	1
			5	4	1		
5	2-A	1	Total	O	S	0	1
			5	4	1		
5	1-B	1	Total	O	S	0	1
			5	4	1		
5	2-B	1	Total	O	S	0	1
			5	4	1		
5	1-B	1	Total	O	S	0	1
			5	4	1		
5	2-B	1	Total	O	S	0	1
			5	4	1		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	1-A	215	Total	O	0	215
			215	215		
6	2-A	213	Total	O	0	0
			213	213		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	1-B	179	Total	O	0	179
			179	179		
6	2-B	181	Total	O	0	0
			181	181		



### 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. 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. 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: PROTEASE

Chain 1-A: 



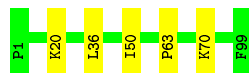
- Molecule 1: PROTEASE

Chain 1-B: 



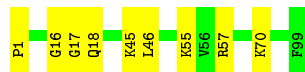
- Molecule 1: PROTEASE

Chain 2-A: 

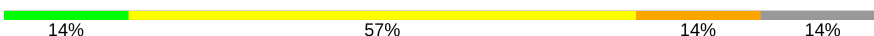


- Molecule 1: PROTEASE

Chain 2-B: 



- Molecule 2: INHIBITOR MOLECULE JG365

Chain 1-C: 



- Molecule 2: INHIBITOR MOLECULE JG365

Chain 2-C: 



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	50.50Å 58.85Å 60.89Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	10.00 – 1.07 9.96 – 1.07	Depositor EDS
% Data completeness (in resolution range)	93.9 (10.00-1.07) 86.0 (9.96-1.07)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.04 (at 1.07Å)	Xtriage
Refinement program	SHELXL-97	Depositor
R, $R_{free}$	0.144 , 0.184 0.212 , (Not available)	Depositor DCC
$R_{free}$ test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	11.3	Xtriage
Anisotropy	0.153	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.48 , 35.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.018 for -h,l,k	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	4236	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	20.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.71% 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 ⓘ

### 5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, VME, NLE, SO4, ACT, JG3, DBU

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	0.83	2/802 (0.2%)	1.40	9/1079 (0.8%)
1	1-B	0.79	1/791 (0.1%)	1.37	8/1064 (0.8%)
2	1-C	3.48	3/28 (10.7%)	1.38	0/35
All	All	0.92	6/1621 (0.4%)	1.39	17/2178 (0.8%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	1-C	1	1
2	2-C	1	1
All	All	2	2

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	1-C	1	SER	CA-CB	15.32	1.75	1.52
2	1-C	1	SER	N-CA	7.87	1.62	1.46
1	1-A	99[A]	PHE	C-OXT	7.42	1.37	1.23
1	1-A	99[B]	PHE	C-OXT	7.42	1.37	1.23
1	1-B	99[A]	PHE	C-OXT	7.08	1.36	1.23

The worst 5 of 17 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1-B	14[A]	ARG	CD-NE-CZ	11.77	140.08	123.60
1	1-A	8[A]	ARG	NE-CZ-NH1	-9.71	115.44	120.30
1	1-A	14[A]	ARG	NE-CZ-NH2	-9.54	115.53	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1-A	14[B]	ARG	NE-CZ-NH2	-9.54	115.53	120.30
1	1-A	57[A]	ARG	NE-CZ-NH1	-8.50	116.05	120.30

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	1-C	4[A]	JG3	C1
2	2-C	4[B]	JG3	C1

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	1-C	3[A]	ASN	Peptide
2	2-C	3[B]	ASN	Peptide

## 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	1-A	810	0	861	7	0
1	1-B	800	0	865	12	0
1	2-A	810	0	850	9	0
1	2-B	800	0	855	9	0
2	1-C	58	0	60	9	0
2	2-C	52	0	52	2	0
3	1-A	8	0	6	0	0
3	1-B	8	0	6	0	0
3	2-A	8	0	6	0	0
3	2-B	8	0	6	0	0
4	1-A	18	0	21	1	0
4	2-A	18	0	21	1	0
5	1-A	15	0	0	1	0
5	1-B	10	0	0	5	0
5	2-A	15	0	0	1	0
5	2-B	10	0	0	5	0
6	1-A	215	0	0	4	0
6	1-B	179	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	2-A	213	0	0	8	0
6	2-B	181	0	0	2	0
All	All	4236	0	3609	46	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 7.

The worst 5 of 46 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:1:SER:CB	2:C:1:SER:CA	1.75	1.64
2:C:6[B]:VME:CM	2:C:6[B]:VME:O	1.68	1.42
2:C:6[B]:VME:O	2:C:6[B]:VME:CM	1.90	1.18
2:C:6[B]:VME:O	2:C:6[B]:VME:CA	2.18	0.92
1:B:84[A]:ILE:HD13	2:C:5[A]:ILE:HD11	1.60	0.81

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	1-A	100/99 (101%)	100 (100%)	0	0	100	100
1	1-B	100/99 (101%)	99 (99%)	1 (1%)	0	100	100
1	2-A	101/99 (102%)	101 (100%)	0	0	100	100
1	2-B	101/99 (102%)	100 (99%)	1 (1%)	0	100	100
2	1-C	3/7 (43%)	3 (100%)	0	0	100	100
2	2-C	2/7 (29%)	2 (100%)	0	0	100	100
All	All	407/410 (99%)	405 (100%)	2 (0%)	0	100	100

There are no Ramachandran outliers to report.

### 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	84/80 (105%)	84 (100%)	0	100	100
1	1-B	84/80 (105%)	84 (100%)	0	100	100
2	1-C	4/4 (100%)	4 (100%)	0	100	100
All	All	172/164 (105%)	172 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	1-A	2[A]	GLN
1	1-A	98[A]	ASN
1	1-B	2[A]	GLN
2	1-C	3[A]	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

18 non-standard protein/DNA/RNA residues 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
1	NLE	1-A	46[A]	1	6,7,8	0.64	0	2,7,9	0.24	0
1	NLE	1-B	46[A]	1	6,7,8	0.84	0	2,7,9	1.17	0
2	JG3	1-C	4[A]	2	19,20,21	3.33	6 (31%)	21,26,28	3.09	6 (28%)
1	DBU	1-A	67[A]	1	4,5,6	6.04	3 (75%)	2,5,7	15.92	1 (50%)
1	NLE	1-A	36[A]	1	6,7,8	0.54	0	2,7,9	0.78	0
1	DBU	1-B	67[A]	1	4,5,6	3.28	2 (50%)	2,5,7	8.18	2 (100%)
1	NLE	1-B	36[A]	1	6,7,8	0.86	0	2,7,9	0.21	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
1	NLE	1-A	46[A]	1	-	0/5/6/8	-
1	NLE	1-B	46[A]	1	-	0/5/6/8	-
2	JG3	1-C	4[A]	2	1/1/4/5	4/12/24/26	0/2/2/2
1	DBU	1-A	67[A]	1	-	0/1/4/6	-
1	NLE	1-A	36[A]	1	-	1/5/6/8	-
2	JG3	2-C	4[B]	-	1/1/4/5	-	-
1	DBU	1-B	67[A]	1	-	1/1/4/6	-
1	NLE	1-B	36[A]	1	-	0/5/6/8	-

The worst 5 of 11 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	1-C	4[A]	JG3	C4-C1	-9.23	1.39	1.52
1	1-A	67[A]	DBU	C-CA	8.75	1.59	1.45
2	1-C	4[A]	JG3	C4-N2	-7.50	1.33	1.47
1	1-A	67[A]	DBU	CG-CB	-7.48	1.21	1.49
2	1-C	4[A]	JG3	O1-C1	-6.65	1.29	1.43

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1-A	67[A]	DBU	CG-CB-CA	-22.46	97.27	126.38
1	1-B	67[A]	DBU	CG-CB-CA	-10.78	112.42	126.38
2	1-C	4[A]	JG3	C-CA-N2	7.85	119.43	112.32
2	1-C	4[A]	JG3	O1-C1-C4	7.38	127.65	109.80
2	1-C	4[A]	JG3	O1-C1-C8	6.32	120.80	109.40



All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	1-C	4[A]	JG3	C1
2	2-C	4[B]	JG3	C1

5 of 6 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	1-C	4[A]	JG3	O1-C1-C4-N2
2	1-C	4[A]	JG3	O1-C1-C8-C10
1	1-A	36[A]	NLE	CE-CD-CG-CB
2	1-C	4[A]	JG3	C1-C4-N2-C3
1	1-B	67[A]	DBU	O-C-CA-CB

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	1-B	46[A]	NLE	1	0
1	1-A	36[A]	NLE	1	0

## 5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

## 5.6 Ligand geometry ⓘ

24 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	$\# Z  > 2$
4	GOL	1-A	1102[A]	-	5,5,5	0.53	0	5,5,5	2.04	2 (40%)
3	ACT	1-A	1101[A]	-	1,3,3	1.74	0	0,3,3	0.00	-
5	SO4	1-B	1103[A]	-	4,4,4	1.51	2 (50%)	6,6,6	1.72	3 (50%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
5	SO4	1-B	1102[A]	-	4,4,4	1.60	2 (50%)	6,6,6	2.43	2 (33%)
3	ACT	1-A	1100[A]	-	1,3,3	1.32	0	0,3,3	0.00	-
4	GOL	1-A	1104[A]	-	5,5,5	0.53	0	5,5,5	2.30	3 (60%)
3	ACT	1-B	1100[A]	-	1,3,3	2.37	1 (100%)	0,3,3	0.00	-
5	SO4	1-A	1112[A]	-	4,4,4	1.81	2 (50%)	6,6,6	6.06	6 (100%)
4	GOL	1-A	1103[A]	-	5,5,5	1.00	0	5,5,5	2.13	2 (40%)
3	ACT	1-B	1101[A]	-	1,3,3	1.04	0	0,3,3	0.00	-
5	SO4	1-A	1105[A]	-	4,4,4	1.30	1 (25%)	6,6,6	1.20	1 (16%)
5	SO4	1-A	1109[A]	-	4,4,4	1.36	0	6,6,6	1.56	1 (16%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	GOL	1-A	1102[A]	-	-	2/4/4/4	-
4	GOL	1-A	1103[A]	-	-	2/4/4/4	-
4	GOL	1-A	1104[A]	-	-	3/4/4/4	-

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	1-A	1112[A]	SO4	O1-S	2.64	1.60	1.46
5	1-A	1112[A]	SO4	O2-S	2.46	1.59	1.46
3	1-B	1100[A]	ACT	CH3-C	2.37	1.51	1.48
5	1-B	1102[A]	SO4	O2-S	2.22	1.58	1.46
5	1-B	1102[A]	SO4	O1-S	2.13	1.57	1.46

The worst 5 of 20 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	1-A	1112[A]	SO4	O4-S-O3	11.04	156.17	109.06
5	1-A	1112[A]	SO4	O4-S-O2	-5.63	79.95	109.31
5	1-A	1112[A]	SO4	O3-S-O2	-5.51	80.53	109.31
5	1-A	1112[A]	SO4	O4-S-O1	-4.75	84.53	109.31
5	1-B	1102[A]	SO4	O4-S-O3	4.42	127.94	109.06

There are no chirality outliers.

5 of 7 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	1-A	1102[A]	GOL	C1-C2-C3-O3
4	1-A	1103[A]	GOL	O1-C1-C2-O2
4	1-A	1103[A]	GOL	C1-C2-C3-O3
4	1-A	1104[A]	GOL	O1-C1-C2-O2
4	1-A	1104[A]	GOL	C1-C2-C3-O3

There are no ring outliers.

4 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	1-A	1102[A]	GOL	1	0
5	1-B	1103[A]	SO4	3	0
5	1-B	1102[A]	SO4	2	0
5	1-A	1112[A]	SO4	1	0

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

### 6.3 Carbohydrates ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

### 6.4 Ligands ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

### 6.5 Other polymers ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.