



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 13, 2026 – 07:55 PM UTC

PDB ID : 4Z50 / pdb_00004z50
Title : Crystal Structure of Multidrug Resistant HIV-1 Protease Clinical Isolate PR20D25N with Tucked Flap
Authors : Agniswamy, J.; Shen, C.-H.; Weber, I.T.
Deposited on : 2015-04-02
Resolution : 1.45 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

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

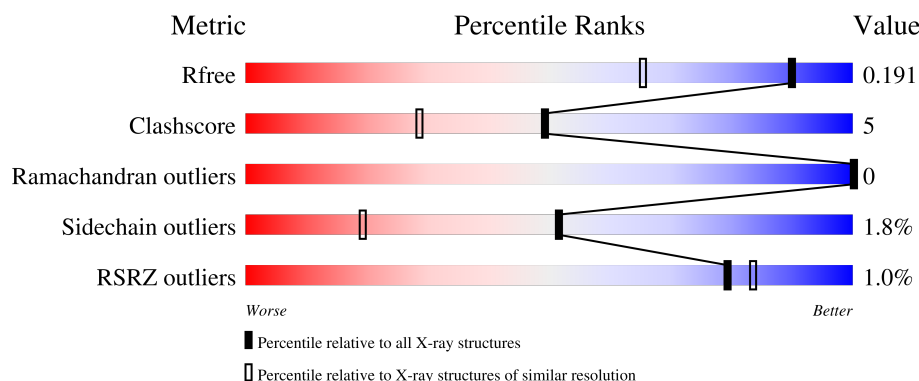
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.45 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}	180053	1756 (1.46-1.46)
Clashscore	190562	1795 (1.46-1.46)
Ramachandran outliers	187476	1776 (1.46-1.46)
Sidechain outliers	187428	1776 (1.46-1.46)
RSRZ outliers	180081	1756 (1.46-1.46)

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

Mol	Chain	Length	Quality of chain
1	A	99	 89% 11%
1	B	99	 2% 87% 12%
1	C	99	 2% 84% 15%
1	D	99	 2% 83% 15%

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
4	GOL	B	206	-	X	-	-
4	GOL	D	204	-	X	-	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 3561 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	A	99	Total	C	N	O	S	0	1	0
			766	496	133	135	2			
1	B	99	Total	C	N	O	S	0	5	0
			780	506	134	138	2			
1	C	99	Total	C	N	O	S	0	7	0
			796	519	135	140	2			
1	D	99	Total	C	N	O	S	0	8	0
			794	514	136	141	3			

There are 48 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	7	LYS	GLN	engineered mutation	UNP Q0PQ60
A	25	ASN	ASP	engineered mutation	UNP Q0PQ60
A	32	ILE	VAL	engineered mutation	UNP Q0PQ60
A	37	ASN	GLU	engineered mutation	UNP Q0PQ60
A	47	VAL	ILE	engineered mutation	UNP Q0PQ60
A	54	LEU	VAL	engineered mutation	UNP Q0PQ60
A	58	GLU	GLN	engineered mutation	UNP Q0PQ60
A	67	ALA	CYS	engineered mutation	UNP Q0PQ60
A	71	VAL	ALA	engineered mutation	UNP Q0PQ60
A	89	THR	PHE	engineered mutation	UNP Q0PQ60
A	93	ILE	LEU	engineered mutation	UNP Q0PQ60
A	95	ALA	CYS	engineered mutation	UNP Q0PQ60
B	107	LYS	GLN	engineered mutation	UNP Q0PQ60
B	125	ASN	ASP	engineered mutation	UNP Q0PQ60
B	132	ILE	VAL	engineered mutation	UNP Q0PQ60
B	137	ASN	GLU	engineered mutation	UNP Q0PQ60
B	147	VAL	ILE	engineered mutation	UNP Q0PQ60
B	154	LEU	VAL	engineered mutation	UNP Q0PQ60
B	158	GLU	GLN	engineered mutation	UNP Q0PQ60
B	167	ALA	CYS	engineered mutation	UNP Q0PQ60
B	171	VAL	ALA	engineered mutation	UNP Q0PQ60

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
B	189	THR	PHE	engineered mutation	UNP Q0PQ60
B	193	ILE	LEU	engineered mutation	UNP Q0PQ60
B	195	ALA	CYS	engineered mutation	UNP Q0PQ60
C	7	LYS	GLN	engineered mutation	UNP Q0PQ60
C	25	ASN	ASP	engineered mutation	UNP Q0PQ60
C	32	ILE	VAL	engineered mutation	UNP Q0PQ60
C	37	ASN	GLU	engineered mutation	UNP Q0PQ60
C	47	VAL	ILE	engineered mutation	UNP Q0PQ60
C	54	LEU	VAL	engineered mutation	UNP Q0PQ60
C	58	GLU	GLN	engineered mutation	UNP Q0PQ60
C	67	ALA	CYS	engineered mutation	UNP Q0PQ60
C	71	VAL	ALA	engineered mutation	UNP Q0PQ60
C	89	THR	PHE	engineered mutation	UNP Q0PQ60
C	93	ILE	LEU	engineered mutation	UNP Q0PQ60
C	95	ALA	CYS	engineered mutation	UNP Q0PQ60
D	107	LYS	GLN	engineered mutation	UNP Q0PQ60
D	125	ASN	ASP	engineered mutation	UNP Q0PQ60
D	132	ILE	VAL	engineered mutation	UNP Q0PQ60
D	137	ASN	GLU	engineered mutation	UNP Q0PQ60
D	147	VAL	ILE	engineered mutation	UNP Q0PQ60
D	154	LEU	VAL	engineered mutation	UNP Q0PQ60
D	158	GLU	GLN	engineered mutation	UNP Q0PQ60
D	167	ALA	CYS	engineered mutation	UNP Q0PQ60
D	171	VAL	ALA	engineered mutation	UNP Q0PQ60
D	189	THR	PHE	engineered mutation	UNP Q0PQ60
D	193	ILE	LEU	engineered mutation	UNP Q0PQ60
D	195	ALA	CYS	engineered mutation	UNP Q0PQ60

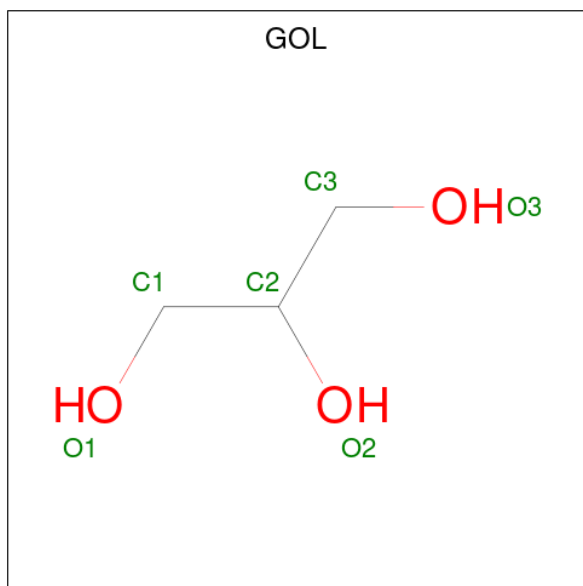
- Molecule 2 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Cl 1 1	0	0
2	B	3	Total Cl 3 3	0	0
2	C	3	Total Cl 3 3	0	0
2	D	2	Total Cl 2 2	0	0

- Molecule 3 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	2	Total Na 2 2	0	0
3	C	1	Total Na 1 1	0	0
3	D	1	Total Na 1 1	0	0

- Molecule 4 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



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

- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	112	Total O 112 112	0	4
5	B	106	Total O 106 106	0	6
5	C	79	Total O 79 79	0	2
5	D	103	Total O 103 103	0	4

3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

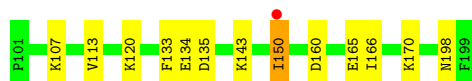
- Molecule 1: Protease

Chain A:  89% 11%



- Molecule 1: Protease

Chain B:  87% 12% .



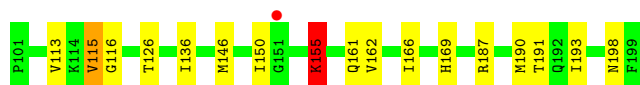
- Molecule 1: Protease

Chain C:  84% 15% .



- Molecule 1: Protease

Chain D:  83% 15% ..



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	54.15Å 48.57Å 69.68Å 90.00° 99.15° 90.00°	Depositor
Resolution (Å)	9.92 – 1.45 9.92 – 1.45	Depositor EDS
% Data completeness (in resolution range)	92.8 (9.92-1.45) 92.6 (9.92-1.45)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.57 (at 1.45Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.138 , 0.191 0.137 , 0.191	Depositor DCC
R_{free} test set	3070 reflections (4.84%)	wwPDB-VP
Wilson B-factor (Å ²)	14.3	Xtriage
Anisotropy	0.056	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.48 , 59.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	3561	wwPDB-VP
Average B, all atoms (Å ²)	18.0	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 36.31 % 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 5.1006e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, NA, CL

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	1.37	3/786 (0.4%)	1.09	0/1066
1	B	1.41	5/819 (0.6%)	1.09	0/1111
1	C	1.38	5/831 (0.6%)	1.12	0/1128
1	D	1.36	2/841 (0.2%)	1.10	2/1139 (0.2%)
All	All	1.38	15/3277 (0.5%)	1.10	2/4444 (0.0%)

All (15) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	46	MET	SD-CE	-7.99	1.59	1.79
1	D	155	LYS	CB-CG	-7.94	1.28	1.52
1	B	150	ILE	CA-CB	6.41	1.61	1.54
1	C	55	LYS	CE-NZ	6.00	1.67	1.49
1	D	116	GLY	CA-C	5.97	1.58	1.51
1	C	42	TRP	N-CA	5.76	1.53	1.45
1	B	107	LYS	CB-CG	-5.64	1.35	1.52
1	A	23	LEU	CG-CD1	-5.57	1.34	1.52
1	B	133	PHE	CA-C	-5.32	1.46	1.52
1	C	49	GLY	N-CA	5.29	1.50	1.45
1	B	135[A]	ASP	N-CA	5.24	1.52	1.46
1	B	135[B]	ASP	N-CA	5.24	1.52	1.46
1	A	67	ALA	C-O	5.20	1.30	1.23
1	A	50	ILE	CA-CB	5.17	1.59	1.54
1	C	82	VAL	CB-CG2	-5.07	1.35	1.52

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	162	VAL	CB-CA-C	-8.29	101.74	110.53
1	D	155	LYS	CB-CG-CD	-6.22	96.99	111.30

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	766	0	801	5	0
1	B	780	0	816	6	0
1	C	796	0	847	12	0
1	D	794	0	821	16	0
2	A	1	0	0	0	0
2	B	3	0	0	0	0
2	C	3	0	0	0	0
2	D	2	0	0	0	0
3	B	2	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
4	B	6	0	8	0	0
4	D	6	0	8	1	0
5	A	112	0	0	1	0
5	B	106	0	0	1	0
5	C	79	0	0	2	0
5	D	103	0	0	2	1
All	All	3561	0	3301	35	1

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 5.

All (35) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:54:LEU:HD22	1:C:79[A]:PRO:HB2	1.41	1.01
1:C:43:LYS:HE3	5:C:202:HOH:O	1.69	0.91
1:C:5:LEU:HD13	1:D:190[A]:MET:HE3	1.52	0.90
1:C:54:LEU:HD13	1:C:79[A]:PRO:O	1.78	0.83
1:D:113:VAL:HG12	1:D:166:ILE:HG12	1.64	0.80
1:D:146:MET:HE1	1:D:155:LYS:CD	2.23	0.69

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:161:GLN:NE2	5:D:303:HOH:O	2.25	0.69
1:D:146:MET:HE1	1:D:155:LYS:HD2	1.77	0.65
1:B:165[B]:GLU:HG2	1:B:170:LYS:HG2	1.80	0.64
1:C:54:LEU:CD1	1:C:79[A]:PRO:O	2.47	0.62
1:D:169[A]:HIS:HD2	4:D:204:GOL:O2	1.81	0.62
1:C:15[A]:VAL:HG13	1:C:36:ILE:HD11	1.80	0.61
1:C:5:LEU:HD13	1:D:190[A]:MET:CE	2.28	0.61
1:D:115:VAL:HG13	1:D:136:ILE:HD11	1.81	0.60
1:C:5:LEU:CD1	1:D:190[A]:MET:HE3	2.28	0.58
1:C:13[B]:VAL:HG12	1:C:66:ILE:HG12	1.88	0.56
1:D:146:MET:HE1	1:D:155:LYS:HD3	1.88	0.56
1:D:161:GLN:OE1	5:D:302:HOH:O	2.18	0.53
1:D:146:MET:CE	1:D:155:LYS:HD2	2.39	0.53
1:A:54:LEU:HD11	1:A:79:PRO:HG2	1.91	0.53
1:A:69[A]:HIS:HD2	5:A:202:HOH:O	1.93	0.51
1:C:38:LEU:HB3	1:C:39:PRO:HD2	1.93	0.51
1:C:13[A]:VAL:HG23	1:C:66:ILE:HG12	1.94	0.50
1:C:43:LYS:CE	5:C:202:HOH:O	2.41	0.48
1:A:63:PRO:HA	1:A:72:ILE:HD13	1.96	0.48
1:D:187:ARG:O	1:D:191:THR:HG23	2.13	0.47
1:D:126:THR:HG22	1:D:190[A]:MET:HE1	1.99	0.45
1:A:2:GLN:HG3	1:B:198:ASN:HD21	1.81	0.45
1:B:120:LYS:NZ	5:B:303[A]:HOH:O	2.43	0.44
1:B:143:LYS:HE2	1:B:160:ASP:OD2	2.18	0.43
1:B:113:VAL:HG12	1:B:166:ILE:HG12	2.00	0.43
1:D:190[A]:MET:HA	1:D:193:ILE:HG12	2.02	0.41
1:A:45:LYS:HD2	1:A:58:GLU:OE1	2.21	0.40

All (1) 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)
5:D:362:HOH:O	5:D:365:HOH:O[2_556]	2.05	0.15

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	A	98/99 (99%)	96 (98%)	2 (2%)	0	100	100
1	B	102/99 (103%)	101 (99%)	1 (1%)	0	100	100
1	C	104/99 (105%)	101 (97%)	3 (3%)	0	100	100
1	D	105/99 (106%)	103 (98%)	2 (2%)	0	100	100
All	All	409/396 (103%)	401 (98%)	8 (2%)	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	A	83/82 (101%)	83 (100%)	0	100	100
1	B	87/82 (106%)	86 (99%)	1 (1%)	65	38
1	C	89/82 (108%)	86 (97%)	3 (3%)	32	5
1	D	89/82 (108%)	86 (97%)	3 (3%)	32	5
All	All	348/328 (106%)	341 (98%)	7 (2%)	51	16

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	150	ILE
1	C	34[A]	GLU
1	C	34[B]	GLU
1	C	55	LYS
1	D	115	VAL
1	D	155	LYS
1	D	198	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	92	GLN
1	B	137	ASN
1	B	161	GLN
1	C	2	GLN
1	D	198	ASN

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 oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 15 ligands modelled in this entry, 13 are monoatomic - leaving 2 for Mogul analysis.

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	B	206	-	5,5,5	0.51	0	5,5,5	1.99	3 (60%)
4	GOL	D	204	-	5,5,5	0.72	0	5,5,5	1.62	2 (40%)

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	B	206	-	-	4/4/4/4	-
4	GOL	D	204	-	-	4/4/4/4	-

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	206	GOL	C3-C2-C1	-3.20	100.08	111.80
4	B	206	GOL	O2-C2-C1	2.24	118.46	109.18
4	D	204	GOL	O2-C2-C1	2.24	118.43	109.18
4	D	204	GOL	C3-C2-C1	2.11	119.52	111.80
4	B	206	GOL	O2-C2-C3	-2.01	100.87	109.18

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	B	206	GOL	C1-C2-C3-O3
4	D	204	GOL	O1-C1-C2-C3
4	D	204	GOL	C1-C2-C3-O3
4	D	204	GOL	O2-C2-C3-O3
4	B	206	GOL	O1-C1-C2-C3
4	B	206	GOL	O2-C2-C3-O3
4	B	206	GOL	O1-C1-C2-O2
4	D	204	GOL	O1-C1-C2-O2

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	D	204	GOL	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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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, 95th 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 ²)	Q<0.9
1	A	99/99 (100%)	-0.79	0 100 100	8, 14, 24, 28	1 (1%)
1	B	99/99 (100%)	-0.63	1 (1%) 79 83	9, 14, 29, 44	5 (5%)
1	C	99/99 (100%)	-0.56	2 (2%) 65 67	6, 15, 32, 44	7 (7%)
1	D	99/99 (100%)	-0.57	1 (1%) 79 83	7, 15, 29, 36	8 (8%)
All	All	396/396 (100%)	-0.64	4 (1%) 79 83	6, 15, 27, 44	21 (5%)

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	150	ILE	4.8
1	D	151[A]	GLY	2.8
1	C	53	PHE	2.7
1	C	51	GLY	2.1

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 oligosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	GOL	B	206	6/6	0.80	0.10	33,36,38,40	0
4	GOL	D	204	6/6	0.91	0.09	23,28,30,31	0
3	NA	B	205	1/1	0.96	0.22	33,33,33,33	1
3	NA	B	204	1/1	0.97	0.05	23,23,23,23	1
3	NA	C	104	1/1	0.97	0.04	24,24,24,24	1
3	NA	D	203	1/1	0.98	0.06	24,24,24,24	1
2	CL	C	103	1/1	0.98	0.09	29,29,29,29	0
2	CL	C	101	1/1	0.98	0.12	28,28,28,28	0
2	CL	C	102	1/1	0.99	0.04	20,20,20,20	0
2	CL	B	203	1/1	0.99	0.07	30,30,30,30	0
2	CL	D	202	1/1	0.99	0.04	32,32,32,32	0
2	CL	D	201	1/1	1.00	0.01	14,14,14,14	0
2	CL	B	201	1/1	1.00	0.06	19,19,19,19	0
2	CL	B	202	1/1	1.00	0.04	11,11,11,11	0
2	CL	A	101	1/1	1.00	0.01	10,10,10,10	0

6.5 Other polymers [i](#)

There are no such residues in this entry.