



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 07:59 AM UTC

PDB ID : 3ECP / pdb_00003ecp
Title : Crystal Structure Of Tn5 Transposase Complexed With 5' Phosphorylated Transposon End DNA
Authors : Klenchin, V.A.
Deposited on : 2008-09-01
Resolution : 2.50 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

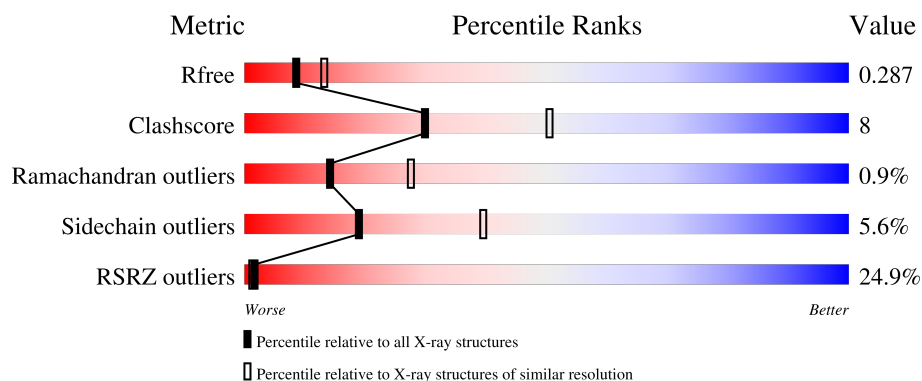
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

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 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	477	25% 75% 19% ••
2	B	20	5% 80% 15% 5%
3	C	20	25% 50% 40% 10%

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	A	502	-	-	X	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 4572 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 Tn5 transposase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	458	Total	C	N	O	S	0	3	0
			3616	2276	660	667	13			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	54	LYS	GLU	engineered mutation	UNP Q08JA5
A	56	ALA	MET	engineered mutation	UNP Q08JA5
A	372	PRO	LEU	engineered mutation	UNP Q08JA5
A	477	GLY	-	cloning artifact	UNP Q08JA5

- Molecule 2 is a DNA chain called DNA transferred strand.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	20	Total	C	N	O	P	0	0	0
			413	198	78	118	19			

- Molecule 3 is a DNA chain called DNA non-transferred strand.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	20	Total	C	N	O	P	0	0	0
			405	194	70	121	20			

- Molecule 4 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



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

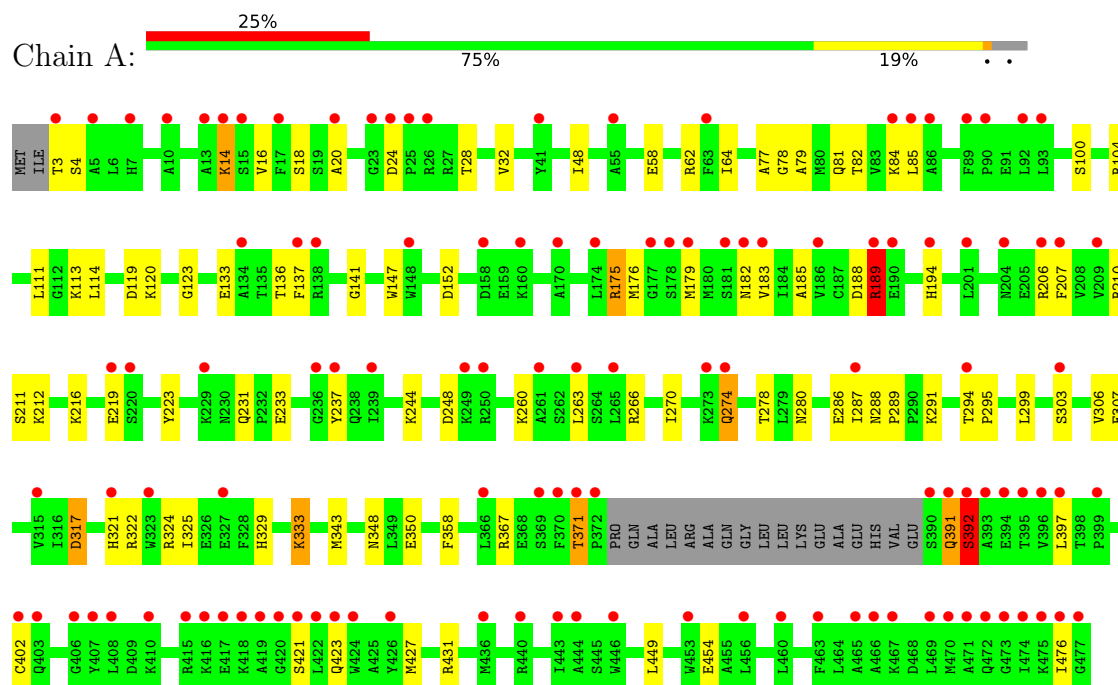
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	100	Total	O	0	0
			100	100		
5	B	9	Total	O	0	0
			9	9		
5	C	11	Total	O	0	0
			11	11		

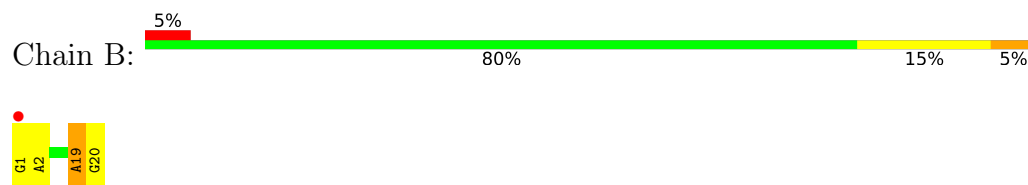
3 Residue-property plots

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.

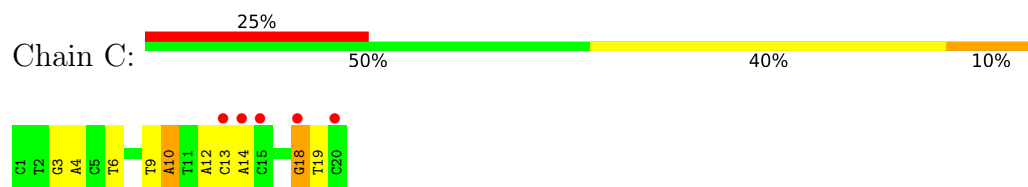
• Molecule 1: Tn5 transposase



• Molecule 2: DNA transferred strand



• Molecule 3: DNA non-transferred strand



4 Data and refinement statistics

Property	Value	Source
Space group	P 65 2 2	Depositor
Cell constants a, b, c, α , β , γ	113.51Å 113.51Å 228.78Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	30.00 – 2.50 30.00 – 2.50	Depositor EDS
% Data completeness (in resolution range)	99.8 (30.00-2.50) 99.6 (30.00-2.50)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	7.41 (at 2.51Å)	Xtriage
Refinement program	REFMAC 5.2	Depositor
R, R_{free}	0.219 , 0.274 0.243 , 0.287	Depositor DCC
R_{free} test set	1556 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	55.7	Xtriage
Anisotropy	0.187	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 67.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	4572	wwPDB-VP
Average B, all atoms (Å ²)	72.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.57% of the height of the origin peak. No significant pseudotranslation is detected.*

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

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	A	0.68	0/3696	0.92	4/4983 (0.1%)
2	B	0.46	0/464	1.31	4/716 (0.6%)
3	C	0.53	0/452	1.29	2/692 (0.3%)
All	All	0.64	0/4612	1.02	10/6391 (0.2%)

There are no bond length outliers.

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	19	DA	C4'-C3'-O3'	9.04	123.55	110.00
2	B	19	DA	O3'-P-O5'	6.36	113.55	104.00
2	B	19	DA	O4'-C1'-N9	6.20	117.70	108.40
1	A	189	ARG	N-CA-C	6.00	118.61	111.71
3	C	18	DG	P-O5'-C5'	-5.75	111.38	120.00
3	C	10	DA	O5'-C5'-C4'	-5.42	102.66	110.80
2	B	19	DA	C5'-C4'-O4'	-5.27	101.49	109.40
1	A	371	THR	N-CA-C	5.21	119.33	112.35
1	A	392	SER	N-CA-C	5.14	118.49	110.32
1	A	141	GLY	N-CA-C	5.03	118.12	110.97

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3616	0	3658	62	0
2	B	413	0	228	6	0
3	C	405	0	227	8	0
4	A	18	0	24	5	0
5	A	100	0	0	1	0
5	B	9	0	0	0	0
5	C	11	0	0	1	0
All	All	4572	0	4137	73	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 8.

All (73) 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:A:3:THR:HG23	1:A:4:SER:H	1.23	1.04
1:A:120:LYS:H	4:A:502:GOL:H32	1.34	0.91
2:B:19:DA:H4'	2:B:20:DG:OP1	1.74	0.87
1:A:104:ARG:HH12	4:A:502:GOL:H31	1.45	0.80
1:A:175:ARG:CG	1:A:175:ARG:HH11	2.01	0.74
1:A:3:THR:HG23	1:A:4:SER:N	2.03	0.71
1:A:3:THR:CG2	1:A:4:SER:H	2.02	0.70
1:A:289:PRO:HG3	1:A:295:PRO:HB3	1.73	0.69
1:A:317:ASP:O	1:A:321:HIS:HD2	1.74	0.69
1:A:81:GLN:NE2	1:A:81:GLN:HA	2.10	0.65
3:C:6:DT:OP2	5:C:724:HOH:O	2.14	0.64
2:B:19:DA:C4'	2:B:20:DG:OP1	2.40	0.62
1:A:175:ARG:HH11	1:A:175:ARG:HG3	1.64	0.61
1:A:104:ARG:NH1	4:A:502:GOL:H31	2.16	0.61
3:C:9:DT:H2''	3:C:10:DA:H5''	1.83	0.60
1:A:397:LEU:HB2	1:A:402[A]:CYS:SG	2.42	0.59
1:A:194:HIS:CD2	1:A:274:GLN:HB2	2.38	0.59
1:A:120:LYS:N	4:A:502:GOL:H32	2.12	0.58
1:A:58:GLU:O	1:A:62:ARG:HG3	2.06	0.56
1:A:333:LYS:HB2	2:B:19:DA:OP1	2.06	0.55
1:A:64:ILE:O	1:A:348:ASN:HA	2.07	0.54
1:A:111:LEU:HD13	1:A:123:GLY:HA2	1.90	0.54
1:A:133:GLU:O	1:A:137:PHE:HA	2.08	0.53
1:A:119:ASP:HA	4:A:502:GOL:H11	1.89	0.53
1:A:179:MET:O	1:A:182:ASN:HB2	2.09	0.53
1:A:280:ASN:HB3	1:A:306:VAL:HG21	1.90	0.53
1:A:14:LYS:O	1:A:18:SER:OG	2.27	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:81:GLN:HA	1:A:81:GLN:HE21	1.74	0.52
1:A:427:MET:HB3	1:A:431:ARG:NH1	2.25	0.51
1:A:237:TYR:CE2	1:A:263:LEU:HD12	2.45	0.51
1:A:211:SER:HB3	1:A:299:LEU:HB3	1.93	0.51
1:A:263:LEU:HD23	1:A:286:GLU:HA	1.92	0.51
3:C:3:DG:H2''	3:C:4:DA:H5'	1.92	0.50
1:A:133:GLU:OE1	1:A:136:THR:OG1	2.26	0.50
1:A:81:GLN:HE22	1:A:84:LYS:HD3	1.77	0.50
1:A:367:ARG:HG3	1:A:449:LEU:HG	1.95	0.49
1:A:427:MET:HB3	1:A:431:ARG:HH12	1.78	0.48
1:A:188:ASP:HB2	5:A:686:HOH:O	2.13	0.48
1:A:194:HIS:NE2	1:A:274:GLN:HB2	2.29	0.48
1:A:137:PHE:O	1:A:324:ARG:NH2	2.40	0.47
1:A:28:THR:O	1:A:32:VAL:HG23	2.14	0.47
1:A:392:SER:HA	1:A:421:SER:HA	1.95	0.47
3:C:12:DA:H2''	3:C:13:DC:H5''	1.96	0.47
1:A:206:ARG:HA	1:A:303:SER:OG	2.15	0.47
1:A:189:ARG:HD2	1:A:210:ARG:HD3	1.97	0.47
1:A:113:LYS:HD3	1:A:152:ASP:HA	1.97	0.45
1:A:147:TRP:CZ3	1:A:350:GLU:HG3	2.51	0.45
1:A:79:ALA:O	1:A:82:THR:HB	2.16	0.45
1:A:189:ARG:HG2	1:A:212:LYS:HB2	1.98	0.45
1:A:244:LYS:NZ	3:C:3:DG:N7	2.58	0.45
1:A:367:ARG:O	1:A:371:THR:HG23	2.18	0.44
1:A:237:TYR:CZ	1:A:263:LEU:HD12	2.54	0.43
1:A:78:GLY:HA3	1:A:358:PHE:CZ	2.53	0.43
1:A:185:ALA:O	1:A:207:PHE:HA	2.19	0.43
2:B:1:DG:H2''	2:B:2:DA:C8	2.53	0.43
2:B:19:DA:H2''	2:B:20:DG:C8	2.54	0.43
3:C:18:DG:H2'	3:C:19:DT:C6	2.54	0.43
1:A:176:MET:HE2	1:A:183:VAL:CG2	2.49	0.43
1:A:329:HIS:ND1	2:B:20:DG:OP2	2.42	0.43
3:C:13:DC:H2'	3:C:14:DA:C8	2.55	0.42
3:C:12:DA:H2''	3:C:13:DC:C5'	2.50	0.42
1:A:175:ARG:HH11	1:A:175:ARG:HG2	1.82	0.42
1:A:231:GLN:O	1:A:266:ARG:NH1	2.54	0.41
1:A:391:GLN:HE21	1:A:392:SER:N	2.17	0.41
1:A:189:ARG:HD2	1:A:210:ARG:CD	2.51	0.41
1:A:20:ALA:HA	1:A:77:ALA:HB2	2.03	0.41
1:A:16:VAL:HA	1:A:81:GLN:HG2	2.03	0.41
1:A:391:GLN:HB2	1:A:392:SER:H	1.68	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:100:SER:HB2	1:A:114:LEU:HD22	2.02	0.40
1:A:322:ARG:O	1:A:325:ILE:HG22	2.21	0.40
1:A:3:THR:CG2	1:A:4:SER:N	2.72	0.40
1:A:216:LYS:HG3	1:A:223:TYR:CD2	2.56	0.40
1:A:248:ASP:OD1	1:A:248:ASP:C	2.65	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	457/477 (96%)	434 (95%)	19 (4%)	4 (1%)	14 27

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	233	GLU
1	A	291	LYS
1	A	333	LYS
1	A	24	ASP

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	377/389 (97%)	356 (94%)	21 (6%)	19	39

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	14	LYS
1	A	48	ILE
1	A	85	LEU
1	A	175	ARG
1	A	189	ARG
1	A	219	GLU
1	A	260	LYS
1	A	270	ILE
1	A	274	GLN
1	A	278	THR
1	A	287	ILE
1	A	288	ASN
1	A	294	THR
1	A	307	GLU
1	A	317	ASP
1	A	343	MET
1	A	391	GLN
1	A	392	SER
1	A	423	GLN
1	A	454	GLU
1	A	476	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	7	HIS
1	A	81	GLN
1	A	182	ASN
1	A	198	GLN
1	A	238	GLN
1	A	288	ASN
1	A	321	HIS
1	A	341	GLN
1	A	391	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

3 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	A	502	-	5,5,5	0.46	0	5,5,5	0.90	0
4	GOL	A	501	-	5,5,5	0.44	0	5,5,5	0.70	0
4	GOL	A	503	-	5,5,5	0.27	0	5,5,5	0.74	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
4	GOL	A	502	-	-	2/4/4/4	-
4	GOL	A	501	-	-	2/4/4/4	-
4	GOL	A	503	-	-	2/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	501	GOL	O1-C1-C2-C3
4	A	502	GOL	C1-C2-C3-O3
4	A	502	GOL	O2-C2-C3-O3
4	A	503	GOL	C1-C2-C3-O3
4	A	501	GOL	O1-C1-C2-O2
4	A	503	GOL	O2-C2-C3-O3

There are no ring outliers.

1 monomer is involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	502	GOL	5	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

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	458/477 (96%)	1.43	118 (25%) 1 1	22, 68, 100, 142	27 (5%)
2	B	20/20 (100%)	0.87	1 (5%) 34 30	49, 74, 140, 148	0
3	C	20/20 (100%)	1.01	5 (25%) 2 1	52, 72, 111, 133	0
All	All	498/517 (96%)	1.39	124 (24%) 2 1	22, 68, 103, 148	27 (5%)

All (124) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	250	ARG	4.9
1	A	273	LYS	4.9
1	A	390	SER	4.5
1	A	418	LYS	4.3
1	A	474	ILE	4.3
1	A	410	LYS	4.2
1	A	372	PRO	4.1
1	A	403	GLN	4.1
1	A	249	LYS	4.0
1	A	463	PHE	3.9
1	A	470	MET	3.9
1	A	263	LEU	3.8
1	A	466	ALA	3.8
1	A	138	ARG	3.8
1	A	236	GLY	3.8
1	A	408	LEU	3.7
1	A	416	LYS	3.7
1	A	237	TYR	3.7
1	A	3	THR	3.6
1	A	219	GLU	3.6
1	A	440	ARG	3.5
1	A	26	ARG	3.5
1	A	239	ILE	3.4

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Mol	Chain	Res	Type	RSRZ
1	A	424	TRP	3.3
1	A	321	HIS	3.3
1	A	160	LYS	3.3
1	A	24	ASP	3.3
1	A	287	ILE	3.2
1	A	158	ASP	3.2
1	A	476	ILE	3.2
1	A	469	LEU	3.2
1	A	370	PHE	3.1
1	A	426	TYR	3.1
1	A	86	ALA	3.1
1	A	415	ARG	3.1
1	A	84	LYS	3.1
1	A	178[A]	SER	3.1
1	A	323	TRP	3.0
1	A	477	GLY	3.0
1	A	396	VAL	3.0
1	A	443	ILE	3.0
1	A	436	MET	3.0
1	A	420	GLY	3.0
1	A	170	ALA	3.0
1	A	423	GLN	3.0
1	A	460	LEU	2.9
1	A	89	PHE	2.9
1	A	137	PHE	2.9
1	A	183	VAL	2.9
1	A	90	PRO	2.9
1	A	393	ALA	2.8
1	A	179	MET	2.8
1	A	366	LEU	2.8
1	A	391	GLN	2.8
1	A	194	HIS	2.8
1	A	394	GLU	2.7
1	A	419	ALA	2.7
1	A	261	ALA	2.7
1	A	85	LEU	2.6
1	A	453	TRP	2.6
1	A	392	SER	2.6
1	A	371	THR	2.6
1	A	407	TYR	2.6
1	A	20	ALA	2.6
3	C	18	DG	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	397	LEU	2.5
1	A	92	LEU	2.5
1	A	204	ASN	2.5
1	A	265	LEU	2.4
1	A	315	VAL	2.4
1	A	399	PRO	2.4
1	A	23	GLY	2.4
1	A	406	GLY	2.4
1	A	395	THR	2.4
1	A	421	SER	2.4
1	A	174	LEU	2.4
1	A	5	ALA	2.4
1	A	369	SER	2.3
1	A	472	GLN	2.3
2	B	1	DG	2.3
1	A	220	SER	2.3
3	C	14	DA	2.3
1	A	186	VAL	2.3
1	A	456	LEU	2.3
1	A	13	ALA	2.3
1	A	55	ALA	2.3
1	A	134	ALA	2.3
1	A	473	GLY	2.3
1	A	15	SER	2.3
1	A	181	SER	2.3
1	A	303	SER	2.3
1	A	471	ALA	2.2
1	A	201	LEU	2.2
1	A	209	VAL	2.2
1	A	10	ALA	2.2
1	A	7	HIS	2.2
1	A	189	ARG	2.2
1	A	17	PHE	2.2
1	A	444	ALA	2.2
1	A	25	PRO	2.2
1	A	402[A]	CYS	2.2
1	A	190[A]	GLU	2.2
1	A	446	TRP	2.2
3	C	13	DC	2.1
3	C	15	DC	2.1
3	C	20	DC	2.1
1	A	41	TYR	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	93	LEU	2.1
1	A	177	GLY	2.1
1	A	422	LEU	2.1
1	A	327	GLU	2.1
1	A	229	LYS	2.1
1	A	207	PHE	2.1
1	A	148	TRP	2.1
1	A	63	PHE	2.1
1	A	274	GLN	2.1
1	A	294	THR	2.1
1	A	467	LYS	2.1
1	A	475	LYS	2.1
1	A	417	GLU	2.0
1	A	14	LYS	2.0
1	A	206	ARG	2.0
1	A	465	ALA	2.0
1	A	182	ASN	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 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	A	501	6/6	0.73	0.19	77,83,84,84	0
4	GOL	A	502	6/6	0.84	0.14	76,77,79,82	0
4	GOL	A	503	6/6	0.87	0.18	68,69,74,77	0

6.5 Other polymers [i](#)

There are no such residues in this entry.