



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 07:44 AM UTC

PDB ID : 2O5C / pdb_00002o5c
Title : Structure of E. coli topoisomerase III in complex with an 8-base single stranded oligonucleotide. Frozen in glucose pH 5.5
Authors : Changela, A.; DiGate, R.J.; Mondragon, A.
Deposited on : 2006-12-05
Resolution : 2.35 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

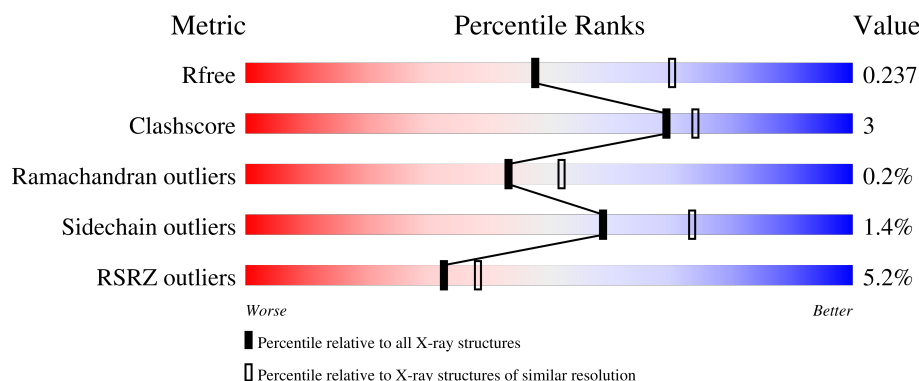
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.35 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	1596 (2.36-2.36)
Clashscore	190562	1663 (2.36-2.36)
Ramachandran outliers	187476	1646 (2.36-2.36)
Sidechain outliers	187428	1646 (2.36-2.36)
RSRZ outliers	180081	1598 (2.36-2.36)

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	C	8	
1	D	8	
2	A	659	
2	B	659	

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
3	TDR	D	799	-	X	-	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 10705 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 DNA chain called 5'-D(*CP*GP*CP*AP*AP*CP*TP*T)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	C	7	Total	C	N	O	P	0	0	0
			138	67	26	39	6			
1	D	7	Total	C	N	O	P	0	0	0
			138	67	26	39	6			

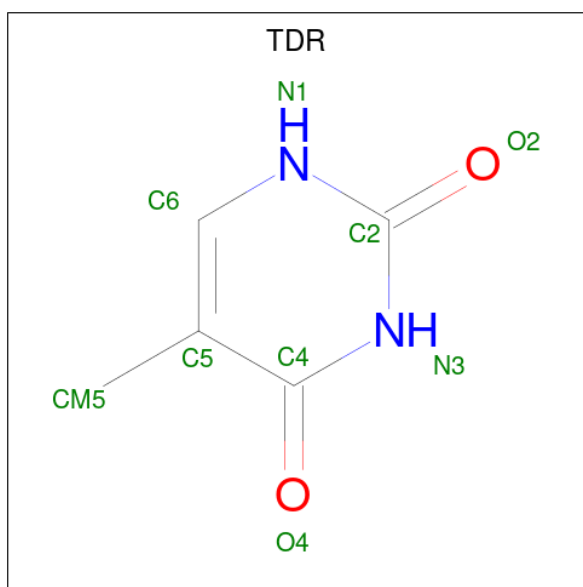
- Molecule 2 is a protein called DNA topoisomerase 3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	A	634	Total	C	N	O	S	0	0	0
			5042	3184	918	920	20			
2	B	631	Total	C	N	O	S	0	0	0
			5020	3170	913	917	20			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	654	HIS	-	expression tag	UNP P14294
A	655	HIS	-	expression tag	UNP P14294
A	656	HIS	-	expression tag	UNP P14294
A	657	HIS	-	expression tag	UNP P14294
A	658	HIS	-	expression tag	UNP P14294
A	659	HIS	-	expression tag	UNP P14294
B	654	HIS	-	expression tag	UNP P14294
B	655	HIS	-	expression tag	UNP P14294
B	656	HIS	-	expression tag	UNP P14294
B	657	HIS	-	expression tag	UNP P14294
B	658	HIS	-	expression tag	UNP P14294
B	659	HIS	-	expression tag	UNP P14294

- Molecule 3 is THYMINE (CCD ID: TDR) (formula: C₅H₆N₂O₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	D	1	Total	C	N	O	0	0
			9	5	2	2		

- Molecule 4 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	2	Total	Cl	0	0
			2	2		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	C	13	Total	O	0	0
			13	13		
5	D	9	Total	O	0	0
			9	9		
5	A	176	Total	O	0	0
			176	176		
5	B	158	Total	O	0	0
			158	158		

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: 5'-D(*CP*GP*CP*AP*AP*CP*TP*T)-3'

Chain C: 

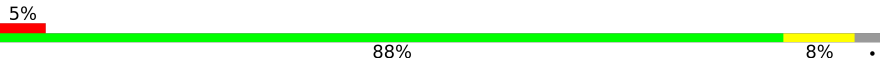


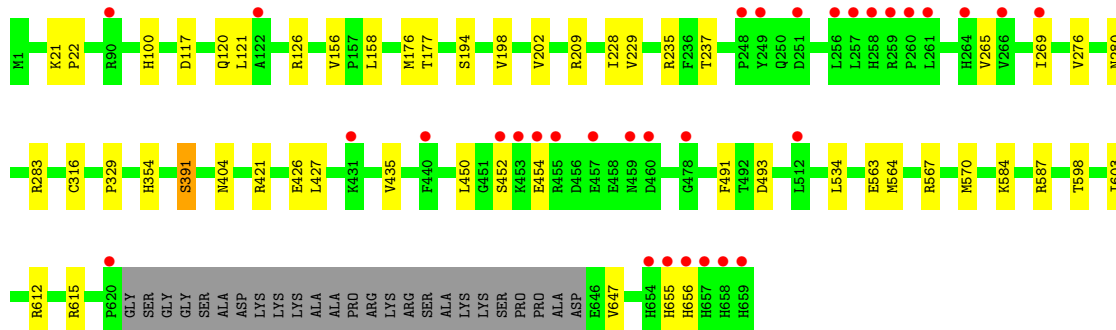
- Molecule 1: 5'-D(*CP*GP*CP*AP*AP*CP*TP*T)-3'

Chain D: 



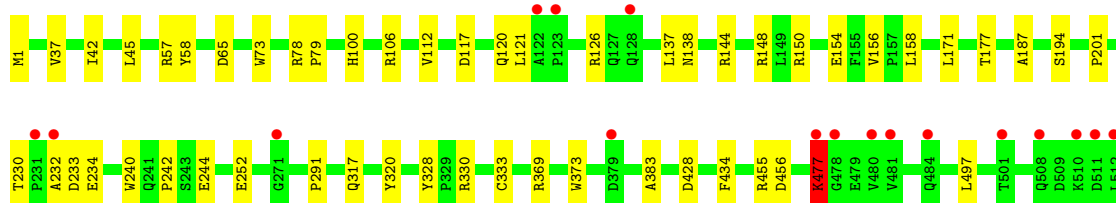
- Molecule 2: DNA topoisomerase 3

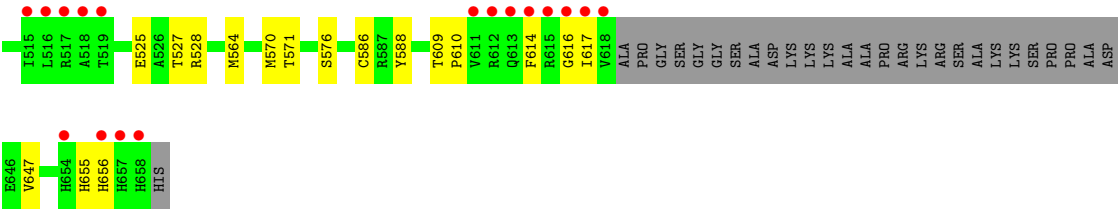
Chain A: 



- Molecule 2: DNA topoisomerase 3

Chain B: 





4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	102.21 Å 102.21 Å 443.75 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.15 – 2.35 29.15 – 2.35	Depositor EDS
% Data completeness (in resolution range)	95.6 (29.15-2.35) 95.6 (29.15-2.35)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	0.05	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.14 (at 2.36 Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.207 , 0.245 0.201 , 0.237	Depositor DCC
R_{free} test set	4758 reflections (4.79%)	wwPDB-VP
Wilson B-factor (Å ²)	44.3	Xtriage
Anisotropy	0.252	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 37.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.43$, $\langle L^2 \rangle = 0.26$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	10705	wwPDB-VP
Average B, all atoms (Å ²)	52.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.92% 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: TDR, 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	C	0.47	0/154	1.12	0/235
1	D	0.42	0/154	1.05	0/235
2	A	0.58	1/5154 (0.0%)	0.83	0/6989
2	B	0.59	2/5130 (0.0%)	0.86	2/6955 (0.0%)
All	All	0.58	3/10592 (0.0%)	0.86	2/14414 (0.0%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	477	LYS	CE-NZ	8.95	1.76	1.49
2	B	156	VAL	CA-CB	6.39	1.57	1.54
2	A	156	VAL	CA-CB	5.28	1.56	1.54

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	138	ASN	CA-C-N	5.28	124.73	119.24
2	B	138	ASN	C-N-CA	5.28	124.73	119.24

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	C	138	0	80	1	0
1	D	138	0	80	2	0
2	A	5042	0	5042	31	0
2	B	5020	0	5023	38	0
3	D	9	0	6	0	0
4	A	2	0	0	0	0
5	A	176	0	0	2	0
5	B	158	0	0	0	0
5	C	13	0	0	1	0
5	D	9	0	0	0	0
All	All	10705	0	10231	71	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 3.

All (71) 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:B:477:LYS:CE	2:B:477:LYS:NZ	1.76	1.47
2:A:176:MET:CE	2:A:603:ILE:HD13	2.16	0.76
2:A:121:LEU:HD21	2:A:126:ARG:HD3	1.68	0.74
2:B:477:LYS:NZ	2:B:477:LYS:CD	2.53	0.72
2:B:564:MET:HE2	2:B:570:MET:SD	2.30	0.72
2:A:117:ASP:HB3	2:A:647:VAL:HG13	1.72	0.71
2:B:230:THR:HG22	2:B:232:ALA:H	1.58	0.68
2:B:588:TYR:HB3	2:B:656:HIS:HE1	1.59	0.66
2:B:201:PRO:HG2	2:B:571:THR:HG21	1.80	0.63
2:A:209:ARG:HG3	2:A:491:PHE:CE2	2.34	0.62
2:A:283:ARG:HG3	2:A:421:ARG:HE	1.65	0.62
2:B:588:TYR:HB3	2:B:656:HIS:CE1	2.36	0.61
2:B:586:CYS:O	2:B:655:HIS:HE1	1.86	0.58
2:B:106:ARG:HG3	2:B:158:LEU:HG	1.86	0.57
2:B:317:GLN:HE22	2:B:330:ARG:HH11	1.54	0.55
2:A:584:LYS:HA	2:A:655:HIS:HE1	1.73	0.54
2:A:176:MET:HE3	2:A:603:ILE:CD1	2.38	0.52
2:B:117:ASP:HB3	2:B:647:VAL:HG13	1.91	0.52
2:B:144:ARG:O	2:B:148:ARG:HG2	2.08	0.52
2:A:176:MET:CE	2:A:603:ILE:CD1	2.87	0.51
2:B:252:GLU:CD	2:B:252:GLU:H	2.19	0.51
2:A:450:LEU:HB3	2:A:454:GLU:HG3	1.93	0.50
2:A:656:HIS:CD2	5:A:863:HOH:O	2.63	0.50
2:B:42:ILE:H	2:B:45:LEU:HD21	1.76	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:73:TRP:HH2	2:B:171:LEU:HG	1.77	0.50
2:B:1:MET:HE1	2:B:37:VAL:HB	1.93	0.50
2:B:240:TRP:HB2	2:B:434:PHE:CE2	2.46	0.50
2:B:100:HIS:CE1	2:B:112:VAL:HB	2.46	0.49
2:B:230:THR:HB	2:B:234:GLU:HB2	1.95	0.49
2:A:176:MET:HA	2:A:176:MET:HE2	1.95	0.49
2:B:137:LEU:HD13	2:B:320:TYR:CZ	2.47	0.49
2:B:525:GLU:HG2	2:B:528:ARG:NH1	2.27	0.49
2:B:317:GLN:NE2	2:B:330:ARG:HH11	2.10	0.49
5:C:10:HOH:O	2:A:534:LEU:HD13	2.13	0.49
2:A:229:VAL:HG21	2:A:235:ARG:HH21	1.77	0.49
2:B:177:THR:HG23	2:B:194:SER:HA	1.94	0.48
2:A:354:HIS:HE1	2:A:391:SER:O	1.96	0.47
2:A:587:ARG:HD2	5:A:871:HOH:O	2.15	0.47
2:B:333:CYS:O	2:B:383:ALA:HA	2.13	0.47
2:A:587:ARG:HD2	2:A:656:HIS:CD2	2.48	0.47
2:B:328:TYR:CZ	2:B:330:ARG:HB2	2.50	0.47
2:A:176:MET:HE3	2:A:603:ILE:HD13	1.94	0.46
2:A:177:THR:HG23	2:A:194:SER:HA	1.98	0.46
2:B:455:ARG:NH1	2:B:456:ASP:OD1	2.49	0.46
2:B:240:TRP:O	2:B:242:PRO:HD3	2.18	0.44
2:B:57:ARG:NH1	2:B:65:ASP:OD1	2.51	0.44
2:B:187:ALA:CB	2:B:614:PHE:HB2	2.47	0.44
1:D:5:DA:C6	1:D:7:DT:H1'	2.52	0.43
2:B:121:LEU:HD23	2:B:126:ARG:HG2	2.00	0.43
2:A:316:CYS:HB3	2:A:329:PRO:CB	2.48	0.43
2:A:426:GLU:HG2	2:A:435:VAL:HG22	2.00	0.43
2:A:612:ARG:HA	2:A:615:ARG:HE	1.83	0.43
2:A:570:MET:SD	2:A:598:THR:HG21	2.58	0.43
2:B:588:TYR:H	2:B:656:HIS:HE1	1.67	0.43
1:C:1:DC:H2''	1:C:2:DG:H5'	2.00	0.42
2:A:563:GLU:HG2	2:A:567:ARG:HG2	2.02	0.42
2:B:291:PRO:HB2	2:B:383:ALA:HB1	2.02	0.42
2:A:265:VAL:O	2:A:269:ILE:HG12	2.19	0.42
2:B:150:ARG:HD2	2:B:154:GLU:OE1	2.20	0.42
2:B:369:ARG:HG3	2:B:373:TRP:CD1	2.55	0.42
1:D:5:DA:C2'	2:B:527:THR:HG21	2.50	0.41
2:B:78:ARG:HA	2:B:79:PRO:HD3	1.90	0.41
2:B:609:THR:HA	2:B:610:PRO:HD3	1.88	0.41
2:A:21:LYS:HB3	2:A:22:PRO:HA	2.02	0.41
2:A:121:LEU:H	2:A:121:LEU:HD23	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:587:ARG:HB3	2:A:656:HIS:CD2	2.55	0.41
2:B:57:ARG:NH1	2:B:58:TYR:HE1	2.18	0.41
2:A:198:VAL:O	2:A:202:VAL:HG23	2.21	0.41
2:A:276:VAL:HA	2:A:427:LEU:HD23	2.03	0.41
2:A:228:ILE:HD13	2:A:427:LEU:HD13	2.04	0.40
2:A:564:MET:HE2	2:A:570:MET:SD	2.61	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	
2	A	630/659 (96%)	618 (98%)	10 (2%)	2 (0%)	36	43
2	B	627/659 (95%)	614 (98%)	12 (2%)	1 (0%)	43	52
All	All	1257/1318 (95%)	1232 (98%)	22 (2%)	3 (0%)	43	52

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	A	452	SER
2	A	120	GLN
2	B	616	GLY

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	
2	A	538/555 (97%)	531 (99%)	7 (1%)	61	76
2	B	536/555 (97%)	528 (98%)	8 (2%)	57	72
All	All	1074/1110 (97%)	1059 (99%)	15 (1%)	59	73

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	A	100	HIS
2	A	158	LEU
2	A	237	THR
2	A	280	ASN
2	A	391	SER
2	A	404	ASN
2	A	493	ASP
2	B	120	GLN
2	B	233	ASP
2	B	244	GLU
2	B	428	ASP
2	B	477	LYS
2	B	497	LEU
2	B	576	SER
2	B	617	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
2	A	227	HIS
2	A	580	GLN
2	A	593	GLN
2	A	655	HIS
2	B	48	GLN
2	B	317	GLN
2	B	345	HIS
2	B	580	GLN
2	B	655	HIS
2	B	656	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 2 are monoatomic - leaving 1 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	$\# Z > 2$
3	TDR	D	799	-	9,9,9	1.94	3 (33%)	12,12,12	3.11	8 (66%)

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
3	TDR	D	799	-	-	-	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	799	TDR	C6-C5	3.71	1.39	1.34
3	D	799	TDR	C4-C5	3.03	1.49	1.44
3	D	799	TDR	C4-N3	-2.16	1.34	1.38

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	799	TDR	N1-C2-N3	6.27	121.79	115.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	799	TDR	C4-N3-C2	-3.94	120.94	126.37
3	D	799	TDR	O2-C2-N1	-3.60	119.07	122.79
3	D	799	TDR	CM5-C5-C4	3.27	122.27	118.78
3	D	799	TDR	C5-C4-N3	3.20	118.10	115.32
3	D	799	TDR	CM5-C5-C6	-3.09	120.05	123.23
3	D	799	TDR	C5-C6-N1	-2.73	119.47	122.42
3	D	799	TDR	O4-C4-C5	-2.68	121.85	124.92

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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	C	7/8 (87%)	-0.94	0 100 100	26, 28, 38, 51	0
1	D	7/8 (87%)	-0.39	0 100 100	29, 34, 46, 62	0
2	A	634/659 (96%)	0.12	32 (5%) 34 40	26, 43, 95, 139	0
2	B	631/659 (95%)	0.18	34 (5%) 31 37	27, 49, 95, 140	0
All	All	1279/1334 (95%)	0.14	66 (5%) 33 38	26, 46, 95, 140	0

All (66) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	618	VAL	7.9
2	A	656	HIS	7.0
2	B	657	HIS	6.0
2	B	611	VAL	5.9
2	B	617	ILE	5.3
2	B	656	HIS	5.2
2	B	614	PHE	5.0
2	A	657	HIS	4.8
2	B	658	HIS	4.6
2	A	658	HIS	4.3
2	A	258	HIS	4.2
2	B	518	ALA	4.1
2	A	257	LEU	3.7
2	B	231	PRO	3.7
2	B	616	GLY	3.6
2	A	659	HIS	3.6
2	B	508	GLN	3.6
2	A	655	HIS	3.6
2	A	260	PRO	3.6
2	A	455	ARG	3.5
2	B	123	PRO	3.4

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Mol	Chain	Res	Type	RSRZ
2	A	249	TYR	3.3
2	B	512	LEU	3.2
2	B	654	HIS	3.2
2	B	519	THR	3.2
2	A	122	ALA	3.1
2	B	510	LYS	3.1
2	A	264	HIS	3.1
2	B	515	ILE	3.0
2	B	379	ASP	3.0
2	B	516	LEU	2.9
2	B	478	GLY	2.9
2	A	454	GLU	2.9
2	A	259	ARG	2.8
2	A	452	SER	2.8
2	B	480	VAL	2.8
2	B	232	ALA	2.7
2	A	256	LEU	2.7
2	A	478	GLY	2.7
2	A	261	LEU	2.7
2	A	453	LYS	2.6
2	A	90	ARG	2.6
2	B	613	GLN	2.5
2	A	460	ASP	2.5
2	B	481	VAL	2.5
2	B	271	GLY	2.5
2	A	266	VAL	2.4
2	B	477	LYS	2.3
2	B	484	GLN	2.3
2	A	440	PHE	2.3
2	A	251	ASP	2.3
2	A	512	LEU	2.2
2	A	431	LYS	2.2
2	B	517	ARG	2.2
2	A	654	HIS	2.2
2	A	269	ILE	2.2
2	B	501	THR	2.2
2	B	511	ASP	2.1
2	B	122	ALA	2.1
2	A	457	GLU	2.1
2	B	128	GLN	2.1
2	A	459	ASN	2.0
2	A	248	PRO	2.0

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Mol	Chain	Res	Type	RSRZ
2	A	620	PRO	2.0
2	B	612	ARG	2.0
2	B	615	ARG	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(Å ²)	Q<0.9
3	TDR	D	799	9/9	0.68	0.29	107,107,107,107	0
4	CL	A	800	1/1	0.96	0.06	34,34,34,34	0
4	CL	A	801	1/1	0.98	0.06	40,40,40,40	0

6.5 Other polymers [i](#)

There are no such residues in this entry.