



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 04:46 AM GMT

PDB ID : 2O59
Title : Structure of E. coli topoisomerase III in complex with an 8-base single stranded oligonucleotide. Frozen in glycerol pH 8.0
Authors : Changela, A.; DiGate, R.J.; Mondragon, A.
Deposited on : 2006-12-05
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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

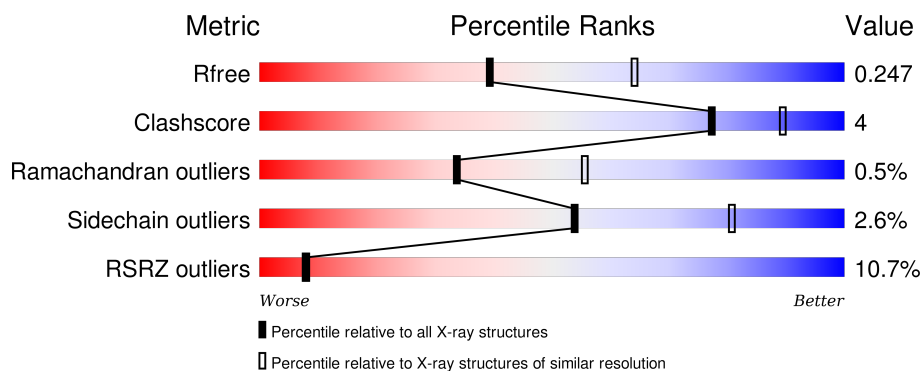
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 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}	91344	3553 (2.50-2.50)
Clashscore	102246	4242 (2.50-2.50)
Ramachandran outliers	100387	4156 (2.50-2.50)
Sidechain outliers	100360	4158 (2.50-2.50)
RSRZ outliers	91569	3562 (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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 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	C	8	<div> <div>13%</div> <div>38%</div> <div>50%</div> <div>13%</div> </div>
1	D	8	<div> <div>63%</div> <div>38%</div> </div>
2	A	659	<div> <div>14%</div> <div>81%</div> <div>12%</div> <div>6%</div> </div>
2	B	659	<div> <div>7%</div> <div>86%</div> <div>9%</div> <div>5%</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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	ACY	B	803	-	-	-	X

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 10353 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	8	Total	C	N	O	P	0	0	0
			158	77	28	46	7			

- Molecule 2 is a protein called DNA topoisomerase 3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	A	619	Total	C	N	O	S	0	0	0
			4927	3117	898	892	20			
2	B	626	Total	C	N	O	S	0	0	0
			4982	3149	904	909	20			

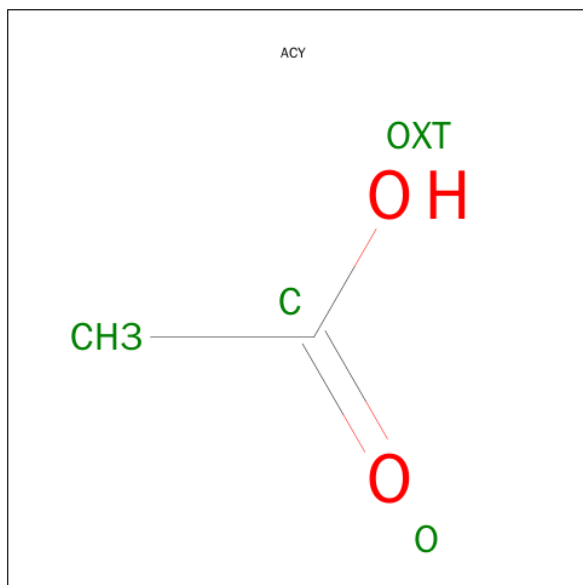
There are 12 discrepancies between the modelled and reference sequences:

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 CHLORIDE ION (three-letter code: CL) (formula: Cl).

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

- Molecule 4 is ACETIC ACID (three-letter code: ACY) (formula: C₂H₄O₂).



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

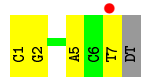
- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	53	Total O 53 53	0	0
5	B	79	Total O 79 79	0	0
5	C	4	Total O 4 4	0	0
5	D	6	Total O 6 6	0	0

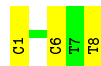
3 Residue-property plots

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.

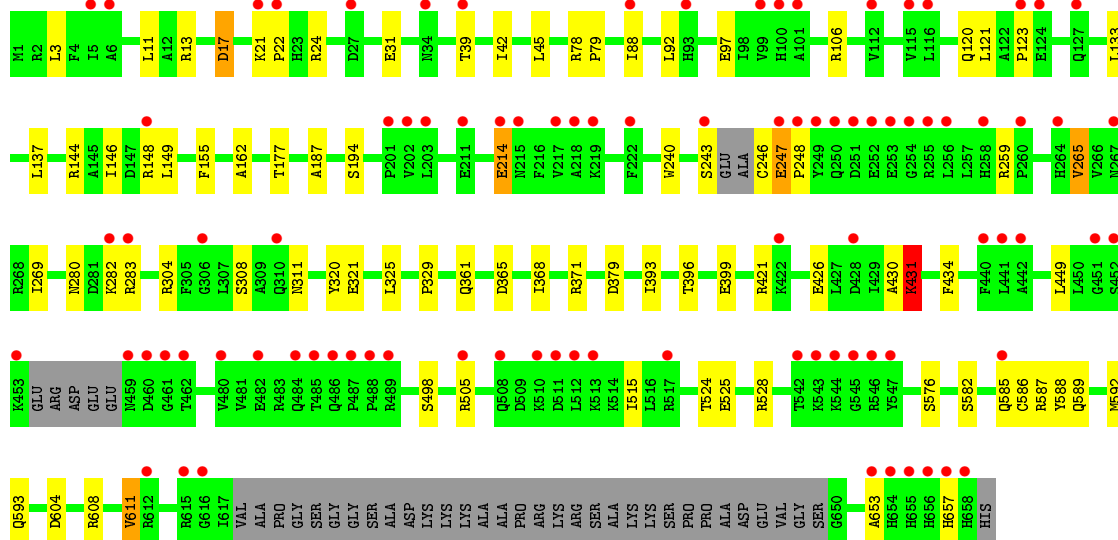
- Molecule 1: 5'-D(*CP*GP*CP*AP*AP*CP*TP*T)-3'



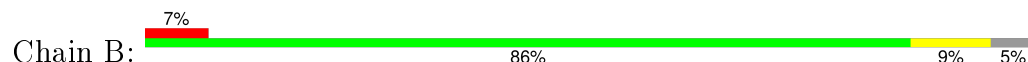
- Molecule 1: 5'-D(*CP*GP*CP*AP*AP*CP*TP*T)-3'

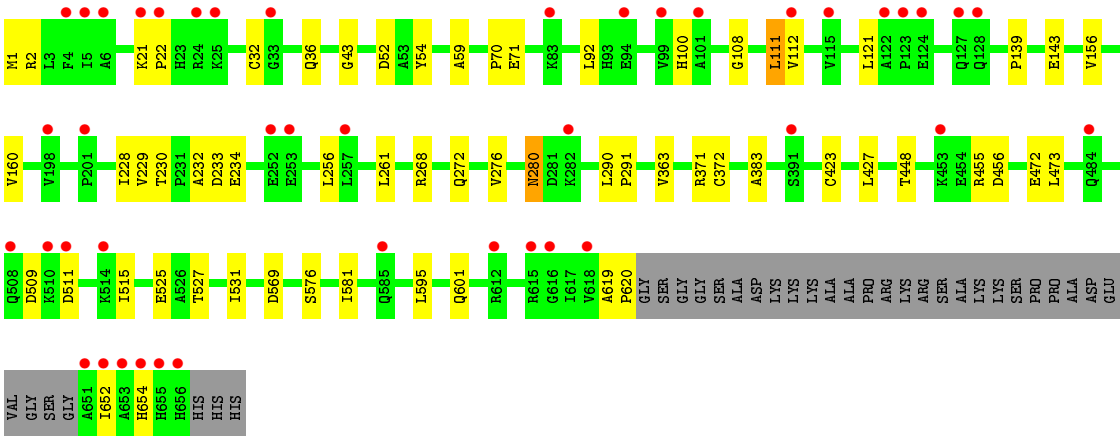


- Molecule 2: DNA topoisomerase 3



- Molecule 2: DNA topoisomerase 3





4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	101.59 Å 101.59 Å 453.59 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.53 – 2.50 29.53 – 2.50	Depositor EDS
% Data completeness (in resolution range)	97.2 (29.53-2.50) 97.3 (29.53-2.50)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	0.05	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.86 (at 2.51 Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.221 , 0.258 0.211 , 0.247	Depositor DCC
R_{free} test set	4038 reflections (5.24%)	DCC
Wilson B-factor (Å ²)	55.9	Xtriage
Anisotropy	0.254	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 40.5	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.43$, $\langle L^2 \rangle = 0.26$	Xtriage
Outliers	0 of 81033 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	10353	wwPDB-VP
Average B, all atoms (Å ²)	62.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.99% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: ACY, 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	1.02	0/154	1.78	4/235 (1.7%)
1	D	1.06	0/176	1.75	6/269 (2.2%)
2	A	0.48	0/5035	0.58	0/6824
2	B	0.50	0/5091	0.62	1/6904 (0.0%)
All	All	0.51	0/10456	0.68	11/14232 (0.1%)

There are no bond length outliers.

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	5	DA	O4'-C4'-C3'	-6.81	101.78	104.50
1	C	7	DT	O4'-C1'-N1	6.41	112.49	108.00
1	D	6	DC	O4'-C4'-C3'	-6.35	101.96	104.50
2	B	595	LEU	CA-CB-CG	-6.09	101.28	115.30
1	C	1	DC	O4'-C1'-N1	5.95	112.17	108.00
1	C	2	DG	O5'-P-OP2	-5.90	100.39	105.70
1	D	1	DC	O4'-C1'-N1	5.86	112.10	108.00
1	D	6	DC	O4'-C1'-N1	5.70	111.99	108.00
1	D	6	DC	C4'-C3'-C2'	-5.69	97.98	103.10
1	D	8	DT	O4'-C4'-C3'	-5.63	102.25	104.50
1	D	6	DC	O5'-P-OP2	-5.57	100.69	105.70

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	0	0
1	D	158	0	92	0	0
2	A	4927	0	4943	46	0
2	B	4982	0	4995	30	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	B	4	0	3	0	0
5	A	53	0	0	2	0
5	B	79	0	0	1	0
5	C	4	0	0	0	0
5	D	6	0	0	0	0
All	All	10353	0	10113	76	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 4.

All (76) 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:A:396:THR:HG23	2:A:399:GLU:H	1.43	0.83
2:B:230:THR:HG22	2:B:232:ALA:H	1.44	0.82
2:A:308:SER:OG	2:A:311:ASN:HB2	1.88	0.72
2:A:187:ALA:HB2	2:A:611:VAL:HG13	1.74	0.70
2:A:24:ARG:HB3	2:A:31:GLU:HG3	1.76	0.66
2:A:396:THR:HG22	2:A:399:GLU:CG	2.29	0.62
2:B:619:ALA:HB1	2:B:620:PRO:HD2	1.81	0.62
2:A:283:ARG:HE	2:A:421:ARG:HH21	1.47	0.61
2:A:430:ALA:O	2:A:431:LYS:HB3	1.99	0.60
2:B:525:GLU:HA	2:B:525:GLU:OE2	2.03	0.59
2:A:396:THR:HG22	2:A:399:GLU:HG3	1.86	0.57
2:B:290:LEU:HB3	2:B:291:PRO:HD2	1.87	0.56
2:A:42:ILE:H	2:A:45:LEU:HD21	1.71	0.56
2:B:256:LEU:HD11	2:B:261:LEU:HD23	1.87	0.56
2:B:32:CYS:HB2	2:B:36:GLN:HB2	1.88	0.55
2:B:43:GLY:C	2:B:111:LEU:HD12	2.27	0.55
2:A:524:THR:O	2:A:528:ARG:HG3	2.08	0.54
2:B:363:VAL:HG21	2:B:448:THR:HG21	1.90	0.53
2:A:88:ILE:O	2:A:92:LEU:HB2	2.09	0.52
2:A:21:LYS:HB3	2:A:22:PRO:HA	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:587:ARG:NH1	5:A:853:HOH:O	2.42	0.51
2:A:361:GLN:HG2	2:A:449:LEU:HD21	1.91	0.51
2:A:265:VAL:O	2:A:269:ILE:HG12	2.11	0.50
2:A:280:ASN:HD21	2:A:282:LYS:HE3	1.77	0.49
2:A:92:LEU:HG	2:A:121:LEU:HD13	1.95	0.48
2:A:396:THR:CG2	2:A:399:GLU:HG3	2.43	0.48
2:B:228:ILE:HG21	2:B:473:LEU:HD23	1.96	0.48
2:A:243:SER:HG	2:A:246:CYS:N	2.12	0.47
2:A:11:LEU:HD12	2:A:137:LEU:HD21	1.96	0.47
2:A:515:ILE:HD13	2:A:576:SER:HB2	1.95	0.47
2:A:13:ARG:O	2:A:17:ASP:HB2	2.15	0.47
2:A:320:TYR:CG	2:A:329:PRO:HD3	2.51	0.46
2:B:455:ARG:HD2	2:B:456:ASP:OD2	2.16	0.45
2:A:106:ARG:HG2	2:A:162:ALA:HB2	1.99	0.45
2:A:246:CYS:SG	2:A:247:GLU:N	2.90	0.45
2:B:100:HIS:NE2	2:B:112:VAL:HB	2.32	0.45
2:A:588:TYR:CE1	2:A:592:MET:HE3	2.52	0.45
2:B:276:VAL:HA	2:B:427:LEU:HD23	2.00	0.44
2:B:156:VAL:HG11	2:B:654:HIS:HB2	1.99	0.44
2:A:3:LEU:HD11	2:A:39:THR:HG22	1.99	0.44
2:B:160:VAL:HG12	2:B:581:ILE:HG21	1.99	0.44
2:B:108:GLY:HA2	2:B:111:LEU:HD22	1.99	0.44
2:A:146:ILE:O	2:A:149:LEU:HG	2.17	0.44
2:B:291:PRO:HB2	2:B:383:ALA:CB	2.48	0.44
2:A:604:ASP:O	2:A:608:ARG:HD2	2.17	0.44
2:A:365:ASP:HB3	2:A:368:ILE:HD12	1.99	0.44
2:B:515:ILE:HD13	2:B:576:SER:HB2	2.00	0.43
2:A:78:ARG:HA	2:A:79:PRO:HD3	1.89	0.43
2:B:92:LEU:HG	2:B:121:LEU:HD13	2.00	0.43
2:A:247:GLU:H	2:A:248:PRO:CD	2.31	0.43
2:B:527:THR:O	2:B:531:ILE:HG12	2.19	0.43
2:B:21:LYS:HE2	2:B:22:PRO:HA	2.01	0.43
2:B:139:PRO:O	2:B:143:GLU:HB2	2.18	0.42
2:B:268:ARG:O	2:B:272:GLN:HG3	2.19	0.42
2:B:509:ASP:C	2:B:509:ASP:OD1	2.58	0.42
2:A:177:THR:HG23	2:A:194:SER:HA	2.00	0.42
2:B:54:TYR:CE2	2:B:70:PRO:HB3	2.54	0.42
2:A:133:LEU:HD11	2:A:155:PHE:CZ	2.54	0.42
2:B:228:ILE:CG2	2:B:229:VAL:N	2.82	0.42
2:A:133:LEU:HD11	2:A:155:PHE:HZ	1.85	0.42
2:B:509:ASP:OD1	2:B:511:ASP:N	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:653:ALA:O	2:A:657:HIS:ND1	2.49	0.42
2:B:52:ASP:HB3	2:B:59:ALA:HB2	2.02	0.41
2:B:371:ARG:HG2	5:B:805:HOH:O	2.19	0.41
2:A:396:THR:CG2	2:A:399:GLU:H	2.22	0.41
2:A:240:TRP:HB2	2:A:434:PHE:CE2	2.55	0.41
2:A:589:GLN:HG3	2:A:593:GLN:HG2	2.02	0.41
2:A:144:ARG:O	2:A:148:ARG:HG3	2.21	0.41
2:B:230:THR:HB	2:B:234:GLU:HG2	2.03	0.41
2:A:79:PRO:HD2	5:A:813:HOH:O	2.20	0.41
2:A:396:THR:HG22	2:A:399:GLU:CD	2.40	0.41
2:A:11:LEU:HD12	2:A:137:LEU:CD2	2.51	0.41
2:A:137:LEU:HD12	2:A:321:GLU:HA	2.03	0.41
2:A:325:LEU:HD21	2:A:393:ILE:HD12	2.03	0.41
2:A:78:ARG:HH11	2:A:78:ARG:HG2	1.87	0.40
2:B:280:ASN:O	2:B:423:CYS:HA	2.21	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	611/659 (93%)	590 (97%)	15 (2%)	6 (1%)	19	34
2	B	622/659 (94%)	606 (97%)	16 (3%)	0	100	100
All	All	1233/1318 (94%)	1196 (97%)	31 (2%)	6 (0%)	34	55

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	A	120	GLN
2	A	247	GLU
2	A	379	ASP

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Mol	Chain	Res	Type
2	A	431	LYS
2	A	214	GLU
2	A	123	PRO

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	
2	A	526/555 (95%)	510 (97%)	16 (3%)	48	76
2	B	532/555 (96%)	521 (98%)	11 (2%)	61	85
All	All	1058/1110 (95%)	1031 (97%)	27 (3%)	54	81

All (27) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	A	17	ASP
2	A	97	GLU
2	A	214	GLU
2	A	259	ARG
2	A	265	VAL
2	A	304	ARG
2	A	371	ARG
2	A	426	GLU
2	A	431	LYS
2	A	498	SER
2	A	505	ARG
2	A	525	GLU
2	A	582	SER
2	A	585	GLN
2	A	586	CYS
2	A	611	VAL
2	B	1	MET
2	B	2	ARG
2	B	71	GLU
2	B	111	LEU

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Mol	Chain	Res	Type
2	B	233	ASP
2	B	280	ASN
2	B	372	CYS
2	B	472	GLU
2	B	569	ASP
2	B	601	GLN
2	B	652	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
2	A	23	HIS
2	A	250	GLN
2	A	280	ASN
2	A	317	GLN
2	A	484	GLN
2	A	585	GLN
2	B	84	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 carbohydrates in this entry.

5.6 Ligand geometry ⓘ

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	$\# Z > 2$
4	ACY	B	803	-	1,3,3	2.57	1 (100%)	0,3,3	0.00	-

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	ACY	B	803	-	-	0/0/0/0	0/0/0/0

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	803	ACY	CH3-C	2.57	1.52	1.48

There are no bond angle outliers.

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%)	0.21	1 (14%) 4 3	41, 43, 74, 104	0
1	D	8/8 (100%)	-0.29	0 100 100	34, 39, 54, 63	0
2	A	619/659 (93%)	0.76	91 (14%) 3 3	33, 66, 120, 164	0
2	B	626/659 (94%)	0.39	43 (6%) 20 22	28, 52, 95, 198	0
All	All	1260/1334 (94%)	0.57	135 (10%) 8 8	28, 58, 103, 198	0

All (135) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	A	656	HIS	10.4
2	A	657	HIS	8.5
2	A	253	GLU	7.9
2	B	656	HIS	7.5
2	A	254	GLY	7.4
2	B	653	ALA	6.7
2	A	654	HIS	6.5
2	B	654	HIS	6.1
2	B	651	ALA	6.0
2	A	655	HIS	5.8
2	A	460	ASP	5.5
2	A	510	LYS	5.5
2	A	461	GLY	5.5
2	A	547	TYR	5.3
2	A	247	GLU	5.3
2	A	612	ARG	5.1
2	A	249	TYR	4.9
2	A	489	ARG	4.9
2	A	615	ARG	4.9
2	A	214	GLU	4.8
2	A	5	ILE	4.7

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Mol	Chain	Res	Type	RSRZ
2	B	655	HIS	4.7
2	A	658	HIS	4.6
2	B	618	VAL	4.5
2	A	459	ASN	4.5
2	B	122	ALA	4.4
2	A	487	PRO	4.4
2	A	486	GLN	4.3
2	A	512	LEU	4.2
2	B	22	PRO	4.2
2	B	124	GLU	4.1
2	A	585	GLN	4.0
2	A	544	LYS	4.0
2	A	260	PRO	4.0
2	B	24	ARG	4.0
2	A	508	GLN	3.9
2	A	545	GLY	3.9
2	B	21	LYS	3.8
2	A	484	GLN	3.8
2	A	482	GLU	3.8
2	B	5	ILE	3.7
2	A	546	ARG	3.7
2	A	513	LYS	3.7
2	A	112	VAL	3.7
2	A	264	HIS	3.6
2	A	282	LYS	3.5
2	A	218	ALA	3.5
2	A	511	ASP	3.4
2	A	124	GLU	3.4
2	A	255	ARG	3.4
2	A	616	GLY	3.3
2	A	452	SER	3.3
2	A	248	PRO	3.2
2	B	510	LYS	3.1
2	B	252	GLU	3.1
2	A	440	PHE	3.0
2	A	211	GLU	3.0
2	B	612	ARG	3.0
2	A	34	ASN	2.9
2	A	219	LYS	2.9
2	A	488	PRO	2.9
2	A	453	LYS	2.8
1	C	7	DT	2.8

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Mol	Chain	Res	Type	RSRZ
2	A	123	PRO	2.8
2	B	127	GLN	2.8
2	B	123	PRO	2.8
2	A	543	LYS	2.8
2	A	441	LEU	2.7
2	B	99	VAL	2.7
2	A	283	ARG	2.7
2	A	222	PHE	2.7
2	B	83	LYS	2.7
2	A	256	LEU	2.7
2	A	462	THR	2.7
2	B	25	LYS	2.7
2	A	217	VAL	2.7
2	A	252	GLU	2.6
2	A	485	THR	2.6
2	A	148	ARG	2.6
2	A	505	ARG	2.6
2	B	6	ALA	2.6
2	A	115	VAL	2.6
2	B	514	LYS	2.5
2	A	267	ASN	2.5
2	B	652	ILE	2.5
2	B	33	GLY	2.5
2	A	451	GLY	2.5
2	A	250	GLN	2.5
2	B	94	GLU	2.5
2	A	517	ARG	2.4
2	A	6	ALA	2.4
2	A	428	ASP	2.4
2	A	215	ASN	2.4
2	A	93	HIS	2.4
2	A	101	ALA	2.4
2	A	653	ALA	2.4
2	A	22	PRO	2.3
2	B	511	ASP	2.3
2	A	243	SER	2.3
2	B	282	LYS	2.3
2	B	616	GLY	2.3
2	B	585	GLN	2.3
2	B	115	VAL	2.3
2	A	116	LEU	2.3
2	A	99	VAL	2.3

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Mol	Chain	Res	Type	RSRZ
2	A	542	THR	2.3
2	A	127	GLN	2.3
2	B	484	GLN	2.3
2	A	258	HIS	2.3
2	B	198	VAL	2.3
2	A	442	ALA	2.2
2	A	21	LYS	2.2
2	A	27	ASP	2.2
2	B	615	ARG	2.2
2	A	203	LEU	2.2
2	B	453	LYS	2.2
2	B	4	PHE	2.2
2	B	253	GLU	2.2
2	A	202	VAL	2.1
2	B	128	GLN	2.1
2	A	88	ILE	2.1
2	A	480	VAL	2.1
2	B	391	SER	2.1
2	A	39	THR	2.1
2	B	257	LEU	2.1
2	B	508	GLN	2.1
2	A	422	LYS	2.1
2	B	112	VAL	2.1
2	A	310	GLN	2.1
2	A	251	ASP	2.1
2	B	101	ALA	2.1
2	A	306	GLY	2.0
2	B	201	PRO	2.0
2	A	100	HIS	2.0
2	A	201	PRO	2.0

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

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

6.3 Carbohydrates ⓘ

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, 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	LLDF	B-factors(Å ²)	Q<0.9
4	ACY	B	803	4/4	0.96	0.31	5.90	45,45,46,46	0
3	CL	B	801	1/1	0.99	0.11	-2.24	39,39,39,39	0
3	CL	A	800	1/1	0.99	0.10	-4.04	37,37,37,37	0

6.5 Other polymers [i](#)

There are no such residues in this entry.