



Full wwPDB X-ray Structure Validation Report ⓘ

May 17, 2020 – 01:53 am BST

PDB ID : 2O5E
Title : Structure of E. coli topoisomerase III in complex with an 8-base single stranded oligonucleotide. Frozen in glucose pH 7.0
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

<https://www.wwpdb.org/validation/2017/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 : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.11
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) : 2.11

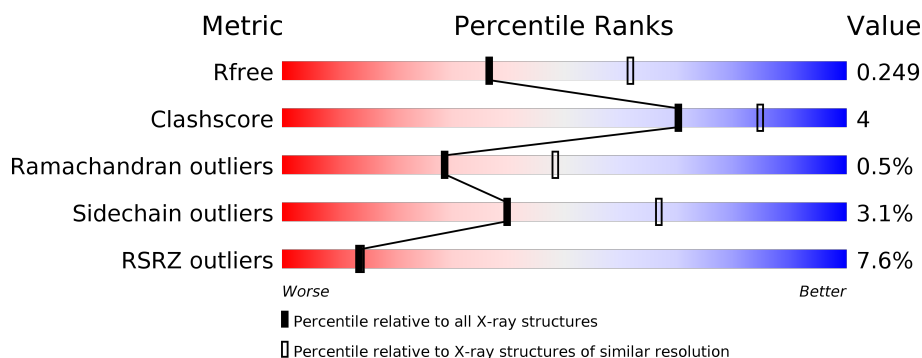
1 Overall quality at a glance

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}	130704	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (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 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	<div> <div>50%</div> <div>38%</div> <div>13%</div> </div>
1	D	8	<div> <div>25%</div> <div>50%</div> <div>13%</div> <div>13%</div> </div>
2	A	659	<div> <div>9%</div> <div>86%</div> <div>10%</div> <div>• •</div> </div>
2	B	659	<div> <div>6%</div> <div>85%</div> <div>10%</div> <div>•</div> </div>

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 10496 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			

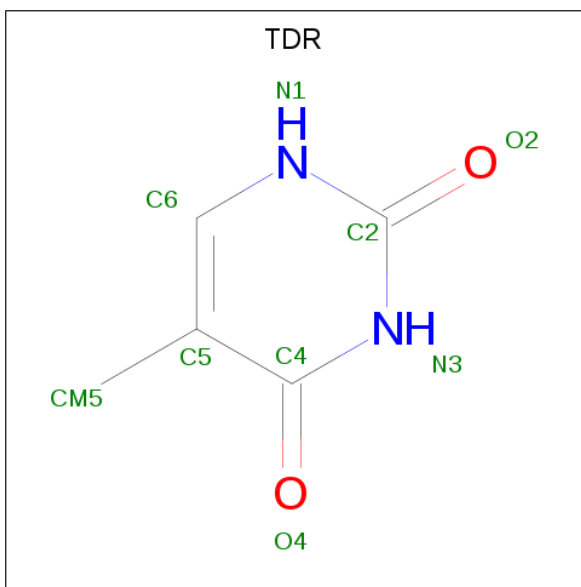
- Molecule 2 is a protein called DNA topoisomerase 3.

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 (three-letter code: 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 (three-letter code: 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	3	Total	O	0	0
			3	3		
5	D	4	Total	O	0	0
			4	4		
5	A	85	Total	O	0	0
			85	85		
5	B	55	Total	O	0	0
			55	55		

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 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: 




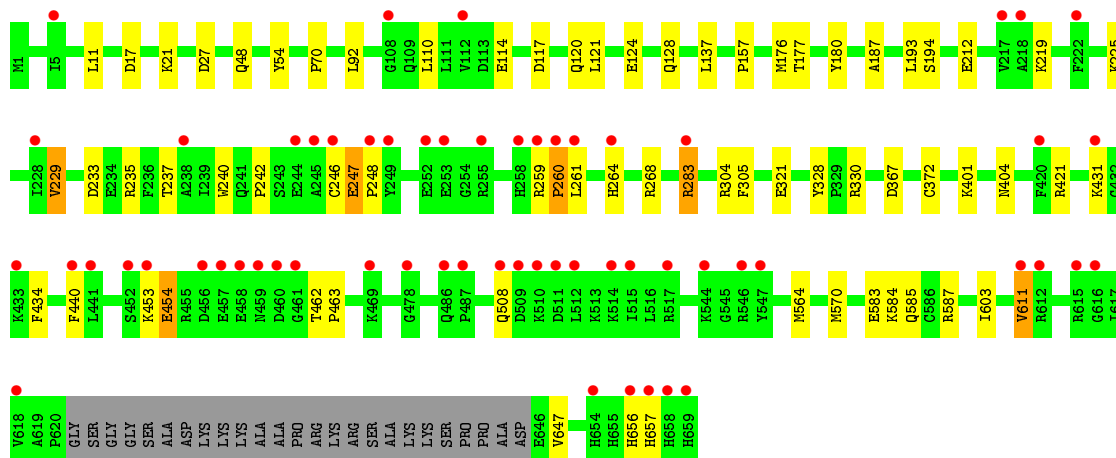
- Molecule 1: 5'-D(*CP*GP*CP*AP*AP*CP*TP*T)-3'

Chain D: 




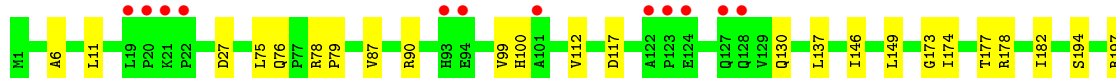
- Molecule 2: DNA topoisomerase 3

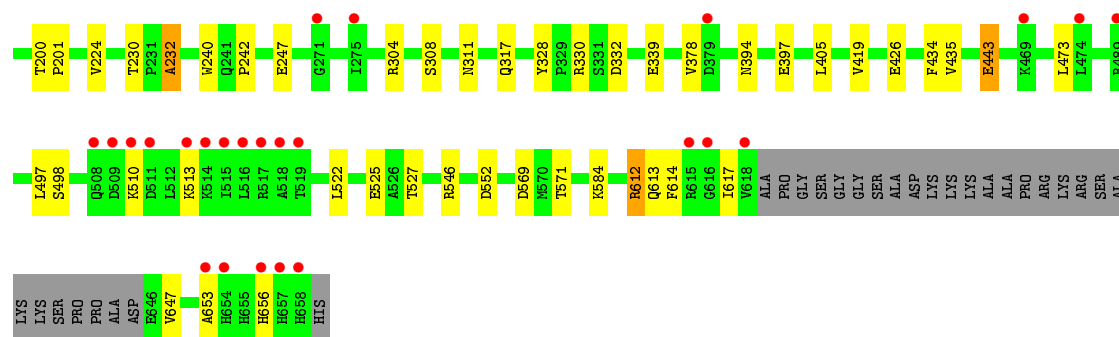
Chain A: 



- 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	102.26 Å 102.26 Å 445.61 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.13 – 2.50 29.13 – 2.50	Depositor EDS
% Data completeness (in resolution range)	95.7 (29.13-2.50) 95.8 (29.13-2.50)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.44 (at 2.51 Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.217 , 0.260 0.209 , 0.249	Depositor DCC
R_{free} test set	3992 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	58.1	Xtriage
Anisotropy	0.184	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 42.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.42$, $\langle L^2 \rangle = 0.24$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	10496	wwPDB-VP
Average B, all atoms (Å ²)	64.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.11% 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	1.11	0/154	1.61	3/235 (1.3%)
1	D	1.04	0/154	1.64	2/235 (0.9%)
2	A	0.52	0/5154	0.60	0/6989
2	B	0.50	0/5130	0.61	0/6955
All	All	0.53	0/10592	0.66	5/14414 (0.0%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	1	DC	O4'-C1'-N1	7.48	113.24	108.00
1	C	5	DA	O4'-C1'-N9	5.80	112.06	108.00
1	C	1	DC	O4'-C1'-N1	5.65	111.96	108.00
1	C	4	DA	O4'-C1'-N9	-5.30	104.29	108.00
1	D	3	DC	O4'-C1'-N1	5.12	111.59	108.00

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	138	0	80	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	5042	0	5042	40	0
2	B	5020	0	5023	32	0
3	D	9	0	6	0	0
4	A	2	0	0	0	0
5	A	85	0	0	3	0
5	B	55	0	0	0	0
5	C	3	0	0	0	0
5	D	4	0	0	0	0
All	All	10496	0	10231	75	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 (75) 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:419:VAL:HB	2:B:443:GLU:HG3	1.55	0.89
2:A:229:VAL:HG23	2:A:235:ARG:HG2	1.66	0.76
2:A:21:LYS:O	5:A:806:HOH:O	2.04	0.75
2:B:75:LEU:HG	2:B:647:VAL:HG21	1.74	0.70
2:B:11:LEU:HD12	2:B:137:LEU:HD21	1.73	0.69
2:A:247:GLU:H	2:A:248:PRO:CD	2.05	0.68
2:A:564:MET:HG3	2:A:570:MET:SD	2.35	0.67
2:A:187:ALA:HB2	2:A:611:VAL:HG13	1.78	0.64
2:A:304:ARG:HG3	2:A:304:ARG:HH11	1.64	0.62
2:A:177:THR:HG23	2:A:194:SER:HA	1.81	0.61
2:B:332:ASP:HB3	2:B:525:GLU:HG3	1.84	0.60
2:A:656:HIS:CD2	5:A:850:HOH:O	2.55	0.58
2:A:259:ARG:C	2:A:261:LEU:H	2.07	0.58
2:B:230:THR:HG22	2:B:232:ALA:H	1.69	0.57
2:B:6:ALA:HB1	2:B:11:LEU:HD23	1.87	0.56
2:A:240:TRP:HB2	2:A:434:PHE:CE2	2.42	0.55
2:A:176:MET:CE	2:A:603:ILE:HD13	2.38	0.54
2:A:11:LEU:HD12	2:A:137:LEU:HD21	1.89	0.54
2:B:653:ALA:HA	2:B:656:HIS:ND1	2.23	0.53
2:A:264:HIS:O	2:A:268:ARG:HB2	2.08	0.53
2:A:304:ARG:HG3	2:A:304:ARG:NH1	2.24	0.53
1:D:6:DC:H4'	1:D:7:DT:C7	2.40	0.52
2:A:247:GLU:H	2:A:248:PRO:HD3	1.73	0.51
2:A:124:GLU:O	2:A:128:GLN:HG2	2.11	0.51
2:A:247:GLU:N	2:A:248:PRO:CD	2.74	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:3:DC:O4'	2:B:173:GLY:HA3	2.11	0.51
2:B:522:LEU:CD1	2:B:571:THR:HG21	2.42	0.50
2:B:197:ARG:HG2	2:B:571:THR:HG23	1.94	0.50
2:B:510:LYS:O	2:B:513:LYS:HB3	2.11	0.50
2:A:117:ASP:HB3	2:A:647:VAL:HG13	1.93	0.49
2:B:308:SER:OG	2:B:311:ASN:HB2	2.12	0.49
2:B:522:LEU:HD11	2:B:571:THR:HG21	1.94	0.49
2:B:328:TYR:CZ	2:B:330:ARG:HB2	2.48	0.49
2:A:176:MET:HE2	2:A:603:ILE:HD13	1.95	0.48
2:A:587:ARG:HB3	2:A:656:HIS:CD2	2.49	0.48
2:B:87:VAL:O	2:B:90:ARG:HB3	2.14	0.48
2:A:225:LYS:CG	2:A:237:THR:HG23	2.44	0.48
2:A:431:LYS:HE2	2:A:431:LYS:HA	1.96	0.48
2:B:177:THR:HG23	2:B:194:SER:HA	1.95	0.47
2:B:240:TRP:HB2	2:B:434:PHE:CE2	2.49	0.47
2:A:92:LEU:HD22	2:A:121:LEU:HD21	1.96	0.47
2:A:110:LEU:O	2:A:114:GLU:HB2	2.14	0.47
2:B:240:TRP:O	2:B:242:PRO:HD3	2.15	0.47
2:A:247:GLU:N	2:A:248:PRO:HD3	2.30	0.46
2:A:137:LEU:HD12	2:A:321:GLU:HA	1.95	0.46
2:A:328:TYR:CZ	2:A:330:ARG:HB2	2.51	0.46
2:A:225:LYS:HG2	2:A:237:THR:HG23	1.97	0.46
2:A:180:TYR:O	2:A:193:LEU:HD12	2.15	0.45
2:A:283:ARG:HG3	2:A:421:ARG:HD3	1.98	0.45
2:A:453:LYS:HG3	2:A:454:GLU:H	1.80	0.45
2:B:612:ARG:O	2:B:614:PHE:N	2.50	0.45
2:A:583:GLU:O	2:A:585:GLN:HG2	2.17	0.45
2:B:230:THR:HA	2:B:473:LEU:HD22	1.98	0.45
2:B:224:VAL:HB	2:B:240:TRP:HB3	2.00	0.44
2:B:99:VAL:HG22	2:B:130:GLN:HB2	2.00	0.44
2:A:440:PHE:CZ	2:A:463:PRO:HD3	2.53	0.43
2:B:614:PHE:O	2:B:617:ILE:HG12	2.17	0.43
2:B:78:ARG:HA	2:B:79:PRO:HD3	1.89	0.43
2:B:426:GLU:HG2	2:B:435:VAL:HG22	2.01	0.43
2:A:176:MET:CE	2:A:603:ILE:CD1	2.96	0.42
2:A:54:TYR:CE1	2:A:70:PRO:HB3	2.54	0.42
2:B:178:ARG:O	2:B:182:ILE:HG13	2.18	0.42
2:B:405:LEU:HA	2:B:405:LEU:HD23	1.94	0.42
2:A:508:GLN:HB2	5:A:877:HOH:O	2.19	0.42
2:A:240:TRP:CZ2	2:A:242:PRO:HA	2.54	0.42
2:B:200:THR:HB	2:B:201:PRO:HD3	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:305:PHE:CD1	2:A:401:LYS:HD3	2.55	0.41
2:B:100:HIS:CE1	2:B:112:VAL:HB	2.56	0.41
2:B:146:ILE:O	2:B:149:LEU:HG	2.21	0.41
2:A:259:ARG:N	2:A:260:PRO:CD	2.83	0.41
1:D:6:DC:H4'	1:D:7:DT:H72	2.03	0.41
1:D:5:DA:H2'	2:B:527:THR:HG21	2.01	0.41
2:B:174:ILE:O	2:B:178:ARG:HG3	2.21	0.41
1:D:6:DC:H4'	1:D:7:DT:H71	2.03	0.41
2:A:157:PRO:HG3	2:A:584:LYS:HG3	2.03	0.40

There are no symmetry-related clashes.

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	
2	A	630/659 (96%)	600 (95%)	27 (4%)	3 (0%)	29	48
2	B	627/659 (95%)	606 (97%)	18 (3%)	3 (0%)	29	48
All	All	1257/1318 (95%)	1206 (96%)	45 (4%)	6 (0%)	29	48

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	A	247	GLU
2	B	612	ARG
2	B	613	GLN
2	B	232	ALA
2	A	260	PRO
2	A	120	GLN

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	538/555 (97%)	522 (97%)	16 (3%)	41	68
2	B	536/555 (97%)	519 (97%)	17 (3%)	39	65
All	All	1074/1110 (97%)	1041 (97%)	33 (3%)	40	67

All (33) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	A	17	ASP
2	A	27	ASP
2	A	48	GLN
2	A	212	GLU
2	A	219	LYS
2	A	229	VAL
2	A	233	ASP
2	A	246	CYS
2	A	283	ARG
2	A	367	ASP
2	A	372	CYS
2	A	404	ASN
2	A	454	GLU
2	A	462	THR
2	A	611	VAL
2	A	657	HIS
2	B	27	ASP
2	B	76	GLN
2	B	117	ASP
2	B	247	GLU
2	B	304	ARG
2	B	317	GLN
2	B	339	GLU
2	B	378	VAL
2	B	394	ASN
2	B	397	GLU
2	B	443	GLU

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Mol	Chain	Res	Type
2	B	497	LEU
2	B	498	SER
2	B	546	ARG
2	B	552	ASP
2	B	569	ASP
2	B	584	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
2	A	48	GLN
2	A	340	HIS
2	A	486	GLN

5.3.3 RNA [i](#)

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 carbohydrates 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	9	-	8,9,9	1.61	1 (12%)	6,12,12	5.55	4 (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	9	-	-	-	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	9	TDR	C4-C5	3.90	1.49	1.41

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	9	TDR	N1-C2-N3	-9.03	121.25	128.43
3	D	9	TDR	C4-N3-C2	7.18	121.20	115.14
3	D	9	TDR	C5-C6-N1	-5.71	119.34	125.16
3	D	9	TDR	C6-N1-C2	4.31	122.47	115.36

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 ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

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%)	-0.35	0	100 100	39, 40, 50, 68	0
1	D	7/8 (87%)	-0.34	0	100 100	40, 44, 61, 78	0
2	A	634/659 (96%)	0.38	60 (9%)	8 8	34, 56, 109, 152	0
2	B	631/659 (95%)	0.20	37 (5%)	22 23	35, 61, 102, 128	0
All	All	1279/1334 (95%)	0.29	97 (7%)	13 14	34, 58, 105, 152	0

All (97) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	A	245	ALA	6.5
2	A	657	HIS	6.4
2	A	461	GLY	6.1
2	B	515	ILE	5.8
2	B	656	HIS	5.7
2	B	654	HIS	5.2
2	B	658	HIS	5.2
2	A	218	ALA	4.8
2	A	658	HIS	4.3
2	A	264	HIS	4.1
2	A	656	HIS	4.0
2	A	260	PRO	4.0
2	B	618	VAL	4.0
2	A	456	ASP	3.8
2	B	514	LYS	3.8
2	B	657	HIS	3.8
2	A	615	ARG	3.7
2	A	249	TYR	3.7
2	B	615	ARG	3.6
2	B	616	GLY	3.6
2	A	486	GLN	3.5

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Mol	Chain	Res	Type	RSRZ
2	A	514	LYS	3.5
2	A	546	ARG	3.4
2	A	244	GLU	3.4
2	A	654	HIS	3.3
2	A	515	ILE	3.3
2	A	460	ASP	3.3
2	A	458	GLU	3.2
2	A	459	ASN	3.2
2	A	441	LEU	3.2
2	A	612	ARG	3.0
2	A	547	TYR	3.0
2	B	517	ARG	3.0
2	A	440	PHE	2.9
2	B	21	LYS	2.9
2	B	508	GLN	2.9
2	A	283	ARG	2.9
2	A	433	LYS	2.8
2	A	112	VAL	2.8
2	A	258	HIS	2.8
2	A	478	GLY	2.8
2	A	248	PRO	2.8
2	A	510	LYS	2.8
2	A	659	HIS	2.8
2	A	457	GLU	2.8
2	B	124	GLU	2.7
2	B	519	THR	2.7
2	B	275	ILE	2.6
2	A	217	VAL	2.6
2	B	93	HIS	2.6
2	A	544	LYS	2.6
2	A	616	GLY	2.6
2	B	20	PRO	2.5
2	A	253	GLU	2.5
2	B	518	ALA	2.5
2	A	509	ASP	2.5
2	B	271	GLY	2.5
2	A	259	ARG	2.5
2	A	222	PHE	2.5
2	B	22	PRO	2.4
2	A	508	GLN	2.4
2	A	469	LYS	2.4
2	B	513	LYS	2.4

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Mol	Chain	Res	Type	RSRZ
2	A	252	GLU	2.4
2	B	510	LYS	2.4
2	B	511	ASP	2.4
2	A	246	CYS	2.4
2	A	452	SER	2.4
2	A	611	VAL	2.3
2	A	618	VAL	2.3
2	A	5	ILE	2.3
2	B	123	PRO	2.3
2	A	255	ARG	2.3
2	B	469	LYS	2.2
2	B	127	GLN	2.2
2	B	474	LEU	2.2
2	B	516	LEU	2.2
2	A	512	LEU	2.2
2	A	238	ALA	2.2
2	B	653	ALA	2.2
2	A	517	ARG	2.2
2	A	511	ASP	2.2
2	A	420	PHE	2.2
2	B	19	LEU	2.1
2	B	94	GLU	2.1
2	A	431	LYS	2.1
2	A	261	LEU	2.1
2	B	379	ASP	2.1
2	A	108	GLY	2.1
2	B	489	ARG	2.1
2	B	101	ALA	2.0
2	B	122	ALA	2.0
2	A	228	ILE	2.0
2	A	453	LYS	2.0
2	B	509	ASP	2.0
2	B	128	GLN	2.0
2	A	487	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 [i](#)

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. 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(\AA^2)	Q<0.9
3	TDR	D	9	9/9	0.82	0.28	107,108,108,108	0
4	CL	A	801	1/1	0.96	0.14	52,52,52,52	0
4	CL	A	800	1/1	0.99	0.10	49,49,49,49	0

6.5 Other polymers [i](#)

There are no such residues in this entry.