



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 10:10 AM GMT

PDB ID : 3L4K
Title : Topoisomerase II-DNA cleavage complex, metal-bound
Authors : Schmidt, B.H.; Burgin, A.B.; Deweese, J.E.; Osheroﬀ, N.; Berger, J.M.
Deposited on : 2009-12-20
Resolution : 2.98 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

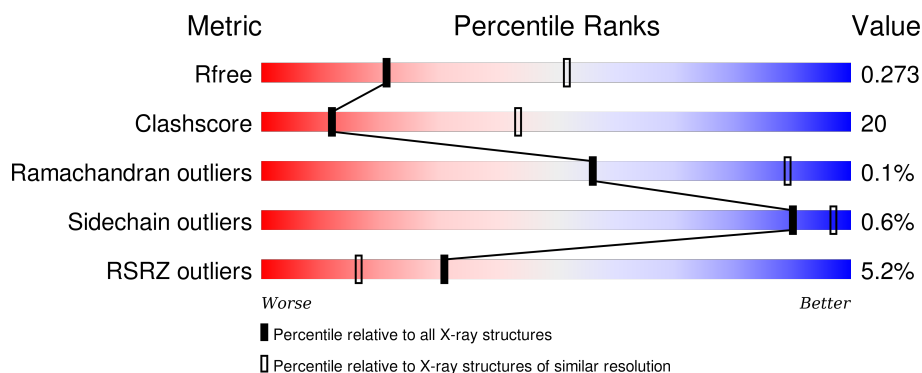
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.98 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	1992 (3.00-2.96)
Clashscore	102246	2349 (3.00-2.96)
Ramachandran outliers	100387	2274 (3.00-2.96)
Sidechain outliers	100360	2277 (3.00-2.96)
RSRZ outliers	91569	2007 (3.00-2.96)

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	A	758	<div> <div>5%</div> <div> <div>61%</div> <div>34%</div> <div>5%</div> </div> </div>
2	B	11	<div> <div>36%</div> <div>27%</div> <div>36%</div> </div>
3	C	15	<div> <div>33%</div> <div>67%</div> </div>
4	D	10	<div> <div>30%</div> <div>30%</div> <div>40%</div> </div>
5	E	15	<div> <div>67%</div> <div>33%</div> </div>

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 7028 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 DNA topoisomerase 2.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	721	Total	C	N	O	P	S	0	1	0
			5941	3829	992	1099	1	20			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	782	PTR	TYR	microheterogeneity	UNP P06786

- Molecule 2 is a DNA chain called DNA (5'-D(P*CP*CP*TP*AP*CP*TP*GP*CP*TP*AP*C)-3').

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	B	11	Total	C	N	O	P		0	11	0
			219	105	36	67	11				

- Molecule 3 is a DNA chain called DNA (5'-D(*CP*GP*CP*GP*GP*TP*AP*GP*CP*AP*GP*TP*AP*GP*G)-3').

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
3	C	15	Total	C	N	O	P		0	15	0
			310	147	63	86	14				

- Molecule 4 is a DNA chain called DNA (5'-D(P*GP*GP*AP*TP*GP*AP*CP*GP*AP*TP*)-3').

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
4	D	10	Total	C	N	O	P		0	10	0
			210	99	42	59	10				

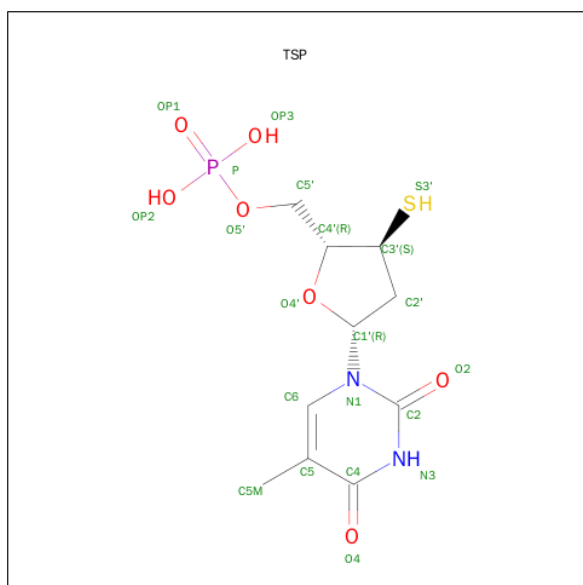
- Molecule 5 is a DNA chain called DNA (5'-D(*CP*GP*CP*GP*AP*AP*TP*CP*GP*TP*CP*AP*TP*CP*C)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	E	15	Total	C	N	O	P	0	15	0
			300	144	54	88	14			

- Molecule 6 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	7	Total	Zn	0	0
			7	7		
6	E	1	Total	Zn	0	0
			1	1		

- Molecule 7 is 3'-THIO-THYMIDINE-5'-PHOSPHATE (three-letter code: TSP) (formula: C₁₀H₁₅N₂O₇PS).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
7	D	1	Total	C	N	O	P	0	1
			20	10	2	6	1		

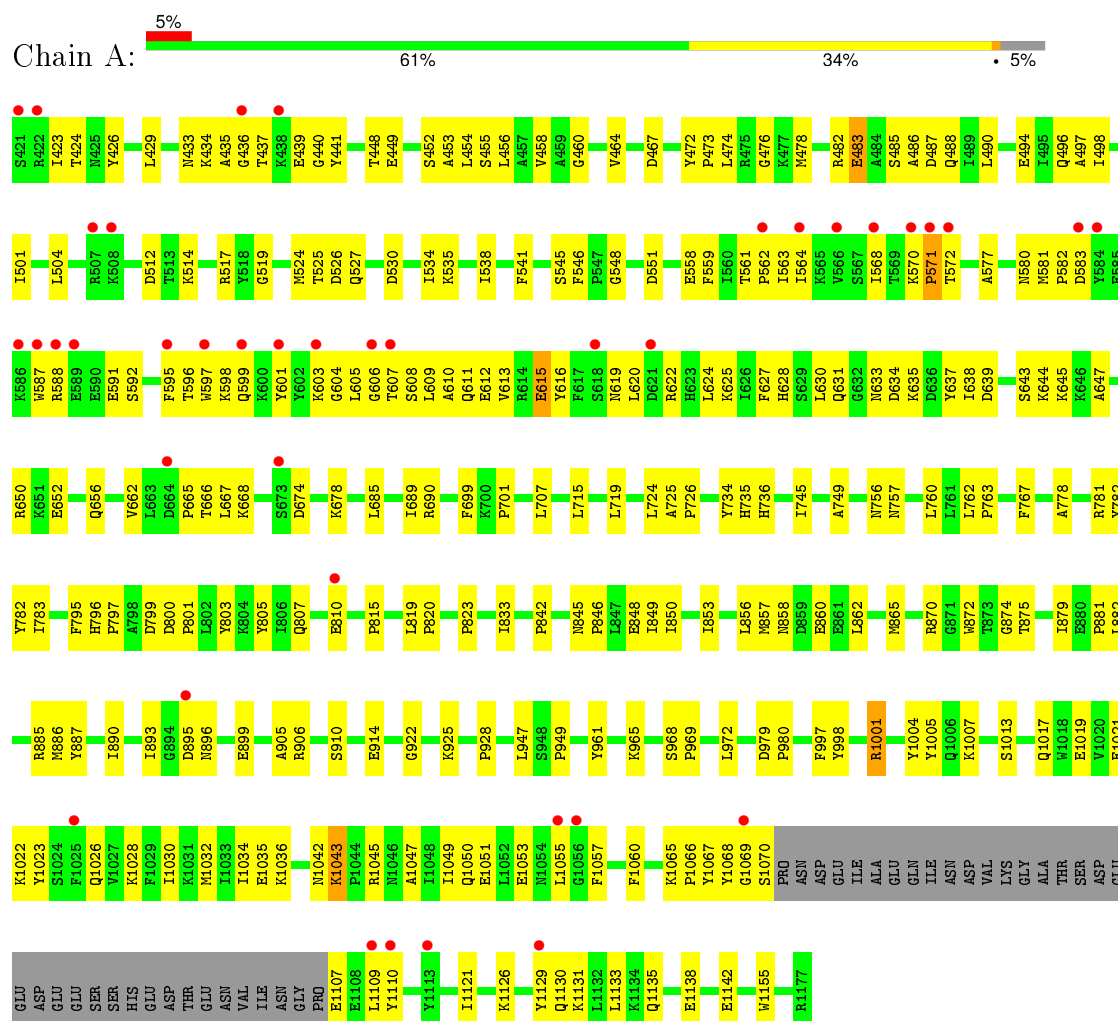
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	17	Total	O	0	0
			17	17		
8	B	2	Total	O	0	0
			2	2		
8	E	1	Total	O	0	0
			1	1		

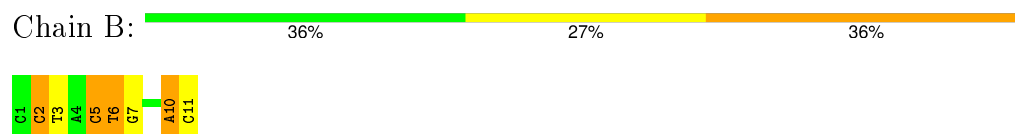
3 Residue-property plots

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: DNA topoisomerase 2



• Molecule 2: DNA (5'-D(P*CP*CP*TP*AP*CP*TP*GP*CP*TP*AP*C)-3')




- Molecule 3: DNA (5'-D(*CP*GP*CP*GP*GP*TP*AP*GP*CP*AP*GP*TP*AP*GP*G)-3')

Chain C:  33% 67%



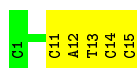
- Molecule 4: DNA (5'-D(P*GP*GP*AP*TP*GP*AP*CP*GP*AP*TP*)-3')

Chain D:  30% 30% 40%



- Molecule 5: DNA (5'-D(*CP*GP*CP*GP*AP*AP*TP*CP*GP*TP*CP*AP*TP*CP*C)-3')

Chain E:  67% 33%



4 Data and refinement statistics

Property	Value	Source
Space group	P 2 ₁ 2 ₁ 2 ₁	Depositor
Cell constants a, b, c, α , β , γ	86.06 Å 91.85 Å 115.94 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.02 – 2.98 49.02 – 2.98	Depositor EDS
% Data completeness (in resolution range)	86.2 (49.02-2.98) 91.2 (49.02-2.98)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.09 (at 3.01 Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.5_2)	Depositor
R, R_{free}	0.239 , 0.273 0.246 , 0.273	Depositor DCC
R_{free} test set	873 reflections (5.21%)	DCC
Wilson B-factor (Å ²)	73.6	Xtriage
Anisotropy	0.301	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 37.3	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.28$	Xtriage
Outliers	0 of 17650 reflections	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	7028	wwPDB-VP
Average B, all atoms (Å ²)	88.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.16% 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: ZN, PTR, TSP

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	0.34	1/6062 (0.0%)	0.46	2/8176 (0.0%)
2	B	0.96	1/243 (0.4%)	1.81	6/371 (1.6%)
3	C	0.80	1/349 (0.3%)	0.94	1/539 (0.2%)
4	D	0.77	1/236 (0.4%)	1.91	9/363 (2.5%)
5	E	0.44	0/335	0.95	0/514
All	All	0.43	4/7225 (0.1%)	0.72	18/9963 (0.2%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	2[A]	DC	P-OP2	-12.37	1.27	1.49
3	C	1[A]	DC	O3'-P	-11.71	1.47	1.61
4	D	6[B]	DA	P-OP2	-7.72	1.35	1.49
1	A	571	PRO	N-CD	-6.29	1.39	1.47

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	6[A]	DT	O5'-P-OP2	-19.89	86.83	110.70
4	D	6[B]	DA	O5'-P-OP2	-19.56	87.23	110.70
4	D	6[B]	DA	O5'-P-OP1	12.03	125.13	110.70
2	B	6[A]	DT	O5'-P-OP1	11.60	124.62	110.70
4	D	6[B]	DA	O5'-C5'-C4'	10.38	136.94	111.00
4	D	1[B]	DG	OP2-P-O3'	-9.06	85.26	105.20
2	B	2[A]	DC	O5'-P-OP2	-8.25	98.27	105.70
4	D	5[B]	DG	OP2-P-O3'	7.98	122.75	105.20
4	D	10[B]	DT	O4'-C4'-C3'	-7.86	101.28	106.00
1	A	572	THR	N-CA-CB	6.97	123.55	110.30
1	A	571	PRO	N-CA-C	6.62	129.30	112.10
2	B	10[A]	DA	O4'-C4'-C3'	-6.17	102.03	104.50

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Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
2	B	2[A]	DC	O5'-P-OP1	5.98	117.88	110.70
4	D	1[B]	DG	OP1-P-O3'	5.97	118.33	105.20
3	C	1[A]	DC	O4'-C4'-C3'	-5.86	102.16	104.50
4	D	10[B]	DT	O4'-C1'-N1	5.42	111.79	108.00
2	B	5[A]	DC	OP2-P-O3'	5.33	116.93	105.20
4	D	10[B]	DT	C1'-O4'-C4'	-5.14	104.96	110.10

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	5941	0	5949	241	0
2	B	219	0	114	9	0
3	C	310	0	149	12	0
4	D	210	0	96	15	0
5	E	300	0	151	15	0
6	A	7	0	0	0	0
6	E	1	0	0	0	0
7	D	20	0	8	2	0
8	A	17	0	0	6	0
8	B	2	0	0	0	0
8	E	1	0	0	2	0
All	All	7028	0	6467	270	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 20.

All (270) 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:482:ARG:NH2	1:A:639:ASP:HA	1.57	1.18
1:A:482:ARG:HH22	1:A:639:ASP:HA	0.98	1.15
3:C:14[A]:DG:H2'	8:E:119:HOH:O	1.50	1.09

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:1[B]:DG:N2	5:E:15[B]:DC:N3	2.03	1.05
1:A:482:ARG:C	1:A:483:GLU:HG2	1.77	1.04
1:A:582:PRO:HG2	1:A:662:VAL:HG21	1.38	1.01
4:D:2[B]:DG:H1	5:E:14[B]:DC:N4	1.60	0.99
1:A:849:ILE:HA	1:A:865:MET:HE1	1.47	0.97
5:E:14[B]:DC:H2'	8:E:119:HOH:O	1.63	0.97
1:A:482:ARG:HH22	1:A:639:ASP:CA	1.80	0.94
1:A:879:ILE:HD11	1:A:885:ARG:HG3	1.50	0.94
1:A:548:GLY:HA2	1:A:551:ASP:OD2	1.70	0.91
1:A:453:ALA:HB2	1:A:605:LEU:HD23	1.53	0.90
4:D:1[B]:DG:H1	5:E:15[B]:DC:N4	1.70	0.88
1:A:453:ALA:CB	1:A:605:LEU:HD23	2.04	0.87
1:A:483:GLU:HB2	1:A:644:LYS:HD2	1.55	0.87
2:B:2[A]:DC:N3	3:C:14[A]:DG:N2	2.23	0.85
1:A:486:ALA:HB3	8:A:108:HOH:O	1.74	0.85
4:D:2[B]:DG:N2	5:E:14[B]:DC:N3	2.25	0.84
1:A:482:ARG:O	1:A:483:GLU:HG2	1.77	0.84
1:A:601:TYR:CE2	1:A:603:LYS:HB2	2.20	0.76
1:A:453:ALA:HA	1:A:605:LEU:HG	1.69	0.75
1:A:715:LEU:HD11	1:A:719:LEU:HD22	1.68	0.74
1:A:570:LYS:HB2	1:A:571:PRO:HD3	1.70	0.74
2:B:3[A]:DT:O4	3:C:13[A]:DA:N1	2.20	0.73
1:A:668:LYS:HG3	1:A:668:LYS:O	1.87	0.73
1:A:482:ARG:C	1:A:483:GLU:CG	2.57	0.73
1:A:1049:ILE:O	1:A:1053:GLU:HG3	1.88	0.72
1:A:609:LEU:O	1:A:613:VAL:HG23	1.88	0.72
1:A:483:GLU:CB	1:A:644:LYS:HD2	2.19	0.72
1:A:619:ASN:HB2	1:A:622:ARG:NH1	2.04	0.72
1:A:423:ILE:HD11	1:A:517:ARG:HH22	1.55	0.72
1:A:625:LYS:HE2	1:A:668:LYS:H	1.54	0.71
1:A:625:LYS:HG2	1:A:668:LYS:HA	1.73	0.71
1:A:628:HIS:HE1	1:A:631:GLN:CD	1.93	0.71
1:A:526:ASP:O	1:A:527:GLN:HB3	1.91	0.70
1:A:512:ASP:HB3	1:A:514:LYS:HG2	1.73	0.70
1:A:452:SER:HB2	1:A:606:GLY:HA3	1.73	0.70
1:A:563:ILE:HG22	1:A:564:ILE:HG13	1.74	0.69
1:A:667:LEU:O	1:A:668:LYS:HB3	1.92	0.69
1:A:668:LYS:CG	1:A:668:LYS:O	2.40	0.69
1:A:483:GLU:HG3	1:A:644:LYS:HB2	1.75	0.68
1:A:561:THR:HB	1:A:562:PRO:HD2	1.77	0.67
1:A:1035:GLU:O	1:A:1036:LYS:HB2	1.94	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:749:ALA:O	1:A:763:PRO:HG3	1.95	0.67
4:D:5[B]:DG:H2''	4:D:6[B]:DA:H5'	1.77	0.67
1:A:620:LEU:HG	1:A:624:LEU:HD12	1.77	0.66
2:B:2[A]:DC:N4	3:C:14[A]:DG:N1	2.31	0.66
1:A:601:TYR:HE2	1:A:603:LYS:HB2	1.61	0.65
1:A:665:PRO:O	1:A:666:THR:OG1	2.15	0.65
1:A:483:GLU:HG3	1:A:644:LYS:CG	2.28	0.64
4:D:4[B]:DT:O4	5:E:12[B]:DA:N1	2.31	0.64
1:A:525:THR:OG1	1:A:535:LYS:HE3	1.97	0.64
1:A:436:GLY:HA2	1:A:517:ARG:HA	1.78	0.64
1:A:583:ASP:OD2	1:A:665:PRO:HG2	1.97	0.64
1:A:604:GLY:O	1:A:605:LEU:CB	2.46	0.63
1:A:778:ALA:HB1	1:A:782[A]:PTR:HD1	1.81	0.63
1:A:527:GLN:O	1:A:527:GLN:HG3	1.97	0.63
1:A:483:GLU:CG	1:A:644:LYS:HD2	2.29	0.62
1:A:699:PHE:CZ	1:A:707:LEU:HD12	2.33	0.62
1:A:592:SER:HB2	1:A:597:TRP:CZ2	2.33	0.62
4:D:3[B]:DA:N1	5:E:13[B]:DT:N3	2.47	0.62
1:A:612:GLU:O	1:A:616:TYR:CD1	2.53	0.62
1:A:563:ILE:HD12	1:A:580:ASN:HA	1.82	0.62
1:A:449:GLU:OE2	1:A:526:ASP:CG	2.38	0.61
1:A:611:GLN:H	1:A:611:GLN:CD	2.03	0.61
1:A:725:ALA:HB3	1:A:726:PRO:HD3	1.82	0.61
1:A:483:GLU:HG3	1:A:644:LYS:HD2	1.81	0.61
1:A:1001:ARG:HD2	1:A:1005:TYR:CE2	2.36	0.60
1:A:486:ALA:O	1:A:490:LEU:HG	2.00	0.60
1:A:1050:GLN:OE1	1:A:1050:GLN:HA	2.00	0.60
1:A:1030:ILE:O	1:A:1034:ILE:HG13	2.02	0.60
1:A:628:HIS:HE1	1:A:631:GLN:CG	2.15	0.60
1:A:609:LEU:HB3	1:A:611:GLN:OE1	2.02	0.59
1:A:476:GLY:HA3	3:C:5[A]:DG:H21	1.67	0.59
2:B:10[A]:DA:H2'	2:B:11[A]:DC:C6	2.37	0.59
1:A:571:PRO:HD3	1:A:596:THR:OG1	2.03	0.59
1:A:603:LYS:NZ	8:A:115:HOH:O	2.35	0.58
1:A:1035:GLU:O	1:A:1036:LYS:CB	2.50	0.58
1:A:979:ASP:HB2	1:A:980:PRO:HD2	1.85	0.58
1:A:588:ARG:NH2	1:A:807:GLN:HG3	2.19	0.58
1:A:800:ASP:HB2	1:A:801:PRO:HD3	1.86	0.58
3:C:12[A]:DT:H2''	3:C:13[A]:DA:C8	2.39	0.57
1:A:490:LEU:HA	1:A:496:GLN:NE2	2.18	0.57
1:A:628:HIS:HE1	1:A:631:GLN:HG3	1.69	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:545:SER:HB2	1:A:546:PHE:CD1	2.39	0.57
1:A:482:ARG:O	1:A:483:GLU:CG	2.50	0.57
1:A:483:GLU:HG3	1:A:644:LYS:CB	2.35	0.57
1:A:633:ASN:O	1:A:637:TYR:HD1	1.88	0.57
1:A:856:LEU:HG	1:A:862:LEU:HD21	1.87	0.57
1:A:603:LYS:HG2	1:A:604:GLY:N	2.20	0.57
1:A:433:ASN:HB2	1:A:467:ASP:HA	1.85	0.57
1:A:823:PRO:HD3	1:A:997:PHE:CE2	2.40	0.57
1:A:526:ASP:O	1:A:527:GLN:CB	2.52	0.56
2:B:10[A]:DA:H2'	2:B:11[A]:DC:H6	1.70	0.56
1:A:485:SER:HB3	1:A:487:ASP:OD2	2.06	0.56
1:A:558:GLU:HB2	1:A:627:PHE:CE1	2.40	0.56
1:A:612:GLU:O	1:A:615:GLU:HG3	2.06	0.56
1:A:628:HIS:CE1	1:A:631:GLN:HG3	2.41	0.56
1:A:893:ILE:HD13	1:A:899:GLU:HB2	1.88	0.56
1:A:1026:GLN:O	1:A:1030:ILE:HG12	2.06	0.56
5:E:11[B]:DC:H2''	5:E:12[B]:DA:C8	2.41	0.55
1:A:845:ASN:HB3	1:A:848:GLU:HG2	1.88	0.55
1:A:799:ASP:CG	1:A:1001:ARG:HH22	2.10	0.55
1:A:1045:ARG:O	1:A:1049:ILE:HG13	2.06	0.55
1:A:583:ASP:OD2	1:A:665:PRO:CG	2.54	0.54
1:A:619:ASN:HB2	1:A:622:ARG:HH12	1.72	0.54
1:A:734:TYR:CZ	1:A:736:HIS:HB2	2.41	0.54
1:A:423:ILE:CD1	1:A:517:ARG:HH22	2.20	0.54
1:A:453:ALA:CB	1:A:605:LEU:CD2	2.83	0.54
1:A:598:LYS:HD3	1:A:599:GLN:N	2.23	0.54
1:A:1067:TYR:HH	1:A:1110:TYR:HE1	1.55	0.54
1:A:582:PRO:CG	1:A:662:VAL:HG21	2.25	0.54
1:A:581:MET:HB2	1:A:582:PRO:HD3	1.89	0.54
1:A:1019:GLU:O	1:A:1023:TYR:HD2	1.90	0.53
1:A:620:LEU:H	1:A:620:LEU:HD23	1.74	0.53
1:A:1021:GLU:OE1	1:A:1066:PRO:HG2	2.08	0.53
4:D:5[B]:DG:N2	5:E:11[B]:DC:O2	2.42	0.53
1:A:474:LEU:HD22	1:A:494:GLU:OE2	2.08	0.53
1:A:483:GLU:HG3	1:A:644:LYS:CD	2.39	0.52
1:A:448:THR:HG21	1:A:454:LEU:HA	1.91	0.52
1:A:598:LYS:HA	1:A:810:GLU:OE1	2.10	0.52
1:A:756:ASN:O	1:A:870:ARG:NH1	2.42	0.52
1:A:487:ASP:OD1	1:A:488:GLN:N	2.43	0.52
1:A:872:TRP:CZ2	1:A:874:GLY:HA3	2.44	0.52
1:A:604:GLY:O	1:A:605:LEU:HB3	2.08	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1107:GLU:HG2	1:A:1109:LEU:H	1.74	0.51
1:A:628:HIS:CE1	1:A:631:GLN:CD	2.81	0.51
1:A:795:PHE:CE2	1:A:820:PRO:HG3	2.46	0.51
1:A:1049:ILE:HG22	1:A:1053:GLU:OE2	2.10	0.51
1:A:456:LEU:HD13	1:A:605:LEU:HD12	1.92	0.51
1:A:512:ASP:N	8:A:106:HOH:O	2.33	0.51
1:A:707:LEU:HD11	1:A:760:LEU:HD13	1.93	0.51
1:A:734:TYR:CE2	1:A:736:HIS:O	2.64	0.51
1:A:613:VAL:O	1:A:616:TYR:N	2.44	0.50
1:A:512:ASP:CB	1:A:514:LYS:HG2	2.42	0.50
1:A:674:ASP:O	1:A:678:LYS:HB2	2.11	0.50
4:D:4[B]:DT:C4	5:E:12[B]:DA:N1	2.79	0.50
1:A:630:LEU:HD13	1:A:635:LYS:HE3	1.92	0.50
1:A:895:ASP:O	1:A:896:ASN:HB2	2.12	0.50
1:A:896:ASN:HD21	1:A:949:PRO:HG3	1.77	0.49
1:A:541:PHE:O	1:A:545:SER:OG	2.27	0.49
4:D:2[B]:DG:N1	5:E:14[B]:DC:N4	2.45	0.49
1:A:423:ILE:HD11	1:A:517:ARG:NH2	2.25	0.49
1:A:734:TYR:CE2	1:A:736:HIS:HB2	2.48	0.49
1:A:715:LEU:HD11	1:A:719:LEU:CD2	2.42	0.49
3:C:2[A]:DG:H2'	3:C:3[A]:DC:C6	2.48	0.49
4:D:4[B]:DT:N3	5:E:12[B]:DA:C2	2.81	0.49
5:E:12[B]:DA:OP2	5:E:12[B]:DA:H8	1.96	0.49
1:A:434:LYS:HD3	1:A:439:GLU:OE1	2.13	0.49
1:A:767:PHE:CE1	1:A:783:ILE:HB	2.47	0.49
1:A:805:TYR:CE2	1:A:815:PRO:HG3	2.48	0.49
1:A:639:ASP:OD2	1:A:643:SER:HB2	2.13	0.48
1:A:896:ASN:HB3	1:A:947:LEU:O	2.12	0.48
1:A:613:VAL:O	1:A:616:TYR:HB2	2.12	0.48
1:A:441:TYR:HA	1:A:519:GLY:HA3	1.96	0.48
1:A:619:ASN:CB	1:A:622:ARG:HH12	2.27	0.48
1:A:1069:GLY:O	1:A:1070:SER:CB	2.61	0.48
1:A:905:ALA:O	1:A:906:ARG:HB2	2.12	0.48
1:A:453:ALA:HB1	1:A:605:LEU:HD23	1.89	0.48
1:A:1068:TYR:N	1:A:1068:TYR:CD2	2.81	0.48
2:B:5[A]:DC:H2'	2:B:6[A]:DT:H71	1.96	0.47
1:A:558:GLU:HB2	1:A:627:PHE:HE1	1.79	0.47
1:A:483:GLU:OE1	1:A:645:LYS:HE3	2.14	0.47
1:A:620:LEU:HD12	1:A:624:LEU:HD11	1.95	0.47
1:A:668:LYS:HD2	1:A:668:LYS:O	2.15	0.47
4:D:10[B]:DT:H2''	7:D:11[B]:TSP:H5'	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:634:ASP:O	1:A:638:ILE:HG13	2.14	0.47
1:A:875:THR:HG23	1:A:887:TYR:HB2	1.96	0.47
1:A:803:TYR:HE1	1:A:819:LEU:HB2	1.79	0.47
1:A:487:ASP:N	8:A:108:HOH:O	2.47	0.46
1:A:1138:GLU:O	1:A:1142:GLU:HG3	2.14	0.46
1:A:922:GLY:HA3	1:A:928:PRO:HD3	1.97	0.46
1:A:690:ARG:HA	1:A:701:PRO:HD2	1.97	0.46
1:A:504:LEU:HB3	1:A:546:PHE:CE2	2.50	0.46
4:D:4[B]:DT:N3	5:E:12[B]:DA:N1	2.63	0.46
1:A:592:SER:HB2	1:A:597:TRP:CE2	2.51	0.46
1:A:925:LYS:NZ	3:C:15[A]:DG:H3'	2.30	0.46
1:A:881:PRO:O	1:A:882:LEU:HB2	2.14	0.46
1:A:872:TRP:CH2	1:A:886:MET:HG3	2.50	0.46
1:A:1022:LYS:HB2	1:A:1060:PHE:CE1	2.52	0.46
1:A:762:LEU:HA	1:A:763:PRO:HD3	1.85	0.45
1:A:699:PHE:CE2	1:A:707:LEU:HD12	2.50	0.45
4:D:10[B]:DT:H2''	7:D:11[B]:TSP:C5'	2.46	0.45
1:A:1001:ARG:O	1:A:1001:ARG:HD3	2.16	0.45
1:A:1042:ASN:O	1:A:1043:LYS:O	2.34	0.45
1:A:979:ASP:HB2	1:A:980:PRO:CD	2.44	0.45
1:A:448:THR:HG22	1:A:524:MET:HE2	1.98	0.45
1:A:667:LEU:O	1:A:668:LYS:CB	2.62	0.45
3:C:6[A]:DT:H2'	3:C:7[A]:DA:C8	2.51	0.45
1:A:1032:MET:HE1	1:A:1057:PHE:HE2	1.82	0.45
1:A:925:LYS:NZ	5:E:15[B]:DC:H3'	2.31	0.45
1:A:607:THR:HG23	1:A:608:SER:N	2.32	0.45
1:A:1126:LYS:O	1:A:1130:GLN:HG2	2.17	0.45
1:A:910:SER:O	1:A:914:GLU:HG3	2.16	0.45
3:C:2[A]:DG:H2'	3:C:3[A]:DC:H6	1.82	0.45
1:A:1004:TYR:HA	1:A:1007:LYS:HB3	1.99	0.45
1:A:1042:ASN:HB3	1:A:1043:LYS:H	1.64	0.44
1:A:1047:ALA:O	1:A:1051:GLU:HG3	2.17	0.44
1:A:534:ILE:O	1:A:538:ILE:HG13	2.18	0.44
1:A:724:LEU:HD23	1:A:745:ILE:HD13	1.98	0.44
1:A:1051:GLU:O	1:A:1055:LEU:HG	2.17	0.44
1:A:541:PHE:O	1:A:541:PHE:CD1	2.71	0.44
1:A:437:THR:O	1:A:440:GLY:N	2.49	0.44
1:A:524:MET:HG3	1:A:559:PHE:HB3	1.99	0.44
1:A:965:LYS:HZ2	3:C:13[A]:DA:H3'	1.83	0.44
1:A:1028:LYS:O	1:A:1032:MET:HG3	2.17	0.44
1:A:1001:ARG:HD2	1:A:1005:TYR:CD2	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:14[A]:DG:H2"	3:C:15[A]:DG:C8	2.53	0.43
1:A:690:ARG:NH1	2:B:10[A]:DA:H4'	2.33	0.43
1:A:603:LYS:HD2	1:A:735:HIS:O	2.18	0.43
1:A:455:SER:O	1:A:458:VAL:HG22	2.17	0.43
1:A:429:LEU:HD13	1:A:501:ILE:HD13	2.00	0.43
1:A:805:TYR:HA	1:A:815:PRO:HA	1.99	0.43
1:A:685:LEU:O	1:A:689:ILE:HG13	2.18	0.43
1:A:1121:ILE:CG1	8:A:116:HOH:O	2.66	0.43
1:A:1121:ILE:N	8:A:116:HOH:O	2.51	0.43
1:A:472:TYR:CD1	1:A:473:PRO:HD2	2.53	0.43
1:A:846:PRO:O	1:A:850:ILE:HG13	2.18	0.43
1:A:707:LEU:HD23	1:A:707:LEU:HA	1.76	0.43
1:A:1067:TYR:CE1	1:A:1110:TYR:HD1	2.37	0.43
1:A:842:PRO:HG3	1:A:972:LEU:HD21	2.01	0.43
1:A:562:PRO:HB3	1:A:577:ALA:HB1	2.01	0.43
1:A:690:ARG:HD2	2:B:10[A]:DA:H5'	2.01	0.43
1:A:568:ILE:HG23	1:A:595:PHE:HB3	2.01	0.42
1:A:643:SER:C	1:A:645:LYS:H	2.22	0.42
1:A:610:ALA:HA	1:A:613:VAL:HB	2.00	0.42
1:A:1005:TYR:CE2	1:A:1155:TRP:CG	3.07	0.42
1:A:426:TYR:CZ	1:A:497:ALA:HA	2.54	0.42
1:A:643:SER:O	1:A:650:ARG:NH2	2.52	0.42
1:A:1013:SER:O	1:A:1017:GLN:HG3	2.19	0.42
1:A:456:LEU:HD22	1:A:524:MET:CE	2.49	0.42
1:A:968:SER:HA	1:A:969:PRO:HD3	1.74	0.42
1:A:570:LYS:HB2	1:A:596:THR:OG1	2.19	0.42
1:A:833:ILE:HD11	2:B:7[A]:DG:C2	2.55	0.42
1:A:545:SER:HB2	1:A:546:PHE:CE1	2.54	0.42
1:A:857:MET:HA	1:A:998:TYR:OH	2.19	0.42
1:A:530:ASP:O	1:A:534:ILE:HG12	2.20	0.42
1:A:478:MET:HE1	1:A:498:ILE:HD12	2.01	0.42
1:A:1065:LYS:HA	1:A:1066:PRO:HD3	1.78	0.42
1:A:611:GLN:CD	1:A:611:GLN:N	2.71	0.42
1:A:796:HIS:HA	1:A:797:PRO:HD3	1.88	0.41
1:A:757:ASN:ND2	1:A:870:ARG:H	2.18	0.41
1:A:436:GLY:HA3	1:A:517:ARG:HD2	2.00	0.41
1:A:853:ILE:O	1:A:857:MET:HG3	2.21	0.41
1:A:482:ARG:O	1:A:644:LYS:HE3	2.19	0.41
1:A:668:LYS:CD	1:A:668:LYS:O	2.67	0.41
1:A:423:ILE:CG1	1:A:517:ARG:HH22	2.33	0.41
1:A:453:ALA:HB1	1:A:605:LEU:CD2	2.48	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:435:ALA:C	1:A:437:THR:H	2.24	0.41
1:A:858:ASN:O	1:A:860:GLU:HG3	2.20	0.41
1:A:1129:TYR:CE1	1:A:1133:LEU:HD11	2.55	0.41
1:A:856:LEU:HD23	1:A:856:LEU:HA	1.79	0.41
1:A:456:LEU:HD13	1:A:605:LEU:CD1	2.51	0.40
1:A:423:ILE:HD12	1:A:429:LEU:CD2	2.51	0.40
1:A:1131:LYS:O	1:A:1135:GLN:HG3	2.21	0.40
1:A:652:GLU:O	1:A:656:GLN:HG2	2.22	0.40
1:A:423:ILE:HG22	1:A:424:THR:N	2.35	0.40
1:A:460:GLY:O	1:A:464:VAL:HG22	2.22	0.40
1:A:570:LYS:N	1:A:571:PRO:CD	2.85	0.40
1:A:782[A]:PTR:O2P	1:A:782[A]:PTR:HE2	2.21	0.40
1:A:690:ARG:NH1	4:D:10[B]:DT:H4'	2.36	0.40
1:A:856:LEU:HD13	1:A:998:TYR:CG	2.56	0.40
1:A:1032:MET:HE1	1:A:1055:LEU:HD13	2.03	0.40
1:A:890:ILE:HG22	1:A:961:TYR:CZ	2.56	0.40
1:A:587:TRP:CD1	1:A:591:GLU:HB2	2.56	0.40
1:A:647:ALA:HA	1:A:650:ARG:NH1	2.37	0.40
1:A:665:PRO:C	1:A:666:THR:HG1	2.21	0.40
1:A:541:PHE:C	1:A:541:PHE:CD1	2.93	0.40
1:A:810:GLU:O	1:A:810:GLU:HG2	2.22	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	
1	A	716/758 (94%)	684 (96%)	31 (4%)	1 (0%)	56	89

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1043	LYS

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	640/672 (95%)	636 (99%)	4 (1%)	90	97

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	483	GLU
1	A	615	GLU
1	A	781	ARG
1	A	1001	ARG

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

Mol	Chain	Res	Type
1	A	496	GLN
1	A	553	GLN
1	A	599	GLN
1	A	619	ASN
1	A	623	HIS
1	A	628	HIS
1	A	677	ASN
1	A	757	ASN
1	A	936	GLN
1	A	1167	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue is 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	$\# Z > 2$
1	PTR	A	782[A]	1	14,16,17	1.94	1 (7%)	18,22,24	0.67	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
1	PTR	A	782[A]	1	-	0/9/11/13	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	782[A]	PTR	OH-CZ	-7.13	1.23	1.40

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	782[A]	PTR	2	0

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry

Of 9 ligands modelled in this entry, 8 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
7	TSP	D	11[B]	6	10,21,22	1.41	3 (30%)	11,30,33	4.97	2 (18%)

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
7	TSP	D	11[B]	6	-	0/3/21/22	0/2/2/2

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	D	11[B]	TSP	C6-C5	-2.13	1.34	1.40
7	D	11[B]	TSP	C6-N1	2.40	1.38	1.35
7	D	11[B]	TSP	C4-N3	2.98	1.38	1.33

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	D	11[B]	TSP	C5-C4-N3	-8.85	115.29	125.14
7	D	11[B]	TSP	C4-N3-C2	13.80	127.17	115.25

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	D	11[B]	TSP	2	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	720/758 (94%)	0.26	40 (5%) 28 14	38, 82, 146, 176	0
2	B	11/11 (100%)	-0.16	0 100 100	50, 71, 168, 172	11 (100%)
3	C	15/15 (100%)	-0.11	0 100 100	52, 69, 173, 176	15 (100%)
4	D	10/10 (100%)	-0.10	0 100 100	49, 83, 168, 172	10 (100%)
5	E	15/15 (100%)	-0.12	0 100 100	52, 69, 174, 177	15 (100%)
All	All	771/809 (95%)	0.23	40 (5%) 31 16	38, 81, 149, 177	51 (6%)

All (40) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	572	THR	6.8
1	A	589	GLU	5.5
1	A	508	LYS	5.5
1	A	587	TRP	5.3
1	A	618	SER	4.9
1	A	607	THR	4.6
1	A	564	ILE	4.4
1	A	570	LYS	4.2
1	A	599	GLN	4.0
1	A	507	ARG	3.6
1	A	1056	GLY	3.5
1	A	586	LYS	3.3
1	A	584	TYR	3.3
1	A	664	ASP	3.0
1	A	422	ARG	3.0
1	A	601	TYR	2.9
1	A	1069	GLY	2.9
1	A	436	GLY	2.9
1	A	597	TRP	2.7
1	A	810	GLU	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	603	LYS	2.6
1	A	595	PHE	2.6
1	A	1109	LEU	2.5
1	A	438	LYS	2.5
1	A	588	ARG	2.4
1	A	895	ASP	2.4
1	A	1129	TYR	2.3
1	A	673	SER	2.2
1	A	1110	TYR	2.2
1	A	621	ASP	2.2
1	A	606	GLY	2.2
1	A	571	PRO	2.2
1	A	1055	LEU	2.2
1	A	421	SER	2.1
1	A	583	ASP	2.1
1	A	562	PRO	2.1
1	A	1025	PHE	2.1
1	A	568	ILE	2.1
1	A	1113	TYR	2.0
1	A	566	VAL	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [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
1	PTR	A	782[A]	16/17	0.90	0.20	-	62,66,71,73	16

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. 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
7	TSP	D	11[B]	20/21	0.95	0.17	-0.36	53,57,58,60	20
6	ZN	A	4	1/1	0.92	0.16	-0.47	129,129,129,129	0
6	ZN	A	7	1/1	0.70	0.11	-1.49	135,135,135,135	0
6	ZN	A	3	1/1	0.95	0.07	-2.44	138,138,138,138	0
6	ZN	A	6	1/1	0.97	0.08	-3.80	106,106,106,106	0
6	ZN	E	16	1/1	0.98	0.21	-	102,102,102,102	0
6	ZN	A	5	1/1	0.78	0.14	-	137,137,137,137	0
6	ZN	A	8	1/1	0.85	0.06	-	125,125,125,125	0
6	ZN	A	1	1/1	0.94	0.05	-	109,109,109,109	0

6.5 Other polymers

There are no such residues in this entry.