



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 10:10 AM GMT

PDB ID : 3L4J  
Title : Topoisomerase II-DNA cleavage complex, apo  
Authors : Schmidt, B.H.; Burgin, A.B.; Deweese, J.E.; Osheroff, N.; Berger, J.M.  
Deposited on : 2009-12-20  
Resolution : 2.48 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](mailto: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.

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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

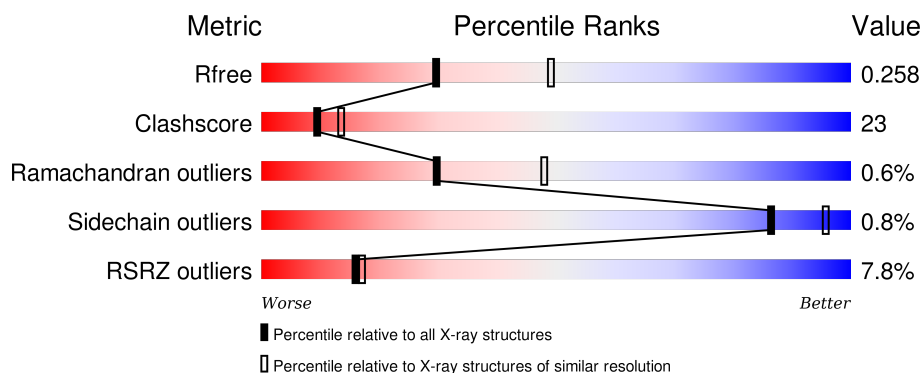
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.48 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	4309 (2.50-2.46)
Clashscore	102246	5050 (2.50-2.46)
Ramachandran outliers	100387	4961 (2.50-2.46)
Sidechain outliers	100360	4963 (2.50-2.46)
RSRZ outliers	91569	4319 (2.50-2.46)

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  $\geq 3$ , 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>8%</div> <div>62%</div> <div>32%</div> <div>• 5%</div> </div>
2	B	11	<div> <div>45%</div> <div>45%</div> <div>9%</div> </div>
3	C	15	<div> <div>13%</div> <div>53%</div> <div>40%</div> <div>7%</div> </div>
4	D	10	<div> <div>40%</div> <div>30%</div> <div>30%</div> </div>
5	E	15	<div> <div>7%</div> <div>47%</div> <div>47%</div> <div>7%</div> </div>

## 2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 7113 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				

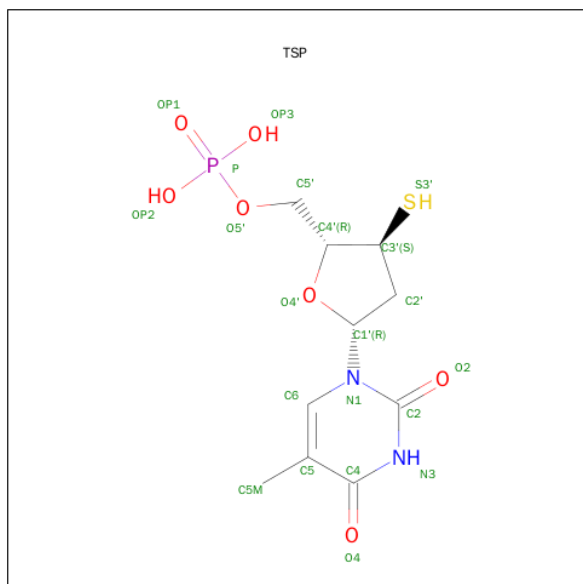
- Molecule 4 is a DNA chain called DNA (5'-D(P\*GP\*GP\*AP\*TP\*GP\*AP\*CP\*GP\*AP\*TP\*)-3').

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 3'-THIO-THYMIDINE-5'-PHOSPHATE (three-letter code: TSP) (formula:  $C_{10}H_{15}N_2O_7PS$ ).



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

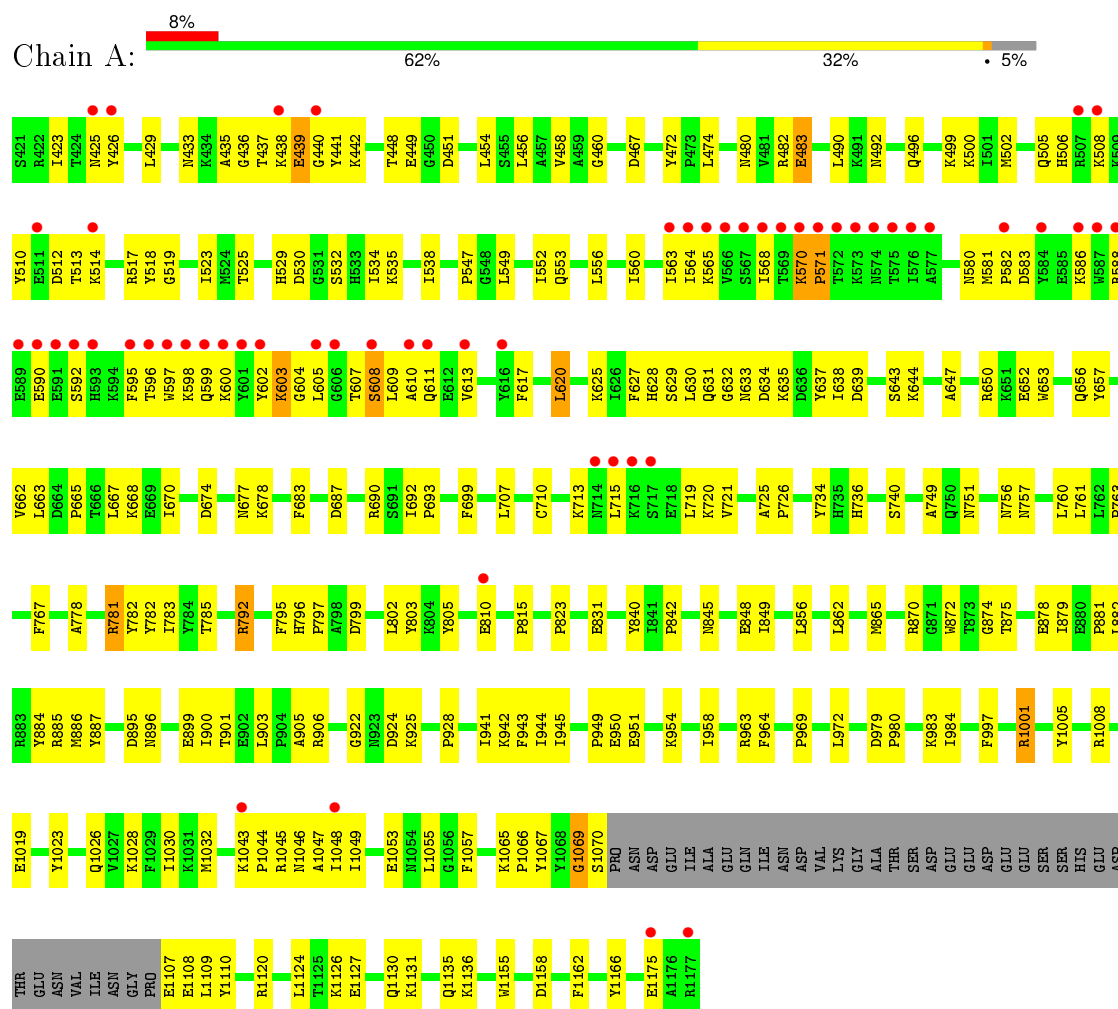
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	100	Total	O	0	0
			100	100		
7	B	6	Total	O	0	0
			6	6		
7	C	2	Total	O	0	0
			2	2		
7	D	5	Total	O	0	0
			5	5		

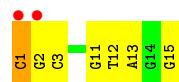
### 3 Residue-property plots

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



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



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



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 2 <sub>1</sub> 2 <sub>1</sub> 2 <sub>1</sub>	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	86.05Å 92.42Å 116.73Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	43.02 – 2.48 43.02 – 2.49	Depositor EDS
% Data completeness (in resolution range)	99.7 (43.02-2.48) 99.7 (43.02-2.49)	Depositor EDS
$R_{merge}$	0.05	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.15 (at 2.48Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.5_2)	Depositor
R, $R_{free}$	0.239 , 0.259 0.240 , 0.258	Depositor DCC
$R_{free}$ test set	1630 reflections (5.14%)	DCC
Wilson B-factor (Å <sup>2</sup> )	52.0	Xtriage
Anisotropy	0.238	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.29 , 47.2	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	0 of 33367 reflections	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	7113	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	77.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.64% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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 ⓘ

### 5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: 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	0.32	0/6062	0.57	4/8176 (0.0%)
2	B	0.56	0/243	1.19	3/371 (0.8%)
3	C	0.78	0/349	1.17	1/539 (0.2%)
4	D	0.61	0/236	1.39	6/363 (1.7%)
5	E	0.68	0/335	1.12	2/514 (0.4%)
All	All	0.40	0/7225	0.73	16/9963 (0.2%)

There are no bond length outliers.

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1120	ARG	NE-CZ-NH2	-17.29	111.66	120.30
4	D	1[B]	DG	OP2-P-O3'	-9.07	85.25	105.20
4	D	10[B]	DT	O4'-C4'-C3'	-8.33	101.00	106.00
3	C	1[A]	DC	P-O3'-C3'	-7.05	111.25	119.70
2	B	10[A]	DA	O4'-C4'-C3'	-7.00	101.70	104.50
1	A	1069	GLY	N-CA-C	6.97	130.53	113.10
1	A	1120	ARG	NH1-CZ-NH2	6.72	126.79	119.40
2	B	9[A]	DT	P-O3'-C3'	6.41	127.39	119.70
4	D	6[B]	DA	O4'-C4'-C3'	-6.21	102.02	104.50
4	D	1[B]	DG	OP1-P-O3'	5.82	118.01	105.20
4	D	10[B]	DT	O4'-C1'-N1	5.72	112.01	108.00
5	E	2[B]	DG	C4'-C3'-C2'	-5.25	98.38	103.10
4	D	10[B]	DT	C4'-C3'-C2'	-5.20	98.42	103.10
5	E	2[B]	DG	O4'-C4'-C3'	-5.13	102.45	104.50
2	B	10[A]	DA	C4'-C3'-C2'	-5.12	98.49	103.10
1	A	620	LEU	N-CA-CB	5.12	120.63	110.40

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	271	0
2	B	219	0	115	13	0
3	C	310	0	151	16	0
4	D	210	0	99	15	0
5	E	300	0	150	17	0
6	D	20	0	8	1	0
7	A	100	0	0	6	0
7	B	6	0	0	1	0
7	C	2	0	0	2	0
7	D	5	0	0	0	0
All	All	7113	0	6472	305	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 23.

All (305) 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:592:SER:HB2	1:A:597:TRP:CZ2	1.78	1.18
1:A:423:ILE:HD11	1:A:517:ARG:NH2	1.69	1.07
1:A:423:ILE:CD1	1:A:517:ARG:HH22	1.68	1.05
1:A:592:SER:HB2	1:A:597:TRP:CE2	1.92	1.04
1:A:699:PHE:CZ	1:A:707:LEU:HD12	1.91	1.04
1:A:423:ILE:HD11	1:A:517:ARG:HH22	0.89	1.04
2:B:3[A]:DT:O4	3:C:13[A]:DA:N1	1.94	1.01
1:A:599:GLN:CG	1:A:810:GLU:HB2	1.95	0.97
1:A:482:ARG:O	1:A:483:GLU:HG2	1.66	0.96
1:A:895:ASP:HB2	7:A:188:HOH:O	1.64	0.95
1:A:599:GLN:HG3	1:A:810:GLU:HB2	1.49	0.94
1:A:699:PHE:CZ	1:A:707:LEU:CD1	2.53	0.90
1:A:441:TYR:O	1:A:519:GLY:HA3	1.71	0.90
1:A:604:GLY:HA3	1:A:607:THR:CG2	2.01	0.89
1:A:437:THR:O	1:A:439:GLU:N	2.05	0.89
1:A:563:ILE:HD12	1:A:580:ASN:HA	1.56	0.87
1:A:607:THR:HG23	1:A:608:SER:N	1.90	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:603:LYS:O	1:A:607:THR:HG21	1.75	0.86
1:A:604:GLY:HA3	1:A:607:THR:HG22	1.56	0.86
1:A:849:ILE:HA	1:A:865:MET:HE1	1.56	0.85
1:A:699:PHE:CE2	1:A:707:LEU:HD12	2.12	0.85
1:A:592:SER:CB	1:A:597:TRP:CZ2	2.60	0.84
1:A:482:ARG:NH2	1:A:639:ASP:HA	1.92	0.83
1:A:483:GLU:HG3	1:A:644:LYS:HB2	1.60	0.83
1:A:512:ASP:HB3	1:A:514:LYS:HG2	1.58	0.83
1:A:592:SER:O	1:A:597:TRP:NE1	2.13	0.82
1:A:563:ILE:HG22	1:A:564:ILE:HG13	1.62	0.82
1:A:483:GLU:HB3	1:A:644:LYS:HD2	1.61	0.81
1:A:474:LEU:HD11	1:A:538:ILE:HD11	1.64	0.80
1:A:571:PRO:HD3	1:A:596:THR:HG1	1.46	0.80
1:A:571:PRO:HD3	1:A:596:THR:OG1	1.81	0.80
1:A:603:LYS:O	1:A:607:THR:CG2	2.32	0.78
1:A:699:PHE:HZ	1:A:707:LEU:CD1	1.95	0.78
3:C:1[A]:DC:H2''	3:C:2[A]:DG:H5'	1.66	0.77
2:B:5[A]:DC:H2''	2:B:6[A]:DT:H5'	1.66	0.76
1:A:1067:TYR:HE1	1:A:1070:SER:H	1.34	0.76
1:A:425:ASN:HB3	1:A:426:TYR:CE2	2.21	0.75
1:A:633:ASN:O	1:A:637:TYR:HD1	1.69	0.75
1:A:749:ALA:O	1:A:763:PRO:HG3	1.88	0.74
1:A:607:THR:HG23	1:A:608:SER:H	1.50	0.73
3:C:3[A]:DC:H5'	7:C:212:HOH:O	1.88	0.72
2:B:3[A]:DT:C4	3:C:13[A]:DA:N1	2.57	0.72
1:A:482:ARG:O	1:A:483:GLU:CG	2.37	0.72
1:A:603:LYS:C	1:A:607:THR:HG21	2.11	0.71
1:A:922:GLY:HA3	1:A:928:PRO:HD3	1.70	0.71
1:A:699:PHE:HZ	1:A:707:LEU:HD11	1.56	0.71
1:A:456:LEU:HD13	1:A:605:LEU:HD12	1.73	0.70
1:A:799:ASP:OD2	1:A:1001:ARG:NH2	2.23	0.70
1:A:879:ILE:HD11	1:A:885:ARG:HG3	1.74	0.69
1:A:608:SER:HB3	7:A:197:HOH:O	1.93	0.69
3:C:1[A]:DC:C2'	3:C:2[A]:DG:H5'	2.22	0.69
2:B:5[A]:DC:N3	3:C:11[A]:DG:N2	2.36	0.68
1:A:607:THR:CG2	1:A:608:SER:N	2.56	0.68
1:A:588:ARG:NH2	1:A:599:GLN:HE22	1.91	0.68
1:A:437:THR:O	1:A:440:GLY:N	2.26	0.68
1:A:725:ALA:HB3	1:A:726:PRO:HD3	1.76	0.68
1:A:756:ASN:O	1:A:870:ARG:NH1	2.27	0.68
1:A:979:ASP:HB2	1:A:980:PRO:HD2	1.76	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:610:ALA:O	1:A:613:VAL:HB	1.93	0.67
1:A:799:ASP:CG	1:A:1001:ARG:HH22	1.97	0.67
4:D:5[B]:DG:N2	5:E:11[B]:DC:O2	2.28	0.67
1:A:663:LEU:HD12	1:A:678:LYS:HD2	1.76	0.67
1:A:568:ILE:CG2	1:A:571:PRO:HG2	2.25	0.67
1:A:437:THR:C	1:A:439:GLU:N	2.46	0.66
1:A:1001:ARG:HD2	1:A:1001:ARG:O	1.96	0.66
1:A:607:THR:CG2	1:A:608:SER:H	2.07	0.66
7:C:212:HOH:O	5:E:3[B]:DC:H5'	1.95	0.66
1:A:482:ARG:HH21	1:A:639:ASP:HA	1.59	0.66
1:A:570:LYS:N	1:A:571:PRO:CD	2.59	0.66
1:A:490:LEU:O	1:A:490:LEU:HD23	1.95	0.66
1:A:792:ARG:NH1	1:A:795:PHE:O	2.28	0.66
1:A:1107:GLU:HG2	1:A:1109:LEU:H	1.60	0.66
1:A:1043:LYS:O	1:A:1048:ILE:HG13	1.96	0.65
1:A:482:ARG:C	1:A:483:GLU:HG2	2.17	0.65
1:A:499:LYS:NZ	1:A:506:HIS:CE1	2.65	0.65
1:A:903:LEU:HG	1:A:941:ILE:HD13	1.78	0.65
1:A:433:ASN:HB2	1:A:467:ASP:HA	1.78	0.64
1:A:598:LYS:NZ	1:A:600:LYS:HG2	2.13	0.63
1:A:608:SER:CB	7:A:197:HOH:O	2.45	0.63
1:A:437:THR:C	1:A:439:GLU:H	2.00	0.63
1:A:634:ASP:O	1:A:638:ILE:HG13	2.00	0.62
1:A:896:ASN:HD21	1:A:949:PRO:HG3	1.65	0.61
4:D:3[B]:DA:N6	5:E:13[B]:DT:N3	2.47	0.61
1:A:736:HIS:CD2	2:B:10[A]:DA:H5''	2.34	0.61
1:A:668:LYS:HG3	1:A:668:LYS:O	2.00	0.61
1:A:767:PHE:CE1	1:A:783:ILE:HB	2.34	0.61
1:A:499:LYS:HZ3	1:A:506:HIS:CE1	2.19	0.61
1:A:583:ASP:OD2	1:A:665:PRO:HG2	2.00	0.61
1:A:482:ARG:O	1:A:483:GLU:CB	2.49	0.61
4:D:1[B]:DG:N2	5:E:15[B]:DC:N3	2.49	0.61
1:A:778:ALA:HB1	1:A:782[A]:PTR:HD1	1.83	0.61
1:A:513:THR:HG23	1:A:552:ILE:HG21	1.82	0.61
1:A:958:ILE:HD12	1:A:963:ARG:HH11	1.65	0.60
1:A:570:LYS:N	1:A:571:PRO:HD2	2.16	0.60
1:A:845:ASN:HB3	1:A:848:GLU:HG2	1.83	0.60
1:A:586:LYS:O	1:A:590:GLU:HG3	2.01	0.60
1:A:647:ALA:HA	1:A:650:ARG:NH1	2.17	0.60
1:A:483:GLU:CB	1:A:644:LYS:HD2	2.32	0.59
1:A:856:LEU:HG	1:A:862:LEU:HD21	1.83	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:875:THR:CG2	1:A:887:TYR:HB2	2.33	0.59
1:A:945:ILE:HD13	1:A:964:PHE:CE1	2.37	0.59
1:A:895:ASP:O	1:A:896:ASN:HB2	2.03	0.59
1:A:736:HIS:CG	4:D:10[B]:DT:H5''	2.37	0.59
1:A:875:THR:HG23	1:A:887:TYR:HB2	1.85	0.58
1:A:823:PRO:HD3	1:A:997:PHE:CE2	2.38	0.58
1:A:1008:ARG:NH2	1:A:1158:ASP:OD2	2.28	0.58
1:A:1026:GLN:O	1:A:1030:ILE:HG12	2.04	0.58
4:D:6[B]:DA:H5'	4:D:6[B]:DA:C8	2.39	0.58
1:A:609:LEU:HG	1:A:611:GLN:HG2	1.86	0.58
1:A:667:LEU:O	1:A:668:LYS:HB3	2.03	0.58
3:C:1[A]:DC:C2'	3:C:2[A]:DG:C5'	2.83	0.57
1:A:979:ASP:HB2	1:A:980:PRO:CD	2.34	0.57
1:A:1032:MET:HE1	1:A:1055:LEU:HD13	1.85	0.57
1:A:736:HIS:CG	2:B:10[A]:DA:H5''	2.39	0.57
1:A:436:GLY:HA2	1:A:517:ARG:HA	1.87	0.57
1:A:581:MET:HB2	1:A:582:PRO:HD3	1.86	0.57
2:B:3[A]:DT:O4	3:C:13[A]:DA:C6	2.57	0.57
1:A:1019:GLU:O	1:A:1023:TYR:HD2	1.86	0.56
1:A:530:ASP:O	1:A:534:ILE:HG12	2.06	0.56
1:A:483:GLU:CG	1:A:644:LYS:HB2	2.32	0.56
1:A:549:LEU:O	1:A:549:LEU:HD12	2.05	0.56
1:A:425:ASN:CB	1:A:426:TYR:CE2	2.88	0.56
1:A:652:GLU:OE2	1:A:656:GLN:NE2	2.39	0.56
1:A:751:ASN:O	1:A:870:ARG:NH2	2.39	0.55
1:A:901:THR:HA	1:A:941:ILE:O	2.06	0.55
2:B:3[A]:DT:N3	3:C:13[A]:DA:C2	2.75	0.55
1:A:663:LEU:HD13	1:A:678:LYS:HB2	1.88	0.55
1:A:872:TRP:CH2	1:A:886:MET:HG3	2.41	0.55
1:A:663:LEU:HD21	1:A:670:ILE:HG23	1.87	0.55
1:A:736:HIS:CD2	4:D:10[B]:DT:H5''	2.40	0.55
1:A:592:SER:HB2	1:A:597:TRP:NE1	2.21	0.55
1:A:423:ILE:CG1	1:A:517:ARG:HH22	2.17	0.55
1:A:878:GLU:HB2	1:A:884:TYR:CE2	2.42	0.55
1:A:715:LEU:HD11	1:A:719:LEU:HD22	1.87	0.55
1:A:592:SER:C	1:A:597:TRP:HE1	2.09	0.55
1:A:608:SER:O	1:A:609:LEU:C	2.41	0.54
1:A:437:THR:O	1:A:438:LYS:C	2.46	0.54
1:A:831:GLU:CG	1:A:840:TYR:HD1	2.20	0.54
1:A:598:LYS:HE2	1:A:810:GLU:OE1	2.08	0.54
1:A:674:ASP:HB2	1:A:678:LYS:HD2	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:663:LEU:CD1	1:A:678:LYS:HD2	2.38	0.54
4:D:5[B]:DG:H2''	4:D:6[B]:DA:C5'	2.39	0.53
1:A:480:ASN:HA	7:A:184:HOH:O	2.08	0.53
1:A:802:LEU:HD11	1:A:1008:ARG:HB2	1.90	0.53
5:E:11[B]:DC:H2''	5:E:12[B]:DA:C8	2.43	0.53
1:A:951:GLU:HG3	7:A:190:HOH:O	2.08	0.53
1:A:1005:TYR:CZ	1:A:1155:TRP:HA	2.44	0.52
1:A:721:VAL:CG2	1:A:783:ILE:HG13	2.39	0.52
1:A:490:LEU:HA	1:A:496:GLN:NE2	2.25	0.52
5:E:1[B]:DC:H2'	5:E:2[B]:DG:O4'	2.10	0.52
1:A:568:ILE:HG22	1:A:571:PRO:HG2	1.90	0.52
1:A:1069:GLY:O	1:A:1070:SER:CB	2.57	0.52
1:A:905:ALA:O	1:A:906:ARG:HB2	2.09	0.52
1:A:529:HIS:HB3	1:A:683:PHE:HA	1.92	0.52
1:A:604:GLY:HA3	1:A:607:THR:CB	2.39	0.51
1:A:740:SER:HB2	7:B:202:HOH:O	2.10	0.51
1:A:570:LYS:HB2	1:A:596:THR:OG1	2.12	0.50
1:A:757:ASN:ND2	1:A:870:ARG:H	2.09	0.50
1:A:436:GLY:CA	1:A:517:ARG:HA	2.42	0.50
1:A:620:LEU:H	1:A:620:LEU:HD23	1.75	0.50
1:A:900:ILE:HB	1:A:943:PHE:HB2	1.94	0.50
1:A:490:LEU:C	1:A:490:LEU:HD23	2.32	0.50
1:A:674:ASP:O	1:A:678:LYS:HB2	2.12	0.50
1:A:720:LYS:HD3	1:A:781:ARG:HA	1.93	0.50
1:A:523:ILE:HG22	1:A:525:THR:HG23	1.94	0.50
1:A:482:ARG:NH2	1:A:639:ASP:CA	2.72	0.50
1:A:570:LYS:N	1:A:596:THR:OG1	2.35	0.50
1:A:707:LEU:HD11	1:A:760:LEU:CD1	2.42	0.49
2:B:4[A]:DA:N1	3:C:12[A]:DT:N3	2.60	0.49
1:A:710:CYS:SG	1:A:715:LEU:HD22	2.53	0.49
1:A:823:PRO:HD3	1:A:997:PHE:CD2	2.47	0.49
1:A:454:LEU:O	1:A:458:VAL:HG13	2.12	0.49
1:A:483:GLU:HG3	1:A:644:LYS:CB	2.38	0.49
1:A:1049:ILE:O	1:A:1053:GLU:HG2	2.13	0.49
1:A:1069:GLY:O	1:A:1070:SER:OG	2.27	0.49
1:A:482:ARG:HH22	1:A:639:ASP:HA	1.75	0.49
1:A:1175:GLU:HB2	7:A:114:HOH:O	2.12	0.49
1:A:565:LYS:HE3	1:A:602:TYR:CD1	2.48	0.49
1:A:429:LEU:HB2	1:A:472:TYR:CD1	2.48	0.48
1:A:426:TYR:OH	1:A:500:LYS:HB2	2.13	0.48
1:A:969:PRO:HG2	5:E:12[B]:DA:O5'	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:598:LYS:HZ3	1:A:600:LYS:HG2	1.76	0.48
1:A:630:LEU:HD13	1:A:635:LYS:HE3	1.95	0.48
1:A:592:SER:CB	1:A:597:TRP:HZ2	2.23	0.48
1:A:1126:LYS:HG3	1:A:1127:GLU:N	2.29	0.48
4:D:1[B]:DG:N2	5:E:15[B]:DC:C2	2.82	0.47
1:A:831:GLU:HG3	1:A:840:TYR:HD1	1.78	0.47
1:A:899:GLU:HG3	1:A:944:ILE:HD13	1.96	0.47
1:A:604:GLY:O	1:A:605:LEU:C	2.51	0.47
1:A:656:GLN:O	1:A:657:TYR:C	2.52	0.47
1:A:426:TYR:OH	1:A:500:LYS:CB	2.63	0.47
1:A:954:LYS:CD	1:A:963:ARG:HH12	2.28	0.47
4:D:5[B]:DG:H2''	4:D:6[B]:DA:H5'	1.97	0.47
1:A:1023:TYR:HB3	1:A:1136:LYS:HB2	1.96	0.46
1:A:448:THR:HG21	1:A:454:LEU:HA	1.96	0.46
1:A:441:TYR:CE2	1:A:442:LYS:HG3	2.49	0.46
1:A:799:ASP:OD1	1:A:1008:ARG:HD3	2.15	0.46
1:A:1044:PRO:O	1:A:1047:ALA:N	2.46	0.46
1:A:512:ASP:CB	1:A:514:LYS:HG2	2.36	0.46
1:A:482:ARG:C	1:A:483:GLU:CG	2.80	0.46
1:A:958:ILE:HD12	1:A:963:ARG:HD2	1.98	0.46
2:B:5[A]:DC:O2	3:C:11[A]:DG:N2	2.48	0.46
1:A:474:LEU:CD1	1:A:538:ILE:HD11	2.39	0.46
4:D:5[B]:DG:N1	5:E:11[B]:DC:N3	2.64	0.46
1:A:715:LEU:HD12	1:A:715:LEU:HA	1.74	0.46
1:A:456:LEU:HD22	1:A:605:LEU:HD11	1.97	0.46
1:A:734:TYR:CE2	1:A:736:HIS:HB2	2.50	0.46
1:A:598:LYS:HZ2	1:A:600:LYS:HG2	1.80	0.46
1:A:761:LEU:HB3	1:A:785:THR:OG1	2.16	0.46
1:A:674:ASP:HB2	1:A:678:LYS:CD	2.45	0.45
1:A:734:TYR:CZ	1:A:736:HIS:HB2	2.51	0.45
3:C:1[A]:DC:H2'	3:C:2[A]:DG:C5'	2.46	0.45
1:A:954:LYS:CG	1:A:963:ARG:HH12	2.30	0.45
3:C:12[A]:DT:H2''	3:C:13[A]:DA:C8	2.51	0.45
1:A:451:ASP:HA	1:A:454:LEU:HB3	1.99	0.45
1:A:425:ASN:C	1:A:426:TYR:CD2	2.90	0.45
5:E:12[B]:DA:OP2	5:E:12[B]:DA:H8	1.98	0.45
1:A:435:ALA:HB3	1:A:517:ARG:HH11	1.82	0.45
1:A:513:THR:HG23	1:A:552:ILE:HD13	1.97	0.45
1:A:568:ILE:HG23	1:A:595:PHE:HB3	1.98	0.45
1:A:1126:LYS:O	1:A:1130:GLN:HG2	2.17	0.45
1:A:499:LYS:HZ1	1:A:506:HIS:CE1	2.34	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1162:PHE:O	1:A:1166:TYR:N	2.49	0.44
1:A:632:GLY:O	1:A:633:ASN:HB2	2.17	0.44
1:A:782[A]:PTR:O3P	1:A:782[A]:PTR:HE2	2.18	0.44
1:A:983:LYS:HA	1:A:983:LYS:HD3	1.69	0.44
1:A:482:ARG:HH22	1:A:639:ASP:CA	2.30	0.44
1:A:1001:ARG:HA	1:A:1001:ARG:HD3	1.52	0.44
1:A:713:LYS:HZ2	1:A:715:LEU:HD12	1.83	0.44
1:A:435:ALA:O	1:A:437:THR:HG23	2.18	0.44
2:B:5[A]:DC:C2	3:C:11[A]:DG:N2	2.74	0.44
1:A:805:TYR:CE2	1:A:815:PRO:HG3	2.52	0.44
1:A:435:ALA:C	1:A:437:THR:H	2.20	0.44
1:A:633:ASN:O	1:A:637:TYR:CD1	2.60	0.44
1:A:707:LEU:HD11	1:A:760:LEU:HD13	1.99	0.44
1:A:872:TRP:CZ2	1:A:874:GLY:HA3	2.53	0.44
1:A:805:TYR:HA	1:A:815:PRO:HA	1.99	0.44
1:A:1032:MET:HE1	1:A:1057:PHE:HE2	1.82	0.43
1:A:1109:LEU:HD23	1:A:1110:TYR:CE2	2.53	0.43
1:A:532:SER:HA	1:A:535:LYS:HD2	2.01	0.43
1:A:436:GLY:HA3	1:A:517:ARG:HD2	2.00	0.43
1:A:607:THR:O	1:A:608:SER:C	2.57	0.43
1:A:881:PRO:O	1:A:882:LEU:HB2	2.19	0.43
1:A:553:GLN:HE22	1:A:629:SER:H	1.66	0.43
1:A:1045:ARG:HG3	1:A:1046:ASN:N	2.33	0.43
1:A:604:GLY:HA3	1:A:607:THR:HB	1.99	0.43
1:A:499:LYS:HZ1	1:A:506:HIS:HE1	1.67	0.43
1:A:958:ILE:HD12	1:A:963:ARG:NH1	2.32	0.43
1:A:1131:LYS:O	1:A:1135:GLN:HG3	2.19	0.43
1:A:692:ILE:HD12	1:A:984:ILE:HD11	2.01	0.43
4:D:4[B]:DT:N3	5:E:12[B]:DA:N1	2.66	0.43
1:A:692:ILE:HG23	1:A:693:PRO:HD2	2.00	0.43
1:A:925:LYS:NZ	3:C:15[A]:DG:H3'	2.34	0.43
1:A:849:ILE:CA	1:A:865:MET:HE1	2.38	0.43
4:D:1[B]:DG:N2	5:E:15[B]:DC:O2	2.52	0.43
1:A:1005:TYR:CE2	1:A:1155:TRP:CG	3.06	0.43
1:A:690:ARG:HD2	2:B:10[A]:DA:H5'	2.01	0.43
1:A:899:GLU:OE1	1:A:942:LYS:HE3	2.18	0.43
1:A:426:TYR:N	1:A:426:TYR:CD2	2.83	0.43
1:A:792:ARG:HA	1:A:792:ARG:HD2	1.70	0.43
1:A:502:MET:SD	1:A:518:TYR:HB2	2.59	0.43
4:D:3[B]:DA:N6	5:E:13[B]:DT:C4	2.87	0.42
1:A:1030:ILE:HG23	1:A:1124:LEU:HD23	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1028:LYS:O	1:A:1032:MET:HG3	2.19	0.42
1:A:803:TYR:HB3	1:A:815:PRO:HB3	2.00	0.42
1:A:449:GLU:OE1	6:D:11[B]:TSP:S3'	2.78	0.42
1:A:492:ASN:O	1:A:496:GLN:HG2	2.20	0.42
1:A:628:HIS:HE2	1:A:631:GLN:CD	2.23	0.42
1:A:560:ILE:CD1	1:A:625:LYS:HE2	2.50	0.42
1:A:950:GLU:OE1	1:A:950:GLU:N	2.50	0.42
1:A:441:TYR:HA	1:A:519:GLY:HA3	2.02	0.41
1:A:1107:GLU:HG2	1:A:1108:GLU:N	2.34	0.41
1:A:1065:LYS:HA	1:A:1066:PRO:HD3	1.81	0.41
1:A:482:ARG:O	1:A:483:GLU:HB2	2.20	0.41
1:A:500:LYS:HD3	1:A:500:LYS:HA	1.81	0.41
4:D:3[B]:DA:N1	5:E:13[B]:DT:N3	2.67	0.41
1:A:831:GLU:HG3	1:A:840:TYR:CD1	2.54	0.41
5:E:1[B]:DC:C2'	5:E:2[B]:DG:H5'	2.50	0.41
1:A:599:GLN:CD	1:A:810:GLU:HB2	2.39	0.41
1:A:643:SER:O	1:A:650:ARG:NH2	2.52	0.41
1:A:699:PHE:CZ	1:A:707:LEU:HD11	2.37	0.41
1:A:441:TYR:C	1:A:519:GLY:HA3	2.37	0.41
1:A:796:HIS:HA	1:A:797:PRO:HD3	1.88	0.41
1:A:690:ARG:NH1	2:B:10[A]:DA:H4'	2.35	0.41
1:A:556:LEU:HG	1:A:627:PHE:CD1	2.55	0.41
1:A:721:VAL:HG21	1:A:783:ILE:HG13	2.01	0.41
4:D:4[B]:DT:O4	5:E:12[B]:DA:N1	2.54	0.41
1:A:954:LYS:HG2	1:A:963:ARG:HH12	1.86	0.41
1:A:845:ASN:HB3	1:A:848:GLU:CG	2.51	0.41
1:A:508:LYS:O	1:A:547:PRO:HG2	2.20	0.41
1:A:650:ARG:NH1	5:E:9[B]:DG:OP1	2.54	0.41
3:C:11[A]:DG:H2''	3:C:12[A]:DT:OP2	2.19	0.41
1:A:460:GLY:HA2	1:A:617:PHE:CD1	2.56	0.41
1:A:683:PHE:O	1:A:687:ASP:N	2.53	0.41
1:A:460:GLY:HA3	1:A:617:PHE:CZ	2.56	0.41
1:A:598:LYS:HZ3	1:A:600:LYS:CG	2.34	0.40
1:A:662:VAL:HG12	1:A:663:LEU:N	2.36	0.40
1:A:713:LYS:NZ	1:A:715:LEU:HD12	2.36	0.40
1:A:653:TRP:HE1	1:A:677:ASN:ND2	2.19	0.40
1:A:564:ILE:HG23	1:A:600:LYS:O	2.22	0.40
1:A:667:LEU:HD23	1:A:667:LEU:HA	1.80	0.40
1:A:951:GLU:HA	1:A:951:GLU:OE1	2.21	0.40
1:A:924:ASP:O	1:A:924:ASP:OD1	2.39	0.40
1:A:505:GLN:H	1:A:510:TYR:HH	1.68	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:842:PRO:HG3	1:A:972:LEU:CD2	2.51	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	716/758 (94%)	688 (96%)	24 (3%)	4 (1%)	30	48

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	571	PRO
1	A	483	GLU
1	A	608	SER
1	A	570	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%)	635 (99%)	5 (1%)	86	96

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	439	GLU
1	A	603	LYS
1	A	781	ARG
1	A	792	ARG
1	A	1001	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	492	ASN
1	A	506	HIS
1	A	553	GLN
1	A	599	GLN
1	A	656	GLN
1	A	677	ASN
1	A	757	ASN
1	A	936	GLN

### 5.3.3 RNA ⓘ

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	1.83	1 (7%)	18,22,24	1.11	3 (16%)

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	-6.70	1.24	1.40

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	782[A]	PTR	O-C-CA	-2.52	118.93	125.49
1	A	782[A]	PTR	O3P-P-OH	2.06	112.61	105.22
1	A	782[A]	PTR	P-OH-CZ	2.06	129.69	123.76

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 [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

1 ligand 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	$\# Z  > 2$
6	TSP	D	11[B]	4	10,21,22	1.40	3 (30%)	11,30,33	4.95	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
6	TSP	D	11[B]	4	-	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)
6	D	11[B]	TSP	C6-C5	-2.12	1.34	1.40
6	D	11[B]	TSP	C6-N1	2.24	1.38	1.35
6	D	11[B]	TSP	C4-N3	3.01	1.38	1.33

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	D	11[B]	TSP	C5-C4-N3	-8.79	115.35	125.14
6	D	11[B]	TSP	C4-N3-C2	13.75	127.14	115.25

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	D	11[B]	TSP	1	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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	720/758 (94%)	0.40	57 (7%) 15 16	27, 61, 151, 274	1 (0%)
2	B	11/11 (100%)	0.36	0 100 100	49, 80, 182, 359	11 (100%)
3	C	15/15 (100%)	0.67	2 (13%) 4 4	39, 103, 252, 288	15 (100%)
4	D	10/10 (100%)	0.48	0 100 100	35, 63, 124, 235	10 (100%)
5	E	15/15 (100%)	0.59	1 (6%) 21 23	54, 71, 130, 132	15 (100%)
All	All	771/809 (95%)	0.41	60 (7%) 16 17	27, 63, 157, 359	52 (6%)

All (60) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	564	ILE	7.7
1	A	602	TYR	7.6
1	A	566	VAL	6.5
1	A	610	ALA	6.3
1	A	507	ARG	6.2
1	A	572	THR	6.0
1	A	569	THR	6.0
1	A	587	TRP	5.8
1	A	563	ILE	5.8
1	A	575	THR	5.8
1	A	588	ARG	5.7
1	A	570	LYS	5.4
1	A	605	LEU	5.3
1	A	592	SER	5.1
1	A	597	TRP	4.9
1	A	571	PRO	4.8
1	A	598	LYS	4.8
1	A	716	LYS	4.7
1	A	596	THR	4.6
1	A	568	ILE	4.3

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Mol	Chain	Res	Type	RSRZ
1	A	606	GLY	4.3
1	A	616	TYR	4.1
1	A	565	LYS	4.1
1	A	591	GLU	4.0
1	A	584	TYR	3.8
1	A	593	HIS	3.8
1	A	611	GLN	3.8
1	A	600	LYS	3.8
1	A	567	SER	3.7
1	A	425	ASN	3.6
1	A	590	GLU	3.6
1	A	573	LYS	3.5
1	A	595	PHE	3.5
1	A	1043	LYS	3.3
1	A	576	ILE	3.2
1	A	601	TYR	3.2
1	A	508	LYS	3.2
1	A	1175	GLU	3.2
1	A	1177	ARG	3.1
1	A	599	GLN	3.0
1	A	577	ALA	3.0
1	A	574	ASN	3.0
1	A	714	ASN	3.0
1	A	810	GLU	2.9
1	A	511	GLU	2.7
5	E	2[B]	DG	2.6
1	A	715	LEU	2.5
3	C	1[A]	DC	2.5
1	A	440	GLY	2.3
1	A	613	VAL	2.3
3	C	2[A]	DG	2.2
1	A	586	LYS	2.2
1	A	608	SER	2.2
1	A	426	TYR	2.2
1	A	1048	ILE	2.2
1	A	438	LYS	2.1
1	A	514	LYS	2.1
1	A	589	GLU	2.1
1	A	717	SER	2.1
1	A	582	PRO	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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	PTR	A	782[A]	16/17	0.90	0.18	-	56,68,90,95	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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
6	TSP	D	11[B]	20/21	0.96	0.18	-0.37	35,44,51,57	20

## 6.5 Other polymers [i](#)

There are no such residues in this entry.