



# Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 04:24 PM UTC

PDB ID : 2XO7 / pdb\_00002xo7  
Title : Crystal structure of a dA:O-allylhydroxylamine-dC basepair in complex with fragment DNA polymerase I from *Bacillus stearothermophilus*  
Authors : Muenzel, M.; Lercher, L.; Mueller, M.; Carell, T.  
Deposited on : 2010-08-10  
Resolution : 2.85 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

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

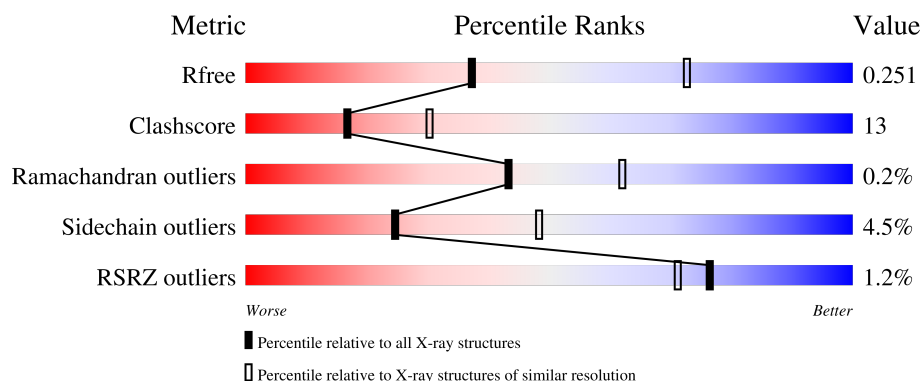
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.85 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	180053	1407 (2.88-2.84)
Clashscore	190562	1446 (2.88-2.84)
Ramachandran outliers	187476	1406 (2.88-2.84)
Sidechain outliers	187428	1407 (2.88-2.84)
RSRZ outliers	180081	1408 (2.88-2.84)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	A	580	<div> <div></div> <div>76%</div> <div>23%</div> <div>.</div> </div>
2	B	10	<div> <div>10%</div> <div>60%</div> <div>30%</div> <div>10%</div> </div>
3	C	11	<div> <div>9%</div> <div>45%</div> <div>45%</div> <div>9%</div> </div>

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 5088 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 POLYMERASE I.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	580	Total	C	N	O	S	0	0	0
			4633	2945	808	863	17			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	512	ARG	GLY	SEE REMARK 999	UNP C3IXT2
A	550	SER	THR	SEE REMARK 999	UNP C3IXT2

- Molecule 2 is a DNA chain called 5'-D(\*GP\*AP\*CP\*CP\*AP\*TP\*47C\*CP\*CP\*T)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	10	Total	C	N	O	P	0	0	0
			200	98	34	59	9			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	11	Total	C	N	O	P	0	0	0
			228	109	47	62	10			

- Molecule 4 is SULFATE ION (CCD ID: SO4) (formula: O<sub>4</sub>S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	O	S	0	0
			5	4	1		
4	A	1	Total	O	S	0	0
			5	4	1		
4	A	1	Total	O	S	0	0
			5	4	1		
4	A	1	Total	O	S	0	0
			5	4	1		

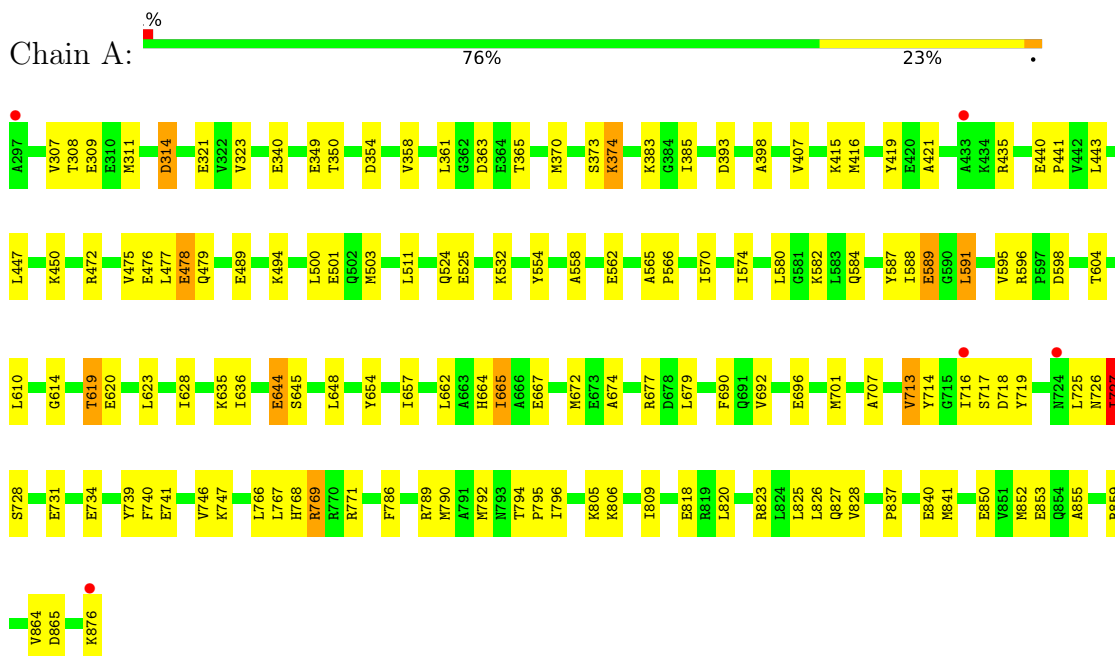
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	7	Total	O	0	0
			7	7		

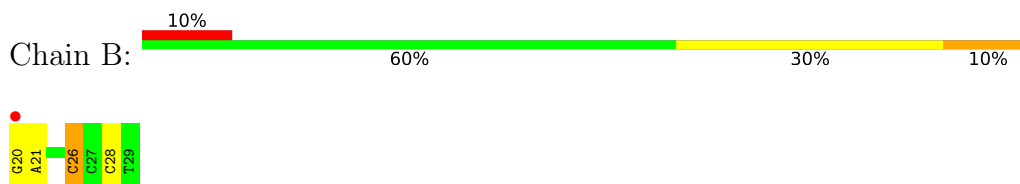
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

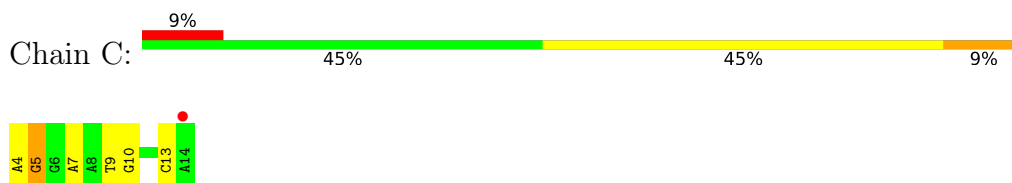
#### • Molecule 1: DNA POLYMERASE I



#### • Molecule 2: 5'-D(\*GP\*AP\*CP\*CP\*AP\*TP\*47C\*CP\*CP\*T)-3'



#### • Molecule 3: 5'-D(\*AP\*GP\*GP\*AP\*AP\*TP\*GP\*GP\*TP\*CP\*A)-3'



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	87.48Å 93.64Å 105.09Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	43.74 – 2.85 43.74 – 2.85	Depositor EDS
% Data completeness (in resolution range)	99.4 (43.74-2.85) 99.3 (43.74-2.85)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.02 (at 2.86Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, $R_{free}$	0.215 , 0.245 0.214 , 0.251	Depositor DCC
$R_{free}$ test set	1047 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	51.1	Xtriage
Anisotropy	0.145	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 36.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	5088	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.67% 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, 0.333 respectively for untwinned datasets, and 0.375, 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: SO4, 47C

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	0.84	0/4715	0.90	2/6371 (0.0%)
2	B	0.55	0/196	1.18	0/297
3	C	0.58	0/257	1.25	2/396 (0.5%)
All	All	0.82	0/5168	0.94	4/7064 (0.1%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	13	DC	P-O3'-C3'	7.82	131.92	120.20
1	A	769	ARG	N-CA-C	-5.84	102.82	110.53
3	C	5	DG	C5'-C4'-O4'	-5.57	101.05	109.40
1	A	478	GLU	N-CA-C	5.07	116.81	111.28

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	4633	0	4688	117	0
2	B	200	0	118	5	0
3	C	228	0	125	7	0
4	A	20	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	A	7	0	0	0	0
All	All	5088	0	4931	126	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 13.

All (126) 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:308:THR:H	1:A:311:MET:CE	1.52	1.21
1:A:308:THR:H	1:A:311:MET:HE1	1.09	1.14
1:A:648:LEU:HB2	1:A:841:MET:HE3	1.50	0.92
1:A:308:THR:N	1:A:311:MET:CE	2.34	0.91
1:A:363:ASP:OD1	1:A:365:THR:OG1	1.88	0.89
1:A:308:THR:H	1:A:311:MET:HE3	1.40	0.85
1:A:308:THR:N	1:A:311:MET:HE1	1.92	0.84
1:A:707:ALA:CB	1:A:725:LEU:HD21	2.12	0.80
1:A:308:THR:N	1:A:311:MET:HE3	1.97	0.79
1:A:713:VAL:HG12	1:A:714:TYR:CD1	2.17	0.78
1:A:818:GLU:CB	1:A:820:LEU:HD13	2.13	0.77
1:A:725:LEU:O	1:A:727:ILE:HD11	1.83	0.77
3:C:4:DA:H2'	3:C:5:DG:H5''	1.64	0.77
1:A:725:LEU:O	1:A:727:ILE:CD1	2.35	0.74
1:A:818:GLU:HB3	1:A:820:LEU:HD13	1.70	0.74
1:A:323:VAL:O	1:A:435:ARG:NH2	2.21	0.73
1:A:727:ILE:HG21	1:A:731:GLU:OE2	1.89	0.72
1:A:588:ILE:HD11	1:A:636:ILE:CD1	2.21	0.70
1:A:472:ARG:NH2	1:A:476:GLU:OE1	2.25	0.69
1:A:727:ILE:CG2	1:A:731:GLU:OE2	2.42	0.68
1:A:726:ASN:C	1:A:727:ILE:HD13	2.21	0.66
1:A:727:ILE:HD13	1:A:727:ILE:N	2.10	0.66
1:A:570:ILE:O	1:A:574:ILE:HD12	1.96	0.66
1:A:383:LYS:O	1:A:385:ILE:HD12	1.95	0.66
1:A:308:THR:OG1	1:A:311:MET:HE2	1.97	0.64
1:A:321:GLU:OE2	1:A:450:LYS:NZ	2.24	0.64
1:A:707:ALA:HB3	1:A:725:LEU:HD21	1.79	0.64
1:A:818:GLU:HB3	1:A:820:LEU:CD1	2.28	0.63
1:A:610:LEU:HD23	1:A:610:LEU:C	2.23	0.63
1:A:308:THR:OG1	1:A:311:MET:CE	2.47	0.63
3:C:4:DA:C2'	3:C:5:DG:H5''	2.29	0.62
1:A:500:LEU:HD22	1:A:588:ILE:HD12	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:837:PRO:HD2	1:A:840:GLU:OE1	2.00	0.62
1:A:478:GLU:OE2	1:A:805:LYS:NZ	2.35	0.60
1:A:667:GLU:C	1:A:672:MET:HE2	2.25	0.60
1:A:818:GLU:HB2	1:A:820:LEU:HD13	1.82	0.60
1:A:588:ILE:HD11	1:A:636:ILE:HD12	1.83	0.60
1:A:588:ILE:HD11	1:A:636:ILE:HD11	1.83	0.60
2:B:26:47C:H4	3:C:7:DA:H61	1.50	0.59
1:A:716:ILE:HG22	1:A:717:SER:O	2.04	0.57
1:A:587:TYR:O	1:A:588:ILE:HD13	2.06	0.56
1:A:674:ALA:HA	1:A:679:LEU:HD12	1.88	0.56
1:A:308:THR:HG23	1:A:311:MET:HE1	1.88	0.55
1:A:503:MET:HE1	1:A:635:LYS:O	2.07	0.55
1:A:853:GLU:HG3	1:A:864:VAL:HG23	1.87	0.55
1:A:786:PHE:CZ	1:A:790:MET:HE2	2.42	0.55
1:A:314:ASP:N	1:A:314:ASP:OD1	2.38	0.54
1:A:398:ALA:HB1	1:A:407:VAL:HG21	1.90	0.54
1:A:358:VAL:HA	1:A:361:LEU:HD12	1.90	0.54
1:A:789:ARG:HA	1:A:792:MET:HE3	1.90	0.53
1:A:570:ILE:HG12	1:A:574:ILE:CD1	2.38	0.53
1:A:558:ALA:O	1:A:562:GLU:HG3	2.08	0.53
1:A:596:ARG:HB3	1:A:598:ASP:OD2	2.09	0.53
1:A:727:ILE:CB	1:A:731:GLU:OE2	2.57	0.53
1:A:374:LYS:HE2	1:A:489:GLU:OE2	2.09	0.52
1:A:598:ASP:OD2	1:A:598:ASP:N	2.42	0.52
1:A:725:LEU:O	1:A:727:ILE:HD13	2.10	0.52
1:A:419:TYR:CE1	1:A:421:ALA:HB3	2.45	0.52
1:A:570:ILE:HG12	1:A:574:ILE:HD11	1.93	0.51
1:A:570:ILE:O	1:A:574:ILE:CD1	2.58	0.51
1:A:440:GLU:N	1:A:441:PRO:CD	2.74	0.50
1:A:628:ILE:HG22	2:B:28:DC:H5''	1.93	0.50
1:A:731:GLU:HA	1:A:734:GLU:CD	2.37	0.50
1:A:419:TYR:CZ	1:A:421:ALA:HB3	2.47	0.50
1:A:728:SER:O	1:A:731:GLU:HG2	2.12	0.49
1:A:677:ARG:NH1	4:A:878:SO4:O3	2.31	0.49
1:A:727:ILE:HB	1:A:731:GLU:OE2	2.12	0.49
1:A:309:GLU:H	1:A:309:GLU:CD	2.21	0.49
1:A:307:VAL:HB	1:A:354:ASP:OD2	2.13	0.48
1:A:740:PHE:CD1	1:A:747:LYS:HB2	2.48	0.48
1:A:644:GLU:OE2	1:A:823:ARG:NH2	2.47	0.48
1:A:308:THR:CA	1:A:311:MET:HE3	2.44	0.47
1:A:477:LEU:HD12	1:A:809:ILE:HD12	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:587:TYR:C	1:A:588:ILE:HD13	2.40	0.47
3:C:9:DT:H2''	3:C:10:DG:C8	2.49	0.47
1:A:825:LEU:O	1:A:826:LEU:HD23	2.14	0.47
1:A:349:GLU:HG2	1:A:350:THR:H	1.78	0.47
1:A:828:VAL:HG12	1:A:828:VAL:O	2.12	0.47
1:A:363:ASP:OD1	1:A:363:ASP:C	2.57	0.46
1:A:614:GLY:HA3	1:A:769:ARG:HD3	1.96	0.46
1:A:443:LEU:HD12	1:A:447:LEU:HD13	1.97	0.46
1:A:664:HIS:O	1:A:859:ARG:NH1	2.48	0.46
1:A:591:LEU:O	1:A:595:VAL:HG23	2.16	0.46
1:A:740:PHE:HE1	1:A:746:VAL:HG12	1.81	0.46
1:A:308:THR:CB	1:A:311:MET:CE	2.95	0.45
1:A:565:ALA:N	1:A:566:PRO:CD	2.79	0.45
1:A:692:VAL:HG21	1:A:701:MET:HE1	1.98	0.45
1:A:665:ILE:HD11	1:A:796:ILE:HG12	1.97	0.45
1:A:806:LYS:NZ	1:A:855:ALA:O	2.45	0.44
1:A:771:ARG:NH1	1:A:794:THR:OG1	2.43	0.44
1:A:662:LEU:HD13	1:A:796:ILE:HD11	2.00	0.44
1:A:614:GLY:CA	1:A:769:ARG:HD3	2.48	0.44
1:A:667:GLU:C	1:A:672:MET:CE	2.91	0.43
1:A:524:GLN:HG2	1:A:525:GLU:N	2.34	0.43
1:A:588:ILE:CD1	1:A:636:ILE:HD12	2.48	0.43
3:C:5:DG:H5'	3:C:5:DG:H8	1.84	0.43
1:A:619:THR:HG23	1:A:620:GLU:HB2	2.00	0.43
1:A:725:LEU:C	1:A:727:ILE:CD1	2.91	0.43
1:A:440:GLU:N	1:A:441:PRO:HD3	2.34	0.43
1:A:584:GLN:O	1:A:589:GLU:HB2	2.20	0.42
1:A:654:TYR:CE2	1:A:852:MET:HE3	2.54	0.42
2:B:26:47C:H6	2:B:26:47C:H2'1	1.77	0.42
1:A:511:LEU:HD21	1:A:580:LEU:HB2	2.02	0.42
1:A:690:PHE:O	1:A:692:VAL:HG13	2.18	0.42
1:A:370:MET:O	1:A:393:ASP:HA	2.19	0.42
3:C:5:DG:H8	3:C:5:DG:C5'	2.32	0.42
1:A:415:LYS:O	1:A:416:MET:C	2.63	0.41
1:A:478:GLU:OE2	1:A:769:ARG:NH2	2.49	0.41
3:C:9:DT:C2'	3:C:10:DG:C8	3.03	0.41
1:A:582:LYS:HE2	2:B:26:47C:O2	2.21	0.41
1:A:786:PHE:CE1	1:A:790:MET:HE2	2.56	0.41
1:A:794:THR:N	1:A:795:PRO:CD	2.83	0.41
1:A:308:THR:CA	1:A:311:MET:CE	2.98	0.41
1:A:692:VAL:HB	1:A:696:GLU:HB2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:864:VAL:HG12	1:A:865:ASP:N	2.35	0.41
1:A:393:ASP:N	1:A:479:GLN:OE1	2.50	0.41
1:A:718:ASP:OD1	1:A:719:TYR:N	2.54	0.41
1:A:604:THR:HB	1:A:623:LEU:HD12	2.02	0.41
1:A:767:LEU:O	1:A:768:HIS:HB2	2.21	0.41
1:A:614:GLY:HA3	1:A:769:ARG:CD	2.51	0.40
1:A:692:VAL:HB	1:A:696:GLU:CB	2.51	0.40
1:A:731:GLU:HA	1:A:734:GLU:HG3	2.03	0.40
1:A:500:LEU:HD11	1:A:591:LEU:HD23	2.02	0.40
1:A:850:GLU:OE1	1:A:850:GLU:HA	2.22	0.40
2:B:20:DG:H2''	2:B:21:DA:OP2	2.21	0.40
1:A:739:TYR:C	1:A:739:TYR:CD1	2.99	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	578/580 (100%)	551 (95%)	26 (4%)	1 (0%)	43 62

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	727	ILE

### 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	
1	A	491/496 (99%)	469 (96%)	22 (4%)	24	48

All (22) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	314	ASP
1	A	340	GLU
1	A	373	SER
1	A	374	LYS
1	A	475	VAL
1	A	494	LYS
1	A	501	GLU
1	A	532	LYS
1	A	554	TYR
1	A	589	GLU
1	A	591	LEU
1	A	619	THR
1	A	644	GLU
1	A	645	SER
1	A	657	ILE
1	A	665	ILE
1	A	713	VAL
1	A	727	ILE
1	A	741	GLU
1	A	766	LEU
1	A	827	GLN
1	A	876	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	529	ASN
1	A	543	GLN
1	A	579	GLN
1	A	603	HIS
1	A	608	GLN
1	A	612	GLN
1	A	691	GLN
1	A	704	GLN
1	A	780	ASN

### 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	$\# Z  > 2$
2	47C	B	26	2,3	21,24,25	1.14	1 (4%)	26,32,35	1.18	2 (7%)

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
2	47C	B	26	2,3	-	3/10/26/27	0/2/2/2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	26	47C	C2-N1	-2.52	1.34	1.40

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	26	47C	C1'-N1-C2	2.36	121.87	117.83
2	B	26	47C	C1'-N1-C6	-2.24	117.12	121.53

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	26	47C	C2'-C1'-N1-C6
2	B	26	47C	O4'-C1'-N1-C6
2	B	26	47C	C2'-C1'-N1-C2

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	26	47C	3	0

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

4 ligands are 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	$\# Z  > 2$
4	SO4	A	878	-	4,4,4	0.30	0	6,6,6	0.47	0
4	SO4	A	877	-	4,4,4	0.19	0	6,6,6	0.31	0
4	SO4	A	887	-	4,4,4	0.24	0	6,6,6	0.25	0
4	SO4	A	879	-	4,4,4	0.24	0	6,6,6	0.32	0

There are no bond length outliers.

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 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	878	SO4	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 [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

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	580/580 (100%)	-0.04	5 (0%) 81 76	27, 37, 49, 55	0
2	B	9/10 (90%)	0.19	1 (11%) 10 8	37, 42, 63, 70	0
3	C	11/11 (100%)	0.06	1 (9%) 15 11	35, 43, 71, 80	0
All	All	600/601 (99%)	-0.04	7 (1%) 76 71	27, 37, 49, 80	0

All (7) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	C	14	DA	4.2
1	A	297	ALA	3.1
1	A	716	ILE	2.7
2	B	20	DG	2.7
1	A	724	ASN	2.5
1	A	433	ALA	2.3
1	A	876	LYS	2.1

### 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. 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	B-factors(Å <sup>2</sup> )	Q<0.9
2	47C	B	26	23/24	0.95	0.11	32,43,60,62	0

### 6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.



## 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 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	B-factors(Å <sup>2</sup> )	Q<0.9
4	SO4	A	887	5/5	0.80	0.20	74,74,76,76	0
4	SO4	A	878	5/5	0.92	0.09	49,50,52,53	0
4	SO4	A	877	5/5	0.93	0.09	52,53,54,55	0
4	SO4	A	879	5/5	0.95	0.07	60,60,61,62	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.