



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 04:41 AM UTC

PDB ID : 8OFU / pdb_00008ofu
Title : Human adenovirus type 53 fiber-knob protein
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Deposited on : 2023-03-16
Resolution : 1.61 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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 types of validation reports are described at

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

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

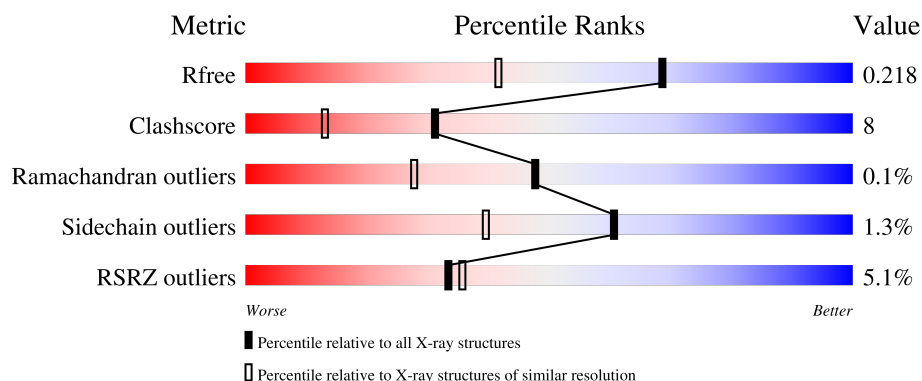
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.61 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	6728 (1.64-1.60)
Clashscore	190562	7023 (1.64-1.60)
Ramachandran outliers	187476	6898 (1.64-1.60)
Sidechain outliers	187428	6896 (1.64-1.60)
RSRZ outliers	180081	6727 (1.64-1.60)

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 ≥ 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	188	3% 82% 15% ..
1	B	188	3% 86% 13% ..
1	C	188	8% 82% 16% .
1	D	188	5% 85% 13% .
1	E	188	2% 90% 9% ..

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Mol	Chain	Length	Quality of chain
1	F	188	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	SO4	A	401	-	-	X	-
2	SO4	F	402	-	-	X	-
3	EDO	A	403	-	-	X	-
3	EDO	A	407	-	-	X	-
3	EDO	C	402	-	-	X	-
3	EDO	D	401	-	-	X	-
3	EDO	D	405	-	-	X	-
3	EDO	F	403	-	-	X	-
4	PEG	C	403	-	-	X	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 10039 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 Fiber protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	184	Total	C	N	O	S	0	2	0
			1475	947	240	280	8			
1	B	188	Total	C	N	O	S	0	2	0
			1509	966	247	289	7			
1	C	184	Total	C	N	O	S	0	0	0
			1461	939	238	278	6			
1	D	184	Total	C	N	O	S	0	1	0
			1467	942	239	279	7			
1	E	188	Total	C	N	O	S	0	4	0
			1526	975	252	292	7			
1	F	184	Total	C	N	O	S	0	0	0
			1461	939	238	278	6			

There are 18 discrepancies between the modelled and reference sequences:

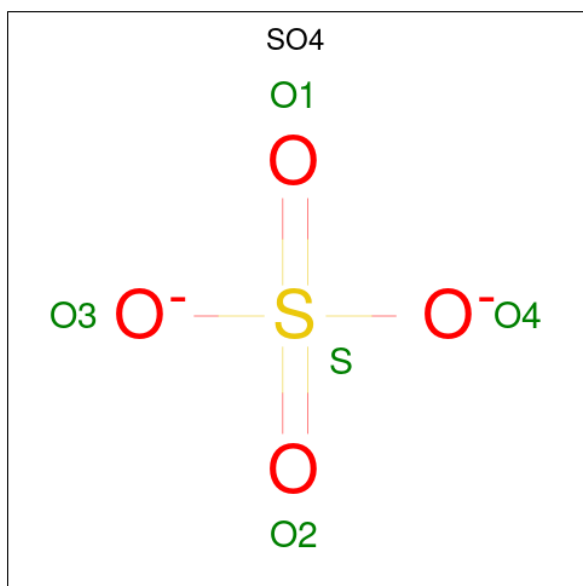
Chain	Residue	Modelled	Actual	Comment	Reference
A	180	ASN	LYS	conflict	UNP E5RWD1
A	181	ASN	GLU	conflict	UNP E5RWD1
A	184	LEU	ARG	conflict	UNP E5RWD1
B	180	ASN	LYS	conflict	UNP E5RWD1
B	181	ASN	GLU	conflict	UNP E5RWD1
B	184	LEU	ARG	conflict	UNP E5RWD1
C	180	ASN	LYS	conflict	UNP E5RWD1
C	181	ASN	GLU	conflict	UNP E5RWD1
C	184	LEU	ARG	conflict	UNP E5RWD1
D	180	ASN	LYS	conflict	UNP E5RWD1
D	181	ASN	GLU	conflict	UNP E5RWD1
D	184	LEU	ARG	conflict	UNP E5RWD1
E	180	ASN	LYS	conflict	UNP E5RWD1
E	181	ASN	GLU	conflict	UNP E5RWD1
E	184	LEU	ARG	conflict	UNP E5RWD1
F	180	ASN	LYS	conflict	UNP E5RWD1
F	181	ASN	GLU	conflict	UNP E5RWD1

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Chain	Residue	Modelled	Actual	Comment	Reference
F	184	LEU	ARG	conflict	UNP E5RWD1

- Molecule 2 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	E	1	Total	O	S	0	0
			5	4	1		
2	F	1	Total	O	S	0	0
			5	4	1		
2	F	1	Total	O	S	0	0
			5	4	1		

- Molecule 3 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



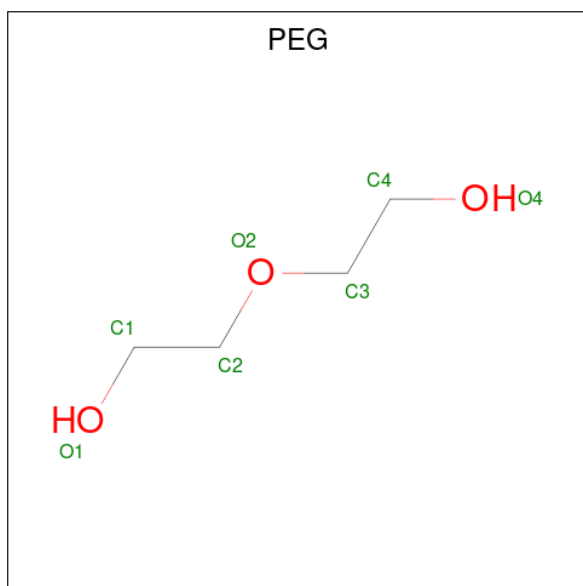
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	B	1	Total	C	O	0	0
			4	2	2		
3	B	1	Total	C	O	0	0
			4	2	2		
3	B	1	Total	C	O	0	0
			4	2	2		
3	B	1	Total	C	O	0	0
			4	2	2		
3	B	1	Total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

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	D	1	Total C O 4 2 2	0	0
3	D	1	Total C O 4 2 2	0	0
3	D	1	Total C O 4 2 2	0	0
3	D	1	Total C O 4 2 2	0	0
3	E	1	Total C O 4 2 2	0	0
3	E	1	Total C O 4 2 2	0	0
3	E	1	Total C O 4 2 2	0	0
3	F	1	Total C O 4 2 2	0	0

- Molecule 4 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: $C_4H_{10}O_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	C	1	Total C O 7 4 3	0	0
4	C	1	Total C O 7 4 3	0	0
4	D	1	Total C O 7 4 3	0	0

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	F	1	Total	C	O	0	0
			7	4	3		
4	F	1	Total	C	O	0	0
			7	4	3		

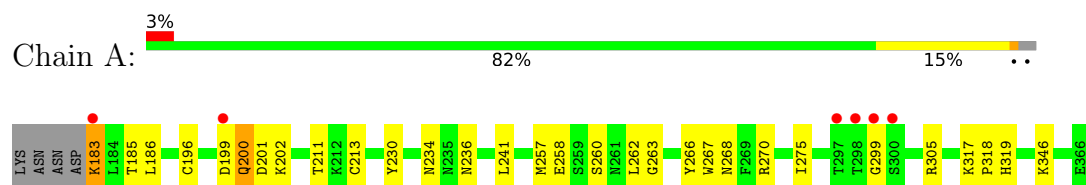
- Molecule 5 is water.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	171	Total	O		0	0
			171	171			
5	B	188	Total	O		0	0
			188	188			
5	C	152	Total	O		0	0
			152	152			
5	D	149	Total	O		0	0
			149	149			
5	E	204	Total	O		0	0
			204	204			
5	F	118	Total	O		0	0
			118	118			

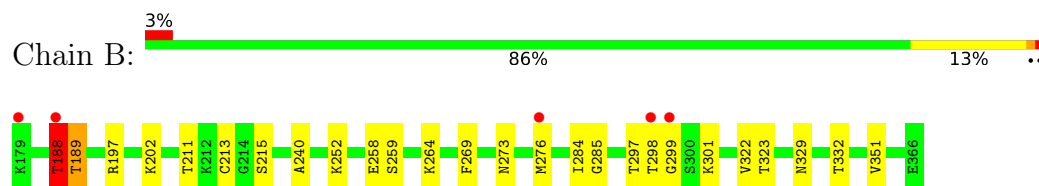
3 Residue-property plots [i](#)

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.

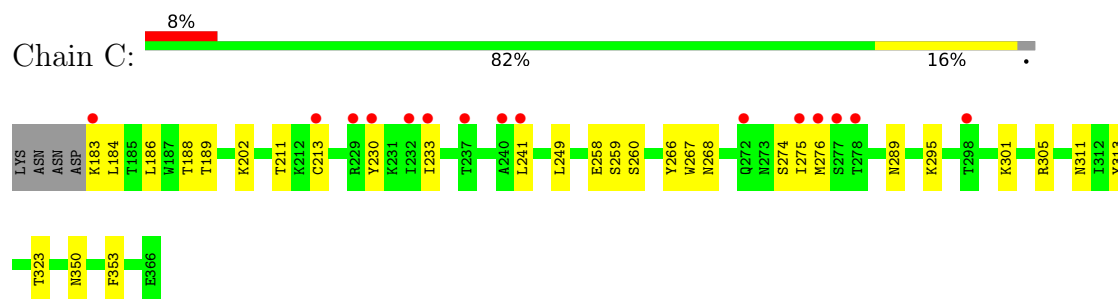
- Molecule 1: Fiber protein



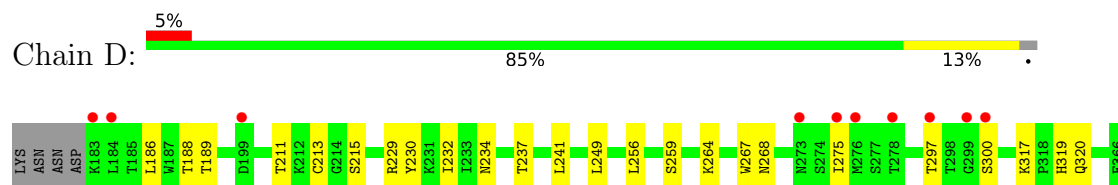
- Molecule 1: Fiber protein



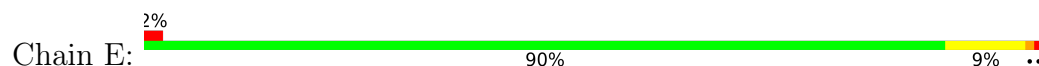
- Molecule 1: Fiber protein

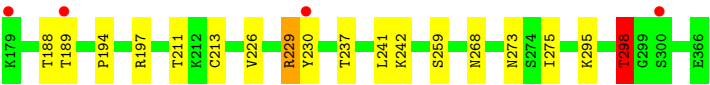


- Molecule 1: Fiber protein

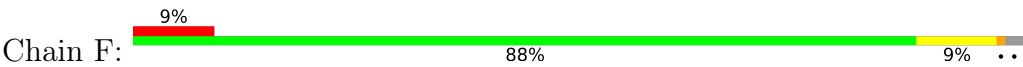


- Molecule 1: Fiber protein





● Molecule 1: Fiber protein



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	206.31Å 60.53Å 93.84Å 90.00° 91.80° 90.00°	Depositor
Resolution (Å)	68.42 – 1.61 68.42 – 1.61	Depositor EDS
% Data completeness (in resolution range)	99.3 (68.42-1.61) 99.4 (68.42-1.61)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.50 (at 1.61Å)	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
R, R_{free}	0.191 , 0.213 0.197 , 0.218	Depositor DCC
R_{free} test set	7463 reflections (4.94%)	wwPDB-VP
Wilson B-factor (Å ²)	19.9	Xtriage
Anisotropy	0.260	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 37.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.018 for -h,-k,l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	10039	wwPDB-VP
Average B, all atoms (Å ²)	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.15% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: PEG, SO4, EDO

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	0.92	0/1509	1.13	1/2046 (0.0%)
1	B	0.94	0/1543	1.16	3/2092 (0.1%)
1	C	0.92	0/1495	1.11	1/2028 (0.0%)
1	D	0.95	0/1501	1.12	0/2036
1	E	0.95	1/1560 (0.1%)	1.21	6/2115 (0.3%)
1	F	0.93	0/1495	1.13	2/2028 (0.1%)
All	All	0.93	1/9103 (0.0%)	1.14	13/12345 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	189	THR	N-CA	6.22	1.54	1.46

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	189	THR	CA-CB-OG1	-14.36	88.06	109.60
1	E	188	THR	CA-C-N	-10.07	97.23	121.80
1	E	188	THR	C-N-CA	-10.07	97.23	121.80
1	E	188	THR	O-C-N	-8.25	110.93	121.74
1	E	298	THR	CB-CA-C	7.84	123.54	109.83

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	188	THR	Mainchain

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	1475	0	1468	32	1
1	B	1509	0	1500	25	0
1	C	1461	0	1456	29	0
1	D	1467	0	1460	24	0
1	E	1526	0	1517	17	0
1	F	1461	0	1456	27	1
2	A	10	0	0	6	0
2	B	5	0	0	1	0
2	C	5	0	0	1	0
2	E	5	0	0	0	0
2	F	10	0	0	2	0
3	A	20	0	30	17	0
3	B	24	0	36	7	0
3	C	4	0	6	5	0
3	D	24	0	36	11	0
3	E	12	0	18	0	0
3	F	4	0	6	4	0
4	C	14	0	20	5	0
4	D	7	0	10	3	0
4	F	14	0	20	1	0
5	A	171	0	0	8	1
5	B	188	0	0	5	0
5	C	152	0	0	3	0
5	D	149	0	0	2	1
5	E	204	0	0	2	0
5	F	118	0	0	1	0
All	All	10039	0	9039	149	2

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 8.

The worst 5 of 149 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)
3:A:403:EDO:H21	5:A:576:HOH:O	1.79	0.81
3:A:403:EDO:C2	5:A:576:HOH:O	2.30	0.80
1:E:273:ASN:HD21	1:F:289:ASN:HD21	1.30	0.80
1:E:237[A]:THR:HG21	5:E:556:HOH:O	1.83	0.79
1:C:258:GLU:O	3:C:402:EDO:H12	1.83	0.78

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:299:GLY:O	1:F:271:ASN:CB[1_554]	2.00	0.20
5:A:652:HOH:O	5:D:570:HOH:O[1_554]	2.16	0.04

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	184/188 (98%)	176 (96%)	8 (4%)	0	100	100
1	B	188/188 (100%)	180 (96%)	7 (4%)	1 (0%)	24	10
1	C	182/188 (97%)	176 (97%)	6 (3%)	0	100	100
1	D	183/188 (97%)	176 (96%)	7 (4%)	0	100	100
1	E	190/188 (101%)	183 (96%)	7 (4%)	0	100	100
1	F	182/188 (97%)	175 (96%)	7 (4%)	0	100	100
All	All	1109/1128 (98%)	1066 (96%)	42 (4%)	1 (0%)	48	28

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	189	THR

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	166/168 (99%)	163 (98%)	3 (2%)	51	28
1	B	170/168 (101%)	165 (97%)	5 (3%)	37	13
1	C	164/168 (98%)	161 (98%)	3 (2%)	51	28
1	D	165/168 (98%)	165 (100%)	0	100	100
1	E	172/168 (102%)	169 (98%)	3 (2%)	53	29
1	F	164/168 (98%)	163 (99%)	1 (1%)	78	66
All	All	1001/1008 (99%)	986 (98%)	15 (2%)	61	34

5 of 15 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	332[B]	THR
1	E	298	THR
1	C	295	LYS
1	F	275	ILE
1	E	229[A]	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	273	ASN
1	F	236	ASN
1	C	311	ASN
1	C	350	ASN
1	D	238	ASN

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

34 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	$\# Z > 2$
3	EDO	A	405	-	3,3,3	0.12	0	2,2,2	0.31	0
3	EDO	E	403	-	3,3,3	0.10	0	2,2,2	0.18	0
2	SO4	B	401	-	4,4,4	0.41	0	6,6,6	0.17	0
3	EDO	B	402	-	3,3,3	0.08	0	2,2,2	0.31	0
2	SO4	A	401	-	4,4,4	0.43	0	6,6,6	0.15	0
3	EDO	E	402	-	3,3,3	0.12	0	2,2,2	0.35	0
3	EDO	D	401	-	3,3,3	0.58	0	2,2,2	0.17	0
3	EDO	D	406	-	3,3,3	0.18	0	2,2,2	0.15	0
2	SO4	F	402	-	4,4,4	0.37	0	6,6,6	0.12	0
3	EDO	D	404	-	3,3,3	0.50	0	2,2,2	0.16	0
2	SO4	F	401	-	4,4,4	0.37	0	6,6,6	0.08	0
3	EDO	B	403	-	3,3,3	0.46	0	2,2,2	0.11	0
4	PEG	F	404	-	6,6,6	0.17	0	5,5,5	0.12	0
3	EDO	A	407	-	3,3,3	0.38	0	2,2,2	0.13	0
3	EDO	A	406	-	3,3,3	0.23	0	2,2,2	0.04	0
3	EDO	D	405	-	3,3,3	0.43	0	2,2,2	0.06	0
3	EDO	B	407	-	3,3,3	0.06	0	2,2,2	0.14	0
3	EDO	B	405	-	3,3,3	0.09	0	2,2,2	0.35	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	EDO	D	403	-	3,3,3	0.23	0	2,2,2	0.03	0
3	EDO	B	404	-	3,3,3	0.36	0	2,2,2	0.18	0
3	EDO	E	404	-	3,3,3	0.04	0	2,2,2	0.24	0
2	SO4	A	402	-	4,4,4	0.46	0	6,6,6	0.12	0
3	EDO	D	402	-	3,3,3	0.24	0	2,2,2	0.31	0
3	EDO	C	402	-	3,3,3	0.28	0	2,2,2	0.57	0
2	SO4	E	401	-	4,4,4	0.32	0	6,6,6	0.08	0
4	PEG	C	404	-	6,6,6	0.15	0	5,5,5	0.10	0
3	EDO	A	403	-	3,3,3	0.51	0	2,2,2	0.12	0
4	PEG	D	407	-	6,6,6	0.30	0	5,5,5	0.19	0
3	EDO	B	406	-	3,3,3	0.20	0	2,2,2	0.30	0
2	SO4	C	401	-	4,4,4	0.41	0	6,6,6	0.09	0
3	EDO	A	404	-	3,3,3	0.34	0	2,2,2	0.09	0
4	PEG	F	405	-	6,6,6	0.25	0	5,5,5	0.13	0
3	EDO	F	403	-	3,3,3	0.49	0	2,2,2	0.04	0
4	PEG	C	403	-	6,6,6	0.13	0	5,5,5	0.15	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
3	EDO	A	405	-	-	1/1/1/1	-
3	EDO	E	403	-	-	1/1/1/1	-
3	EDO	B	402	-	-	1/1/1/1	-
3	EDO	E	402	-	-	0/1/1/1	-
3	EDO	D	401	-	-	1/1/1/1	-
3	EDO	D	406	-	-	0/1/1/1	-
3	EDO	D	404	-	-	0/1/1/1	-
3	EDO	B	403	-	-	0/1/1/1	-
4	PEG	F	404	-	-	2/4/4/4	-
3	EDO	A	407	-	-	1/1/1/1	-
3	EDO	A	406	-	-	0/1/1/1	-
3	EDO	D	405	-	-	0/1/1/1	-
3	EDO	B	407	-	-	0/1/1/1	-
3	EDO	B	405	-	-	1/1/1/1	-
3	EDO	D	403	-	-	1/1/1/1	-
3	EDO	B	404	-	-	1/1/1/1	-
3	EDO	E	404	-	-	1/1/1/1	-
3	EDO	D	402	-	-	0/1/1/1	-
3	EDO	C	402	-	-	1/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	PEG	C	404	-	-	2/4/4/4	-
3	EDO	A	403	-	-	0/1/1/1	-
4	PEG	D	407	-	-	2/4/4/4	-
3	EDO	B	406	-	-	1/1/1/1	-
4	PEG	F	405	-	-	3/4/4/4	-
3	EDO	A	404	-	-	0/1/1/1	-
3	EDO	F	403	-	-	0/1/1/1	-
4	PEG	C	403	-	-	3/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 23 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	C	404	PEG	O1-C1-C2-O2
4	C	403	PEG	O2-C3-C4-O4
4	F	404	PEG	O2-C3-C4-O4
4	D	407	PEG	O1-C1-C2-O2
3	A	405	EDO	O1-C1-C2-O2

There are no ring outliers.

25 monomers are involved in 63 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	405	EDO	2	0
2	B	401	SO4	1	0
3	B	402	EDO	1	0
2	A	401	SO4	5	0
3	D	401	EDO	4	0
2	F	402	SO4	2	0
3	D	404	EDO	2	0
3	B	403	EDO	1	0
4	F	404	PEG	1	0
3	A	407	EDO	5	0
3	A	406	EDO	2	0
3	D	405	EDO	4	0
3	B	407	EDO	1	0
3	B	405	EDO	2	0
3	B	404	EDO	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	402	SO4	1	0
3	D	402	EDO	1	0
3	C	402	EDO	5	0
4	C	404	PEG	1	0
3	A	403	EDO	8	0
4	D	407	PEG	3	0
3	B	406	EDO	1	0
2	C	401	SO4	1	0
3	F	403	EDO	4	0
4	C	403	PEG	4	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, 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	184/188 (97%)	0.03	6 (3%)	49	53	12, 20, 37, 71	2 (1%)
1	B	188/188 (100%)	0.00	5 (2%)	56	60	12, 21, 33, 58	2 (1%)
1	C	184/188 (97%)	0.42	15 (8%)	17	18	17, 29, 52, 59	0
1	D	184/188 (97%)	0.21	10 (5%)	31	33	14, 24, 49, 67	1 (0%)
1	E	188/188 (100%)	-0.08	4 (2%)	63	68	12, 20, 30, 54	4 (2%)
1	F	184/188 (97%)	0.61	17 (9%)	14	15	17, 30, 56, 91	0
All	All	1112/1128 (98%)	0.20	57 (5%)	33	36	12, 24, 48, 91	9 (0%)

The worst 5 of 57 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	275	ILE	7.0
1	F	273	ASN	6.5
1	F	272	GLN	5.3
1	F	279	ALA	4.8
1	F	274	SER	4.4

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

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(Å ²)	Q<0.9
2	SO4	E	401	5/5	0.67	0.17	69,72,77,81	0
4	PEG	F	405	7/7	0.75	0.19	47,50,53,53	0
3	EDO	C	402	4/4	0.76	0.18	39,39,40,40	0
3	EDO	B	402	4/4	0.76	0.16	42,43,44,47	0
3	EDO	A	405	4/4	0.77	0.17	34,41,43,44	0
3	EDO	D	406	4/4	0.80	0.16	36,40,41,41	0
3	EDO	E	404	4/4	0.80	0.17	43,44,45,46	0
3	EDO	B	407	4/4	0.80	0.16	41,41,42,42	0
3	EDO	B	405	4/4	0.81	0.16	40,40,41,41	0
2	SO4	B	401	5/5	0.82	0.20	31,32,33,35	5
2	SO4	F	402	5/5	0.82	0.15	33,33,34,34	5
4	PEG	D	407	7/7	0.84	0.18	24,32,46,46	0
3	EDO	E	402	4/4	0.84	0.14	35,35,36,39	0
4	PEG	F	404	7/7	0.85	0.15	38,40,44,44	0
2	SO4	C	401	5/5	0.86	0.15	33,35,36,37	5
3	EDO	E	403	4/4	0.87	0.15	42,43,43,44	0
3	EDO	D	404	4/4	0.87	0.22	29,32,34,38	0
3	EDO	D	405	4/4	0.87	0.21	28,32,33,33	0
2	SO4	F	401	5/5	0.87	0.15	33,34,35,37	5
3	EDO	D	402	4/4	0.87	0.14	31,34,36,41	0
3	EDO	A	403	4/4	0.88	0.22	26,29,30,35	0
3	EDO	D	401	4/4	0.88	0.16	23,26,27,28	0
3	EDO	A	404	4/4	0.88	0.14	33,41,42,45	0
4	PEG	C	403	7/7	0.89	0.14	37,40,42,42	0
3	EDO	A	407	4/4	0.89	0.16	28,30,31,31	0
3	EDO	B	406	4/4	0.89	0.12	28,32,34,35	0
3	EDO	D	403	4/4	0.89	0.14	26,32,37,41	0
3	EDO	B	404	4/4	0.90	0.16	27,32,33,37	0
4	PEG	C	404	7/7	0.91	0.10	36,37,39,40	0
2	SO4	A	402	5/5	0.91	0.20	23,29,30,31	5
3	EDO	F	403	4/4	0.92	0.21	25,27,27,27	0
2	SO4	A	401	5/5	0.93	0.16	23,26,27,28	5
3	EDO	B	403	4/4	0.93	0.14	29,30,30,30	0
3	EDO	A	406	4/4	0.94	0.08	35,35,35,37	0

6.5 Other polymers [i](#)

There are no such residues in this entry.