



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 09:04 AM UTC

PDB ID : 7PWX / pdb_00007pwx
Title : dUTPase from M. tuberculosis in complex with Stl
Authors : Marina, A.; Sanz-Frasquet, C.
Deposited on : 2021-10-07
Resolution : 2.75 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

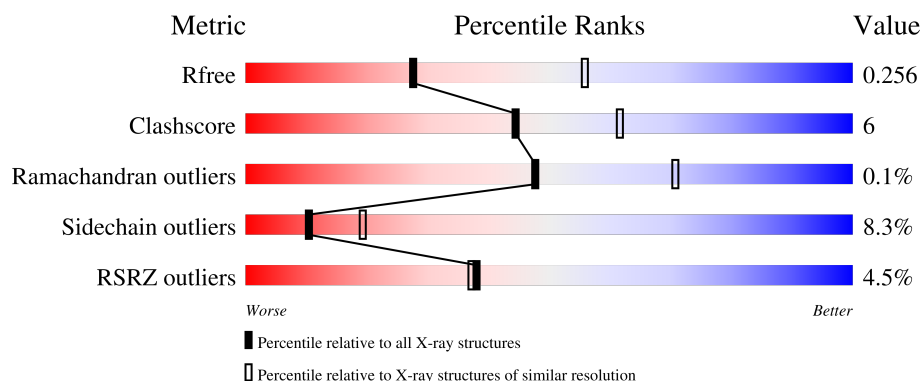
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.75 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	1009 (2.76-2.76)
Clashscore	190562	1044 (2.76-2.76)
Ramachandran outliers	187476	1024 (2.76-2.76)
Sidechain outliers	187428	1024 (2.76-2.76)
RSRZ outliers	180081	1009 (2.76-2.76)

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	HHH	136	5% 85% 12% ..
1	III	136	% 73% 21% ..
1	JJJ	136	% 82% 13% ..
1	KKK	136	2% 79% 18% ..
1	LLL	136	3% 87% 12% .

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Mol	Chain	Length	Quality of chain
1	MMM	136	
2	AAA	147	
2	CCC	147	
2	DDD	147	
2	EEE	147	
2	FFF	147	
2	GGG	147	

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
3	TRS	HHH	201	-	-	X	-

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 12287 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 Deoxyuridine 5'-triphosphate nucleotidohydrolase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	HHH	134	Total	C	N	O	S	0	0	0
			946	602	167	176	1			
1	III	131	Total	C	N	O	S	0	0	0
			950	606	167	176	1			
1	JJJ	131	Total	C	N	O	S	0	0	0
			952	604	168	179	1			
1	KKK	135	Total	C	N	O	S	0	0	0
			946	604	172	169	1			
1	LLL	136	Total	C	N	O	S	0	0	0
			977	620	178	177	2			
1	MMM	131	Total	C	N	O	S	0	0	0
			950	603	172	174	1			

- Molecule 2 is a protein called Orf20.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	CCC	146	Total	C	N	O	S	0	0	0
			1174	757	186	229	2			
2	DDD	145	Total	C	N	O	S	0	0	0
			1167	757	180	228	2			
2	EEE	146	Total	C	N	O	S	0	0	0
			1148	742	178	226	2			
2	FFF	146	Total	C	N	O	S	0	2	0
			1184	768	186	228	2			
2	GGG	128	Total	C	N	O	S	0	0	0
			919	588	145	184	2			
2	AAA	118	Total	C	N	O	S	0	0	0
			787	499	130	156	2			

- Molecule 3 is 2-AMINO-2-HYDROXYMETHYL-PROPANE-1,3-DIOL (CCD ID: TRS) (formula: C₄H₁₂NO₃).



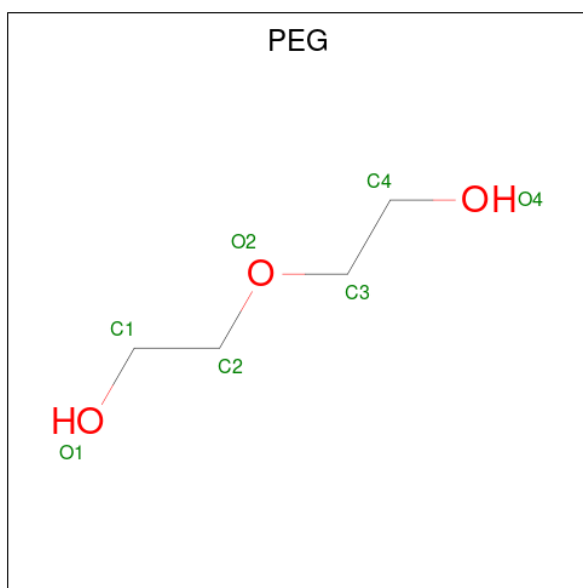
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	HHH	1	Total	C	N	O	0	0
			8	4	1	3		
3	JJJ	1	Total	C	N	O	0	0
			8	4	1	3		
3	LLL	1	Total	C	N	O	0	0
			8	4	1	3		
3	LLL	1	Total	C	N	O	0	0
			8	4	1	3		

- Molecule 4 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	III	1	Total C O 4 2 2	0	0
4	JJJ	1	Total C O 4 2 2	0	0
4	JJJ	1	Total C O 4 2 2	0	0
4	JJJ	1	Total C O 4 2 2	0	0
4	DDD	1	Total C O 4 2 2	0	0
4	DDD	1	Total C O 4 2 2	0	0
4	FFF	1	Total C O 4 2 2	0	0
4	GGG	1	Total C O 4 2 2	0	0

- Molecule 5 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: $C_4H_{10}O_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	JJJ	1	Total C O 7 4 3	0	0
5	KKK	1	Total C O 7 4 3	0	0
5	MMM	1	Total C O 7 4 3	0	0
5	FFF	1	Total C O 7 4 3	0	0

- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	HHH	7	Total O 7 7	0	0
6	III	8	Total O 8 8	0	0
6	JJJ	9	Total O 9 9	0	0
6	KKK	2	Total O 2 2	0	0
6	LLL	8	Total O 8 8	0	0
6	MMM	7	Total O 7 7	0	0
6	CCC	7	Total O 7 7	0	0
6	DDD	12	Total O 12 12	0	0
6	EEE	4	Total O 4 4	0	0
6	FFF	17	Total O 17 17	0	0
6	GGG	8	Total O 8 8	0	0
6	AAA	6	Total O 6 6	0	0

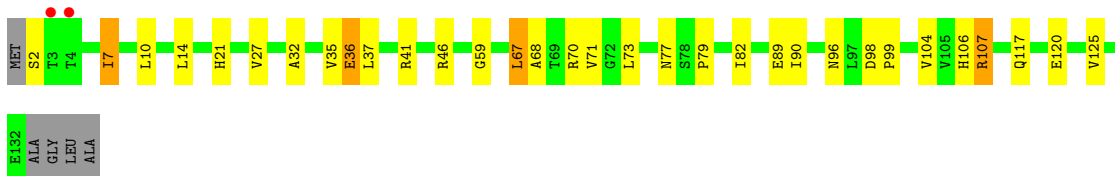
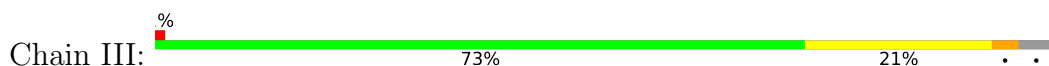
3 Residue-property plots [i](#)

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.

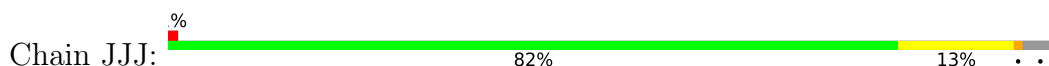
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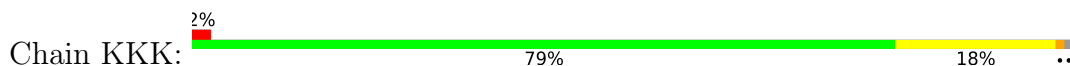
- Molecule 1: Deoxyuridine 5'-triphosphate nucleotidohydrolase



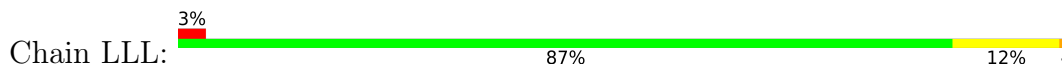
- Molecule 1: Deoxyuridine 5'-triphosphate nucleotidohydrolase



- Molecule 1: Deoxyuridine 5'-triphosphate nucleotidohydrolase

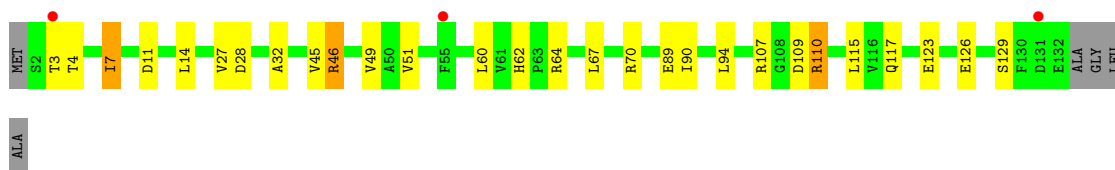
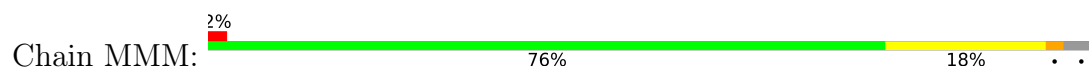


- Molecule 1: Deoxyuridine 5'-triphosphate nucleotidohydrolase

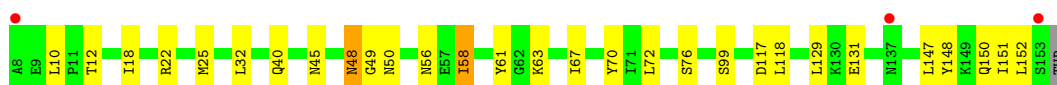
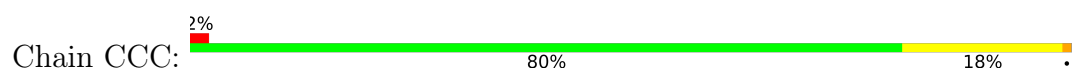




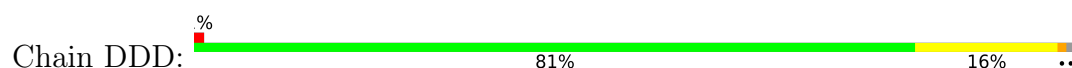
- Molecule 1: Deoxyuridine 5'-triphosphate nucleotidohydrolase



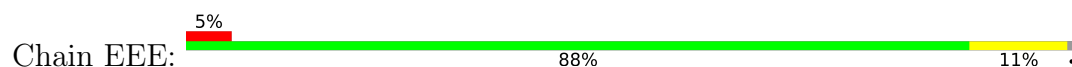
- Molecule 2: Orf20



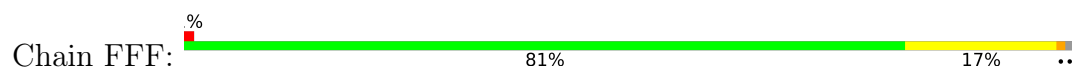
- Molecule 2: Orf20



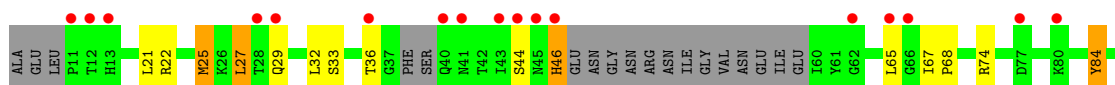
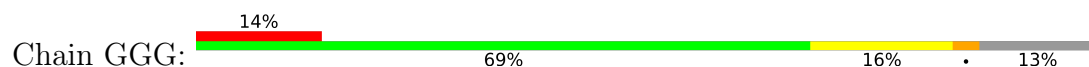
- Molecule 2: Orf20

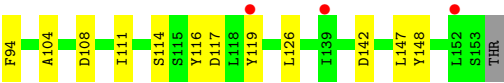


- Molecule 2: Orf20

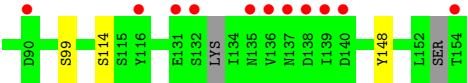
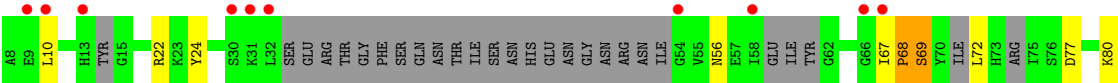
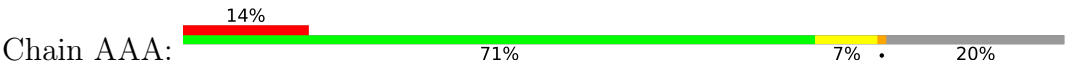


- Molecule 2: Orf20





● Molecule 2: Orf20



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	79.41Å 150.43Å 107.37Å 90.00° 98.85° 90.00°	Depositor
Resolution (Å)	75.33 – 2.75 75.33 – 2.75	Depositor EDS
% Data completeness (in resolution range)	95.1 (75.33-2.75) 95.1 (75.33-2.75)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.88 (at 2.73Å)	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
R, R_{free}	0.201 , 0.259 0.203 , 0.256	Depositor DCC
R_{free} test set	3102 reflections (4.80%)	wwPDB-VP
Wilson B-factor (Å ²)	63.7	Xtriage
Anisotropy	0.113	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 47.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	12287	wwPDB-VP
Average B, all atoms (Å ²)	63.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.72% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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	HHH	1.07	0/960	1.37	0/1311
1	III	1.01	0/964	1.34	1/1314 (0.1%)
1	JJJ	1.01	0/967	1.37	0/1322
1	KKK	1.07	0/960	1.42	0/1312
1	LLL	1.05	0/992	1.39	0/1354
1	MMM	1.05	0/965	1.38	0/1319
2	AAA	1.13	0/795	1.59	0/1076
2	CCC	1.00	0/1199	1.49	2/1622 (0.1%)
2	DDD	1.02	1/1192 (0.1%)	1.55	2/1611 (0.1%)
2	EEE	1.02	0/1173	1.49	2/1590 (0.1%)
2	FFF	0.99	0/1214	1.54	2/1640 (0.1%)
2	GGG	1.17	1/937 (0.1%)	1.66	2/1273 (0.2%)
All	All	1.04	2/12318 (0.0%)	1.47	11/16744 (0.1%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	GGG	46	HIS	CE1-NE2	5.65	1.38	1.32
2	DDD	67	ILE	N-CA	5.22	1.50	1.45

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	FFF	48[A]	ASN	CB-CA-C	7.04	120.90	109.07
2	FFF	48[B]	ASN	CB-CA-C	7.04	120.90	109.07
2	EEE	11	PRO	CB-CA-C	-6.38	102.91	112.04
2	DDD	63	LYS	CA-C-N	5.71	126.28	120.00
2	DDD	63	LYS	C-N-CA	5.71	126.28	120.00

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	HHH	946	0	934	13	0
1	III	950	0	964	18	0
1	JJJ	952	0	968	15	0
1	KKK	946	0	960	15	0
1	LLL	977	0	1002	17	0
1	MMM	950	0	979	19	0
2	AAA	787	0	572	4	0
2	CCC	1174	0	1112	14	0
2	DDD	1167	0	1088	13	0
2	EEE	1148	0	1046	7	0
2	FFF	1184	0	1119	12	0
2	GGG	919	0	735	16	0
3	HHH	8	0	12	6	0
3	JJJ	8	0	12	0	0
3	LLL	16	0	24	5	0
4	DDD	8	0	12	0	0
4	FFF	4	0	6	0	0
4	GGG	4	0	6	0	0
4	III	4	0	6	0	0
4	JJJ	12	0	18	0	0
5	FFF	7	0	10	0	0
5	JJJ	7	0	10	0	0
5	KKK	7	0	10	0	0
5	MMM	7	0	10	2	0
6	AAA	6	0	0	0	0
6	CCC	7	0	0	0	0
6	DDD	12	0	0	0	0
6	EEE	4	0	0	0	0
6	FFF	17	0	0	0	0
6	GGG	8	0	0	1	0
6	HHH	7	0	0	0	0
6	III	8	0	0	0	0
6	JJJ	9	0	0	0	0
6	KKK	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	LLL	8	0	0	0	0
6	MMM	7	0	0	0	0
All	All	12287	0	11615	143	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 6.

The worst 5 of 143 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:LLL:122:VAL:HG12	1:MMM:3:THR:HG22	1.30	1.08
1:LLL:122:VAL:CG1	1:MMM:3:THR:HG22	1.99	0.92
2:FFF:10:LEU:HD21	2:FFF:55:VAL:HA	1.61	0.82
2:GGG:27:LEU:HD13	2:GGG:27:LEU:O	1.87	0.74
3:LLL:202:TRS:H12	1:MMM:60:LEU:HD13	1.70	0.73

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	HHH	132/136 (97%)	127 (96%)	5 (4%)	0	100	100
1	III	129/136 (95%)	122 (95%)	7 (5%)	0	100	100
1	JJJ	129/136 (95%)	125 (97%)	4 (3%)	0	100	100
1	KKK	133/136 (98%)	131 (98%)	2 (2%)	0	100	100
1	LLL	134/136 (98%)	128 (96%)	6 (4%)	0	100	100
1	MMM	129/136 (95%)	116 (90%)	13 (10%)	0	100	100
2	AAA	102/147 (69%)	90 (88%)	11 (11%)	1 (1%)	12	24
2	CCC	144/147 (98%)	138 (96%)	6 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	DDD	143/147 (97%)	136 (95%)	7 (5%)	0	100	100
2	EEE	144/147 (98%)	138 (96%)	6 (4%)	0	100	100
2	FFF	146/147 (99%)	142 (97%)	4 (3%)	0	100	100
2	GGG	122/147 (83%)	110 (90%)	12 (10%)	0	100	100
All	All	1587/1698 (94%)	1503 (95%)	83 (5%)	1 (0%)	48	71

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	AAA	68	PRO

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	HHH	92/106 (87%)	87 (95%)	5 (5%)	20	38
1	III	98/106 (92%)	84 (86%)	14 (14%)	3	5
1	JJJ	98/106 (92%)	93 (95%)	5 (5%)	21	40
1	KKK	90/106 (85%)	81 (90%)	9 (10%)	7	14
1	LLL	98/106 (92%)	94 (96%)	4 (4%)	27	49
1	MMM	99/106 (93%)	90 (91%)	9 (9%)	9	17
2	AAA	51/135 (38%)	43 (84%)	8 (16%)	2	4
2	CCC	122/135 (90%)	109 (89%)	13 (11%)	6	12
2	DDD	117/135 (87%)	110 (94%)	7 (6%)	17	32
2	EEE	111/135 (82%)	107 (96%)	4 (4%)	31	55
2	FFF	121/135 (90%)	110 (91%)	11 (9%)	9	17
2	GGG	75/135 (56%)	67 (89%)	8 (11%)	6	12
All	All	1172/1446 (81%)	1075 (92%)	97 (8%)	10	19

5 of 97 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	CCC	150	GLN
2	FFF	57	GLU
2	DDD	12	THR
2	DDD	147	LEU
2	FFF	115	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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](#)

16 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	EDO	DDD	202	-	3,3,3	0.15	0	2,2,2	0.31	0
4	EDO	III	201	-	3,3,3	0.10	0	2,2,2	0.20	0
4	EDO	JJJ	203	-	3,3,3	0.18	0	2,2,2	0.26	0
3	TRS	JJJ	201	-	7,7,7	0.26	0	9,9,9	0.38	0
4	EDO	FFF	202	-	3,3,3	0.11	0	2,2,2	0.21	0
5	PEG	FFF	201	-	6,6,6	0.17	0	5,5,5	0.08	0
5	PEG	KKK	201	-	6,6,6	0.15	0	5,5,5	0.13	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	EDO	DDD	201	-	3,3,3	0.09	0	2,2,2	0.23	0
3	TRS	HHH	201	-	7,7,7	0.17	0	9,9,9	0.42	0
4	EDO	JJJ	205	-	3,3,3	0.11	0	2,2,2	0.25	0
5	PEG	JJJ	202	-	6,6,6	0.21	0	5,5,5	0.14	0
5	PEG	MMM	201	-	6,6,6	0.22	0	5,5,5	0.18	0
4	EDO	GGG	201	-	3,3,3	0.11	0	2,2,2	0.22	0
3	TRS	LLL	201	-	7,7,7	0.18	0	9,9,9	0.29	0
4	EDO	JJJ	204	-	3,3,3	0.14	0	2,2,2	0.08	0
3	TRS	LLL	202	-	7,7,7	0.20	0	9,9,9	0.30	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
4	EDO	DDD	202	-	-	1/1/1/1	-
4	EDO	III	201	-	-	1/1/1/1	-
4	EDO	JJJ	203	-	-	1/1/1/1	-
3	TRS	JJJ	201	-	-	6/9/9/9	-
4	EDO	FFF	202	-	-	1/1/1/1	-
5	PEG	FFF	201	-	-	1/4/4/4	-
5	PEG	KKK	201	-	-	2/4/4/4	-
4	EDO	DDD	201	-	-	1/1/1/1	-
3	TRS	HHH	201	-	-	4/9/9/9	-
4	EDO	JJJ	205	-	-	1/1/1/1	-
5	PEG	JJJ	202	-	-	1/4/4/4	-
5	PEG	MMM	201	-	-	3/4/4/4	-
4	EDO	GGG	201	-	-	1/1/1/1	-
3	TRS	LLL	201	-	-	2/9/9/9	-
4	EDO	JJJ	204	-	-	0/1/1/1	-
3	TRS	LLL	202	-	-	3/9/9/9	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 29 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	LLL	201	TRS	N-C-C2-O2

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Mol	Chain	Res	Type	Atoms
5	MMM	201	PEG	C4-C3-O2-C2
5	KKK	201	PEG	O1-C1-C2-O2
3	HHH	201	TRS	C3-C-C1-O1
3	JJJ	201	TRS	C2-C-C1-O1

There are no ring outliers.

4 monomers are involved in 13 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	HHH	201	TRS	6	0
5	MMM	201	PEG	2	0
3	LLL	201	TRS	1	0
3	LLL	202	TRS	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 ⓘ

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	HHH	134/136 (98%)	0.01	7 (5%) 33 32	39, 52, 70, 118	0
1	III	131/136 (96%)	-0.18	2 (1%) 72 71	37, 52, 90, 115	0
1	JJJ	131/136 (96%)	-0.09	1 (0%) 82 82	40, 58, 80, 113	0
1	KKK	135/136 (99%)	0.15	3 (2%) 62 60	41, 68, 94, 106	0
1	LLL	136/136 (100%)	-0.06	4 (2%) 53 52	32, 51, 77, 123	0
1	MMM	131/136 (96%)	-0.05	3 (2%) 61 59	34, 56, 86, 110	0
2	AAA	118/147 (80%)	1.23	21 (17%) 4 3	58, 93, 136, 160	1 (0%)
2	CCC	146/147 (99%)	-0.25	3 (2%) 63 61	35, 51, 81, 104	0
2	DDD	145/147 (98%)	-0.06	1 (0%) 84 84	40, 61, 91, 105	0
2	EEE	146/147 (99%)	0.11	7 (4%) 35 35	44, 63, 98, 116	0
2	FFF	146/147 (99%)	-0.16	1 (0%) 84 84	24, 54, 90, 116	2 (1%)
2	GGG	128/147 (87%)	0.82	20 (15%) 5 4	50, 81, 124, 140	0
All	All	1627/1698 (95%)	0.10	73 (4%) 38 37	24, 59, 103, 160	3 (0%)

The worst 5 of 73 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	AAA	32	LEU	8.0
1	HHH	131	ASP	4.9
2	GGG	43	ILE	4.6
1	KKK	136	ALA	4.5
2	GGG	77	ASP	4.2

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

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

6.3 Carbohydrates [i](#)

There are no 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, 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
4	EDO	GGG	201	4/4	0.53	0.15	94,95,96,98	0
4	EDO	JJJ	204	4/4	0.60	0.28	95,102,104,106	0
4	EDO	DDD	202	4/4	0.62	0.16	93,96,96,96	0
4	EDO	JJJ	203	4/4	0.73	0.19	75,85,88,89	0
4	EDO	III	201	4/4	0.75	0.10	76,80,82,82	0
4	EDO	JJJ	205	4/4	0.75	0.17	93,98,99,100	0
5	PEG	MMM	201	7/7	0.82	0.23	98,108,115,119	0
4	EDO	FFF	202	4/4	0.83	0.14	71,76,79,82	0
5	PEG	JJJ	202	7/7	0.86	0.12	98,104,108,111	0
5	PEG	FFF	201	7/7	0.88	0.17	86,97,101,103	0
5	PEG	KKK	201	7/7	0.89	0.16	76,87,104,105	0
3	TRS	JJJ	201	8/8	0.92	0.15	62,70,78,78	0
3	TRS	LLL	202	8/8	0.94	0.12	55,59,61,62	0
3	TRS	LLL	201	8/8	0.94	0.14	70,76,81,85	0
4	EDO	DDD	201	4/4	0.95	0.10	65,68,71,72	0
3	TRS	HHH	201	8/8	0.95	0.12	63,65,68,73	0

6.5 Other polymers [i](#)

There are no such residues in this entry.