



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 2, 2026 – 02:50 PM UTC

PDB ID : 6XI1 / pdb_00006xi1
Title : Crystal structure of tetra-tandem repeat in extending RTX adhesin from *Aeromonas hydrophila*
Authors : Ye, Q.; Vance, T.D.R.; Conroy, B.; Davies, P.L.
Deposited on : 2020-06-19
Resolution : 1.75 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

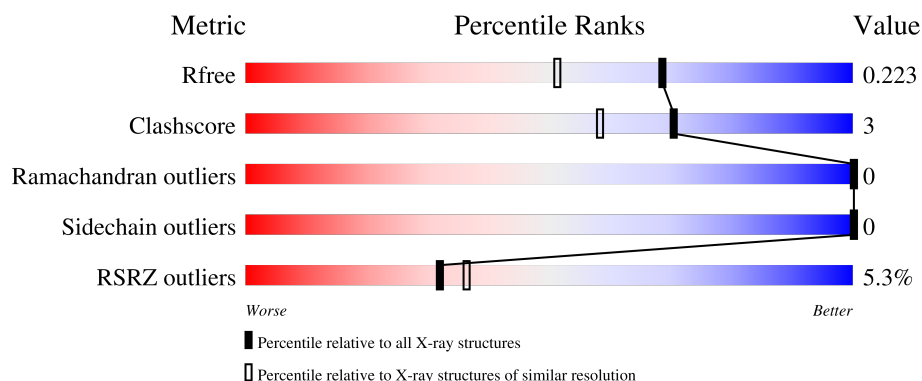
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.75 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	3183 (1.76-1.76)
Clashscore	190562	3299 (1.76-1.76)
Ramachandran outliers	187476	3274 (1.76-1.76)
Sidechain outliers	187428	3274 (1.76-1.76)
RSRZ outliers	180081	3183 (1.76-1.76)

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	AAA	449	6% 88% 6% 5%
1	BBB	449	4% 90% 5% 5%

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	GOL	AAA	505	-	-	X	-
2	GOL	AAA	506	-	-	X	-
2	GOL	BBB	507	-	-	X	-
6	PEG	BBB	508	-	-	X	-

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 7100 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 Flagellin hook IN motif family.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
1	AAA	425	Total	C	N	O	0	0	0
			3002	1832	474	696			
1	BBB	426	Total	C	N	O	0	0	0
			3010	1836	475	699			

There are 42 discrepancies between the modelled and reference sequences:

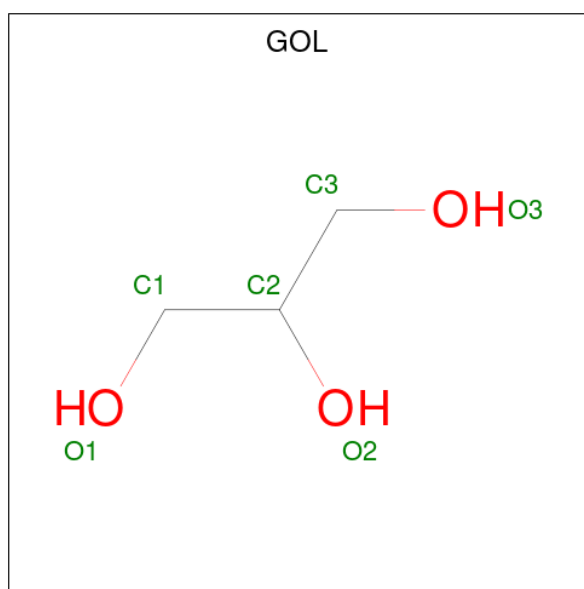
Chain	Residue	Modelled	Actual	Comment	Reference
AAA	1	MET	-	expression tag	UNP A0KNW4
AAA	2	ALA	-	expression tag	UNP A0KNW4
AAA	3	SER	-	expression tag	UNP A0KNW4
AAA	4	SER	-	expression tag	UNP A0KNW4
AAA	5	HIS	-	expression tag	UNP A0KNW4
AAA	6	HIS	-	expression tag	UNP A0KNW4
AAA	7	HIS	-	expression tag	UNP A0KNW4
AAA	8	HIS	-	expression tag	UNP A0KNW4
AAA	9	HIS	-	expression tag	UNP A0KNW4
AAA	10	HIS	-	expression tag	UNP A0KNW4
AAA	11	SER	-	expression tag	UNP A0KNW4
AAA	12	SER	-	expression tag	UNP A0KNW4
AAA	13	GLY	-	expression tag	UNP A0KNW4
AAA	14	LEU	-	expression tag	UNP A0KNW4
AAA	15	VAL	-	expression tag	UNP A0KNW4
AAA	16	PRO	-	expression tag	UNP A0KNW4
AAA	17	ARG	-	expression tag	UNP A0KNW4
AAA	18	GLY	-	expression tag	UNP A0KNW4
AAA	19	SER	-	expression tag	UNP A0KNW4
AAA	20	HIS	-	expression tag	UNP A0KNW4
AAA	21	MET	-	expression tag	UNP A0KNW4
BBB	1	MET	-	expression tag	UNP A0KNW4
BBB	2	ALA	-	expression tag	UNP A0KNW4
BBB	3	SER	-	expression tag	UNP A0KNW4
BBB	4	SER	-	expression tag	UNP A0KNW4

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Chain	Residue	Modelled	Actual	Comment	Reference
BBB	5	HIS	-	expression tag	UNP A0KNW4
BBB	6	HIS	-	expression tag	UNP A0KNW4
BBB	7	HIS	-	expression tag	UNP A0KNW4
BBB	8	HIS	-	expression tag	UNP A0KNW4
BBB	9	HIS	-	expression tag	UNP A0KNW4
BBB	10	HIS	-	expression tag	UNP A0KNW4
BBB	11	SER	-	expression tag	UNP A0KNW4
BBB	12	SER	-	expression tag	UNP A0KNW4
BBB	13	GLY	-	expression tag	UNP A0KNW4
BBB	14	LEU	-	expression tag	UNP A0KNW4
BBB	15	VAL	-	expression tag	UNP A0KNW4
BBB	16	PRO	-	expression tag	UNP A0KNW4
BBB	17	ARG	-	expression tag	UNP A0KNW4
BBB	18	GLY	-	expression tag	UNP A0KNW4
BBB	19	SER	-	expression tag	UNP A0KNW4
BBB	20	HIS	-	expression tag	UNP A0KNW4
BBB	21	MET	-	expression tag	UNP A0KNW4

- Molecule 2 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	AAA	1	Total	C	O	0	0
			6	3	3		
2	AAA	1	Total	C	O	0	0
			6	3	3		
2	AAA	1	Total	C	O	0	0
			6	3	3		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	AAA	1	Total	C	O	0	0
			6	3	3		
2	AAA	1	Total	C	O	0	0
			6	3	3		
2	AAA	1	Total	C	O	0	0
			6	3	3		
2	BBB	1	Total	C	O	0	0
			6	3	3		
2	BBB	1	Total	C	O	0	0
			6	3	3		
2	BBB	1	Total	C	O	0	0
			6	3	3		
2	BBB	1	Total	C	O	0	0
			6	3	3		
2	BBB	1	Total	C	O	0	0
			6	3	3		

- Molecule 3 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	AAA	1	Total	Cl	0	0
			1	1		

- Molecule 4 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	AAA	1	Total	Na	0	0
			1	1		
4	BBB	1	Total	Na	0	0
			1	1		

- Molecule 5 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	AAA	13	Total	Ca	0	0
			13	13		
5	BBB	13	Total	Ca	0	0
			13	13		

- Molecule 6 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: $C_4H_{10}O_3$).



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

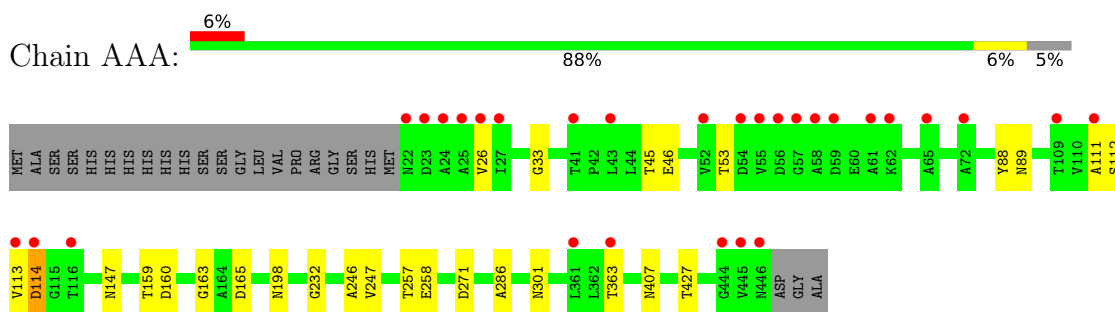
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	AAA	505	Total	O	0	0
			505	505		
7	BBB	469	Total	O	0	0
			469	469		

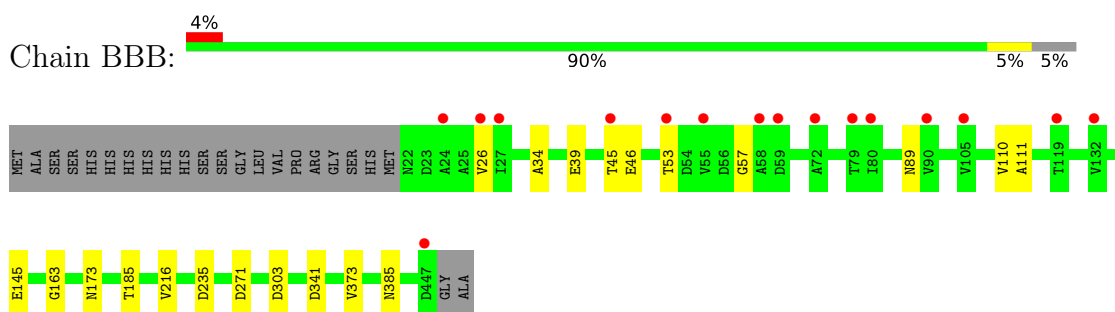
3 Residue-property plots [i](#)

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: Flagellin hook IN motif family



- Molecule 1: Flagellin hook IN motif family



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	47.67Å 50.37Å 124.60Å 97.56° 98.24° 101.72°	Depositor
Resolution (Å)	48.64 – 1.75 48.64 – 1.75	Depositor EDS
% Data completeness (in resolution range)	97.3 (48.64-1.75) 97.3 (48.64-1.75)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.42 (at 1.75Å)	Xtriage
Refinement program	REFMAC 5.8.0253	Depositor
R, R_{free}	0.181 , 0.210 0.196 , 0.223	Depositor DCC
R_{free} test set	5436 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	17.9	Xtriage
Anisotropy	0.070	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 37.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.000 for -h,-k,h+k+l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	7100	wwPDB-VP
Average B, all atoms (Å ²)	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.97% 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: CL, CA, GOL, NA, PEG

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	AAA	1.15	3/3036 (0.1%)	1.25	6/4167 (0.1%)
1	BBB	1.14	2/3044 (0.1%)	1.23	2/4178 (0.0%)
All	All	1.15	5/6080 (0.1%)	1.24	8/8345 (0.1%)

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	AAA	163	GLY	C-O	7.55	1.30	1.23
1	BBB	235	ASP	C-O	5.90	1.31	1.24
1	AAA	286	ALA	C-O	5.83	1.30	1.23
1	AAA	232	GLY	C-O	5.31	1.31	1.23
1	BBB	163	GLY	C-O	5.20	1.28	1.23

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AAA	113	VAL	CA-C-N	7.54	130.24	120.44
1	AAA	113	VAL	C-N-CA	7.54	130.24	120.44
1	AAA	427	THR	CA-CB-OG1	-6.72	99.53	109.60
1	AAA	271	ASP	CA-CB-CG	5.36	117.96	112.60
1	AAA	114	ASP	CA-CB-CG	5.34	117.94	112.60

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	AAA	3002	0	2843	22	0
1	BBB	3010	0	2847	18	0
2	AAA	36	0	48	12	0
2	BBB	42	0	56	7	0
3	AAA	1	0	0	0	0
4	AAA	1	0	0	0	0
4	BBB	1	0	0	0	0
5	AAA	13	0	0	0	0
5	BBB	13	0	0	0	0
6	BBB	7	0	9	4	0
7	AAA	505	0	0	2	0
7	BBB	469	0	0	1	0
All	All	7100	0	5803	40	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 3.

The worst 5 of 40 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:AAA:159:THR:HB	2:AAA:505:GOL:O3	1.75	0.86
1:AAA:114:ASP:HB3	7:AAA:624:HOH:O	1.75	0.84
1:AAA:363:THR:HG22	1:AAA:407:ASN:OD1	1.79	0.83
1:AAA:258:GLU:OE2	2:AAA:506:GOL:H11	1.84	0.78
1:AAA:160:ASP:H	2:AAA:505:GOL:H32	1.54	0.72

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	AAA	423/449 (94%)	421 (100%)	2 (0%)	0	100	100
1	BBB	424/449 (94%)	421 (99%)	3 (1%)	0	100	100
All	All	847/898 (94%)	842 (99%)	5 (1%)	0	100	100

There are no Ramachandran outliers to report.

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	AAA	329/348 (94%)	329 (100%)	0	100	100
1	BBB	330/348 (95%)	330 (100%)	0	100	100
All	All	659/696 (95%)	659 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

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

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 43 ligands modelled in this entry, 29 are monoatomic - leaving 14 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	GOL	AAA	505	-	5,5,5	0.20	0	5,5,5	0.52	0
2	GOL	BBB	505	-	5,5,5	0.15	0	5,5,5	0.46	0
2	GOL	AAA	503	-	5,5,5	0.15	0	5,5,5	0.81	0
2	GOL	BBB	504	-	5,5,5	0.28	0	5,5,5	0.47	0
2	GOL	BBB	507	-	5,5,5	0.20	0	5,5,5	0.32	0
2	GOL	AAA	501	-	5,5,5	0.60	0	5,5,5	1.61	1 (20%)
2	GOL	AAA	506	-	5,5,5	0.17	0	5,5,5	0.50	0
2	GOL	AAA	502	-	5,5,5	0.25	0	5,5,5	0.83	0
2	GOL	BBB	502	-	5,5,5	0.20	0	5,5,5	0.40	0
2	GOL	BBB	503	-	5,5,5	0.19	0	5,5,5	0.35	0
6	PEG	BBB	508	-	6,6,6	0.73	0	5,5,5	0.49	0
2	GOL	BBB	506	4	5,5,5	0.10	0	5,5,5	0.24	0
2	GOL	AAA	504	-	5,5,5	0.13	0	5,5,5	0.21	0
2	GOL	BBB	501	-	5,5,5	0.20	0	5,5,5	0.33	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
2	GOL	AAA	505	-	-	0/4/4/4	-
2	GOL	BBB	505	-	-	0/4/4/4	-
2	GOL	AAA	503	-	-	3/4/4/4	-
2	GOL	BBB	504	-	-	2/4/4/4	-
2	GOL	BBB	507	-	-	0/4/4/4	-
2	GOL	AAA	501	-	-	4/4/4/4	-
2	GOL	AAA	506	-	-	2/4/4/4	-
2	GOL	AAA	502	-	-	4/4/4/4	-
2	GOL	BBB	502	-	-	2/4/4/4	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	GOL	BBB	503	-	-	3/4/4/4	-
6	PEG	BBB	508	-	-	3/4/4/4	-
2	GOL	BBB	506	4	-	2/4/4/4	-
2	GOL	AAA	504	-	-	2/4/4/4	-
2	GOL	BBB	501	-	-	0/4/4/4	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	AAA	501	GOL	O2-C2-C3	2.93	121.31	109.18

There are no chirality outliers.

5 of 27 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	AAA	502	GOL	O1-C1-C2-C3
2	AAA	502	GOL	C1-C2-C3-O3
2	AAA	502	GOL	O2-C2-C3-O3
2	AAA	503	GOL	O1-C1-C2-O2
2	AAA	503	GOL	O1-C1-C2-C3

There are no ring outliers.

7 monomers are involved in 23 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	AAA	505	GOL	4	0
2	BBB	507	GOL	4	0
2	AAA	506	GOL	7	0
2	BBB	502	GOL	1	0
2	BBB	503	GOL	2	0
6	BBB	508	PEG	4	0
2	AAA	504	GOL	1	0

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

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	AAA	425/449 (94%)	0.30	29 (6%)	23 27	12, 22, 47, 76	0
1	BBB	426/449 (94%)	0.38	16 (3%)	44 50	14, 26, 42, 68	0
All	All	851/898 (94%)	0.34	45 (5%)	32 36	12, 24, 45, 76	0

The worst 5 of 45 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	AAA	55	VAL	6.0
1	AAA	113	VAL	4.6
1	AAA	57	GLY	4.5
1	AAA	58	ALA	4.3
1	BBB	55	VAL	3.7

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 [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($\text{\AA}^2$)	Q<0.9
2	GOL	BBB	506	6/6	0.66	0.23	49,64,68,71	0
2	GOL	AAA	505	6/6	0.81	0.19	37,43,48,51	0
2	GOL	BBB	505	6/6	0.82	0.21	43,47,51,52	0
2	GOL	AAA	504	6/6	0.82	0.19	51,57,58,61	0
6	PEG	BBB	508	7/7	0.82	0.16	28,34,41,51	0
2	GOL	BBB	507	6/6	0.84	0.15	48,51,52,52	0
2	GOL	AAA	506	6/6	0.84	0.16	39,44,46,53	0
2	GOL	AAA	501	6/6	0.85	0.16	21,28,33,34	0
2	GOL	BBB	503	6/6	0.85	0.15	30,39,42,56	0
3	CL	AAA	507	1/1	0.88	0.13	63,63,63,63	0
2	GOL	AAA	503	6/6	0.88	0.14	26,37,41,47	0
5	CA	AAA	509	1/1	0.89	0.11	55,55,55,55	0
2	GOL	BBB	504	6/6	0.91	0.11	22,26,27,38	0
2	GOL	BBB	502	6/6	0.92	0.12	19,31,37,40	0
2	GOL	AAA	502	6/6	0.92	0.12	22,33,35,36	0
2	GOL	BBB	501	6/6	0.92	0.11	25,28,35,36	0
4	NA	BBB	509	1/1	0.93	0.08	31,31,31,31	0
5	CA	BBB	514	1/1	0.95	0.06	31,31,31,31	0
5	CA	BBB	510	1/1	0.96	0.11	33,33,33,33	0
5	CA	BBB	511	1/1	0.97	0.05	34,34,34,34	0
5	CA	BBB	522	1/1	0.98	0.03	22,22,22,22	0
5	CA	AAA	521	1/1	0.98	0.06	38,38,38,38	0
5	CA	AAA	515	1/1	0.99	0.02	18,18,18,18	0
5	CA	AAA	518	1/1	0.99	0.02	17,17,17,17	0
4	NA	AAA	508	1/1	0.99	0.04	20,20,20,20	0
5	CA	AAA	510	1/1	0.99	0.02	19,19,19,19	0
5	CA	AAA	511	1/1	0.99	0.03	26,26,26,26	0
5	CA	BBB	512	1/1	0.99	0.06	30,30,30,30	0
5	CA	BBB	513	1/1	0.99	0.05	33,33,33,33	0
5	CA	AAA	512	1/1	0.99	0.08	23,23,23,23	0
5	CA	BBB	515	1/1	0.99	0.04	25,25,25,25	0
5	CA	BBB	516	1/1	0.99	0.03	21,21,21,21	0
5	CA	BBB	517	1/1	0.99	0.04	22,22,22,22	0
5	CA	BBB	521	1/1	0.99	0.05	24,24,24,24	0
5	CA	AAA	513	1/1	0.99	0.02	14,14,14,14	0
5	CA	AAA	514	1/1	0.99	0.03	15,15,15,15	0
5	CA	AAA	517	1/1	1.00	0.01	21,21,21,21	0
5	CA	BBB	518	1/1	1.00	0.01	15,15,15,15	0
5	CA	BBB	519	1/1	1.00	0.02	16,16,16,16	0
5	CA	BBB	520	1/1	1.00	0.01	15,15,15,15	0
5	CA	AAA	516	1/1	1.00	0.01	14,14,14,14	0
5	CA	AAA	519	1/1	1.00	0.07	25,25,25,25	0
5	CA	AAA	520	1/1	1.00	0.02	17,17,17,17	0

6.5 Other polymers [i](#)

There are no such residues in this entry.