



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 12:08 PM UTC

PDB ID : 9KW6 / pdb_00009kw6
Title : Polyether epoxide hydrolase MonBI-MonBII complex
Authors : Yao, M.; Oikawa, A.; Minami, A.; Ozaki, T.; Maenaka, K.; Kumeta, H.;
Oikawa, H.; Ose, T.
Deposited on : 2024-12-05
Resolution : 3.01 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

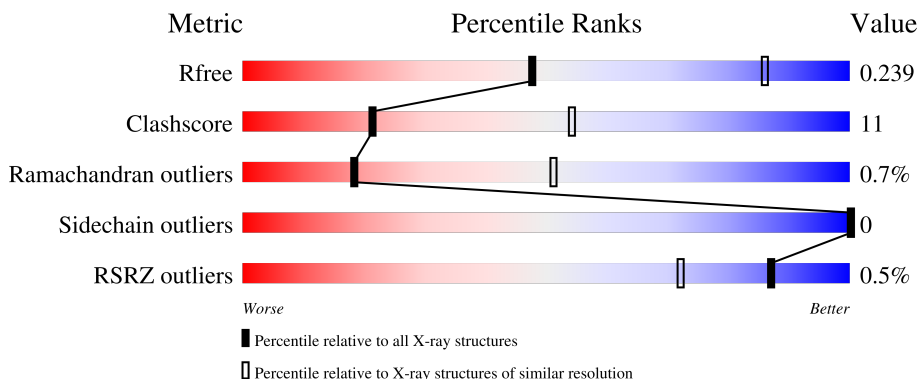
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.01 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	3131 (3.04-3.00)
Clashscore	190562	3444 (3.04-3.00)
Ramachandran outliers	187476	3319 (3.04-3.00)
Sidechain outliers	187428	3322 (3.04-3.00)
RSRZ outliers	180081	3130 (3.04-3.00)

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	302	% 69% 21% • 10%
1	B	302	70% 20% 11%
1	D	302	68% 21% • 11%
2	C	302	% 65% 24% • 11%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 8545 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 MonBI,MonBII.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	273	Total	C	N	O	S	0	1	0
			2096	1312	378	395	11			
1	B	270	Total	C	N	O	S	0	0	0
			2076	1301	372	392	11			
1	D	270	Total	C	N	O	S	0	1	0
			2090	1309	376	394	11			

There are 117 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-14	MET	-	initiating methionine	UNP Q846W7
A	-13	ASN	-	expression tag	UNP Q846W7
A	-12	HIS	-	expression tag	UNP Q846W7
A	-11	LYS	-	expression tag	UNP Q846W7
A	-10	VAL	-	expression tag	UNP Q846W7
A	-9	HIS	-	expression tag	UNP Q846W7
A	-8	HIS	-	expression tag	UNP Q846W7
A	-7	HIS	-	expression tag	UNP Q846W7
A	-6	HIS	-	expression tag	UNP Q846W7
A	-5	HIS	-	expression tag	UNP Q846W7
A	-4	HIS	-	expression tag	UNP Q846W7
A	-3	ILE	-	expression tag	UNP Q846W7
A	-2	GLU	-	expression tag	UNP Q846W7
A	-1	GLY	-	expression tag	UNP Q846W7
A	0	ALA	-	expression tag	UNP Q846W7
A	1	ALA	-	expression tag	UNP Q846W7
A	142	SER	-	linker	UNP Q846W7
A	143	GLY	-	linker	UNP Q846W7
A	144	GLY	-	linker	UNP Q846W7
A	160	SER	-	linker	UNP Q846W7
A	161	GLY	-	linker	UNP Q846W7
A	162	PRO	-	linker	UNP Q846W7
A	163	ALA	-	linker	UNP Q846W7

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Chain	Residue	Modelled	Actual	Comment	Reference
A	164	ALA	-	linker	UNP Q846W7
A	288	ARG	-	expression tag	UNP Q846W8
A	289	VAL	-	expression tag	UNP Q846W8
A	290	GLN	-	expression tag	UNP Q846W8
A	291	ALA	-	expression tag	UNP Q846W8
A	292	PHE	-	expression tag	UNP Q846W8
A	293	TRP	-	expression tag	UNP Q846W8
A	294	GLY	-	expression tag	UNP Q846W8
A	295	VAL	-	expression tag	UNP Q846W8
A	296	THR	-	expression tag	UNP Q846W8
A	297	ASP	-	expression tag	UNP Q846W8
A	298	VAL	-	expression tag	UNP Q846W8
A	299	THR	-	expression tag	UNP Q846W8
A	300	MET	-	expression tag	UNP Q846W8
A	301	ASP	-	expression tag	UNP Q846W8
A	302	ASP	-	expression tag	UNP Q846W8
B	-14	MET	-	initiating methionine	UNP Q846W7
B	-13	ASN	-	expression tag	UNP Q846W7
B	-12	HIS	-	expression tag	UNP Q846W7
B	-11	LYS	-	expression tag	UNP Q846W7
B	-10	VAL	-	expression tag	UNP Q846W7
B	-9	HIS	-	expression tag	UNP Q846W7
B	-8	HIS	-	expression tag	UNP Q846W7
B	-7	HIS	-	expression tag	UNP Q846W7
B	-6	HIS	-	expression tag	UNP Q846W7
B	-5	HIS	-	expression tag	UNP Q846W7
B	-4	HIS	-	expression tag	UNP Q846W7
B	-3	ILE	-	expression tag	UNP Q846W7
B	-2	GLU	-	expression tag	UNP Q846W7
B	-1	GLY	-	expression tag	UNP Q846W7
B	0	ALA	-	expression tag	UNP Q846W7
B	1	ALA	-	expression tag	UNP Q846W7
B	142	SER	-	linker	UNP Q846W7
B	158	GLY	-	linker	UNP Q846W7
B	159	GLY	-	linker	UNP Q846W7
B	160	SER	-	linker	UNP Q846W7
B	161	GLY	-	linker	UNP Q846W7
B	162	PRO	-	linker	UNP Q846W7
B	163	ALA	-	linker	UNP Q846W7
B	164	ALA	-	linker	UNP Q846W7
B	288	ARG	-	expression tag	UNP Q846W8
B	289	VAL	-	expression tag	UNP Q846W8

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Chain	Residue	Modelled	Actual	Comment	Reference
B	290	GLN	-	expression tag	UNP Q846W8
B	291	ALA	-	expression tag	UNP Q846W8
B	292	PHE	-	expression tag	UNP Q846W8
B	293	TRP	-	expression tag	UNP Q846W8
B	294	GLY	-	expression tag	UNP Q846W8
B	295	VAL	-	expression tag	UNP Q846W8
B	296	THR	-	expression tag	UNP Q846W8
B	297	ASP	-	expression tag	UNP Q846W8
B	298	VAL	-	expression tag	UNP Q846W8
B	299	THR	-	expression tag	UNP Q846W8
B	300	MET	-	expression tag	UNP Q846W8
B	301	ASP	-	expression tag	UNP Q846W8
B	302	ASP	-	expression tag	UNP Q846W8
D	-14	MET	-	initiating methionine	UNP Q846W7
D	-13	ASN	-	expression tag	UNP Q846W7
D	-12	HIS	-	expression tag	UNP Q846W7
D	-11	LYS	-	expression tag	UNP Q846W7
D	-10	VAL	-	expression tag	UNP Q846W7
D	-9	HIS	-	expression tag	UNP Q846W7
D	-8	HIS	-	expression tag	UNP Q846W7
D	-7	HIS	-	expression tag	UNP Q846W7
D	-6	HIS	-	expression tag	UNP Q846W7
D	-5	HIS	-	expression tag	UNP Q846W7
D	-4	HIS	-	expression tag	UNP Q846W7
D	-3	ILE	-	expression tag	UNP Q846W7
D	-2	GLU	-	expression tag	UNP Q846W7
D	-1	GLY	-	expression tag	UNP Q846W7
D	0	ALA	-	expression tag	UNP Q846W7
D	1	ALA	-	expression tag	UNP Q846W7
D	142	SER	-	linker	UNP Q846W7
D	143	GLY	-	linker	UNP Q846W7
D	159	GLY	-	linker	UNP Q846W7
D	160	SER	-	linker	UNP Q846W7
D	161	GLY	-	linker	UNP Q846W7
D	162	PRO	-	linker	UNP Q846W7
D	163	ALA	-	linker	UNP Q846W7
D	164	ALA	-	linker	UNP Q846W7
D	288	ARG	-	expression tag	UNP Q846W8
D	289	VAL	-	expression tag	UNP Q846W8
D	290	GLN	-	expression tag	UNP Q846W8
D	291	ALA	-	expression tag	UNP Q846W8
D	292	PHE	-	expression tag	UNP Q846W8

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Chain	Residue	Modelled	Actual	Comment	Reference
D	293	TRP	-	expression tag	UNP Q846W8
D	294	GLY	-	expression tag	UNP Q846W8
D	295	VAL	-	expression tag	UNP Q846W8
D	296	THR	-	expression tag	UNP Q846W8
D	297	ASP	-	expression tag	UNP Q846W8
D	298	VAL	-	expression tag	UNP Q846W8
D	299	THR	-	expression tag	UNP Q846W8
D	300	MET	-	expression tag	UNP Q846W8
D	301	ASP	-	expression tag	UNP Q846W8
D	302	ASP	-	expression tag	UNP Q846W8

- Molecule 2 is a protein called MonBI,MonBII.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	270	Total	C	N	O	S	0	0	0
			2075	1301	373	390	11			

There are 38 discrepancies between the modelled and reference sequences:

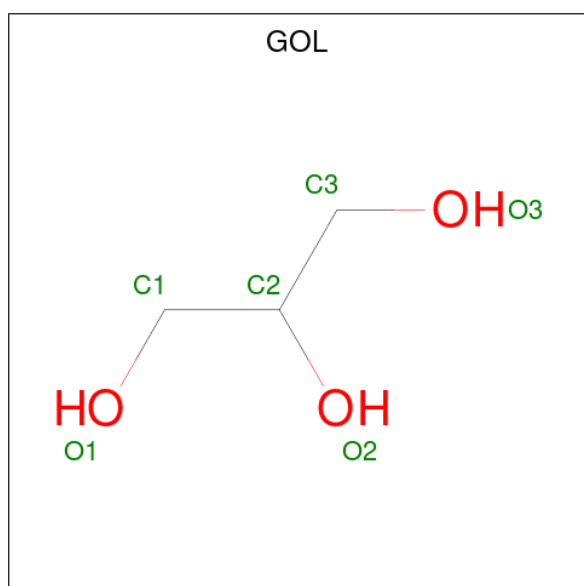
Chain	Residue	Modelled	Actual	Comment	Reference
C	-14	MET	-	initiating methionine	UNP Q846W7
C	-13	ASN	-	expression tag	UNP Q846W7
C	-12	HIS	-	expression tag	UNP Q846W7
C	-11	LYS	-	expression tag	UNP Q846W7
C	-10	VAL	-	expression tag	UNP Q846W7
C	-9	HIS	-	expression tag	UNP Q846W7
C	-8	HIS	-	expression tag	UNP Q846W7
C	-7	HIS	-	expression tag	UNP Q846W7
C	-6	HIS	-	expression tag	UNP Q846W7
C	-5	HIS	-	expression tag	UNP Q846W7
C	-4	HIS	-	expression tag	UNP Q846W7
C	-3	ILE	-	expression tag	UNP Q846W7
C	-2	GLU	-	expression tag	UNP Q846W7
C	-1	GLY	-	expression tag	UNP Q846W7
C	0	ALA	-	expression tag	UNP Q846W7
C	1	ALA	-	expression tag	UNP Q846W7
C	142	SER	-	linker	UNP Q846W7
C	143	GLY	-	linker	UNP Q846W7
C	144	GLY	-	linker	UNP Q846W7
C	160	SER	-	linker	UNP Q846W7
C	161	GLY	-	linker	UNP Q846W7
C	162	PRO	-	linker	UNP Q846W7

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Chain	Residue	Modelled	Actual	Comment	Reference
C	163	ALA	-	linker	UNP Q846W7
C	288	ARG	-	expression tag	UNP Q846W8
C	289	VAL	-	expression tag	UNP Q846W8
C	290	GLN	-	expression tag	UNP Q846W8
C	291	ALA	-	expression tag	UNP Q846W8
C	292	PHE	-	expression tag	UNP Q846W8
C	293	TRP	-	expression tag	UNP Q846W8
C	294	GLY	-	expression tag	UNP Q846W8
C	295	VAL	-	expression tag	UNP Q846W8
C	296	THR	-	expression tag	UNP Q846W8
C	297	ASP	-	expression tag	UNP Q846W8
C	298	VAL	-	expression tag	UNP Q846W8
C	299	THR	-	expression tag	UNP Q846W8
C	300	MET	-	expression tag	UNP Q846W8
C	301	ASP	-	expression tag	UNP Q846W8
C	302	ASP	-	expression tag	UNP Q846W8

- Molecule 3 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



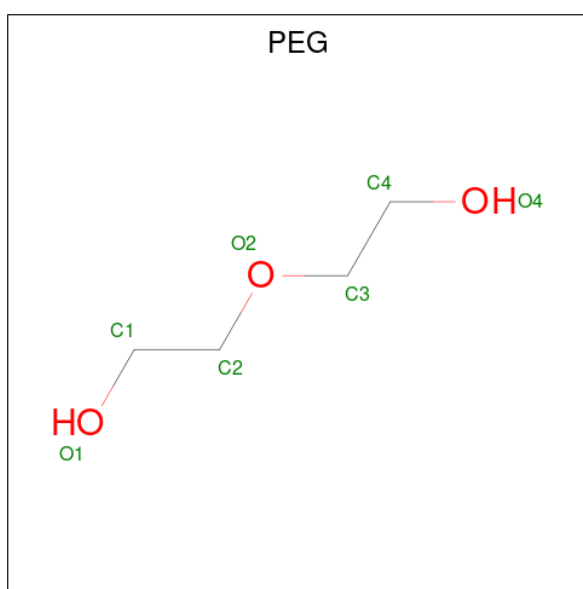
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		

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

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



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

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	38	Total	O	0	0
			38	38		
5	B	37	Total	O	0	0
			37	37		

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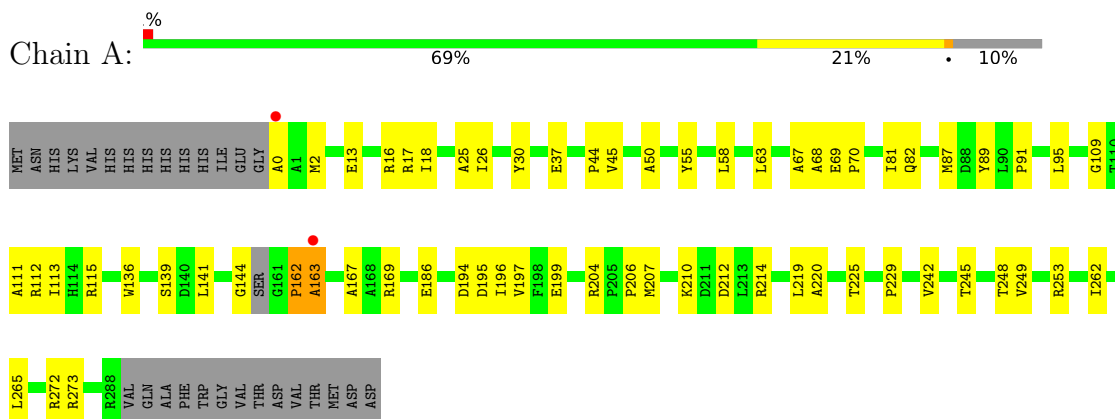
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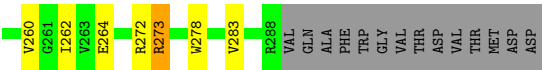
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	C	36	Total	O	0	0
			36	36		
5	D	34	Total	O	0	0
			34	34		

3 Residue-property plots [i](#)

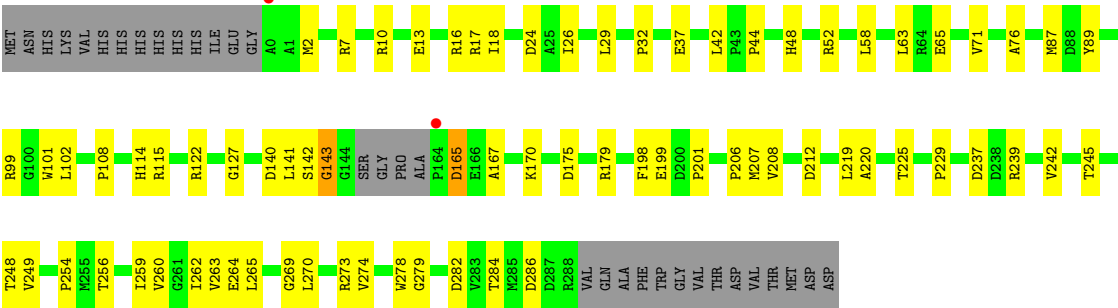
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: MonBI,MonBII





● Molecule 2: MonBI,MonBII



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	126.81Å 177.68Å 62.56Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	44.53 – 3.01 44.53 – 3.02	Depositor EDS
% Data completeness (in resolution range)	99.4 (44.53-3.01) 99.4 (44.53-3.02)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.95 (at 3.01Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.176 , 0.235 0.179 , 0.239	Depositor DCC
R_{free} test set	1464 reflections (5.10%)	wwPDB-VP
Wilson B-factor (Å ²)	61.1	Xtriage
Anisotropy	0.099	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 42.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	8545	wwPDB-VP
Average B, all atoms (Å ²)	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.99% 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: GOL, 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	A	0.46	0/2145	0.68	0/2921
1	B	0.47	0/2122	0.68	0/2891
1	D	0.46	0/2139	0.68	0/2911
2	C	0.45	0/2121	0.65	0/2887
All	All	0.46	0/8527	0.67	0/11610

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	D	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	D	273	ARG	Sidechain

5.2 Too-close contacts [i](#)

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	2096	0	2057	47	1
1	B	2076	0	2036	45	0
1	D	2090	0	2056	49	1
2	C	2075	0	2041	51	0
3	A	6	0	8	2	0
3	B	12	0	16	5	0
3	C	6	0	8	1	0
3	D	18	0	24	2	0
4	B	7	0	10	0	0
4	D	14	0	20	2	0
5	A	38	0	0	2	0
5	B	37	0	0	0	0
5	C	36	0	0	2	0
5	D	34	0	0	1	0
All	All	8545	0	8276	182	1

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 11.

The worst 5 of 182 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:163:ALA:HB1	1:A:167:ALA:HB2	1.36	1.07
1:B:58:LEU:HD22	1:B:87:MET:HE1	1.47	0.96
1:A:58:LEU:HD22	1:A:87:MET:HE1	1.46	0.93
2:C:58:LEU:HD22	2:C:87:MET:HE1	1.50	0.93
1:A:273:ARG:NH1	5:A:501:HOH:O	2.01	0.91

All (1) 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:109:GLY:O	1:D:112:ARG:NH2[4_545]	2.16	0.04

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	270/302 (89%)	260 (96%)	8 (3%)	2 (1%)	18	51
1	B	266/302 (88%)	260 (98%)	6 (2%)	0	100	100
1	D	267/302 (88%)	257 (96%)	9 (3%)	1 (0%)	30	63
2	C	266/302 (88%)	253 (95%)	9 (3%)	4 (2%)	8	33
All	All	1069/1208 (88%)	1030 (96%)	32 (3%)	7 (1%)	18	51

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	162	PRO
1	A	163	ALA
2	C	165	ASP
2	C	167	ALA
2	C	286	ASP

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	218/246 (89%)	218 (100%)	0	100	100
1	B	217/246 (88%)	217 (100%)	0	100	100
1	D	220/246 (89%)	220 (100%)	0	100	100
2	C	217/247 (88%)	217 (100%)	0	100	100
All	All	872/985 (88%)	872 (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. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	74	GLN
1	B	74	GLN
2	C	131	HIS
1	D	268	HIS

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 ⓘ

10 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	GOL	A	401	-	5,5,5	1.10	0	5,5,5	0.91	0
3	GOL	B	403	-	5,5,5	0.95	0	5,5,5	1.18	1 (20%)
4	PEG	B	401	-	6,6,6	0.47	0	5,5,5	0.54	0
3	GOL	B	402	-	5,5,5	0.98	0	5,5,5	1.05	0
4	PEG	D	402	-	6,6,6	0.51	0	5,5,5	0.39	0
3	GOL	D	405	-	5,5,5	0.85	0	5,5,5	1.24	0
4	PEG	D	401	-	6,6,6	0.52	0	5,5,5	0.44	0
3	GOL	D	403	-	5,5,5	1.43	1 (20%)	5,5,5	0.93	0
3	GOL	C	401	-	5,5,5	1.68	1 (20%)	5,5,5	1.05	0
3	GOL	D	404	-	5,5,5	1.19	1 (20%)	5,5,5	1.09	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	GOL	A	401	-	-	0/4/4/4	-
3	GOL	B	403	-	-	2/4/4/4	-
4	PEG	B	401	-	-	3/4/4/4	-
3	GOL	B	402	-	-	4/4/4/4	-
4	PEG	D	402	-	-	2/4/4/4	-
3	GOL	D	405	-	-	4/4/4/4	-
4	PEG	D	401	-	-	1/4/4/4	-
3	GOL	D	403	-	-	4/4/4/4	-
3	GOL	C	401	-	-	0/4/4/4	-
3	GOL	D	404	-	-	3/4/4/4	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	401	GOL	C3-C2	3.20	1.64	1.51
3	D	403	GOL	C1-C2	2.36	1.60	1.51
3	D	404	GOL	C3-C2	2.24	1.60	1.51

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	403	GOL	C3-C2-C1	-2.32	103.28	111.80

There are no chirality outliers.

5 of 23 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	D	403	GOL	O1-C1-C2-C3
3	D	403	GOL	C1-C2-C3-O3
3	D	404	GOL	C1-C2-C3-O3
3	D	405	GOL	O1-C1-C2-C3
3	D	405	GOL	O2-C2-C3-O3

There are no ring outliers.

7 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	401	GOL	2	0
3	B	403	GOL	3	0
3	B	402	GOL	2	0
4	D	402	PEG	2	0
3	D	405	GOL	1	0
3	C	401	GOL	1	0
3	D	404	GOL	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, 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	273/302 (90%)	-0.48	2 (0%) 84 66	25, 49, 77, 104	1 (0%)
1	B	270/302 (89%)	-0.54	1 (0%) 88 76	32, 46, 69, 111	0
1	D	270/302 (89%)	-0.46	0 100 100	23, 50, 70, 106	1 (0%)
2	C	270/302 (89%)	-0.47	2 (0%) 84 66	37, 50, 72, 102	0
All	All	1083/1208 (89%)	-0.49	5 (0%) 87 72	23, 49, 73, 111	2 (0%)

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	C	0	ALA	2.5
1	B	1	ALA	2.3
1	A	163	ALA	2.2
1	A	0	ALA	2.2
2	C	164	PRO	2.2

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(Å ²)	Q<0.9
3	GOL	D	403	6/6	0.81	0.15	59,65,71,73	0
4	PEG	D	401	7/7	0.82	0.18	51,59,69,73	0
3	GOL	D	405	6/6	0.83	0.13	66,72,74,80	0
3	GOL	D	404	6/6	0.85	0.16	54,61,64,67	0
3	GOL	B	402	6/6	0.88	0.13	52,64,65,67	0
3	GOL	C	401	6/6	0.89	0.17	53,56,62,68	0
4	PEG	B	401	7/7	0.90	0.15	48,56,63,63	0
4	PEG	D	402	7/7	0.94	0.14	45,50,61,65	0
3	GOL	B	403	6/6	0.95	0.14	36,40,47,52	0
3	GOL	A	401	6/6	0.95	0.16	45,47,57,61	0

6.5 Other polymers ⓘ

There are no such residues in this entry.