



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 7, 2026 – 02:10 AM UTC

PDB ID : 6BUM / pdb_00006bum
Title : Crystal structures of cyanuric acid hydrolase from Moorella thermoacetica
Authors : Shi, K.; Cho, S.; Seffernick, J.L.; Bera, A.; Wackett, L.P.; Aihara, H.
Deposited on : 2017-12-11
Resolution : 1.51 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

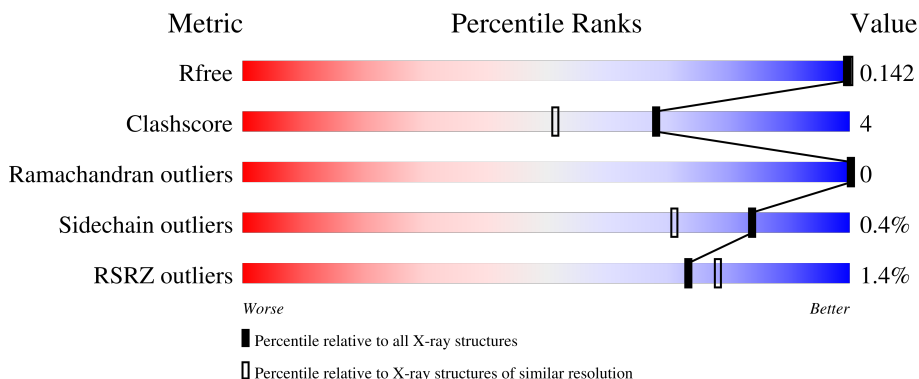
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.51 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	5890 (1.54-1.50)
Clashscore	190562	6116 (1.54-1.50)
Ramachandran outliers	187476	6002 (1.54-1.50)
Sidechain outliers	187428	5999 (1.54-1.50)
RSRZ outliers	180081	5891 (1.54-1.50)

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	363	 2% 93% 6%
1	B	363	 % 96% .
1	C	363	 % 94% 6%
1	D	363	 2% 92% 8%

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
4	PDO	A	410	-	-	X	-
4	PDO	C	405	-	-	X	-
4	PDO	C	409	-	-	X	-
4	PDO	D	405	-	-	X	-

2 Entry composition i

There are 6 unique types of molecules in this entry. The entry contains 23325 atoms, of which 11152 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 Cyanuric acid amidohydrolase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
			Total	C	H	N	O				S
1	A	362	5468	1681	2749	489	533	16	0	6	0
1	B	363	5469	1682	2750	489	533	15	3	6	0
1	C	363	5456	1680	2741	485	533	17	0	5	0
1	D	362	5409	1669	2712	481	531	16	0	3	0

There are 64 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	HIS	-	expression tag	UNP Q2RGM7
A	103	ALA	GLN	engineered mutation	UNP Q2RGM7
A	104	ALA	GLU	engineered mutation	UNP Q2RGM7
A	107	ALA	LYS	engineered mutation	UNP Q2RGM7
A	279	ILE	LEU	engineered mutation	UNP Q2RGM7
A	280	ARG	LYS	engineered mutation	UNP Q2RGM7
A	281	SER	PHE	engineered mutation	UNP Q2RGM7
A	?	-	CYS	deletion	UNP Q2RGM7
A	?	-	CYS	deletion	UNP Q2RGM7
A	?	-	PRO	deletion	UNP Q2RGM7
A	?	-	PRO	deletion	UNP Q2RGM7
A	?	-	ALA	deletion	UNP Q2RGM7
A	283	ASP	GLU	engineered mutation	UNP Q2RGM7
A	290	MET	LEU	engineered mutation	UNP Q2RGM7
A	291	ASP	ALA	engineered mutation	UNP Q2RGM7
A	292	ARG	LYS	engineered mutation	UNP Q2RGM7
B	0	HIS	-	expression tag	UNP Q2RGM7
B	103	ALA	GLN	engineered mutation	UNP Q2RGM7
B	104	ALA	GLU	engineered mutation	UNP Q2RGM7
B	107	ALA	LYS	engineered mutation	UNP Q2RGM7
B	279	ILE	LEU	engineered mutation	UNP Q2RGM7

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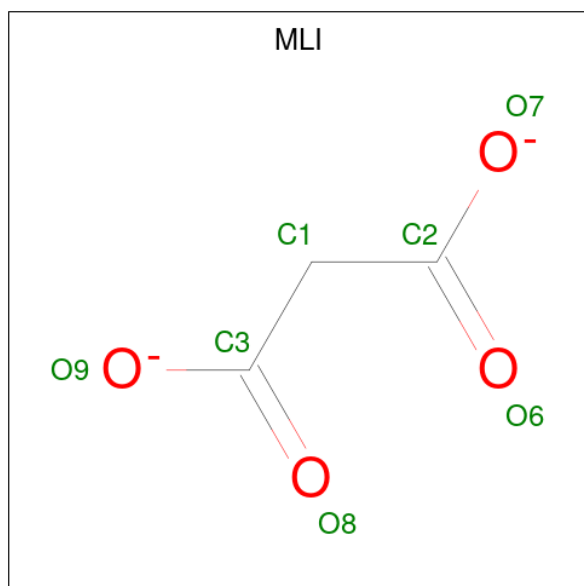
Chain	Residue	Modelled	Actual	Comment	Reference
B	280	ARG	LYS	engineered mutation	UNP Q2RGM7
B	281	SER	PHE	engineered mutation	UNP Q2RGM7
B	?	-	CYS	deletion	UNP Q2RGM7
B	?	-	CYS	deletion	UNP Q2RGM7
B	?	-	PRO	deletion	UNP Q2RGM7
B	?	-	PRO	deletion	UNP Q2RGM7
B	?	-	ALA	deletion	UNP Q2RGM7
B	283	ASP	GLU	engineered mutation	UNP Q2RGM7
B	290	MET	LEU	engineered mutation	UNP Q2RGM7
B	291	ASP	ALA	engineered mutation	UNP Q2RGM7
B	292	ARG	LYS	engineered mutation	UNP Q2RGM7
C	0	HIS	-	expression tag	UNP Q2RGM7
C	103	ALA	GLN	engineered mutation	UNP Q2RGM7
C	104	ALA	GLU	engineered mutation	UNP Q2RGM7
C	107	ALA	LYS	engineered mutation	UNP Q2RGM7
C	279	ILE	LEU	engineered mutation	UNP Q2RGM7
C	280	ARG	LYS	engineered mutation	UNP Q2RGM7
C	281	SER	PHE	engineered mutation	UNP Q2RGM7
C	?	-	CYS	deletion	UNP Q2RGM7
C	?	-	CYS	deletion	UNP Q2RGM7
C	?	-	PRO	deletion	UNP Q2RGM7
C	?	-	PRO	deletion	UNP Q2RGM7
C	?	-	ALA	deletion	UNP Q2RGM7
C	283	ASP	GLU	engineered mutation	UNP Q2RGM7
C	290	MET	LEU	engineered mutation	UNP Q2RGM7
C	291	ASP	ALA	engineered mutation	UNP Q2RGM7
C	292	ARG	LYS	engineered mutation	UNP Q2RGM7
D	0	HIS	-	expression tag	UNP Q2RGM7
D	103	ALA	GLN	engineered mutation	UNP Q2RGM7
D	104	ALA	GLU	engineered mutation	UNP Q2RGM7
D	107	ALA	LYS	engineered mutation	UNP Q2RGM7
D	279	ILE	LEU	engineered mutation	UNP Q2RGM7
D	280	ARG	LYS	engineered mutation	UNP Q2RGM7
D	281	SER	PHE	engineered mutation	UNP Q2RGM7
D	?	-	CYS	deletion	UNP Q2RGM7
D	?	-	CYS	deletion	UNP Q2RGM7
D	?	-	PRO	deletion	UNP Q2RGM7
D	?	-	PRO	deletion	UNP Q2RGM7
D	?	-	ALA	deletion	UNP Q2RGM7
D	283	ASP	GLU	engineered mutation	UNP Q2RGM7
D	290	MET	LEU	engineered mutation	UNP Q2RGM7
D	291	ASP	ALA	engineered mutation	UNP Q2RGM7

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Chain	Residue	Modelled	Actual	Comment	Reference
D	292	ARG	LYS	engineered mutation	UNP Q2RGM7

- Molecule 2 is MALONATE ION (CCD ID: MLI) (formula: $C_3H_2O_4$).

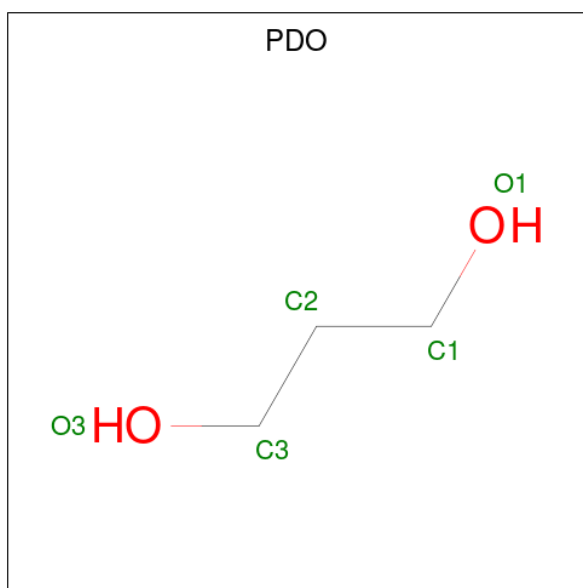


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	H	O		
2	A	1	9	3	2	4	0	0
2	B	1	9	3	2	4	0	0
2	C	1	9	3	2	4	0	0
2	D	1	9	3	2	4	0	0

- Molecule 3 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Ca		
3	A	1	1	1	0	0
3	B	1	1	1	0	0
3	C	1	1	1	0	0
3	D	1	1	1	0	0

- Molecule 4 is 1,3-PROPANDIOL (CCD ID: PDO) (formula: $C_3H_8O_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	H	O	0	0
			13	3	8	2		
4	A	1	Total	C	H	O	0	0
			13	3	8	2		
4	A	1	Total	C	H	O	0	0
			13	3	8	2		
4	A	1	Total	C	H	O	0	0
			13	3	8	2		
4	A	1	Total	C	H	O	0	0
			13	3	8	2		
4	A	1	Total	C	H	O	0	0
			13	3	8	2		
4	A	1	Total	C	H	O	0	0
			13	3	8	2		
4	B	1	Total	C	H	O	0	0
			13	3	8	2		
4	B	1	Total	C	H	O	0	0
			13	3	8	2		
4	B	1	Total	C	H	O	0	0
			13	3	8	2		
4	B	1	Total	C	H	O	0	0
			13	3	8	2		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	B	1	Total	C	H	O	0	0
			13	3	8	2		
4	C	1	Total	C	H	O	0	0
			13	3	8	2		
4	C	1	Total	C	H	O	0	0
			13	3	8	2		
4	C	1	Total	C	H	O	0	0
			13	3	8	2		
4	C	1	Total	C	H	O	0	0
			13	3	8	2		
4	C	1	Total	C	H	O	0	0
			13	3	8	2		
4	C	1	Total	C	H	O	0	0
			13	3	8	2		
4	D	1	Total	C	H	O	0	0
			13	3	8	2		
4	D	1	Total	C	H	O	0	0
			13	3	8	2		
4	D	1	Total	C	H	O	0	0
			13	3	8	2		

- Molecule 5 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	1	Total	Cl	0	0
			1	1		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	332	Total	O	0	0
			332	332		
6	B	329	Total	O	0	0
			329	329		
6	C	314	Total	O	0	2
			316	316		
6	D	192	Total	O	0	1
			193	193		

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.

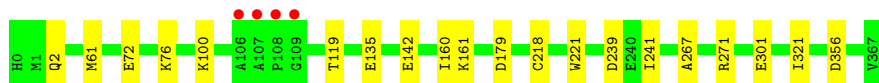
- Molecule 1: Cyanuric acid amidohydrolase



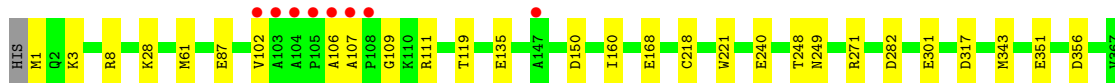
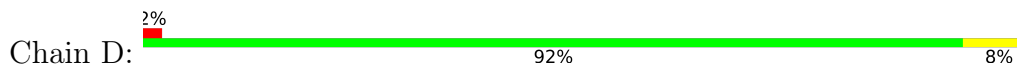
- Molecule 1: Cyanuric acid amidohydrolase



- Molecule 1: Cyanuric acid amidohydrolase



- Molecule 1: Cyanuric acid amidohydrolase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	81.44Å 88.69Å 204.28Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.99 – 1.51 29.99 – 1.51	Depositor EDS
% Data completeness (in resolution range)	91.7 (29.99-1.51) 95.7 (29.99-1.51)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	0.04	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.39 (at 1.51Å)	Xtrriage
Refinement program	PHENIX (1.13rc2_2975: ???)	Depositor
R, R_{free}	0.126 , 0.141 0.127 , 0.142	Depositor DCC
R_{free} test set	11226 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å ²)	19.2	Xtrriage
Anisotropy	0.104	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.40 , 41.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.98	EDS
Total number of atoms	23325	wwPDB-VP
Average B, all atoms (Å ²)	30.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.37% 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: CA, CL, MLI, PDO

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	0.22	0/2769	0.49	0/3745
1	B	0.20	0/2782	0.48	0/3763
1	C	0.19	0/2769	0.46	0/3746
1	D	0.17	0/2742	0.41	0/3710
All	All	0.19	0/11062	0.46	0/14964

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	2719	2749	2733	23	0
1	B	2719	2750	2728	11	0
1	C	2715	2741	2718	17	0
1	D	2697	2712	2713	22	0
2	A	7	2	2	0	0
2	B	7	2	2	0	0
2	C	7	2	2	0	0
2	D	7	2	2	0	0
3	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
4	A	40	64	64	10	0
4	B	30	48	48	3	0
4	C	35	56	56	10	0
4	D	15	24	24	7	0
5	B	1	0	0	1	0
6	A	332	0	0	14	2
6	B	329	0	0	6	2
6	C	316	0	0	3	0
6	D	193	0	0	6	0
All	All	12173	11152	11092	80	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 4.

The worst 5 of 80 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:B:2:GLN:OE1	6:B:501:HOH:O	1.73	1.06
5:B:403:CL:CL	6:B:597:HOH:O	2.15	0.98
1:D:168:GLU:OE1	6:D:501:HOH:O	1.89	0.90
1:A:142:GLU:OE2	6:A:501:HOH:O	1.89	0.90
1:A:138[B]:ARG:NH1	6:A:505:HOH:O	2.11	0.83

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)
6:A:525:HOH:O	6:B:505:HOH:O[3_645]	1.90	0.30
6:A:794:HOH:O	6:B:573:HOH:O[1_455]	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	366/363 (101%)	357 (98%)	9 (2%)	0	100	100
1	B	367/363 (101%)	359 (98%)	8 (2%)	0	100	100
1	C	366/363 (101%)	357 (98%)	9 (2%)	0	100	100
1	D	363/363 (100%)	354 (98%)	9 (2%)	0	100	100
All	All	1462/1452 (101%)	1427 (98%)	35 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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	290/286 (101%)	290 (100%)	0	100	100
1	B	292/286 (102%)	292 (100%)	0	100	100
1	C	291/286 (102%)	289 (99%)	2 (1%)	76	57
1	D	288/286 (101%)	286 (99%)	2 (1%)	76	57
All	All	1161/1144 (102%)	1157 (100%)	4 (0%)	84	75

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	100	LYS
1	C	179	ASP
1	D	28	LYS
1	D	150	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	57	GLN
1	B	57	GLN
1	B	148	GLN
1	B	249	ASN
1	C	148	GLN

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](#)

Of 33 ligands modelled in this entry, 5 are monoatomic - leaving 28 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	$\# Z > 2$
4	PDO	D	403	-	4,4,4	0.34	0	3,3,3	0.45	0
4	PDO	B	404	-	4,4,4	0.36	0	3,3,3	0.23	0
2	MLI	D	401	-	6,6,6	1.42	0	7,7,7	1.19	1 (14%)
4	PDO	C	404	-	4,4,4	0.44	0	3,3,3	0.41	0
4	PDO	A	409	-	4,4,4	0.38	0	3,3,3	0.36	0
4	PDO	C	406	-	4,4,4	0.36	0	3,3,3	0.29	0
4	PDO	A	410	-	4,4,4	0.30	0	3,3,3	0.59	0
2	MLI	C	401	-	6,6,6	1.56	0	7,7,7	1.12	0
4	PDO	C	409	-	4,4,4	0.35	0	3,3,3	0.25	0
4	PDO	B	405	-	4,4,4	0.33	0	3,3,3	0.47	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	PDO	A	404	-	4,4,4	0.34	0	3,3,3	0.48	0
4	PDO	B	409	-	4,4,4	0.34	0	3,3,3	0.49	0
2	MLI	B	401	-	6,6,6	1.30	0	7,7,7	1.25	1 (14%)
4	PDO	A	405	-	4,4,4	0.40	0	3,3,3	0.36	0
4	PDO	A	403	-	4,4,4	0.36	0	3,3,3	0.26	0
4	PDO	C	407	-	4,4,4	0.36	0	3,3,3	0.36	0
4	PDO	B	407	-	4,4,4	0.40	0	3,3,3	0.32	0
4	PDO	A	408	-	4,4,4	0.35	0	3,3,3	0.29	0
2	MLI	A	401	-	6,6,6	1.35	0	7,7,7	1.18	0
4	PDO	B	406	-	4,4,4	0.34	0	3,3,3	0.48	0
4	PDO	A	407	-	4,4,4	0.35	0	3,3,3	0.44	0
4	PDO	C	405	3	4,4,4	0.43	0	3,3,3	0.61	0
4	PDO	C	408	-	4,4,4	0.35	0	3,3,3	0.39	0
4	PDO	B	408	-	4,4,4	0.37	0	3,3,3	0.46	0
4	PDO	D	405	3	4,4,4	0.39	0	3,3,3	0.41	0
4	PDO	C	403	-	4,4,4	0.35	0	3,3,3	0.24	0
4	PDO	D	404	-	4,4,4	0.35	0	3,3,3	0.35	0
4	PDO	A	406	-	4,4,4	0.34	0	3,3,3	0.38	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	PDO	D	403	-	-	0/2/2/2	-
4	PDO	B	404	-	-	0/2/2/2	-
2	MLI	D	401	-	-	2/4/4/4	-
4	PDO	C	404	-	-	1/2/2/2	-
4	PDO	A	409	-	-	0/2/2/2	-
4	PDO	C	406	-	-	0/2/2/2	-
4	PDO	A	410	-	-	1/2/2/2	-
2	MLI	C	401	-	-	2/4/4/4	-
4	PDO	C	409	-	-	1/2/2/2	-
4	PDO	B	405	-	-	0/2/2/2	-
4	PDO	A	404	-	-	0/2/2/2	-
4	PDO	B	409	-	-	0/2/2/2	-
2	MLI	B	401	-	-	2/4/4/4	-
4	PDO	A	405	-	-	1/2/2/2	-
4	PDO	A	403	-	-	0/2/2/2	-
4	PDO	C	407	-	-	2/2/2/2	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	PDO	B	407	-	-	1/2/2/2	-
4	PDO	A	408	-	-	0/2/2/2	-
2	MLI	A	401	-	-	2/4/4/4	-
4	PDO	B	406	-	-	0/2/2/2	-
4	PDO	A	407	-	-	0/2/2/2	-
4	PDO	C	405	3	-	0/2/2/2	-
4	PDO	C	408	-	-	0/2/2/2	-
4	PDO	B	408	-	-	1/2/2/2	-
4	PDO	D	405	3	-	0/2/2/2	-
4	PDO	C	403	-	-	0/2/2/2	-
4	PDO	D	404	-	-	1/2/2/2	-
4	PDO	A	406	-	-	1/2/2/2	-

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	401	MLI	O8-C3-C1	-2.15	115.98	122.11
2	B	401	MLI	O6-C2-C1	-2.09	116.15	122.11

There are no chirality outliers.

5 of 18 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	406	PDO	C1-C2-C3-O3
4	A	410	PDO	C1-C2-C3-O3
4	B	407	PDO	O1-C1-C2-C3
4	B	408	PDO	O1-C1-C2-C3
4	C	404	PDO	C1-C2-C3-O3

There are no ring outliers.

12 monomers are involved in 30 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	D	403	PDO	1	0
4	C	404	PDO	1	0
4	A	409	PDO	3	0
4	A	410	PDO	6	0
4	C	409	PDO	5	0
4	B	409	PDO	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	407	PDO	1	0
4	C	405	PDO	4	0
4	B	408	PDO	1	0
4	D	405	PDO	5	0
4	D	404	PDO	1	0
4	A	406	PDO	2	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	362/363 (99%)	-0.73	6 (1%) 69 74	12, 20, 44, 92	4 (1%)
1	B	363/363 (100%)	-0.80	2 (0%) 85 89	12, 22, 41, 65	4 (1%)
1	C	363/363 (100%)	-0.64	4 (1%) 78 82	9, 25, 48, 89	3 (0%)
1	D	362/363 (99%)	-0.14	8 (2%) 62 68	9, 37, 68, 100	2 (0%)
All	All	1450/1452 (99%)	-0.58	20 (1%) 73 78	9, 24, 55, 100	13 (0%)

The worst 5 of 20 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	107	ALA	6.2
1	A	106	ALA	5.7
1	A	107	ALA	4.1
1	C	106	ALA	3.8
1	D	104	ALA	3.8

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(\AA^2)	Q<0.9
4	PDO	A	408	5/5	0.64	0.26	59,71,74,74	0
4	PDO	A	409	5/5	0.69	0.22	72,86,90,91	0
4	PDO	C	406	5/5	0.78	0.18	51,62,66,66	0
4	PDO	B	409	5/5	0.80	0.16	43,52,61,63	0
4	PDO	C	404	5/5	0.82	0.17	27,39,45,47	0
4	PDO	B	408	5/5	0.82	0.13	53,63,64,65	0
4	PDO	C	409	5/5	0.84	0.13	45,55,56,60	0
4	PDO	A	410	5/5	0.85	0.16	37,49,58,61	0
4	PDO	C	407	5/5	0.85	0.17	38,49,58,58	0
4	PDO	C	405	5/5	0.85	0.16	37,44,49,52	0
4	PDO	A	406	5/5	0.86	0.19	81,97,100,101	0
4	PDO	A	407	5/5	0.86	0.15	62,74,79,79	0
4	PDO	D	403	5/5	0.86	0.15	76,92,93,94	0
4	PDO	B	407	5/5	0.87	0.15	27,40,46,48	0
4	PDO	B	405	5/5	0.88	0.15	60,72,74,75	0
4	PDO	D	405	5/5	0.88	0.12	48,57,59,63	0
4	PDO	A	405	5/5	0.89	0.12	30,41,46,49	0
4	PDO	C	408	5/5	0.91	0.13	60,72,75,75	0
4	PDO	D	404	5/5	0.92	0.11	56,67,75,77	0
4	PDO	A	404	5/5	0.93	0.09	33,42,52,54	0
4	PDO	B	406	5/5	0.94	0.10	39,49,57,59	0
5	CL	B	403	1/1	0.95	0.12	73,73,73,73	0
4	PDO	A	403	5/5	0.96	0.07	25,34,41,41	0
4	PDO	C	403	5/5	0.97	0.07	27,32,38,39	0
4	PDO	B	404	5/5	0.98	0.05	25,30,35,35	0
2	MLI	B	401	7/7	0.99	0.03	17,18,22,22	0
2	MLI	C	401	7/7	0.99	0.04	18,19,23,23	0
2	MLI	D	401	7/7	0.99	0.04	20,21,25,25	0
2	MLI	A	401	7/7	0.99	0.03	16,17,21,21	0
3	CA	B	402	1/1	1.00	0.02	18,18,18,18	1
3	CA	C	402	1/1	1.00	0.02	19,19,19,19	1
3	CA	D	402	1/1	1.00	0.02	27,27,27,27	1
3	CA	A	402	1/1	1.00	0.01	18,18,18,18	1

6.5 Other polymers i

There are no such residues in this entry.