



wwPDB X-ray Structure Validation Summary Report ⓘ

Jun 3, 2020 – 07:35 pm BST

PDB ID : 6DXS
Title : Crystal structure of the LigJ hydratase E284Q mutant substrate complex with (3Z)-2-keto-4-carboxy-3-hexenedioate
Authors : Mabanglo, M.F.; Raushel, F.M.; Hogancamp, T.N.
Deposited on : 2018-06-29
Resolution : 1.65 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : **FAILED**
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

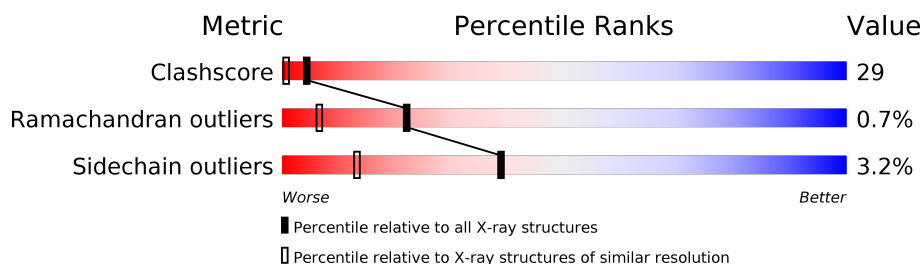
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.65 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))
Clashscore	141614	1931 (1.66-1.66)
Ramachandran outliers	138981	1891 (1.66-1.66)
Sidechain outliers	138945	1891 (1.66-1.66)

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 on 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 $\leq 5\%$.

Note EDS failed to run properly.

Mol	Chain	Length	Quality of chain
1	A	342	
1	B	342	
1	C	342	
1	D	342	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 11540 atoms, of which 11 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 4-oxalomesaconate hydratase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	342	Total	C	N	O	S	0	0	0
			2683	1709	464	490	20			
1	B	342	Total	C	N	O	S	0	0	0
			2683	1709	464	490	20			
1	C	342	Total	C	N	O	S	0	0	0
			2683	1709	464	490	20			
1	D	342	Total	C	N	O	S	0	0	0
			2683	1709	464	490	20			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	284	GLN	GLU	engineered mutation	UNP G2IQQ5
A	342	LEU	-	expression tag	UNP G2IQQ5
A	343	GLU	-	expression tag	UNP G2IQQ5
B	284	GLN	GLU	engineered mutation	UNP G2IQQ5
B	342	LEU	-	expression tag	UNP G2IQQ5
B	343	GLU	-	expression tag	UNP G2IQQ5
C	284	GLN	GLU	engineered mutation	UNP G2IQQ5
C	342	LEU	-	expression tag	UNP G2IQQ5
C	343	GLU	-	expression tag	UNP G2IQQ5
D	284	GLN	GLU	engineered mutation	UNP G2IQQ5
D	342	LEU	-	expression tag	UNP G2IQQ5
D	343	GLU	-	expression tag	UNP G2IQQ5

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

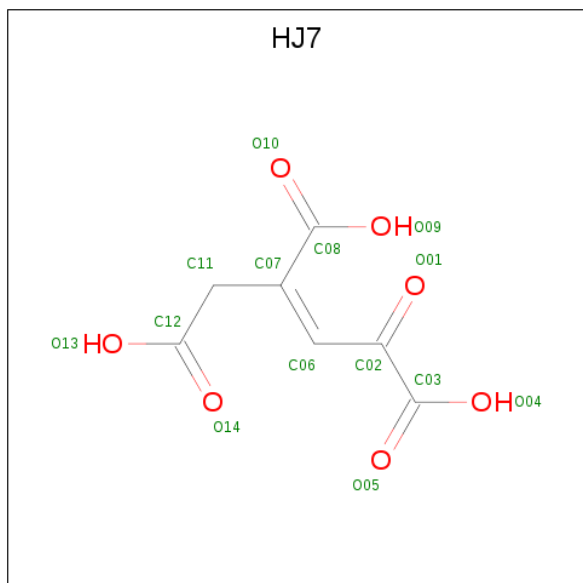
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total	Zn	0	0
			1	1		
2	A	1	Total	Zn	0	0
			1	1		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	D	1	Total	Zn	0	0
			1	1		
2	C	1	Total	Zn	0	0
			1	1		

- Molecule 3 is (2Z)-4-oxobut-2-ene-1,2,4-tricarboxylic acid (three-letter code: HJ7) (formula: C₇H₆O₇).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	H	O	0	0
			17	7	3	7		
3	B	1	Total	C	H	O	0	0
			17	7	3	7		
3	C	1	Total	C	H	O	0	0
			17	7	3	7		
3	D	1	Total	C	H	O	0	0
			16	7	2	7		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	181	Total	O	0	0
			181	181		
4	B	192	Total	O	0	0
			192	192		
4	C	169	Total	O	0	0
			169	169		

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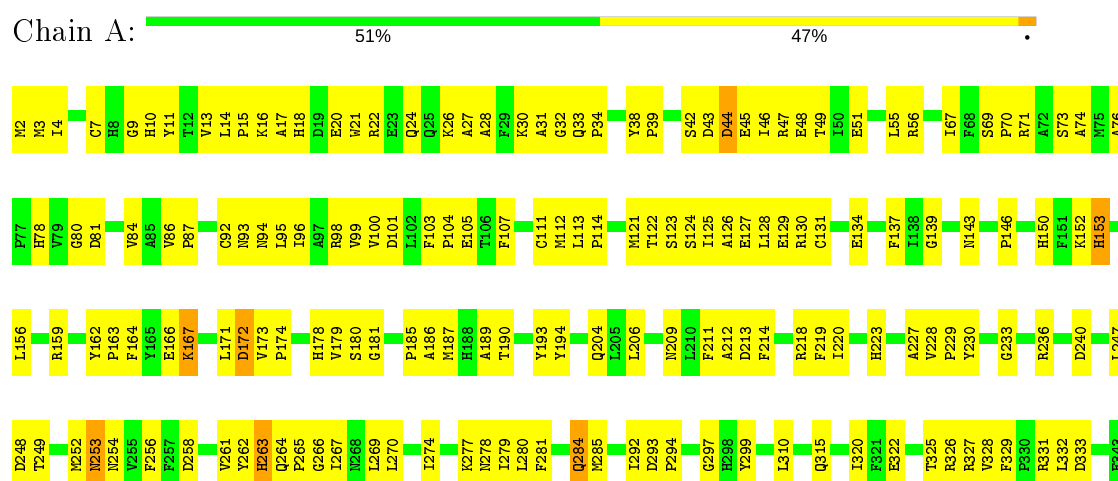
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	D	195	Total 195	O 195	0	0

3 Residue-property plots

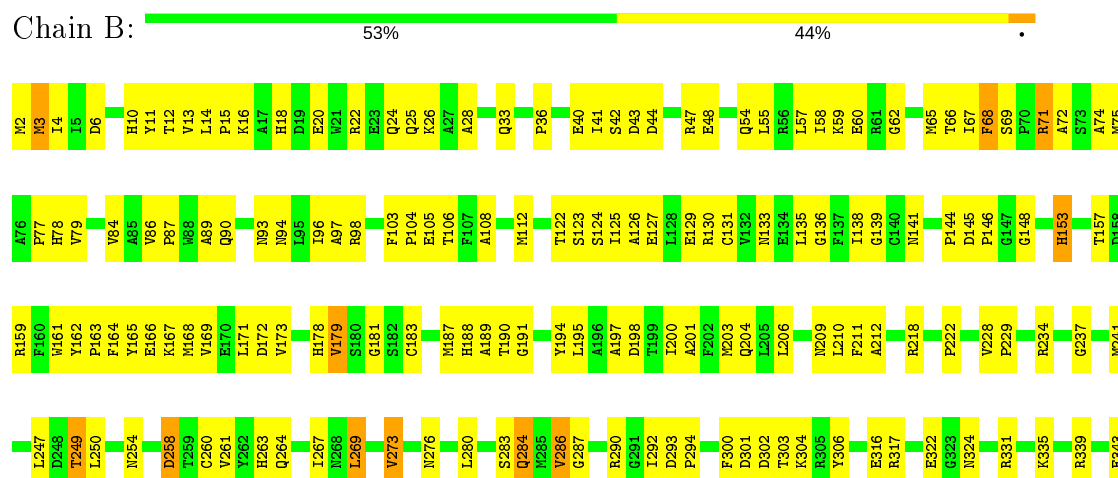
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded according 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. 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.

Note EDS failed to run properly.

- Molecule 1: 4-oxalomesaconate hydratase

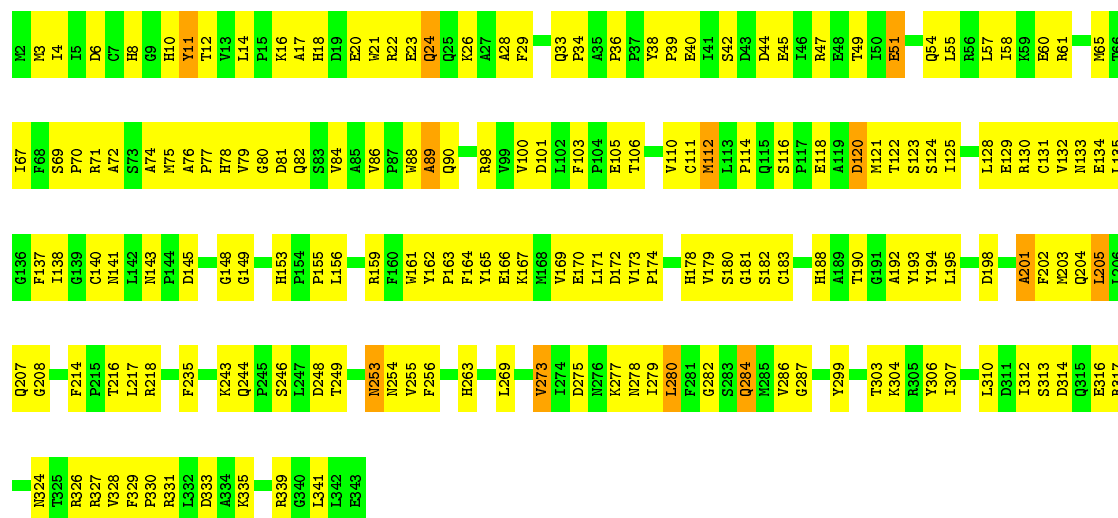


- Molecule 1: 4-oxalomesaconate hydratase



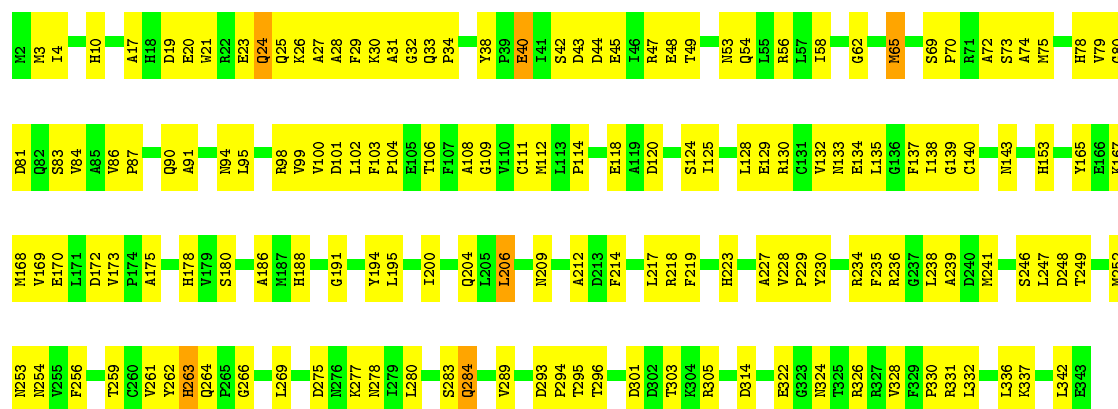
- Molecule 1: 4-oxalomesaconate hydratase





• Molecule 1: 4-oxalomesaconate hydratase

Chain D: 54% 44%



4 Data and refinement statistics

EDS failed to run properly - this section is therefore incomplete.

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	82.69Å 78.25Å 136.22Å 90.00° 89.98° 90.00°	Depositor
Resolution (Å)	43.63 – 1.65	Depositor
% Data completeness (in resolution range)	97.8 (43.63-1.65)	Depositor
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.40 (at 1.64Å)	Xtriage
Refinement program	PHENIX (1.13_2998: ???)	Depositor
R, R_{free}	0.202 , 0.266	Depositor
Wilson B-factor (Å ²)	20.5	Xtriage
Anisotropy	0.770	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.41$, $\langle L^2 \rangle = 0.24$	Xtriage
Estimated twinning fraction	0.479 for h,-k,-l	Xtriage
Total number of atoms	11540	wwPDB-VP
Average B, all atoms (Å ²)	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 55.95 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 2.9363e-05.*

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: HJ7, ZN

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	0.39	0/2757	0.56	0/3748
1	B	0.40	0/2757	0.59	0/3748
1	C	0.40	0/2757	0.57	0/3748
1	D	0.39	0/2757	0.59	0/3748
All	All	0.40	0/11028	0.58	0/14992

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	2683	0	2602	160	0
1	B	2683	0	2602	140	1
1	C	2683	0	2602	162	0
1	D	2683	0	2602	157	1
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	A	14	3	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	14	3	0	4	0
3	C	14	3	0	2	0
3	D	14	2	0	4	0
4	A	181	0	0	40	0
4	B	192	0	0	39	3
4	C	169	0	0	33	2
4	D	195	0	0	49	1
All	All	11529	11	10408	614	4

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 29.

The worst 5 of 614 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:C:75:MET:SD	4:C:632:HOH:O	2.08	1.11
1:C:145:ASP:OD1	4:C:501:HOH:O	1.69	1.08
1:D:195:LEU:O	4:D:501:HOH:O	1.73	1.06
1:D:112:MET:SD	4:D:629:HOH:O	2.13	1.05
1:D:40:GLU:OE1	4:D:502:HOH:O	1.73	1.04

All (4) 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:D:102:LEU:O	4:B:668:HOH:O[1_655]	1.93	0.27
1:B:234:ARG:NH2	4:C:564:HOH:O[1_565]	2.11	0.09
4:B:523:HOH:O	4:C:621:HOH:O[1_565]	2.16	0.04
4:B:564:HOH:O	4:D:613:HOH:O[1_455]	2.17	0.03

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	340/342 (99%)	307 (90%)	30 (9%)	3 (1%)	17	4
1	B	340/342 (99%)	307 (90%)	31 (9%)	2 (1%)	25	8
1	C	340/342 (99%)	300 (88%)	37 (11%)	3 (1%)	17	4
1	D	340/342 (99%)	310 (91%)	29 (8%)	1 (0%)	41	22
All	All	1360/1368 (99%)	1224 (90%)	127 (9%)	9 (1%)	22	6

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	172	ASP
1	B	3	MET
1	C	201	ALA
1	A	80	GLY
1	C	89	ALA

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	284/284 (100%)	278 (98%)	6 (2%)	53	29
1	B	284/284 (100%)	274 (96%)	10 (4%)	36	11
1	C	284/284 (100%)	271 (95%)	13 (5%)	27	6
1	D	284/284 (100%)	277 (98%)	7 (2%)	47	22
All	All	1136/1136 (100%)	1100 (97%)	36 (3%)	39	13

5 of 36 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	11	TYR
1	C	120	ASP
1	D	206	LEU
1	C	51	GLU
1	C	153	HIS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	133	ASN
1	D	150	HIS
1	C	150	HIS
1	B	284	GLN
1	D	133	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 8 ligands modelled in this entry, 4 are monoatomic - leaving 4 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	$\# Z > 2$
3	HJ7	C	402	2	4,13,13	2.19	2 (50%)	4,17,17	1.82	1 (25%)
3	HJ7	D	402	2	4,13,13	2.19	1 (25%)	4,17,17	1.69	1 (25%)
3	HJ7	A	402	2	4,13,13	2.45	1 (25%)	4,17,17	1.93	1 (25%)
3	HJ7	B	402	2	4,13,13	2.24	2 (50%)	4,17,17	1.79	1 (25%)

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	HJ7	C	402	2	-	2/6/16/16	-
3	HJ7	D	402	2	-	2/6/16/16	-
3	HJ7	A	402	2	-	2/6/16/16	-
3	HJ7	B	402	2	-	2/6/16/16	-

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	402	HJ7	C06-C02	4.03	1.56	1.43
3	D	402	HJ7	C06-C02	3.84	1.55	1.43
3	C	402	HJ7	C06-C02	3.46	1.54	1.43
3	B	402	HJ7	C06-C02	3.40	1.54	1.43
3	B	402	HJ7	O01-C02	-2.50	1.18	1.24

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	402	HJ7	C11-C07-C06	-3.50	117.83	125.83
3	C	402	HJ7	C11-C07-C06	-3.24	118.44	125.83
3	B	402	HJ7	C11-C07-C06	-2.95	119.09	125.83
3	D	402	HJ7	C11-C07-C06	-2.69	119.68	125.83

There are no chirality outliers.

5 of 8 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	402	HJ7	C06-C07-C11-C12
3	A	402	HJ7	C08-C07-C11-C12
3	B	402	HJ7	C06-C07-C11-C12
3	B	402	HJ7	C08-C07-C11-C12
3	C	402	HJ7	C06-C07-C11-C12

There are no ring outliers.

4 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	402	HJ7	2	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	402	HJ7	4	0
3	A	402	HJ7	1	0
3	B	402	HJ7	4	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

EDS failed to run properly - this section is therefore empty.

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

EDS failed to run properly - this section is therefore empty.

6.3 Carbohydrates [i](#)

EDS failed to run properly - this section is therefore empty.

6.4 Ligands [i](#)

EDS failed to run properly - this section is therefore empty.

6.5 Other polymers [i](#)

EDS failed to run properly - this section is therefore empty.