



wwPDB X-ray Structure Validation Summary Report ⓘ

May 15, 2020 – 08:03 pm BST

PDB ID : 5Z5C
Title : Crystal structure of hydrogen sulfide-producing enzyme (Fn1055) from *Fusobacterium nucleatum*: lysine-dimethylated form
Authors : Kezuka, Y.; Yoshida, Y.; Nonaka, T.
Deposited on : 2018-01-17
Resolution : 2.07 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 : 2.11
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

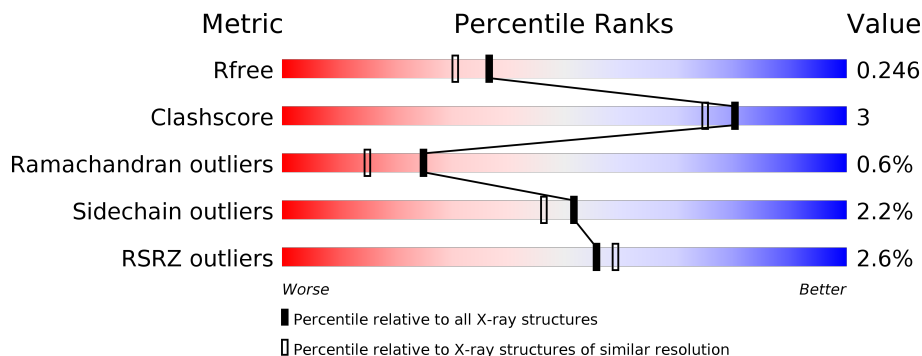
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.07 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}	130704	2684 (2.08-2.04)
Clashscore	141614	2801 (2.08-2.04)
Ramachandran outliers	138981	2768 (2.08-2.04)
Sidechain outliers	138945	2768 (2.08-2.04)
RSRZ outliers	127900	2646 (2.08-2.04)

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 $\leq 5\%$. 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	340	
1	B	340	
1	C	340	
1	D	340	

2 Entry composition i

There are 4 unique types of molecules in this entry. The entry contains 10840 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.

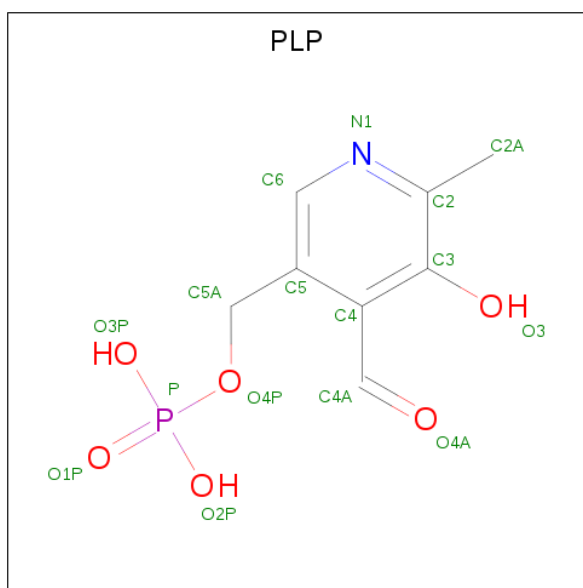
- Molecule 1 is a protein called Cysteine synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	331	2590	1663	427	487	13	0	0	0
1	B	336	2622	1678	434	496	14	0	1	0
1	C	332	2591	1661	429	488	13	0	0	0
1	D	332	2601	1671	429	488	13	0	0	0

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-3	GLY	-	expression tag	UNP Q8REP3
A	-2	PRO	-	expression tag	UNP Q8REP3
A	-1	LEU	-	expression tag	UNP Q8REP3
A	0	GLY	-	expression tag	UNP Q8REP3
A	1	SER	-	expression tag	UNP Q8REP3
B	-3	GLY	-	expression tag	UNP Q8REP3
B	-2	PRO	-	expression tag	UNP Q8REP3
B	-1	LEU	-	expression tag	UNP Q8REP3
B	0	GLY	-	expression tag	UNP Q8REP3
B	1	SER	-	expression tag	UNP Q8REP3
C	-3	GLY	-	expression tag	UNP Q8REP3
C	-2	PRO	-	expression tag	UNP Q8REP3
C	-1	LEU	-	expression tag	UNP Q8REP3
C	0	GLY	-	expression tag	UNP Q8REP3
C	1	SER	-	expression tag	UNP Q8REP3
D	-3	GLY	-	expression tag	UNP Q8REP3
D	-2	PRO	-	expression tag	UNP Q8REP3
D	-1	LEU	-	expression tag	UNP Q8REP3
D	0	GLY	-	expression tag	UNP Q8REP3
D	1	SER	-	expression tag	UNP Q8REP3

- Molecule 2 is PYRIDOXAL-5'-PHOSPHATE (three-letter code: PLP) (formula: C₈H₁₀NO₆P).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
2	A	1	Total	C	N	O	P	0	0
			15	8	1	5	1		
2	B	1	Total	C	N	O	P	0	0
			15	8	1	5	1		
2	C	1	Total	C	N	O	P	0	0
			15	8	1	5	1		
2	D	1	Total	C	N	O	P	0	0
			15	8	1	5	1		

- Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

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

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
4	A	122	Total	O	0	0
			122	122		
4	B	68	Total	O	0	0
			68	68		

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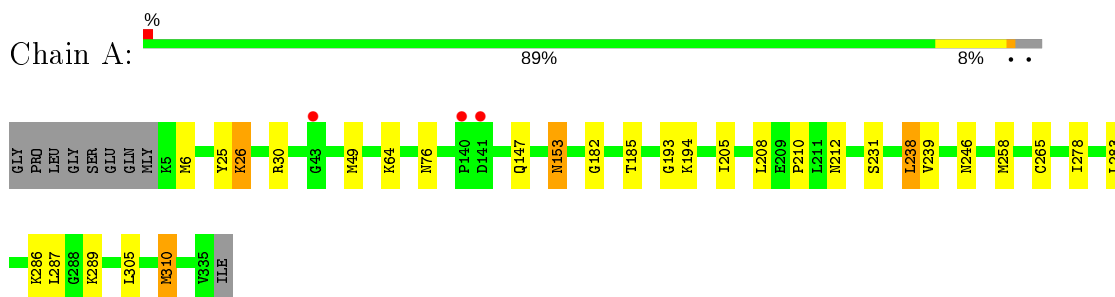
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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	C	99	Total O 99 99	0	0
4	D	84	Total O 84 84	0	0

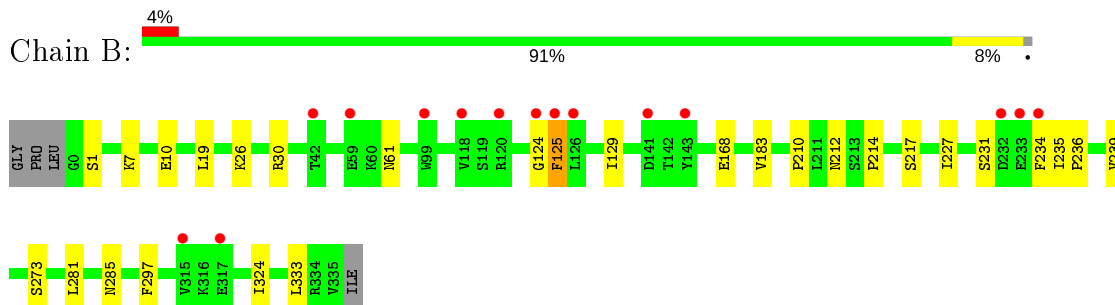
3 Residue-property plots [i](#)

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 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.

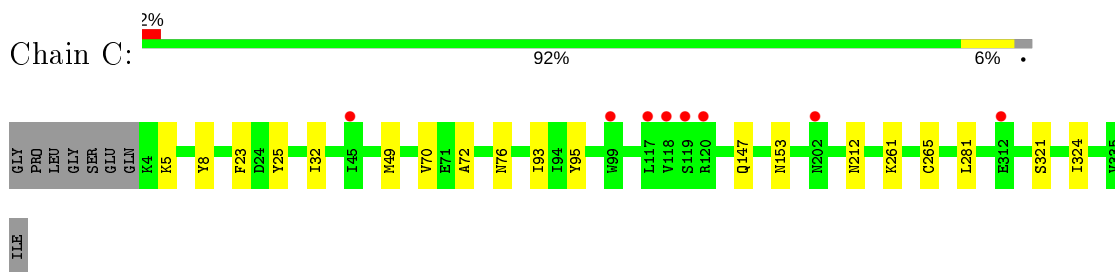
- Molecule 1: Cysteine synthase



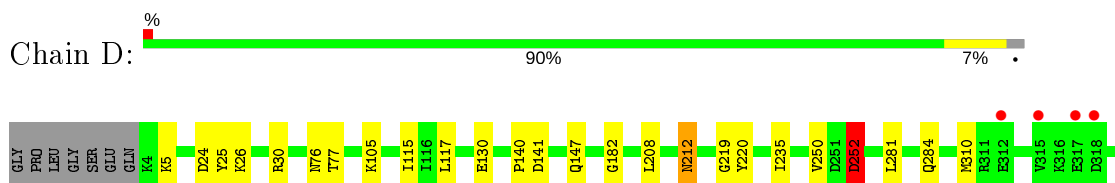
- Molecule 1: Cysteine synthase

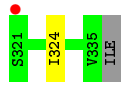


- Molecule 1: Cysteine synthase



- Molecule 1: Cysteine synthase





4 Data and refinement statistics

Property	Value	Source
Space group	P 2 21 21	Depositor
Cell constants a, b, c, α , β , γ	57.76Å 136.16Å 171.68Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.93 – 2.07 40.93 – 2.07	Depositor EDS
% Data completeness (in resolution range)	99.5 (40.93-2.07) 99.5 (40.93-2.07)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.06 (at 2.06Å)	Xtrriage
Refinement program	REFMAC 5.8.0189	Depositor
R, R_{free}	0.186 , 0.242 0.194 , 0.246	Depositor DCC
R_{free} test set	4180 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	30.8	Xtrriage
Anisotropy	0.580	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 43.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	10840	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.46% 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, MLY, PLP

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	0.76	0/2299	0.74	0/3128
1	B	0.63	0/2332	0.73	0/3170
1	C	0.74	0/2299	0.74	0/3128
1	D	0.67	0/2299	0.71	0/3128
All	All	0.70	0/9229	0.73	0/12554

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	A	0	1
1	B	0	1
All	All	0	2

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	26	MLY	Peptide
1	B	26	MLY	Peptide

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	A	2590	0	2587	20	0
1	B	2622	0	2602	10	0
1	C	2591	0	2575	11	0
1	D	2601	0	2605	16	0
2	A	15	0	6	1	0
2	B	15	0	6	0	0
2	C	15	0	6	1	0
2	D	15	0	7	1	0
3	A	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
4	A	122	0	0	1	0
4	B	68	0	0	0	0
4	C	99	0	0	0	0
4	D	84	0	0	1	0
All	All	10840	0	10394	57	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 57 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:D:105:MLY:HE2	1:D:117:LEU:HD11	1.72	0.71
1:B:236:PRO:HG2	1:B:239:VAL:HG23	1.82	0.62
1:A:283:LEU:O	1:A:287:LEU:HD12	2.02	0.60
1:D:30:ARG:HH11	1:D:284:GLN:HE21	1.49	0.59
1:A:153:ASN:HB3	1:A:238:LEU:HD11	1.85	0.58

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	A	295/340 (87%)	281 (95%)	14 (5%)	0	100	100
1	B	299/340 (88%)	284 (95%)	11 (4%)	4 (1%)	12	4
1	C	295/340 (87%)	287 (97%)	8 (3%)	0	100	100
1	D	295/340 (87%)	279 (95%)	13 (4%)	3 (1%)	15	6
All	All	1184/1360 (87%)	1131 (96%)	46 (4%)	7 (1%)	25	15

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	125	PHE
1	D	252	ASP
1	B	1	SER
1	B	61	ASN
1	B	231	SER

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	248/254 (98%)	240 (97%)	8 (3%)	39	32
1	B	252/254 (99%)	247 (98%)	5 (2%)	55	51
1	C	248/254 (98%)	245 (99%)	3 (1%)	71	69
1	D	248/254 (98%)	242 (98%)	6 (2%)	49	43
All	All	996/1016 (98%)	974 (98%)	22 (2%)	52	46

5 of 22 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	129	ILE
1	B	235	ILE
1	D	252	ASP
1	B	212	ASN
1	B	234	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	139	ASN
1	D	284	GLN
1	D	147	GLN
1	B	285	ASN
1	C	147	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](#)

143 non-standard protein/DNA/RNA residues 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	$\# Z > 2$
1	MLY	B	224	1	7,8,11	0.45	0	3,8,13	0.33	0
1	MLY	B	204	1	7,8,11	0.47	0	3,8,13	0.49	0
1	MLY	D	264	1	7,8,11	0.29	0	3,8,13	0.41	0
1	MLY	D	114	1	9,10,11	0.56	0	6,11,13	0.54	0
1	MLY	A	303	1	7,8,11	0.48	0	3,8,13	0.31	0
1	MLY	B	121	1	7,8,11	0.55	0	3,8,13	0.38	0
1	MLY	A	114	1	7,8,11	0.45	0	3,8,13	0.27	0
1	MLY	B	316	1	7,8,11	0.46	0	3,8,13	0.42	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	MLY	D	322	1	7,8,11	0.40	0	3,8,13	0.50	0
1	MLY	A	131	1	9,10,11	0.65	0	6,11,13	0.61	0
1	MLY	C	194	1	9,10,11	0.47	0	6,11,13	0.82	0
1	MLY	A	55	1	7,8,11	0.39	0	3,8,13	0.62	0
1	MLY	B	314	1	7,8,11	0.50	0	3,8,13	0.32	0
1	MLY	A	194	1	9,10,11	0.70	0	6,11,13	0.61	0
1	MLY	B	15	1	7,8,11	0.43	0	3,8,13	0.48	0
1	MLY	A	56	1	7,8,11	0.29	0	3,8,13	0.29	0
1	MLY	A	197	1	7,8,11	0.52	0	3,8,13	0.61	0
1	MLY	B	197	1	7,8,11	0.40	0	3,8,13	0.45	0
1	MLY	D	327	1	7,8,11	0.37	0	3,8,13	0.50	0
1	MLY	C	15	1	7,8,11	0.58	0	3,8,13	0.42	0
1	MLY	A	15	1	9,10,11	0.64	0	6,11,13	0.82	0
1	MLY	C	26	1	7,8,11	0.26	0	3,8,13	0.47	0
1	MLY	D	64	1	7,8,11	0.64	0	3,8,13	0.27	0
1	MLY	C	131	1	7,8,11	0.27	0	3,8,13	0.40	0
1	MLY	B	5	1	7,8,11	0.49	0	3,8,13	0.36	0
1	MLY	A	224	1	7,8,11	0.54	0	3,8,13	0.51	0
1	MLY	B	35	1	7,8,11	0.67	0	3,8,13	0.43	0
1	MLY	C	105	1	7,8,11	0.59	0	3,8,13	0.42	0
1	MLY	B	114	1	7,8,11	0.51	0	3,8,13	0.42	0
1	MLY	D	65	1	7,8,11	0.47	0	3,8,13	0.42	0
1	MLY	C	327	1	7,8,11	0.42	0	3,8,13	0.49	0
1	MLY	B	55	1	9,10,11	0.64	0	6,11,13	0.48	0
1	MLY	A	261	1	9,10,11	0.59	0	6,11,13	0.51	0
1	MLY	B	137	1	7,8,11	0.38	0	3,8,13	0.43	0
1	MLY	C	286	1	9,10,11	0.50	0	6,11,13	0.66	0
1	MLY	C	289	1	7,8,11	0.52	0	3,8,13	0.55	0
1	MLY	B	303	1	7,8,11	0.42	0	3,8,13	0.44	0
1	MLY	C	35	1	7,8,11	0.45	0	3,8,13	0.62	0
1	MLY	B	60	1	7,8,11	0.41	0	3,8,13	0.38	0
1	MLY	B	302	1	7,8,11	0.26	0	3,8,13	0.50	0
1	MLY	D	302	1	7,8,11	0.53	0	3,8,13	0.73	0
1	MLY	C	314	1	7,8,11	0.47	0	3,8,13	0.31	0
1	MLY	B	170	1	7,8,11	0.36	0	3,8,13	0.40	0
1	MLY	D	316	1	7,8,11	0.55	0	3,8,13	0.59	0
1	MLY	A	64	1	7,8,11	0.56	0	3,8,13	0.19	0
1	MLY	C	60	1	7,8,11	0.46	0	3,8,13	0.36	0
1	MLY	B	261	1	9,10,11	0.56	0	6,11,13	0.60	0
1	MLY	A	133	1	7,8,11	0.33	0	3,8,13	0.64	0
1	MLY	A	330	1	7,8,11	0.42	0	3,8,13	0.42	0
1	MLY	B	330	1	7,8,11	0.37	0	3,8,13	0.48	0
1	MLY	D	289	1	7,8,11	0.51	0	3,8,13	0.65	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	MLY	D	5	1	9,10,11	0.66	0	6,11,13	0.48	0
1	MLY	B	221	1	7,8,11	0.58	0	3,8,13	0.41	0
1	MLY	D	243	1	7,8,11	0.52	0	3,8,13	0.50	0
1	MLY	A	5	1	7,8,11	0.83	0	3,8,13	0.37	0
1	MLY	D	15	1	9,10,11	0.46	0	6,11,13	0.71	0
1	MLY	B	327	1	7,8,11	0.74	0	3,8,13	0.45	0
1	MLY	D	4	1	7,8,11	0.32	0	3,8,13	0.52	0
1	MLY	D	133	1	7,8,11	0.36	0	3,8,13	0.46	0
1	MLY	D	221	1	7,8,11	0.41	0	3,8,13	0.64	0
1	MLY	B	194	1	9,10,11	0.52	0	6,11,13	0.43	0
1	MLY	A	286	1	9,10,11	0.51	0	6,11,13	0.48	0
1	MLY	A	314	1	7,8,11	0.45	0	3,8,13	0.46	0
1	MLY	C	5	1	7,8,11	0.49	0	3,8,13	0.62	0
1	MLY	C	121	1	7,8,11	0.40	0	3,8,13	0.47	0
1	MLY	D	314	1	7,8,11	0.51	0	3,8,13	0.46	0
1	MLY	D	131	1	7,8,11	0.48	0	3,8,13	0.51	0
1	MLY	B	65	1	7,8,11	0.33	0	3,8,13	0.51	0
1	MLY	B	286	1	7,8,11	0.52	0	3,8,13	0.38	0
1	MLY	D	286	1	9,10,11	0.41	0	6,11,13	0.76	0
1	MLY	C	137	1	7,8,11	0.28	0	3,8,13	0.50	0
1	MLY	A	316	1	7,8,11	0.45	0	3,8,13	0.56	0
1	MLY	C	322	1	7,8,11	0.23	0	3,8,13	0.68	0
1	MLY	D	330	1	7,8,11	0.42	0	3,8,13	0.54	0
1	MLY	D	26	1	9,10,11	0.62	0	6,11,13	0.58	0
1	MLY	A	204	1	7,8,11	0.66	0	3,8,13	0.11	0
1	MLY	C	114	1	7,8,11	0.50	0	3,8,13	0.39	0
1	MLY	C	224	1	7,8,11	0.48	0	3,8,13	0.55	0
1	MLY	C	330	1	7,8,11	0.37	0	3,8,13	0.45	0
1	MLY	A	35	1	7,8,11	0.53	0	3,8,13	0.42	0
1	MLY	A	327	1	7,8,11	0.50	0	3,8,13	0.34	0
1	MLY	C	261	1	9,10,11	0.48	0	6,11,13	0.67	0
1	MLY	C	197	1	7,8,11	0.39	0	3,8,13	0.53	0
1	MLY	C	264	1	7,8,11	0.50	0	3,8,13	0.31	0
1	MLY	B	264	1	7,8,11	0.28	0	3,8,13	0.64	0
1	MLY	C	55	1	7,8,11	0.74	0	3,8,13	0.63	0
1	MLY	C	204	1	9,10,11	0.77	0	6,11,13	0.57	0
1	MLY	A	289	1	7,8,11	0.49	0	3,8,13	0.42	0
1	MLY	A	105	1	9,10,11	0.73	0	6,11,13	0.46	0
1	MLY	B	4	1	7,8,11	0.37	0	3,8,13	0.57	0
1	MLY	A	240	1	9,10,11	0.56	0	6,11,13	0.49	0
1	MLY	C	240	1	7,8,11	0.58	0	3,8,13	0.35	0
1	MLY	B	105	1	9,10,11	0.59	0	6,11,13	0.44	0
1	MLY	C	303	1	7,8,11	0.58	0	3,8,13	0.14	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	MLY	B	131	1	7,8,11	0.38	0	3,8,13	0.53	0
1	MLY	B	56	1	9,10,11	0.67	0	6,11,13	0.59	0
1	MLY	D	121	1	7,8,11	0.35	0	3,8,13	0.67	0
1	MLY	B	322	1	7,8,11	0.34	0	3,8,13	0.50	0
1	MLY	C	302	1	7,8,11	0.59	0	3,8,13	0.57	0
1	MLY	B	64	1	7,8,11	0.37	0	3,8,13	0.63	0
1	MLY	A	26	1	9,10,11	0.51	0	6,11,13	0.71	0
1	MLY	B	7	1	7,8,11	0.64	0	3,8,13	0.39	0
1	MLY	A	170	1	7,8,11	0.65	0	3,8,13	0.66	0
1	MLY	A	65	1	7,8,11	0.36	0	3,8,13	0.46	0
1	MLY	B	133	1	7,8,11	0.47	0	3,8,13	0.48	0
1	MLY	A	302	1	7,8,11	0.26	0	3,8,13	0.56	0
1	MLY	C	65	1	7,8,11	0.38	0	3,8,13	0.47	0
1	MLY	C	316	1	7,8,11	0.52	0	3,8,13	0.49	0
1	MLY	D	194	1	9,10,11	0.64	0	6,11,13	0.51	0
1	MLY	D	170	1	7,8,11	0.50	0	3,8,13	0.39	0
1	MLY	A	264	1	7,8,11	0.49	0	3,8,13	0.65	0
1	MLY	C	170	1	7,8,11	0.62	0	3,8,13	0.33	0
1	MLY	A	137	1	7,8,11	0.33	0	3,8,13	0.47	0
1	MLY	C	133	1	9,10,11	0.43	0	6,11,13	0.80	0
1	MLY	D	137	1	9,10,11	0.42	0	6,11,13	0.60	0
1	MLY	A	60	1	9,10,11	0.57	0	6,11,13	0.30	0
1	MLY	D	261	1	9,10,11	0.59	0	6,11,13	0.50	0
1	MLY	B	240	1	7,8,11	0.68	0	3,8,13	0.31	0
1	MLY	D	240	1	9,10,11	0.55	0	6,11,13	0.43	0
1	MLY	A	7	1	7,8,11	0.73	0	3,8,13	0.58	0
1	MLY	D	303	1	7,8,11	0.67	0	3,8,13	0.33	0
1	MLY	C	56	1	7,8,11	0.72	0	3,8,13	0.44	0
1	MLY	C	221	1	7,8,11	0.54	0	3,8,13	0.51	0
1	MLY	A	322	1	7,8,11	0.47	0	3,8,13	0.46	0
1	MLY	D	224	1	7,8,11	0.56	0	3,8,13	0.55	0
1	MLY	D	7	1	7,8,11	0.54	0	3,8,13	0.29	0
1	MLY	D	197	1	7,8,11	0.36	0	3,8,13	0.42	0
1	MLY	A	243	1	7,8,11	0.26	0	3,8,13	0.50	0
1	MLY	D	60	1	7,8,11	0.56	0	3,8,13	0.38	0
1	MLY	C	243	1	7,8,11	0.34	0	3,8,13	0.51	0
1	MLY	D	105	1	7,8,11	0.67	0	3,8,13	0.70	0
1	MLY	D	55	1	7,8,11	0.79	0	3,8,13	0.53	0
1	MLY	D	56	1	9,10,11	0.58	0	6,11,13	0.61	0
1	MLY	B	243	1	7,8,11	0.49	0	3,8,13	0.38	0
1	MLY	B	289	1	7,8,11	0.46	0	3,8,13	0.50	0
1	MLY	A	121	1	7,8,11	0.57	0	3,8,13	0.69	0
1	MLY	C	4	1	7,8,11	0.80	0	3,8,13	0.42	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	MLY	C	7	1	7,8,11	0.70	0	3,8,13	0.53	0
1	MLY	B	26	1	7,8,11	0.47	0	3,8,13	0.55	0
1	MLY	A	221	1	7,8,11	0.52	0	3,8,13	0.39	0
1	MLY	D	204	1	7,8,11	0.52	0	3,8,13	0.43	0
1	MLY	C	64	1	7,8,11	0.58	0	3,8,13	0.38	0
1	MLY	D	35	1	7,8,11	0.37	0	3,8,13	0.35	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
1	MLY	B	224	1	-	2/6/7/11	-
1	MLY	B	204	1	-	0/6/7/11	-
1	MLY	D	264	1	-	2/6/7/11	-
1	MLY	D	114	1	-	2/8/9/11	-
1	MLY	A	303	1	-	1/6/7/11	-
1	MLY	B	121	1	-	2/6/7/11	-
1	MLY	A	114	1	-	5/6/7/11	-
1	MLY	B	316	1	-	1/6/7/11	-
1	MLY	D	322	1	-	1/6/7/11	-
1	MLY	A	131	1	-	0/8/9/11	-
1	MLY	C	194	1	-	0/8/9/11	-
1	MLY	A	55	1	-	0/6/7/11	-
1	MLY	B	314	1	-	1/6/7/11	-
1	MLY	A	194	1	-	2/8/9/11	-
1	MLY	B	15	1	-	2/6/7/11	-
1	MLY	A	56	1	-	0/6/7/11	-
1	MLY	A	197	1	-	3/6/7/11	-
1	MLY	B	197	1	-	2/6/7/11	-
1	MLY	D	327	1	-	4/6/7/11	-
1	MLY	C	15	1	-	1/6/7/11	-
1	MLY	A	15	1	-	0/8/9/11	-
1	MLY	C	26	1	-	1/6/7/11	-
1	MLY	D	64	1	-	4/6/7/11	-
1	MLY	C	131	1	-	3/6/7/11	-
1	MLY	B	5	1	-	1/6/7/11	-
1	MLY	A	224	1	-	2/6/7/11	-
1	MLY	B	35	1	-	1/6/7/11	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	MLY	C	105	1	-	1/6/7/11	-
1	MLY	B	114	1	-	2/6/7/11	-
1	MLY	D	65	1	-	1/6/7/11	-
1	MLY	C	327	1	-	2/6/7/11	-
1	MLY	B	55	1	-	0/8/9/11	-
1	MLY	A	261	1	-	2/8/9/11	-
1	MLY	B	137	1	-	1/6/7/11	-
1	MLY	C	286	1	-	0/8/9/11	-
1	MLY	C	289	1	-	0/6/7/11	-
1	MLY	B	303	1	-	0/6/7/11	-
1	MLY	C	35	1	-	1/6/7/11	-
1	MLY	B	60	1	-	3/6/7/11	-
1	MLY	B	302	1	-	0/6/7/11	-
1	MLY	D	302	1	-	1/6/7/11	-
1	MLY	C	314	1	-	2/6/7/11	-
1	MLY	B	170	1	-	2/6/7/11	-
1	MLY	D	316	1	-	0/6/7/11	-
1	MLY	A	64	1	-	1/6/7/11	-
1	MLY	C	60	1	-	0/6/7/11	-
1	MLY	B	261	1	-	2/8/9/11	-
1	MLY	A	133	1	-	0/6/7/11	-
1	MLY	A	330	1	-	2/6/7/11	-
1	MLY	B	330	1	-	0/6/7/11	-
1	MLY	D	289	1	-	3/6/7/11	-
1	MLY	D	5	1	-	3/8/9/11	-
1	MLY	B	221	1	-	2/6/7/11	-
1	MLY	D	243	1	-	1/6/7/11	-
1	MLY	A	5	1	-	3/6/7/11	-
1	MLY	D	15	1	-	1/8/9/11	-
1	MLY	B	327	1	-	2/6/7/11	-
1	MLY	D	4	1	-	3/6/7/11	-
1	MLY	D	133	1	-	0/6/7/11	-
1	MLY	D	221	1	-	0/6/7/11	-
1	MLY	B	194	1	-	0/8/9/11	-
1	MLY	A	286	1	-	2/8/9/11	-
1	MLY	A	314	1	-	2/6/7/11	-
1	MLY	C	5	1	-	1/6/7/11	-
1	MLY	C	121	1	-	2/6/7/11	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	MLY	D	314	1	-	3/6/7/11	-
1	MLY	D	131	1	-	0/6/7/11	-
1	MLY	B	65	1	-	2/6/7/11	-
1	MLY	B	286	1	-	1/6/7/11	-
1	MLY	D	286	1	-	1/8/9/11	-
1	MLY	C	137	1	-	2/6/7/11	-
1	MLY	A	316	1	-	1/6/7/11	-
1	MLY	C	322	1	-	2/6/7/11	-
1	MLY	D	330	1	-	0/6/7/11	-
1	MLY	D	26	1	-	3/8/9/11	-
1	MLY	A	204	1	-	2/6/7/11	-
1	MLY	C	114	1	-	0/6/7/11	-
1	MLY	C	224	1	-	4/6/7/11	-
1	MLY	C	330	1	-	1/6/7/11	-
1	MLY	A	35	1	-	1/6/7/11	-
1	MLY	A	327	1	-	3/6/7/11	-
1	MLY	C	261	1	-	2/8/9/11	-
1	MLY	C	197	1	-	2/6/7/11	-
1	MLY	C	264	1	-	2/6/7/11	-
1	MLY	B	264	1	-	1/6/7/11	-
1	MLY	C	55	1	-	0/6/7/11	-
1	MLY	C	204	1	-	1/8/9/11	-
1	MLY	A	289	1	-	1/6/7/11	-
1	MLY	A	105	1	-	1/8/9/11	-
1	MLY	B	4	1	-	3/6/7/11	-
1	MLY	A	240	1	-	3/8/9/11	-
1	MLY	C	240	1	-	1/6/7/11	-
1	MLY	B	105	1	-	0/8/9/11	-
1	MLY	C	303	1	-	1/6/7/11	-
1	MLY	B	131	1	-	1/6/7/11	-
1	MLY	B	56	1	-	0/8/9/11	-
1	MLY	D	121	1	-	2/6/7/11	-
1	MLY	B	322	1	-	2/6/7/11	-
1	MLY	C	302	1	-	1/6/7/11	-
1	MLY	B	64	1	-	1/6/7/11	-
1	MLY	A	26	1	-	3/8/9/11	-
1	MLY	B	7	1	-	0/6/7/11	-
1	MLY	A	170	1	-	4/6/7/11	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	MLY	A	65	1	-	2/6/7/11	-
1	MLY	B	133	1	-	1/6/7/11	-
1	MLY	A	302	1	-	0/6/7/11	-
1	MLY	C	65	1	-	2/6/7/11	-
1	MLY	C	316	1	-	1/6/7/11	-
1	MLY	D	194	1	-	1/8/9/11	-
1	MLY	D	170	1	-	2/6/7/11	-
1	MLY	A	264	1	-	2/6/7/11	-
1	MLY	C	170	1	-	2/6/7/11	-
1	MLY	A	137	1	-	3/6/7/11	-
1	MLY	C	133	1	-	2/8/9/11	-
1	MLY	D	137	1	-	5/8/9/11	-
1	MLY	A	60	1	-	2/8/9/11	-
1	MLY	D	261	1	-	2/8/9/11	-
1	MLY	B	240	1	-	3/6/7/11	-
1	MLY	D	240	1	-	2/8/9/11	-
1	MLY	A	7	1	-	0/6/7/11	-
1	MLY	D	303	1	-	0/6/7/11	-
1	MLY	C	56	1	-	0/6/7/11	-
1	MLY	C	221	1	-	3/6/7/11	-
1	MLY	A	322	1	-	3/6/7/11	-
1	MLY	D	224	1	-	3/6/7/11	-
1	MLY	D	7	1	-	3/6/7/11	-
1	MLY	D	197	1	-	2/6/7/11	-
1	MLY	A	243	1	-	2/6/7/11	-
1	MLY	D	60	1	-	0/6/7/11	-
1	MLY	C	243	1	-	1/6/7/11	-
1	MLY	D	105	1	-	1/6/7/11	-
1	MLY	D	55	1	-	0/6/7/11	-
1	MLY	D	56	1	-	0/8/9/11	-
1	MLY	B	243	1	-	2/6/7/11	-
1	MLY	B	289	1	-	2/6/7/11	-
1	MLY	A	121	1	-	3/6/7/11	-
1	MLY	C	4	1	-	3/6/7/11	-
1	MLY	C	7	1	-	2/6/7/11	-
1	MLY	B	26	1	-	2/6/7/11	-
1	MLY	A	221	1	-	1/6/7/11	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	MLY	D	204	1	-	1/6/7/11	-
1	MLY	C	64	1	-	2/6/7/11	-
1	MLY	D	35	1	-	1/6/7/11	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 218 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	114	MLY	C-CA-CB-CG
1	A	197	MLY	C-CA-CB-CG
1	A	197	MLY	O-C-CA-CB
1	D	327	MLY	N-CA-CB-CG
1	D	327	MLY	C-CA-CB-CG

There are no ring outliers.

11 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	194	MLY	1	0
1	A	64	MLY	1	0
1	D	5	MLY	1	0
1	A	286	MLY	1	0
1	C	5	MLY	1	0
1	D	26	MLY	1	0
1	C	261	MLY	1	0
1	A	289	MLY	1	0
1	A	26	MLY	1	0
1	B	7	MLY	1	0
1	D	105	MLY	2	0

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 7 ligands modelled in this entry, 3 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
2	PLP	A	401	1	15,15,16	2.80	4 (26%)	20,22,23	1.62	5 (25%)
2	PLP	B	401	1	15,15,16	2.78	3 (20%)	20,22,23	1.37	3 (15%)
2	PLP	C	401	1	15,15,16	3.06	3 (20%)	20,22,23	1.43	5 (25%)
2	PLP	D	401	1	15,15,16	3.10	3 (20%)	20,22,23	1.60	5 (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
2	PLP	A	401	1	-	0/6/6/8	0/1/1/1
2	PLP	B	401	1	-	0/6/6/8	0/1/1/1
2	PLP	C	401	1	-	0/6/6/8	0/1/1/1
2	PLP	D	401	1	-	0/6/6/8	0/1/1/1

The worst 5 of 13 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	401	PLP	C3-C2	8.28	1.49	1.40
2	C	401	PLP	C3-C2	7.85	1.48	1.40
2	C	401	PLP	C5-C4	7.64	1.48	1.40
2	A	401	PLP	C5-C4	7.39	1.48	1.40
2	D	401	PLP	C5-C4	7.39	1.48	1.40

The worst 5 of 18 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	401	PLP	O3-C3-C2	3.08	124.21	117.49
2	A	401	PLP	O3-C3-C2	2.87	123.74	117.49
2	D	401	PLP	C6-N1-C2	2.71	124.19	119.17
2	A	401	PLP	C6-N1-C2	2.68	124.13	119.17
2	D	401	PLP	O4P-C5A-C5	2.64	114.39	109.35

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	401	PLP	1	0
2	C	401	PLP	1	0
2	D	401	PLP	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	296/340 (87%)	0.01	3 (1%) 82 83	20, 30, 47, 72	0
1	B	300/340 (88%)	0.42	15 (5%) 28 29	26, 42, 70, 92	0
1	C	296/340 (87%)	0.17	8 (2%) 54 57	21, 35, 54, 66	0
1	D	296/340 (87%)	0.17	5 (1%) 70 71	23, 39, 61, 78	0
All	All	1188/1360 (87%)	0.19	31 (2%) 56 59	20, 36, 61, 92	0

The worst 5 of 31 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	120	ARG	4.8
1	B	234	PHE	4.4
1	C	99	TRP	4.0
1	D	315	VAL	3.5
1	B	232	ASP	3.5

6.2 Non-standard residues in protein, DNA, RNA chains [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
1	MLY	A	5	9/12	0.47	0.25	58,63,65,67	0
1	MLY	C	4	9/12	0.57	0.23	62,64,65,66	0
1	MLY	D	316	9/12	0.76	0.27	73,76,77,77	0
1	MLY	D	314	9/12	0.77	0.39	72,77,83,83	0
1	MLY	A	7	9/12	0.78	0.26	43,50,56,57	0
1	MLY	D	224	9/12	0.79	0.29	55,59,68,68	0
1	MLY	D	4	9/12	0.79	0.15	45,47,48,48	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
1	MLY	D	26	11/12	0.83	0.35	70,75,82,83	0
1	MLY	C	314	9/12	0.83	0.32	59,61,70,71	0
1	MLY	C	7	9/12	0.83	0.30	46,51,54,55	0
1	MLY	D	64	9/12	0.84	0.32	48,52,64,66	0
1	MLY	B	289	9/12	0.84	0.24	41,46,56,56	0
1	MLY	B	137	9/12	0.85	0.25	68,72,76,79	0
1	MLY	D	221	9/12	0.86	0.21	62,65,75,77	0
1	MLY	A	322	9/12	0.86	0.18	46,49,61,62	0
1	MLY	C	121	9/12	0.86	0.43	55,58,65,66	0
1	MLY	D	7	9/12	0.86	0.23	31,34,42,43	0
1	MLY	B	170	9/12	0.86	0.27	40,42,55,55	0
1	MLY	A	114	9/12	0.86	0.22	29,31,41,41	0
1	MLY	D	133	9/12	0.86	0.18	45,47,48,48	0
1	MLY	C	60	9/12	0.87	0.16	42,44,48,51	0
1	MLY	B	221	9/12	0.87	0.16	51,52,53,54	0
1	MLY	B	60	9/12	0.87	0.35	61,63,66,66	0
1	MLY	B	121	9/12	0.87	0.41	83,87,92,92	0
1	MLY	D	105	9/12	0.87	0.20	37,40,50,50	0
1	MLY	B	243	9/12	0.87	0.23	57,58,67,69	0
1	MLY	D	322	9/12	0.87	0.37	58,60,70,71	0
1	MLY	A	204	9/12	0.87	0.16	33,36,39,40	0
1	MLY	A	137	9/12	0.87	0.21	35,38,47,47	0
1	MLY	C	224	9/12	0.88	0.26	39,40,50,51	0
1	MLY	D	121	9/12	0.88	0.14	57,59,67,69	0
1	MLY	D	327	9/12	0.88	0.18	49,51,61,62	0
1	MLY	C	286	11/12	0.89	0.13	47,48,48,49	0
1	MLY	C	316	9/12	0.89	0.16	59,61,62,63	0
1	MLY	A	264	9/12	0.89	0.18	35,42,51,54	0
1	MLY	B	5	9/12	0.89	0.14	47,49,51,54	0
1	MLY	D	137	11/12	0.89	0.22	54,59,64,64	0
1	MLY	B	240	9/12	0.89	0.18	55,57,60,60	0
1	MLY	C	137	9/12	0.89	0.16	41,45,51,53	0
1	MLY	A	316	9/12	0.89	0.18	61,63,64,64	0
1	MLY	A	286	11/12	0.89	0.22	42,44,46,46	0
1	MLY	C	105	9/12	0.89	0.15	41,43,50,50	0
1	MLY	B	314	9/12	0.89	0.22	52,56,67,68	0
1	MLY	C	114	9/12	0.89	0.23	44,48,60,62	0
1	MLY	A	64	9/12	0.89	0.24	34,40,50,51	0
1	MLY	A	289	9/12	0.89	0.25	45,49,60,63	0
1	MLY	B	4	9/12	0.89	0.23	52,54,59,59	0
1	MLY	C	221	9/12	0.90	0.19	38,40,51,52	0
1	MLY	A	26	11/12	0.90	0.14	52,55,61,61	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
1	MLY	A	327	9/12	0.90	0.14	43,49,56,57	0
1	MLY	B	224	9/12	0.90	0.17	46,51,58,60	0
1	MLY	B	286	9/12	0.90	0.21	44,47,53,54	0
1	MLY	A	240	11/12	0.90	0.16	32,34,42,42	0
1	MLY	D	261	11/12	0.90	0.19	39,43,51,52	0
1	MLY	A	121	9/12	0.90	0.14	38,39,46,47	0
1	MLY	D	289	9/12	0.90	0.17	50,53,57,57	0
1	MLY	B	64	9/12	0.90	0.20	62,63,69,71	0
1	MLY	B	26	9/12	0.90	0.29	47,51,55,57	0
1	MLY	D	204	9/12	0.90	0.14	38,40,45,46	0
1	MLY	A	60	11/12	0.91	0.17	35,39,48,48	0
1	MLY	D	131	9/12	0.91	0.13	44,46,50,50	0
1	MLY	B	264	9/12	0.91	0.15	31,34,42,43	0
1	MLY	C	55	9/12	0.91	0.14	35,37,40,41	0
1	MLY	D	15	11/12	0.91	0.16	25,29,41,42	0
1	MLY	B	55	11/12	0.91	0.17	41,43,45,46	0
1	MLY	C	26	9/12	0.91	0.16	49,53,55,56	0
1	MLY	C	322	9/12	0.91	0.16	48,52,59,60	0
1	MLY	D	197	9/12	0.91	0.15	41,43,51,54	0
1	MLY	A	243	9/12	0.91	0.28	42,43,55,56	0
1	MLY	B	114	9/12	0.91	0.23	49,51,58,60	0
1	MLY	D	330	9/12	0.91	0.16	38,40,51,52	0
1	MLY	B	7	9/12	0.91	0.21	41,45,48,49	0
1	MLY	A	170	9/12	0.91	0.25	38,42,52,53	0
1	MLY	A	314	9/12	0.91	0.27	53,57,62,63	0
1	MLY	C	5	9/12	0.91	0.17	56,60,63,63	0
1	MLY	D	243	9/12	0.91	0.18	51,53,59,63	0
1	MLY	C	327	9/12	0.91	0.15	38,41,54,56	0
1	MLY	A	133	9/12	0.92	0.11	27,30,33,33	0
1	MLY	B	194	11/12	0.92	0.16	41,44,49,49	0
1	MLY	B	131	9/12	0.92	0.18	65,66,67,67	0
1	MLY	B	133	9/12	0.92	0.24	64,67,68,71	0
1	MLY	C	65	9/12	0.92	0.30	49,54,64,66	0
1	MLY	D	303	9/12	0.92	0.22	30,30,32,34	0
1	MLY	B	56	11/12	0.92	0.21	44,48,52,52	0
1	MLY	D	286	11/12	0.92	0.12	53,55,58,58	0
1	MLY	C	170	9/12	0.92	0.19	40,42,51,54	0
1	MLY	A	15	11/12	0.92	0.17	25,29,40,41	0
1	MLY	B	65	9/12	0.93	0.20	60,64,70,70	0
1	MLY	D	60	9/12	0.93	0.23	42,43,47,48	0
1	MLY	C	243	9/12	0.93	0.16	45,47,52,52	0
1	MLY	C	264	9/12	0.93	0.18	32,35,49,52	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
1	MLY	D	55	9/12	0.93	0.13	29,29,30,32	0
1	MLY	B	197	9/12	0.93	0.18	43,47,51,51	0
1	MLY	C	56	9/12	0.93	0.13	36,37,40,41	0
1	MLY	B	15	9/12	0.93	0.16	29,32,41,41	0
1	MLY	D	65	9/12	0.93	0.26	48,52,61,62	0
1	MLY	C	289	9/12	0.93	0.15	45,49,57,59	0
1	MLY	A	197	9/12	0.93	0.13	34,37,47,50	0
1	MLY	A	221	9/12	0.93	0.16	34,36,46,49	0
1	MLY	B	105	11/12	0.93	0.14	45,47,53,54	0
1	MLY	B	330	9/12	0.94	0.12	32,34,42,44	0
1	MLY	A	105	11/12	0.94	0.15	28,31,41,42	0
1	MLY	A	131	11/12	0.94	0.11	26,28,35,35	0
1	MLY	D	170	9/12	0.94	0.12	40,42,44,45	0
1	MLY	D	5	11/12	0.94	0.13	35,43,51,51	0
1	MLY	A	224	9/12	0.94	0.17	33,36,45,49	0
1	MLY	C	330	9/12	0.94	0.17	28,31,41,43	0
1	MLY	C	133	11/12	0.94	0.14	35,37,50,50	0
1	MLY	B	303	9/12	0.94	0.19	30,32,33,33	0
1	MLY	C	261	11/12	0.94	0.13	30,35,46,47	0
1	MLY	B	322	9/12	0.94	0.20	38,40,45,45	0
1	MLY	D	114	11/12	0.94	0.15	38,41,50,51	0
1	MLY	D	240	11/12	0.94	0.12	45,48,54,54	0
1	MLY	D	264	9/12	0.94	0.15	39,41,49,51	0
1	MLY	A	330	9/12	0.94	0.12	39,41,51,53	0
1	MLY	C	204	11/12	0.94	0.16	35,39,49,51	0
1	MLY	A	65	9/12	0.94	0.20	35,39,49,51	0
1	MLY	C	197	9/12	0.95	0.12	40,43,47,49	0
1	MLY	A	194	11/12	0.95	0.12	27,29,36,36	0
1	MLY	C	240	9/12	0.95	0.10	35,37,37,38	0
1	MLY	D	302	9/12	0.95	0.23	28,29,31,32	0
1	MLY	C	303	9/12	0.95	0.16	28,28,30,31	0
1	MLY	B	261	11/12	0.95	0.14	27,30,34,36	0
1	MLY	B	316	9/12	0.95	0.10	51,54,56,56	0
1	MLY	A	56	9/12	0.95	0.12	26,27,36,39	0
1	MLY	D	194	11/12	0.95	0.15	35,37,43,44	0
1	MLY	B	204	9/12	0.95	0.20	41,42,46,48	0
1	MLY	C	64	9/12	0.95	0.16	47,52,58,59	0
1	MLY	A	55	9/12	0.96	0.11	25,27,32,34	0
1	MLY	C	194	11/12	0.96	0.10	34,36,42,44	0
1	MLY	C	15	9/12	0.96	0.12	22,24,31,33	0
1	MLY	A	261	11/12	0.96	0.14	30,36,46,47	0
1	MLY	A	302	9/12	0.96	0.22	27,28,31,32	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
1	MLY	C	302	9/12	0.96	0.23	25,27,27,28	0
1	MLY	C	131	9/12	0.96	0.09	36,38,45,46	0
1	MLY	B	327	9/12	0.96	0.21	35,37,49,52	0
1	MLY	A	35	9/12	0.97	0.17	23,24,26,26	0
1	MLY	B	302	9/12	0.97	0.22	27,28,30,30	0
1	MLY	D	56	11/12	0.97	0.19	31,33,36,37	0
1	MLY	B	35	9/12	0.97	0.14	27,27,28,28	0
1	MLY	D	35	9/12	0.97	0.17	26,28,29,29	0
1	MLY	C	35	9/12	0.98	0.17	23,23,24,24	0
1	MLY	A	303	9/12	0.98	0.19	24,25,26,27	0

6.3 Carbohydrates [i](#)

There are no carbohydrates 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	CL	C	402	1/1	0.94	0.09	48,48,48,48	0
2	PLP	D	401	15/16	0.96	0.15	31,31,32,33	0
3	CL	D	402	1/1	0.97	0.10	47,47,47,47	0
2	PLP	A	401	15/16	0.98	0.11	20,20,21,21	0
2	PLP	B	401	15/16	0.98	0.15	33,35,36,36	0
2	PLP	C	401	15/16	0.98	0.11	23,24,24,24	0
3	CL	A	402	1/1	0.99	0.12	32,32,32,32	0

6.5 Other polymers [i](#)

There are no such residues in this entry.