



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 27, 2022 – 04:21 PM EDT

PDB ID : 7MKV
Title : Engineered PLP-dependent decarboxylative aldolase from *Aspergillus flavus*, UstD2.0, bound as the internal aldimine
Authors : Ellis, J.M.; Buller, A.R.; Bingman, C.A.
Deposited on : 2021-04-27
Resolution : 2.25 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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 : 2.28.1
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) : 2.28.1

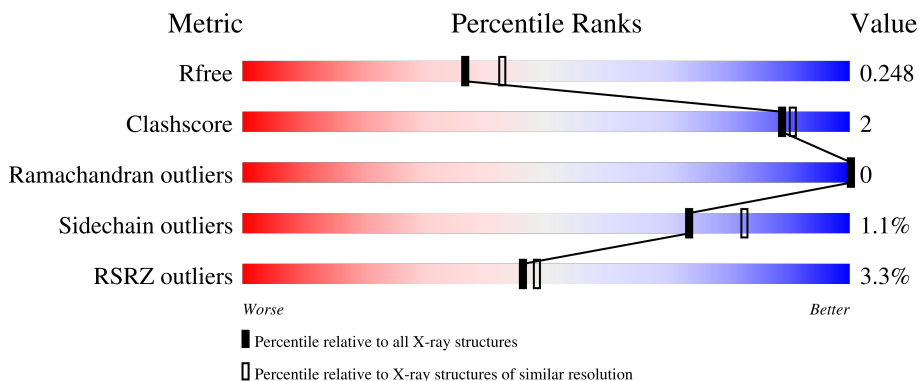
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.25 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	1377 (2.26-2.26)
Clashscore	141614	1487 (2.26-2.26)
Ramachandran outliers	138981	1449 (2.26-2.26)
Sidechain outliers	138945	1450 (2.26-2.26)
RSRZ outliers	127900	1356 (2.26-2.26)

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	447	 2% 86% 9%
1	B	447	 4% 85% 6% 9%
1	C	447	 3% 87% 9%

2 Entry composition i

There are 2 unique types of molecules in this entry. The entry contains 9782 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 desulfurase-like protein ustD.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	P	S			
1	A	407	3180	2025	538	599	1	17	0	2	0
1	B	407	3165	2019	532	595	1	18	0	3	0
1	C	406	3162	2017	534	592	1	18	0	3	0

There are 42 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	122	ALA	CYS	engineered mutation	UNP B8NM72
A	227	ALA	CYS	engineered mutation	UNP B8NM72
A	236	SER	CYS	engineered mutation	UNP B8NM72
A	391	THR	ILE	engineered mutation	UNP B8NM72
A	392	LEU	CYS	engineered mutation	UNP B8NM72
A	393	MET	LEU	engineered mutation	UNP B8NM72
A	440	LEU	-	expression tag	UNP B8NM72
A	441	GLU	-	expression tag	UNP B8NM72
A	442	HIS	-	expression tag	UNP B8NM72
A	443	HIS	-	expression tag	UNP B8NM72
A	444	HIS	-	expression tag	UNP B8NM72
A	445	HIS	-	expression tag	UNP B8NM72
A	446	HIS	-	expression tag	UNP B8NM72
A	447	HIS	-	expression tag	UNP B8NM72
B	122	ALA	CYS	engineered mutation	UNP B8NM72
B	227	ALA	CYS	engineered mutation	UNP B8NM72
B	236	SER	CYS	engineered mutation	UNP B8NM72
B	391	THR	ILE	engineered mutation	UNP B8NM72
B	392	LEU	CYS	engineered mutation	UNP B8NM72
B	393	MET	LEU	engineered mutation	UNP B8NM72
B	440	LEU	-	expression tag	UNP B8NM72
B	441	GLU	-	expression tag	UNP B8NM72
B	442	HIS	-	expression tag	UNP B8NM72

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Chain	Residue	Modelled	Actual	Comment	Reference
B	443	HIS	-	expression tag	UNP B8NM72
B	444	HIS	-	expression tag	UNP B8NM72
B	445	HIS	-	expression tag	UNP B8NM72
B	446	HIS	-	expression tag	UNP B8NM72
B	447	HIS	-	expression tag	UNP B8NM72
C	122	ALA	CYS	engineered mutation	UNP B8NM72
C	227	ALA	CYS	engineered mutation	UNP B8NM72
C	236	SER	CYS	engineered mutation	UNP B8NM72
C	391	THR	ILE	engineered mutation	UNP B8NM72
C	392	LEU	CYS	engineered mutation	UNP B8NM72
C	393	MET	LEU	engineered mutation	UNP B8NM72
C	440	LEU	-	expression tag	UNP B8NM72
C	441	GLU	-	expression tag	UNP B8NM72
C	442	HIS	-	expression tag	UNP B8NM72
C	443	HIS	-	expression tag	UNP B8NM72
C	444	HIS	-	expression tag	UNP B8NM72
C	445	HIS	-	expression tag	UNP B8NM72
C	446	HIS	-	expression tag	UNP B8NM72
C	447	HIS	-	expression tag	UNP B8NM72

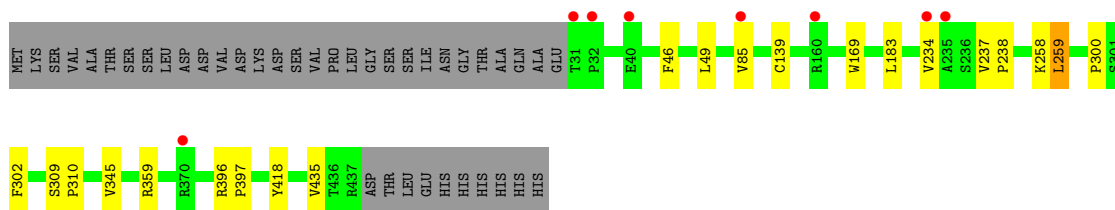
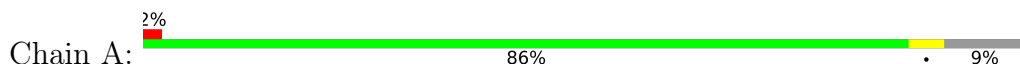
- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	85	Total O 85 85	0	0
2	B	94	Total O 94 94	0	0
2	C	96	Total O 96 96	0	0

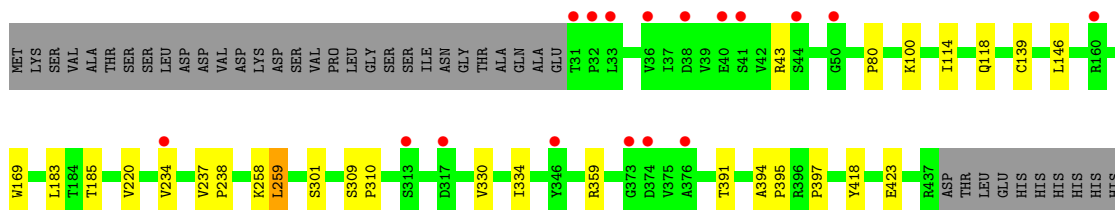
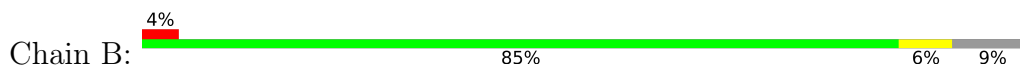
3 Residue-property plots [i](#)

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.

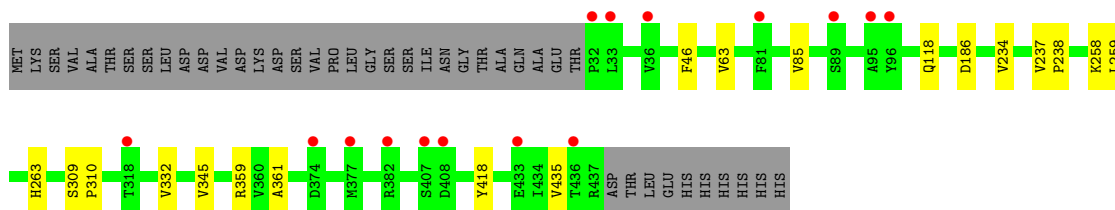
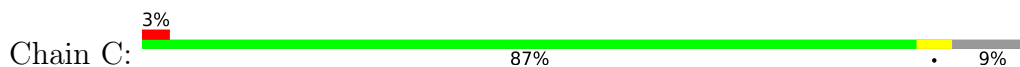
- Molecule 1: Cysteine desulfurase-like protein ustD



- Molecule 1: Cysteine desulfurase-like protein ustD



- Molecule 1: Cysteine desulfurase-like protein ustD



4 Data and refinement statistics i

Property	Value	Source
Space group	I 4 2 2	Depositor
Cell constants a, b, c, α , β , γ	162.09Å 162.09Å 221.00Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	39.81 – 2.25 39.78 – 2.25	Depositor EDS
% Data completeness (in resolution range)	99.6 (39.81-2.25) 99.6 (39.78-2.25)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.36 (at 2.24Å)	Xtrriage
Refinement program	REFMAC 5.8.0267	Depositor
R, R_{free}	0.214 , 0.246 0.218 , 0.248	Depositor DCC
R_{free} test set	3418 reflections (4.95%)	wwPDB-VP
Wilson B-factor (Å ²)	39.7	Xtrriage
Anisotropy	0.147	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 22.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	0.000 for $-1/2^*h+1/2^*k-1/2^*l, 1/2^*h-1/2^*k-1/2^*l, -h-k$ 0.000 for $-1/2^*h-1/2^*k+1/2^*l, -1/2^*h-1/2^*k-1/2^*l, h-k$	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	9782	wwPDB-VP
Average B, all atoms (Å ²)	46.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 33.66 % 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 $7.7247e-04$. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: LLP, CSD

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	0.65	0/3223	0.70	0/4398
1	B	0.66	0/3211	0.71	0/4384
1	C	0.66	0/3208	0.71	0/4378
All	All	0.65	0/9642	0.71	0/13160

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	3180	0	3151	11	0
1	B	3165	0	3130	16	0
1	C	3162	0	3136	11	0
2	A	85	0	0	0	0
2	B	94	0	0	0	0
2	C	96	0	0	0	0
All	All	9782	0	9417	35	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 2.

All (35) 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:237:VAL:N	1:A:238:PRO:HD2	2.16	0.61
1:B:118:GLN:HB2	1:C:118:GLN:HB2	1.86	0.56
1:C:309:SER:OG	1:C:310:PRO:HD3	2.08	0.54
1:B:309:SER:OG	1:B:310:PRO:HD3	2.08	0.53
1:A:396:ARG:HB2	1:A:397:PRO:HD3	1.93	0.51
1:C:85:VAL:HG12	1:C:85:VAL:O	2.11	0.50
1:B:80:PRO:HD3	1:C:63:VAL:HG12	1.94	0.48
1:C:46:PHE:HB3	1:C:63:VAL:HG21	1.95	0.48
1:C:332:VAL:HG11	1:C:361:ALA:HA	1.95	0.47
1:B:237:VAL:N	1:B:238:PRO:CD	2.78	0.47
1:B:146:LEU:HA	1:B:397:PRO:HB3	1.97	0.46
1:A:169:TRP:CZ2	1:A:183:LEU:HG	2.51	0.46
1:B:169:TRP:CZ2	1:B:183:LEU:HG	2.51	0.46
1:A:309:SER:OG	1:A:310:PRO:HD3	2.15	0.46
1:C:332:VAL:CG1	1:C:361:ALA:HA	2.46	0.45
1:B:237:VAL:HG12	1:B:259:LEU:HD21	1.99	0.44
1:A:300:PRO:HG2	1:A:302:PHE:CE1	2.53	0.43
1:B:100:LYS:HE2	1:B:114:ILE:HG13	2.00	0.43
1:A:345:VAL:CG1	1:A:435:VAL:HG11	2.48	0.43
1:C:237:VAL:N	1:C:238:PRO:CD	2.81	0.43
1:B:330:VAL:O	1:B:334:ILE:HG12	2.19	0.43
1:A:234:VAL:CG1	1:A:258:LLP:HD3	2.49	0.43
1:B:234:VAL:CG1	1:B:258:LLP:HD3	2.48	0.42
1:B:391:THR:CG2	1:B:395:PRO:HA	2.50	0.42
1:A:309:SER:N	1:A:310:PRO:CD	2.83	0.42
1:C:345:VAL:HG11	1:C:435:VAL:HG11	2.01	0.41
1:A:46:PHE:HB2	1:A:49:LEU:HD12	2.03	0.41
1:C:234:VAL:CG1	1:C:258:LLP:HD3	2.50	0.41
1:A:85:VAL:O	1:A:85:VAL:HG12	2.21	0.41
1:B:185:THR:HB	1:B:220:VAL:HG21	2.03	0.41
1:B:394:ALA:HB1	1:B:397:PRO:HG2	2.03	0.41
1:B:43:ARG:HH22	1:B:423:GLU:CD	2.25	0.40
1:B:301:SER:HA	1:C:263:HIS:HB2	2.02	0.40
1:A:237:VAL:HG12	1:A:259:LEU:HD21	2.03	0.40
1:B:237:VAL:HG12	1:B:259:LEU:HD11	2.04	0.40

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	405/447 (91%)	396 (98%)	9 (2%)	0	100	100
1	B	406/447 (91%)	398 (98%)	8 (2%)	0	100	100
1	C	405/447 (91%)	398 (98%)	7 (2%)	0	100	100
All	All	1216/1341 (91%)	1192 (98%)	24 (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	356/393 (91%)	351 (99%)	5 (1%)	67	76
1	B	353/393 (90%)	348 (99%)	5 (1%)	67	76
1	C	353/393 (90%)	349 (99%)	4 (1%)	73	82
All	All	1062/1179 (90%)	1048 (99%)	14 (1%)	73	79

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	139[A]	CYS
1	A	139[B]	CYS
1	A	259	LEU
1	A	359	ARG
1	A	418	TYR

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Mol	Chain	Res	Type
1	B	139[A]	CYS
1	B	139[B]	CYS
1	B	259	LEU
1	B	359	ARG
1	B	418	TYR
1	C	186	ASP
1	C	259	LEU
1	C	359	ARG
1	C	418	TYR

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

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

6 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	CSD	A	147	1	3,7,8	0.82	0	1,8,10	0.12	0
1	LLP	B	258	1	23,24,25	0.48	0	25,32,34	0.55	0
1	CSD	C	147	1	3,7,8	0.86	0	1,8,10	0.02	0
1	CSD	B	147	1	3,7,8	0.88	0	1,8,10	0.15	0
1	LLP	C	258	1	23,24,25	0.50	0	25,32,34	0.50	0
1	LLP	A	258	1	23,24,25	0.48	0	25,32,34	0.50	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	CSD	A	147	1	-	2/2/6/8	-
1	LLP	B	258	1	-	3/16/17/19	0/1/1/1
1	CSD	C	147	1	-	2/2/6/8	-
1	CSD	B	147	1	-	2/2/6/8	-
1	LLP	C	258	1	-	1/16/17/19	0/1/1/1
1	LLP	A	258	1	-	1/16/17/19	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (11) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	147	CSD	CA-CB-SG-OD1
1	A	258	LLP	C4-C4'-NZ-CE
1	B	147	CSD	N-CA-CB-SG
1	B	147	CSD	CA-CB-SG-OD1
1	B	258	LLP	C4-C4'-NZ-CE
1	B	258	LLP	C5'-OP4-P-OP1
1	C	147	CSD	CA-CB-SG-OD1
1	C	258	LLP	C4-C4'-NZ-CE
1	B	258	LLP	C5'-OP4-P-OP2
1	A	147	CSD	N-CA-CB-SG
1	C	147	CSD	N-CA-CB-SG

There are no ring outliers.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	B	258	LLP	1	0
1	C	258	LLP	1	0
1	A	258	LLP	1	0

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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

6.1 Protein, DNA and RNA chains

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	405/447 (90%)	0.16	8 (1%) 65 68	29, 43, 72, 93	0
1	B	405/447 (90%)	0.23	17 (4%) 36 38	31, 44, 70, 97	0
1	C	404/447 (90%)	0.16	15 (3%) 41 44	32, 44, 69, 96	0
All	All	1214/1341 (90%)	0.18	40 (3%) 46 48	29, 44, 71, 97	0

All (40) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	32	PRO	4.1
1	C	374	ASP	4.0
1	A	32	PRO	3.2
1	C	377	MET	3.2
1	B	41	SER	3.2
1	C	81	PHE	3.2
1	C	89	SER	3.1
1	A	370	ARG	3.1
1	B	40	GLU	3.1
1	C	436	THR	3.1
1	B	36	VAL	3.1
1	C	33	LEU	2.9
1	B	44	SER	2.8
1	C	36	VAL	2.8
1	B	313	SER	2.7
1	B	317	ASP	2.7
1	B	33	LEU	2.7
1	A	235	ALA	2.6
1	B	31	THR	2.6
1	B	32	PRO	2.6
1	A	160	ARG	2.6
1	B	346	TYR	2.6
1	B	373	GLY	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	40	GLU	2.6
1	C	433	GLU	2.6
1	C	96	TYR	2.5
1	C	95	ALA	2.4
1	C	407	SER	2.4
1	A	85	VAL	2.2
1	B	234	VAL	2.2
1	A	31	THR	2.2
1	C	408	ASP	2.1
1	B	376	ALA	2.1
1	C	318	THR	2.1
1	C	382	ARG	2.1
1	B	38	ASP	2.1
1	B	374	ASP	2.1
1	B	50	GLY	2.0
1	A	234	VAL	2.0
1	B	160	ARG	2.0

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	LLP	C	258	24/25	0.90	0.20	40,42,43,44	0
1	LLP	A	258	24/25	0.92	0.20	37,41,42,44	0
1	LLP	B	258	24/25	0.93	0.21	40,42,44,44	0
1	CSD	B	147	8/9	0.95	0.11	38,39,39,39	0
1	CSD	C	147	8/9	0.97	0.12	38,38,39,39	0
1	CSD	A	147	8/9	0.97	0.14	36,37,37,37	0

6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.