



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 15, 2017 – 12:36 am GMT

PDB ID : 3MOG
Title : Crystal structure of 3-hydroxybutyryl-CoA dehydrogenase from Escherichia coli K12 substr. MG1655
Authors : Patskovsky, Y.; Ramagopal, U.; Toro, R.; Gilmore, M.; Miller, S.; Sauder, J.M.; Burley, S.K.; Almo, S.C.; New York SGX Research Center for Structural Genomics (NYSGXRC)
Deposited on : 2010-04-22
Resolution : 2.20 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

<http://wwpdb.org/validation/2016/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	:	1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix)	:	1.9-1692
EDS	:	trunk28620
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	recalc28949

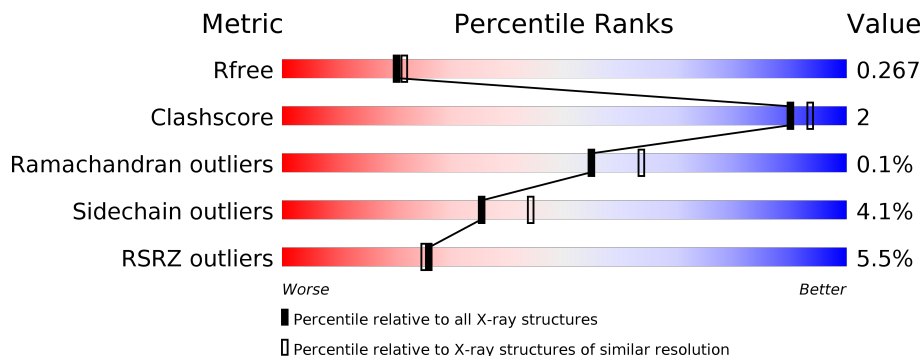
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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}	100719	4002 (2.20-2.20)
Clashscore	112137	4730 (2.20-2.20)
Ramachandran outliers	110173	4656 (2.20-2.20)
Sidechain outliers	110143	4657 (2.20-2.20)
RSRZ outliers	101464	4033 (2.20-2.20)

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. 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	483	<div> <div>3%</div> <div> <div></div> <div>91%</div> <div>6% . .</div> </div> </div>
1	B	483	<div> <div>10%</div> <div> <div></div> <div>91%</div> <div>6% . .</div> </div> </div>
1	C	483	<div> <div>2%</div> <div> <div></div> <div>92%</div> <div>5% . .</div> </div> </div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 11211 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 Probable 3-hydroxybutyryl-CoA dehydrogenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	470	Total	C	N	O	S	0	1	0
			3604	2284	634	672	14			
1	B	470	Total	C	N	O	S	0	4	0
			3624	2297	638	675	14			
1	C	472	Total	C	N	O	S	0	5	0
			3650	2314	644	678	14			

There are 33 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	EXPRESSION TAG	UNP P76083
A	2	SER	-	EXPRESSION TAG	UNP P76083
A	3	LEU	-	EXPRESSION TAG	UNP P76083
A	476	GLU	-	EXPRESSION TAG	UNP P76083
A	477	GLY	-	EXPRESSION TAG	UNP P76083
A	478	HIS	-	EXPRESSION TAG	UNP P76083
A	479	HIS	-	EXPRESSION TAG	UNP P76083
A	480	HIS	-	EXPRESSION TAG	UNP P76083
A	481	HIS	-	EXPRESSION TAG	UNP P76083
A	482	HIS	-	EXPRESSION TAG	UNP P76083
A	483	HIS	-	EXPRESSION TAG	UNP P76083
B	1	MET	-	EXPRESSION TAG	UNP P76083
B	2	SER	-	EXPRESSION TAG	UNP P76083
B	3	LEU	-	EXPRESSION TAG	UNP P76083
B	476	GLU	-	EXPRESSION TAG	UNP P76083
B	477	GLY	-	EXPRESSION TAG	UNP P76083
B	478	HIS	-	EXPRESSION TAG	UNP P76083
B	479	HIS	-	EXPRESSION TAG	UNP P76083
B	480	HIS	-	EXPRESSION TAG	UNP P76083
B	481	HIS	-	EXPRESSION TAG	UNP P76083
B	482	HIS	-	EXPRESSION TAG	UNP P76083
B	483	HIS	-	EXPRESSION TAG	UNP P76083
C	1	MET	-	EXPRESSION TAG	UNP P76083

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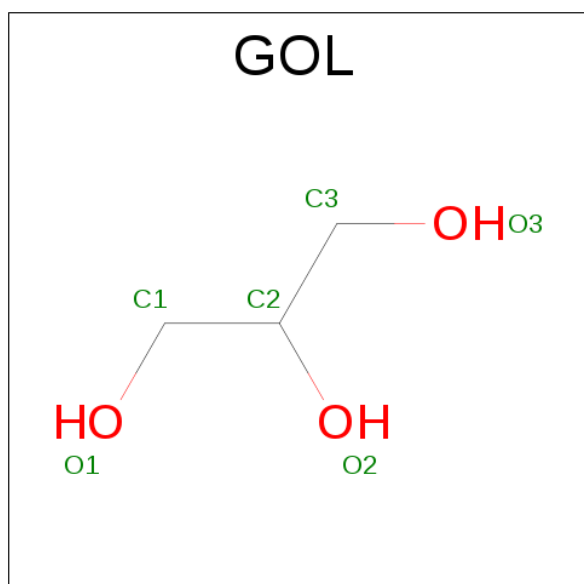
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Chain	Residue	Modelled	Actual	Comment	Reference
C	2	SER	-	EXPRESSION TAG	UNP P76083
C	3	LEU	-	EXPRESSION TAG	UNP P76083
C	476	GLU	-	EXPRESSION TAG	UNP P76083
C	477	GLY	-	EXPRESSION TAG	UNP P76083
C	478	HIS	-	EXPRESSION TAG	UNP P76083
C	479	HIS	-	EXPRESSION TAG	UNP P76083
C	480	HIS	-	EXPRESSION TAG	UNP P76083
C	481	HIS	-	EXPRESSION TAG	UNP P76083
C	482	HIS	-	EXPRESSION TAG	UNP P76083
C	483	HIS	-	EXPRESSION TAG	UNP P76083

- Molecule 2 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

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

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



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

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

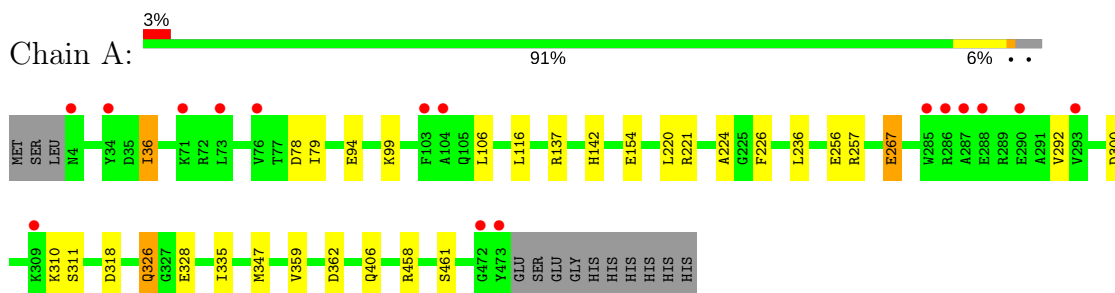
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	112	Total	O	0	0
			112	112		
4	B	77	Total	O	0	0
			77	77		
4	C	129	Total	O	0	0
			129	129		

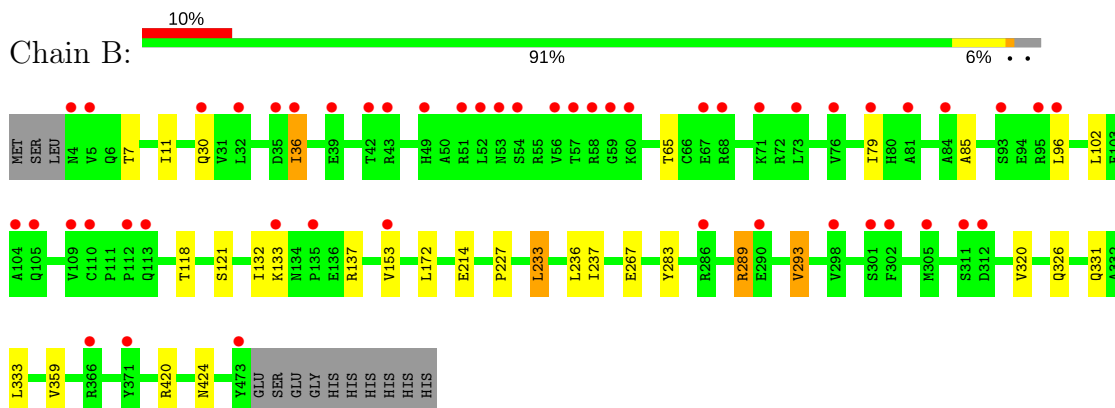
3 Residue-property plots [i](#)

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.

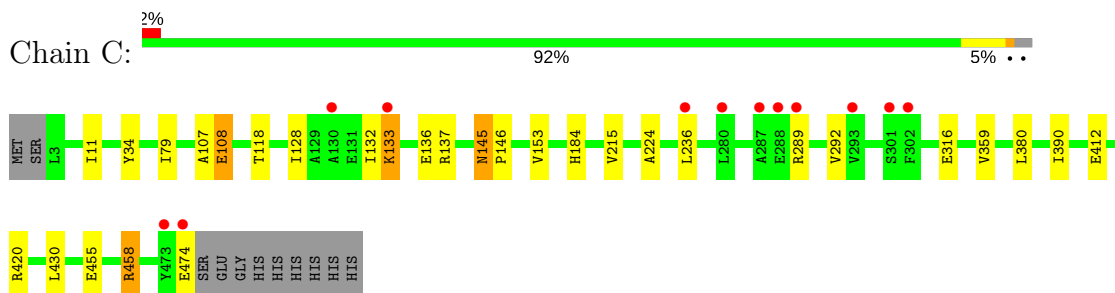
- Molecule 1: Probable 3-hydroxybutyryl-CoA dehydrogenase



- Molecule 1: Probable 3-hydroxybutyryl-CoA dehydrogenase



- Molecule 1: Probable 3-hydroxybutyryl-CoA dehydrogenase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	71.30Å 145.75Å 148.78Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.20 38.76 – 2.19	Depositor EDS
% Data completeness (in resolution range)	99.3 (20.00-2.20) 98.7 (38.76-2.19)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.48 (at 2.20Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.216 , 0.266 0.216 , 0.267	Depositor DCC
R_{free} test set	2370 reflections (3.10%)	DCC
Wilson B-factor (Å ²)	53.1	Xtriage
Anisotropy	0.173	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 40.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.007 for -h,l,k	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	11211	wwPDB-VP
Average B, all atoms (Å ²)	69.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.24% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, CL

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.46	0/3671	0.60	0/4993
1	B	0.44	0/3700	0.59	0/5031
1	C	0.47	0/3730	0.62	0/5072
All	All	0.46	0/11101	0.60	0/15096

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	3604	0	3667	13	0
1	B	3624	0	3694	19	0
1	C	3650	0	3723	16	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
3	B	6	0	8	1	0
3	C	6	0	8	0	0
4	A	112	0	0	1	0
4	B	77	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	C	129	0	0	1	0
All	All	11211	0	11100	47	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 (47) 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:420[B]:ARG:HH11	1:B:420[B]:ARG:CG	1.59	1.15
1:C:420[B]:ARG:HG2	1:C:420[B]:ARG:HH11	0.88	1.05
1:B:420[B]:ARG:HH11	1:B:420[B]:ARG:HG2	1.24	1.01
1:C:420[B]:ARG:CG	1:C:420[B]:ARG:HH11	1.76	0.98
1:C:420[B]:ARG:NH1	1:C:420[B]:ARG:HG2	1.70	0.97
1:B:420[B]:ARG:HH11	1:B:420[B]:ARG:HG3	1.39	0.85
1:C:145:ASN:HD22	1:C:146:PRO:HA	1.46	0.81
1:B:420[B]:ARG:NH1	1:B:420[B]:ARG:CG	2.31	0.77
1:C:455:GLU:HG3	1:C:458[B]:ARG:HD3	1.73	0.69
1:A:406:GLN:HE22	1:A:461:SER:HB3	1.57	0.68
1:A:310:LYS:HG2	1:A:311:SER:H	1.61	0.66
1:B:420[B]:ARG:NH1	1:B:420[B]:ARG:HG3	2.01	0.66
1:B:326[B]:GLN:HE21	1:B:326[B]:GLN:HA	1.62	0.65
1:B:420[B]:ARG:NH1	1:B:420[B]:ARG:HG2	2.01	0.63
1:C:145:ASN:HD22	1:C:146:PRO:CA	2.13	0.61
1:B:233:LEU:HD22	1:B:237:ILE:CD1	2.36	0.56
1:C:420[B]:ARG:NH1	1:C:420[B]:ARG:CG	2.45	0.54
1:B:233:LEU:O	1:B:233:LEU:HD23	2.08	0.52
1:B:289:ARG:HD3	3:B:485:GOL:H2	1.92	0.52
1:A:310:LYS:CG	1:A:311:SER:H	2.24	0.50
1:B:326[A]:GLN:HE22	1:B:333:LEU:HD21	1.77	0.50
1:C:107:ALA:HB1	1:C:133:LYS:HB2	1.95	0.48
1:A:94:GLU:HA	1:A:99:LYS:HE3	1.96	0.47
1:B:7:THR:HB	1:B:85:ALA:HA	1.97	0.46
1:C:224:ALA:HB2	1:C:390:ILE:HG23	1.97	0.46
1:A:224:ALA:HA	1:A:347:MET:HE2	1.98	0.46
1:C:420[A]:ARG:NH2	4:C:599:HOH:O	2.49	0.46
1:B:233:LEU:CD2	1:B:237:ILE:HG13	2.45	0.45
1:C:412:GLU:HG3	1:C:430:LEU:HD13	1.97	0.45
1:B:233:LEU:HD22	1:B:237:ILE:HD11	1.97	0.45
1:A:267:GLU:OE2	1:C:184[A]:HIS:NE2	2.49	0.45
1:C:11:ILE:HG23	1:C:34:TYR:HD1	1.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:106:LEU:HD12	1:A:116:LEU:HD22	1.99	0.43
1:B:214:GLU:HG3	1:B:283:TYR:HE2	1.83	0.43
1:A:256:GLU:OE2	1:A:458:ARG:NH2	2.50	0.43
1:C:108:GLU:HG2	1:C:108:GLU:H	1.62	0.43
1:B:36:ILE:HG13	1:B:36:ILE:H	1.53	0.42
1:A:142:HIS:HB3	1:A:154:GLU:HB2	2.00	0.42
4:A:488:HOH:O	1:B:331:GLN:HG2	2.18	0.42
1:A:326:GLN:NE2	1:A:328:GLU:OE2	2.53	0.41
1:A:36:ILE:HG13	1:A:36:ILE:H	1.57	0.41
1:B:11:ILE:HG21	1:B:102:LEU:HD21	2.03	0.41
1:C:215:VAL:HG13	1:C:380:LEU:HD13	2.03	0.41
1:B:227:PRO:HG3	1:B:424:ASN:HB2	2.02	0.41
1:A:221:ARG:HA	1:A:226:PHE:O	2.21	0.40
1:A:220:LEU:O	1:A:224:ALA:HB3	2.22	0.40
1:C:118:THR:HG21	1:C:128:ILE:HD13	2.03	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	469/483 (97%)	452 (96%)	16 (3%)	1 (0%)	51	58
1	B	472/483 (98%)	453 (96%)	18 (4%)	1 (0%)	51	58
1	C	475/483 (98%)	461 (97%)	14 (3%)	0	100	100
All	All	1416/1449 (98%)	1366 (96%)	48 (3%)	2 (0%)	55	63

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	318	ASP
1	B	293	VAL

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	378/389 (97%)	365 (97%)	13 (3%)	42	53
1	B	381/389 (98%)	362 (95%)	19 (5%)	28	34
1	C	384/389 (99%)	368 (96%)	16 (4%)	34	43
All	All	1143/1167 (98%)	1095 (96%)	48 (4%)	35	43

All (48) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	36	ILE
1	A	78	ASP
1	A	79	ILE
1	A	137	ARG
1	A	236	LEU
1	A	257	ARG
1	A	267	GLU
1	A	292	VAL
1	A	300	ASP
1	A	326	GLN
1	A	335	ILE
1	A	359	VAL
1	A	362	ASP
1	B	30	GLN
1	B	36	ILE
1	B	65	THR
1	B	79	ILE
1	B	96	LEU
1	B	118	THR
1	B	121	SER
1	B	132	ILE
1	B	133	LYS
1	B	137	ARG
1	B	153	VAL
1	B	172	LEU
1	B	233	LEU

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Mol	Chain	Res	Type
1	B	236	LEU
1	B	267	GLU
1	B	289	ARG
1	B	293	VAL
1	B	320	VAL
1	B	359	VAL
1	C	79	ILE
1	C	108	GLU
1	C	132	ILE
1	C	133	LYS
1	C	136	GLU
1	C	137	ARG
1	C	145	ASN
1	C	153	VAL
1	C	236	LEU
1	C	289	ARG
1	C	292	VAL
1	C	316	GLU
1	C	359	VAL
1	C	458[A]	ARG
1	C	458[B]	ARG
1	C	474	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	105	GLN
1	A	251	ASN
1	A	255	GLN
1	A	406	GLN
1	B	30	GLN
1	B	105	GLN
1	C	105	GLN
1	C	145	ASN
1	C	449	GLN
1	C	465	GLN

5.3.3 RNA ⓘ

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 5 ligands modelled in this entry, 3 are monoatomic - leaving 2 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	GOL	B	485	-	5,5,5	0.31	0	5,5,5	0.53	0
3	GOL	C	485	-	5,5,5	0.30	0	5,5,5	0.44	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	GOL	B	485	-	-	0/4/4/4	0/0/0/0
3	GOL	C	485	-	-	0/4/4/4	0/0/0/0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	485	GOL	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

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	470/483 (97%)	0.16	16 (3%) 46 43	37, 65, 106, 125	0
1	B	470/483 (97%)	0.39	50 (10%) 7 6	42, 71, 139, 161	0
1	C	472/483 (97%)	-0.19	12 (2%) 58 55	36, 54, 87, 128	0
All	All	1412/1449 (97%)	0.12	78 (5%) 26 25	36, 62, 120, 161	0

All (78) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	52	LEU	7.1
1	A	473	TYR	6.6
1	C	473	TYR	5.8
1	B	57	THR	5.3
1	B	53	ASN	4.9
1	B	84	ALA	4.8
1	B	81	ALA	4.4
1	B	312	ASP	4.3
1	C	289	ARG	4.1
1	A	288	GLU	3.8
1	A	287	ALA	3.8
1	B	59	GLY	3.8
1	B	76	VAL	3.7
1	A	472	GLY	3.6
1	B	93	SER	3.6
1	C	287	ALA	3.5
1	A	71	LYS	3.5
1	B	473	TYR	3.4
1	A	104	ALA	3.3
1	C	474	GLU	3.3
1	B	298	VAL	3.3
1	B	104	ALA	3.2
1	C	133	LYS	3.2

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Mol	Chain	Res	Type	RSRZ
1	B	54	SER	3.2
1	B	4	ASN	3.2
1	B	5	VAL	3.2
1	B	35	ASP	3.2
1	B	133	LYS	3.1
1	B	68	ARG	3.0
1	B	311	SER	3.0
1	B	36	ILE	3.0
1	B	301	SER	2.9
1	B	113	GLN	2.9
1	B	58	ARG	2.9
1	B	49	HIS	2.9
1	B	290	GLU	2.9
1	A	293	VAL	2.9
1	B	302	PHE	2.8
1	B	112	PRO	2.8
1	C	301	SER	2.7
1	A	286	ARG	2.7
1	B	56	VAL	2.7
1	B	109	VAL	2.6
1	B	51	ARG	2.6
1	A	290	GLU	2.5
1	B	67	GLU	2.5
1	B	366	ARG	2.5
1	C	302	PHE	2.5
1	B	32	LEU	2.5
1	B	73	LEU	2.5
1	B	153	VAL	2.5
1	B	60	LYS	2.4
1	B	30	GLN	2.4
1	B	286	ARG	2.4
1	B	105	GLN	2.4
1	B	371	TYR	2.4
1	C	288	GLU	2.4
1	B	95	ARG	2.4
1	A	103	PHE	2.4
1	B	79	ILE	2.4
1	A	285	TRP	2.3
1	B	71	LYS	2.3
1	B	42	THR	2.3
1	B	96	LEU	2.2
1	B	305	MET	2.2

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Mol	Chain	Res	Type	RSRZ
1	C	293	VAL	2.2
1	B	39	GLU	2.2
1	A	73	LEU	2.2
1	B	43	ARG	2.2
1	B	110	CYS	2.2
1	C	236	LEU	2.2
1	A	34	TYR	2.1
1	A	309	LYS	2.1
1	C	130	ALA	2.1
1	A	76	VAL	2.1
1	A	4	ASN	2.1
1	B	135	PRO	2.0
1	C	280	LEU	2.0

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 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(\AA^2)	Q<0.9
3	GOL	B	485	6/6	0.84	0.16	-0.20	73,82,85,86	0
3	GOL	C	485	6/6	0.93	0.16	-0.60	73,77,80,85	0
2	CL	A	484	1/1	0.99	0.11	-1.24	58,58,58,58	0
2	CL	C	484	1/1	0.97	0.09	-1.49	65,65,65,65	0
2	CL	B	484	1/1	0.98	0.05	-3.19	59,59,59,59	0

6.5 Other polymers [i](#)

There are no such residues in this entry.