



Full wwPDB X-ray Structure Validation Report ⓘ

Sep 15, 2017 – 12:37 PM EDT

PDB ID : 5HLD
Title : E. coli PBP1b in complex with acyl-CENTA and moenomycin
Authors : King, D.T.; Strynadka, N.C.J.
Deposited on : unknown
Resolution : 2.31 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 : rb-20029824
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) : rb-20029824

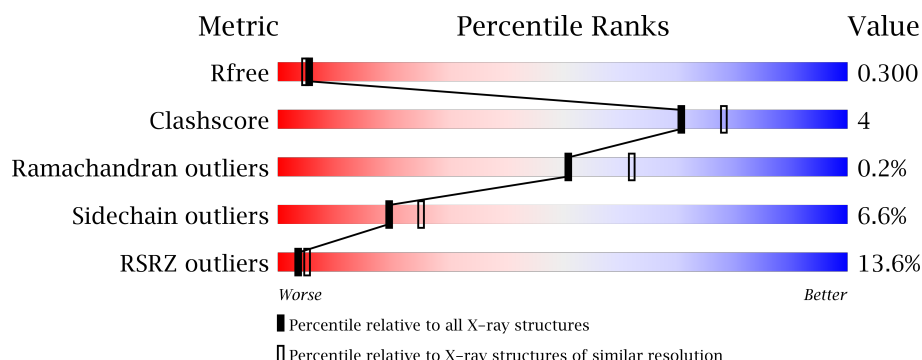
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.31 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	4787 (2.34-2.30)
Clashscore	112137	5439 (2.34-2.30)
Ramachandran outliers	110173	5386 (2.34-2.30)
Sidechain outliers	110143	5385 (2.34-2.30)
RSRZ outliers	101464	4814 (2.34-2.30)

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	747	<div> <div>12%</div> <div>76%</div> <div>10%</div> <div>13%</div> </div>

2 Entry composition [i](#)

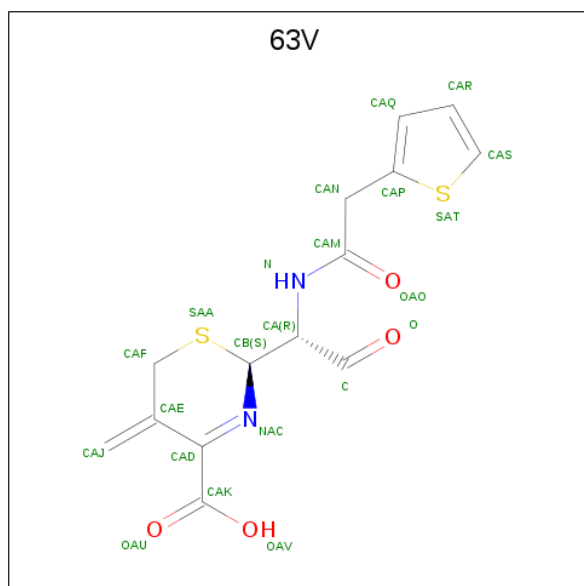
There are 4 unique types of molecules in this entry. The entry contains 5349 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Penicillin-binding protein 1B.

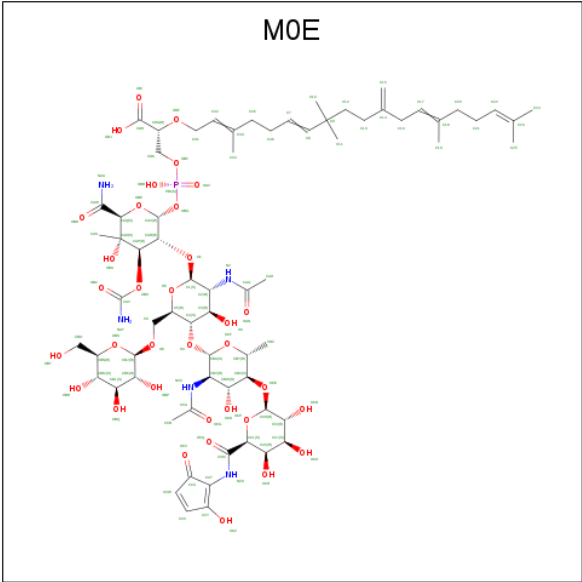
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	649	5063	3209	887	942	25	0	0	0

- Molecule 2 is (2S)-5-methylidene-2-{(1R)-2-oxo-1-[(thiophen-2-ylacetyl)amino]ethyl}-5,6-dihydro-2H-1,3-thiazine-4-carboxylic acid (three-letter code: 63V) (formula: C₁₄H₁₄N₂O₄S₂).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	S		
2	A	1	22	14	2	4	2	0	0

- Molecule 3 is MOENOMYCIN (three-letter code: M0E) (formula: C₆₉H₁₀₆N₅O₃₄P).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
3	A	1	77	39	5	32	1	0	0

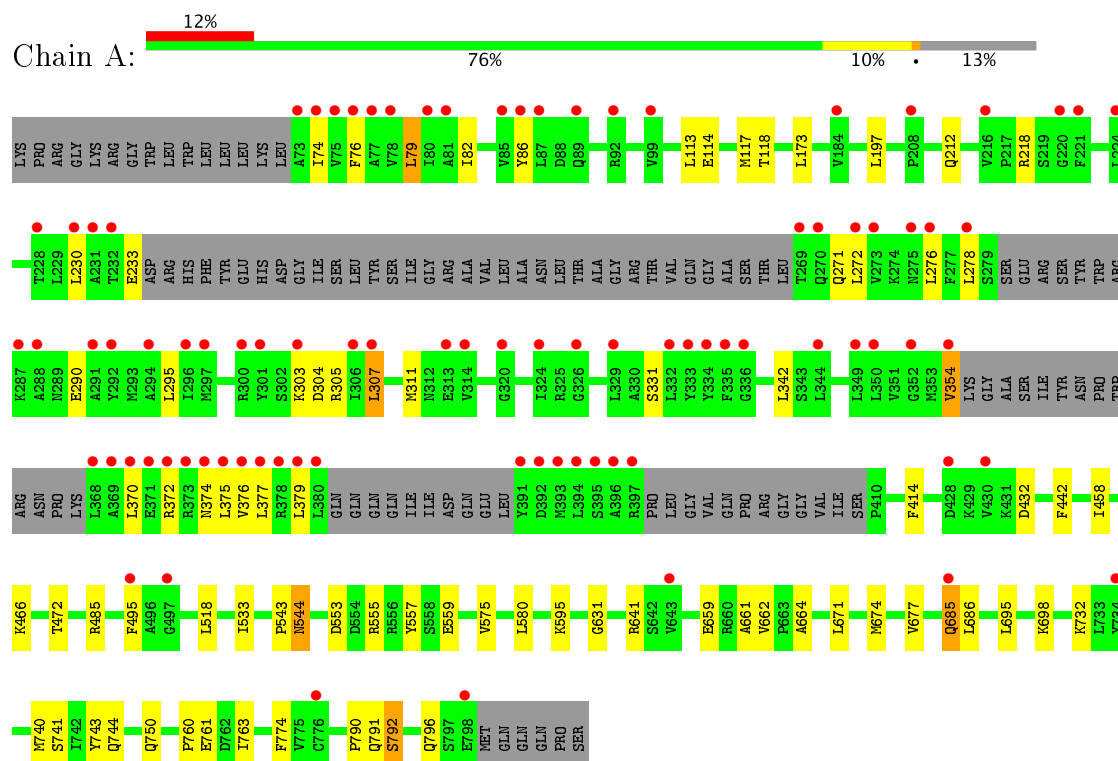
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	187	Total	O	0	0
			187	187		

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: Penicillin-binding protein 1B



4 Data and refinement statistics

Property	Value	Source
Space group	P 2 21 21	Depositor
Cell constants a, b, c, α , β , γ	62.34Å 63.94Å 294.63Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	33.82 – 2.31 62.49 – 2.31	Depositor EDS
% Data completeness (in resolution range)	91.2 (33.82-2.31) 85.7 (62.49-2.31)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.62 (at 2.32Å)	Xtriage
Refinement program	BUSTER 2.10.0	Depositor
R, R_{free}	0.253 , 0.279 0.272 , 0.300	Depositor DCC
R_{free} test set	2384 reflections (5.20%)	DCC
Wilson B-factor (Å ²)	34.6	Xtriage
Anisotropy	0.853	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 35.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.42$, $\langle L^2 \rangle = 0.25$	Xtriage
Estimated twinning fraction	0.049 for k,h,-l	Xtriage
F_o, F_c correlation	0.88	EDS
Total number of atoms	5349	wwPDB-VP
Average B, all atoms (Å ²)	61.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.04% 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: M0E, 63V

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	0.43	0/5157	0.67	0/6992

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

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	5063	0	5111	29	0
2	A	22	0	0	1	0
3	A	77	0	58	16	0
4	A	187	0	0	0	0
All	All	5349	0	5169	42	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 4.

All (42) 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)
3:A:902:M0E:CAV	3:A:902:M0E:OBH	1.63	1.44
3:A:902:M0E:CAX	3:A:902:M0E:OBG	1.67	1.42
3:A:902:M0E:O1	3:A:902:M0E:CAR	1.65	1.41
3:A:902:M0E:C1	3:A:902:M0E:CAR	2.27	1.12
3:A:902:M0E:CAP	3:A:902:M0E:CAV	2.54	0.85
1:A:278:LEU:HD11	1:A:290:GLU:HB3	1.65	0.77
1:A:741:SER:O	1:A:744:GLN:HG2	1.90	0.71
3:A:902:M0E:O1	3:A:902:M0E:CAP	2.37	0.70
1:A:233:GLU:OE2	1:A:271:GLN:NE2	2.34	0.61
1:A:595:LYS:HB3	1:A:661:ALA:HB1	1.86	0.58
3:A:902:M0E:HAS2	3:A:902:M0E:OBD	2.04	0.56
3:A:902:M0E:HBJ	3:A:902:M0E:HCB2	1.87	0.56
3:A:902:M0E:H1	3:A:902:M0E:CAR	2.32	0.55
3:A:902:M0E:PBI	3:A:902:M0E:CAX	2.93	0.55
1:A:271:GLN:HG3	3:A:902:M0E:HAT2	1.76	0.50
1:A:79:LEU:HA	1:A:82:ILE:HG12	1.94	0.49
1:A:760:PRO:HD2	1:A:763:ILE:HG13	1.94	0.49
1:A:761:GLU:CD	1:A:761:GLU:H	2.17	0.48
1:A:674:MET:HA	1:A:677:VAL:HG13	1.94	0.48
1:A:271:GLN:CG	3:A:902:M0E:HAT2	2.26	0.47
1:A:686:LEU:HD11	1:A:743:TYR:HD2	1.79	0.47
1:A:553:ASP:HB3	2:A:901:63V:SAA	2.56	0.46
1:A:374:ASN:HA	1:A:377:LEU:HD12	1.98	0.46
1:A:113:LEU:HD13	1:A:173:LEU:HD21	1.98	0.46
1:A:114:GLU:H	1:A:117:MET:HE2	1.81	0.46
1:A:790:PRO:C	1:A:792:SER:H	2.20	0.45
3:A:902:M0E:O1	3:A:902:M0E:CAX	2.56	0.44
1:A:376:VAL:HA	1:A:379:LEU:HD12	1.99	0.44
1:A:533:ILE:HD12	1:A:580:LEU:HD13	1.99	0.44
1:A:458:ILE:HD11	1:A:472:THR:HB	1.99	0.44
1:A:543:PRO:HA	1:A:544:ASN:HA	1.71	0.44
1:A:774:PHE:N	1:A:796:GLN:HG2	2.32	0.44
1:A:685:GLN:HG3	1:A:740:MET:CE	2.48	0.43
1:A:331:SER:HB3	1:A:342:LEU:HD11	2.00	0.43
3:A:902:M0E:OCD	3:A:902:M0E:OCP	2.18	0.42
1:A:518:LEU:HD21	1:A:662:VAL:HG21	2.02	0.42
3:A:902:M0E:CAR	3:A:902:M0E:OBG	2.55	0.42
1:A:414:PHE:CE1	1:A:442:PHE:HB2	2.55	0.41
1:A:354:VAL:HG22	3:A:902:M0E:HAH3	2.02	0.41
1:A:557:TYR:HE2	1:A:575:VAL:HG21	1.86	0.41
1:A:631:GLY:O	1:A:664:ALA:HA	2.21	0.41
1:A:307:LEU:O	1:A:311:MET:HG3	2.21	0.41

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	637/747 (85%)	618 (97%)	18 (3%)	1 (0%)	51 62

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	791	GLN

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	544/627 (87%)	508 (93%)	36 (7%)	19 25

All (36) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	74	ILE
1	A	76	PHE
1	A	79	LEU
1	A	86	TYR
1	A	118	THR
1	A	197	LEU
1	A	212	GLN

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Mol	Chain	Res	Type
1	A	218	ARG
1	A	230	LEU
1	A	272	LEU
1	A	276	LEU
1	A	295	LEU
1	A	303	LYS
1	A	304	ASP
1	A	305	ARG
1	A	307	LEU
1	A	354	VAL
1	A	370	LEU
1	A	372	ARG
1	A	375	LEU
1	A	432	ASP
1	A	466	LYS
1	A	485	ARG
1	A	495	PHE
1	A	544	ASN
1	A	555	ARG
1	A	559	GLU
1	A	641	ARG
1	A	659	GLU
1	A	671	LEU
1	A	685	GLN
1	A	695	LEU
1	A	698	LYS
1	A	732	LYS
1	A	750	GLN
1	A	792	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	189	ASN

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](#)

2 ligands 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	$\# Z > 2$
2	63V	A	901	1	16,23,23	3.65	3 (18%)	13,31,31	2.89	6 (46%)
3	M0E	A	902	-	76,81,114	4.05	40 (52%)	103,122,166	2.43	18 (17%)

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	63V	A	901	1	-	0/6/31/31	0/1/2/2
3	M0E	A	902	-	-	2/47/158/206	0/5/5/6

All (43) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	902	M0E	O1-C1	-11.14	1.12	1.41
2	A	901	63V	CA-C	-8.85	1.38	1.50
3	A	902	M0E	ODF-CDG	-8.33	1.23	1.42
3	A	902	M0E	CCL-CCM	-7.57	1.41	1.52
3	A	902	M0E	OBR-CBM	-6.61	1.27	1.43
3	A	902	M0E	CAR-CAP	-5.11	1.41	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	902	M0E	CBK-CBL	-3.97	1.42	1.52
3	A	902	M0E	CDK-CDG	-3.76	1.37	1.50
3	A	902	M0E	CAO-CAP	-3.20	1.49	1.53
3	A	902	M0E	CCK-CCJ	-2.89	1.45	1.52
3	A	902	M0E	C6-C5	-2.48	1.43	1.51
3	A	902	M0E	CBW-CBV	-2.30	1.48	1.53
3	A	902	M0E	OCQ-CCM	-2.28	1.19	1.23
3	A	902	M0E	O4-CBU	-2.17	1.35	1.41
3	A	902	M0E	OBS-CBJ	2.00	1.46	1.41
3	A	902	M0E	CBX-CBY	2.05	1.56	1.52
3	A	902	M0E	OCN-CCI	2.09	1.47	1.43
3	A	902	M0E	OBE-CAQ	2.11	1.47	1.44
3	A	902	M0E	OCF-CBU	2.19	1.47	1.41
3	A	902	M0E	CCH-CCI	2.20	1.58	1.52
3	A	902	M0E	OBD-CAW	2.39	1.28	1.23
3	A	902	M0E	OCO-CCJ	2.60	1.48	1.43
3	A	902	M0E	CBJ-CBK	2.60	1.60	1.52
3	A	902	M0E	OCE-CBX	2.85	1.50	1.43
3	A	902	M0E	CAG-N2	2.95	1.45	1.34
3	A	902	M0E	O5-C5	3.33	1.52	1.44
3	A	902	M0E	O6-CBJ	3.35	1.46	1.40
3	A	902	M0E	CCK-CCL	3.52	1.59	1.53
3	A	902	M0E	OBH-CAP	3.79	1.52	1.45
3	A	902	M0E	CBZ-CBY	4.10	1.61	1.51
3	A	902	M0E	PBI-OBG	4.30	1.71	1.60
3	A	902	M0E	CCA-NCC	4.33	1.50	1.34
3	A	902	M0E	OCP-CCL	4.96	1.51	1.43
3	A	902	M0E	O6-C6	5.12	1.52	1.43
3	A	902	M0E	CBV-NCC	5.31	1.54	1.45
2	A	901	63V	CAM-N	5.66	1.45	1.34
3	A	902	M0E	CAH-CAG	6.38	1.64	1.50
3	A	902	M0E	CAV-NAT	7.35	1.47	1.33
3	A	902	M0E	OCD-CBW	7.57	1.60	1.43
3	A	902	M0E	O1-CAR	8.97	1.65	1.43
2	A	901	63V	CAJ-CAE	9.33	1.53	1.32
3	A	902	M0E	OBH-CAV	11.84	1.63	1.35
3	A	902	M0E	CAW-NAU	13.87	1.59	1.32

All (24) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	902	M0E	CAS-CAO-CAP	-11.21	99.63	111.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	902	M0E	OBC-CAV-NAT	-10.59	107.69	125.49
2	A	901	63V	CAF-SAA-CB	-4.97	84.56	94.48
2	A	901	63V	CAR-CAS-SAT	-4.76	108.06	113.18
3	A	902	M0E	CBU-O4-C4	-3.87	108.56	118.00
3	A	902	M0E	C1-O1-CAR	-3.82	108.70	118.00
2	A	901	63V	CAP-CAN-CAM	-3.68	106.47	112.88
3	A	902	M0E	CCH-OCE-CBX	-3.55	109.34	118.00
3	A	902	M0E	CBV-NCC-CCA	-2.67	116.42	123.19
3	A	902	M0E	CBZ-CBY-CBX	-2.56	109.42	113.36
3	A	902	M0E	CBU-OCF-CBY	-2.44	109.36	113.67
3	A	902	M0E	O1-C1-O5	-2.40	104.88	110.70
3	A	902	M0E	OAN-CAG-CAH	-2.32	117.84	122.06
3	A	902	M0E	OCG-CCA-NCC	-2.29	117.51	121.92
3	A	902	M0E	OCQ-CCM-NCS	-2.18	119.72	123.06
3	A	902	M0E	O1-CAR-CAP	-2.07	101.26	106.79
3	A	902	M0E	O4-CBU-CBV	2.04	112.21	108.23
2	A	901	63V	CA-N-CAM	2.05	125.49	123.28
2	A	901	63V	CAE-CAF-SAA	2.35	116.49	111.65
3	A	902	M0E	CCL-CCM-NCS	2.47	120.93	116.77
3	A	902	M0E	CCB-CCA-NCC	2.81	121.19	116.11
2	A	901	63V	CAS-SAT-CAP	5.56	95.01	91.95
3	A	902	M0E	OBA-CAO-CAP	6.31	123.81	107.90
3	A	902	M0E	OBH-CAV-NAT	12.16	129.11	110.56

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	902	M0E	CAP-OBH-CAV-OBC
3	A	902	M0E	CAP-OBH-CAV-NAT

There are no ring outliers.

2 monomers are involved in 17 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	901	63V	1	0
3	A	902	M0E	16	0

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

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	649/747 (86%)	0.95	88 (13%) 3 5	21, 52, 122, 158	0

All (88) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	86	TYR	11.4
1	A	370	LEU	11.0
1	A	368	LEU	10.0
1	A	393	MET	9.5
1	A	373	ARG	9.2
1	A	374	ASN	7.2
1	A	495	PHE	6.4
1	A	378	ARG	6.1
1	A	392	ASP	5.8
1	A	335	PHE	5.4
1	A	76	PHE	5.4
1	A	377	LEU	5.4
1	A	224	LEU	5.4
1	A	273	VAL	5.4
1	A	380	LEU	5.3
1	A	369	ALA	4.8
1	A	326	GLY	4.8
1	A	89	GLN	4.7
1	A	375	LEU	4.6
1	A	272	LEU	4.5
1	A	287	LYS	4.5
1	A	230	LEU	4.4
1	A	270	GLN	4.3
1	A	379	LEU	4.3
1	A	75	VAL	4.2
1	A	288	ALA	4.2
1	A	371	GLU	4.2

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Mol	Chain	Res	Type	RSRZ
1	A	297	MET	4.0
1	A	74	ILE	4.0
1	A	394	LEU	4.0
1	A	303	LYS	4.0
1	A	306	ILE	3.9
1	A	275	ASN	3.9
1	A	300	ARG	3.9
1	A	430	VAL	3.9
1	A	334	TYR	3.9
1	A	372	ARG	3.8
1	A	87	LEU	3.8
1	A	301	TYR	3.8
1	A	391	TYR	3.8
1	A	428	ASP	3.7
1	A	231	ALA	3.6
1	A	776	CYS	3.6
1	A	336	GLY	3.6
1	A	376	VAL	3.5
1	A	314	VAL	3.4
1	A	276	LEU	3.3
1	A	734	TYR	3.2
1	A	307	LEU	3.2
1	A	396	ALA	3.2
1	A	278	LEU	3.2
1	A	77	ALA	3.2
1	A	208	PRO	3.0
1	A	80	ILE	3.0
1	A	296	ILE	3.0
1	A	221	PHE	3.0
1	A	216	VAL	2.9
1	A	73	ALA	2.9
1	A	324	ILE	2.9
1	A	352	GLY	2.8
1	A	397	ARG	2.7
1	A	232	THR	2.7
1	A	81	ALA	2.6
1	A	643	VAL	2.6
1	A	320	GLY	2.5
1	A	344	LEU	2.5
1	A	184	VAL	2.5
1	A	292	TYR	2.5
1	A	350	LEU	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	228	THR	2.5
1	A	220	GLY	2.5
1	A	395	SER	2.5
1	A	92	ARG	2.5
1	A	78	VAL	2.4
1	A	333	TYR	2.4
1	A	497	GLY	2.4
1	A	313	GLU	2.3
1	A	354	VAL	2.3
1	A	332	LEU	2.2
1	A	85	VAL	2.2
1	A	269	THR	2.2
1	A	291	ALA	2.2
1	A	294	ALA	2.2
1	A	685	GLN	2.2
1	A	99	VAL	2.1
1	A	329	LEU	2.1
1	A	349	LEU	2.1
1	A	798	GLU	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(Å ²)	Q<0.9
2	63V	A	901	22/22	0.93	0.17	0.16	28,34,42,44	0
3	M0E	A	902	77/109	0.69	0.21	-0.47	79,106,125,132	0

6.5 Other polymers [i](#)

There are no such residues in this entry.