



Full wwPDB X-ray Structure Validation Report ⓘ

Sep 11, 2023 – 04:57 pm BST

PDB ID : 8BVB
Title : Crystal structure of the apo form of SmbA loop deletion mutant.
Authors : Dubey, B.N.; Schirmer, T.
Deposited on : 2022-12-02
Resolution : 1.80 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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Xtriage (Phenix) : 1.13
EDS : 2.35
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) : 2.35

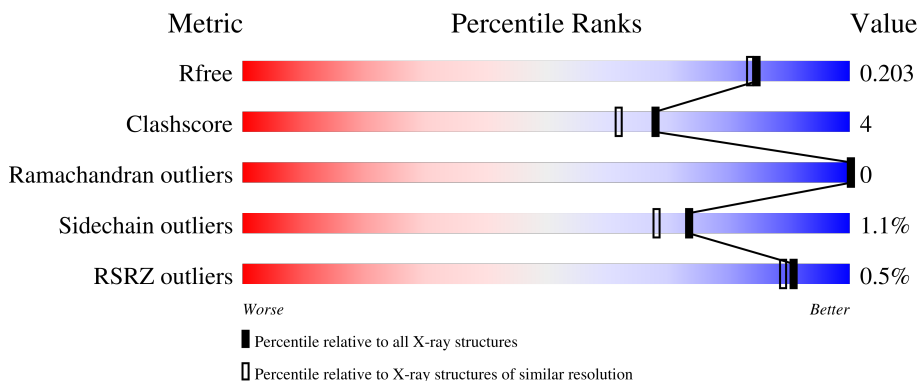
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 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	5950 (1.80-1.80)
Clashscore	141614	6793 (1.80-1.80)
Ramachandran outliers	138981	6697 (1.80-1.80)
Sidechain outliers	138945	6696 (1.80-1.80)
RSRZ outliers	127900	5850 (1.80-1.80)

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	291	91% 8% .
1	B	291	90% 8% ..
1	C	291	2% 90% 8% ..
1	D	291	92% 7% .

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 10222 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 Aldo_ket_red domain-containing protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	289	2238	1402	411	420	5	0	0	0
1	B	289	2238	1402	411	420	5	0	0	0
1	C	289	2238	1402	411	420	5	0	0	0
1	D	289	2238	1402	411	420	5	0	0	0

There are 124 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	VAL	deletion	UNP Q9A5E6
A	?	-	ALA	deletion	UNP Q9A5E6
A	?	-	ASP	deletion	UNP Q9A5E6
A	?	-	LYS	deletion	UNP Q9A5E6
A	?	-	ALA	deletion	UNP Q9A5E6
A	?	-	PRO	deletion	UNP Q9A5E6
A	?	-	PRO	deletion	UNP Q9A5E6
A	?	-	LYS	deletion	UNP Q9A5E6
A	?	-	PRO	deletion	UNP Q9A5E6
A	?	-	SER	deletion	UNP Q9A5E6
A	?	-	PHE	deletion	UNP Q9A5E6
A	?	-	TRP	deletion	UNP Q9A5E6
A	?	-	GLN	deletion	UNP Q9A5E6
A	?	-	ARG	deletion	UNP Q9A5E6
A	?	-	ARG	deletion	UNP Q9A5E6
A	?	-	THR	deletion	UNP Q9A5E6
A	?	-	ASP	deletion	UNP Q9A5E6
A	?	-	PRO	deletion	UNP Q9A5E6
A	297	LYS	-	expression tag	UNP Q9A5E6
A	298	LEU	-	expression tag	UNP Q9A5E6
A	299	ALA	-	expression tag	UNP Q9A5E6

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Chain	Residue	Modelled	Actual	Comment	Reference
A	300	ALA	-	expression tag	UNP Q9A5E6
A	301	ALA	-	expression tag	UNP Q9A5E6
A	302	LEU	-	expression tag	UNP Q9A5E6
A	303	GLU	-	expression tag	UNP Q9A5E6
A	304	HIS	-	expression tag	UNP Q9A5E6
A	305	HIS	-	expression tag	UNP Q9A5E6
A	306	HIS	-	expression tag	UNP Q9A5E6
A	307	HIS	-	expression tag	UNP Q9A5E6
A	308	GLU	-	expression tag	UNP Q9A5E6
A	309	LYS	-	expression tag	UNP Q9A5E6
B	?	-	VAL	deletion	UNP Q9A5E6
B	?	-	ALA	deletion	UNP Q9A5E6
B	?	-	ASP	deletion	UNP Q9A5E6
B	?	-	LYS	deletion	UNP Q9A5E6
B	?	-	ALA	deletion	UNP Q9A5E6
B	?	-	PRO	deletion	UNP Q9A5E6
B	?	-	PRO	deletion	UNP Q9A5E6
B	?	-	LYS	deletion	UNP Q9A5E6
B	?	-	PRO	deletion	UNP Q9A5E6
B	?	-	SER	deletion	UNP Q9A5E6
B	?	-	PHE	deletion	UNP Q9A5E6
B	?	-	TRP	deletion	UNP Q9A5E6
B	?	-	GLN	deletion	UNP Q9A5E6
B	?	-	ARG	deletion	UNP Q9A5E6
B	?	-	ARG	deletion	UNP Q9A5E6
B	?	-	THR	deletion	UNP Q9A5E6
B	?	-	ASP	deletion	UNP Q9A5E6
B	?	-	PRO	deletion	UNP Q9A5E6
B	297	LYS	-	expression tag	UNP Q9A5E6
B	298	LEU	-	expression tag	UNP Q9A5E6
B	299	ALA	-	expression tag	UNP Q9A5E6
B	300	ALA	-	expression tag	UNP Q9A5E6
B	301	ALA	-	expression tag	UNP Q9A5E6
B	302	LEU	-	expression tag	UNP Q9A5E6
B	303	GLU	-	expression tag	UNP Q9A5E6
B	304	HIS	-	expression tag	UNP Q9A5E6
B	305	HIS	-	expression tag	UNP Q9A5E6
B	306	HIS	-	expression tag	UNP Q9A5E6
B	307	HIS	-	expression tag	UNP Q9A5E6
B	308	GLU	-	expression tag	UNP Q9A5E6
B	309	LYS	-	expression tag	UNP Q9A5E6
C	?	-	VAL	deletion	UNP Q9A5E6

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Chain	Residue	Modelled	Actual	Comment	Reference
C	?	-	ALA	deletion	UNP Q9A5E6
C	?	-	ASP	deletion	UNP Q9A5E6
C	?	-	LYS	deletion	UNP Q9A5E6
C	?	-	ALA	deletion	UNP Q9A5E6
C	?	-	PRO	deletion	UNP Q9A5E6
C	?	-	PRO	deletion	UNP Q9A5E6
C	?	-	LYS	deletion	UNP Q9A5E6
C	?	-	PRO	deletion	UNP Q9A5E6
C	?	-	SER	deletion	UNP Q9A5E6
C	?	-	PHE	deletion	UNP Q9A5E6
C	?	-	TRP	deletion	UNP Q9A5E6
C	?	-	GLN	deletion	UNP Q9A5E6
C	?	-	ARG	deletion	UNP Q9A5E6
C	?	-	ARG	deletion	UNP Q9A5E6
C	?	-	THR	deletion	UNP Q9A5E6
C	?	-	ASP	deletion	UNP Q9A5E6
C	?	-	PRO	deletion	UNP Q9A5E6
C	297	LYS	-	expression tag	UNP Q9A5E6
C	298	LEU	-	expression tag	UNP Q9A5E6
C	299	ALA	-	expression tag	UNP Q9A5E6
C	300	ALA	-	expression tag	UNP Q9A5E6
C	301	ALA	-	expression tag	UNP Q9A5E6
C	302	LEU	-	expression tag	UNP Q9A5E6
C	303	GLU	-	expression tag	UNP Q9A5E6
C	304	HIS	-	expression tag	UNP Q9A5E6
C	305	HIS	-	expression tag	UNP Q9A5E6
C	306	HIS	-	expression tag	UNP Q9A5E6
C	307	HIS	-	expression tag	UNP Q9A5E6
C	308	GLU	-	expression tag	UNP Q9A5E6
C	309	LYS	-	expression tag	UNP Q9A5E6
D	?	-	VAL	deletion	UNP Q9A5E6
D	?	-	ALA	deletion	UNP Q9A5E6
D	?	-	ASP	deletion	UNP Q9A5E6
D	?	-	LYS	deletion	UNP Q9A5E6
D	?	-	ALA	deletion	UNP Q9A5E6
D	?	-	PRO	deletion	UNP Q9A5E6
D	?	-	PRO	deletion	UNP Q9A5E6
D	?	-	LYS	deletion	UNP Q9A5E6
D	?	-	PRO	deletion	UNP Q9A5E6
D	?	-	SER	deletion	UNP Q9A5E6
D	?	-	PHE	deletion	UNP Q9A5E6
D	?	-	TRP	deletion	UNP Q9A5E6

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Chain	Residue	Modelled	Actual	Comment	Reference
D	?	-	GLN	deletion	UNP Q9A5E6
D	?	-	ARG	deletion	UNP Q9A5E6
D	?	-	ARG	deletion	UNP Q9A5E6
D	?	-	THR	deletion	UNP Q9A5E6
D	?	-	ASP	deletion	UNP Q9A5E6
D	?	-	PRO	deletion	UNP Q9A5E6
D	297	LYS	-	expression tag	UNP Q9A5E6
D	298	LEU	-	expression tag	UNP Q9A5E6
D	299	ALA	-	expression tag	UNP Q9A5E6
D	300	ALA	-	expression tag	UNP Q9A5E6
D	301	ALA	-	expression tag	UNP Q9A5E6
D	302	LEU	-	expression tag	UNP Q9A5E6
D	303	GLU	-	expression tag	UNP Q9A5E6
D	304	HIS	-	expression tag	UNP Q9A5E6
D	305	HIS	-	expression tag	UNP Q9A5E6
D	306	HIS	-	expression tag	UNP Q9A5E6
D	307	HIS	-	expression tag	UNP Q9A5E6
D	308	GLU	-	expression tag	UNP Q9A5E6
D	309	LYS	-	expression tag	UNP Q9A5E6

- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	344	Total O 344 344	0	0
2	B	306	Total O 306 306	0	0
2	C	307	Total O 307 307	0	0
2	D	313	Total O 313 313	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: Aldo_ket_red domain-containing protein

Chain A:  91% 8%




- Molecule 1: Aldo_ket_red domain-containing protein

Chain B:  90% 8%



- Molecule 1: Aldo_ket_red domain-containing protein

Chain C:  90% 8% 2%



- Molecule 1: Aldo_ket_red domain-containing protein

Chain D:  92% 7%



4 Data and refinement statistics i

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	61.38Å 208.10Å 64.23Å 90.00° 117.58° 90.00°	Depositor
Resolution (Å)	56.94 – 1.80 56.94 – 1.80	Depositor EDS
% Data completeness (in resolution range)	97.8 (56.94-1.80) 97.8 (56.94-1.80)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.48 (at 1.80Å)	Xtrriage
Refinement program	PHENIX 1.19.2	Depositor
R, R_{free}	0.169 , 0.203 0.169 , 0.203	Depositor DCC
R_{free} test set	6163 reflections (4.79%)	wwPDB-VP
Wilson B-factor (Å ²)	20.4	Xtrriage
Anisotropy	0.248	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 51.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtrriage
Estimated twinning fraction	0.036 for h,-k,-h-l	Xtrriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	10222	wwPDB-VP
Average B, all atoms (Å ²)	23.0	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 i

5.1 Standard geometry i

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	0.48	0/2283	0.70	1/3098 (0.0%)
1	B	0.46	0/2283	0.70	1/3098 (0.0%)
1	C	0.45	0/2283	0.69	2/3098 (0.1%)
1	D	0.46	0/2283	0.68	1/3098 (0.0%)
All	All	0.46	0/9132	0.70	5/12392 (0.0%)

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	C	0	1

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	281	MET	CA-CB-CG	8.07	127.02	113.30
1	C	281	MET	CB-CG-SD	-7.79	89.04	112.40
1	A	281	MET	CA-CB-CG	7.67	126.34	113.30
1	C	281	MET	CG-SD-CE	7.40	112.04	100.20
1	D	281	MET	CG-SD-CE	5.21	108.53	100.20

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	289	ARG	Sidechain

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	2238	0	2209	16	0
1	B	2238	0	2209	20	1
1	C	2238	0	2209	18	1
1	D	2238	0	2209	15	0
2	A	344	0	0	5	5
2	B	306	0	0	5	4
2	C	307	0	0	7	3
2	D	313	0	0	5	6
All	All	10222	0	8836	68	10

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 (68) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:67:GLU:OE2	2:C:401:HOH:O	1.99	0.80
1:D:90:ASP:HB3	1:D:94:ARG:NH1	1.96	0.80
1:C:289:ARG:HG2	1:C:290:GLU:O	1.82	0.79
1:C:67:GLU:OE1	2:C:402:HOH:O	2.03	0.75
1:C:289:ARG:NH2	2:C:404:HOH:O	2.19	0.74
1:B:288:GLU:OE2	2:B:401:HOH:O	2.11	0.69
1:D:90:ASP:HB3	1:D:94:ARG:HH12	1.58	0.67
1:B:296:PRO:HD2	1:B:297:LYS:HE3	1.77	0.65
1:D:257:ARG:NH2	2:D:402:HOH:O	2.18	0.65
1:C:57:LYS:O	1:C:61:GLU:HG3	1.98	0.63
1:A:84:LEU:HD22	1:A:88:THR:HG21	1.81	0.62
1:A:21:ALA:O	1:A:31:TRP:HH2	1.87	0.57
1:C:291:LYS:NZ	2:C:409:HOH:O	2.31	0.57
1:D:268:GLU:OE1	2:D:401:HOH:O	2.18	0.57
1:A:127:GLN:O	1:A:131:LYS:HG3	2.06	0.56
1:D:80:ASP:OD1	1:D:82:LYS:NZ	2.31	0.54
1:B:297:LYS:N	1:B:297:LYS:HD2	2.23	0.53
1:B:93:LYS:HA	1:B:97:PHE:HD2	1.73	0.53
1:D:258:GLN:HG2	1:D:262:ARG:NH1	2.24	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:239:GLY:O	1:C:243:THR:HG23	2.10	0.52
1:B:8:SER:HB2	1:C:69:HIS:CG	2.45	0.52
1:C:303:GLU:HG3	2:C:449:HOH:O	2.10	0.51
1:D:86:PRO:HA	1:D:89:LEU:HD12	1.94	0.50
1:D:84:LEU:HD22	1:D:88:THR:HG21	1.94	0.49
1:C:256:ASN:OD1	1:C:259:GLU:HG3	2.13	0.49
1:B:297:LYS:HD2	1:B:297:LYS:H	1.77	0.49
1:C:23:ASN:HD21	1:C:25:ARG:HD3	1.76	0.48
1:B:130:GLN:NE2	2:B:415:HOH:O	2.47	0.47
1:D:238:LEU:HD22	1:D:263:LEU:HD22	1.97	0.47
1:C:23:ASN:C	1:C:23:ASN:HD22	2.18	0.47
1:C:262:ARG:HD3	2:C:627:HOH:O	2.14	0.47
1:A:96:ALA:O	1:A:100:LEU:HB2	2.16	0.46
1:A:284:PHE:CE1	1:A:286:ALA:HB2	2.51	0.46
1:D:258:GLN:NE2	2:D:411:HOH:O	2.43	0.46
1:B:84:LEU:HD22	1:B:88:THR:HG21	1.99	0.45
1:D:239:GLY:O	1:D:243:THR:HG23	2.17	0.45
1:A:284:PHE:HE1	1:A:286:ALA:HB2	1.82	0.45
1:A:21:ALA:O	1:A:31:TRP:CH2	2.70	0.45
1:D:258:GLN:O	1:D:262:ARG:HG3	2.16	0.45
1:D:307:HIS:O	2:D:403:HOH:O	2.21	0.45
1:A:67:GLU:HB3	1:A:69:HIS:CE1	2.52	0.44
1:A:81:ALA:HA	1:A:84:LEU:HG	1.98	0.44
1:A:94:ARG:NH1	2:A:419:HOH:O	2.50	0.44
1:A:67:GLU:HG2	2:A:574:HOH:O	2.16	0.44
1:B:89:LEU:HD23	1:B:89:LEU:HA	1.77	0.44
1:A:86:PRO:HA	1:A:89:LEU:HD12	1.99	0.44
1:B:218:ASP:OD2	2:B:403:HOH:O	2.21	0.44
1:B:127:GLN:O	1:B:131:LYS:HG3	2.18	0.43
1:B:190:PHE:CE1	1:B:191:TRP:HB2	2.53	0.43
1:B:90:ASP:O	1:B:94:ARG:HG3	2.18	0.43
1:C:6:PHE:HB3	1:C:11:VAL:HG13	2.00	0.43
1:C:258:GLN:NE2	2:C:407:HOH:O	2.29	0.43
1:D:257:ARG:HB2	2:D:500:HOH:O	2.18	0.43
1:A:258:GLN:O	1:A:262:ARG:HG3	2.19	0.43
1:B:8:SER:OG	2:B:402:HOH:O	2.21	0.42
1:A:22:ASP:HB2	2:A:428:HOH:O	2.18	0.42
1:A:294:ARG:NH2	2:A:411:HOH:O	2.45	0.42
1:C:31:TRP:CD1	1:C:55:LEU:HA	2.53	0.42
1:C:89:LEU:HD13	1:C:125:GLY:HA3	2.02	0.42
1:A:218:ASP:HA	2:A:420:HOH:O	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:191:TRP:CZ2	1:B:196:ARG:HG2	2.54	0.42
1:B:67:GLU:HG3	2:B:616:HOH:O	2.20	0.42
1:B:82:LYS:HB2	1:B:82:LYS:HE2	1.90	0.41
1:B:96:ALA:O	1:B:100:LEU:HB2	2.21	0.41
1:B:297:LYS:HD2	1:B:298:LEU:H	1.85	0.41
1:C:23:ASN:HD22	1:C:25:ARG:H	1.69	0.41
1:D:21:ALA:O	1:D:31:TRP:HH2	2.04	0.40
1:B:297:LYS:H	1:B:297:LYS:CD	2.34	0.40

All (10) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:412:HOH:O	2:C:401:HOH:O[1_655]	1.98	0.22
2:B:650:HOH:O	2:D:459:HOH:O[1_656]	2.10	0.10
2:A:436:HOH:O	2:D:559:HOH:O[1_656]	2.11	0.09
2:A:581:HOH:O	2:D:539:HOH:O[1_656]	2.12	0.08
1:B:2:ARG:NH1	1:C:292:ALA:O[1_655]	2.14	0.06
2:A:659:HOH:O	2:D:627:HOH:O[1_656]	2.15	0.05
2:B:563:HOH:O	2:D:684:HOH:O[2_547]	2.15	0.05
2:A:578:HOH:O	2:D:645:HOH:O[1_656]	2.17	0.03
2:A:503:HOH:O	2:C:644:HOH:O[1_655]	2.18	0.02
2:B:515:HOH:O	2:C:596:HOH:O[1_655]	2.19	0.01

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	287/291 (99%)	282 (98%)	5 (2%)	0	100	100
1	B	287/291 (99%)	284 (99%)	3 (1%)	0	100	100
1	C	287/291 (99%)	280 (98%)	7 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	D	287/291 (99%)	282 (98%)	5 (2%)	0	100	100
All	All	1148/1164 (99%)	1128 (98%)	20 (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	229/231 (99%)	228 (100%)	1 (0%)	91	89
1	B	229/231 (99%)	226 (99%)	3 (1%)	69	62
1	C	229/231 (99%)	224 (98%)	5 (2%)	52	39
1	D	229/231 (99%)	228 (100%)	1 (0%)	91	89
All	All	916/924 (99%)	906 (99%)	10 (1%)	73	68

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	289	ARG
1	B	130	GLN
1	B	161	SER
1	B	297	LYS
1	C	23	ASN
1	C	25	ARG
1	C	219	VAL
1	C	258	GLN
1	C	288	GLU
1	D	297	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	306	HIS

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Mol	Chain	Res	Type
1	C	23	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no 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 [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	289/291 (99%)	-0.59	0	100 100	9, 18, 36, 65	0
1	B	289/291 (99%)	-0.55	0	100 100	10, 20, 37, 57	0
1	C	289/291 (99%)	-0.48	6 (2%)	63 59	10, 20, 44, 72	0
1	D	289/291 (99%)	-0.57	0	100 100	10, 20, 39, 59	0
All	All	1156/1164 (99%)	-0.55	6 (0%)	91 89	9, 20, 39, 72	0

All (6) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	289	ARG	6.6
1	C	288	GLU	3.5
1	C	294	ARG	2.9
1	C	287	GLN	2.6
1	C	9	THR	2.4
1	C	290	GLU	2.1

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 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.