



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 21, 2016 – 12:31 PM EDT

PDB ID : 5DXJ
Title : Crystal structure of CARM1 and sinefungin
Authors : Boriack-Sjodin, P.A.
Deposited on : 2015-09-23
Resolution : 1.95 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 : 1.7.1 (RC1), CSD as537be (2016)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20027107
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0122
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20027107

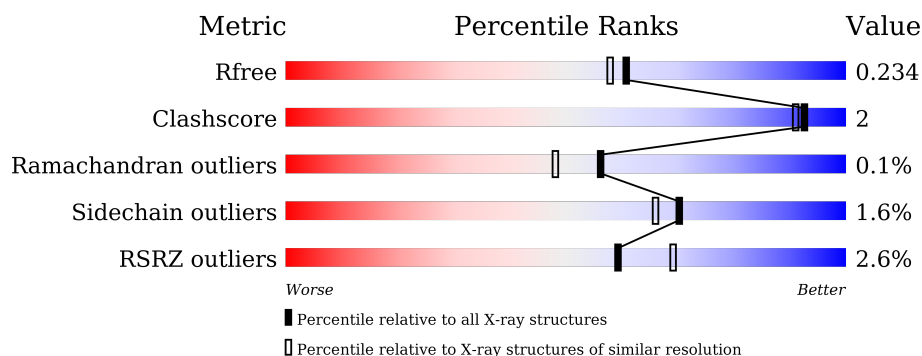
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.95 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}	91344	1833 (1.96-1.96)
Clashscore	102246	1953 (1.96-1.96)
Ramachandran outliers	100387	1936 (1.96-1.96)
Sidechain outliers	100360	1936 (1.96-1.96)
RSRZ outliers	91569	1835 (1.96-1.96)

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	349	<div> <div>2%</div> <div> <div></div> <div>91%</div> <div>7%</div> <div></div> </div> </div>
1	B	349	<div> <div>%</div> <div> <div></div> <div>92%</div> <div>6%</div> <div></div> </div> </div>
1	C	349	<div> <div>4%</div> <div> <div></div> <div>94%</div> <div></div> <div></div> </div> </div>
1	D	349	<div> <div>3%</div> <div> <div></div> <div>93%</div> <div>5%</div> <div></div> </div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	GOL	B	502	-	-	-	X

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 12312 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.

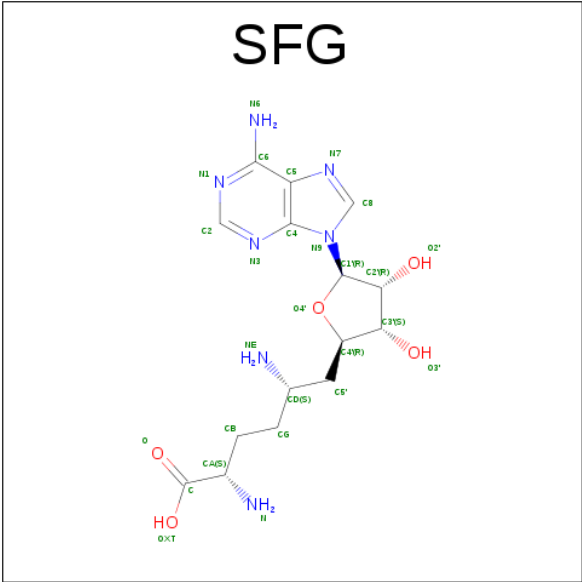
- Molecule 1 is a protein called Histone-arginine methyltransferase CARM1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	344	Total	C	N	O	S	0	14	0
			2869	1842	477	534	16			
1	B	344	Total	C	N	O	S	0	19	0
			2917	1880	481	539	17			
1	C	343	Total	C	N	O	S	0	7	0
			2814	1811	471	515	17			
1	D	344	Total	C	N	O	S	0	5	0
			2809	1813	464	517	15			

There are 12 discrepancies between the modelled and reference sequences:

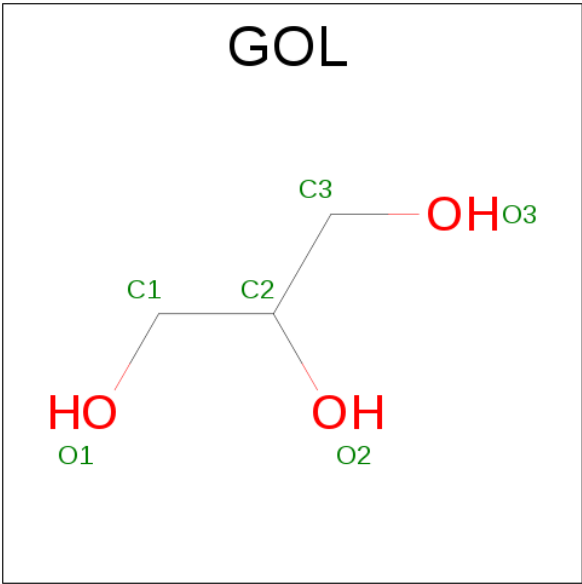
Chain	Residue	Modelled	Actual	Comment	Reference
A	131	SER	-	expression tag	UNP Q86X55
A	132	ILE	-	expression tag	UNP Q86X55
A	133	ALA	-	expression tag	UNP Q86X55
B	131	SER	-	expression tag	UNP Q86X55
B	132	ILE	-	expression tag	UNP Q86X55
B	133	ALA	-	expression tag	UNP Q86X55
C	131	SER	-	expression tag	UNP Q86X55
C	132	ILE	-	expression tag	UNP Q86X55
C	133	ALA	-	expression tag	UNP Q86X55
D	131	SER	-	expression tag	UNP Q86X55
D	132	ILE	-	expression tag	UNP Q86X55
D	133	ALA	-	expression tag	UNP Q86X55

- Molecule 2 is SINEFUNGIN (three-letter code: SFG) (formula: C₁₅H₂₃N₇O₅).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			27	15	7	5		
2	B	1	Total	C	N	O	0	0
			27	15	7	5		
2	C	1	Total	C	N	O	0	0
			27	15	7	5		
2	D	1	Total	C	N	O	0	0
			27	15	7	5		

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



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

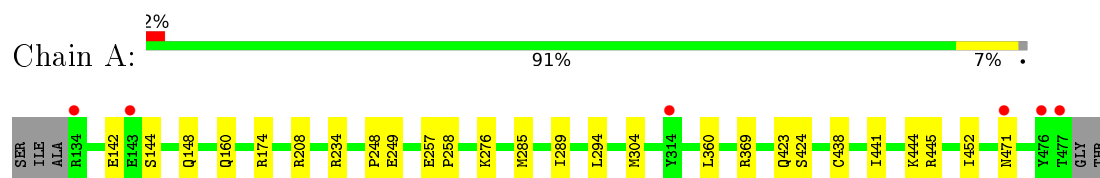
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	231	Total 231	O 231	0	0
4	B	239	Total 240	O 240	0	1
4	C	134	Total 134	O 134	0	0
4	D	160	Total 160	O 160	0	0

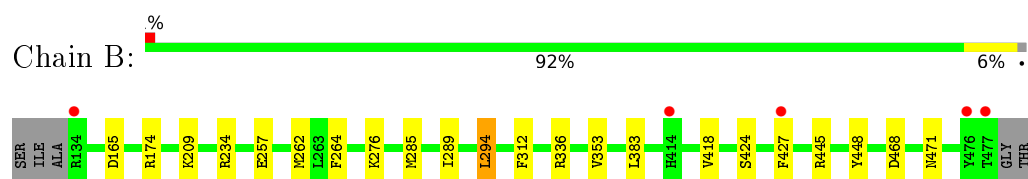
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

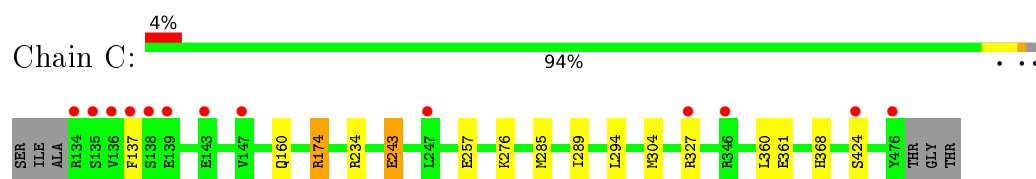
- Molecule 1: Histone-arginine methyltransferase CARM1



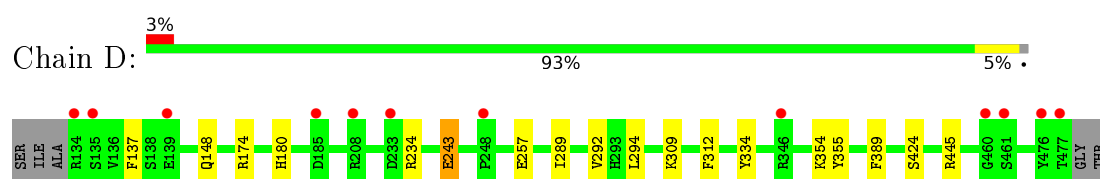
- Molecule 1: Histone-arginine methyltransferase CARM1



- Molecule 1: Histone-arginine methyltransferase CARM1



- Molecule 1: Histone-arginine methyltransferase CARM1



4 Data and refinement statistics

Property	Value	Source
Space group	P 2 ₁ 2 ₁ 2	Depositor
Cell constants a, b, c, α , β , γ	74.92Å 97.88Å 207.38Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 1.95 38.11 – 1.95	Depositor EDS
% Data completeness (in resolution range)	98.8 (50.00-1.95) 98.9 (38.11-1.95)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.01 (at 1.95Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.198 , 0.231 0.204 , 0.234	Depositor DCC
R_{free} test set	5555 reflections (5.28%)	DCC
Wilson B-factor (Å ²)	27.3	Xtriage
Anisotropy	0.010	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 40.7	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	1 of 110736 reflections (0.001%)	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	12312	wwPDB-VP
Average B, all atoms (Å ²)	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 31.75 % 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 1.0509e-03. 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, 0.375 respectively for untwinned datasets, and 0.333, 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: GOL, SFG

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	0.57	0/2940	0.91	6/3982 (0.2%)
1	B	0.56	0/2997	0.80	7/4061 (0.2%)
1	C	0.51	0/2885	0.77	5/3906 (0.1%)
1	D	0.52	0/2881	0.78	5/3904 (0.1%)
All	All	0.54	0/11703	0.82	23/15853 (0.1%)

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

There are no bond length outliers.

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	234	ARG	NE-CZ-NH2	21.46	131.03	120.30
1	A	234	ARG	NE-CZ-NH1	-19.48	110.56	120.30
1	B	294[A]	LEU	CA-CB-CG	8.83	135.61	115.30
1	B	294[B]	LEU	CA-CB-CG	8.83	135.61	115.30
1	C	174	ARG	NE-CZ-NH2	8.65	124.62	120.30
1	C	234	ARG	NE-CZ-NH2	-8.46	116.07	120.30
1	A	174	ARG	NE-CZ-NH1	-7.90	116.35	120.30
1	A	174	ARG	NE-CZ-NH2	7.84	124.22	120.30
1	C	174	ARG	NE-CZ-NH1	-7.47	116.56	120.30
1	B	234	ARG	NE-CZ-NH2	-7.39	116.60	120.30
1	D	234	ARG	NE-CZ-NH2	-7.21	116.70	120.30
1	C	234	ARG	NE-CZ-NH1	6.22	123.41	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	445	ARG	NE-CZ-NH1	6.16	123.38	120.30
1	B	234	ARG	NE-CZ-NH1	6.13	123.36	120.30
1	D	234	ARG	NE-CZ-NH1	6.00	123.30	120.30
1	D	174	ARG	NE-CZ-NH1	5.95	123.27	120.30
1	B	174	ARG	NE-CZ-NH1	5.70	123.15	120.30
1	B	165	ASP	CB-CG-OD1	5.51	123.26	118.30
1	C	327	ARG	CB-CG-CD	5.45	125.78	111.60
1	A	208	ARG	NE-CZ-NH2	5.42	123.01	120.30
1	D	174	ARG	NE-CZ-NH2	-5.27	117.66	120.30
1	D	445	ARG	NE-CZ-NH1	5.27	122.93	120.30
1	A	445	ARG	NE-CZ-NH1	5.18	122.89	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	248	PRO	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	2869	0	2798	13	0
1	B	2917	0	2837	19	0
1	C	2814	0	2754	8	1
1	D	2809	0	2745	9	1
2	A	27	0	22	0	0
2	B	27	0	22	0	0
2	C	27	0	22	0	0
2	D	27	0	22	0	0
3	A	6	0	8	0	0
3	B	12	0	16	0	0
3	C	6	0	8	0	0
3	D	6	0	8	0	0
4	A	231	0	0	4	0
4	B	240	0	0	0	0
4	C	134	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	D	160	0	0	1	0
All	All	12312	0	11262	46	1

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 (46) 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:383[B]:LEU:HD11	1:B:427[B]:PHE:CE1	1.18	1.64
1:B:383[B]:LEU:CD1	1:B:427[B]:PHE:CE1	2.04	1.39
1:B:383[B]:LEU:CD1	1:B:427[B]:PHE:CD1	2.41	1.02
1:B:383[B]:LEU:HD11	1:B:427[B]:PHE:CD1	1.95	1.01
1:B:383[B]:LEU:CD1	1:B:427[B]:PHE:HE1	1.53	1.00
1:B:383[B]:LEU:HD12	1:B:427[B]:PHE:CD1	2.19	0.75
1:B:383[B]:LEU:CG	1:B:427[B]:PHE:CE1	2.70	0.74
1:D:137:PHE:HB2	1:D:243:GLU:CG	2.22	0.70
1:C:137:PHE:HB2	1:C:243:GLU:CG	2.21	0.69
1:A:471[B]:ASN:O	1:A:471[B]:ASN:CG	2.37	0.61
1:B:262[A]:MET:HE3	1:B:418:VAL:HG11	1.86	0.57
1:C:137:PHE:HB2	1:C:243:GLU:HG2	1.88	0.55
1:D:137:PHE:HB2	1:D:243:GLU:HG2	1.89	0.54
1:B:383[B]:LEU:HD12	1:B:427[B]:PHE:HD1	1.69	0.52
1:C:174:ARG:NH1	4:C:603:HOH:O	2.41	0.52
1:D:294:LEU:HG	1:D:389:PHE:CE2	2.46	0.50
1:A:249:GLU:HG3	4:A:617:HOH:O	2.11	0.50
1:C:276:LYS:HD3	1:C:285[B]:MET:SD	2.53	0.49
1:A:276:LYS:HD3	1:A:285[B]:MET:SD	2.52	0.49
1:B:262[A]:MET:CE	1:B:418:VAL:HG11	2.42	0.48
1:B:294[B]:LEU:HD22	1:B:353:VAL:O	2.13	0.48
1:A:423:GLN:HG3	4:A:615:HOH:O	2.13	0.48
1:B:336:ARG:NH2	1:B:468[B]:ASP:OD1	2.45	0.47
1:A:285[B]:MET:HG3	1:A:360:LEU:HD23	1.96	0.47
1:C:137:PHE:HB2	1:C:243:GLU:HG3	1.97	0.47
1:A:304:MET:HE1	1:C:304:MET:HE1	1.96	0.46
1:D:292:VAL:CG1	1:D:355:TYR:HB3	2.45	0.46
1:B:471[B]:ASN:CG	1:B:471[B]:ASN:O	2.52	0.46
1:A:438[B]:CYS:SG	1:A:452:ILE:HG12	2.56	0.44
1:D:180:HIS:HD2	4:D:742:HOH:O	2.00	0.44
1:A:369[B]:ARG:HG3	1:A:441:ILE:CD1	2.48	0.43
1:D:137:PHE:HB2	1:D:243:GLU:HG3	1.98	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:148:GLN:NE2	4:A:611:HOH:O	2.52	0.43
1:A:369[A]:ARG:HG3	1:A:441:ILE:CD1	2.49	0.43
1:D:309:LYS:HE3	1:D:334:TYR:CE1	2.54	0.43
1:C:285[B]:MET:HG3	1:C:360:LEU:HD23	2.00	0.42
1:B:276:LYS:HD3	1:B:285[B]:MET:SD	2.60	0.42
1:A:142[B]:GLU:HG2	1:A:444:LYS:HB3	2.00	0.42
1:A:369[B]:ARG:NH2	4:A:610:HOH:O	2.52	0.41
1:B:294[A]:LEU:HD12	1:B:353:VAL:HB	2.01	0.41
1:C:160:GLN:HG3	1:D:312:PHE:CD2	2.56	0.41
1:B:383[B]:LEU:HG	1:B:427[B]:PHE:CE1	2.52	0.41
1:A:160:GLN:HG3	1:B:312:PHE:CD2	2.55	0.41
1:B:336:ARG:NE	1:B:468[B]:ASP:OD2	2.54	0.40
1:D:292:VAL:HG13	1:D:355:TYR:HB3	2.02	0.40
1:B:264:PHE:HB3	1:B:448:TYR:CE1	2.56	0.40

All (1) 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)
1:C:361:GLU:OE1	1:D:354:LYS:NZ[1_655]	2.15	0.05

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	356/349 (102%)	338 (95%)	15 (4%)	3 (1%)	24	11
1	B	361/349 (103%)	351 (97%)	10 (3%)	0	100	100
1	C	348/349 (100%)	338 (97%)	10 (3%)	0	100	100
1	D	347/349 (99%)	336 (97%)	11 (3%)	0	100	100
All	All	1412/1396 (101%)	1363 (96%)	46 (3%)	3 (0%)	56	43

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	144[A]	SER
1	A	144[B]	SER
1	A	258	PRO

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	314/303 (104%)	310 (99%)	4 (1%)	76	72
1	B	319/303 (105%)	315 (99%)	4 (1%)	76	72
1	C	306/303 (101%)	300 (98%)	6 (2%)	63	55
1	D	305/303 (101%)	300 (98%)	5 (2%)	70	66
All	All	1244/1212 (103%)	1225 (98%)	19 (2%)	70	68

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	257	GLU
1	A	289	ILE
1	A	294	LEU
1	A	424	SER
1	B	209	LYS
1	B	257	GLU
1	B	289	ILE
1	B	424	SER
1	C	243	GLU
1	C	257	GLU
1	C	289	ILE
1	C	294	LEU
1	C	368	HIS
1	C	424	SER
1	D	148	GLN
1	D	243	GLU
1	D	257	GLU

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Mol	Chain	Res	Type
1	D	289	ILE
1	D	424	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	148	GLN
1	A	160	GLN
1	A	164	GLN
1	B	148	GLN
1	B	178	GLN
1	B	265	ASN
1	C	158	GLN
1	C	160	GLN
1	C	178	GLN
1	C	265	ASN
1	D	148	GLN
1	D	178	GLN
1	D	265	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

9 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	SFG	A	501	-	23,29,29	0.86	1 (4%)	20,42,42	2.47	7 (35%)
3	GOL	A	502	-	5,5,5	0.27	0	5,5,5	0.29	0
2	SFG	B	501	-	23,29,29	1.03	2 (8%)	20,42,42	2.11	5 (25%)
3	GOL	B	502	-	5,5,5	0.43	0	5,5,5	0.95	0
3	GOL	B	503	-	5,5,5	0.30	0	5,5,5	0.19	0
2	SFG	C	501	-	23,29,29	1.00	2 (8%)	20,42,42	2.22	3 (15%)
3	GOL	C	502	-	5,5,5	0.26	0	5,5,5	0.23	0
2	SFG	D	501	-	23,29,29	1.10	2 (8%)	20,42,42	2.43	6 (30%)
3	GOL	D	502	-	5,5,5	0.20	0	5,5,5	0.30	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
2	SFG	A	501	-	-	0/9/33/33	0/3/3/3
3	GOL	A	502	-	-	0/4/4/4	0/0/0/0
2	SFG	B	501	-	-	0/9/33/33	0/3/3/3
3	GOL	B	502	-	-	0/4/4/4	0/0/0/0
3	GOL	B	503	-	-	0/4/4/4	0/0/0/0
2	SFG	C	501	-	-	0/9/33/33	0/3/3/3
3	GOL	C	502	-	-	0/4/4/4	0/0/0/0
2	SFG	D	501	-	-	0/9/33/33	0/3/3/3
3	GOL	D	502	-	-	0/4/4/4	0/0/0/0

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	501	SFG	CD-NE	-2.62	1.39	1.47
2	B	501	SFG	CD-NE	-2.22	1.40	1.47
2	A	501	SFG	C5-C4	2.06	1.45	1.40
2	B	501	SFG	C5-C4	2.12	1.45	1.40
2	C	501	SFG	C2-N3	2.21	1.36	1.32
2	C	501	SFG	C5-C4	2.64	1.46	1.40
2	D	501	SFG	C5-C4	2.88	1.47	1.40

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
2	A	501	SFG	N3-C2-N1	-8.55	122.15	128.87
2	D	501	SFG	N3-C2-N1	-8.51	122.18	128.87
2	C	501	SFG	N3-C2-N1	-8.13	122.49	128.87
2	B	501	SFG	N3-C2-N1	-7.46	123.01	128.87
2	D	501	SFG	C1'-N9-C4	-3.46	122.94	126.81
2	A	501	SFG	C5'-CD-NE	-2.73	101.33	108.96
2	A	501	SFG	C1'-N9-C4	-2.53	123.99	126.81
2	B	501	SFG	C1'-N9-C4	-2.49	124.02	126.81
2	A	501	SFG	CG-CD-NE	-2.31	102.49	108.92
2	D	501	SFG	C5'-CD-NE	-2.22	102.75	108.96
2	B	501	SFG	C5'-CD-NE	-2.15	102.95	108.96
2	A	501	SFG	C5'-CD-CG	2.05	116.64	110.43
2	D	501	SFG	C5'-CD-CG	2.11	116.84	110.43
2	C	501	SFG	C2-N1-C6	2.18	122.66	118.77
2	D	501	SFG	C2-N1-C6	2.29	122.85	118.77
2	B	501	SFG	C2-N1-C6	2.31	122.89	118.77
2	D	501	SFG	N6-C6-N1	2.34	122.44	118.52
2	A	501	SFG	C2-N1-C6	2.38	123.02	118.77
2	A	501	SFG	N6-C6-N1	2.61	122.89	118.52
2	B	501	SFG	N6-C6-N1	2.72	123.08	118.52
2	C	501	SFG	N6-C6-N1	3.36	124.15	118.52

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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	344/349 (98%)	0.22	6 (1%) 73 81	18, 29, 44, 74	0
1	B	344/349 (98%)	0.01	5 (1%) 76 84	15, 25, 40, 74	0
1	C	343/349 (98%)	0.26	13 (3%) 44 56	26, 35, 52, 88	0
1	D	344/349 (98%)	0.28	12 (3%) 48 58	25, 36, 54, 90	0
All	All	1375/1396 (98%)	0.19	36 (2%) 59 69	15, 32, 49, 90	0

All (36) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	477	THR	6.7
1	D	134	ARG	6.4
1	C	134	ARG	6.3
1	D	476[A]	TYR	5.1
1	D	477	THR	4.4
1	A	134	ARG	4.0
1	C	136	VAL	4.0
1	B	134	ARG	3.4
1	C	476	TYR	3.4
1	C	147	VAL	3.4
1	C	139	GLU	3.3
1	A	476	TYR	3.3
1	C	137	PHE	3.3
1	B	477	THR	3.1
1	D	233	ASP	3.0
1	D	248	PRO	2.9
1	C	135	SER	2.9
1	D	346	ARG	2.9
1	B	476[A]	TYR	2.9
1	C	247	LEU	2.8
1	A	143[A]	GLU	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	314	TYR	2.6
1	D	139	GLU	2.6
1	C	138	SER	2.6
1	C	424	SER	2.5
1	C	346	ARG	2.5
1	B	427[A]	PHE	2.4
1	D	135	SER	2.4
1	C	327	ARG	2.4
1	D	185	ASP	2.3
1	A	471[A]	ASN	2.2
1	D	460	GLY	2.1
1	C	143	GLU	2.1
1	D	461	SER	2.1
1	D	208	ARG	2.0
1	B	414[A]	HIS	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
3	GOL	B	502	6/6	0.89	0.26	4.91	48,48,53,62	0
2	SFG	D	501	27/27	0.93	0.12	0.39	26,30,33,34	0
2	SFG	B	501	27/27	0.97	0.10	0.33	15,19,23,27	0
2	SFG	A	501	27/27	0.94	0.10	-0.25	18,20,25,28	0
2	SFG	C	501	27/27	0.93	0.10	-0.43	29,31,32,33	0
3	GOL	C	502	6/6	0.85	0.12	-	47,54,56,58	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
3	GOL	D	502	6/6	0.83	0.32	-	59,62,65,66	0
3	GOL	A	502	6/6	0.90	0.11	-	47,48,49,49	0
3	GOL	B	503	6/6	0.89	0.12	-	47,49,51,52	0

6.5 Other polymers [i](#)

There are no such residues in this entry.