



Full wwPDB X-ray Structure Validation Report ⓘ

May 17, 2020 – 01:32 am BST

PDB ID : 5F39
Title : Crystal structure of human KDM4A in complex with compound 37
Authors : Le Bihan, Y.-V.; Dempster, S.; Westwood, I.M.; van Montfort, R.L.M.
Deposited on : 2015-12-02
Resolution : 2.65 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 : 2.11
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) : 2.11

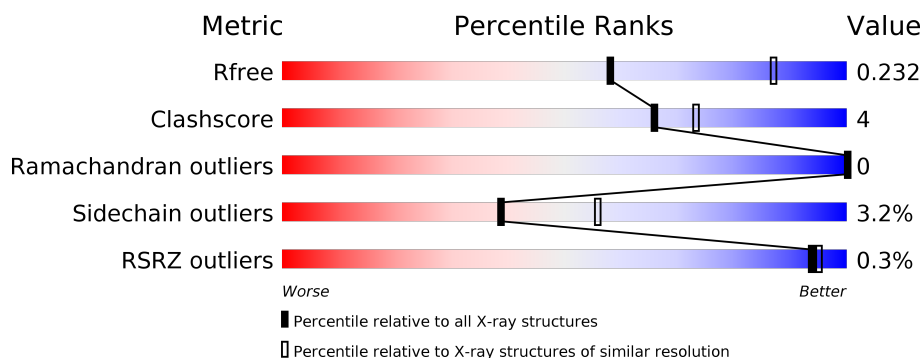
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.65 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	1332 (2.68-2.64)
Clashscore	141614	1374 (2.68-2.64)
Ramachandran outliers	138981	1349 (2.68-2.64)
Sidechain outliers	138945	1349 (2.68-2.64)
RSRZ outliers	127900	1318 (2.68-2.64)

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 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	360	
1	B	360	
1	C	360	
1	D	360	

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 11319 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 Lysine-specific demethylase 4A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	343	Total	C	N	O	S	0	0	0
			2694	1754	432	493	15			
1	B	344	Total	C	N	O	S	0	1	0
			2716	1764	446	491	15			
1	C	348	Total	C	N	O	S	0	0	0
			2730	1781	439	495	15			
1	D	344	Total	C	N	O	S	0	1	0
			2726	1771	452	489	14			

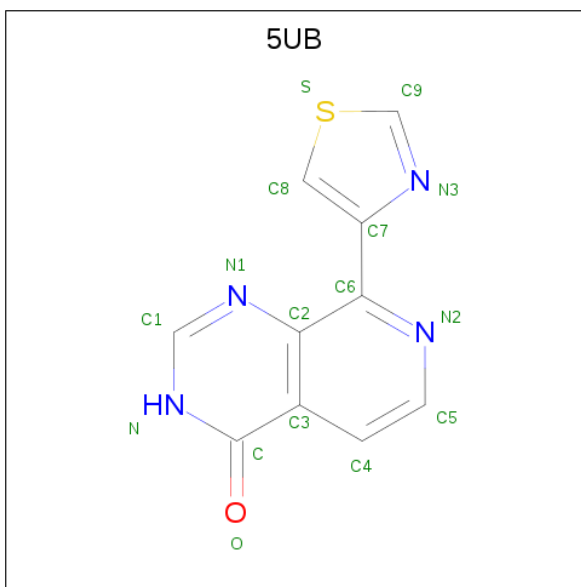
There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	SER	-	expression tag	UNP O75164
B	0	SER	-	expression tag	UNP O75164
C	0	SER	-	expression tag	UNP O75164
D	0	SER	-	expression tag	UNP O75164

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

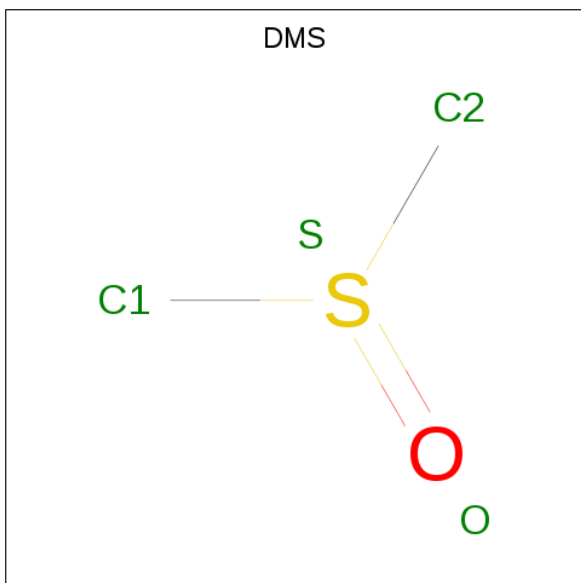
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	2	Total	Zn	0	0
			2	2		
2	A	2	Total	Zn	0	0
			2	2		
2	D	2	Total	Zn	0	0
			2	2		
2	C	2	Total	Zn	0	0
			2	2		

- Molecule 3 is 8-(1,3-thiazol-4-yl)-3 {H}-pyrido[3,4-d]pyrimidin-4-one (three-letter code: 5UB) (formula: C₁₀H₆N₄OS).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	S	0	0
			16	10	4	1	1		
3	B	1	Total	C	N	O	S	0	0
			16	10	4	1	1		
3	C	1	Total	C	N	O	S	0	0
			16	10	4	1	1		
3	D	1	Total	C	N	O	S	0	0
			16	10	4	1	1		

- Molecule 4 is DIMETHYL SULFOXIDE (three-letter code: DMS) (formula: C_2H_6OS).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O S 4 2 1 1	0	0
4	A	1	Total C O S 4 2 1 1	0	0
4	A	1	Total C O S 4 2 1 1	0	0
4	A	1	Total C O S 4 2 1 1	0	0
4	B	1	Total C O S 4 2 1 1	0	0
4	B	1	Total C O S 4 2 1 1	0	0
4	C	1	Total C O S 4 2 1 1	0	0
4	C	1	Total C O S 4 2 1 1	0	0
4	C	1	Total C O S 4 2 1 1	0	0
4	C	1	Total C O S 4 2 1 1	0	0
4	C	1	Total C O S 4 2 1 1	0	0
4	D	1	Total C O S 4 2 1 1	0	0
4	D	1	Total C O S 4 2 1 1	0	0
4	D	1	Total C O S 4 2 1 1	0	0

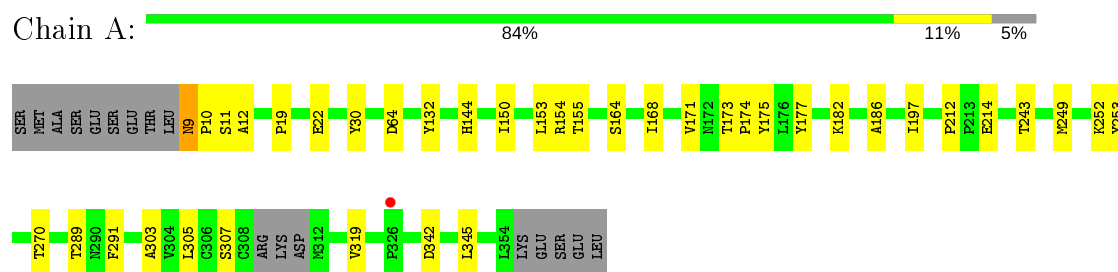
- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	82	Total O 82 82	0	0
5	B	84	Total O 84 84	0	0
5	C	80	Total O 80 80	0	0
5	D	79	Total O 79 79	0	0

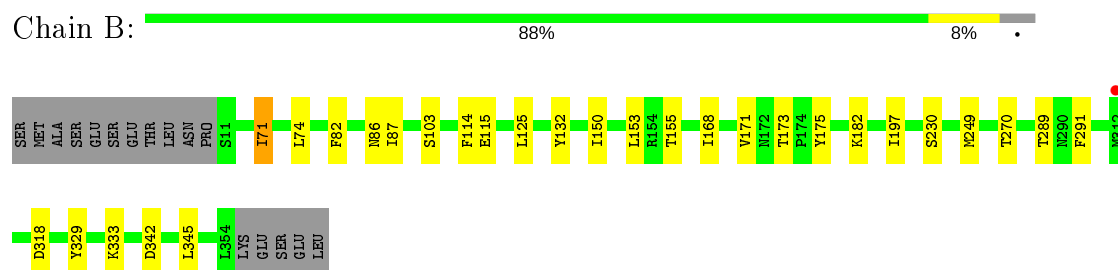
3 Residue-property plots

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.

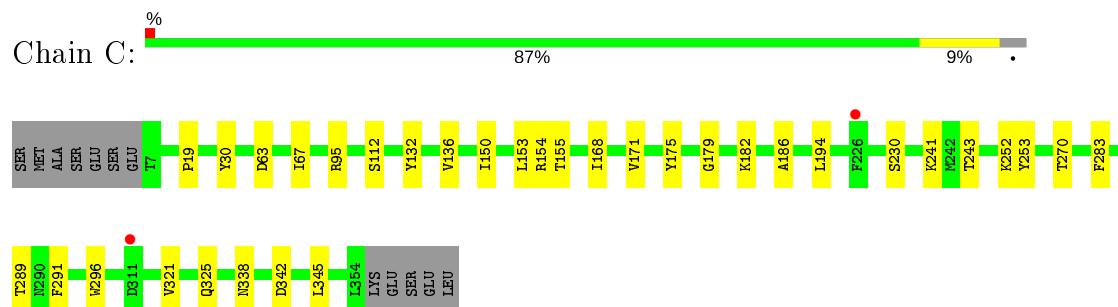
• Molecule 1: Lysine-specific demethylase 4A



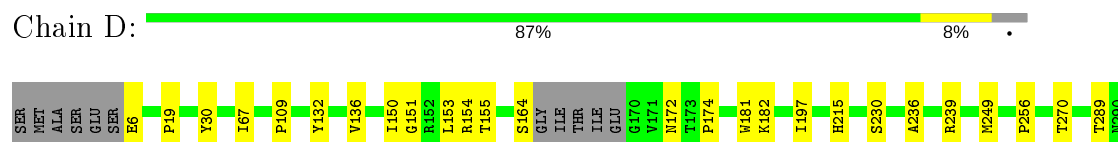
• Molecule 1: Lysine-specific demethylase 4A



• Molecule 1: Lysine-specific demethylase 4A



• Molecule 1: Lysine-specific demethylase 4A



F291					
E327					
D342					
L345					
L354					
LYS					
GLU					
SER					
GLU					
LEU					

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	58.41 Å 102.06 Å 143.47 Å 90.00° 99.82° 90.00°	Depositor
Resolution (Å)	49.63 – 2.65 49.63 – 2.65	Depositor EDS
% Data completeness (in resolution range)	96.3 (49.63-2.65) 96.3 (49.63-2.65)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.09 (at 2.65 Å)	Xtriage
Refinement program	BUSTER 2.10.2	Depositor
R, R_{free}	0.169 , 0.210 0.185 , 0.232	Depositor DCC
R_{free} test set	2353 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	66.2	Xtriage
Anisotropy	0.226	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 53.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.028 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	11319	wwPDB-VP
Average B, all atoms (Å ²)	73.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 19.55% 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: ZN, DMS, 5UB

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	0.50	0/2780	0.69	0/3787
1	B	0.51	0/2802	0.69	0/3818
1	C	0.52	0/2816	0.70	0/3835
1	D	0.54	0/2812	0.70	0/3828
All	All	0.52	0/11210	0.69	0/15268

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	2694	0	2454	27	0
1	B	2716	0	2485	14	0
1	C	2730	0	2513	20	0
1	D	2726	0	2506	14	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
2	C	2	0	0	0	0
2	D	2	0	0	0	0
3	A	16	0	6	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	16	0	6	2	0
3	C	16	0	6	3	0
3	D	16	0	6	2	0
4	A	16	0	24	0	0
4	B	8	0	12	1	0
4	C	20	0	30	1	0
4	D	12	0	18	0	0
5	A	82	0	0	3	0
5	B	84	0	0	1	0
5	C	80	0	0	1	0
5	D	79	0	0	0	0
All	All	11319	0	10066	84	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 (84) 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:9:ASN:HB2	1:A:12:ALA:HB3	1.40	1.00
1:B:74:LEU:HD11	1:B:87:ILE:HD11	1.48	0.95
1:B:74:LEU:HD11	1:B:87:ILE:CD1	2.03	0.88
1:C:19:PRO:HB3	1:C:30:TYR:CE2	2.24	0.73
1:C:150:ILE:HG23	1:C:289:THR:HG22	1.73	0.71
1:A:305:LEU:HD22	1:A:305:LEU:N	2.07	0.70
1:A:12:ALA:HB1	1:A:212:PRO:HG3	1.75	0.68
1:B:150:ILE:HG23	1:B:289:THR:HG22	1.77	0.67
1:A:9:ASN:HD22	1:A:9:ASN:N	1.97	0.61
1:A:150:ILE:HG22	1:A:174:PRO:HB3	1.82	0.61
1:D:150:ILE:HG23	1:D:289:THR:HG22	1.81	0.61
1:C:153:LEU:O	1:C:154:ARG:HB2	2.03	0.58
1:D:327:GLU:OE1	1:D:327:GLU:N	2.26	0.57
1:D:67:ILE:HG23	1:D:136:VAL:CG2	2.36	0.56
3:B:403:5UB:N1	3:B:403:5UB:H6	2.22	0.55
3:A:403:5UB:N1	3:A:403:5UB:H6	2.23	0.54
1:C:63:ASP:HB3	1:C:95:ARG:NH1	2.23	0.54
3:D:403:5UB:N1	3:D:403:5UB:H6	2.24	0.53
1:A:19:PRO:HB3	1:A:30:TYR:CE1	2.44	0.53
1:C:241:LYS:HE2	3:C:403:5UB:S	2.50	0.52
1:B:153:LEU:HD11	1:B:197:ILE:HG21	1.92	0.51
3:C:403:5UB:H6	3:C:403:5UB:N1	2.25	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:19:PRO:HB3	1:D:30:TYR:CE1	2.45	0.51
1:C:186:ALA:HB1	1:C:243:THR:O	2.11	0.51
1:C:150:ILE:HG23	1:C:289:THR:CG2	2.41	0.51
1:A:12:ALA:HB1	1:A:212:PRO:CG	2.40	0.50
1:B:74:LEU:HD11	1:B:87:ILE:HD12	1.93	0.50
1:B:150:ILE:HG23	1:B:289:THR:CG2	2.42	0.49
1:D:150:ILE:HG23	1:D:289:THR:CG2	2.42	0.49
1:A:153:LEU:O	1:A:154:ARG:HB2	2.13	0.49
1:B:74:LEU:CD1	1:B:87:ILE:HD11	2.33	0.49
1:A:144:HIS:HB3	5:A:576:HOH:O	2.12	0.49
1:A:186:ALA:HB1	1:A:243:THR:O	2.12	0.48
1:C:175:TYR:HB2	4:C:405:DMS:C1	2.43	0.48
1:A:305:LEU:N	1:A:305:LEU:CD2	2.75	0.48
1:A:9:ASN:ND2	1:A:9:ASN:N	2.60	0.48
1:C:67:ILE:HG23	1:C:136:VAL:CG2	2.43	0.48
1:A:177:TYR:CE2	3:A:403:5UB:H3	2.48	0.48
1:A:303:ALA:O	1:A:305:LEU:HD22	2.13	0.48
1:C:155:THR:HG21	1:C:291:PHE:HB2	1.96	0.48
1:C:179:GLY:O	1:C:283:PHE:HA	2.13	0.48
1:D:150:ILE:HG22	1:D:174:PRO:HB3	1.96	0.48
1:A:214:GLU:HG3	5:A:507:HOH:O	2.14	0.47
1:B:155:THR:HG21	1:B:291:PHE:HB2	1.97	0.47
1:A:155:THR:HG21	1:A:291:PHE:HB2	1.96	0.47
1:C:321:VAL:O	1:C:325:GLN:C	2.53	0.47
1:D:151:GLY:HA2	1:D:174:PRO:HG3	1.96	0.47
1:D:342:ASP:HB3	1:D:345:LEU:HD12	1.96	0.46
3:D:403:5UB:N1	3:D:403:5UB:C8	2.79	0.46
1:A:64:ASP:HB2	5:A:528:HOH:O	2.16	0.45
1:A:153:LEU:HD11	1:A:197:ILE:HG21	1.97	0.45
3:B:403:5UB:N1	3:B:403:5UB:C8	2.77	0.45
3:A:403:5UB:N1	3:A:403:5UB:C8	2.79	0.45
4:B:405:DMS:H23	5:B:510:HOH:O	2.17	0.44
1:A:303:ALA:O	1:A:305:LEU:CD2	2.65	0.44
1:D:215:HIS:CD2	1:D:256:PRO:HG2	2.53	0.44
1:B:71:ILE:CG2	1:B:86:ASN:HB3	2.48	0.44
1:C:342:ASP:HB3	1:C:345:LEU:HD12	1.99	0.44
1:A:177:TYR:CE2	3:A:403:5UB:C1	3.01	0.44
1:B:342:ASP:HB3	1:B:345:LEU:HD12	2.01	0.43
1:C:168:ILE:HB	1:C:171:VAL:HB	2.00	0.43
1:A:150:ILE:HG23	1:A:289:THR:HG22	1.99	0.43
1:B:82:PHE:CZ	1:B:125:LEU:HD21	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:114:PHE:O	1:B:115:GLU:C	2.54	0.43
3:C:403:5UB:N1	3:C:403:5UB:C8	2.80	0.43
1:D:236:ALA:HB1	1:D:239:ARG:HG3	2.00	0.42
1:B:168:ILE:HB	1:B:171:VAL:HB	2.02	0.42
1:A:10:PRO:HG2	1:A:11:SER:H	1.84	0.42
1:A:168:ILE:HB	1:A:171:VAL:HB	2.01	0.42
1:A:342:ASP:HB3	1:A:345:LEU:HD12	2.01	0.42
1:C:19:PRO:HB3	1:C:30:TYR:CZ	2.55	0.42
1:C:252:LYS:HG2	1:C:253:TYR:CE1	2.54	0.41
1:D:153:LEU:O	1:D:154:ARG:HB2	2.20	0.41
1:C:153:LEU:HA	1:C:153:LEU:HD23	1.83	0.41
1:B:329:TYR:CZ	1:B:333:LYS:HD3	2.55	0.41
1:D:153:LEU:HD11	1:D:197:ILE:HG21	2.03	0.41
1:C:112:SER:HB3	5:C:577:HOH:O	2.21	0.41
1:D:155:THR:HG21	1:D:291:PHE:HB2	2.02	0.41
1:A:10:PRO:CG	1:A:11:SER:N	2.84	0.40
1:A:10:PRO:HG2	1:A:11:SER:N	2.36	0.40
1:D:109:PRO:HD3	1:D:181:TRP:CE2	2.57	0.40
1:A:252:LYS:HG2	1:A:253:TYR:CE1	2.57	0.40
1:C:194:LEU:HA	1:C:296:TRP:CD1	2.57	0.40
1:C:321:VAL:O	1:C:325:GLN:O	2.39	0.40

There are no symmetry-related clashes.

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	339/360 (94%)	333 (98%)	6 (2%)	0	100	100
1	B	343/360 (95%)	336 (98%)	7 (2%)	0	100	100
1	C	346/360 (96%)	338 (98%)	8 (2%)	0	100	100
1	D	341/360 (95%)	335 (98%)	6 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	1369/1440 (95%)	1342 (98%)	27 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	261/316 (83%)	250 (96%)	11 (4%)	30	45
1	B	262/316 (83%)	252 (96%)	10 (4%)	33	49
1	C	267/316 (84%)	262 (98%)	5 (2%)	57	74
1	D	264/316 (84%)	255 (97%)	9 (3%)	37	53
All	All	1054/1264 (83%)	1019 (97%)	35 (3%)	39	54

All (35) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	9	ASN
1	A	22	GLU
1	A	132	TYR
1	A	164	SER
1	A	173	THR
1	A	175	TYR
1	A	182	LYS
1	A	249	MET
1	A	270	THR
1	A	307	SER
1	A	319	VAL
1	B	71	ILE
1	B	103	SER
1	B	132	TYR
1	B	173	THR
1	B	175	TYR
1	B	182	LYS

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Mol	Chain	Res	Type
1	B	230	SER
1	B	249	MET
1	B	270	THR
1	B	318	ASP
1	C	132	TYR
1	C	182	LYS
1	C	230	SER
1	C	270	THR
1	C	338	ASN
1	D	6	GLU
1	D	132	TYR
1	D	164	SER
1	D	172[A]	ASN
1	D	172[B]	ASN
1	D	182	LYS
1	D	230	SER
1	D	249	MET
1	D	270	THR

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

Mol	Chain	Res	Type
1	D	215	HIS

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](#)

Of 26 ligands modelled in this entry, 8 are monoatomic - leaving 18 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	5UB	A	403	2	13,18,18	1.31	1 (7%)	14,25,25	1.95	4 (28%)
4	DMS	D	405	-	3,3,3	0.37	0	3,3,3	0.75	0
4	DMS	D	406	-	3,3,3	0.29	0	3,3,3	0.54	0
4	DMS	A	404	-	3,3,3	0.20	0	3,3,3	0.39	0
4	DMS	C	407	-	3,3,3	0.27	0	3,3,3	0.18	0
4	DMS	A	407	-	3,3,3	0.35	0	3,3,3	0.20	0
3	5UB	B	403	2	13,18,18	1.30	1 (7%)	14,25,25	2.00	5 (35%)
4	DMS	A	406	-	3,3,3	0.28	0	3,3,3	0.44	0
4	DMS	B	404	-	3,3,3	0.19	0	3,3,3	0.48	0
4	DMS	D	404	-	3,3,3	0.40	0	3,3,3	0.45	0
3	5UB	D	403	2	13,18,18	1.30	1 (7%)	14,25,25	1.95	4 (28%)
4	DMS	C	406	-	3,3,3	0.34	0	3,3,3	0.32	0
4	DMS	A	405	-	3,3,3	0.25	0	3,3,3	0.44	0
4	DMS	B	405	-	3,3,3	0.28	0	3,3,3	0.71	0
4	DMS	C	405	-	3,3,3	0.31	0	3,3,3	0.76	0
4	DMS	C	408	-	3,3,3	0.34	0	3,3,3	0.28	0
3	5UB	C	403	2	13,18,18	1.34	1 (7%)	14,25,25	1.93	4 (28%)
4	DMS	C	404	-	3,3,3	0.18	0	3,3,3	0.41	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	5UB	A	403	2	-	0/1/4/4	0/3/3/3
3	5UB	D	403	2	-	0/1/4/4	0/3/3/3
3	5UB	B	403	2	-	0/1/4/4	0/3/3/3
3	5UB	C	403	2	-	0/1/4/4	0/3/3/3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	403	5UB	C6-C7	-3.12	1.47	1.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	403	5UB	C6-C7	-3.09	1.47	1.50
3	C	403	5UB	C6-C7	-3.09	1.47	1.50
3	B	403	5UB	C6-C7	-3.00	1.47	1.50

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	403	5UB	C1-N-C	4.17	122.87	115.88
3	B	403	5UB	C1-N-C	4.17	122.86	115.88
3	D	403	5UB	C1-N-C	4.15	122.83	115.88
3	C	403	5UB	C1-N-C	4.15	122.82	115.88
3	B	403	5UB	C5-C4-C3	-3.53	116.72	119.77
3	A	403	5UB	C5-C4-C3	-3.50	116.75	119.77
3	D	403	5UB	C5-C4-C3	-3.45	116.79	119.77
3	C	403	5UB	C5-C4-C3	-3.40	116.84	119.77
3	B	403	5UB	C4-C3-C2	2.51	120.29	118.14
3	A	403	5UB	C4-C3-C2	2.39	120.19	118.14
3	D	403	5UB	C4-C3-C2	2.38	120.18	118.14
3	C	403	5UB	C4-C3-C2	2.35	120.15	118.14
3	C	403	5UB	N1-C1-N	-2.29	125.10	128.68
3	B	403	5UB	N1-C1-N	-2.24	125.18	128.68
3	A	403	5UB	N1-C1-N	-2.23	125.19	128.68
3	D	403	5UB	N1-C1-N	-2.21	125.22	128.68
3	B	403	5UB	C5-N2-C6	2.05	119.47	117.99

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

6 monomers are involved in 13 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	403	5UB	4	0
3	B	403	5UB	2	0
3	D	403	5UB	2	0
4	B	405	DMS	1	0
4	C	405	DMS	1	0
3	C	403	5UB	3	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 [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	343/360 (95%)	-0.29	1 (0%) 94 95	48, 72, 112, 140	0
1	B	344/360 (95%)	-0.44	1 (0%) 94 95	48, 72, 112, 133	0
1	C	348/360 (96%)	-0.42	2 (0%) 89 89	46, 70, 111, 130	0
1	D	344/360 (95%)	-0.41	0 100 100	48, 67, 100, 123	0
All	All	1379/1440 (95%)	-0.39	4 (0%) 94 95	46, 71, 110, 140	0

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	226	PHE	2.9
1	B	312	MET	2.3
1	A	326	PRO	2.1
1	C	311	ASP	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 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. 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(\AA^2)	Q<0.9
4	DMS	C	406	4/4	0.82	0.32	121,122,123,123	0
4	DMS	C	407	4/4	0.89	0.18	96,97,97,97	4
4	DMS	D	406	4/4	0.89	0.24	99,103,104,104	0
4	DMS	A	407	4/4	0.90	0.25	90,91,91,92	4
4	DMS	A	406	4/4	0.91	0.22	93,96,96,97	4
4	DMS	C	408	4/4	0.92	0.41	81,83,84,85	4
4	DMS	B	405	4/4	0.94	0.24	82,83,84,85	4
4	DMS	A	404	4/4	0.96	0.22	75,75,78,78	4
3	5UB	A	403	16/16	0.96	0.17	53,58,74,76	16
4	DMS	D	404	4/4	0.96	0.15	83,85,85,87	4
4	DMS	C	405	4/4	0.97	0.20	88,88,89,91	4
3	5UB	D	403	16/16	0.97	0.18	36,42,68,70	16
3	5UB	C	403	16/16	0.97	0.16	35,41,63,63	16
3	5UB	B	403	16/16	0.97	0.14	40,45,67,67	16
4	DMS	D	405	4/4	0.97	0.34	78,78,78,79	4
4	DMS	C	404	4/4	0.98	0.20	85,85,87,87	0
4	DMS	A	405	4/4	0.98	0.34	81,84,86,86	4
2	ZN	D	401	1/1	0.99	0.14	64,64,64,64	0
2	ZN	A	401	1/1	0.99	0.17	64,64,64,64	0
2	ZN	B	402	1/1	0.99	0.10	68,68,68,68	1
2	ZN	A	402	1/1	0.99	0.17	66,66,66,66	1
2	ZN	C	402	1/1	0.99	0.12	75,75,75,75	0
2	ZN	B	401	1/1	0.99	0.15	62,62,62,62	0
2	ZN	C	401	1/1	0.99	0.15	63,63,63,63	0
4	DMS	B	404	4/4	0.99	0.16	76,79,79,82	4
2	ZN	D	402	1/1	1.00	0.15	67,67,67,67	0

6.5 Other polymers ⓘ

There are no such residues in this entry.