



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 3, 2018 – 02:37 PM EST

PDB ID : 5UZ0
Title : Crystal structure of AICARFT bound to an antifolate
Authors : Atwell, S.; Wang, Y.; Fales, K.R.; Clawson, D.; Wang, J.
Deposited on : 2017-02-24
Resolution : 1.79 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-20030736
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-20030736

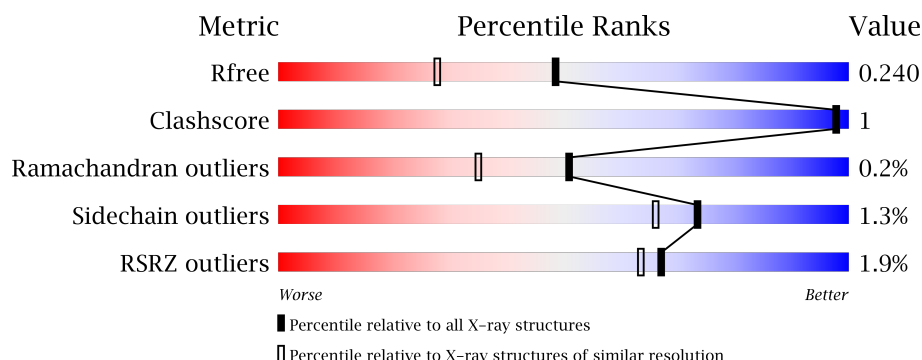
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.79 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	4827 (1.80-1.80)
Clashscore	112137	5742 (1.80-1.80)
Ramachandran outliers	110173	5676 (1.80-1.80)
Sidechain outliers	110143	5675 (1.80-1.80)
RSRZ outliers	101464	4906 (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 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	601	<div> <div>0.2%</div> <div>95%</div> <div>0.2%</div> </div>
1	B	601	<div> <div>2%</div> <div>95%</div> <div>0.2%</div> </div>
1	C	601	<div> <div>0.2%</div> <div>95%</div> <div>0.2%</div> </div>
1	D	601	<div> <div>2%</div> <div>94%</div> <div>0.2%</div> </div>

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 18813 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 Bifunctional purine biosynthesis protein PURH.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	589	Total	C	N	O	S	0	1	0
			4503	2849	782	853	19			
1	B	589	Total	C	N	O	S	0	2	0
			4495	2844	782	850	19			
1	C	589	Total	C	N	O	S	0	1	0
			4484	2840	782	843	19			
1	D	588	Total	C	N	O	S	0	1	0
			4469	2831	781	838	19			

There are 40 discrepancies between the modelled and reference sequences:

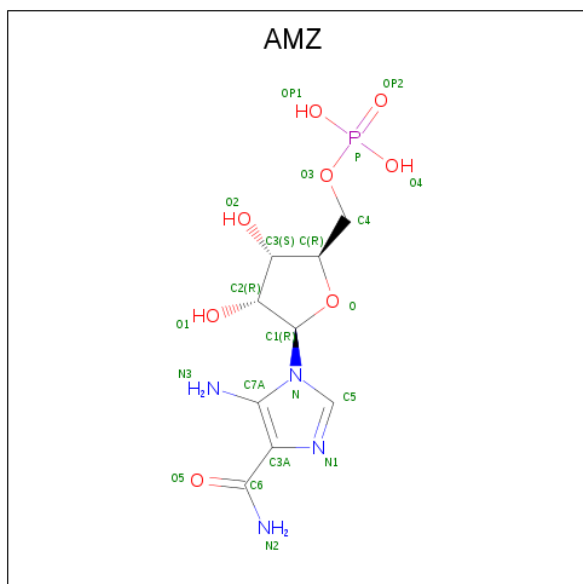
Chain	Residue	Modelled	Actual	Comment	Reference
A	-8	MET	-	expression tag	UNP P31939
A	-7	ALA	-	expression tag	UNP P31939
A	-6	HIS	-	expression tag	UNP P31939
A	-5	HIS	-	expression tag	UNP P31939
A	-4	HIS	-	expression tag	UNP P31939
A	-3	HIS	-	expression tag	UNP P31939
A	-2	HIS	-	expression tag	UNP P31939
A	-1	HIS	-	expression tag	UNP P31939
A	0	SER	-	expression tag	UNP P31939
A	1	LEU	-	expression tag	UNP P31939
B	-8	MET	-	expression tag	UNP P31939
B	-7	ALA	-	expression tag	UNP P31939
B	-6	HIS	-	expression tag	UNP P31939
B	-5	HIS	-	expression tag	UNP P31939
B	-4	HIS	-	expression tag	UNP P31939
B	-3	HIS	-	expression tag	UNP P31939
B	-2	HIS	-	expression tag	UNP P31939
B	-1	HIS	-	expression tag	UNP P31939
B	0	SER	-	expression tag	UNP P31939
B	1	LEU	-	expression tag	UNP P31939
C	-8	MET	-	expression tag	UNP P31939

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-7	ALA	-	expression tag	UNP P31939
C	-6	HIS	-	expression tag	UNP P31939
C	-5	HIS	-	expression tag	UNP P31939
C	-4	HIS	-	expression tag	UNP P31939
C	-3	HIS	-	expression tag	UNP P31939
C	-2	HIS	-	expression tag	UNP P31939
C	-1	HIS	-	expression tag	UNP P31939
C	0	SER	-	expression tag	UNP P31939
C	1	LEU	-	expression tag	UNP P31939
D	-8	MET	-	expression tag	UNP P31939
D	-7	ALA	-	expression tag	UNP P31939
D	-6	HIS	-	expression tag	UNP P31939
D	-5	HIS	-	expression tag	UNP P31939
D	-4	HIS	-	expression tag	UNP P31939
D	-3	HIS	-	expression tag	UNP P31939
D	-2	HIS	-	expression tag	UNP P31939
D	-1	HIS	-	expression tag	UNP P31939
D	0	SER	-	expression tag	UNP P31939
D	1	LEU	-	expression tag	UNP P31939

- Molecule 2 is AMINOIMIDAZOLE 4-CARBOXAMIDE RIBONUCLEOTIDE (three-letter code: AMZ) (formula: C₉H₁₅N₄O₈P).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			22	9	4	8	1		

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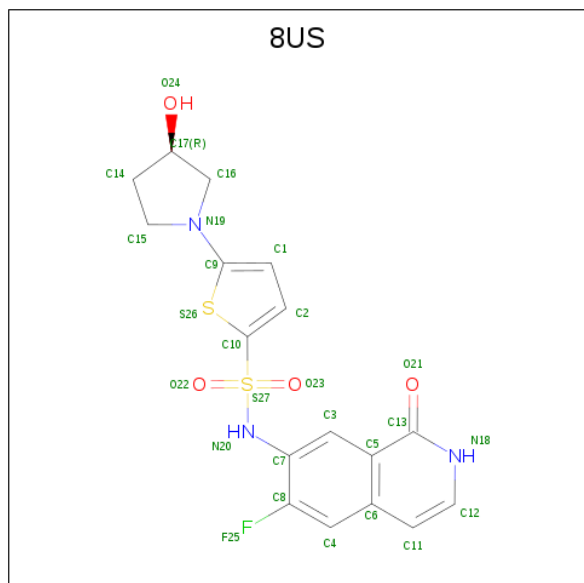
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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			22	9	4	8	1		
2	B	1	Total	C	N	O	P	0	0
			22	9	4	8	1		
2	C	1	Total	C	N	O	P	0	0
			22	9	4	8	1		
2	C	1	Total	C	N	O	P	0	0
			22	9	4	8	1		
2	D	1	Total	C	N	O	P	0	0
			22	9	4	8	1		
2	D	1	Total	C	N	O	P	0	0
			22	9	4	8	1		

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

- Molecule 4 is N-(6-fluoro-1-oxo-1,2-dihydroisoquinolin-7-yl)-5-[(3R)-3-hydroxypyrrolidin-1-yl]thiophene-2-sulfonamide (three-letter code: 8US) (formula: C₁₇H₁₆FN₃O₄S₂).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
4	B	1	Total	C	F	N	O	S	0	0
			27	17	1	3	4	2		
4	B	1	Total	C	F	N	O	S	0	0
			27	17	1	3	4	2		
4	D	1	Total	C	F	N	O	S	0	0
			27	17	1	3	4	2		
4	D	1	Total	C	F	N	O	S	0	0
			27	17	1	3	4	2		

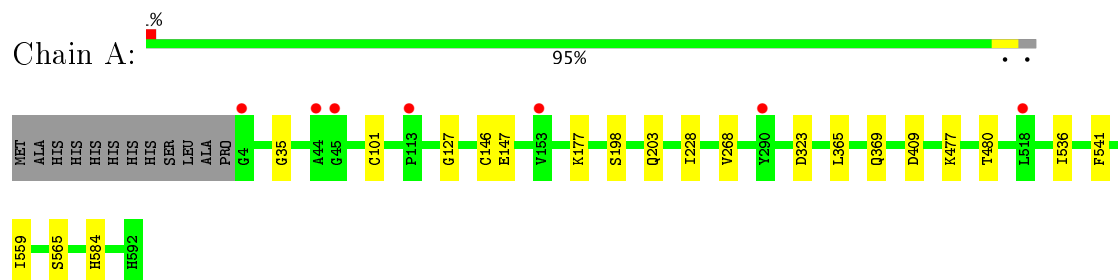
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	156	Total	O	0	0
			156	156		
5	B	144	Total	O	0	0
			144	144		
5	C	154	Total	O	0	0
			154	154		
5	D	142	Total	O	0	0
			142	142		

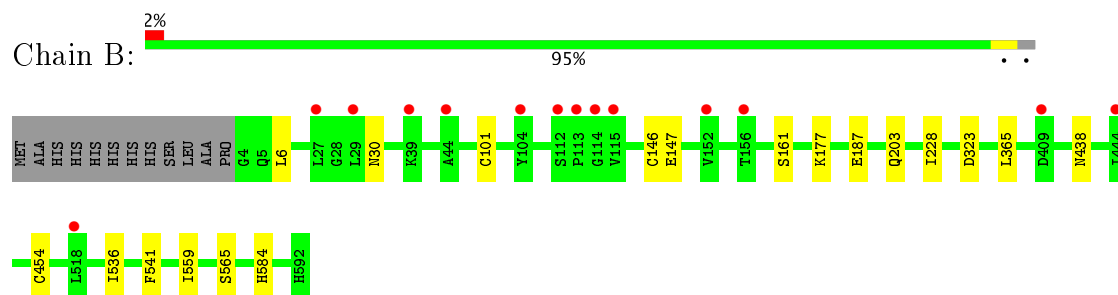
3 Residue-property plots [i](#)

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.

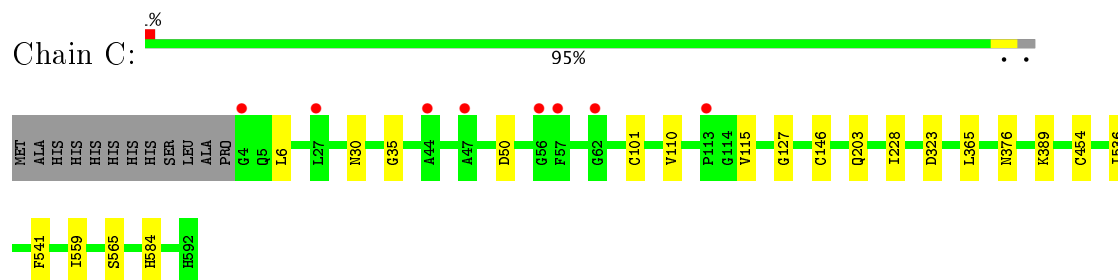
- Molecule 1: Bifunctional purine biosynthesis protein PURH



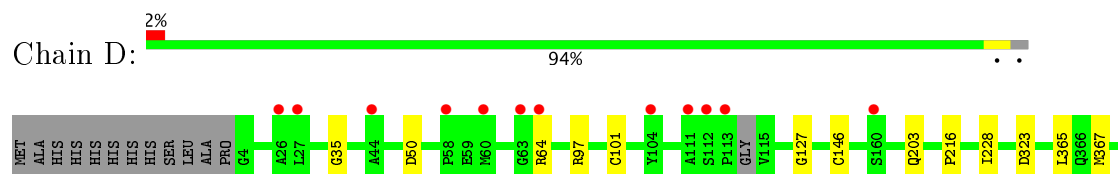
- Molecule 1: Bifunctional purine biosynthesis protein PURH

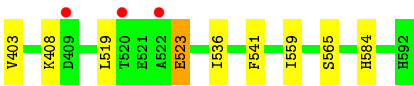


- Molecule 1: Bifunctional purine biosynthesis protein PURH



- Molecule 1: Bifunctional purine biosynthesis protein PURH





4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	61.80Å 105.12Å 105.65Å 113.48° 99.42° 95.52°	Depositor
Resolution (Å)	18.04 – 1.79 42.44 – 1.79	Depositor EDS
% Data completeness (in resolution range)	95.6 (18.04-1.79) 81.5 (42.44-1.79)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.46 (at 1.79Å)	Xtriage
Refinement program	BUSTER 2.11.5	Depositor
R, R_{free}	0.202 , 0.225 0.216 , 0.240	Depositor DCC
R_{free} test set	10759 reflections (5.32%)	DCC
Wilson B-factor (Å ²)	13.2	Xtriage
Anisotropy	0.388	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 39.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.016 for -h,-l,-k	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	18813	wwPDB-VP
Average B, all atoms (Å ²)	17.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.48% 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: MG, AMZ, 8US

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	0/4589	0.60	0/6227
1	B	0.49	0/4585	0.61	0/6224
1	C	0.48	0/4570	0.60	0/6203
1	D	0.49	0/4554	0.61	1/6181 (0.0%)
All	All	0.48	0/18298	0.61	1/24835 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	367	MET	CG-SD-CE	6.00	109.80	100.20

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	4503	0	4519	7	0
1	B	4495	0	4502	7	0
1	C	4484	0	4501	9	0
1	D	4469	0	4480	9	0
2	A	44	0	26	1	0
2	B	22	0	13	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	C	44	0	26	2	0
2	D	44	0	26	1	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
4	B	54	0	0	0	0
4	D	54	0	0	0	0
5	A	156	0	0	0	0
5	B	144	0	0	0	0
5	C	154	0	0	1	0
5	D	142	0	0	0	0
All	All	18813	0	18093	31	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 1.

All (31) 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:D:519:LEU:HD22	1:D:523:GLU:HG3	1.82	0.62
1:D:541:PHE:CD1	1:D:565:SER:HB2	2.37	0.60
1:C:541:PHE:CD1	1:C:565:SER:HB2	2.37	0.59
1:A:541:PHE:CD1	1:A:565:SER:HB2	2.38	0.58
1:B:536:ILE:HG12	1:B:559:ILE:HG12	1.87	0.56
1:C:536:ILE:HG12	1:C:559:ILE:HG12	1.89	0.55
1:A:536:ILE:HG12	1:A:559:ILE:HG12	1.89	0.54
1:D:536:ILE:HG12	1:D:559:ILE:HG12	1.88	0.54
1:B:147:GLU:HG3	1:B:177:LYS:HD3	1.90	0.53
1:D:101:CYS:O	1:D:146:CYS:HA	2.10	0.52
1:D:228:ILE:HD11	1:D:365:LEU:HD13	1.91	0.52
1:A:480:THR:HG21	1:D:97:ARG:HH11	1.76	0.50
1:C:127:GLY:HA3	2:C:602:AMZ:C6	2.41	0.50
1:C:101:CYS:O	1:C:146:CYS:HA	2.11	0.50
1:A:228:ILE:HD11	1:A:365:LEU:HD13	1.95	0.48
1:C:228:ILE:HD11	1:C:365:LEU:HD13	1.96	0.48
1:B:228:ILE:HD11	1:B:365:LEU:HD13	1.95	0.48
1:B:101:CYS:O	1:B:146:CYS:HA	2.14	0.47
1:A:147:GLU:HG3	1:A:177:LYS:HD3	1.96	0.47
1:C:6:LEU:HD23	1:C:30:ASN:HB2	1.96	0.47
1:B:541:PHE:CD1	1:B:565:SER:HB2	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:101:CYS:O	1:A:146:CYS:HA	2.15	0.46
1:D:127:GLY:HA3	2:D:604:AMZ:C6	2.46	0.46
1:A:127:GLY:HA3	2:A:602:AMZ:C6	2.46	0.45
1:C:389:LYS:HE3	1:D:216:PRO:HD2	2.00	0.44
1:C:376:ASN:HB2	5:C:848:HOH:O	2.17	0.43
1:B:541:PHE:CD1	1:B:541:PHE:C	2.93	0.41
2:C:602:AMZ:H9	2:C:602:AMZ:H12	1.67	0.41
1:B:6:LEU:HD23	1:B:30:ASN:HB2	2.03	0.41
1:D:403:VAL:HG11	1:D:408:LYS:HA	2.03	0.41
1:C:110:VAL:HA	1:C:115:VAL:HG11	2.02	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	588/601 (98%)	576 (98%)	10 (2%)	2 (0%)	44	29
1	B	589/601 (98%)	575 (98%)	14 (2%)	0	100	100
1	C	588/601 (98%)	577 (98%)	10 (2%)	1 (0%)	51	35
1	D	585/601 (97%)	571 (98%)	12 (2%)	2 (0%)	44	29
All	All	2350/2404 (98%)	2299 (98%)	46 (2%)	5 (0%)	51	35

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	35	GLY
1	D	35	GLY
1	D	64	ARG
1	A	35	GLY
1	A	268	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	479/496 (97%)	472 (98%)	7 (2%)	70	61
1	B	477/496 (96%)	469 (98%)	8 (2%)	66	55
1	C	474/496 (96%)	469 (99%)	5 (1%)	78	72
1	D	471/496 (95%)	466 (99%)	5 (1%)	78	72
All	All	1901/1984 (96%)	1876 (99%)	25 (1%)	73	66

All (25) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	198	SER
1	A	203	GLN
1	A	323	ASP
1	A	369	GLN
1	A	409	ASP
1	A	477	LYS
1	A	584	HIS
1	B	161	SER
1	B	187	GLU
1	B	203	GLN
1	B	323	ASP
1	B	438[A]	ASN
1	B	438[B]	ASN
1	B	454	CYS
1	B	584	HIS
1	C	50	ASP
1	C	203	GLN
1	C	323	ASP
1	C	454	CYS
1	C	584	HIS
1	D	50	ASP
1	D	203	GLN
1	D	323	ASP
1	D	523	GLU
1	D	584	HIS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	181	HIS
1	A	369	GLN
1	A	431	ASN
1	B	123	GLN
1	B	181	HIS
1	C	181	HIS
1	C	196	GLN

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 15 ligands modelled in this entry, 4 are monoatomic - leaving 11 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	$\# Z > 2$
2	AMZ	A	601	-	19,23,23	0.79	0	21,35,35	0.91	1 (4%)
2	AMZ	A	602	-	19,23,23	0.78	0	21,35,35	1.37	3 (14%)
4	8US	B	601	-	27,30,30	1.59	4 (14%)	29,45,45	1.47	6 (20%)
4	8US	B	602	-	27,30,30	1.63	6 (22%)	29,45,45	1.65	6 (20%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	AMZ	B	603	-	19,23,23	0.81	0	21,35,35	0.98	1 (4%)
2	AMZ	C	601	-	19,23,23	0.80	0	21,35,35	0.97	1 (4%)
2	AMZ	C	602	-	19,23,23	0.80	0	21,35,35	1.48	2 (9%)
4	8US	D	601	-	27,30,30	1.48	4 (14%)	29,45,45	1.49	5 (17%)
4	8US	D	602	-	27,30,30	1.48	5 (18%)	29,45,45	1.68	5 (17%)
2	AMZ	D	603	-	19,23,23	0.79	0	21,35,35	0.91	1 (4%)
2	AMZ	D	604	-	19,23,23	0.86	1 (5%)	21,35,35	1.53	2 (9%)

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	AMZ	A	601	-	-	0/6/30/30	0/2/2/2
2	AMZ	A	602	-	-	0/6/30/30	0/2/2/2
4	8US	B	601	-	-	0/5/24/24	0/4/4/4
4	8US	B	602	-	-	0/5/24/24	0/4/4/4
2	AMZ	B	603	-	-	0/6/30/30	0/2/2/2
2	AMZ	C	601	-	-	0/6/30/30	0/2/2/2
2	AMZ	C	602	-	-	0/6/30/30	0/2/2/2
4	8US	D	601	-	-	0/5/24/24	0/4/4/4
4	8US	D	602	-	-	0/5/24/24	0/4/4/4
2	AMZ	D	603	-	-	0/6/30/30	0/2/2/2
2	AMZ	D	604	-	-	0/6/30/30	0/2/2/2

All (20) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	602	8US	C11-C6	2.01	1.46	1.41
4	D	602	8US	C11-C6	2.03	1.46	1.41
4	D	602	8US	O22-S27	2.06	1.45	1.43
4	D	601	8US	C11-C6	2.19	1.47	1.41
4	B	601	8US	C11-C6	2.42	1.47	1.41
4	B	602	8US	O22-S27	2.43	1.46	1.43
2	D	604	AMZ	C3A-C7A	2.46	1.48	1.44
4	B	602	8US	O23-S27	2.59	1.46	1.43
4	D	602	8US	C4-C8	3.01	1.40	1.35
4	B	601	8US	C4-C8	3.15	1.40	1.35
4	B	602	8US	C4-C8	3.38	1.40	1.35
4	D	601	8US	C4-C8	3.47	1.40	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	602	8US	C13-N18	3.57	1.39	1.33
4	D	601	8US	C13-N18	3.72	1.39	1.33
4	B	602	8US	C13-N18	3.78	1.39	1.33
4	D	601	8US	S27-N20	3.94	1.70	1.63
4	D	602	8US	S27-N20	3.96	1.70	1.63
4	B	602	8US	S27-N20	4.04	1.70	1.63
4	B	601	8US	C13-N18	4.33	1.40	1.33
4	B	601	8US	S27-N20	4.36	1.71	1.63

All (33) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	602	8US	C5-C13-N18	-4.44	114.80	123.48
4	D	601	8US	C5-C13-N18	-4.05	115.55	123.48
4	B	602	8US	O22-S27-C10	-3.94	101.07	107.60
4	B	601	8US	C5-C13-N18	-3.83	115.99	123.48
4	D	602	8US	C8-C7-N20	-3.80	113.40	119.83
4	B	602	8US	C5-C13-N18	-3.68	116.28	123.48
4	B	602	8US	C8-C7-N20	-3.18	114.45	119.83
4	D	602	8US	C4-C8-C7	-2.82	120.64	123.45
4	B	601	8US	C4-C8-C7	-2.74	120.71	123.45
4	B	601	8US	O22-S27-C10	-2.49	103.48	107.60
4	D	601	8US	C4-C8-C7	-2.49	120.97	123.45
4	D	601	8US	C8-C7-N20	-2.47	115.65	119.83
4	B	602	8US	C11-C12-N18	-2.23	121.48	123.80
4	B	601	8US	C8-C7-N20	-2.21	116.10	119.83
2	A	602	AMZ	O2-C3-C	-2.03	105.17	111.09
2	D	603	AMZ	C5-N1-C3A	2.12	107.49	103.35
4	B	602	8US	C3-C5-C6	2.15	121.75	117.74
4	D	601	8US	O22-S27-N20	2.18	112.28	106.74
4	D	602	8US	O22-S27-N20	2.26	112.50	106.74
2	B	603	AMZ	C5-N1-C3A	2.58	108.38	103.35
4	B	601	8US	O22-S27-N20	2.59	113.33	106.74
2	C	601	AMZ	C5-N1-C3A	2.59	108.40	103.35
2	A	601	AMZ	C5-N1-C3A	2.76	108.73	103.35
2	A	602	AMZ	C5-N1-C3A	2.77	108.75	103.35
4	B	601	8US	C12-N18-C13	2.80	122.96	116.60
2	C	602	AMZ	C5-N1-C3A	3.00	109.20	103.35
2	D	604	AMZ	C5-N1-C3A	3.01	109.21	103.35
4	D	601	8US	C12-N18-C13	3.27	124.03	116.60
4	B	602	8US	C12-N18-C13	3.36	124.23	116.60
2	A	602	AMZ	C3A-C6-N2	3.63	121.55	115.75

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	602	8US	C12-N18-C13	3.72	125.05	116.60
2	C	602	AMZ	C3A-C6-N2	4.41	122.79	115.75
2	D	604	AMZ	C3A-C6-N2	4.49	122.92	115.75

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	602	AMZ	1	0
2	C	602	AMZ	2	0
2	D	604	AMZ	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	589/601 (98%)	-0.03	7 (1%) 79 77	6, 15, 31, 42	0
1	B	589/601 (98%)	0.09	14 (2%) 59 55	6, 15, 33, 44	0
1	C	589/601 (98%)	-0.01	8 (1%) 75 72	6, 15, 33, 49	0
1	D	588/601 (97%)	0.05	15 (2%) 56 52	5, 15, 35, 58	0
All	All	2355/2404 (97%)	0.02	44 (1%) 67 63	5, 15, 33, 58	0

All (44) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	113	PRO	6.6
1	D	113	PRO	5.3
1	C	4	GLY	4.8
1	D	112	SER	4.2
1	A	113	PRO	4.1
1	D	63	GLY	4.0
1	D	58	PRO	3.7
1	D	27	LEU	3.6
1	B	104	TYR	3.4
1	B	113	PRO	3.3
1	B	114	GLY	3.3
1	C	62	GLY	3.3
1	B	27	LEU	3.2
1	C	56	GLY	3.2
1	C	47	ALA	3.1
1	B	409	ASP	3.0
1	B	112	SER	3.0
1	A	4	GLY	2.9
1	D	522	ALA	2.8
1	A	518	LEU	2.7
1	C	44	ALA	2.6

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Mol	Chain	Res	Type	RSRZ
1	D	26	ALA	2.6
1	D	104	TYR	2.6
1	D	409	ASP	2.6
1	A	44	ALA	2.5
1	B	152	VAL	2.5
1	A	290	TYR	2.5
1	D	160	SER	2.4
1	B	518	LEU	2.3
1	C	57	PHE	2.3
1	B	29	LEU	2.2
1	D	520	THR	2.2
1	B	44	ALA	2.2
1	B	115	VAL	2.2
1	B	39	LYS	2.1
1	D	64	ARG	2.1
1	A	45	GLY	2.0
1	A	153	VAL	2.0
1	C	27	LEU	2.0
1	B	444	ILE	2.0
1	D	60	MET	2.0
1	D	44	ALA	2.0
1	D	111	ALA	2.0
1	B	156	THR	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
2	AMZ	D	604	22/22	0.90	0.13	-0.08	16,23,29,30	0
2	AMZ	C	602	22/22	0.93	0.10	-0.21	16,19,22,23	0
2	AMZ	A	601	22/22	0.97	0.08	-0.37	7,10,13,14	0
2	AMZ	D	603	22/22	0.98	0.07	-0.84	7,12,16,17	0
2	AMZ	B	603	22/22	0.98	0.07	-0.87	6,10,12,15	0
4	8US	B	601	27/27	0.98	0.09	-0.90	6,10,15,16	0
2	AMZ	A	602	22/22	0.96	0.07	-0.91	11,15,21,22	0
4	8US	D	602	27/27	0.98	0.08	-0.97	7,11,14,14	0
4	8US	D	601	27/27	0.98	0.08	-1.02	4,8,13,15	0
3	MG	B	604	1/1	0.97	0.09	-1.08	16,16,16,16	0
4	8US	B	602	27/27	0.98	0.07	-1.25	4,9,13,15	0
2	AMZ	C	601	22/22	0.97	0.06	-1.42	6,9,12,14	0
3	MG	D	605	1/1	0.99	0.07	-1.80	17,17,17,17	0
3	MG	A	603	1/1	0.99	0.07	-2.39	15,15,15,15	0
3	MG	C	603	1/1	0.99	0.05	-3.49	20,20,20,20	0

6.5 Other polymers [i](#)

There are no such residues in this entry.