



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 14, 2026 – 10:07 AM UTC

PDB ID : 2E2L / pdb_00002e2l
Title : Helicobacter pylori formamidase AmiF contains a fine-tuned cysteine-glutamate-lysine catalytic triad
Authors : Wang, W.C.; Hung, C.L.
Deposited on : 2006-11-14
Resolution : 2.29 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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 : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

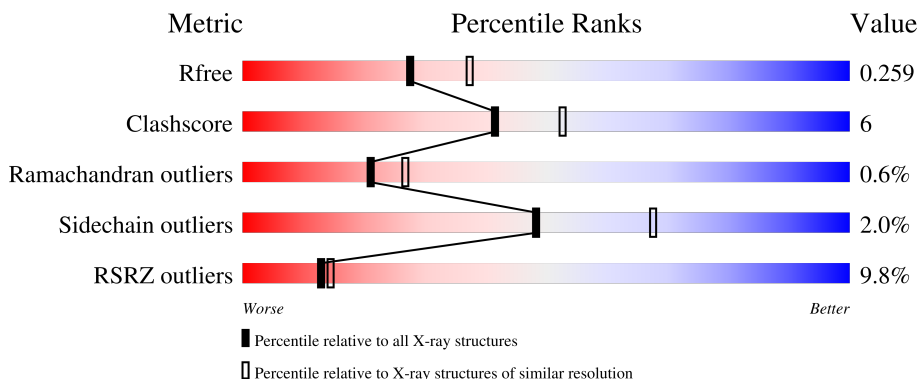
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.29 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.



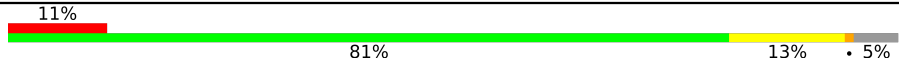
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	6319 (2.30-2.30)
Clashscore	190562	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (2.30-2.30)
RSRZ outliers	180081	6325 (2.30-2.30)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments 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	334	 10% 81% 13% 5%
1	B	334	 8% 80% 15% 5%
1	C	334	 10% 79% 14% • 5%
1	D	334	 7% 83% 11% • 5%
1	E	334	 10% 83% 10% • 5%

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Mol	Chain	Length	Quality of chain
1	F	334	

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 criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	ARF	A	1335	-	-	X	-

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 15751 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.

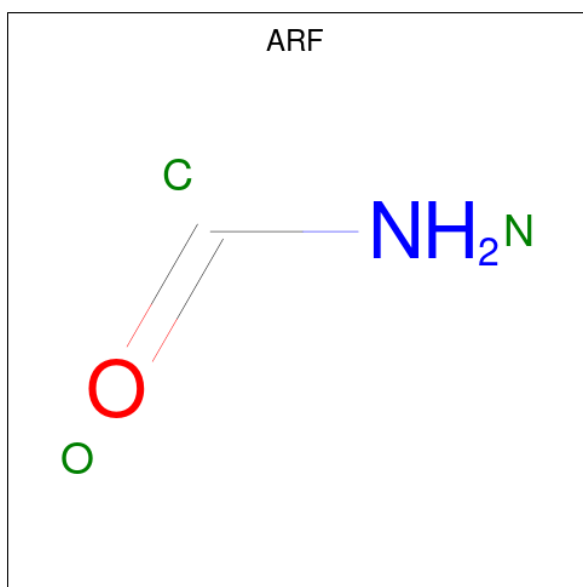
- Molecule 1 is a protein called Formamidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	317	2503	1610	421	461	11	0	0	0
1	B	317	2503	1610	421	461	11	0	0	0
1	C	317	2503	1610	421	461	11	0	0	0
1	D	317	2503	1610	421	461	11	0	0	0
1	E	316	2492	1604	417	460	11	0	0	0
1	F	317	2503	1610	421	461	11	0	0	0

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	166	SER	CYS	engineered mutation	UNP O25836
B	166	SER	CYS	engineered mutation	UNP O25836
C	166	SER	CYS	engineered mutation	UNP O25836
D	166	SER	CYS	engineered mutation	UNP O25836
E	166	SER	CYS	engineered mutation	UNP O25836
F	166	SER	CYS	engineered mutation	UNP O25836

- Molecule 2 is FORMAMIDE (CCD ID: ARF) (formula: CH₃NO).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
2	A	1	3	1	1	1	0	0
2	C	1	3	1	1	1	0	0
2	F	1	3	1	1	1	0	0

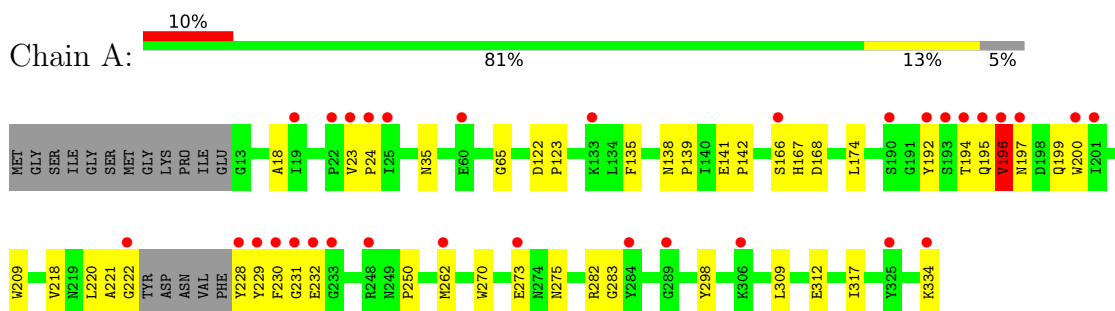
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	A	133	133	133	0	0
3	B	131	131	131	0	0
3	C	143	143	143	0	0
3	D	102	102	102	0	0
3	E	114	114	114	0	0
3	F	112	112	112	0	0

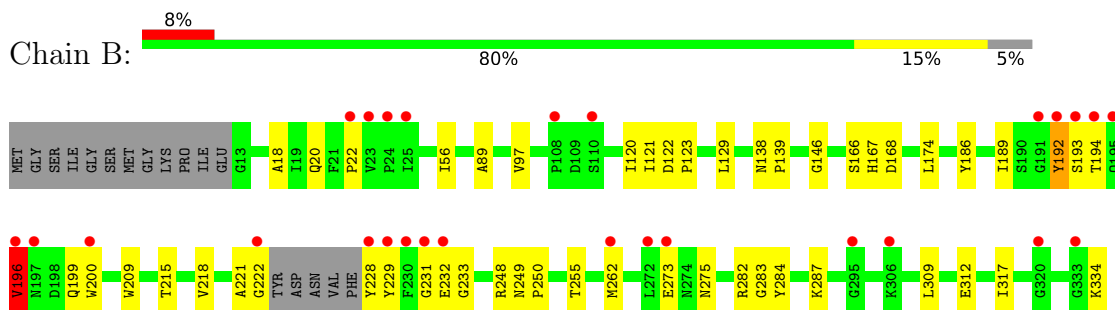
3 Residue-property plots [i](#)

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.

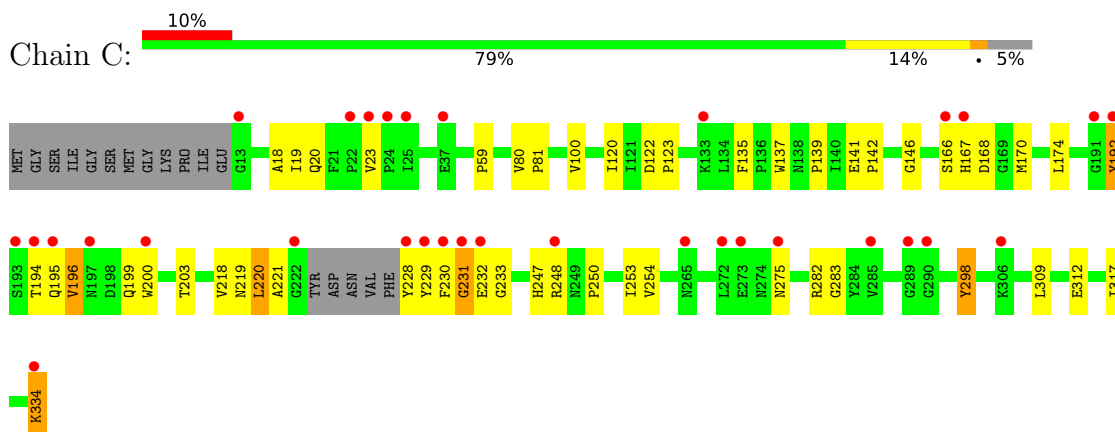
- Molecule 1: Formamidase



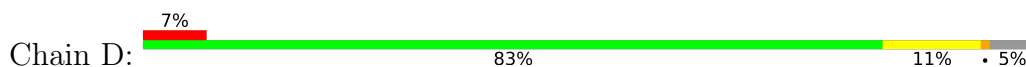
- Molecule 1: Formamidase

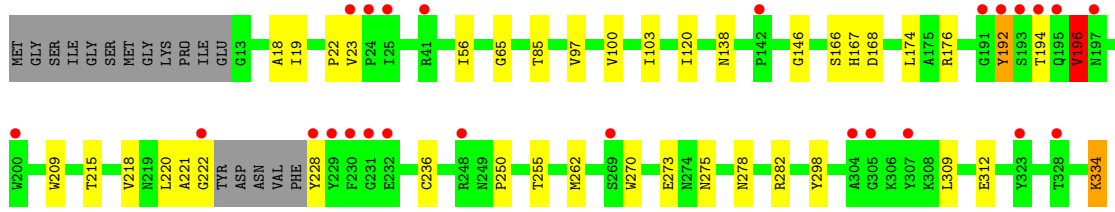


- Molecule 1: Formamidase

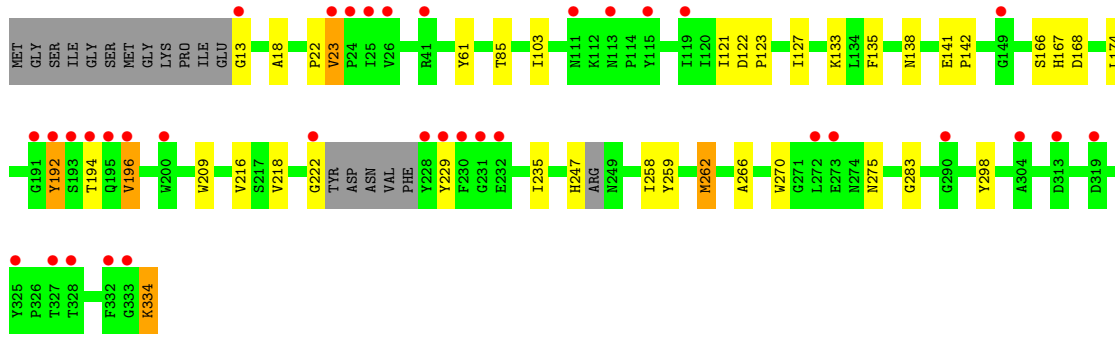
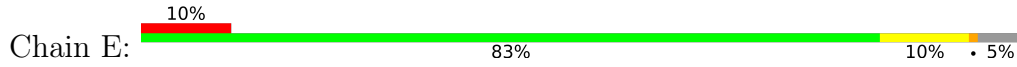


- Molecule 1: Formamidase

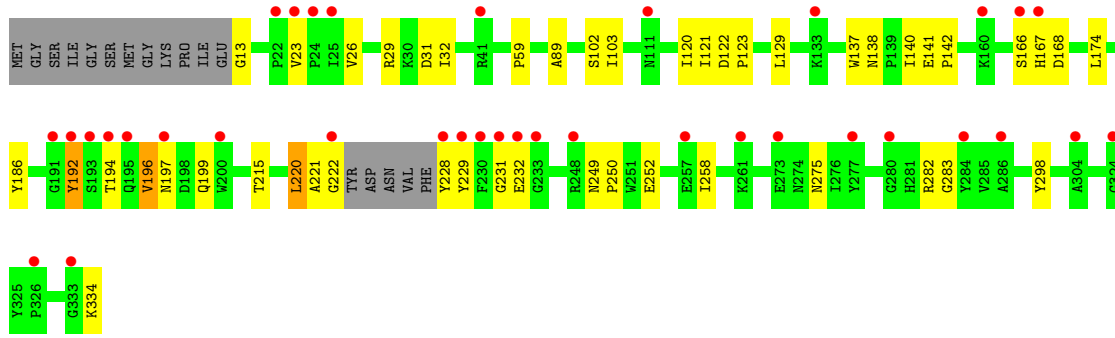
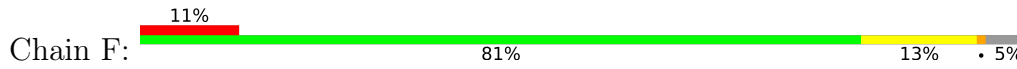




• Molecule 1: Formamidase



• Molecule 1: Formamidase



4 Data and refinement statistics i

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	83.09Å 151.79Å 89.08Å 90.00° 114.99° 90.00°	Depositor
Resolution (Å)	30.00 – 2.29 30.00 – 2.29	Depositor EDS
% Data completeness (in resolution range)	90.9 (30.00-2.29) 91.1 (30.00-2.29)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.23 (at 2.29Å)	Xtrriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.253 , 0.285 0.252 , 0.259	Depositor DCC
R_{free} test set	4091 reflections (4.54%)	wwPDB-VP
Wilson B-factor (Å ²)	35.7	Xtrriage
Anisotropy	0.612	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 46.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	0.016 for h,-k,-h-l	Xtrriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	15751	wwPDB-VP
Average B, all atoms (Å ²)	36.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.54% 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: ARF

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	0.45	0/2574	0.79	1/3498 (0.0%)
1	B	0.45	0/2574	0.75	0/3498
1	C	0.45	0/2574	0.77	0/3498
1	D	0.45	0/2574	0.78	1/3498 (0.0%)
1	E	0.44	0/2562	0.76	0/3481
1	F	0.44	0/2574	0.75	0/3498
All	All	0.45	0/15432	0.77	2/20971 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	D	196	VAL	N-CA-C	-5.46	107.41	112.43
1	A	196	VAL	N-CA-C	-5.23	107.62	112.43

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	2503	0	2442	43	0
1	B	2503	0	2442	49	0
1	C	2503	0	2442	49	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	2503	0	2442	41	0
1	E	2492	0	2428	25	0
1	F	2503	0	2442	32	0
2	A	3	0	3	2	0
2	C	3	0	3	1	0
2	F	3	0	3	0	0
3	A	133	0	0	3	0
3	B	131	0	0	1	0
3	C	143	0	0	1	0
3	D	102	0	0	2	0
3	E	114	0	0	1	0
3	F	112	0	0	0	0
All	All	15751	0	14647	190	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 6.

The worst 5 of 190 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:170:MET:CE	1:D:209:TRP:HE1	1.66	1.08
1:C:170:MET:HE2	1:D:209:TRP:HE1	1.24	0.98
1:C:170:MET:HE2	1:D:209:TRP:NE1	1.94	0.81
1:A:192:TYR:HD2	2:A:1335:ARF:HN2	1.27	0.81
1:C:170:MET:CE	1:D:209:TRP:NE1	2.47	0.77

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	313/334 (94%)	300 (96%)	12 (4%)	1 (0%)	36	46
1	B	313/334 (94%)	298 (95%)	11 (4%)	4 (1%)	9	10
1	C	313/334 (94%)	298 (95%)	13 (4%)	2 (1%)	21	27
1	D	313/334 (94%)	302 (96%)	10 (3%)	1 (0%)	36	46
1	E	310/334 (93%)	299 (96%)	9 (3%)	2 (1%)	21	27
1	F	313/334 (94%)	299 (96%)	13 (4%)	1 (0%)	36	46
All	All	1875/2004 (94%)	1796 (96%)	68 (4%)	11 (1%)	21	27

5 of 11 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	166	SER
1	B	193	SER
1	C	231	GLY
1	E	166	SER
1	F	166	SER

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	263/277 (95%)	258 (98%)	5 (2%)	50	69
1	B	263/277 (95%)	260 (99%)	3 (1%)	65	81
1	C	263/277 (95%)	257 (98%)	6 (2%)	44	63
1	D	263/277 (95%)	257 (98%)	6 (2%)	44	63
1	E	262/277 (95%)	256 (98%)	6 (2%)	44	63
1	F	263/277 (95%)	257 (98%)	6 (2%)	44	63
All	All	1577/1662 (95%)	1545 (98%)	32 (2%)	48	67

5 of 32 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	197	ASN

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Mol	Chain	Res	Type
1	F	220	LEU
1	C	298	TYR
1	C	220	LEU
1	F	298	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 43 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	281	HIS
1	F	20	GLN
1	E	138	ASN
1	E	245	GLN
1	F	124	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

3 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	ARF	F	3335	-	2,2,2	2.45	1 (50%)	1,1,1	0.76	0
2	ARF	A	1335	-	2,2,2	2.37	1 (50%)	1,1,1	0.79	0
2	ARF	C	2335	-	2,2,2	2.37	1 (50%)	1,1,1	0.79	0

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	3335	ARF	O-C	3.41	1.33	1.22
2	C	2335	ARF	O-C	3.31	1.33	1.22
2	A	1335	ARF	O-C	3.30	1.33	1.22

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1335	ARF	2	0
2	C	2335	ARF	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 [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	317/334 (94%)	0.80	32 (10%) 12 14	24, 34, 42, 49	0
1	B	317/334 (94%)	0.87	27 (8%) 16 18	24, 35, 49, 52	0
1	C	317/334 (94%)	0.83	32 (10%) 12 14	25, 34, 44, 47	0
1	D	317/334 (94%)	0.85	25 (7%) 18 20	27, 36, 51, 56	0
1	E	316/334 (94%)	1.07	35 (11%) 10 11	28, 39, 55, 59	0
1	F	317/334 (94%)	1.02	36 (11%) 10 11	28, 39, 48, 51	0
All	All	1901/2004 (94%)	0.91	187 (9%) 13 14	24, 36, 48, 59	0

The worst 5 of 187 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	193	SER	13.9
1	A	229	TYR	11.5
1	F	228	TYR	9.6
1	B	228	TYR	9.1
1	C	193	SER	9.1

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 oligosaccharides 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
2	ARF	F	3335	3/3	0.76	0.25	40,40,40,40	0
2	ARF	C	2335	3/3	0.79	0.20	41,41,44,44	0
2	ARF	A	1335	3/3	0.83	0.17	36,36,40,40	0

6.5 Other polymers [i](#)

There are no such residues in this entry.