



Full wwPDB X-ray Structure Validation Report

May 20, 2014 – 01:20 AM EDT

PDB ID : 4NX3
Title : Structure of the core ectodomain of the hepatitis C virus envelope glycoprotein 2
Authors : Khan, A.G.; Miller, M.T.; Marcotrigiano, J.
Deposited on : 2013-12-08
Resolution : 2.40 Å(reported)

This is a full wwPDB 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/ValidationPDFNotes.html>

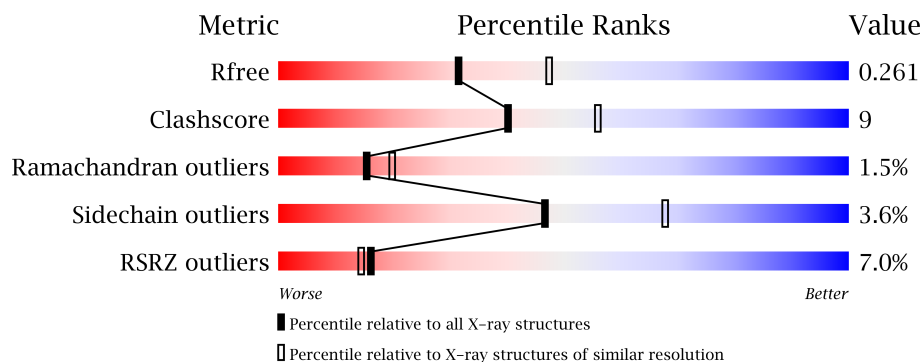
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.16 November 2013
Xtriage (Phenix) : dev-1439
EDS : stable22978
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22978

1 Overall quality at a glance

The reported resolution of this entry is 2.40 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}	66092	2207 (2.40-2.40)
Clashscore	79885	2789 (2.40-2.40)
Ramachandran outliers	78287	2736 (2.40-2.40)
Sidechain outliers	78261	2737 (2.40-2.40)
RSRZ outliers	66119	2210 (2.40-2.40)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	D	217	
2	B	467	
3	A	240	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
4	NAG	D	701	-	X
4	NAG	D	702	-	X
5	ARF	B	502	-	X

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 4317 atoms, of which 0 are hydrogen and 0 are deuterium.

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 HCV E2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	D	119	Total	C	N	O	S	0	0	0
			870	561	140	157	12			

There are 17 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	450	THR	-	EXPRESSION TAG	UNP Q9QF35
D	451	PRO	-	EXPRESSION TAG	UNP Q9QF35
D	452	VAL	-	EXPRESSION TAG	UNP Q9QF35
D	453	GLY	-	EXPRESSION TAG	UNP Q9QF35
D	454	LEU	-	EXPRESSION TAG	UNP Q9QF35
D	455	ALA	-	EXPRESSION TAG	UNP Q9QF35
D	656	GLY	-	EXPRESSION TAG	UNP Q9QF35
D	657	SER	-	EXPRESSION TAG	UNP Q9QF35
D	658	ALA	-	EXPRESSION TAG	UNP Q9QF35
D	659	SER	-	EXPRESSION TAG	UNP Q9QF35
D	660	GLY	-	EXPRESSION TAG	UNP Q9QF35
D	661	LEU	-	EXPRESSION TAG	UNP Q9QF35
D	662	GLU	-	EXPRESSION TAG	UNP Q9QF35
D	663	VAL	-	EXPRESSION TAG	UNP Q9QF35
D	664	LEU	-	EXPRESSION TAG	UNP Q9QF35
D	665	PHE	-	EXPRESSION TAG	UNP Q9QF35
D	666	GLN	-	EXPRESSION TAG	UNP Q9QF35

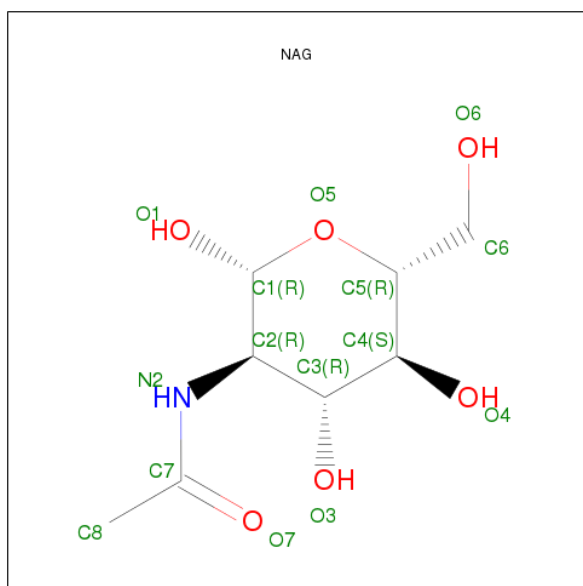
- Molecule 2 is a protein called Mouse Fab Heavy Chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	216	Total	C	N	O	S	0	0	0
			1616	1015	264	332	5			

- Molecule 3 is a protein called Mouse Fab Light Chain.

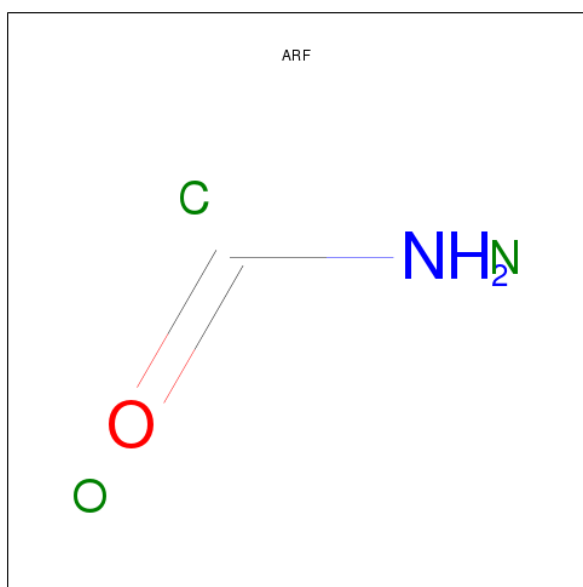
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	A	217	Total	C	N	O	S	0	0	0
			1648	1025	273	342	8			

- Molecule 4 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	D	1	Total	C	N	O	0	0
			14	8	1	5		
4	D	1	Total	C	N	O	0	0
			14	8	1	5		

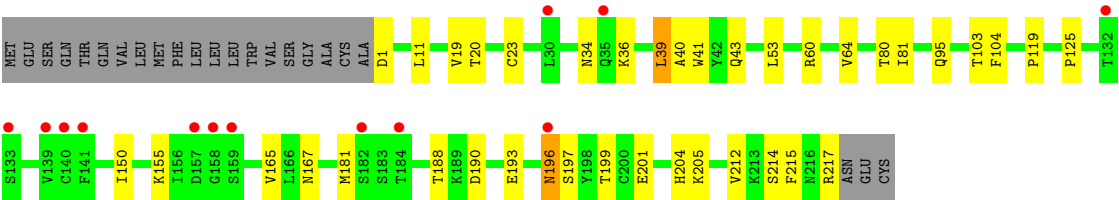
- Molecule 5 is FORMAMIDE (three-letter code: ARF) (formula: CH_3NO).



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

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	D	14	Total	O	0	0
			14	14		
6	B	60	Total	O	0	0
			60	60		
6	A	63	Total	O	0	0
			63	63		



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	85.96Å 194.57Å 37.92Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.91 – 2.40 29.91 – 2.40	Depositor EDS
% Data completeness (in resolution range)	94.2 (29.91-2.40) 94.2 (29.91-2.40)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.83 (at 2.39Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.4_1496)	Depositor
R, R_{free}	0.198 , 0.261 0.198 , 0.261	Depositor DCC
R_{free} test set	1998 reflections (8.21%)	DCC
Wilson B-factor (Å ²)	45.9	Xtriage
Anisotropy	0.338	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 46.0	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 24344 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	4317	wwPDB-VP
Average B, all atoms (Å ²)	50.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.00% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: NAG, 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	D	0.39	0/899	0.68	1/1239 (0.1%)
2	B	0.45	0/1655	0.65	0/2268
3	A	0.44	0/1685	0.61	0/2295
All	All	0.44	0/4239	0.64	1/5802 (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	643	ARG	NE-CZ-NH2	-5.81	117.39	120.30

There are no chirality outliers.

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	870	0	804	25	0
2	B	1616	0	1561	34	0
3	A	1648	0	1535	19	0
4	D	28	0	26	1	0
5	A	6	0	6	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	B	9	0	9	0	0
5	D	3	0	3	1	0
6	A	63	0	0	1	0
6	B	60	0	0	0	0
6	D	14	0	0	3	0
All	All	4317	0	3944	76	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 9.

All (76) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:B:124:PRO:HB3	2:B:150:TYR:HB3	1.70	0.74
1:D:499:VAL:O	1:D:539:PHE:HB3	1.91	0.69
1:D:501:ALA:HB2	1:D:539:PHE:HE2	1.59	0.68
2:B:55:ASN:HB3	2:B:57:HIS:H	1.60	0.67
1:D:501:ALA:HB2	1:D:539:PHE:CE2	2.30	0.66
3:A:43:GLN:HB2	3:A:53:LEU:HD11	1.76	0.66
3:A:1:ASP:OD2	6:A:455:HOH:O	2.15	0.62
1:D:520:THR:HG1	1:D:538:VAL:N	1.98	0.62
1:D:596:THR:HG22	1:D:598:TYR:H	1.64	0.61
3:A:201:GLU:HG2	3:A:212:VAL:HG12	1.82	0.60
1:D:546:PRO:HA	1:D:549:GLY:O	2.03	0.58
5:D:703:ARF:H	6:D:804:HOH:O	2.03	0.58
1:D:643:ARG:HH22	2:B:106:ASP:CG	2.09	0.56
2:B:218:ARG:CZ	3:A:125:PRO:HG2	2.35	0.56
1:D:643:ARG:HD2	6:D:813:HOH:O	2.05	0.56
1:D:496:CYS:HB3	1:D:541:LEU:HB2	1.88	0.55
2:B:149:GLY:HA2	2:B:179:LEU:HB3	1.88	0.55
1:D:508:VAL:HG22	1:D:556:TRP:HB3	1.89	0.55
2:B:175:LEU:HB3	2:B:176:GLN:HB2	1.89	0.54
1:D:624:CYS:SG	6:D:810:HOH:O	2.57	0.54
2:B:137:THR:HG22	2:B:139:SER:H	1.73	0.53
1:D:513:PRO:HD3	1:D:637:VAL:HG21	1.90	0.53
2:B:52:ASP:HB3	2:B:55:ASN:HB2	1.91	0.52
2:B:194:PRO:O	2:B:195:SER:OG	2.14	0.52
3:A:34:ASN:OD1	3:A:36:LYS:HB2	2.11	0.51
1:D:643:ARG:NH2	2:B:106:ASP:OD1	2.43	0.51
2:B:61:ASP:OD1	2:B:63:LYS:HG2	2.10	0.50
2:B:67:LYS:HG2	2:B:84:SER:O	2.11	0.50
1:D:496:CYS:HA	1:D:566:CYS:HB2	1.93	0.50
2:B:24:ALA:HB1	2:B:27:PHE:CE1	2.47	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:A:150:ILE:HD12	3:A:204:HIS:HD2	1.77	0.49
2:B:28:ASN:OD1	2:B:30:LYS:HB2	2.12	0.49
3:A:196:ASN:ND2	3:A:217:ARG:O	2.44	0.49
1:D:540:LEU:HD11	1:D:542:ASN:ND2	2.29	0.48
2:B:189:THR:C	2:B:191:SER:H	2.17	0.47
2:B:129:LEU:HB2	2:B:144:GLY:C	2.35	0.47
2:B:197:SER:HB2	2:B:214:LYS:HE3	1.96	0.47
2:B:159:TRP:CZ3	2:B:200:CYS:HB3	2.50	0.47
1:D:648:CYS:HB3	1:D:649:ASN:H	1.55	0.47
2:B:214:LYS:HE2	2:B:216:GLU:OE1	2.15	0.46
1:D:540:LEU:HD12	1:D:540:LEU:HA	1.64	0.46
3:A:190:ASP:HA	3:A:193:GLU:HB2	1.97	0.46
3:A:197:SER:HB2	3:A:215:PHE:O	2.16	0.46
2:B:153:GLU:HG3	2:B:154:PRO:HA	1.99	0.45
1:D:628:TYR:CG	1:D:648:CYS:O	2.69	0.45
2:B:119:ALA:HB3	2:B:151:PHE:CE2	2.52	0.45
3:A:39:LEU:HG	3:A:40:ALA:N	2.31	0.45
2:B:175:LEU:CG	2:B:176:GLN:HA	2.47	0.45
2:B:12:VAL:HG21	2:B:86:LEU:HD12	2.00	0.43
3:A:155:LYS:N	3:A:199:THR:O	2.50	0.43
2:B:160:ASN:OD1	2:B:198:ILE:HA	2.19	0.43
2:B:47:TRP:CH2	2:B:49:GLY:HA2	2.54	0.43
3:A:150:ILE:HD12	3:A:204:HIS:CD2	2.52	0.43
1:D:546:PRO:HG2	1:D:552:PHE:CD2	2.53	0.43
1:D:569:PRO:HA	1:D:570:PRO:HD3	1.78	0.43
3:A:23:CYS:HB2	3:A:41:TRP:CH2	2.53	0.42
2:B:175:LEU:HB3	2:B:176:GLN:CB	2.49	0.42
2:B:198:ILE:O	2:B:215:ILE:HG12	2.18	0.42
2:B:145:CYS:HB2	2:B:159:TRP:CH2	2.54	0.42
2:B:197:SER:CB	2:B:214:LYS:HE3	2.49	0.42
3:A:167:ASN:HB3	3:A:181:MET:HE2	2.00	0.42
1:D:618:ARG:O	1:D:622:TYR:N	2.51	0.42
3:A:95:GLN:HB2	3:A:104:PHE:CD1	2.55	0.41
1:D:514:SER:HA	1:D:515:PRO:HD3	1.83	0.41
2:B:199:THR:HG23	2:B:213:LYS:C	2.41	0.41
3:A:19:VAL:HB	3:A:81:ILE:HB	2.02	0.41
3:A:60:ARG:HD3	3:A:64:VAL:O	2.20	0.41
2:B:179:LEU:HA	2:B:179:LEU:HD23	1.90	0.41
1:D:559:SER:HB2	4:D:701:NAG:H82	2.02	0.41
3:A:119:PRO:HG3	3:A:150:ILE:HD11	2.03	0.41
1:D:498:VAL:HB	1:D:540:LEU:HD13	2.03	0.40
2:B:193:TRP:HA	2:B:194:PRO:HA	1.89	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:B:174:VAL:O	2:B:181:THR:N	2.44	0.40
2:B:188:VAL:HG22	2:B:189:THR:H	1.85	0.40
3:A:11:LEU:HA	3:A:11:LEU:HD23	1.78	0.40
1:D:614:ASP:OD1	1:D:615:TYR:N	2.55	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	D	113/217 (52%)	95 (84%)	15 (13%)	3 (3%)	8	7
2	B	212/467 (45%)	196 (92%)	12 (6%)	4 (2%)	12	14
3	A	215/240 (90%)	205 (95%)	9 (4%)	1 (0%)	38	53
All	All	540/924 (58%)	496 (92%)	36 (7%)	8 (2%)	15	20

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	502	LYS
1	D	540	LEU
2	B	177	SER
2	B	176	GLN
2	B	195	SER
3	A	196	ASN
2	B	137	THR
1	D	512	THR

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	D	95/186 (51%)	92 (97%)	3 (3%)	51	72
2	B	185/420 (44%)	179 (97%)	6 (3%)	51	72
3	A	186/214 (87%)	178 (96%)	8 (4%)	40	59
All	All	466/820 (57%)	449 (96%)	17 (4%)	47	68

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	498	VAL
1	D	503	THR
1	D	544	THR
2	B	17	SER
2	B	166	SER
2	B	188	VAL
2	B	192	THR
2	B	201	ASN
2	B	213	LYS
3	A	20	THR
3	A	39	LEU
3	A	80	THR
3	A	103	THR
3	A	165	VAL
3	A	188	THR
3	A	205	LYS
3	A	214	SER

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

Mol	Chain	Res	Type
2	B	38	ASN
3	A	37	ASN

5.3.3 RNA ⓘ

There are no RNA chains in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

8 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$
5	ARF	A	301	-	2,2,2	1.44	1 (50%)	1,1,1	0.74	0
5	ARF	A	302	-	2,2,2	1.70	1 (50%)	1,1,1	0.41	0
5	ARF	B	501	-	2,2,2	1.54	1 (50%)	1,1,1	0.64	0
5	ARF	B	502	-	2,2,2	1.50	1 (50%)	1,1,1	0.91	0
5	ARF	B	503	-	2,2,2	1.60	1 (50%)	1,1,1	0.46	0
4	NAG	D	701	1	12,14,15	0.40	0	15,19,21	0.49	0
4	NAG	D	702	1	12,14,15	0.43	0	15,19,21	0.33	0
5	ARF	D	703	-	2,2,2	1.43	1 (50%)	1,1,1	0.67	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
5	ARF	A	301	-	-	0/0/0/0	0/0/0/0
5	ARF	A	302	-	-	0/0/0/0	0/0/0/0
5	ARF	B	501	-	-	0/0/0/0	0/0/0/0
5	ARF	B	502	-	-	0/0/0/0	0/0/0/0
5	ARF	B	503	-	-	0/0/0/0	0/0/0/0
4	NAG	D	701	1	-	0/6/23/26	0/1/1/1
4	NAG	D	702	1	-	0/6/23/26	0/1/1/1
5	ARF	D	703	-	-	0/0/0/0	0/0/0/0

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	302	ARF	C-N	2.36	1.43	1.30
5	B	503	ARF	C-N	2.26	1.43	1.30
5	B	501	ARF	C-N	2.18	1.42	1.30
5	B	502	ARF	C-N	2.09	1.42	1.30
5	A	301	ARF	C-N	2.04	1.42	1.30
5	D	703	ARF	C-N	2.03	1.42	1.30

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

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	D	119/217 (54%)	0.76	17 (14%) 3 3	34, 71, 105, 112	0
2	B	216/467 (46%)	-0.00	9 (4%) 35 32	24, 41, 78, 107	0
3	A	217/240 (90%)	0.17	13 (5%) 21 19	24, 41, 79, 88	0
All	All	552/924 (59%)	0.23	39 (7%) 16 14	24, 45, 91, 112	0

All (39) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	596	THR	5.3
1	D	539	PHE	5.2
1	D	538	VAL	5.0
1	D	521	THR	4.6
1	D	522	ASP	4.1
1	D	599	LEU	4.1
3	A	158	GLY	4.1
1	D	619	LEU	3.8
3	A	139	VAL	3.8
1	D	501	ALA	3.7
2	B	137	THR	3.4
1	D	571	CYS	3.4
1	D	493	PRO	3.3
1	D	617	TYR	3.2
3	A	132	THR	2.9
2	B	163	SER	2.9
3	A	157	ASP	2.9
3	A	140	CYS	2.9
2	B	164	LEU	2.7
1	D	500	SER	2.7
1	D	570	PRO	2.7
3	A	30	LEU	2.7
3	A	141	PHE	2.7

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Mol	Chain	Res	Type	RSRZ
2	B	161	SER	2.6
3	A	35	GLN	2.5
2	B	175	LEU	2.4
3	A	133	SER	2.3
1	D	520	THR	2.3
2	B	136	THR	2.3
2	B	162	GLY	2.2
1	D	492	PRO	2.2
1	D	569	PRO	2.2
1	D	597	THR	2.1
3	A	159	SER	2.1
3	A	184	THR	2.1
3	A	182	SER	2.0
2	B	176	GLN	2.0
3	A	196	ASN	2.0
2	B	183	SER	2.0

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

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	RSR	LLDF	B-factors(Å ²)	Q<0.9
4	NAG	D	702	14/15	0.40	5.35	86,94,101,104	0
5	ARF	B	502	3/3	0.16	4.30	35,35,36,44	0
4	NAG	D	701	14/15	0.34	3.38	96,98,105,106	0
5	ARF	A	301	3/3	0.19	0.51	51,51,53,54	0
5	ARF	B	503	3/3	0.18	0.21	32,32,36,42	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
5	ARF	D	703	3/3	0.13	0.05	40,40,48,49	0
5	ARF	A	302	3/3	0.12	-0.84	34,34,36,42	0
5	ARF	B	501	3/3	0.10	-1.89	31,31,36,36	0

6.5 Other polymers

There are no such residues in this entry.