



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 14, 2017 – 09:19 pm GMT

PDB ID : 4FMF
Title : Crystal structure of human nectin-1 full ectodomain (D1-D3)
Authors : Harrison, O.J.; Brasch, J.; Shapiro, L.
Deposited on : 2012-06-16
Resolution : 3.20 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

<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 : trunk28620
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) : recalc28949

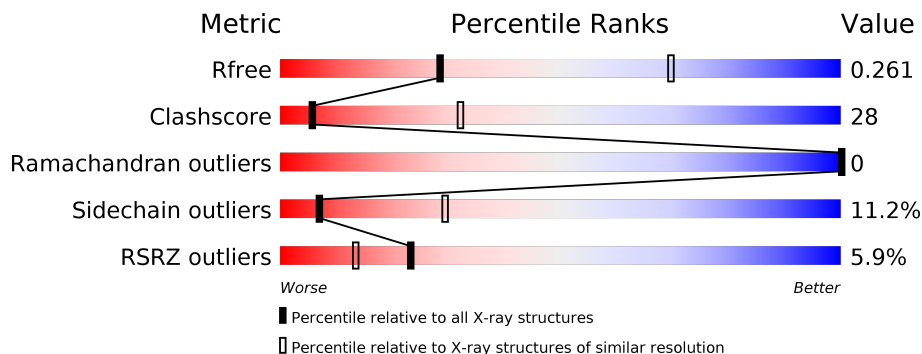
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.20 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	1015 (3.22-3.18)
Clashscore	112137	1009 (3.20-3.20)
Ramachandran outliers	110173	1118 (3.22-3.18)
Sidechain outliers	110143	1117 (3.22-3.18)
RSRZ outliers	101464	1020 (3.22-3.18)

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	313	<div> <div>4%</div> <div> <div>59%</div> <div>28%</div> <div>8%</div> <div>• •</div> </div> </div>
1	B	313	<div> <div>10%</div> <div> <div>62%</div> <div>27%</div> <div>5%</div> <div>• •</div> </div> </div>
1	C	313	<div> <div>3%</div> <div> <div>61%</div> <div>28%</div> <div>6%</div> <div>• •</div> </div> </div>
1	D	313	<div> <div>5%</div> <div> <div>65%</div> <div>28%</div> <div>• •</div> </div> </div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 9598 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 Poliovirus receptor-related protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	302	Total	C	N	O	S	0	0	0
			2376	1497	410	458	11			
1	B	299	Total	C	N	O	S	0	0	0
			2349	1478	407	453	11			
1	C	301	Total	C	N	O	S	0	0	0
			2369	1492	409	457	11			
1	D	302	Total	C	N	O	S	0	0	0
			2376	1497	410	458	11			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	338	HIS	-	EXPRESSION TAG	UNP Q15223
A	339	HIS	-	EXPRESSION TAG	UNP Q15223
A	340	HIS	-	EXPRESSION TAG	UNP Q15223
A	341	HIS	-	EXPRESSION TAG	UNP Q15223
A	342	HIS	-	EXPRESSION TAG	UNP Q15223
A	343	HIS	-	EXPRESSION TAG	UNP Q15223
B	338	HIS	-	EXPRESSION TAG	UNP Q15223
B	339	HIS	-	EXPRESSION TAG	UNP Q15223
B	340	HIS	-	EXPRESSION TAG	UNP Q15223
B	341	HIS	-	EXPRESSION TAG	UNP Q15223
B	342	HIS	-	EXPRESSION TAG	UNP Q15223
B	343	HIS	-	EXPRESSION TAG	UNP Q15223
C	338	HIS	-	EXPRESSION TAG	UNP Q15223
C	339	HIS	-	EXPRESSION TAG	UNP Q15223
C	340	HIS	-	EXPRESSION TAG	UNP Q15223
C	341	HIS	-	EXPRESSION TAG	UNP Q15223
C	342	HIS	-	EXPRESSION TAG	UNP Q15223
C	343	HIS	-	EXPRESSION TAG	UNP Q15223
D	338	HIS	-	EXPRESSION TAG	UNP Q15223
D	339	HIS	-	EXPRESSION TAG	UNP Q15223
D	340	HIS	-	EXPRESSION TAG	UNP Q15223

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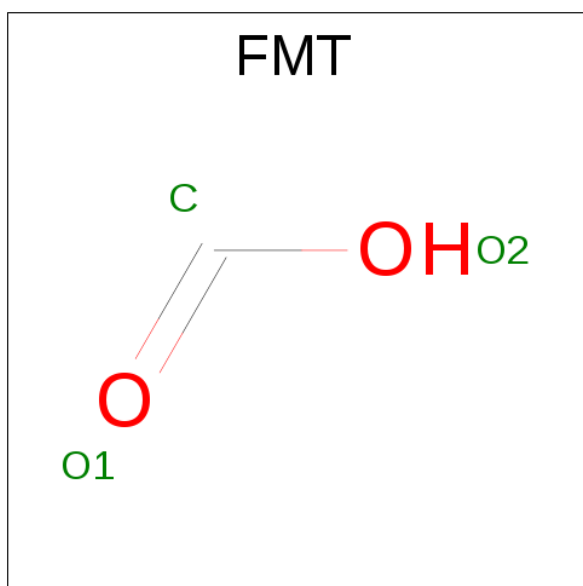
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Chain	Residue	Modelled	Actual	Comment	Reference
D	341	HIS	-	EXPRESSION TAG	UNP Q15223
D	342	HIS	-	EXPRESSION TAG	UNP Q15223
D	343	HIS	-	EXPRESSION TAG	UNP Q15223

- Molecule 2 is a polymer of unknown type called SUGAR (2-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	2	Total	C	N	O	0	0
			28	16	2	10		
2	B	2	Total	C	N	O	0	0
			28	16	2	10		
2	C	2	Total	C	N	O	0	0
			28	16	2	10		
2	D	2	Total	C	N	O	0	0
			28	16	2	10		

- Molecule 3 is FORMIC ACID (three-letter code: FMT) (formula: CH₂O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			3	1	2		
3	B	1	Total	C	O	0	0
			3	1	2		
3	C	1	Total	C	O	0	0
			3	1	2		
3	D	1	Total	C	O	0	0
			3	1	2		

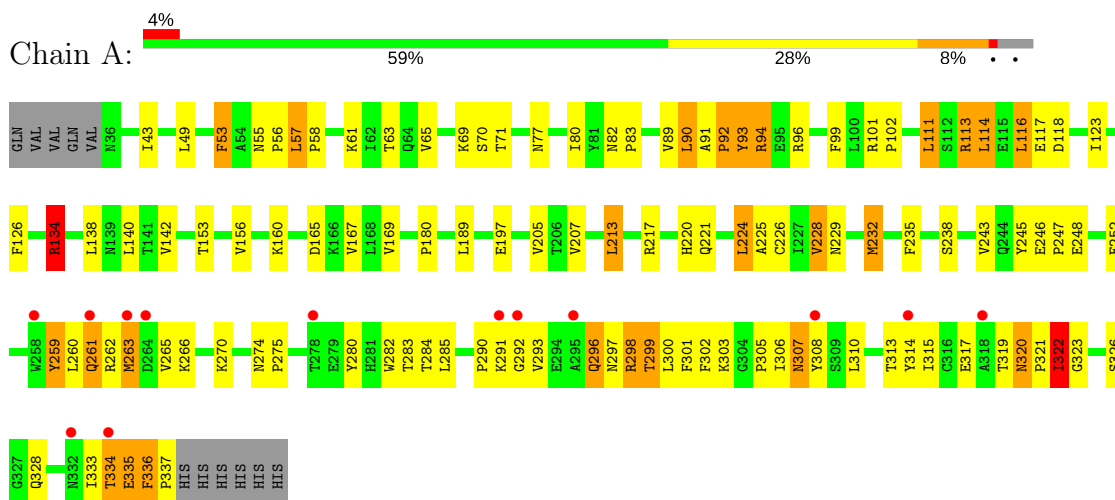
- Molecule 4 is water.

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

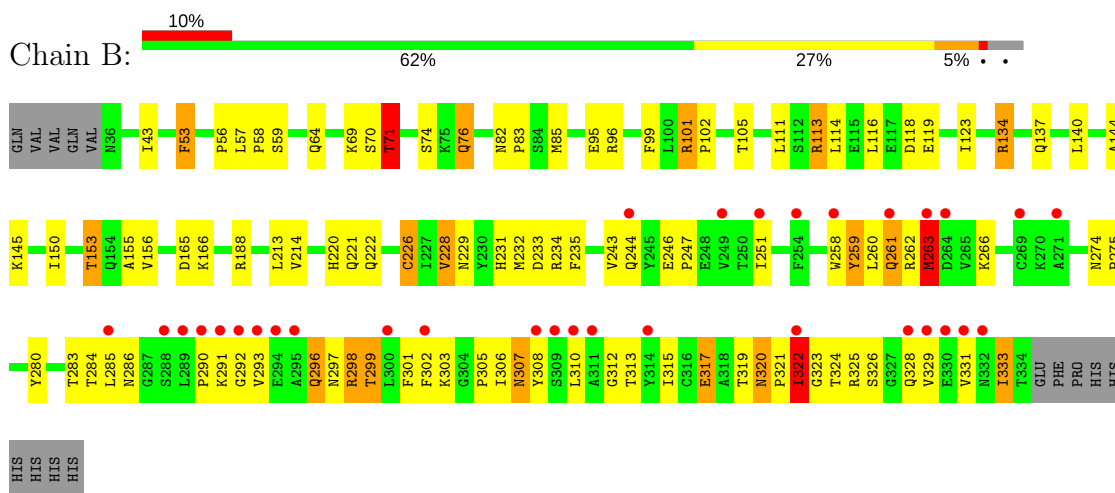
3 Residue-property plots

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.

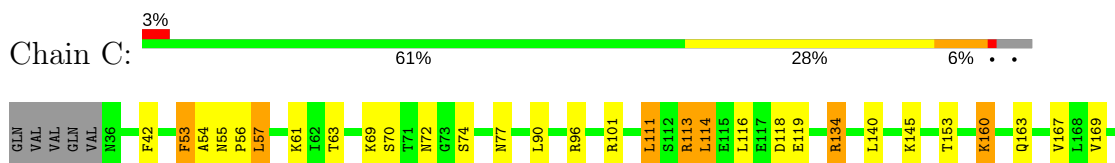
• Molecule 1: Poliovirus receptor-related protein 1

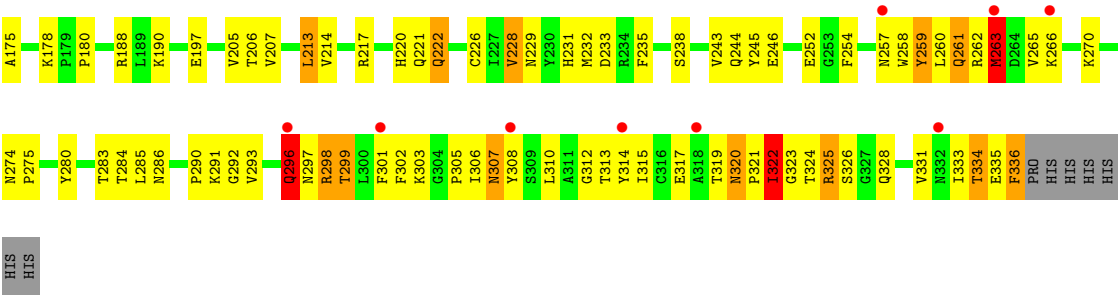


• Molecule 1: Poliovirus receptor-related protein 1

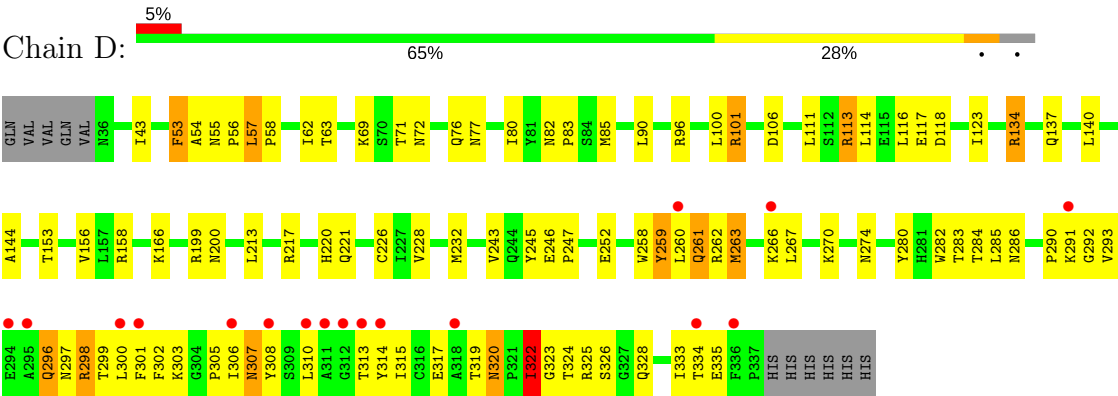


• Molecule 1: Poliovirus receptor-related protein 1





● Molecule 1: Poliovirus receptor-related protein 1



4 Data and refinement statistics

Property	Value	Source
Space group	P 63	Depositor
Cell constants a, b, c, α , β , γ	106.29Å 106.29Å 334.62Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	20.00 – 3.20 38.47 – 3.20	Depositor EDS
% Data completeness (in resolution range)	98.9 (20.00-3.20) 98.9 (38.47-3.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.42 (at 3.18Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.233 , 0.258 0.233 , 0.261	Depositor DCC
R_{free} test set	1749 reflections (5.29%)	DCC
Wilson B-factor (Å ²)	74.6	Xtriage
Anisotropy	0.390	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 32.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	0.330 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	9598	wwPDB-VP
Average B, all atoms (Å ²)	96.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.10% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: FMT, NAG

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	0.80	1/2430 (0.0%)	0.86	5/3308 (0.2%)
1	B	0.74	0/2401	0.81	1/3268 (0.0%)
1	C	0.80	0/2422	0.86	1/3296 (0.0%)
1	D	0.73	1/2430 (0.0%)	0.82	2/3308 (0.1%)
All	All	0.77	2/9683 (0.0%)	0.83	9/13180 (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	3
1	B	0	4
1	C	0	3
1	D	0	2
All	All	0	12

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	282	TRP	CD2-CE2	5.24	1.47	1.41
1	A	282	TRP	CD2-CE2	5.08	1.47	1.41

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	232	MET	CG-SD-CE	7.19	111.71	100.20
1	C	296	GLN	N-CA-C	-6.82	92.59	111.00
1	A	296	GLN	N-CA-C	-6.36	93.84	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	72	ASN	N-CA-C	5.85	126.80	111.00
1	B	296	GLN	N-CA-C	-5.84	95.24	111.00

There are no chirality outliers.

5 of 12 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	259	TYR	Peptide
1	A	263	MET	Peptide
1	A	322	ILE	Peptide
1	B	259	TYR	Peptide
1	B	71	THR	Peptide

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	2376	0	2324	164	1
1	B	2349	0	2302	129	0
1	C	2369	0	2316	149	0
1	D	2376	0	2324	104	0
2	A	28	0	25	0	0
2	B	28	0	25	0	0
2	C	28	0	24	0	0
2	D	28	0	25	2	0
3	A	3	0	1	0	0
3	B	3	0	1	0	0
3	C	3	0	1	0	0
3	D	3	0	1	0	0
4	A	2	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
All	All	9598	0	9369	533	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 28.

The worst 5 of 533 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:260:LEU:HD21	1:A:308:TYR:CE1	1.27	1.63
1:C:260:LEU:HD21	1:C:308:TYR:CE1	1.10	1.63
1:C:260:LEU:HD21	1:C:308:TYR:CD1	1.46	1.49
1:C:266:LYS:HE2	1:C:301:PHE:CE1	1.46	1.49
1:B:57:LEU:CD2	1:B:58:PRO:HD2	1.45	1.46

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:A:229:ASN:OD1	1:A:232:MET:CE[3_565]	2.01	0.19

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	300/313 (96%)	286 (95%)	14 (5%)	0	100	100
1	B	297/313 (95%)	287 (97%)	10 (3%)	0	100	100
1	C	299/313 (96%)	288 (96%)	11 (4%)	0	100	100
1	D	300/313 (96%)	293 (98%)	7 (2%)	0	100	100
All	All	1196/1252 (96%)	1154 (96%)	42 (4%)	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	264/275 (96%)	234 (89%)	30 (11%)	7	28
1	B	261/275 (95%)	232 (89%)	29 (11%)	7	30
1	C	263/275 (96%)	231 (88%)	32 (12%)	6	25
1	D	264/275 (96%)	237 (90%)	27 (10%)	8	34
All	All	1052/1100 (96%)	934 (89%)	118 (11%)	7	29

5 of 118 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	307	ASN
1	C	134	ARG
1	D	298	ARG
1	B	317	GLU
1	C	53	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 18 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	222	GLN
1	B	229	ASN
1	C	307	ASN
1	B	139	ASN
1	B	163	GLN

5.3.3 RNA ⓘ

There are no RNA molecules 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 ⓘ

8 carbohydrates 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	NAG	A	401	1,2	14,14,15	0.84	0	15,19,21	1.97	6 (40%)
2	NAG	A	402	2	14,14,15	0.81	0	15,19,21	2.18	3 (20%)
2	NAG	B	401	1,2	14,14,15	0.64	0	15,19,21	1.38	2 (13%)
2	NAG	B	402	2	14,14,15	0.76	0	15,19,21	2.16	5 (33%)
2	NAG	C	401	1,2	14,14,15	0.99	1 (7%)	15,19,21	2.40	7 (46%)
2	NAG	C	402	2	14,14,15	0.75	0	15,19,21	2.28	5 (33%)
2	NAG	D	401	1,2	14,14,15	1.57	1 (7%)	15,19,21	1.89	3 (20%)
2	NAG	D	402	2	14,14,15	0.87	1 (7%)	15,19,21	2.45	5 (33%)

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	NAG	A	401	1,2	-	0/6/23/26	0/1/1/1
2	NAG	A	402	2	-	0/6/23/26	0/1/1/1
2	NAG	B	401	1,2	-	0/6/23/26	0/1/1/1
2	NAG	B	402	2	-	0/6/23/26	0/1/1/1
2	NAG	C	401	1,2	-	0/6/23/26	0/1/1/1
2	NAG	C	402	2	-	0/6/23/26	0/1/1/1
2	NAG	D	401	1,2	-	0/6/23/26	0/1/1/1
2	NAG	D	402	2	-	0/6/23/26	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	401	NAG	O5-C1	-5.15	1.35	1.43
2	C	401	NAG	C1-C2	-2.42	1.49	1.52
2	D	402	NAG	C1-C2	2.39	1.55	1.52

The worst 5 of 36 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	402	NAG	C4-C3-C2	-5.14	103.48	111.02
2	C	401	NAG	O7-C7-N2	-5.09	112.13	121.92
2	C	402	NAG	C4-C3-C2	-4.85	103.92	111.02
2	D	402	NAG	C4-C3-C2	-4.26	104.77	111.02
2	B	402	NAG	O5-C1-C2	-3.87	106.08	111.47

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	401	NAG	2	0

5.6 Ligand geometry [i](#)

4 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	$\# Z > 2$
3	FMT	A	403	-	0,2,2	0.00	-	0,1,1	0.00	-
3	FMT	B	403	-	0,2,2	0.00	-	0,1,1	0.00	-
3	FMT	C	403	-	0,2,2	0.00	-	0,1,1	0.00	-
3	FMT	D	403	-	0,2,2	0.00	-	0,1,1	0.00	-

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	FMT	A	403	-	-	0/0/0/0	0/0/0/0
3	FMT	B	403	-	-	0/0/0/0	0/0/0/0
3	FMT	C	403	-	-	0/0/0/0	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	FMT	D	403	-	-	0/0/0/0	0/0/0/0

There are no bond length outliers.

There are no bond angle outliers.

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 [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	302/313 (96%)	0.35	13 (4%) 36 23	48, 67, 183, 204	0
1	B	299/313 (95%)	0.66	32 (10%) 7 4	48, 78, 230, 255	0
1	C	301/313 (96%)	0.26	9 (2%) 51 35	46, 66, 152, 178	0
1	D	302/313 (96%)	0.34	17 (5%) 25 14	50, 81, 159, 181	0
All	All	1204/1252 (96%)	0.40	71 (5%) 23 13	46, 73, 201, 255	0

The worst 5 of 71 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	310	LEU	8.2
1	B	261	GLN	7.8
1	B	311	ALA	7.4
1	B	289	LEU	7.3
1	B	300	LEU	7.2

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](#)

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	NAG	A	401	14/15	0.92	0.27	0.42	73,78,82,89	0
2	NAG	D	401	14/15	0.86	0.23	-0.10	90,95,105,107	0
2	NAG	C	401	14/15	0.89	0.21	-0.61	75,79,88,92	0
2	NAG	B	401	14/15	0.91	0.22	-0.79	75,80,86,91	0
2	NAG	A	402	14/15	0.89	0.32	-	81,90,98,101	0
2	NAG	C	402	14/15	0.81	0.25	-	85,98,109,114	0
2	NAG	D	402	14/15	0.79	0.23	-	93,105,111,116	0
2	NAG	B	402	14/15	0.90	0.24	-	86,96,106,110	0

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
3	FMT	B	403	3/3	0.94	0.27	0.58	60,60,63,64	0
3	FMT	C	403	3/3	0.89	0.24	0.20	44,44,44,45	0
3	FMT	A	403	3/3	0.85	0.22	-0.82	32,32,34,35	0
3	FMT	D	403	3/3	0.92	0.17	-2.12	57,57,60,60	0

6.5 Other polymers [i](#)

There are no such residues in this entry.