wwPDB X-ray Structure Validation Summary Report (i)

Sep 24, 2023 – 06:15 PM EDT

PDB ID	:	5UMN
Title	:	Crystal structure of C05 VPGSGW mutant bound to H3 influenza hemagglutinin, HA1 subunit
Authors	:	Wu, N.C.; Wilson, I.A.
Deposited on	:	2017-01-27
Resolution	:	1.97 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 (i) 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 (i)) were used in the production of this report:

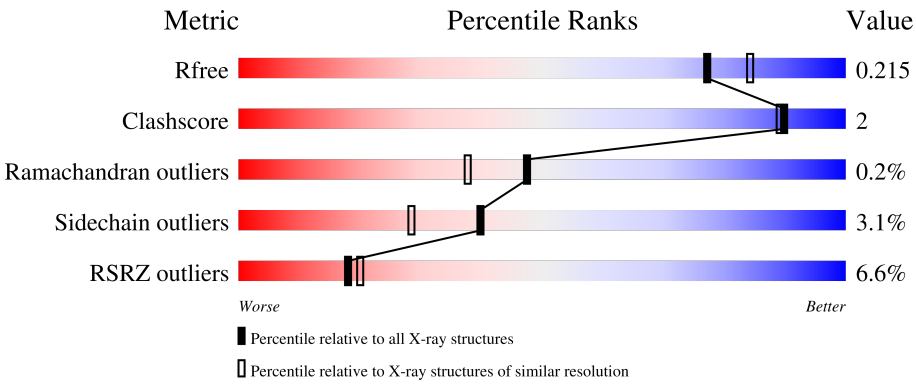
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35.1

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.97 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	11647 (2.00-1.96)
Clashscore	141614	1014 (1.98-1.98)
Ramachandran outliers	138981	1006 (1.98-1.98)
Sidechain outliers	138945	1006 (1.98-1.98)
RSRZ outliers	127900	11410 (2.00-1.96)

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 <=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	274	10% 93% • • •
1	B	274	11% 80% 8% • 11%
2	C	247	7% 91% • • •
2	E	247	5% 89% 6% • •
3	D	214	2% 92% 7%

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Mol	Chain	Length	Quality of chain
3	F	214	% 93% 6%

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
4	NAG	A	402	-	-	-	X
7	FLC	C	301	-	-	-	X
7	FLC	C	302	-	-	-	X

2 Entry composition (i)

There are 8 unique types of molecules in this entry. The entry contains 12093 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 Hemagglutinin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	267	2087	1310	366	400	11	0	2	0
1	B	243	1900	1194	333	361	12	0	1	0

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	310	GLY	-	expression tag	UNP Q91MA7
A	311	HIS	-	expression tag	UNP Q91MA7
A	312	HIS	-	expression tag	UNP Q91MA7
A	313	HIS	-	expression tag	UNP Q91MA7
A	314	HIS	-	expression tag	UNP Q91MA7
A	315	HIS	-	expression tag	UNP Q91MA7
A	316	HIS	-	expression tag	UNP Q91MA7
B	310	GLY	-	expression tag	UNP Q91MA7
B	311	HIS	-	expression tag	UNP Q91MA7
B	312	HIS	-	expression tag	UNP Q91MA7
B	313	HIS	-	expression tag	UNP Q91MA7
B	314	HIS	-	expression tag	UNP Q91MA7
B	315	HIS	-	expression tag	UNP Q91MA7
B	316	HIS	-	expression tag	UNP Q91MA7

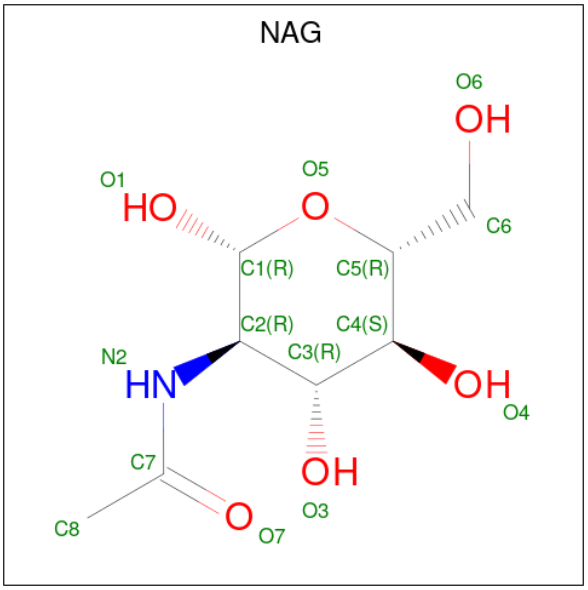
- Molecule 2 is a protein called Antibody C05 VPGSGW mutant, heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	C	238	1791	1118	304	361	8	0	3	0
2	E	238	1774	1110	298	357	9	0	1	0

- Molecule 3 is a protein called Antibody C05, light chain.

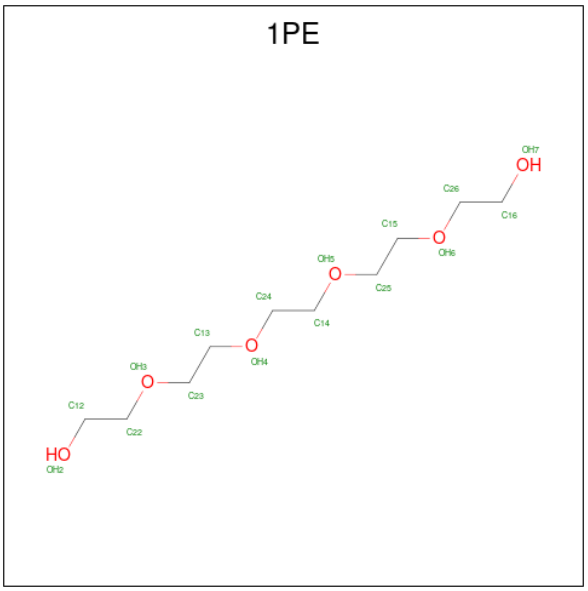
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	D	213	1637	1027	277	329	4	0	0	0
			Total	C	N	O	S			
3	F	213	1644	1031	278	331	4	0	1	0

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



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

- Molecule 5 is PENTAETHYLENE GLYCOL (three-letter code: 1PE) (formula: $C_{10}H_{22}O_6$).

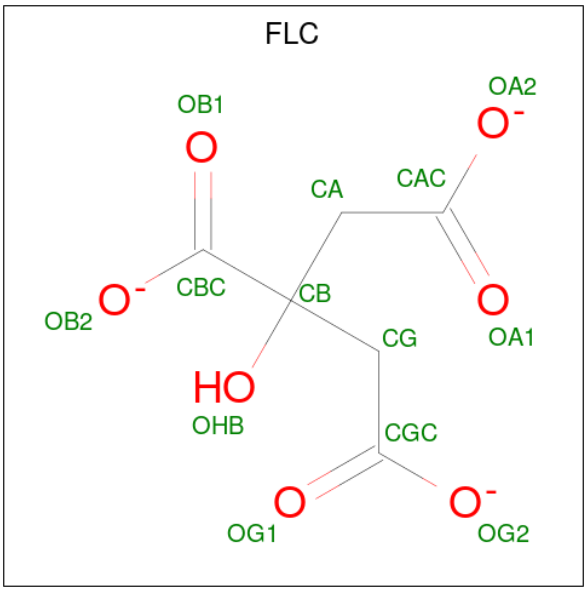


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
5	A	1	16	10	6	0	0
			Total	C	O		
5	B	1	16	10	6	0	0
			Total	C	O		
5	B	1	16	10	6	0	0
			Total	C	O		
5	B	1	16	10	6	0	0

- Molecule 6 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Na		
6	B	1	1	1	0	0

- Molecule 7 is CITRATE ANION (three-letter code: FLC) (formula: $C_6H_5O_7$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	C	1	Total C O 13 6 7	0	0
7	C	1	Total C O 13 6 7	0	0

- Molecule 8 is water.

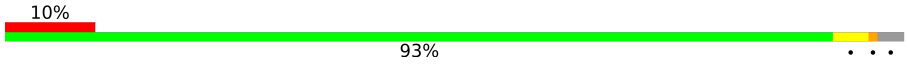
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	A	191	Total O 191 191	0	0
8	B	154	Total O 154 154	0	0
8	C	183	Total O 183 183	0	0
8	D	152	Total O 152 152	0	0
8	E	201	Total O 201 201	0	0
8	F	232	Total O 232 232	0	0

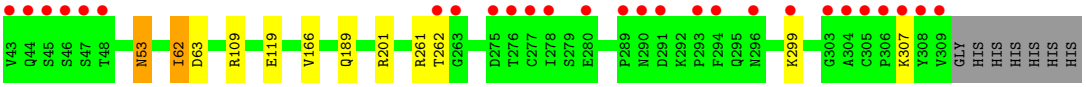
3 Residue-property plots (i)

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: Hemagglutinin

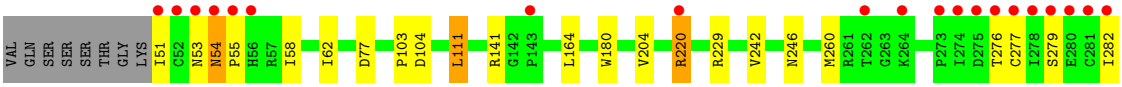
Chain A:

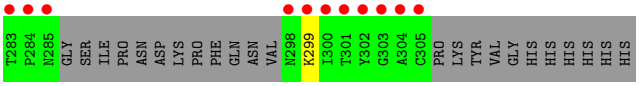




• Molecule 1: Hemagglutinin

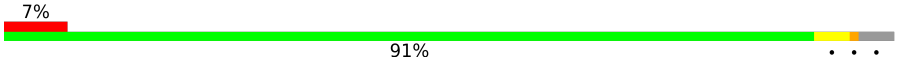
Chain B:

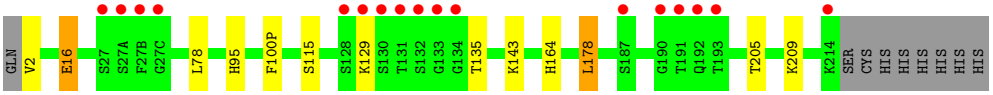




• Molecule 2: Antibody C05 VPGSGW mutant, heavy chain

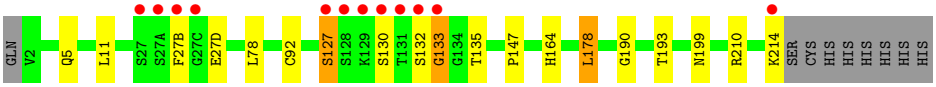
Chain C:





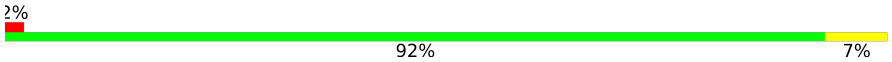
• Molecule 2: Antibody C05 VPGSGW mutant, heavy chain

Chain E:



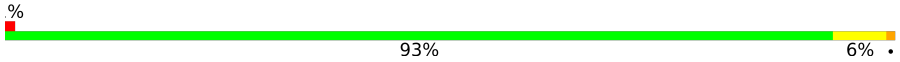
• Molecule 3: Antibody C05, light chain

Chain D:



• Molecule 3: Antibody C05, light chain

Chain F:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 43	Depositor
Cell constants a, b, c, α, β, γ	88.34Å 88.34Å 255.04Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	88.34 – 1.97 39.51 – 1.97	Depositor EDS
% Data completeness (in resolution range)	99.5 (88.34-1.97) 99.5 (39.51-1.97)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.15	Depositor
$< I/\sigma(I) >$ [1]	1.98 (at 1.97Å)	Xtriage
Refinement program	REFMAC 5.8.0158	Depositor
R, R_{free}	0.181 , 0.208 0.189 , 0.215	Depositor DCC
R_{free} test set	6721 reflections (4.93%)	wwPDB-VP
Wilson B-factor (Å^2)	25.9	Xtriage
Anisotropy	0.017	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 43.3	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.039 for h,-k,-l	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	12093	wwPDB-VP
Average B, all atoms (Å^2)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.71% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ 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: 1PE, NAG, NA, FLC

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	0.61	0/2139	0.76	2/2914 (0.1%)
1	B	0.62	0/1946	0.76	3/2649 (0.1%)
2	C	0.68	1/1830 (0.1%)	0.80	2/2489 (0.1%)
2	E	0.68	1/1813 (0.1%)	0.84	2/2466 (0.1%)
3	D	0.60	0/1671	0.77	1/2266 (0.0%)
3	F	0.68	0/1678	0.85	2/2276 (0.1%)
All	All	0.65	2/11077 (0.0%)	0.80	12/15060 (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
2	E	0	3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	16	GLU	CD-OE1	8.34	1.34	1.25
2	E	92	CYS	CB-SG	-5.29	1.73	1.81

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	E	178	LEU	CA-CB-CG	7.89	133.44	115.30
2	C	178	LEU	CB-CG-CD2	7.11	123.08	111.00
3	F	28	ASP	CB-CG-OD1	6.94	124.54	118.30
2	C	178	LEU	CA-CB-CG	6.53	130.32	115.30
1	B	220	ARG	NE-CZ-NH2	-6.50	117.05	120.30

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	E	132	SER	Peptide
2	E	190	GLY	Peptide
2	E	27(B)	PHE	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	2087	0	2022	5	0
1	B	1900	0	1838	10	0
2	C	1791	0	1733	6	0
2	E	1774	0	1721	5	1
3	D	1637	0	1602	9	1
3	F	1644	0	1608	8	0
4	A	28	0	26	0	0
4	B	28	0	26	0	0
5	A	16	0	22	0	0
5	B	48	0	66	0	0
6	B	1	0	0	0	0
7	C	26	0	10	0	0
8	A	191	0	0	0	0
8	B	154	0	0	0	0
8	C	183	0	0	3	0
8	D	152	0	0	1	0
8	E	201	0	0	0	0
8	F	232	0	0	1	0
All	All	12093	0	10674	38	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 2.

The worst 5 of 38 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)
2:C:2:VAL:N	8:C:401:HOH:O	2.20	0.74
3:F:155:GLN:HE21	3:F:158:ASN:HD21	1.40	0.68
2:C:16:GLU:HG2	8:C:578:HOH:O	2.00	0.61
3:F:55:GLN:HE21	3:F:55:GLN:HA	1.66	0.61
2:E:127:SER:N	2:E:130:SER:OG	2.35	0.60

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)
3:D:17:ASP:OD1	2:E:133:GLY:O[1_645]	1.85	0.35

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	267/274 (97%)	260 (97%)	6 (2%)	1 (0%)	34	22
1	B	240/274 (88%)	228 (95%)	11 (5%)	1 (0%)	34	22
2	C	239/247 (97%)	233 (98%)	6 (2%)	0	100	100
2	E	237/247 (96%)	228 (96%)	8 (3%)	1 (0%)	34	22
3	D	211/214 (99%)	205 (97%)	6 (3%)	0	100	100
3	F	212/214 (99%)	206 (97%)	6 (3%)	0	100	100
All	All	1406/1470 (96%)	1360 (97%)	43 (3%)	3 (0%)	47	38

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	E	133	GLY
1	A	62	ILE
1	B	62	ILE

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	238/242 (98%)	233 (98%)	5 (2%)	53	47
1	B	215/242 (89%)	207 (96%)	8 (4%)	34	22
2	C	201/207 (97%)	194 (96%)	7 (4%)	36	24
2	E	199/207 (96%)	191 (96%)	8 (4%)	31	19
3	D	186/187 (100%)	181 (97%)	5 (3%)	44	35
3	F	187/187 (100%)	182 (97%)	5 (3%)	44	35
All	All	1226/1272 (96%)	1188 (97%)	38 (3%)	40	28

5 of 38 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	E	135	THR
3	F	137	ASN
2	E	178	LEU
2	E	214	LYS
3	F	154	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 21 such sidechains are listed below:

Mol	Chain	Res	Type
3	D	155	GLN
3	F	124	GLN
3	F	155	GLN
3	F	137	ASN
3	F	55	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 11 ligands modelled in this entry, 1 is monoatomic - leaving 10 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	$\#\|Z\| > 2$
5	1PE	B	404	-	15,15,15	0.49	0	14,14,14	0.26	0
4	NAG	B	401	1	14,14,15	0.77	0	17,19,21	1.06	2 (11%)
4	NAG	A	402	1	14,14,15	0.57	0	17,19,21	1.07	1 (5%)
5	1PE	A	403	-	15,15,15	0.56	0	14,14,14	0.40	0
7	FLC	C	301	-	12,12,12	1.00	0	17,17,17	1.23	2 (11%)
4	NAG	B	402	1	14,14,15	0.60	0	17,19,21	1.22	3 (17%)
7	FLC	C	302	-	12,12,12	1.04	0	17,17,17	1.22	2 (11%)
4	NAG	A	401	1	14,14,15	0.76	0	17,19,21	1.95	3 (17%)
5	1PE	B	403	-	15,15,15	0.53	0	14,14,14	0.37	0
5	1PE	B	405	-	15,15,15	0.53	0	14,14,14	0.34	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	1PE	B	404	-	-	3/13/13/13	-
4	NAG	B	401	1	-	0/6/23/26	0/1/1/1
4	NAG	A	402	1	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	1PE	A	403	-	-	5/13/13/13	-
7	FLC	C	301	-	-	0/16/16/16	-
4	NAG	B	402	1	-	2/6/23/26	0/1/1/1
7	FLC	C	302	-	-	6/16/16/16	-
4	NAG	A	401	1	-	0/6/23/26	0/1/1/1
5	1PE	B	403	-	-	5/13/13/13	-
5	1PE	B	405	-	-	2/13/13/13	-

There are no bond length outliers.

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	A	401	NAG	C1-O5-C5	6.46	120.94	112.19
7	C	301	FLC	OB2-CBC-CB	3.30	118.78	113.05
4	A	401	NAG	O5-C1-C2	2.97	115.97	111.29
7	C	302	FLC	OB2-CBC-CB	2.68	117.71	113.05
4	B	402	NAG	C1-O5-C5	2.58	115.69	112.19

There are no chirality outliers.

5 of 23 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	B	402	NAG	O5-C5-C6-O6
4	B	402	NAG	C4-C5-C6-O6
5	B	405	1PE	OH4-C13-C23-OH3
5	A	403	1PE	OH4-C13-C23-OH3
5	B	404	1PE	OH7-C16-C26-OH6

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	267/274 (97%)	0.54	27 (10%)	7	7	16, 27, 64, 78	0
1	B	243/274 (88%)	1.13	31 (12%)	3	4	19, 32, 137, 166	0
2	C	238/247 (96%)	0.42	17 (7%)	16	17	20, 28, 63, 98	0
2	E	238/247 (96%)	0.29	12 (5%)	28	31	19, 27, 58, 100	0
3	D	213/214 (99%)	0.08	4 (1%)	66	68	22, 32, 54, 76	0
3	F	213/214 (99%)	-0.05	2 (0%)	84	85	17, 24, 35, 53	0
All	All	1412/1470 (96%)	0.42	93 (6%)	18	20	16, 28, 63, 166	0

The worst 5 of 93 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	305	CYS	16.7
1	B	52	CYS	15.7
1	B	282	ILE	15.2
1	B	300	ILE	14.2
1	B	278	ILE	14.0

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 monosaccharides 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(Å^2)	Q<0.9
5	1PE	A	403	16/16	0.53	0.30	69,73,79,79	0
7	FLC	C	302	13/13	0.62	0.41	47,73,77,80	0
4	NAG	A	401	14/15	0.66	0.33	64,74,79,80	0
5	1PE	B	405	16/16	0.69	0.27	71,81,86,88	0
5	1PE	B	403	16/16	0.70	0.29	70,76,82,82	0
7	FLC	C	301	13/13	0.72	0.42	70,80,85,88	0
4	NAG	B	401	14/15	0.73	0.25	60,68,70,73	0
4	NAG	A	402	14/15	0.79	0.50	65,70,74,75	0
5	1PE	B	404	16/16	0.81	0.25	74,78,80,80	0
4	NAG	B	402	14/15	0.81	0.41	74,83,87,87	0
6	NA	B	406	1/1	0.90	0.27	46,46,46,46	0

6.5 Other polymers (i)

There are no such residues in this entry.