



Full wwPDB X-ray Structure Validation Report ⓘ

Sep 15, 2017 – 12:54 PM EDT

PDB ID : 5VTU
Title : Crystal structure of the A/Hong Kong/1/1968 (H3N2) influenza virus hemagglutinin G225L/L226S mutant apo form
Authors : Wu, N.C.; Wilson, I.A.
Deposited on : unknown
Resolution : 2.45 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-20029824
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-20029824

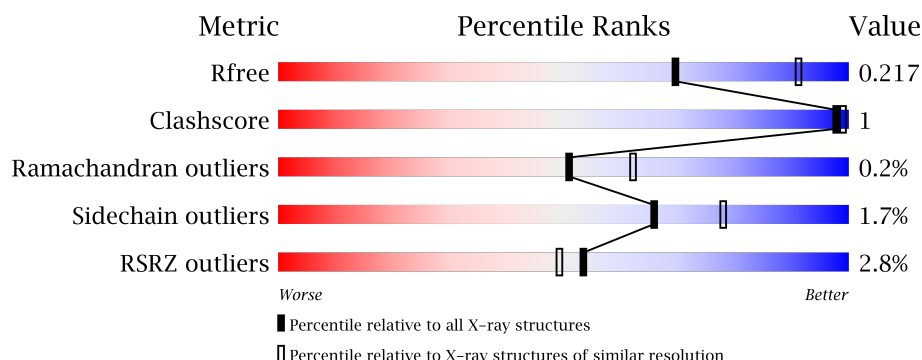
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.45 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	1119 (2.48-2.44)
Clashscore	112137	1193 (2.48-2.44)
Ramachandran outliers	110173	1185 (2.48-2.44)
Sidechain outliers	110143	1185 (2.48-2.44)
RSRZ outliers	101464	1126 (2.48-2.44)

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	323	<div> <div>0.2%</div> <div>92%</div> <div>6%</div> <div>.</div> </div>
1	C	323	<div> <div>2%</div> <div>93%</div> <div>5%</div> <div>.</div> </div>
1	E	323	<div> <div>2%</div> <div>93%</div> <div>5%</div> <div>.</div> </div>
2	B	174	<div> <div>2%</div> <div>98%</div> <div>..</div> </div>
2	D	174	<div> <div>9%</div> <div>97%</div> <div>...</div> </div>

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Mol	Chain	Length	Quality of chain
2	F	174	<div> <div>4%</div> <div>98%</div> <div>..</div> </div>

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
3	NAG	A	402	-	-	-	X
3	NAG	A	406	-	-	-	X
3	NAG	E	501	-	-	-	X

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 12078 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 HA1 chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	317	Total	C	N	O	S	0	0	0
			2445	1532	429	471	13			
1	C	316	Total	C	N	O	S	0	0	0
			2438	1527	428	470	13			
1	E	317	Total	C	N	O	S	0	0	0
			2445	1532	429	471	13			

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	7	ALA	-	expression tag	UNP Q91MA7
A	8	ASP	-	expression tag	UNP Q91MA7
A	9	PRO	-	expression tag	UNP Q91MA7
A	10	GLY	-	expression tag	UNP Q91MA7
A	225	LEU	GLY	engineered mutation	UNP Q91MA7
A	226	SER	LEU	engineered mutation	UNP Q91MA7
C	7	ALA	-	expression tag	UNP Q91MA7
C	8	ASP	-	expression tag	UNP Q91MA7
C	9	PRO	-	expression tag	UNP Q91MA7
C	10	GLY	-	expression tag	UNP Q91MA7
C	225	LEU	GLY	engineered mutation	UNP Q91MA7
C	226	SER	LEU	engineered mutation	UNP Q91MA7
E	7	ALA	-	expression tag	UNP Q91MA7
E	8	ASP	-	expression tag	UNP Q91MA7
E	9	PRO	-	expression tag	UNP Q91MA7
E	10	GLY	-	expression tag	UNP Q91MA7
E	225	LEU	GLY	engineered mutation	UNP Q91MA7
E	226	SER	LEU	engineered mutation	UNP Q91MA7

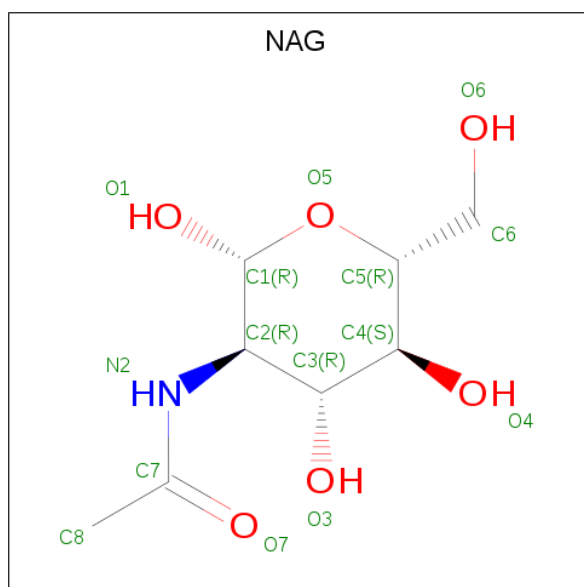
- Molecule 2 is a protein called Hemagglutinin HA2 chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	172	Total	C	N	O	S	0	0	0
			1391	863	243	279	6			
2	D	171	Total	C	N	O	S	0	0	0
			1382	858	241	277	6			
2	F	171	Total	C	N	O	S	0	0	0
			1382	858	241	277	6			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	123	GLY	ARG	conflict	UNP Q91MA7
D	123	GLY	ARG	conflict	UNP Q91MA7
F	123	GLY	ARG	conflict	UNP Q91MA7

- Molecule 3 is N-ACETYL-D-GLUCOSAMINE (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



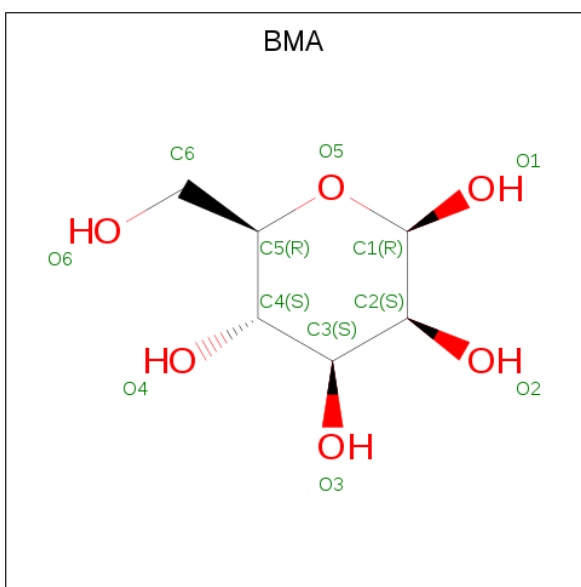
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O		0	0
			14	8	1	5			
3	A	1	Total	C	N	O		0	0
			14	8	1	5			
3	A	1	Total	C	N	O		0	0
			14	8	1	5			
3	A	1	Total	C	N	O		0	0
			14	8	1	5			
3	A	1	Total	C	N	O		0	0
			14	8	1	5			

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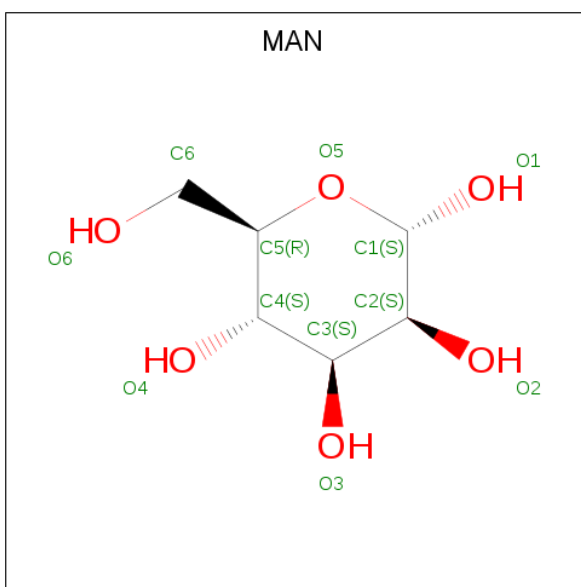
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
3	C	1	Total	C	N	O	0	0
			14	8	1	5		
3	C	1	Total	C	N	O	0	0
			14	8	1	5		
3	C	1	Total	C	N	O	0	0
			14	8	1	5		
3	C	1	Total	C	N	O	0	0
			14	8	1	5		
3	E	1	Total	C	N	O	0	0
			14	8	1	5		
3	E	1	Total	C	N	O	0	0
			14	8	1	5		
3	E	1	Total	C	N	O	0	0
			14	8	1	5		
3	E	1	Total	C	N	O	0	0
			14	8	1	5		
3	E	1	Total	C	N	O	0	0
			14	8	1	5		
3	E	1	Total	C	N	O	0	0
			14	8	1	5		
3	F	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 4 is BETA-D-MANNOSE (three-letter code: BMA) (formula: C₆H₁₂O₆).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			11	6	5		
4	C	1	Total	C	O	0	0
			11	6	5		
4	E	1	Total	C	O	0	0
			11	6	5		

- Molecule 5 is ALPHA-D-MANNOSE (three-letter code: MAN) (formula: C₆H₁₂O₆).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	C	1	Total	C	O	0	0
			11	6	5		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	E	1	Total	C	O	0	0
			11	6	5		

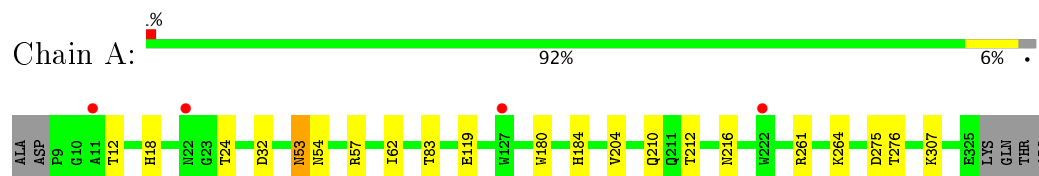
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	48	Total	O	0	0
			48	48		
6	B	31	Total	O	0	0
			31	31		
6	C	53	Total	O	0	0
			53	53		
6	D	39	Total	O	0	0
			39	39		
6	E	70	Total	O	0	0
			70	70		
6	F	33	Total	O	0	0
			33	33		

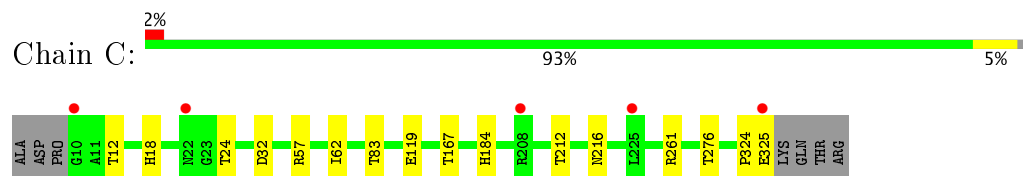
3 Residue-property plots [i](#)

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.

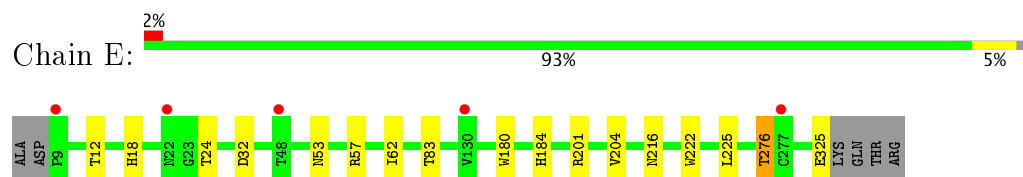
- Molecule 1: Hemagglutinin HA1 chain



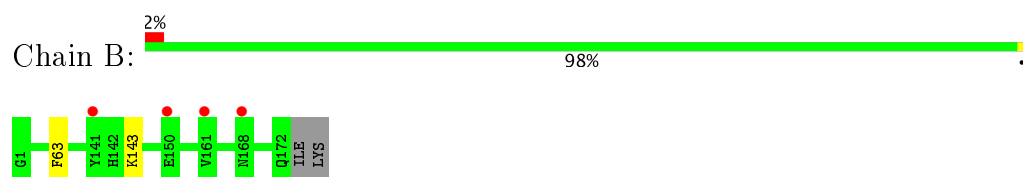
- Molecule 1: Hemagglutinin HA1 chain



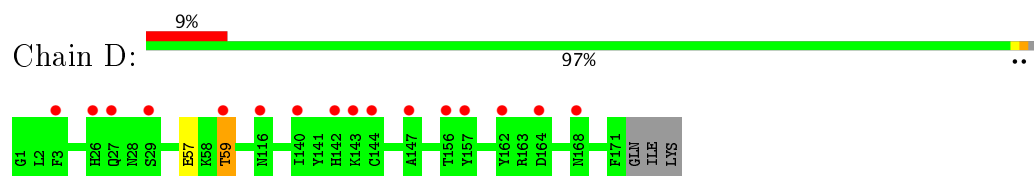
- Molecule 1: Hemagglutinin HA1 chain



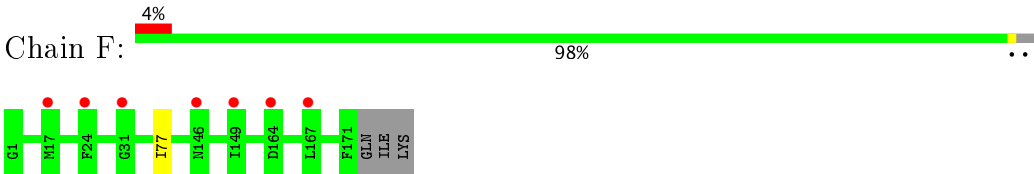
- Molecule 2: Hemagglutinin HA2 chain



- Molecule 2: Hemagglutinin HA2 chain



- Molecule 2: Hemagglutinin HA2 chain



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	205.55Å 129.39Å 72.89Å 90.00° 102.66° 90.00°	Depositor
Resolution (Å)	50.00 – 2.45 46.00 – 2.45	Depositor EDS
% Data completeness (in resolution range)	97.9 (50.00-2.45) 97.9 (46.00-2.45)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.11 (at 2.45Å)	Xtriage
Refinement program	REFMAC 5.8.0155	Depositor
R, R_{free}	0.198 , 0.220 0.199 , 0.217	Depositor DCC
R_{free} test set	3348 reflections (5.28%)	DCC
Wilson B-factor (Å ²)	52.3	Xtriage
Anisotropy	0.171	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 30.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	12078	wwPDB-VP
Average B, all atoms (Å ²)	61.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.22% 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: BMA, NAG, MAN

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	0.50	0/2502	0.74	1/3410 (0.0%)
1	C	0.48	0/2494	0.71	0/3399
1	E	0.50	0/2502	0.72	0/3410
2	B	0.48	0/1415	0.69	0/1902
2	D	0.49	0/1406	0.68	0/1890
2	F	0.48	0/1406	0.67	0/1890
All	All	0.49	0/11725	0.71	1/15901 (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	A	275	ASP	CB-CG-OD1	5.17	122.95	118.30

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	2445	0	2392	7	0
1	C	2438	0	2385	7	0
1	E	2445	0	2392	6	0
2	B	1391	0	1307	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	D	1382	0	1299	1	0
2	F	1382	0	1298	1	0
3	A	84	0	75	0	0
3	C	70	0	62	1	0
3	E	98	0	87	0	0
3	F	14	0	13	0	0
4	A	11	0	10	0	0
4	C	11	0	9	0	0
4	E	11	0	9	0	0
5	C	11	0	10	0	0
5	E	11	0	10	0	0
6	A	48	0	0	0	0
6	B	31	0	0	0	0
6	C	53	0	0	0	0
6	D	39	0	0	0	0
6	E	70	0	0	0	0
6	F	33	0	0	1	0
All	All	12078	0	11358	20	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 (20) 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:D:57:GLU:O	2:D:59:THR:HG22	1.95	0.67
1:C:324:PRO:O	1:C:325:GLU:HB2	2.00	0.61
1:C:167:THR:OG1	3:C:502:NAG:H62	2.00	0.61
1:C:119:GLU:OE2	1:C:261:ARG:NH2	2.40	0.54
1:A:212:THR:HG21	1:C:216:ASN:HB3	1.90	0.54
1:A:119:GLU:OE2	1:A:261:ARG:NH2	2.43	0.52
1:E:57:ARG:NH1	1:E:83:THR:O	2.46	0.49
1:A:57:ARG:NH1	1:A:83:THR:O	2.46	0.48
1:C:57:ARG:NH1	1:C:83:THR:O	2.47	0.48
1:E:53:ASN:HD21	1:E:276:THR:HG23	1.78	0.47
1:E:184:HIS:HD1	1:E:216:ASN:H	1.64	0.45
1:C:184:HIS:HD1	1:C:216:ASN:H	1.65	0.44
1:A:184:HIS:HD1	1:A:216:ASN:H	1.66	0.43
2:F:77:ILE:HG22	6:F:322:HOH:O	2.20	0.41
1:A:53:ASN:HD22	1:A:54:ASN:N	2.18	0.41
1:A:180:TRP:CE2	1:A:204:VAL:HG21	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:222:TRP:CZ2	1:E:225:LEU:HA	2.56	0.41
1:C:212:THR:HB	1:E:216:ASN:ND2	2.35	0.40
1:E:180:TRP:CE2	1:E:204:VAL:HG21	2.57	0.40
1:A:264:LYS:HG2	2:B:63:PHE:CD2	2.56	0.40

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	315/323 (98%)	305 (97%)	9 (3%)	1 (0%)	44	55
1	C	314/323 (97%)	303 (96%)	10 (3%)	1 (0%)	44	55
1	E	315/323 (98%)	305 (97%)	9 (3%)	1 (0%)	44	55
2	B	170/174 (98%)	159 (94%)	11 (6%)	0	100	100
2	D	169/174 (97%)	160 (95%)	9 (5%)	0	100	100
2	F	169/174 (97%)	160 (95%)	9 (5%)	0	100	100
All	All	1452/1491 (97%)	1392 (96%)	57 (4%)	3 (0%)	51	62

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	62	ILE
1	C	62	ILE
1	E	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	279/284 (98%)	271 (97%)	8 (3%)	48	61
1	C	278/284 (98%)	273 (98%)	5 (2%)	64	77
1	E	279/284 (98%)	272 (98%)	7 (2%)	53	67
2	B	146/148 (99%)	145 (99%)	1 (1%)	87	92
2	D	145/148 (98%)	144 (99%)	1 (1%)	87	92
2	F	145/148 (98%)	145 (100%)	0	100	100
All	All	1272/1296 (98%)	1250 (98%)	22 (2%)	66	78

All (22) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	12	THR
1	A	18	HIS
1	A	24	THR
1	A	32	ASP
1	A	53	ASN
1	A	210	GLN
1	A	276	THR
1	A	307	LYS
2	B	143	LYS
1	C	12	THR
1	C	18	HIS
1	C	24	THR
1	C	32	ASP
1	C	276	THR
2	D	59	THR
1	E	12	THR
1	E	18	HIS
1	E	24	THR
1	E	32	ASP
1	E	201	ARG
1	E	276	THR
1	E	325	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	18	HIS
1	A	53	ASN
1	A	216	ASN
2	B	53	ASN
2	B	125	GLN
1	C	18	HIS
2	D	53	ASN
2	D	125	GLN
1	E	18	HIS
1	E	33	GLN
1	E	216	ASN
2	F	53	ASN
2	F	125	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](#)

24 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	NAG	A	401	1	14,14,15	0.67	0	15,19,21	1.03	2 (13%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	NAG	A	402	1	14,14,15	0.50	0	15,19,21	1.80	2 (13%)
3	NAG	A	403	1,3	14,14,15	0.48	0	15,19,21	1.17	1 (6%)
3	NAG	A	404	3,4	14,14,15	0.43	0	15,19,21	0.88	0
4	BMA	A	405	3	11,11,12	0.40	0	13,15,17	0.88	1 (7%)
3	NAG	A	406	1,3	14,14,15	0.47	0	15,19,21	1.38	2 (13%)
3	NAG	A	407	3	14,14,15	0.44	0	15,19,21	1.85	5 (33%)
3	NAG	C	501	1	14,14,15	0.61	0	15,19,21	3.19	8 (53%)
3	NAG	C	502	1,3	14,14,15	0.45	0	15,19,21	1.57	2 (13%)
3	NAG	C	503	3,4	14,14,15	0.41	0	15,19,21	1.02	0
4	BMA	C	504	3,5	11,11,12	0.58	0	13,15,17	1.43	2 (15%)
5	MAN	C	505	4	11,11,12	0.56	0	13,15,17	2.40	3 (23%)
3	NAG	C	506	1,3	14,14,15	0.37	0	15,19,21	0.80	0
3	NAG	C	507	3	14,14,15	0.41	0	15,19,21	1.97	1 (6%)
3	NAG	E	501	1	14,14,15	0.36	0	15,19,21	1.37	1 (6%)
3	NAG	E	502	1,3	14,14,15	0.51	0	15,19,21	1.63	2 (13%)
3	NAG	E	503	3,4	14,14,15	0.56	0	15,19,21	1.60	2 (13%)
4	BMA	E	504	3,5	11,11,12	0.83	1 (9%)	13,15,17	2.19	2 (15%)
5	MAN	E	505	4	11,11,12	0.47	0	13,15,17	1.86	1 (7%)
3	NAG	E	506	1,3	14,14,15	0.73	0	15,19,21	1.14	2 (13%)
3	NAG	E	507	3	14,14,15	0.66	0	15,19,21	2.26	2 (13%)
3	NAG	E	508	1,3	14,14,15	0.44	0	15,19,21	1.13	2 (13%)
3	NAG	E	509	3	14,14,15	0.42	0	15,19,21	1.21	2 (13%)
3	NAG	F	201	2	14,14,15	0.69	1 (7%)	15,19,21	1.03	2 (13%)

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	NAG	A	401	1	-	0/6/23/26	0/1/1/1
3	NAG	A	402	1	-	0/6/23/26	0/1/1/1
3	NAG	A	403	1,3	-	0/6/23/26	0/1/1/1
3	NAG	A	404	3,4	-	0/6/23/26	0/1/1/1
4	BMA	A	405	3	-	0/2/19/22	0/1/1/1
3	NAG	A	406	1,3	-	0/6/23/26	0/1/1/1
3	NAG	A	407	3	-	0/6/23/26	0/1/1/1
3	NAG	C	501	1	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAG	C	502	1,3	-	0/6/23/26	0/1/1/1
3	NAG	C	503	3,4	-	0/6/23/26	0/1/1/1
4	BMA	C	504	3,5	-	0/2/19/22	0/1/1/1
5	MAN	C	505	4	-	0/2/19/22	0/1/1/1
3	NAG	C	506	1,3	-	0/6/23/26	0/1/1/1
3	NAG	C	507	3	-	0/6/23/26	0/1/1/1
3	NAG	E	501	1	-	0/6/23/26	0/1/1/1
3	NAG	E	502	1,3	-	0/6/23/26	0/1/1/1
3	NAG	E	503	3,4	-	0/6/23/26	0/1/1/1
4	BMA	E	504	3,5	-	0/2/19/22	0/1/1/1
5	MAN	E	505	4	-	0/2/19/22	0/1/1/1
3	NAG	E	506	1,3	-	0/6/23/26	0/1/1/1
3	NAG	E	507	3	-	0/6/23/26	0/1/1/1
3	NAG	E	508	1,3	-	0/6/23/26	0/1/1/1
3	NAG	E	509	3	-	0/6/23/26	0/1/1/1
3	NAG	F	201	2	-	0/6/23/26	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	E	504	BMA	C2-C3	2.08	1.55	1.52
3	F	201	NAG	C1-C2	2.13	1.55	1.52

All (47) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	501	NAG	C4-C3-C2	-4.56	104.34	111.02
3	E	502	NAG	O5-C1-C2	-4.30	105.48	111.47
3	C	501	NAG	O7-C7-N2	-3.09	115.96	121.92
3	C	501	NAG	C1-C2-N2	-2.87	105.58	110.49
3	C	502	NAG	O4-C4-C5	-2.50	102.97	109.28
3	E	508	NAG	O5-C1-C2	-2.36	108.19	111.47
3	A	407	NAG	O5-C1-C2	-2.26	108.33	111.47
3	A	407	NAG	C6-C5-C4	-2.13	108.02	113.00
3	E	507	NAG	C4-C3-C2	-2.11	107.93	111.02
3	A	401	NAG	C6-C5-C4	-2.10	108.09	113.00
3	F	201	NAG	C3-C4-C5	-2.08	106.56	110.22
3	A	402	NAG	C6-C5-C4	-2.03	108.24	113.00
3	E	506	NAG	O4-C4-C5	2.00	114.33	109.28
3	E	509	NAG	C4-C3-C2	2.03	114.00	111.02
3	F	201	NAG	C1-O5-C5	2.06	115.00	112.17
4	A	405	BMA	C1-C2-C3	2.17	112.41	109.65

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	E	506	NAG	C1-C2-N2	2.23	114.29	110.49
4	C	504	BMA	C1-C2-C3	2.25	112.50	109.65
3	A	407	NAG	C1-C2-N2	2.28	114.39	110.49
3	A	407	NAG	C3-C4-C5	2.38	114.41	110.22
3	A	406	NAG	C3-C4-C5	2.46	114.55	110.22
3	E	508	NAG	C1-C2-N2	2.47	114.71	110.49
4	C	504	BMA	C3-C4-C5	2.47	114.58	110.22
3	C	501	NAG	O5-C1-C2	2.49	114.94	111.47
3	E	503	NAG	C1-C2-N2	2.56	114.86	110.49
3	E	509	NAG	C1-O5-C5	2.57	115.71	112.17
5	C	505	MAN	O5-C1-C2	2.72	115.05	110.79
3	A	401	NAG	C1-O5-C5	2.73	115.92	112.17
3	C	501	NAG	C3-C4-C5	3.11	115.70	110.22
3	E	502	NAG	C1-O5-C5	3.18	116.55	112.17
3	A	406	NAG	C1-C2-N2	3.18	115.92	110.49
4	E	504	BMA	C2-C3-C4	3.39	116.80	110.88
3	A	403	NAG	C1-O5-C5	3.56	117.08	112.17
3	C	502	NAG	C1-O5-C5	4.36	118.17	112.17
3	E	501	NAG	C1-O5-C5	4.64	118.56	112.17
3	A	407	NAG	C1-O5-C5	4.78	118.75	112.17
3	E	503	NAG	C1-O5-C5	4.99	119.05	112.17
3	C	501	NAG	C8-C7-N2	5.24	125.56	116.11
3	C	501	NAG	C2-N2-C7	5.42	130.86	122.94
5	C	505	MAN	C1-C2-C3	5.59	116.74	109.65
5	C	505	MAN	C1-O5-C5	5.63	119.93	112.17
3	A	402	NAG	C1-O5-C5	5.82	120.19	112.17
3	C	501	NAG	C1-O5-C5	5.90	120.30	112.17
5	E	505	MAN	C1-O5-C5	6.22	120.75	112.17
3	C	507	NAG	C1-O5-C5	6.23	120.75	112.17
4	E	504	BMA	C1-C2-C3	6.42	117.80	109.65
3	E	507	NAG	C1-O5-C5	7.62	122.67	112.17

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	502	NAG	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	317/323 (98%)	0.13	4 (1%) 77 76	38, 59, 84, 106	0
1	C	316/323 (97%)	0.13	5 (1%) 72 70	40, 55, 72, 108	0
1	E	317/323 (98%)	0.06	5 (1%) 72 70	37, 53, 72, 115	0
2	B	172/174 (98%)	0.34	4 (2%) 61 57	35, 62, 103, 115	0
2	D	171/174 (98%)	0.73	16 (9%) 9 7	35, 70, 118, 131	0
2	F	171/174 (98%)	0.37	7 (4%) 38 35	36, 62, 93, 109	0
All	All	1464/1491 (98%)	0.24	41 (2%) 53 49	35, 57, 97, 131	0

All (41) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	22	ASN	6.1
2	D	27	GLN	5.3
2	F	31	GLY	4.8
2	D	164	ASP	4.1
2	D	140	ILE	3.5
1	C	10	GLY	3.4
1	A	22	ASN	3.2
2	B	168	ASN	3.0
2	B	161	VAL	3.0
2	F	146	ASN	2.9
1	C	325	GLU	2.9
2	F	17	MET	2.9
2	B	141	TYR	2.8
1	E	130	VAL	2.8
2	D	143	LYS	2.8
2	D	162	TYR	2.8
2	D	142	HIS	2.8
2	F	164	ASP	2.7
2	D	157	TYR	2.6

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Mol	Chain	Res	Type	RSRZ
2	D	29	SER	2.6
2	F	167	LEU	2.4
2	D	147	ALA	2.4
1	A	222	TRP	2.4
1	E	277	CYS	2.4
1	C	208	ARG	2.3
1	C	225	LEU	2.3
2	F	24	PHE	2.3
2	D	3	PHE	2.2
2	D	156	THR	2.2
1	E	9	PRO	2.2
1	E	22	ASN	2.1
1	A	11	ALA	2.1
1	E	48	THR	2.1
2	D	144	CYS	2.1
2	F	149	ILE	2.1
1	A	127	TRP	2.1
2	D	168	ASN	2.1
2	B	150	GLU	2.0
2	D	59	THR	2.0
2	D	26	HIS	2.0
2	D	116	ASN	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
3	NAG	E	501	14/15	0.82	0.27	3.61	74,86,90,91	0
3	NAG	A	402	14/15	0.90	0.33	2.36	68,80,89,89	0
3	NAG	A	406	14/15	0.93	0.20	2.11	57,64,71,88	0
3	NAG	E	503	14/15	0.94	0.27	1.67	66,78,82,89	0
3	NAG	F	201	14/15	0.91	0.34	1.53	80,88,100,104	0
3	NAG	E	506	14/15	0.95	0.16	0.63	57,62,70,83	0
3	NAG	A	403	14/15	0.93	0.20	0.21	61,69,77,77	0
3	NAG	C	506	14/15	0.96	0.16	-0.33	54,59,71,76	0
3	NAG	C	502	14/15	0.95	0.12	-1.02	47,52,59,61	0
3	NAG	C	503	14/15	0.95	0.12	-1.38	60,66,76,83	0
3	NAG	E	508	14/15	0.95	0.11	-1.53	67,76,81,88	0
5	MAN	E	505	11/12	0.85	0.32	-	116,122,124,125	0
4	BMA	C	504	11/12	0.86	0.16	-	93,101,106,106	0
3	NAG	A	407	14/15	0.79	0.30	-	89,100,104,106	0
3	NAG	E	509	14/15	0.84	0.22	-	92,99,101,101	0
3	NAG	E	502	14/15	0.95	0.27	-	63,70,72,74	0
3	NAG	C	501	14/15	0.90	0.14	-	73,81,89,97	0
3	NAG	E	507	14/15	0.80	0.32	-	82,98,108,109	0
5	MAN	C	505	11/12	0.80	0.25	-	103,109,114,115	0
3	NAG	A	404	14/15	0.94	0.17	-	73,82,94,94	0
3	NAG	C	507	14/15	0.81	0.24	-	74,91,98,102	0
4	BMA	A	405	11/12	0.88	0.17	-	94,102,106,109	0
4	BMA	E	504	11/12	0.80	0.21	-	96,101,113,115	0
3	NAG	A	401	14/15	0.88	0.23	-	63,71,76,78	0

6.5 Other polymers [i](#)

There are no such residues in this entry.