



wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 17, 2017 – 01:47 PM EST

PDB ID : 5UGY
Title : Influenza hemagglutinin in complex with a neutralizing antibody
Authors : Whittle, J.R.R.; Jenni, S.; Harrison, S.C.
Deposited on : 2017-01-10
Resolution : 2.80 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	:	1.7.1 (RC1), CSD as537be (2016)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20028442
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
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-20028442

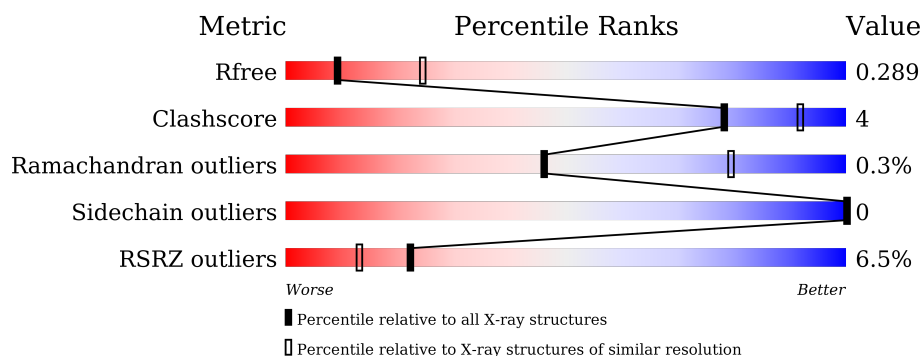
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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.



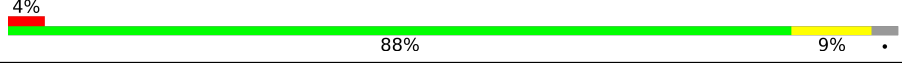
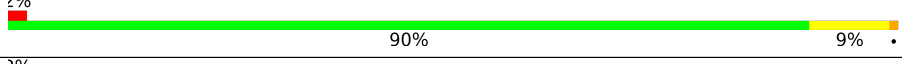
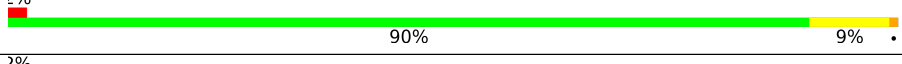

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	2393 (2.80-2.80)
Clashscore	102246	2827 (2.80-2.80)
Ramachandran outliers	100387	2782 (2.80-2.80)
Sidechain outliers	100360	2784 (2.80-2.80)
RSRZ outliers	91569	2404 (2.80-2.80)

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>8%</div> <div>93%</div> <div>7%</div> </div>
1	C	323	<div> <div>5%</div> <div>92%</div> <div>8%</div> </div>
1	E	323	<div> <div>6%</div> <div>94%</div> <div>6%</div> </div>
2	B	173	<div> <div>13%</div> <div>88%</div> <div>12%</div> </div>
2	D	173	<div> <div>16%</div> <div>88%</div> <div>12%</div> </div>
2	F	173	<div> <div>16%</div> <div>88%</div> <div>12%</div> </div>

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Mol	Chain	Length	Quality of chain
3	H	227	
3	I	227	
3	J	227	
4	L	210	
4	M	210	
4	N	210	

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
5	NAG	A	406	-	-	-	X
5	NAG	A	407	-	-	-	X
5	NAG	A	408	-	-	-	X
5	NAG	C	406	-	-	-	X
5	NAG	C	407	-	-	-	X
5	NAG	C	408	-	-	-	X
5	NAG	C	409	-	-	-	X
5	NAG	E	407	-	-	-	X
5	NAG	E	408	-	-	-	X
5	NAG	E	409	-	-	-	X

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 42918 atoms, of which 21036 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.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	323	Total	C	H	N	O	S	0	0	0
			4975	1597	2440	441	486	11			
1	C	323	Total	C	H	N	O	S	0	0	0
			4975	1597	2440	441	486	11			
1	E	323	Total	C	H	N	O	S	0	0	0
			4975	1597	2440	441	486	11			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	4	GLU	-	expression tag	UNP A7UPX0
C	4	GLU	-	expression tag	UNP A7UPX0
E	4	GLU	-	expression tag	UNP A7UPX0

- Molecule 2 is a protein called Hemagglutinin HA2.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	B	173	Total	C	H	N	O	S	0	0	0
			2718	874	1324	238	275	7			
2	D	173	Total	C	H	N	O	S	0	0	0
			2718	874	1324	238	275	7			
2	F	173	Total	C	H	N	O	S	0	0	0
			2718	874	1324	238	275	7			

- Molecule 3 is a protein called CH65 heavy chain.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
3	H	221	Total	C	H	N	O	S	0	0	0
			3294	1062	1617	279	328	8			
3	I	221	Total	C	H	N	O	S	0	0	0
			3294	1062	1617	279	328	8			

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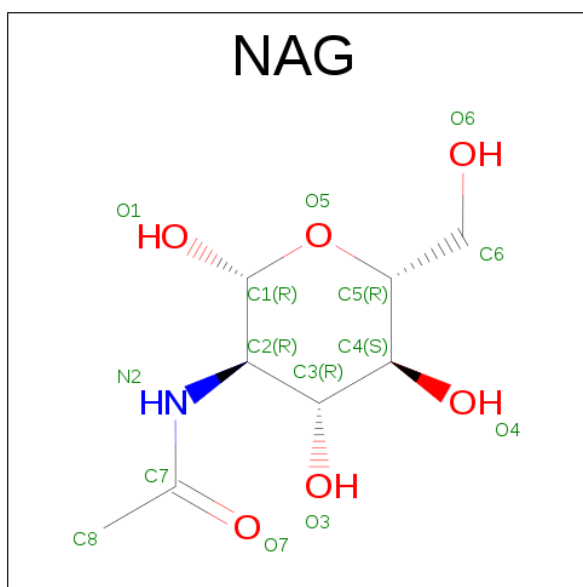
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Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
3	J	221	Total	C	H	N	O	S	0	0	0
			3294	1062	1617	279	328	8			

- Molecule 4 is a protein called CH65 light chain.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
4	L	210	Total	C	H	N	O	S	0	0	0
			3078	973	1513	269	318	5			
4	M	210	Total	C	H	N	O	S	0	0	0
			3078	973	1513	269	318	5			
4	N	210	Total	C	H	N	O	S	0	0	0
			3078	973	1513	269	318	5			

- Molecule 5 is N-ACETYL-D-GLUCOSAMINE (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



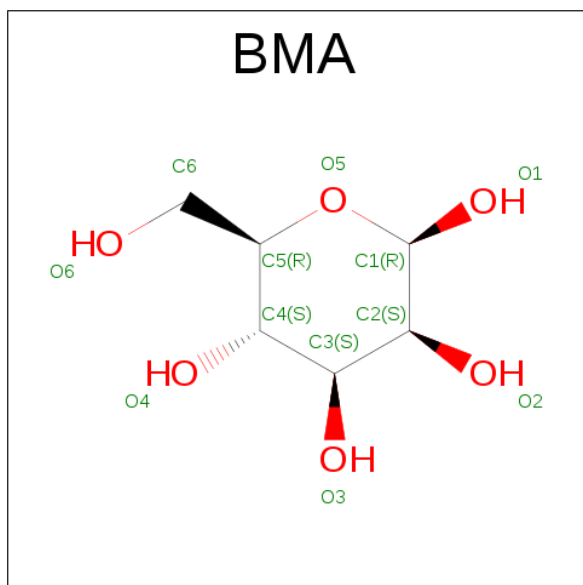
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total	C	H	N	O	0	0
			28	8	14	1	5		
5	A	1	Total	C	H	N	O	0	0
			27	8	13	1	5		
5	A	1	Total	C	H	N	O	0	0
			27	8	13	1	5		
5	A	1	Total	C	H	N	O	0	0
			27	8	13	1	5		
5	A	1	Total	C	H	N	O	0	0
			28	8	14	1	5		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total	C	H	N	O	0	0
			28	8	14	1	5		
5	A	1	Total	C	H	N	O	0	0
			28	8	14	1	5		
5	A	1	Total	C	H	N	O	0	0
			27	8	13	1	5		
5	C	1	Total	C	H	N	O	0	0
			28	8	14	1	5		
5	C	1	Total	C	H	N	O	0	0
			27	8	13	1	5		
5	C	1	Total	C	H	N	O	0	0
			27	8	13	1	5		
5	C	1	Total	C	H	N	O	0	0
			27	8	13	1	5		
5	C	1	Total	C	H	N	O	0	0
			28	8	14	1	5		
5	C	1	Total	C	H	N	O	0	0
			28	8	14	1	5		
5	C	1	Total	C	H	N	O	0	0
			28	8	14	1	5		
5	C	1	Total	C	H	N	O	0	0
			27	8	13	1	5		
5	E	1	Total	C	H	N	O	0	0
			28	8	14	1	5		
5	E	1	Total	C	H	N	O	0	0
			27	8	13	1	5		
5	E	1	Total	C	H	N	O	0	0
			27	8	13	1	5		
5	E	1	Total	C	H	N	O	0	0
			27	8	13	1	5		
5	E	1	Total	C	H	N	O	0	0
			28	8	14	1	5		
5	E	1	Total	C	H	N	O	0	0
			28	8	14	1	5		
5	E	1	Total	C	H	N	O	0	0
			28	8	14	1	5		
5	E	1	Total	C	H	N	O	0	0
			27	8	13	1	5		

- Molecule 6 is BETA-D-MANNOSE (three-letter code: BMA) (formula: C₆H₁₂O₆).

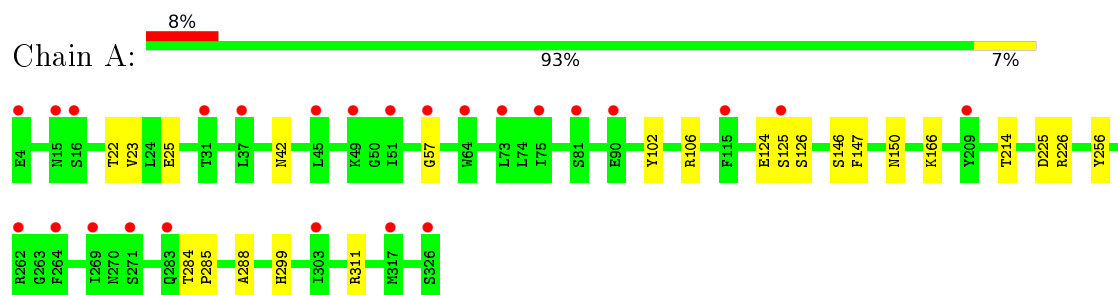


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	A	1	Total	C	H	O	0	0
			21	6	10	5		
6	C	1	Total	C	H	O	0	0
			21	6	10	5		
6	E	1	Total	C	H	O	0	0
			21	6	10	5		

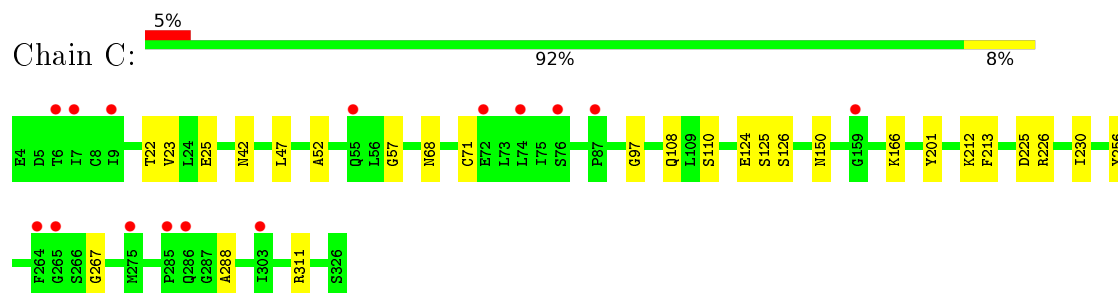
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

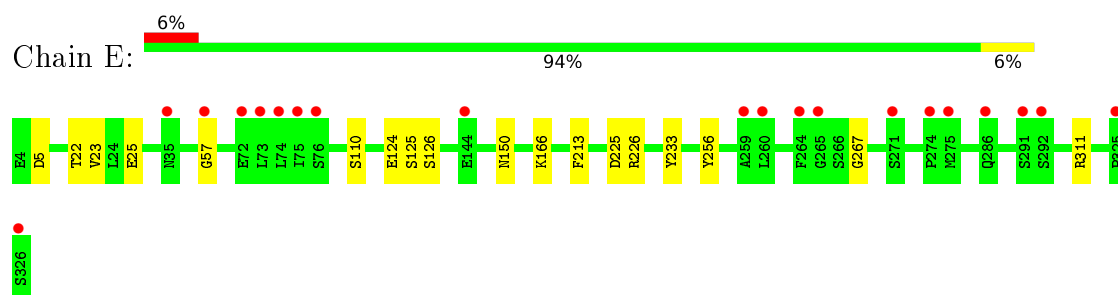
• Molecule 1: Hemagglutinin HA1



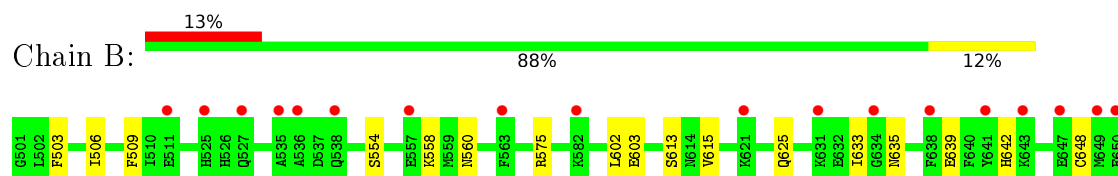
• Molecule 1: Hemagglutinin HA1

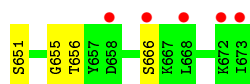


• Molecule 1: Hemagglutinin HA1

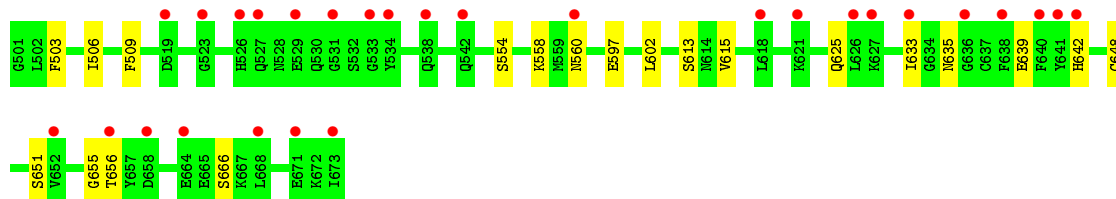
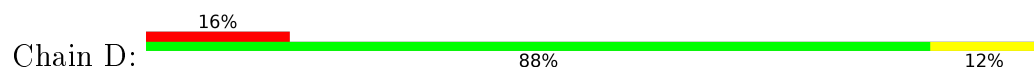


• Molecule 2: Hemagglutinin HA2

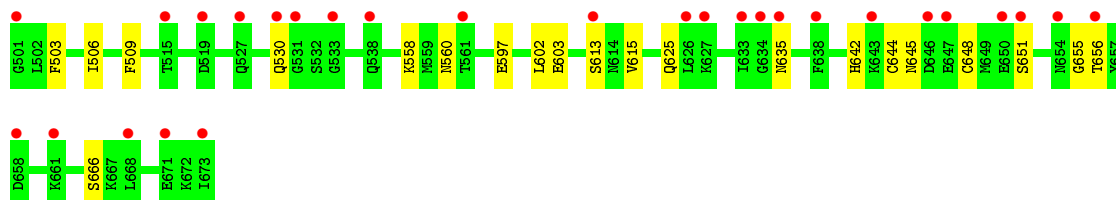
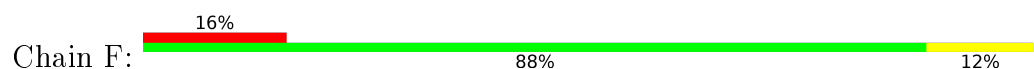




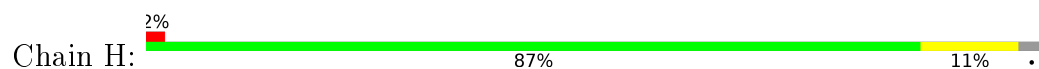
- Molecule 2: Hemagglutinin HA2



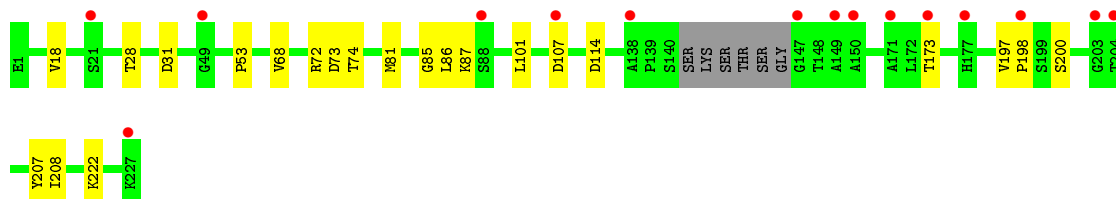
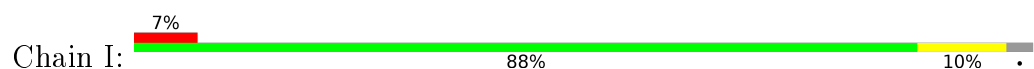
- Molecule 2: Hemagglutinin HA2



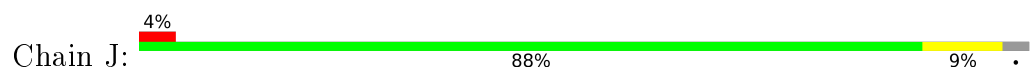
- Molecule 3: CH65 heavy chain



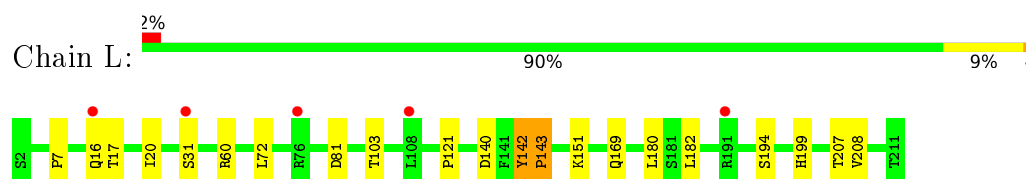
- Molecule 3: CH65 heavy chain



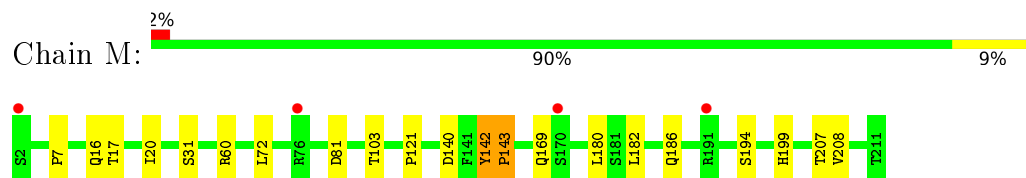
- Molecule 3: CH65 heavy chain



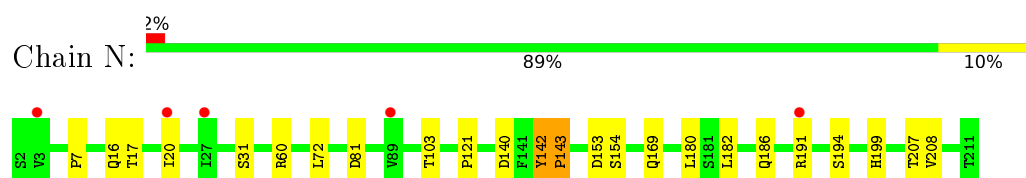
- Molecule 4: CH65 light chain



- Molecule 4: CH65 light chain



- Molecule 4: CH65 light chain



4 Data and refinement statistics

Property	Value	Source
Space group	I 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	154.82Å 192.19Å 333.22Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.92 – 2.80 166.61 – 2.80	Depositor EDS
% Data completeness (in resolution range)	91.7 (29.92-2.80) 91.7 (166.61-2.80)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.01 (at 2.82Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.259 , 0.289 0.258 , 0.289	Depositor DCC
R_{free} test set	2756 reflections (2.47%)	DCC
Wilson B-factor (Å ²)	40.0	Xtriage
Anisotropy	0.000	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 39.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.84	EDS
Total number of atoms	42918	wwPDB-VP
Average B, all atoms (Å ²)	49.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.93% 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: BMA, 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	0.25	0/2601	0.47	0/3540
1	C	0.25	0/2601	0.47	0/3540
1	E	0.25	0/2601	0.47	0/3540
2	B	0.27	0/1421	0.46	0/1909
2	D	0.27	0/1421	0.46	0/1909
2	F	0.27	0/1421	0.46	0/1909
3	H	0.26	0/1722	0.49	0/2351
3	I	0.27	0/1722	0.50	0/2351
3	J	0.27	0/1722	0.49	0/2351
4	L	0.26	0/1603	0.50	0/2192
4	M	0.26	0/1603	0.50	0/2192
4	N	0.26	0/1603	0.50	0/2192
All	All	0.26	0/22041	0.48	0/29976

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
4	L	0	1
4	M	0	1
4	N	0	1
All	All	0	3

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	L	142	TYR	Peptide
4	M	142	TYR	Peptide
4	N	142	TYR	Peptide

5.2 Too-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 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	2535	2440	2440	14	0
1	C	2535	2440	2440	16	0
1	E	2535	2440	2440	11	0
2	B	1394	1324	1323	16	0
2	D	1394	1324	1323	14	0
2	F	1394	1324	1323	17	0
3	H	1677	1617	1617	14	1
3	I	1677	1617	1617	13	2
3	J	1677	1617	1617	12	1
4	L	1565	1513	1513	14	0
4	M	1565	1513	1513	14	0
4	N	1565	1513	1513	17	0
5	A	112	108	100	0	0
5	C	112	108	100	0	0
5	E	112	108	100	0	0
6	A	11	10	10	0	0
6	C	11	10	10	0	0
6	E	11	10	10	0	0
All	All	21882	21036	21009	155	2

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 4.

The worst 5 of 155 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:B:625:GLN:NE2	2:B:655:GLY:O	2.04	0.91
2:D:625:GLN:NE2	2:D:655:GLY:O	2.09	0.86
2:F:625:GLN:NE2	2:F:655:GLY:O	2.11	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:225:ASP:O	1:E:226:ARG:NH1	2.12	0.81
1:C:225:ASP:O	1:C:226:ARG:NH1	2.13	0.79

All (2) 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:H:173:THR:OG1	3:I:173:THR:OG1[8_555]	2.11	0.09
3:I:200:SER:OG	3:J:185:SER:OG[3_545]	2.13	0.07

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	321/323 (99%)	304 (95%)	16 (5%)	1 (0%)	46	79
1	C	321/323 (99%)	305 (95%)	15 (5%)	1 (0%)	46	79
1	E	321/323 (99%)	305 (95%)	15 (5%)	1 (0%)	46	79
2	B	171/173 (99%)	157 (92%)	14 (8%)	0	100	100
2	D	171/173 (99%)	157 (92%)	14 (8%)	0	100	100
2	F	171/173 (99%)	157 (92%)	14 (8%)	0	100	100
3	H	217/227 (96%)	205 (94%)	12 (6%)	0	100	100
3	I	217/227 (96%)	207 (95%)	10 (5%)	0	100	100
3	J	217/227 (96%)	206 (95%)	11 (5%)	0	100	100
4	L	208/210 (99%)	196 (94%)	10 (5%)	2 (1%)	19	52
4	M	208/210 (99%)	197 (95%)	9 (4%)	2 (1%)	19	52
4	N	208/210 (99%)	197 (95%)	9 (4%)	2 (1%)	19	52
All	All	2751/2799 (98%)	2593 (94%)	149 (5%)	9 (0%)	46	79

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	L	143	PRO
4	M	143	PRO
4	N	143	PRO
4	L	31	SER
4	M	31	SER

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	283/283 (100%)	283 (100%)	0	100	100
1	C	283/283 (100%)	283 (100%)	0	100	100
1	E	283/283 (100%)	283 (100%)	0	100	100
2	B	149/149 (100%)	149 (100%)	0	100	100
2	D	149/149 (100%)	149 (100%)	0	100	100
2	F	149/149 (100%)	149 (100%)	0	100	100
3	H	185/190 (97%)	185 (100%)	0	100	100
3	I	185/190 (97%)	185 (100%)	0	100	100
3	J	185/190 (97%)	185 (100%)	0	100	100
4	L	177/177 (100%)	177 (100%)	0	100	100
4	M	177/177 (100%)	177 (100%)	0	100	100
4	N	177/177 (100%)	177 (100%)	0	100	100
All	All	2382/2397 (99%)	2382 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA ⓘ

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](#)

27 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	NAG	A	401	5	14,14,15	0.24	0	15,19,21	0.34	0
5	NAG	A	402	1,5	14,14,15	0.26	0	15,19,21	0.39	0
6	BMA	A	403	5	11,11,12	0.53	0	15,15,17	1.03	0
5	NAG	A	404	5,6	14,14,15	0.20	0	15,19,21	0.30	0
5	NAG	A	405	1,5	14,14,15	0.17	0	15,19,21	0.35	0
5	NAG	A	406	1	14,14,15	0.24	0	15,19,21	0.43	0
5	NAG	A	407	1	14,14,15	0.15	0	15,19,21	0.38	0
5	NAG	A	408	5	14,14,15	0.17	0	15,19,21	0.41	0
5	NAG	A	409	1,5	14,14,15	0.30	0	15,19,21	0.57	0
5	NAG	C	401	5	14,14,15	0.22	0	15,19,21	0.34	0
5	NAG	C	402	1,5	14,14,15	0.24	0	15,19,21	0.41	0
6	BMA	C	403	5	11,11,12	0.54	0	15,15,17	1.03	0
5	NAG	C	404	5,6	14,14,15	0.22	0	15,19,21	0.32	0
5	NAG	C	405	1,5	14,14,15	0.16	0	15,19,21	0.35	0
5	NAG	C	406	1	14,14,15	0.24	0	15,19,21	0.40	0
5	NAG	C	407	1	14,14,15	0.16	0	15,19,21	0.39	0
5	NAG	C	408	5	14,14,15	0.16	0	15,19,21	0.40	0
5	NAG	C	409	1,5	14,14,15	0.27	0	15,19,21	0.62	0
5	NAG	E	401	5	14,14,15	0.25	0	15,19,21	0.33	0
5	NAG	E	402	1,5	14,14,15	0.25	0	15,19,21	0.38	0
6	BMA	E	403	5	11,11,12	0.56	0	15,15,17	1.03	0
5	NAG	E	404	5,6	14,14,15	0.20	0	15,19,21	0.32	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	NAG	E	405	1,5	14,14,15	0.17	0	15,19,21	0.36	0
5	NAG	E	406	1	14,14,15	0.23	0	15,19,21	0.43	0
5	NAG	E	407	1	14,14,15	0.15	0	15,19,21	0.37	0
5	NAG	E	408	5	14,14,15	0.17	0	15,19,21	0.41	0
5	NAG	E	409	1,5	14,14,15	0.31	0	15,19,21	0.60	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	NAG	A	401	5	-	0/6/23/26	0/1/1/1
5	NAG	A	402	1,5	-	0/6/23/26	0/1/1/1
6	BMA	A	403	5	-	0/2/19/22	0/1/1/1
5	NAG	A	404	5,6	-	0/6/23/26	0/1/1/1
5	NAG	A	405	1,5	-	0/6/23/26	0/1/1/1
5	NAG	A	406	1	-	0/6/23/26	0/1/1/1
5	NAG	A	407	1	-	0/6/23/26	0/1/1/1
5	NAG	A	408	5	-	0/6/23/26	0/1/1/1
5	NAG	A	409	1,5	-	0/6/23/26	0/1/1/1
5	NAG	C	401	5	-	0/6/23/26	0/1/1/1
5	NAG	C	402	1,5	-	0/6/23/26	0/1/1/1
6	BMA	C	403	5	-	0/2/19/22	0/1/1/1
5	NAG	C	404	5,6	-	0/6/23/26	0/1/1/1
5	NAG	C	405	1,5	-	0/6/23/26	0/1/1/1
5	NAG	C	406	1	-	0/6/23/26	0/1/1/1
5	NAG	C	407	1	-	0/6/23/26	0/1/1/1
5	NAG	C	408	5	-	0/6/23/26	0/1/1/1
5	NAG	C	409	1,5	-	0/6/23/26	0/1/1/1
5	NAG	E	401	5	-	0/6/23/26	0/1/1/1
5	NAG	E	402	1,5	-	0/6/23/26	0/1/1/1
6	BMA	E	403	5	-	0/2/19/22	0/1/1/1
5	NAG	E	404	5,6	-	0/6/23/26	0/1/1/1
5	NAG	E	405	1,5	-	0/6/23/26	0/1/1/1
5	NAG	E	406	1	-	0/6/23/26	0/1/1/1
5	NAG	E	407	1	-	0/6/23/26	0/1/1/1
5	NAG	E	408	5	-	0/6/23/26	0/1/1/1
5	NAG	E	409	1,5	-	0/6/23/26	0/1/1/1

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

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 [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	323/323 (100%)	0.79	25 (7%)	16 8	31, 51, 78, 104	0
1	C	323/323 (100%)	0.67	15 (4%)	36 25	17, 38, 70, 99	0
1	E	323/323 (100%)	0.69	20 (6%)	24 15	17, 36, 70, 106	0
2	B	173/173 (100%)	1.01	23 (13%)	4 2	18, 55, 91, 108	0
2	D	173/173 (100%)	1.15	28 (16%)	3 1	12, 54, 103, 123	0
2	F	173/173 (100%)	1.09	28 (16%)	3 1	16, 45, 108, 114	0
3	H	221/227 (97%)	0.56	4 (1%)	71 61	15, 33, 57, 81	0
3	I	221/227 (97%)	0.70	15 (6%)	20 12	13, 28, 75, 106	0
3	J	221/227 (97%)	0.62	9 (4%)	41 29	12, 28, 67, 90	0
4	L	210/210 (100%)	0.65	5 (2%)	62 50	26, 51, 77, 103	0
4	M	210/210 (100%)	0.60	4 (1%)	70 59	20, 42, 67, 96	0
4	N	210/210 (100%)	0.61	5 (2%)	62 50	16, 36, 58, 78	0
All	All	2781/2799 (99%)	0.74	181 (6%)	22 13	12, 40, 83, 123	0

The worst 5 of 181 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	673	ILE	8.9
2	D	527	GLN	7.7
1	A	326	SER	7.1
1	E	75	ILE	5.6
2	D	533	GLY	5.5

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 ⓘ

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	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
5	NAG	C	407	14/15	0.56	0.55	12.00	51,107,132,155	0
5	NAG	C	408	14/15	0.50	0.69	8.80	82,115,142,153	0
5	NAG	A	406	14/15	0.59	0.55	8.49	75,111,140,149	0
5	NAG	E	408	14/15	0.66	0.75	7.43	61,123,160,162	0
5	NAG	E	407	14/15	0.43	0.43	6.30	58,104,151,154	0
5	NAG	A	407	14/15	0.53	0.40	6.28	53,97,139,154	0
5	NAG	A	408	14/15	0.68	0.55	5.62	55,110,137,139	0
5	NAG	C	409	14/15	0.67	0.46	4.79	61,87,116,133	0
5	NAG	C	406	14/15	0.71	0.29	2.84	83,108,138,146	0
5	NAG	E	409	14/15	0.75	0.47	2.22	50,81,120,127	0
5	NAG	E	405	14/15	0.92	0.28	1.22	36,56,93,103	0
5	NAG	A	409	14/15	0.83	0.29	0.69	56,87,110,121	0
5	NAG	A	405	14/15	0.90	0.28	0.60	40,73,120,125	0
5	NAG	C	405	14/15	0.91	0.24	0.42	33,60,97,103	0
5	NAG	A	401	14/15	0.47	0.42	-	67,127,159,164	0
6	BMA	A	403	11/12	0.75	0.39	-	74,97,115,138	0
5	NAG	C	401	14/15	0.43	0.56	-	85,134,170,175	0
6	BMA	E	403	11/12	0.78	0.24	-	64,98,117,123	0
5	NAG	A	404	14/15	0.78	0.32	-	55,92,118,125	0
5	NAG	C	404	14/15	0.78	0.36	-	50,97,117,124	0
5	NAG	E	401	14/15	0.48	0.50	-	81,127,159,167	0
5	NAG	E	406	14/15	0.65	0.54	-	78,110,139,143	0
6	BMA	C	403	11/12	0.77	0.39	-	85,106,127,130	0
5	NAG	E	402	14/15	0.83	0.25	-	73,97,122,140	0
5	NAG	C	402	14/15	0.61	0.39	-	91,111,135,155	0
5	NAG	A	402	14/15	0.69	0.34	-	76,116,140,147	0
5	NAG	E	404	14/15	0.86	0.29	-	51,82,101,117	0

6.5 Other polymers [i](#)

There are no such residues in this entry.