



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 05:55 PM GMT

PDB ID : 4JUG
Title : Crystal structure of 1918 pandemic influenza virus hemagglutinin mutant D225G
Authors : Zhang, W.; Shi, Y.; Qi, J.; Gao, F.; Li, Q.; Fan, Z.; Yan, J.; Gao, G.F.
Deposited on : 2013-03-24
Resolution : 2.70 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 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
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) : trunk26865

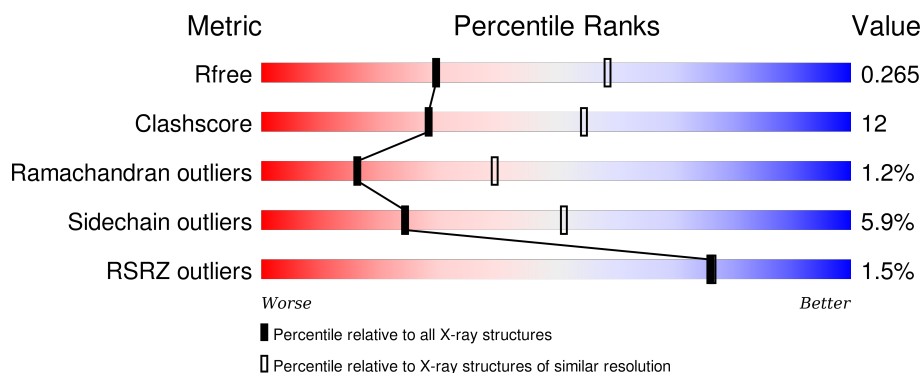
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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.




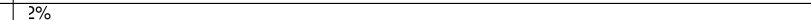

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	2103 (2.70-2.70)
Clashscore	102246	2422 (2.70-2.70)
Ramachandran outliers	100387	2382 (2.70-2.70)
Sidechain outliers	100360	2382 (2.70-2.70)
RSRZ outliers	91569	2107 (2.70-2.70)

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	324	<div> <div>2%</div> <div>76%</div> <div>22%</div> <div>.</div> </div>
1	C	324	<div> <div>77%</div> <div>19%</div> <div>..</div> </div>
1	E	324	<div> <div>%</div> <div>77%</div> <div>22%</div> <div>.</div> </div>
1	G	324	<div> <div>2%</div> <div>77%</div> <div>19%</div> <div>.</div> </div>
1	I	324	<div> <div>%</div> <div>76%</div> <div>21%</div> <div>.</div> </div>

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Mol	Chain	Length	Quality of chain	
1	K	324	 75% 23%	.
2	B	170	 75% 24%	.
2	D	170	 69% 25%	..
2	F	170	 69% 25%	...
2	H	170	 74% 23%	.
2	J	170	 71% 24%	..
2	L	170	 69% 22% 5%	...

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 23611 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
1	A	324	Total	C	N	O	S	0	0	0
			2512	1584	434	483	11			
1	C	324	Total	C	N	O	S	0	0	0
			2512	1584	434	483	11			
1	E	324	Total	C	N	O	S	0	0	0
			2512	1584	434	483	11			
1	G	324	Total	C	N	O	S	0	0	0
			2512	1584	434	483	11			
1	I	324	Total	C	N	O	S	0	0	0
			2512	1584	434	483	11			
1	K	324	Total	C	N	O	S	0	0	0
			2512	1584	434	483	11			

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	225	GLY	ASP	ENGINEERED MUTATION	UNP Q9WFX3
A	326	ALA	-	EXPRESSION TAG	UNP Q9WFX3
A	327	ARG	-	EXPRESSION TAG	UNP Q9WFX3
C	225	GLY	ASP	ENGINEERED MUTATION	UNP Q9WFX3
C	326	ALA	-	EXPRESSION TAG	UNP Q9WFX3
C	327	ARG	-	EXPRESSION TAG	UNP Q9WFX3
E	225	GLY	ASP	ENGINEERED MUTATION	UNP Q9WFX3
E	326	ALA	-	EXPRESSION TAG	UNP Q9WFX3
E	327	ARG	-	EXPRESSION TAG	UNP Q9WFX3
G	225	GLY	ASP	ENGINEERED MUTATION	UNP Q9WFX3
G	326	ALA	-	EXPRESSION TAG	UNP Q9WFX3
G	327	ARG	-	EXPRESSION TAG	UNP Q9WFX3
I	225	GLY	ASP	ENGINEERED MUTATION	UNP Q9WFX3
I	326	ALA	-	EXPRESSION TAG	UNP Q9WFX3
I	327	ARG	-	EXPRESSION TAG	UNP Q9WFX3
K	225	GLY	ASP	ENGINEERED MUTATION	UNP Q9WFX3
K	326	ALA	-	EXPRESSION TAG	UNP Q9WFX3

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Chain	Residue	Modelled	Actual	Comment	Reference
K	327	ARG	-	EXPRESSION TAG	UNP Q9WFX3

- Molecule 2 is a protein called Hemagglutinin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	170	Total	C	N	O	S	0	0	0
			1368	855	236	271	6			
2	D	169	Total	C	N	O	S	0	0	0
			1357	849	232	270	6			
2	F	165	Total	C	N	O	S	0	0	0
			1326	830	226	264	6			
2	H	170	Total	C	N	O	S	0	0	0
			1368	855	236	271	6			
2	J	167	Total	C	N	O	S	0	0	0
			1341	839	229	267	6			
2	L	165	Total	C	N	O	S	0	0	0
			1326	830	226	264	6			

- Molecule 3 is a polymer of unknown type called SUGAR (2-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	2	Total	C	N	O	0	0
			28	16	2	10		
3	C	2	Total	C	N	O	0	0
			28	16	2	10		
3	E	2	Total	C	N	O	0	0
			28	16	2	10		
3	G	2	Total	C	N	O	0	0
			28	16	2	10		
3	I	2	Total	C	N	O	0	0
			28	16	2	10		
3	K	2	Total	C	N	O	0	0
			28	16	2	10		

- Molecule 4 is a polymer of unknown type called SUGAR (3-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	D	3	Total	C	N	O	0	0
			39	22	2	15		
4	J	3	Total	C	N	O	0	0
			39	22	2	15		

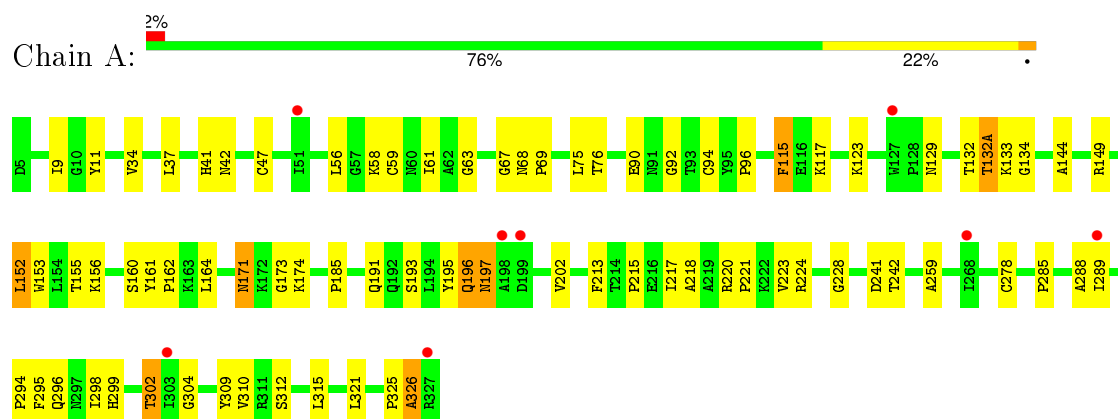
- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	16	Total O 16 16	0	0
5	B	6	Total O 6 6	0	0
5	C	35	Total O 35 35	0	0
5	D	19	Total O 19 19	0	0
5	E	18	Total O 18 18	0	0
5	F	6	Total O 6 6	0	0
5	G	14	Total O 14 14	0	0
5	H	5	Total O 5 5	0	0
5	I	45	Total O 45 45	0	0
5	J	24	Total O 24 24	0	0
5	K	12	Total O 12 12	0	0
5	L	7	Total O 7 7	0	0

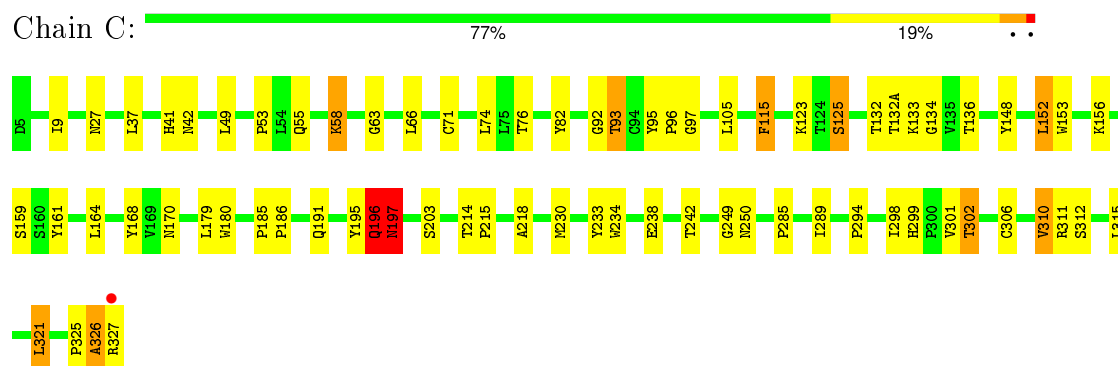
3 Residue-property plots [i](#)

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 ($\text{RSRZ} > 2$). 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.

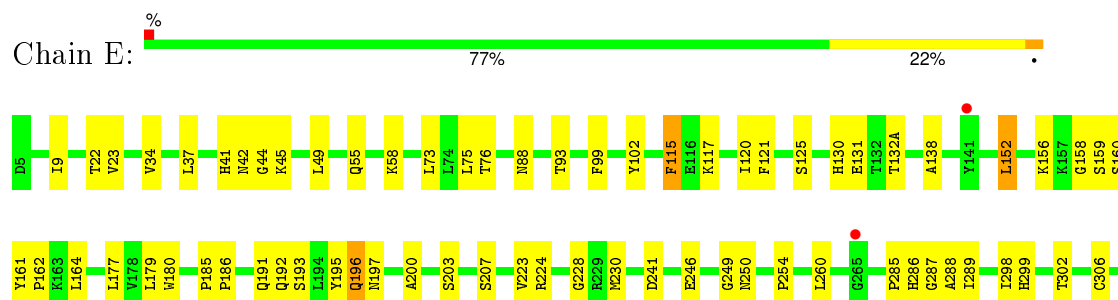
• Molecule 1: Hemagglutinin



• Molecule 1: Hemagglutinin

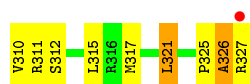
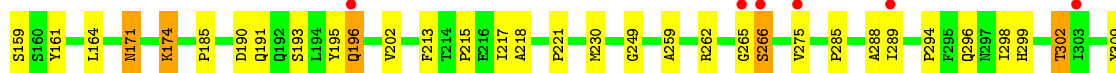
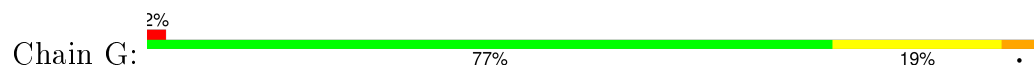


• Molecule 1: Hemagglutinin

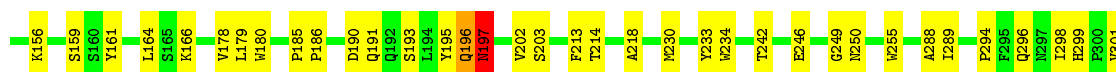
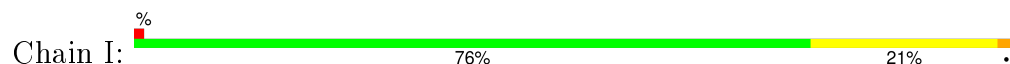




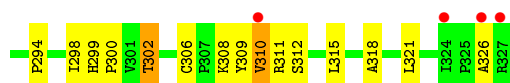
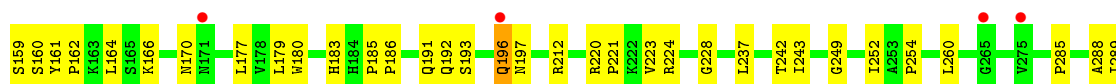
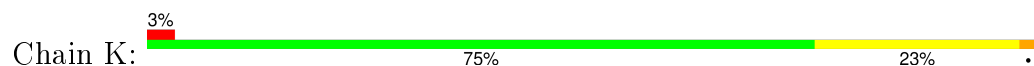
• Molecule 1: Hemagglutinin



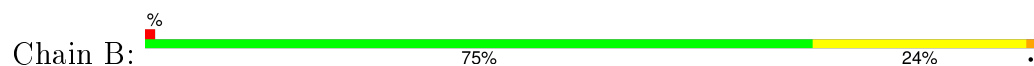
• Molecule 1: Hemagglutinin

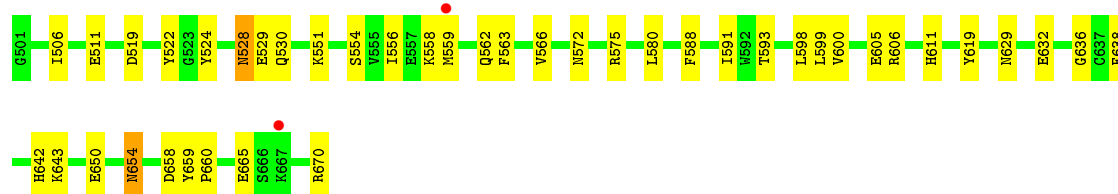


• Molecule 1: Hemagglutinin

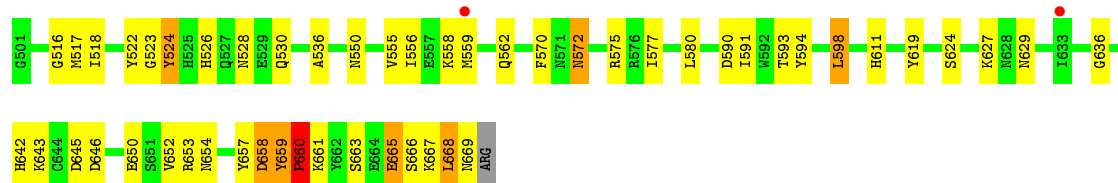


• Molecule 2: Hemagglutinin

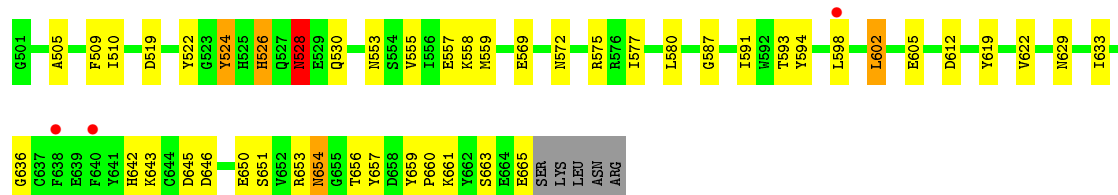




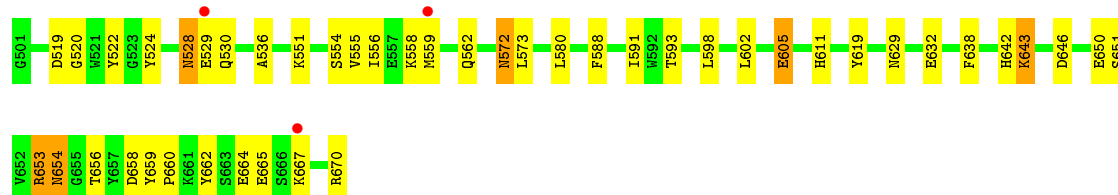
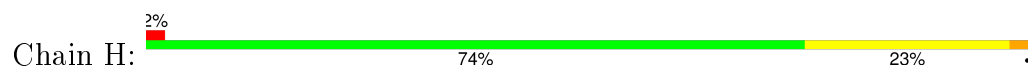
- Molecule 2: Hemagglutinin



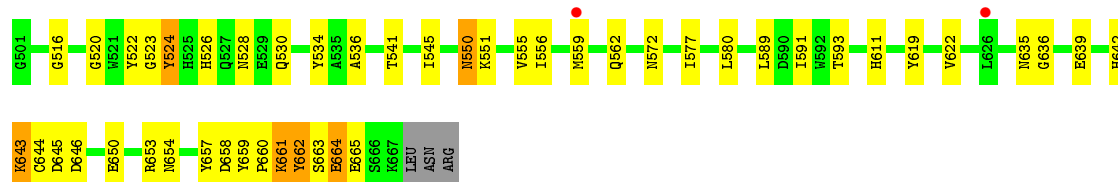
- Molecule 2: Hemagglutinin



- Molecule 2: Hemagglutinin



- Molecule 2: Hemagglutinin



- Molecule 2: Hemagglutinin



4 Data and refinement statistics

Property	Value	Source
Space group	P 3	Depositor
Cell constants a, b, c, α , β , γ	120.86Å 120.86Å 235.72Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	47.90 – 2.70 47.90 – 2.70	Depositor EDS
% Data completeness (in resolution range)	92.0 (47.90-2.70) 98.6 (47.90-2.70)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.49 (at 2.69Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.5_2)	Depositor
R, R_{free}	0.207 , 0.267 0.210 , 0.265	Depositor DCC
R_{free} test set	5228 reflections (5.27%)	DCC
Wilson B-factor (Å ²)	53.1	Xtriage
Anisotropy	0.543	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 27.7	EDS
Estimated twinning fraction	0.477 for -h,-k,l 0.028 for h,-h-k,-l 0.025 for -k,-h,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	0 of 104392 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	23611	wwPDB-VP
Average B, all atoms (Å ²)	63.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 20.98 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 7.7261e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹ Intensities estimated from amplitudes.

² Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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	0.27	0/2576	0.43	0/3508
1	C	0.30	0/2576	0.44	1/3508 (0.0%)
1	E	0.31	0/2576	0.49	1/3508 (0.0%)
1	G	0.29	0/2576	0.45	2/3508 (0.1%)
1	I	0.30	0/2576	0.46	1/3508 (0.0%)
1	K	0.31	0/2576	0.45	3/3508 (0.1%)
2	B	0.24	0/1395	0.39	0/1878
2	D	0.28	0/1384	0.52	2/1864 (0.1%)
2	F	0.26	0/1353	0.48	1/1823 (0.1%)
2	H	0.23	0/1395	0.40	0/1878
2	J	0.30	0/1368	0.45	0/1842
2	L	0.25	0/1353	0.54	2/1823 (0.1%)
All	All	0.28	0/23704	0.46	13/32156 (0.0%)

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	C	0	1
1	I	0	1
All	All	0	2

There are no bond length outliers.

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	197	ASN	N-CA-CB	14.84	137.31	110.60
2	L	663	SER	N-CA-C	12.43	144.57	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	196	GLN	N-CA-C	8.54	134.06	111.00
2	D	660	PRO	N-CA-C	8.42	133.98	112.10
2	F	528	ASN	CB-CA-C	7.41	125.21	110.40

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	196	GLN	Peptide
1	I	196	GLN	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	2512	0	2440	68	0
1	C	2512	0	2440	59	0
1	E	2512	0	2440	50	0
1	G	2512	0	2440	63	0
1	I	2512	0	2440	69	0
1	K	2512	0	2440	49	0
2	B	1368	0	1285	33	0
2	D	1357	0	1270	46	0
2	F	1326	0	1237	33	0
2	H	1368	0	1285	46	0
2	J	1341	0	1253	51	0
2	L	1326	0	1237	37	0
3	A	28	0	25	0	0
3	C	28	0	25	0	0
3	E	28	0	25	1	0
3	G	28	0	25	2	0
3	I	28	0	25	0	0
3	K	28	0	25	1	0
4	D	39	0	34	0	0
4	J	39	0	34	0	0
5	A	16	0	0	1	0
5	B	6	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	C	35	0	0	0	0
5	D	19	0	0	0	0
5	E	18	0	0	1	0
5	F	6	0	0	0	0
5	G	14	0	0	0	0
5	H	5	0	0	0	0
5	I	45	0	0	1	0
5	J	24	0	0	0	0
5	K	12	0	0	0	0
5	L	7	0	0	0	0
All	All	23611	0	22425	530	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 12.

The worst 5 of 530 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:C:196:GLN:CG	1:C:196:GLN:O	1.94	1.07
2:D:629:ASN:HA	2:D:665:GLU:HG2	1.36	1.05
2:F:528:ASN:ND2	2:F:646:ASP:OD1	1.93	1.00
1:G:196:GLN:HG2	1:G:196:GLN:O	1.61	1.00
1:E:41:HIS:HB3	1:E:298:ILE:HD13	1.45	0.96

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	322/324 (99%)	298 (92%)	21 (6%)	3 (1%)	21 49
1	C	322/324 (99%)	301 (94%)	18 (6%)	3 (1%)	21 49

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	E	322/324 (99%)	299 (93%)	18 (6%)	5 (2%)	12	30
1	G	322/324 (99%)	296 (92%)	23 (7%)	3 (1%)	21	49
1	I	322/324 (99%)	303 (94%)	17 (5%)	2 (1%)	30	59
1	K	322/324 (99%)	296 (92%)	24 (8%)	2 (1%)	30	59
2	B	168/170 (99%)	156 (93%)	10 (6%)	2 (1%)	16	39
2	D	167/170 (98%)	149 (89%)	13 (8%)	5 (3%)	5	13
2	F	163/170 (96%)	145 (89%)	13 (8%)	5 (3%)	5	12
2	H	168/170 (99%)	156 (93%)	11 (6%)	1 (1%)	30	59
2	J	165/170 (97%)	151 (92%)	13 (8%)	1 (1%)	30	59
2	L	163/170 (96%)	147 (90%)	12 (7%)	4 (2%)	7	18
All	All	2926/2964 (99%)	2697 (92%)	193 (7%)	36 (1%)	16	39

5 of 36 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	197	ASN
2	D	658	ASP
2	D	659	TYR
2	D	661	LYS
2	D	668	LEU

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	278/278 (100%)	267 (96%)	11 (4%)	38	69
1	C	278/278 (100%)	263 (95%)	15 (5%)	27	56
1	E	278/278 (100%)	265 (95%)	13 (5%)	32	63
1	G	278/278 (100%)	264 (95%)	14 (5%)	30	60
1	I	278/278 (100%)	264 (95%)	14 (5%)	30	60
1	K	278/278 (100%)	265 (95%)	13 (5%)	32	63

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	B	145/145 (100%)	132 (91%)	13 (9%)	12	27
2	D	144/145 (99%)	135 (94%)	9 (6%)	22	48
2	F	140/145 (97%)	129 (92%)	11 (8%)	15	34
2	H	145/145 (100%)	134 (92%)	11 (8%)	16	37
2	J	142/145 (98%)	133 (94%)	9 (6%)	22	48
2	L	140/145 (97%)	125 (89%)	15 (11%)	8	19
All	All	2524/2538 (99%)	2376 (94%)	148 (6%)	24	51

5 of 148 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	F	572	ASN
1	G	190	ASP
2	L	569	GLU
2	F	580	LEU
1	G	115	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 74 such sidechains are listed below:

Mol	Chain	Res	Type
2	F	560	ASN
1	G	191	GLN
2	L	528	ASN
2	F	572	ASN
2	F	654	ASN

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 ⓘ

18 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	$\# Z > 2$
3	NAG	A	801	1,3	14,14,15	0.54	0	15,19,21	0.57	0
3	NAG	A	802	3	14,14,15	0.51	0	15,19,21	0.85	0
3	NAG	C	801	1,3	14,14,15	0.48	0	15,19,21	0.78	0
3	NAG	C	802	3	14,14,15	0.45	0	15,19,21	0.90	1 (6%)
4	NAG	D	801	2,4	14,14,15	0.47	0	15,19,21	1.31	1 (6%)
4	NAG	D	802	4	14,14,15	0.57	0	15,19,21	0.73	0
4	BMA	D	803	4	11,11,12	0.26	0	14,15,17	0.59	0
3	NAG	E	801	1,3	14,14,15	0.53	0	15,19,21	0.78	0
3	NAG	E	802	3	14,14,15	0.48	0	15,19,21	0.71	0
3	NAG	G	801	1,3	14,14,15	0.56	0	15,19,21	0.59	0
3	NAG	G	802	3	14,14,15	0.44	0	15,19,21	1.00	1 (6%)
3	NAG	I	801	1,3	14,14,15	0.47	0	15,19,21	0.83	0
3	NAG	I	802	3	14,14,15	0.51	0	15,19,21	0.65	0
4	NAG	J	801	2,4	14,14,15	0.48	0	15,19,21	1.36	2 (13%)
4	NAG	J	802	4	14,14,15	0.56	0	15,19,21	0.73	0
4	BMA	J	803	4	11,11,12	0.27	0	14,15,17	0.60	0
3	NAG	K	801	1,3	14,14,15	0.51	0	15,19,21	0.88	0
3	NAG	K	802	3	14,14,15	0.49	0	15,19,21	0.70	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
3	NAG	A	801	1,3	-	0/6/23/26	0/1/1/1
3	NAG	A	802	3	-	0/6/23/26	0/1/1/1
3	NAG	C	801	1,3	-	0/6/23/26	0/1/1/1
3	NAG	C	802	3	-	0/6/23/26	0/1/1/1
4	NAG	D	801	2,4	-	0/6/23/26	0/1/1/1
4	NAG	D	802	4	-	0/6/23/26	0/1/1/1
4	BMA	D	803	4	-	0/2/19/22	0/1/1/1
3	NAG	E	801	1,3	-	0/6/23/26	0/1/1/1
3	NAG	E	802	3	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAG	G	801	1,3	-	0/6/23/26	0/1/1/1
3	NAG	G	802	3	-	0/6/23/26	0/1/1/1
3	NAG	I	801	1,3	-	0/6/23/26	0/1/1/1
3	NAG	I	802	3	-	0/6/23/26	0/1/1/1
4	NAG	J	801	2,4	-	0/6/23/26	0/1/1/1
4	NAG	J	802	4	-	0/6/23/26	0/1/1/1
4	BMA	J	803	4	-	0/2/19/22	0/1/1/1
3	NAG	K	801	1,3	-	0/6/23/26	0/1/1/1
3	NAG	K	802	3	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	G	802	NAG	C2-N2-C7	-2.15	120.27	123.04
3	C	802	NAG	C1-O5-C5	2.50	115.42	112.25
4	J	801	NAG	C4-C3-C2	2.69	115.42	111.23
4	J	801	NAG	C1-O5-C5	3.17	116.27	112.25
4	D	801	NAG	C1-O5-C5	3.75	117.00	112.25

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	E	801	NAG	1	0
3	G	801	NAG	2	0
3	G	802	NAG	2	0
3	K	801	NAG	1	0

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	324/324 (100%)	0.34	8 (2%) 61 61	43, 70, 106, 159	0
1	C	324/324 (100%)	0.04	1 (0%) 94 95	27, 46, 68, 153	0
1	E	324/324 (100%)	0.20	4 (1%) 81 81	38, 65, 94, 153	0
1	G	324/324 (100%)	0.26	7 (2%) 65 66	44, 69, 106, 146	0
1	I	324/324 (100%)	0.05	2 (0%) 90 91	25, 47, 70, 143	0
1	K	324/324 (100%)	0.18	9 (2%) 56 57	40, 63, 93, 135	0
2	B	170/170 (100%)	0.20	2 (1%) 81 81	33, 70, 107, 129	0
2	D	169/170 (99%)	0.07	2 (1%) 81 81	37, 55, 81, 116	0
2	F	165/170 (97%)	0.30	3 (1%) 71 72	40, 67, 102, 133	0
2	H	170/170 (100%)	0.15	3 (1%) 71 72	35, 66, 105, 129	0
2	J	167/170 (98%)	0.14	2 (1%) 81 81	35, 54, 84, 112	0
2	L	165/170 (97%)	0.20	1 (0%) 90 91	39, 62, 96, 130	0
All	All	2950/2964 (99%)	0.18	44 (1%) 76 76	25, 61, 99, 159	0

The worst 5 of 44 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	327	ARG	9.9
1	C	327	ARG	9.2
1	E	327	ARG	7.3
1	I	327	ARG	6.8
1	G	327	ARG	5.7

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

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

6.3 Carbohydrates [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(Å ²)	Q<0.9
3	NAG	E	801	14/15	0.96	0.21	1.76	71,81,99,105	0
3	NAG	K	801	14/15	0.95	0.20	0.91	65,79,94,98	0
3	NAG	G	801	14/15	0.96	0.17	-0.12	59,69,81,83	0
3	NAG	A	801	14/15	0.96	0.15	-0.70	60,70,82,86	0
3	NAG	I	801	14/15	0.96	0.14	-0.81	39,45,53,54	0
3	NAG	C	801	14/15	0.97	0.14	-1.01	40,48,59,60	0
3	NAG	A	802	14/15	0.89	0.19	-	103,115,126,129	0
4	BMA	J	803	11/12	0.86	0.21	-	97,112,119,130	0
3	NAG	G	802	14/15	0.81	0.35	-	100,120,126,131	0
3	NAG	I	802	14/15	0.88	0.18	-	69,80,87,91	0
3	NAG	E	802	14/15	0.89	0.15	-	107,117,122,125	0
4	BMA	D	803	11/12	0.75	0.19	-	91,104,110,121	0
4	NAG	J	801	14/15	0.92	0.25	-	73,80,87,90	0
4	NAG	D	801	14/15	0.89	0.23	-	72,79,84,89	0
3	NAG	C	802	14/15	0.94	0.14	-	66,73,78,81	0
4	NAG	J	802	14/15	0.88	0.25	-	78,92,99,100	0
3	NAG	K	802	14/15	0.84	0.26	-	106,111,117,122	0
4	NAG	D	802	14/15	0.90	0.19	-	65,76,81,83	0

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.