



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 15, 2017 – 04:31 am GMT

PDB ID : 4JTX  
Title : Crystal structure of 2009 pandemic influenza virus hemagglutinin mutant D225E  
Authors : Zhang, W.; Shi, Y.; Qi, J.; Gao, F.; Li, Q.; Fan, Z.; Yan, J.; Gao, G.F.  
Deposited on : 2013-03-24  
Resolution : 3.00 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](mailto: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.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.7.2 (RC1), CSD as538be (2017)  
Xtriage (Phenix) : 1.9-1692  
EDS : trunk28620  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : recalc28949

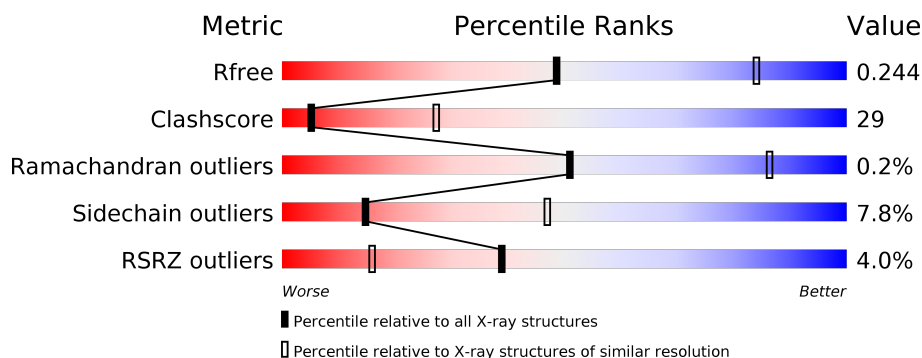
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.00 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	1692 (3.00-3.00)
Clashscore	112137	2037 (3.00-3.00)
Ramachandran outliers	110173	1973 (3.00-3.00)
Sidechain outliers	110143	1976 (3.00-3.00)
RSRZ outliers	101464	1716 (3.00-3.00)

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  $\geq 3$ , 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>3%</div> <div>55%</div> <div>38%</div> <div>7%</div> </div>
1	C	323	<div> <div>3%</div> <div>55%</div> <div>39%</div> <div>5%</div> </div>
1	E	323	<div> <div>3%</div> <div>51%</div> <div>43%</div> <div>5%</div> </div>
1	G	323	<div> <div>3%</div> <div>55%</div> <div>40%</div> <div>•</div> </div>
1	I	323	<div> <div>3%</div> <div>55%</div> <div>39%</div> <div>5%</div> </div>
1	K	323	<div> <div>3%</div> <div>52%</div> <div>42%</div> <div>5%</div> </div>

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Mol	Chain	Length	Quality of chain
2	B	166	
2	D	166	
2	F	166	
2	H	166	
2	J	166	
2	L	166	

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	K	601	-	-	X	X
4	NAG	I	601	-	-	X	-

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 23277 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	323	Total	C	N	O	S	0	0	0
			2525	1597	438	479	11			
1	C	322	Total	C	N	O	S	0	0	0
			2517	1592	434	480	11			
1	E	321	Total	C	N	O	S	0	0	0
			2510	1587	433	479	11			
1	G	322	Total	C	N	O	S	0	0	0
			2513	1590	434	478	11			
1	I	322	Total	C	N	O	S	0	0	0
			2517	1592	434	480	11			
1	K	322	Total	C	N	O	S	0	0	0
			2517	1592	434	480	11			

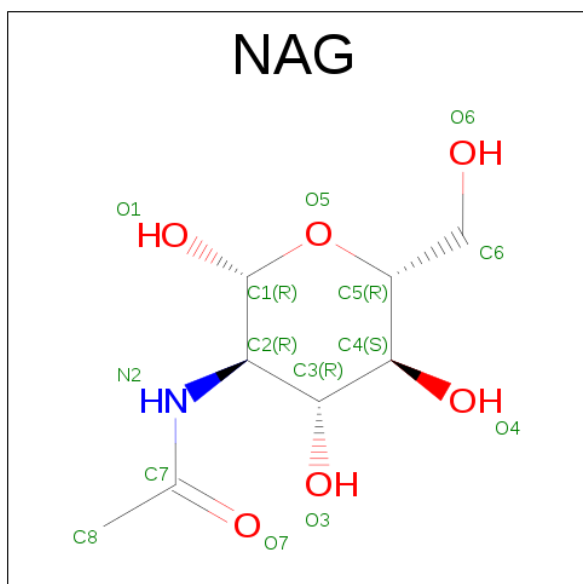
There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	6	ARG	-	EXPRESSION TAG	UNP C3W5S1
A	228	GLU	ASP	ENGINEERED MUTATION	UNP C3W5S1
C	6	ARG	-	EXPRESSION TAG	UNP C3W5S1
C	228	GLU	ASP	ENGINEERED MUTATION	UNP C3W5S1
E	6	ARG	-	EXPRESSION TAG	UNP C3W5S1
E	228	GLU	ASP	ENGINEERED MUTATION	UNP C3W5S1
G	6	ARG	-	EXPRESSION TAG	UNP C3W5S1
G	228	GLU	ASP	ENGINEERED MUTATION	UNP C3W5S1
I	6	ARG	-	EXPRESSION TAG	UNP C3W5S1
I	228	GLU	ASP	ENGINEERED MUTATION	UNP C3W5S1
K	6	ARG	-	EXPRESSION TAG	UNP C3W5S1
K	228	GLU	ASP	ENGINEERED MUTATION	UNP C3W5S1

- Molecule 2 is a protein called Hemagglutinin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	162	Total	C	N	O	S	0	0	0
			1305	822	220	257	6			
2	D	164	Total	C	N	O	S	0	0	0
			1315	826	221	262	6			
2	F	161	Total	C	N	O	S	0	0	0
			1302	821	219	256	6			
2	H	162	Total	C	N	O	S	0	0	0
			1305	822	220	257	6			
2	J	166	Total	C	N	O	S	0	0	0
			1334	838	224	266	6			
2	L	161	Total	C	N	O	S	0	0	0
			1302	821	219	256	6			

- Molecule 3 is SUGAR (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	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	G	1	Total	C	N	O	0	0
			14	8	1	5		
3	I	1	Total	C	N	O	0	0
			14	8	1	5		

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

- Molecule 4 is a polymer of unknown type called SUGAR (2-MER).

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

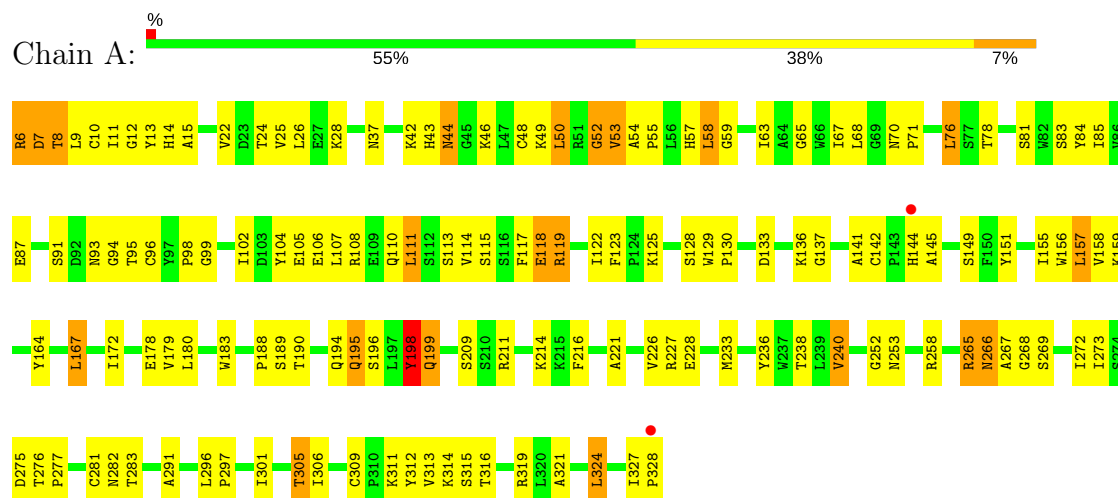
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	18	Total	O	0	0
			18	18		
5	B	10	Total	O	0	0
			10	10		
5	C	16	Total	O	0	0
			16	16		
5	D	9	Total	O	0	0
			9	9		
5	E	14	Total	O	0	0
			14	14		
5	F	11	Total	O	0	0
			11	11		
5	G	14	Total	O	0	0
			14	14		
5	H	5	Total	O	0	0
			5	5		
5	I	11	Total	O	0	0
			11	11		
5	J	9	Total	O	0	0
			9	9		
5	K	21	Total	O	0	0
			21	21		
5	L	9	Total	O	0	0
			9	9		

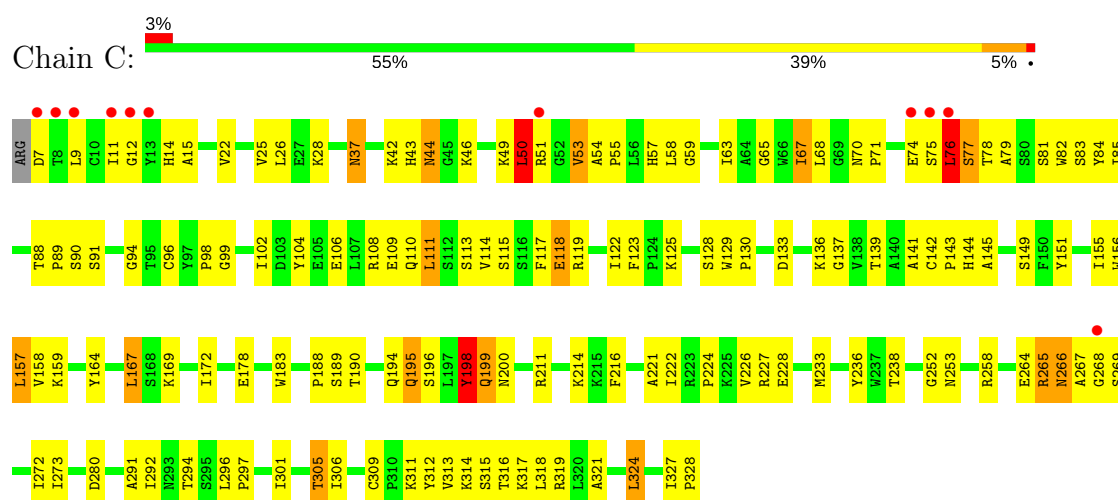
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

#### • Molecule 1: Hemagglutinin

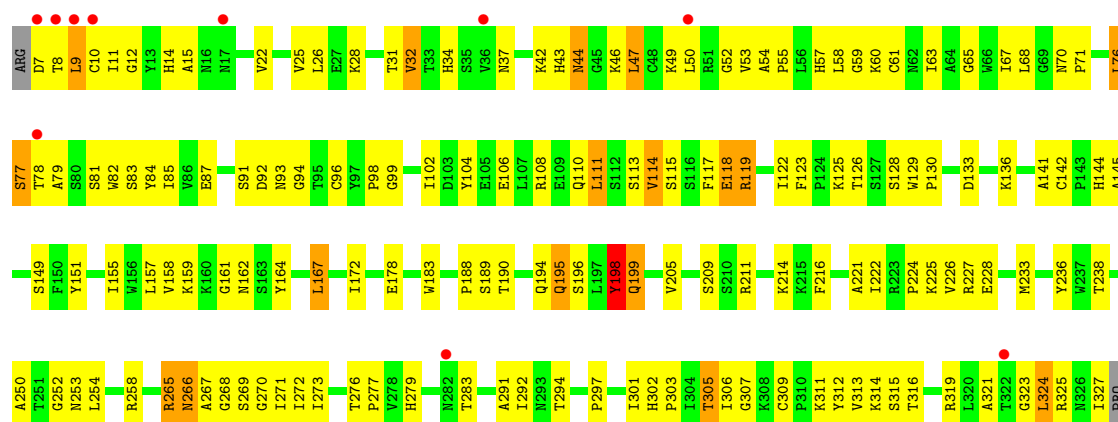


#### • Molecule 1: Hemagglutinin

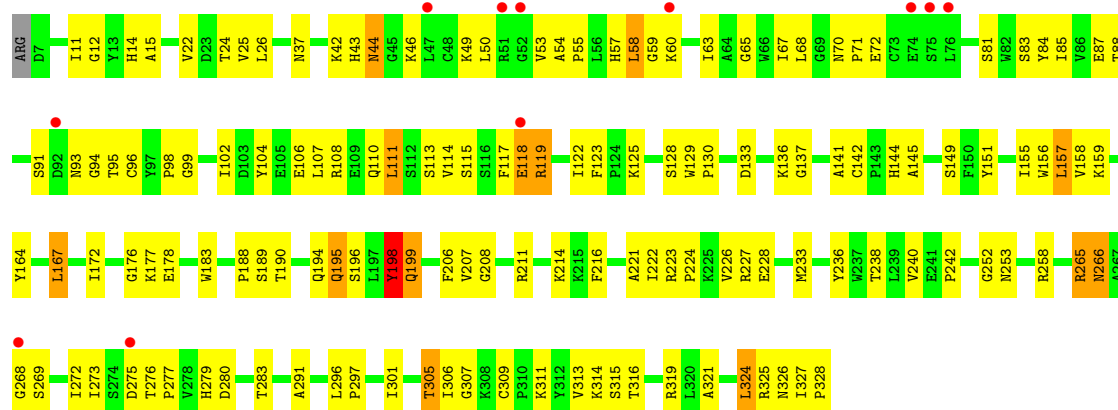


#### • Molecule 1: Hemagglutinin

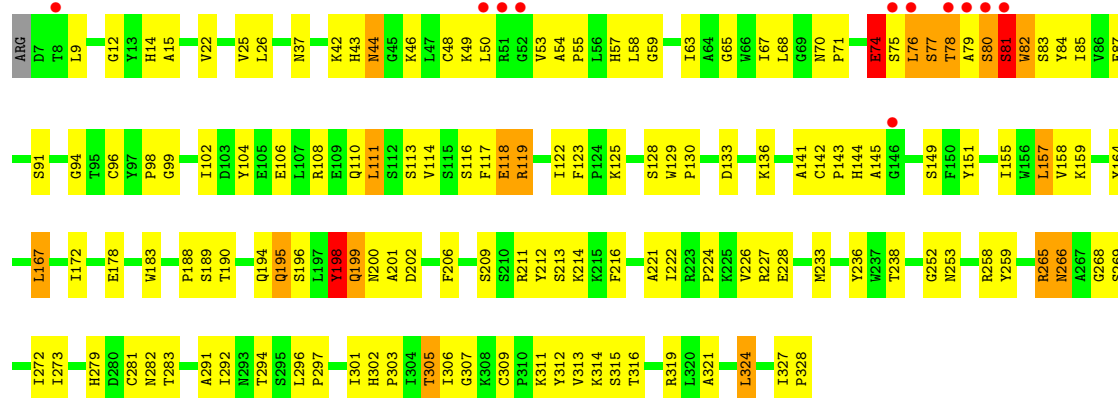




• Molecule 1: Hemagglutinin



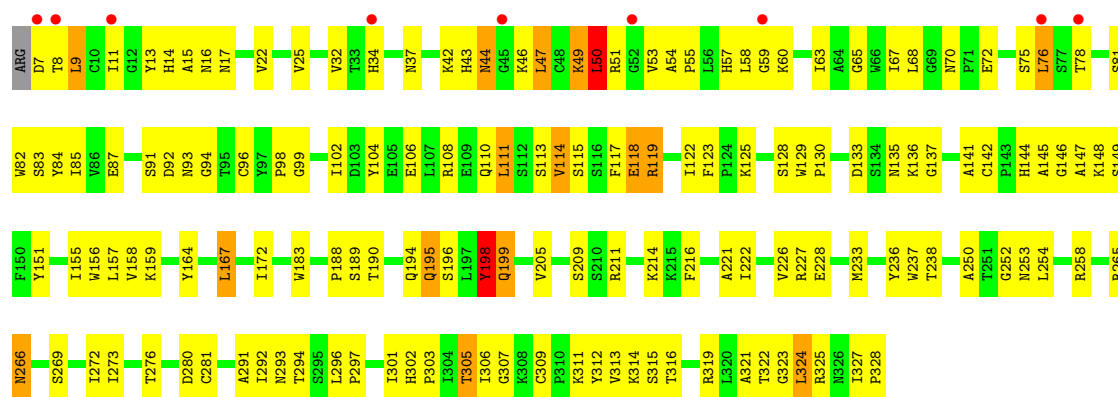
• Molecule 1: Hemagglutinin



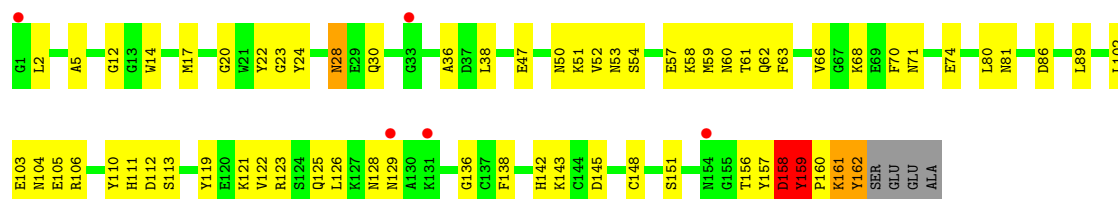
• Molecule 1: Hemagglutinin



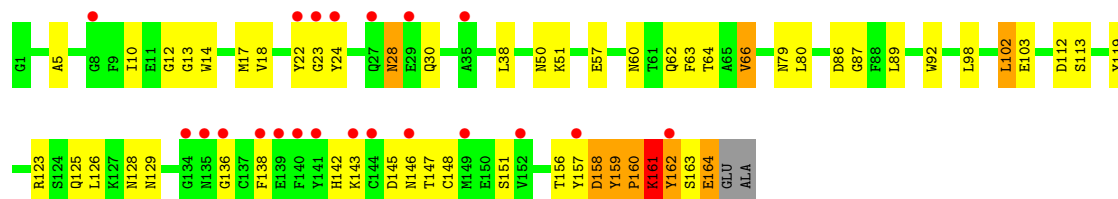




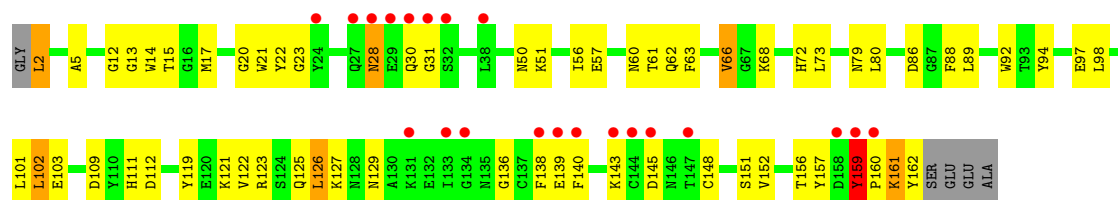
### • Molecule 2: Hemagglutinin



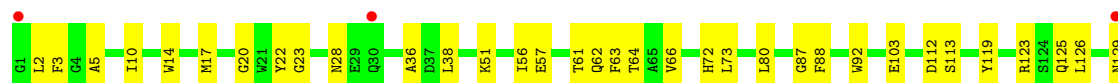
### • Molecule 2: Hemagglutinin



### • Molecule 2: Hemagglutinin



### • Molecule 2: Hemagglutinin

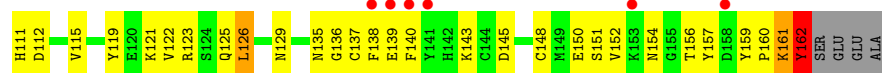




• Molecule 2: Hemagglutinin



• Molecule 2: Hemagglutinin



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	67.69Å 119.01Å 123.61Å 115.14° 94.96° 96.78°	Depositor
Resolution (Å)	46.75 – 3.00 46.75 – 3.00	Depositor EDS
% Data completeness (in resolution range)	88.1 (46.75-3.00) 79.9 (46.75-3.00)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.08 (at 3.01Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.5_2)	Depositor
R, $R_{free}$	0.210 , 0.243 0.212 , 0.244	Depositor DCC
$R_{free}$ test set	3273 reflections (5.09%)	DCC
Wilson B-factor (Å <sup>2</sup> )	54.4	Xtriage
Anisotropy	0.524	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.29 , 44.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.004 for -h,-l,-k	Xtriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	23277	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	60.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.66% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: 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	0/2589	0.70	8/3517 (0.2%)
1	C	0.27	0/2581	0.70	13/3506 (0.4%)
1	E	0.25	0/2573	0.63	9/3494 (0.3%)
1	G	0.25	0/2577	0.66	5/3501 (0.1%)
1	I	0.29	0/2581	0.69	11/3506 (0.3%)
1	K	0.26	0/2581	0.66	8/3506 (0.2%)
2	B	0.25	0/1333	0.54	3/1797 (0.2%)
2	D	0.24	0/1343	0.45	0/1811
2	F	0.24	0/1330	0.49	1/1794 (0.1%)
2	H	0.24	0/1333	0.48	1/1797 (0.1%)
2	J	0.32	0/1362	0.58	3/1836 (0.2%)
2	L	0.24	0/1330	0.53	1/1794 (0.1%)
All	All	0.26	0/23513	0.62	63/31859 (0.2%)

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	I	0	1

There are no bond length outliers.

The worst 5 of 63 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	119	ARG	NE-CZ-NH1	-15.90	112.35	120.30
1	A	119	ARG	NE-CZ-NH1	-15.77	112.41	120.30
1	G	119	ARG	NE-CZ-NH2	15.37	127.99	120.30
1	A	119	ARG	NE-CZ-NH2	15.17	127.88	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	I	76	LEU	CB-CA-C	-13.19	85.14	110.20

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	I	81	SER	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	2525	0	2471	157	0
1	C	2517	0	2457	145	4
1	E	2510	0	2452	181	5
1	G	2513	0	2456	161	0
1	I	2517	0	2458	158	0
1	K	2517	0	2459	211	0
2	B	1305	0	1228	105	0
2	D	1315	0	1227	77	0
2	F	1302	0	1226	97	0
2	H	1305	0	1228	44	0
2	J	1334	0	1250	75	0
2	L	1302	0	1226	96	0
3	A	14	0	13	0	0
3	C	14	0	13	0	0
3	E	14	0	13	0	0
3	G	14	0	13	0	0
3	I	14	0	13	0	0
3	K	14	0	13	9	0
4	A	28	0	25	6	0
4	C	28	0	25	4	0
4	I	28	0	25	7	0
5	A	18	0	0	23	0
5	B	10	0	0	28	0
5	C	16	0	0	33	0
5	D	9	0	0	26	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	E	14	0	0	37	0
5	F	11	0	0	24	0
5	G	14	0	0	46	0
5	H	5	0	0	6	0
5	I	11	0	0	15	1
5	J	9	0	0	16	0
5	K	21	0	0	65	0
5	L	9	0	0	21	0
All	All	23277	0	22291	1339	5

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 29.

The worst 5 of 1339 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:145:ASP:HB2	5:B:204:HOH:O	1.29	1.28
1:C:227:ARG:HD3	5:C:714:HOH:O	1.12	1.27
1:K:238:THR:HB	5:K:718:HOH:O	1.10	1.25
1:A:178:GLU:HA	5:A:713:HOH:O	1.10	1.25
2:D:160:PRO:O	2:D:161:LYS:HG2	1.35	1.24

All (5) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:76:LEU:CG	1:E:225:LYS:CE[1_455]	1.33	0.87
1:C:76:LEU:CG	1:E:225:LYS:NZ[1_455]	1.38	0.82
1:C:76:LEU:CD1	1:E:225:LYS:NZ[1_455]	1.73	0.47
1:C:76:LEU:CD2	1:E:225:LYS:CE[1_455]	1.86	0.34
1:E:279:HIS:NE2	5:I:710:HOH:O[1_655]	2.17	0.03

## 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%)	44	81
1	C	320/323 (99%)	300 (94%)	19 (6%)	1 (0%)	44	81
1	E	319/323 (99%)	300 (94%)	19 (6%)	0	100	100
1	G	320/323 (99%)	299 (93%)	21 (7%)	0	100	100
1	I	320/323 (99%)	299 (93%)	21 (7%)	0	100	100
1	K	320/323 (99%)	303 (95%)	17 (5%)	0	100	100
2	B	160/166 (96%)	151 (94%)	9 (6%)	0	100	100
2	D	162/166 (98%)	149 (92%)	10 (6%)	3 (2%)	9	41
2	F	159/166 (96%)	150 (94%)	9 (6%)	0	100	100
2	H	160/166 (96%)	150 (94%)	9 (6%)	1 (1%)	28	70
2	J	164/166 (99%)	151 (92%)	13 (8%)	0	100	100
2	L	159/166 (96%)	149 (94%)	10 (6%)	0	100	100
All	All	2884/2934 (98%)	2705 (94%)	173 (6%)	6 (0%)	51	86

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	D	159	TYR
2	D	160	PRO
2	H	160	PRO
1	C	75	SER
2	D	161	LYS

### 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	283/284 (100%)	259 (92%)	24 (8%)	12	43
1	C	283/284 (100%)	262 (93%)	21 (7%)	16	49

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	E	282/284 (99%)	261 (93%)	21 (7%)	16	49
1	G	282/284 (99%)	262 (93%)	20 (7%)	17	52
1	I	283/284 (100%)	259 (92%)	24 (8%)	12	43
1	K	283/284 (100%)	260 (92%)	23 (8%)	14	45
2	B	139/142 (98%)	129 (93%)	10 (7%)	17	51
2	D	140/142 (99%)	127 (91%)	13 (9%)	10	38
2	F	139/142 (98%)	128 (92%)	11 (8%)	14	46
2	H	139/142 (98%)	132 (95%)	7 (5%)	28	67
2	J	142/142 (100%)	130 (92%)	12 (8%)	12	43
2	L	139/142 (98%)	127 (91%)	12 (9%)	12	42
All	All	2534/2556 (99%)	2336 (92%)	198 (8%)	15	47

5 of 198 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	F	2	LEU
1	G	190	THR
1	K	266	ASN
2	F	57	GLU
1	G	37	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 104 such sidechains are listed below:

Mol	Chain	Res	Type
2	F	28	ASN
1	G	162	ASN
1	K	253	ASN
2	F	30	GLN
2	F	146	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 ⓘ

6 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$
4	NAG	A	602	1,4	14,14,15	0.66	0	15,19,21	1.97	2 (13%)
4	NAG	A	603	4	14,14,15	0.45	0	15,19,21	2.01	4 (26%)
4	NAG	C	602	1,4	14,14,15	0.91	1 (7%)	15,19,21	2.01	6 (40%)
4	NAG	C	603	4	14,14,15	0.49	0	15,19,21	1.30	1 (6%)
4	NAG	I	601	1,4	14,14,15	0.82	1 (7%)	15,19,21	2.34	5 (33%)
4	NAG	I	602	4	14,14,15	0.61	0	15,19,21	0.91	1 (6%)

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
4	NAG	A	602	1,4	-	0/6/23/26	0/1/1/1
4	NAG	A	603	4	-	0/6/23/26	0/1/1/1
4	NAG	C	602	1,4	-	0/6/23/26	0/1/1/1
4	NAG	C	603	4	-	0/6/23/26	0/1/1/1
4	NAG	I	601	1,4	-	0/6/23/26	0/1/1/1
4	NAG	I	602	4	-	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	I	601	NAG	C1-C2	2.44	1.55	1.52
4	C	602	NAG	C1-C2	3.13	1.56	1.52

The worst 5 of 19 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	603	NAG	C2-N2-C7	-5.79	114.49	122.94
4	A	602	NAG	C2-N2-C7	-4.77	115.98	122.94
4	C	602	NAG	C4-C3-C2	-3.69	105.60	111.02
4	C	603	NAG	C1-O5-C5	-3.61	107.19	112.17
4	C	602	NAG	C2-N2-C7	-2.98	118.59	122.94

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

6 monomers are involved in 17 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	602	NAG	6	0
4	A	603	NAG	5	0
4	C	602	NAG	4	0
4	C	603	NAG	3	0
4	I	601	NAG	7	0
4	I	602	NAG	2	0

## 5.6 Ligand geometry

6 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	601	1	14,14,15	0.63	0	15,19,21	2.74	4 (26%)
3	NAG	C	601	1	14,14,15	0.63	0	15,19,21	2.02	4 (26%)
3	NAG	E	601	1	14,14,15	0.76	1 (7%)	15,19,21	1.16	1 (6%)
3	NAG	G	601	1	14,14,15	0.50	0	15,19,21	1.53	3 (20%)
3	NAG	I	603	1	14,14,15	0.79	1 (7%)	15,19,21	2.52	4 (26%)
3	NAG	K	601	1	14,14,15	0.42	0	15,19,21	2.19	1 (6%)

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	601	1	-	0/6/23/26	0/1/1/1
3	NAG	C	601	1	-	0/6/23/26	0/1/1/1
3	NAG	E	601	1	-	0/6/23/26	0/1/1/1
3	NAG	G	601	1	-	0/6/23/26	0/1/1/1
3	NAG	I	603	1	-	0/6/23/26	0/1/1/1
3	NAG	K	601	1	-	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)
3	E	601	NAG	C1-C2	2.18	1.55	1.52
3	I	603	NAG	C1-C2	2.63	1.56	1.52

The worst 5 of 17 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	K	601	NAG	C2-N2-C7	-7.80	111.56	122.94
3	I	603	NAG	C4-C3-C2	-4.01	105.14	111.02
3	A	601	NAG	C2-N2-C7	-3.79	117.42	122.94
3	E	601	NAG	C2-N2-C7	-2.40	119.44	122.94
3	I	603	NAG	C3-C4-C5	-2.39	106.01	110.22

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	K	601	NAG	9	0

## 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q < 0.9
1	A	323/323 (100%)	-0.03	2 (0%) 89 71	20, 50, 95, 142	0
1	C	322/323 (99%)	0.03	11 (3%) 46 20	17, 47, 94, 172	0
1	E	321/323 (99%)	0.11	10 (3%) 49 22	22, 48, 88, 152	0
1	G	322/323 (99%)	0.14	11 (3%) 46 20	23, 54, 99, 155	0
1	I	322/323 (99%)	0.05	11 (3%) 46 20	22, 52, 87, 212	0
1	K	322/323 (99%)	0.00	9 (2%) 53 25	23, 52, 98, 160	0
2	B	162/166 (97%)	0.26	5 (3%) 49 22	21, 60, 109, 160	0
2	D	164/166 (98%)	0.61	21 (12%) 4 2	20, 71, 137, 180	0
2	F	161/166 (96%)	0.52	21 (13%) 4 1	23, 73, 141, 203	0
2	H	162/166 (97%)	0.11	5 (3%) 49 22	24, 61, 116, 160	0
2	J	166/166 (100%)	0.17	2 (1%) 79 53	19, 58, 102, 132	0
2	L	161/166 (96%)	0.38	9 (5%) 25 10	26, 68, 132, 199	0
All	All	2908/2934 (99%)	0.15	117 (4%) 39 16	17, 54, 115, 212	0

The worst 5 of 117 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	I	79	ALA	9.7
1	C	8	THR	6.3
1	C	76	LEU	6.3
2	D	24	TYR	6.2
1	E	9	LEU	6.2

### 6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

### 6.3 Carbohydrates [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
4	NAG	I	601	14/15	0.88	0.23	1.89	54,67,82,89	0
4	NAG	A	602	14/15	0.90	0.21	0.24	50,55,73,87	0
4	NAG	C	602	14/15	0.85	0.18	-0.28	61,91,103,103	0
4	NAG	C	603	14/15	0.65	0.34	-	119,145,155,170	0
4	NAG	A	603	14/15	0.82	0.24	-	70,99,123,128	0
4	NAG	I	602	14/15	0.76	0.28	-	65,96,112,114	0

### 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
3	NAG	K	601	14/15	0.79	0.28	4.28	69,93,112,117	0
3	NAG	C	601	14/15	0.73	0.33	-	108,149,162,165	0
3	NAG	E	601	14/15	0.69	0.35	-	127,145,172,172	0
3	NAG	I	603	14/15	0.78	0.27	-	67,95,120,122	0
3	NAG	G	601	14/15	0.76	0.25	-	67,103,119,122	0
3	NAG	A	601	14/15	0.84	0.33	-	111,124,137,141	0

### 6.5 Other polymers [i](#)

There are no such residues in this entry.