



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 04:40 PM GMT

PDB ID : 4FP8  
Title : Crystal structure of broadly neutralizing antibody C05 bound to H3 influenza hemagglutinin, HA1 subunit  
Authors : Ekiert, D.C.; Wilson, I.A.  
Deposited on : 2012-06-21  
Resolution : 2.95 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 (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

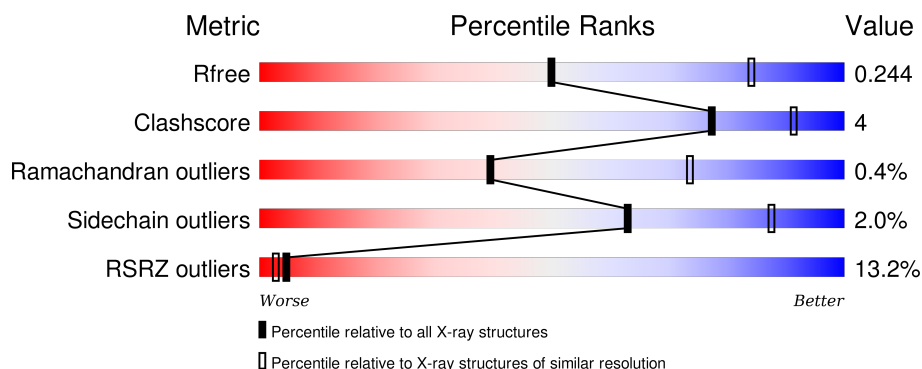
# 1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.95 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	2057 (2.98-2.90)
Clashscore	102246	2308 (2.98-2.90)
Ramachandran outliers	100387	2245 (2.98-2.90)
Sidechain outliers	100360	2247 (2.98-2.90)
RSRZ outliers	91569	2065 (2.98-2.90)

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	278	<div> <div>7%</div> <div>88%</div> <div>8%</div> <div>.</div> </div>
1	B	278	<div> <div>11%</div> <div>92%</div> <div>.</div> <div>.</div> </div>
1	C	278	<div> <div>15%</div> <div>86%</div> <div>9%</div> <div>5%</div> </div>
1	D	278	<div> <div>19%</div> <div>88%</div> <div>8%</div> <div>.</div> </div>
2	H	241	<div> <div>3%</div> <div>88%</div> <div>9%</div> <div>..</div> </div>

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Mol	Chain	Length	Quality of chain
2	I	241	<p>4% 92% 7% •</p>
2	J	241	<p>5% 91% 7% •</p>
2	K	241	<p>31% 89% 9% ••</p>
3	L	214	<p>88% 10% •</p>
3	M	214	<p>89% 9% •</p>
3	N	214	<p>90% 8% •</p>
3	O	214	<p>60% 87% 11% •</p>

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 22406 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	267	Total	C	N	O	S	0	8	0
			2141	1346	375	408	12			
1	B	267	Total	C	N	O	S	0	8	0
			2141	1346	375	408	12			
1	C	265	Total	C	N	O	S	0	7	0
			2116	1330	369	405	12			
1	D	266	Total	C	N	O	S	0	8	0
			2128	1335	374	407	12			

There are 44 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	39	ALA	-	EXPRESSION TAG	UNP Q91MA7
A	40	ASP	-	EXPRESSION TAG	UNP Q91MA7
A	41	PRO	-	EXPRESSION TAG	UNP Q91MA7
A	42	GLY	-	EXPRESSION TAG	UNP Q91MA7
A	310	GLY	-	EXPRESSION TAG	UNP Q91MA7
A	311	HIS	-	EXPRESSION TAG	UNP Q91MA7
A	312	HIS	-	EXPRESSION TAG	UNP Q91MA7
A	313	HIS	-	EXPRESSION TAG	UNP Q91MA7
A	314	HIS	-	EXPRESSION TAG	UNP Q91MA7
A	315	HIS	-	EXPRESSION TAG	UNP Q91MA7
A	316	HIS	-	EXPRESSION TAG	UNP Q91MA7
B	39	ALA	-	EXPRESSION TAG	UNP Q91MA7
B	40	ASP	-	EXPRESSION TAG	UNP Q91MA7
B	41	PRO	-	EXPRESSION TAG	UNP Q91MA7
B	42	GLY	-	EXPRESSION TAG	UNP Q91MA7
B	310	GLY	-	EXPRESSION TAG	UNP Q91MA7
B	311	HIS	-	EXPRESSION TAG	UNP Q91MA7
B	312	HIS	-	EXPRESSION TAG	UNP Q91MA7
B	313	HIS	-	EXPRESSION TAG	UNP Q91MA7
B	314	HIS	-	EXPRESSION TAG	UNP Q91MA7
B	315	HIS	-	EXPRESSION TAG	UNP Q91MA7

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Chain	Residue	Modelled	Actual	Comment	Reference
B	316	HIS	-	EXPRESSION TAG	UNP Q91MA7
C	39	ALA	-	EXPRESSION TAG	UNP Q91MA7
C	40	ASP	-	EXPRESSION TAG	UNP Q91MA7
C	41	PRO	-	EXPRESSION TAG	UNP Q91MA7
C	42	GLY	-	EXPRESSION TAG	UNP Q91MA7
C	310	GLY	-	EXPRESSION TAG	UNP Q91MA7
C	311	HIS	-	EXPRESSION TAG	UNP Q91MA7
C	312	HIS	-	EXPRESSION TAG	UNP Q91MA7
C	313	HIS	-	EXPRESSION TAG	UNP Q91MA7
C	314	HIS	-	EXPRESSION TAG	UNP Q91MA7
C	315	HIS	-	EXPRESSION TAG	UNP Q91MA7
C	316	HIS	-	EXPRESSION TAG	UNP Q91MA7
D	39	ALA	-	EXPRESSION TAG	UNP Q91MA7
D	40	ASP	-	EXPRESSION TAG	UNP Q91MA7
D	41	PRO	-	EXPRESSION TAG	UNP Q91MA7
D	42	GLY	-	EXPRESSION TAG	UNP Q91MA7
D	310	GLY	-	EXPRESSION TAG	UNP Q91MA7
D	311	HIS	-	EXPRESSION TAG	UNP Q91MA7
D	312	HIS	-	EXPRESSION TAG	UNP Q91MA7
D	313	HIS	-	EXPRESSION TAG	UNP Q91MA7
D	314	HIS	-	EXPRESSION TAG	UNP Q91MA7
D	315	HIS	-	EXPRESSION TAG	UNP Q91MA7
D	316	HIS	-	EXPRESSION TAG	UNP Q91MA7

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	239	Total	C	N	O	S	0	4	0
			1806	1127	306	365	8			
2	I	239	Total	C	N	O	S	0	4	0
			1806	1127	306	365	8			
2	J	239	Total	C	N	O	S	0	4	0
			1806	1127	306	365	8			
2	K	239	Total	C	N	O	S	0	4	0
			1806	1127	306	365	8			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	L	213	Total	C	N	O	S	0	1	0
			1648	1033	281	330	4			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	M	213	Total	C	N	O	S	0	1	0
			1648	1033	281	330	4			
3	N	213	Total	C	N	O	S	0	1	0
			1648	1033	281	330	4			
3	O	213	Total	C	N	O	S	0	1	0
			1648	1033	281	330	4			

- Molecule 4 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula:  $C_8H_{15}NO_6$ ).



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

- Molecule 5 is a polymer of unknown type called SUGAR (2-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	C	2	Total	C	N	O	0	0
			28	16	2	10		

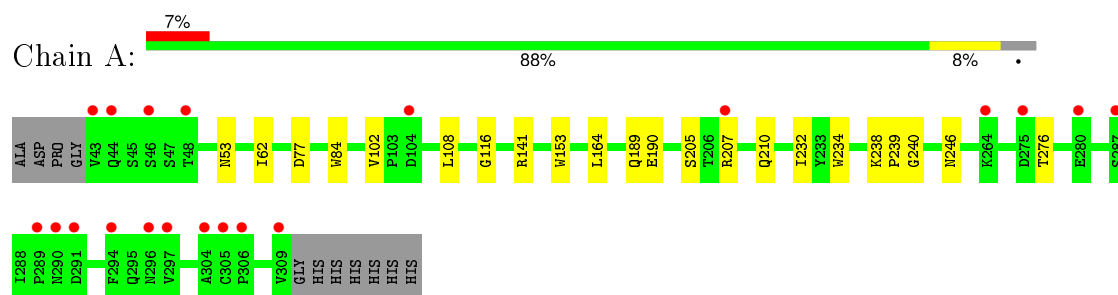
- Molecule 6 is ZINC ION (three-letter code: ZN) (formula:  $Zn$ ).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	J	1	Total 1	Zn 1	0	0
6	H	1	Total 1	Zn 1	0	0
6	N	2	Total 2	Zn 2	0	0
6	O	1	Total 1	Zn 1	0	0
6	L	2	Total 2	Zn 2	0	0
6	M	1	Total 1	Zn 1	0	0

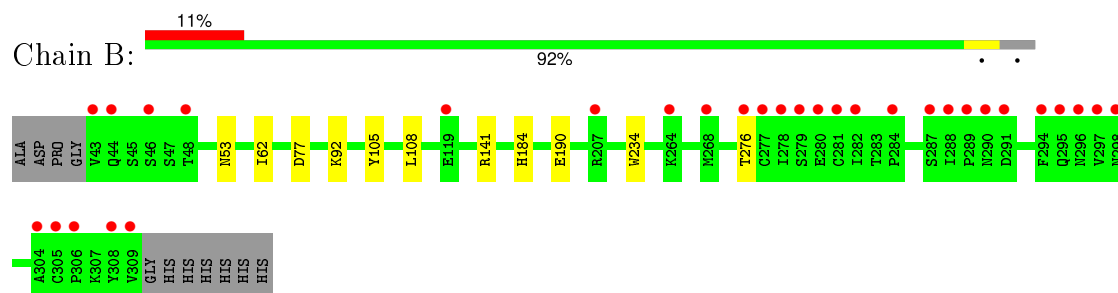
### 3 Residue-property plots [i](#)

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 ( $RSRZ > 2$ ). 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.

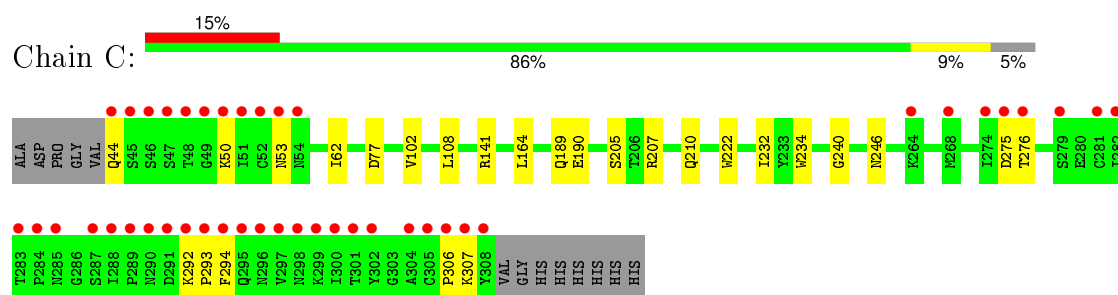
- Molecule 1: Hemagglutinin HA1 chain



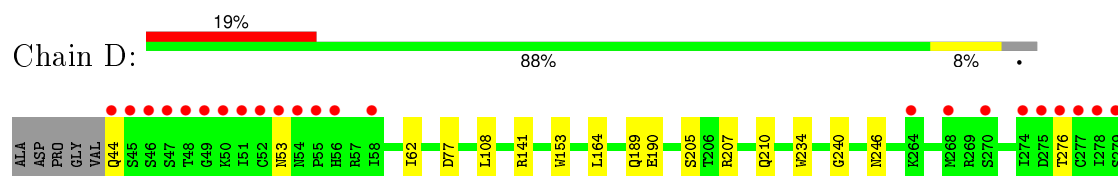
- Molecule 1: Hemagglutinin HA1 chain



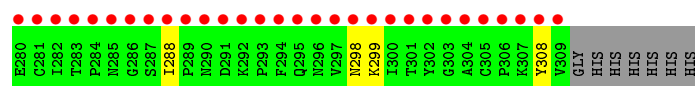
- Molecule 1: Hemagglutinin HA1 chain



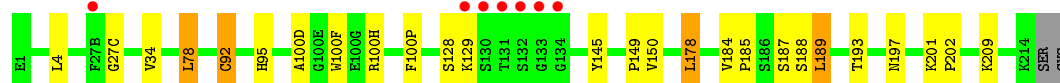
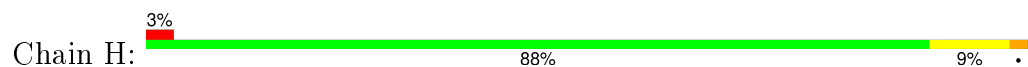
- Molecule 1: Hemagglutinin HA1 chain



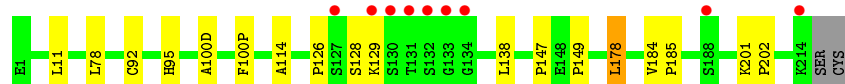
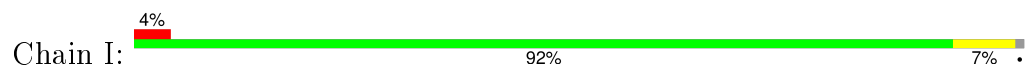




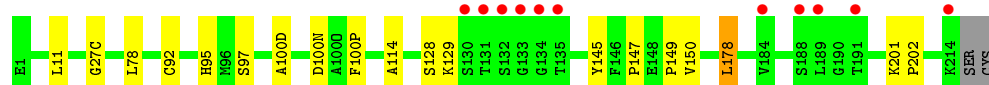
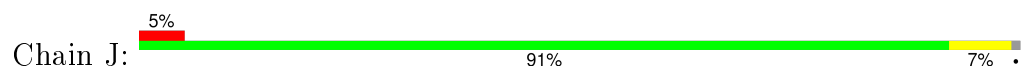
- Molecule 2: Antibody C05, heavy chain



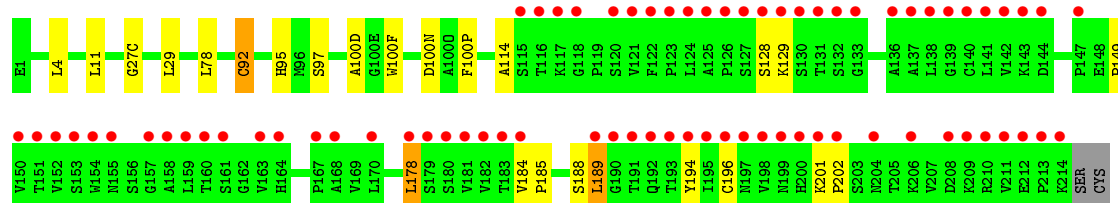
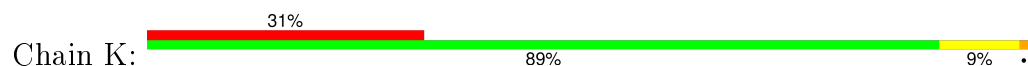
- Molecule 2: Antibody C05, heavy chain



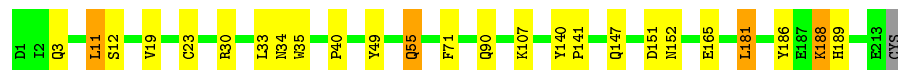
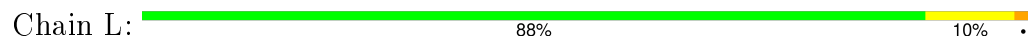
- Molecule 2: Antibody C05, heavy chain



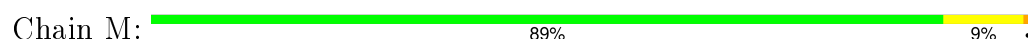
- Molecule 2: Antibody C05, heavy chain



- Molecule 3: Antibody C05, light chain



- Molecule 3: Antibody C05, light chain




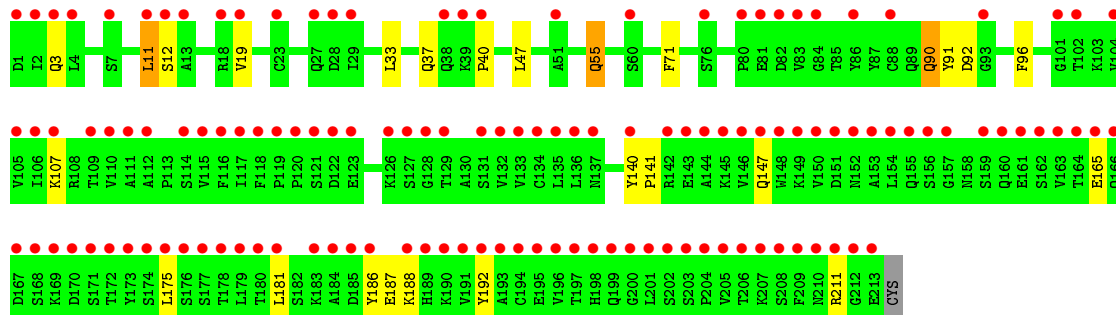
- Molecule 3: Antibody C05, light chain

Chain N:  90% 8%



- Molecule 3: Antibody C05, light chain

Chain O:  60% 87% 11%



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	90.79Å 247.72Å 95.38Å 90.00° 91.33° 90.00°	Depositor
Resolution (Å)	44.49 – 2.95 44.49 – 2.95	Depositor EDS
% Data completeness (in resolution range)	95.1 (44.49-2.95) 95.0 (44.49-2.95)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.10	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.64 (at 2.96Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7.2_869)	Depositor
R, $R_{free}$	0.212 , 0.241 0.214 , 0.244	Depositor DCC
$R_{free}$ test set	4192 reflections (5.24%)	DCC
Wilson B-factor (Å <sup>2</sup> )	56.8	Xtriage
Anisotropy	0.240	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.29 , 36.7	EDS
Estimated twinning fraction	0.008 for l,k,-h 0.028 for h,-k,-l 0.021 for l,-k,h	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 84219 reflections	Xtriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	22406	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	83.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.89% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: ZN, PCA, 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	0.30	0/2195	0.58	0/2990
1	B	0.29	0/2195	0.57	0/2990
1	C	0.29	0/2170	0.59	0/2956
1	D	0.31	0/2181	0.58	0/2971
2	H	0.31	0/1837	0.58	1/2500 (0.0%)
2	I	0.28	0/1837	0.54	0/2500
2	J	0.28	0/1837	0.54	0/2500
2	K	0.26	0/1837	0.51	0/2500
3	L	0.34	0/1682	0.59	0/2280
3	M	0.32	0/1682	0.57	0/2280
3	N	0.30	0/1682	0.56	0/2280
3	O	0.26	0/1682	0.52	0/2280
All	All	0.30	0/22817	0.56	1/31027 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	100(H)	ARG	NE-CZ-NH2	-5.03	117.78	120.30

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	2141	0	2074	13	0
1	B	2141	0	2075	12	0
1	C	2116	0	2044	21	0
1	D	2128	0	2058	18	0
2	H	1806	0	1749	16	0
2	I	1806	0	1749	13	0
2	J	1806	0	1749	13	0
2	K	1806	0	1749	20	0
3	L	1648	0	1614	19	0
3	M	1648	0	1614	15	0
3	N	1648	0	1614	12	0
3	O	1648	0	1614	15	0
4	A	14	0	13	0	0
4	D	14	0	13	0	0
5	C	28	0	25	0	0
6	H	1	0	0	0	0
6	J	1	0	0	0	0
6	L	2	0	0	0	0
6	M	1	0	0	0	0
6	N	2	0	0	0	0
6	O	1	0	0	0	0
All	All	22406	0	21754	165	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 4.

The worst 5 of 165 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:205:SER:HB3	1:C:210:GLN:HG3	1.64	0.80
1:A:77:ASP:OD2	1:A:141:ARG:NH1	2.16	0.78
3:M:11:LEU:C	3:M:11:LEU:HD12	2.09	0.72
1:D:299:LYS:HA	1:D:308:TYR:CG	2.28	0.69
2:J:11:LEU:HD21	2:J:114:ALA:O	1.96	0.65

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	273/278 (98%)	266 (97%)	6 (2%)	1 (0%)	39	73
1	B	273/278 (98%)	266 (97%)	6 (2%)	1 (0%)	39	73
1	C	270/278 (97%)	264 (98%)	5 (2%)	1 (0%)	39	73
1	D	272/278 (98%)	265 (97%)	6 (2%)	1 (0%)	39	73
2	H	241/241 (100%)	234 (97%)	5 (2%)	2 (1%)	24	58
2	I	241/241 (100%)	234 (97%)	6 (2%)	1 (0%)	39	73
2	J	241/241 (100%)	235 (98%)	5 (2%)	1 (0%)	39	73
2	K	241/241 (100%)	233 (97%)	6 (2%)	2 (1%)	24	58
3	L	212/214 (99%)	208 (98%)	4 (2%)	0	100	100
3	M	212/214 (99%)	208 (98%)	4 (2%)	0	100	100
3	N	212/214 (99%)	207 (98%)	5 (2%)	0	100	100
3	O	212/214 (99%)	207 (98%)	5 (2%)	0	100	100
All	All	2900/2932 (99%)	2827 (98%)	63 (2%)	10 (0%)	39	78

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	H	189	LEU
2	K	189	LEU
1	A	62	ILE
1	B	62	ILE
1	C	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	244/244 (100%)	243 (100%)	1 (0%)	93	98
1	B	244/244 (100%)	243 (100%)	1 (0%)	93	98
1	C	241/244 (99%)	240 (100%)	1 (0%)	93	98
1	D	242/244 (99%)	241 (100%)	1 (0%)	93	98
2	H	202/200 (101%)	195 (96%)	7 (4%)	43	77
2	I	202/200 (101%)	199 (98%)	3 (2%)	72	91
2	J	202/200 (101%)	199 (98%)	3 (2%)	72	91
2	K	202/200 (101%)	198 (98%)	4 (2%)	63	87
3	L	187/187 (100%)	180 (96%)	7 (4%)	41	75
3	M	187/187 (100%)	180 (96%)	7 (4%)	41	75
3	N	187/187 (100%)	180 (96%)	7 (4%)	41	75
3	O	187/187 (100%)	180 (96%)	7 (4%)	41	75
All	All	2527/2524 (100%)	2478 (98%)	49 (2%)	63	88

5 of 49 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	M	11	LEU
3	M	188	LYS
3	O	90	GLN
3	M	90	GLN
2	J	78	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 26 such sidechains are listed below:

Mol	Chain	Res	Type
2	H	192	GLN
3	L	138	ASN
3	O	189	HIS
3	L	55	GLN
3	L	137	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

4 non-standard protein/DNA/RNA residues 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	$\# Z  > 2$
2	PCA	H	1	2	7,8,9	1.90	2 (28%)	9,10,12	2.08	4 (44%)
2	PCA	I	1	2	7,8,9	1.90	2 (28%)	9,10,12	2.11	4 (44%)
2	PCA	J	1	2	7,8,9	1.91	2 (28%)	9,10,12	2.09	4 (44%)
2	PCA	K	1	2	7,8,9	1.92	2 (28%)	9,10,12	2.10	4 (44%)

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
2	PCA	H	1	2	-	0/0/11/13	0/1/1/1
2	PCA	I	1	2	-	0/0/11/13	0/1/1/1
2	PCA	J	1	2	-	0/0/11/13	0/1/1/1
2	PCA	K	1	2	-	0/0/11/13	0/1/1/1

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	I	1	PCA	CA-N	2.97	1.50	1.46
2	J	1	PCA	CA-N	3.01	1.50	1.46
2	K	1	PCA	CA-N	3.07	1.50	1.46
2	H	1	PCA	CA-N	3.10	1.50	1.46
2	H	1	PCA	CD-N	3.85	1.46	1.33

The worst 5 of 16 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	I	1	PCA	CA-N-CD	-3.40	102.43	113.81
2	J	1	PCA	CA-N-CD	-3.30	102.75	113.81

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	1	PCA	CA-N-CD	-3.29	102.77	113.81
2	K	1	PCA	CA-N-CD	-3.20	103.09	113.81
2	K	1	PCA	CB-CA-C	-2.95	108.73	112.76

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.5 Carbohydrates [i](#)

2 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	$\# Z  > 2$
5	NAG	C	701	1,5	14,14,15	0.52	0	15,19,21	0.56	0
5	NAG	C	702	5	14,14,15	0.51	0	15,19,21	0.65	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	C	701	1,5	-	0/6/23/26	0/1/1/1
5	NAG	C	702	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.

## 5.6 Ligand geometry

Of 10 ligands modelled in this entry, 8 are monoatomic - leaving 2 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
4	NAG	A	701	1	14,14,15	0.56	0	15,19,21	0.54	0
4	NAG	D	701	1	14,14,15	0.54	0	15,19,21	0.49	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
4	NAG	A	701	1	-	0/6/23/26	0/1/1/1
4	NAG	D	701	1	-	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, 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	267/278 (96%)	0.34	20 (7%) 17 13	30, 54, 125, 181	0
1	B	267/278 (96%)	0.47	31 (11%) 6 4	29, 60, 146, 202	0
1	C	265/278 (95%)	0.84	43 (16%) 3 1	33, 59, 237, 285	0
1	D	266/278 (95%)	1.23	53 (19%) 1 1	31, 62, 281, 438	0
2	H	238/241 (98%)	0.10	7 (2%) 55 51	31, 50, 97, 265	0
2	I	238/241 (98%)	0.26	9 (3%) 44 40	31, 63, 133, 250	0
2	J	238/241 (98%)	0.29	11 (4%) 36 32	35, 68, 131, 246	0
2	K	238/241 (98%)	2.39	74 (31%) 1 0	36, 100, 312, 488	0
3	L	213/214 (99%)	-0.00	0 100 100	30, 46, 75, 106	0
3	M	213/214 (99%)	0.01	1 (0%) 91 91	27, 46, 86, 147	0
3	N	213/214 (99%)	0.13	1 (0%) 91 91	49, 69, 113, 140	0
3	O	213/214 (99%)	3.24	129 (60%) 0 0	89, 178, 276, 356	0
All	All	2869/2932 (97%)	0.77	379 (13%) 4 3	27, 62, 228, 488	0

The worst 5 of 379 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	K	182	VAL	23.2
2	K	138	LEU	22.3
2	K	139	GLY	16.1
2	K	140	CYS	15.8
2	K	158	ALA	13.9

### 6.2 Non-standard residues in protein, DNA, RNA chains [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
2	PCA	I	1	8/9	0.92	0.20	-	61,81,87,88	0
2	PCA	H	1	8/9	0.95	0.22	-	79,96,104,105	0
2	PCA	K	1	8/9	0.82	0.20	-	122,139,147,148	0
2	PCA	J	1	8/9	0.86	0.19	-	86,98,103,106	0

### 6.3 Carbohydrates

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
5	NAG	C	701	14/15	0.80	0.32	-	109,120,130,136	0
5	NAG	C	702	14/15	0.82	0.31	-	120,125,127,128	0

### 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, 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
6	ZN	N	302	1/1	0.94	0.08	-2.27	104,104,104,104	0
6	ZN	L	301	1/1	0.94	0.09	-3.00	106,106,106,106	0
6	ZN	M	301	1/1	0.98	0.09	-3.17	94,94,94,94	0
4	NAG	A	701	14/15	0.70	0.28	-	122,134,148,154	0
4	NAG	D	701	14/15	0.85	0.27	-	100,115,129,135	0
6	ZN	L	302	1/1	0.94	0.14	-	72,72,72,72	0
6	ZN	N	301	1/1	0.95	0.12	-	102,102,102,102	0
6	ZN	O	301	1/1	0.95	0.13	-	133,133,133,133	0
6	ZN	J	301	1/1	0.94	0.04	-	143,143,143,143	0
6	ZN	H	301	1/1	0.85	0.18	-	134,134,134,134	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.