



# wwPDB X-ray Structure Validation Summary Report ⓘ

Sep 3, 2017 – 11:56 PM EDT

PDB ID : 5MWF  
Title : Human Jagged2 C2-EGF2  
Authors : Suckling, R.J.; Handford, P.A.; Lea, S.M.  
Deposited on : unknown  
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](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	:	rb-20029824
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	rb-20029824

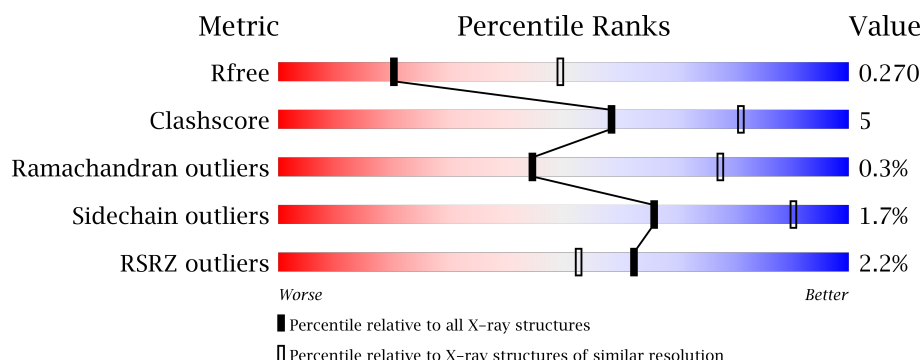
# 1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.80 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))
$R_{free}$	100719	2583 (2.80-2.80)
Clashscore	112137	3033 (2.80-2.80)
Ramachandran outliers	110173	2983 (2.80-2.80)
Sidechain outliers	110143	2985 (2.80-2.80)
RSRZ outliers	101464	2610 (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  $\geq 3$ , 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	293	<div> <div>86%</div> <div>8%</div> <div>6%</div> </div>
1	B	293	<div> <div>84%</div> <div>10%</div> <div>6%</div> </div>
1	C	293	<div> <div>82%</div> <div>7%</div> <div>11%</div> </div>
1	D	293	<div> <div>3%</div> <div>80%</div> <div>10%</div> <div>9%</div> </div>
1	E	293	<div> <div>3%</div> <div>77%</div> <div>10%</div> <div>11%</div> </div>

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Mol	Chain	Length	Quality of chain
1	F	293	

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
2	NAG	E	401	X	-	-	-
3	FUC	A	403	X	-	-	-
3	FUC	D	403	X	-	-	-
3	FUC	E	403	X	-	-	-

## 2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 12890 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 Protein jagged-2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	276	Total	C	N	O	S	0	0	0
			2136	1326	379	403	28			
1	B	275	Total	C	N	O	S	0	1	0
			2133	1325	381	399	28			
1	C	262	Total	C	N	O	S	0	0	0
			2038	1272	355	383	28			
1	D	266	Total	C	N	O	S	0	0	0
			2068	1290	364	386	28			
1	E	260	Total	C	N	O	S	0	0	0
			2024	1265	351	380	28			
1	F	253	Total	C	N	O	S	0	0	0
			1979	1238	342	371	28			

There are 60 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	310	GLY	-	expression tag	UNP Q9Y219
A	311	SER	-	expression tag	UNP Q9Y219
A	312	HIS	-	expression tag	UNP Q9Y219
A	313	HIS	-	expression tag	UNP Q9Y219
A	314	HIS	-	expression tag	UNP Q9Y219
A	315	HIS	-	expression tag	UNP Q9Y219
A	316	HIS	-	expression tag	UNP Q9Y219
A	317	HIS	-	expression tag	UNP Q9Y219
A	318	HIS	-	expression tag	UNP Q9Y219
A	319	HIS	-	expression tag	UNP Q9Y219
B	310	GLY	-	expression tag	UNP Q9Y219
B	311	SER	-	expression tag	UNP Q9Y219
B	312	HIS	-	expression tag	UNP Q9Y219
B	313	HIS	-	expression tag	UNP Q9Y219
B	314	HIS	-	expression tag	UNP Q9Y219
B	315	HIS	-	expression tag	UNP Q9Y219
B	316	HIS	-	expression tag	UNP Q9Y219

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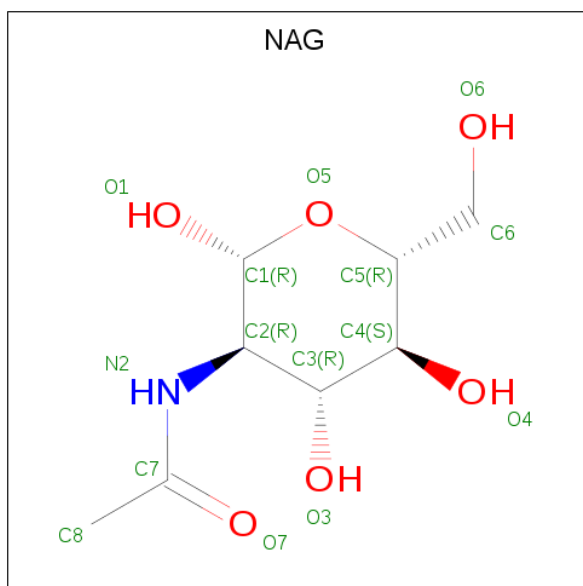
Chain	Residue	Modelled	Actual	Comment	Reference
B	317	HIS	-	expression tag	UNP Q9Y219
B	318	HIS	-	expression tag	UNP Q9Y219
B	319	HIS	-	expression tag	UNP Q9Y219
C	310	GLY	-	expression tag	UNP Q9Y219
C	311	SER	-	expression tag	UNP Q9Y219
C	312	HIS	-	expression tag	UNP Q9Y219
C	313	HIS	-	expression tag	UNP Q9Y219
C	314	HIS	-	expression tag	UNP Q9Y219
C	315	HIS	-	expression tag	UNP Q9Y219
C	316	HIS	-	expression tag	UNP Q9Y219
C	317	HIS	-	expression tag	UNP Q9Y219
C	318	HIS	-	expression tag	UNP Q9Y219
C	319	HIS	-	expression tag	UNP Q9Y219
D	310	GLY	-	expression tag	UNP Q9Y219
D	311	SER	-	expression tag	UNP Q9Y219
D	312	HIS	-	expression tag	UNP Q9Y219
D	313	HIS	-	expression tag	UNP Q9Y219
D	314	HIS	-	expression tag	UNP Q9Y219
D	315	HIS	-	expression tag	UNP Q9Y219
D	316	HIS	-	expression tag	UNP Q9Y219
D	317	HIS	-	expression tag	UNP Q9Y219
D	318	HIS	-	expression tag	UNP Q9Y219
D	319	HIS	-	expression tag	UNP Q9Y219
E	310	GLY	-	expression tag	UNP Q9Y219
E	311	SER	-	expression tag	UNP Q9Y219
E	312	HIS	-	expression tag	UNP Q9Y219
E	313	HIS	-	expression tag	UNP Q9Y219
E	314	HIS	-	expression tag	UNP Q9Y219
E	315	HIS	-	expression tag	UNP Q9Y219
E	316	HIS	-	expression tag	UNP Q9Y219
E	317	HIS	-	expression tag	UNP Q9Y219
E	318	HIS	-	expression tag	UNP Q9Y219
E	319	HIS	-	expression tag	UNP Q9Y219
F	310	GLY	-	expression tag	UNP Q9Y219
F	311	SER	-	expression tag	UNP Q9Y219
F	312	HIS	-	expression tag	UNP Q9Y219
F	313	HIS	-	expression tag	UNP Q9Y219
F	314	HIS	-	expression tag	UNP Q9Y219
F	315	HIS	-	expression tag	UNP Q9Y219
F	316	HIS	-	expression tag	UNP Q9Y219
F	317	HIS	-	expression tag	UNP Q9Y219
F	318	HIS	-	expression tag	UNP Q9Y219

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Chain	Residue	Modelled	Actual	Comment	Reference
F	319	HIS	-	expression tag	UNP Q9Y219

- Molecule 2 is N-ACETYL-D-GLUCOSAMINE (three-letter code: NAG) (formula:  $C_8H_{15}NO_6$ ).



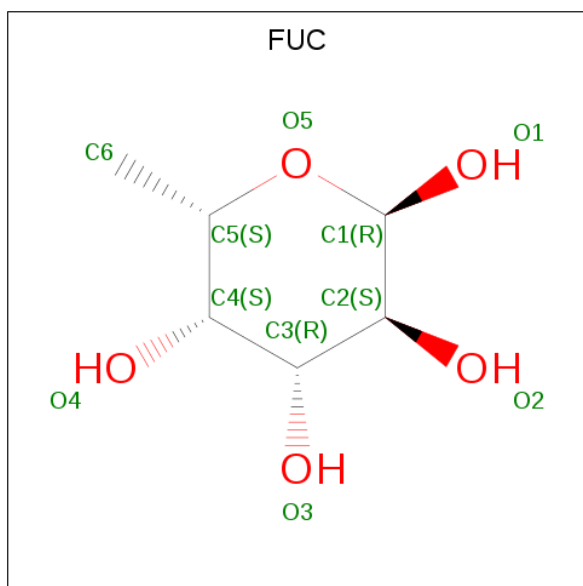
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	B	1	Total	C	N	O	0	0
			14	8	1	5		
2	B	1	Total	C	N	O	0	0
			14	8	1	5		
2	C	1	Total	C	N	O	0	0
			14	8	1	5		
2	C	1	Total	C	N	O	0	0
			14	8	1	5		
2	D	1	Total	C	N	O	0	0
			14	8	1	5		
2	D	1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

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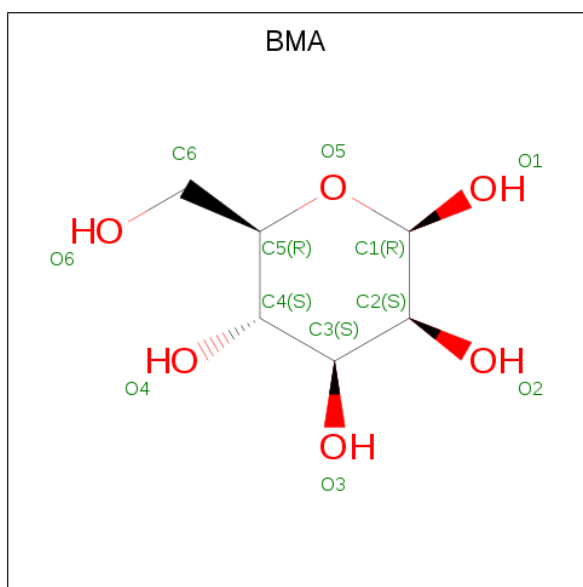
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	F	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 3 is ALPHA-L-FUCOSE (three-letter code: FUC) (formula:  $C_6H_{12}O_5$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			10	6	4		
3	B	1	Total	C	O	0	0
			10	6	4		
3	C	1	Total	C	O	0	0
			10	6	4		
3	D	1	Total	C	O	0	0
			10	6	4		
3	E	1	Total	C	O	0	0
			10	6	4		
3	F	1	Total	C	O	0	0
			10	6	4		

- Molecule 4 is BETA-D-MANNOSE (three-letter code: BMA) (formula:  $C_6H_{12}O_6$ ).



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

- Molecule 5 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	D	3	Total	Ca	0	0
			3	3		
5	E	3	Total	Ca	0	0
			3	3		
5	B	3	Total	Ca	0	0
			3	3		
5	C	3	Total	Ca	0	0
			3	3		
5	A	3	Total	Ca	0	0
			3	3		
5	F	2	Total	Ca	0	0
			2	2		

- Molecule 6 is CHLORIDE ION (three-letter code: CL) (formula: Cl).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	B	1	Total	Cl	0	0
			1	1		
6	A	1	Total	Cl	0	0
			1	1		

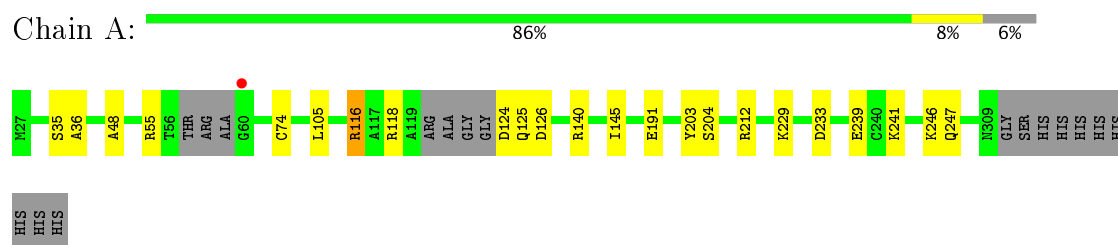
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	61	Total	O	0	0
			61	61		
7	B	34	Total	O	0	0
			34	34		
7	C	33	Total	O	0	0
			33	33		
7	D	32	Total	O	0	0
			32	32		
7	E	35	Total	O	0	0
			35	35		
7	F	37	Total	O	0	0
			37	37		

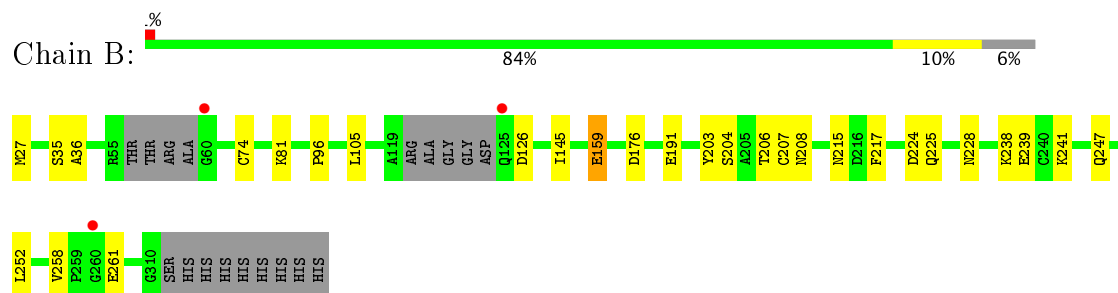
### 3 Residue-property plots [i](#)

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

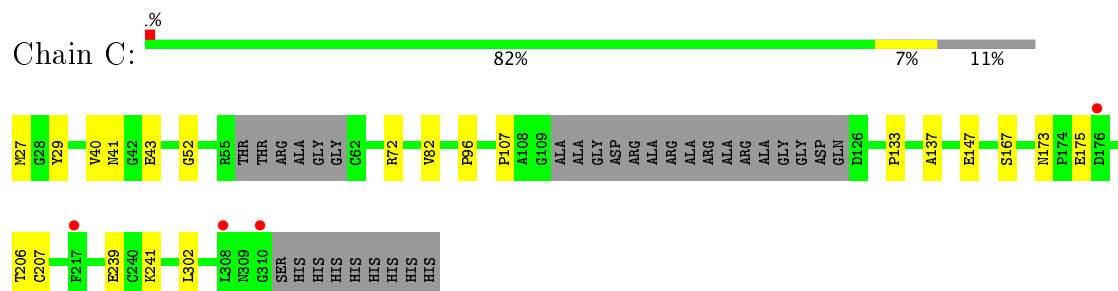
#### • Molecule 1: Protein jagged-2



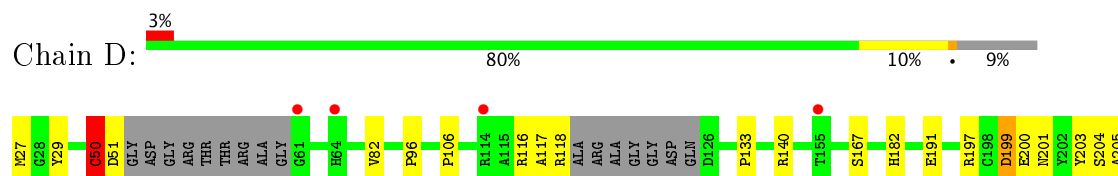
#### • Molecule 1: Protein jagged-2



#### • Molecule 1: Protein jagged-2



#### • Molecule 1: Protein jagged-2





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	62.63Å 92.93Å 97.00Å 71.68° 83.16° 82.68°	Depositor
Resolution (Å)	38.01 – 2.80 38.01 – 2.80	Depositor EDS
% Data completeness (in resolution range)	97.7 (38.01-2.80) 87.6 (38.01-2.80)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.68 (at 2.81Å)	Xtriage
Refinement program	PHENIX (1.10_2155: ???)	Depositor
R, $R_{free}$	0.217 , 0.275 0.212 , 0.270	Depositor DCC
$R_{free}$ test set	2392 reflections (4.85%)	DCC
Wilson B-factor (Å <sup>2</sup> )	48.7	Xtriage
Anisotropy	0.255	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 49.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.055 for -h,-l,-k	Xtriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	12890	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.29% 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 [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: FUC, CA, BMA, NAG, CL

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	0.32	0/2194	0.50	0/2975
1	B	0.34	2/2194 (0.1%)	0.51	0/2973
1	C	0.28	0/2096	0.48	0/2844
1	D	0.37	0/2126	0.57	2/2884 (0.1%)
1	E	0.40	3/2082 (0.1%)	0.57	1/2826 (0.0%)
1	F	0.28	0/2036	0.53	0/2763
All	All	0.34	5/12728 (0.0%)	0.53	3/17265 (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	E	0	1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	159	GLU	CD-OE1	-6.73	1.18	1.25
1	E	239	GLU	CD-OE1	-5.79	1.19	1.25
1	B	159	GLU	CD-OE2	-5.52	1.19	1.25
1	E	197	ARG	CA-CB	5.29	1.65	1.53
1	E	29	TYR	CB-CG	-5.26	1.43	1.51

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	212	ARG	NE-CZ-NH1	-10.46	115.07	120.30
1	D	212	ARG	NE-CZ-NH2	8.79	124.69	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	197	ARG	CA-CB-CG	5.67	125.87	113.40

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	E	64	HIS	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	2136	0	1946	15	0
1	B	2133	0	1951	17	1
1	C	2038	0	1853	12	1
1	D	2068	0	1889	24	0
1	E	2024	0	1840	26	0
1	F	1979	0	1798	38	0
2	A	28	0	23	0	0
2	B	28	0	23	0	0
2	C	28	0	23	0	0
2	D	28	0	24	0	0
2	E	28	0	24	0	0
2	F	28	0	24	0	0
3	A	10	0	10	0	0
3	B	10	0	10	1	0
3	C	10	0	10	1	0
3	D	10	0	10	1	0
3	E	10	0	10	0	0
3	F	10	0	10	1	0
4	A	11	0	10	0	0
4	B	11	0	10	0	0
4	C	11	0	10	0	0
5	A	3	0	0	0	0
5	B	3	0	0	0	0
5	C	3	0	0	0	0
5	D	3	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	E	3	0	0	0	0
5	F	2	0	0	0	0
6	A	1	0	0	0	0
6	B	1	0	0	0	0
7	A	61	0	0	1	1
7	B	34	0	0	0	0
7	C	33	0	0	0	0
7	D	32	0	0	0	0
7	E	35	0	0	0	1
7	F	37	0	0	0	0
All	All	12890	0	11508	132	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 5.

The worst 5 of 132 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:E:229:LYS:NZ	1:E:239:GLU:OE2	1.96	0.98
1:D:197:ARG:HH11	1:D:197:ARG:HG3	1.31	0.95
1:E:29:TYR:HB3	1:E:133:PRO:HA	1.60	0.82
1:B:217:PHE:O	1:B:241:LYS:NZ	2.13	0.82
1:F:182:HIS:HD2	1:F:191:GLU:HG2	1.46	0.80

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)
1:B:81:LYS:NZ	1:C:52:GLY:O[1_546]	2.17	0.03
7:A:550:HOH:O	7:E:533:HOH:O[1_455]	2.18	0.02

## 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	270/293 (92%)	253 (94%)	17 (6%)	0	100	100
1	B	270/293 (92%)	253 (94%)	17 (6%)	0	100	100
1	C	256/293 (87%)	233 (91%)	22 (9%)	1 (0%)	38	72
1	D	260/293 (89%)	238 (92%)	21 (8%)	1 (0%)	38	72
1	E	254/293 (87%)	230 (91%)	23 (9%)	1 (0%)	38	72
1	F	247/293 (84%)	220 (89%)	25 (10%)	2 (1%)	22	55
All	All	1557/1758 (89%)	1427 (92%)	125 (8%)	5 (0%)	44	77

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	107	PRO
1	D	50	CYS
1	F	50	CYS
1	F	127	PRO
1	E	127	PRO

### 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	227/239 (95%)	221 (97%)	6 (3%)	51	83
1	B	226/239 (95%)	222 (98%)	4 (2%)	64	90
1	C	220/239 (92%)	219 (100%)	1 (0%)	91	97
1	D	221/239 (92%)	215 (97%)	6 (3%)	50	83
1	E	219/239 (92%)	216 (99%)	3 (1%)	71	92
1	F	215/239 (90%)	212 (99%)	3 (1%)	71	92
All	All	1328/1434 (93%)	1305 (98%)	23 (2%)	66	90

5 of 23 residues with a non-rotameric sidechain are listed below:



Mol	Chain	Res	Type
1	C	302	LEU
1	D	140	ARG
1	F	103	PHE
1	D	50	CYS
1	D	199	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	182	HIS
1	F	201	ASN
1	F	79	GLN
1	E	101	ASN
1	E	247	GLN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 40 ligands modelled in this entry, 19 are monoatomic - leaving 21 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
2	NAG	A	401	1,3,2	14,14,15	0.25	0	15,19,21	0.47	0
2	NAG	A	402	2,4	14,14,15	0.25	0	15,19,21	0.47	0
3	FUC	A	403	2	9,10,11	0.92	1 (11%)	13,14,16	0.81	0
4	BMA	A	404	2	11,11,12	0.67	0	13,15,17	0.79	0
2	NAG	B	401	1,3,2	14,14,15	0.28	0	15,19,21	0.42	0
2	NAG	B	402	2,4	14,14,15	0.41	0	15,19,21	0.38	0
3	FUC	B	403	2	9,10,11	0.56	0	13,14,16	0.95	1 (7%)
4	BMA	B	404	2	11,11,12	0.74	0	13,15,17	0.85	0
2	NAG	C	401	1,3,2	14,14,15	0.58	0	15,19,21	0.44	0
2	NAG	C	402	2,4	14,14,15	0.24	0	15,19,21	0.52	0
3	FUC	C	403	2	9,10,11	0.68	0	13,14,16	0.90	0
4	BMA	C	404	2	11,11,12	0.65	0	13,15,17	0.94	0
2	NAG	D	401	3,2	14,14,15	0.27	0	15,19,21	0.46	0
2	NAG	D	402	2	14,14,15	0.35	0	15,19,21	0.46	0
3	FUC	D	403	2	9,10,11	0.85	0	13,14,16	0.93	0
2	NAG	E	401	1,3,2	14,14,15	0.18	0	15,19,21	0.52	0
2	NAG	E	402	2	14,14,15	0.21	0	15,19,21	0.44	0
3	FUC	E	403	2	9,10,11	0.78	0	13,14,16	0.94	0
2	NAG	F	401	1,3,2	14,14,15	0.29	0	15,19,21	0.51	0
2	NAG	F	402	2	14,14,15	0.22	0	15,19,21	0.50	0
3	FUC	F	403	2	9,10,11	0.82	0	13,14,16	0.97	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
2	NAG	A	401	1,3,2	-	0/6/23/26	0/1/1/1
2	NAG	A	402	2,4	-	0/6/23/26	0/1/1/1
3	FUC	A	403	2	1/1/4/5	0/0/17/20	0/1/1/1
4	BMA	A	404	2	-	0/2/19/22	0/1/1/1
2	NAG	B	401	1,3,2	-	0/6/23/26	0/1/1/1
2	NAG	B	402	2,4	-	0/6/23/26	0/1/1/1
3	FUC	B	403	2	-	0/0/17/20	0/1/1/1
4	BMA	B	404	2	-	0/2/19/22	0/1/1/1
2	NAG	C	401	1,3,2	-	0/6/23/26	0/1/1/1
2	NAG	C	402	2,4	-	0/6/23/26	0/1/1/1
3	FUC	C	403	2	-	0/0/17/20	0/1/1/1
4	BMA	C	404	2	-	0/2/19/22	0/1/1/1
2	NAG	D	401	3,2	-	0/6/23/26	0/1/1/1
2	NAG	D	402	2	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	FUC	D	403	2	1/1/4/5	0/0/17/20	0/1/1/1
2	NAG	E	401	1,3,2	1/1/5/7	0/6/23/26	0/1/1/1
2	NAG	E	402	2	-	0/6/23/26	0/1/1/1
3	FUC	E	403	2	1/1/4/5	0/0/17/20	0/1/1/1
2	NAG	F	401	1,3,2	-	0/6/23/26	0/1/1/1
2	NAG	F	402	2	-	0/6/23/26	0/1/1/1
3	FUC	F	403	2	-	0/0/17/20	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	403	FUC	O5-C1	-2.27	1.40	1.43

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	403	FUC	C1-O5-C5	2.02	116.85	112.39

All (4) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	D	403	FUC	C1
3	A	403	FUC	C1
2	E	401	NAG	C1
3	E	403	FUC	C1

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	B	403	FUC	1	0
3	C	403	FUC	1	0
3	D	403	FUC	1	0
3	F	403	FUC	1	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	276/293 (94%)	-0.13	1 (0%) 92 90	21, 41, 69, 94	0
1	B	275/293 (93%)	-0.06	3 (1%) 80 74	23, 44, 78, 88	0
1	C	262/293 (89%)	-0.07	4 (1%) 74 67	21, 46, 81, 93	0
1	D	266/293 (90%)	0.09	8 (3%) 51 39	25, 52, 92, 108	0
1	E	260/293 (88%)	0.05	8 (3%) 49 38	24, 46, 97, 113	0
1	F	253/293 (86%)	0.16	11 (4%) 36 26	26, 52, 101, 120	0
All	All	1592/1758 (90%)	0.00	35 (2%) 62 52	21, 47, 88, 120	0

The worst 5 of 35 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	310	GLY	8.7
1	F	61	GLY	5.5
1	A	60	GLY	4.7
1	C	310	GLY	4.0
1	F	297	THR	3.9

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

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

### 6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 6.4 Ligands

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	CA	C	405	1/1	0.73	0.18	0.62	70,70,70,70	0
5	CA	B	405	1/1	0.92	0.13	-1.57	42,42,42,42	0
5	CA	E	406	1/1	0.74	0.07	-1.78	96,96,96,96	0
5	CA	F	405	1/1	0.75	0.10	-1.93	97,97,97,97	0
5	CA	F	404	1/1	0.66	0.08	-1.99	108,108,108,108	0
5	CA	D	405	1/1	0.81	0.05	-2.33	96,96,96,96	0
5	CA	A	406	1/1	0.90	0.09	-2.59	34,34,34,34	0
5	CA	C	406	1/1	0.82	0.06	-2.67	69,69,69,69	0
5	CA	E	405	1/1	0.71	0.09	-2.73	110,110,110,110	0
5	CA	D	406	1/1	0.89	0.07	-3.00	100,100,100,100	0
2	NAG	C	402	14/15	0.91	0.24	-	74,84,89,90	0
3	FUC	A	403	10/11	0.93	0.15	-	30,38,43,45	0
2	NAG	A	401	14/15	0.95	0.13	-	42,50,60,65	0
2	NAG	E	401	14/15	0.75	0.34	-	101,113,124,125	0
2	NAG	B	401	14/15	0.95	0.15	-	40,51,66,69	0
5	CA	B	407	1/1	0.86	0.21	-	70,70,70,70	0
6	CL	B	408	1/1	0.94	0.18	-	57,57,57,57	0
2	NAG	E	402	14/15	0.76	0.24	-	91,99,104,105	0
5	CA	E	404	1/1	0.75	0.14	-	89,89,89,89	0
5	CA	B	406	1/1	0.97	0.06	-	32,32,32,32	0
3	FUC	D	403	10/11	0.86	0.30	-	83,91,96,97	0
4	BMA	A	404	11/12	0.87	0.15	-	55,62,67,69	0
4	BMA	B	404	11/12	0.87	0.12	-	64,71,75,76	0
5	CA	A	405	1/1	0.97	0.10	-	36,36,36,36	0
2	NAG	F	402	14/15	0.84	0.21	-	75,81,87,88	0
5	CA	C	407	1/1	0.96	0.08	-	68,68,68,68	0
3	FUC	F	403	10/11	0.79	0.25	-	92,94,98,106	0
5	CA	A	407	1/1	0.77	0.12	-	60,60,60,60	0
2	NAG	F	401	14/15	0.81	0.22	-	84,92,96,96	0
4	BMA	C	404	11/12	0.77	0.30	-	93,97,100,102	0
2	NAG	A	402	14/15	0.97	0.12	-	38,42,47,56	0
3	FUC	E	403	10/11	0.89	0.19	-	83,90,94,94	0
3	FUC	B	403	10/11	0.96	0.19	-	29,42,53,56	0
6	CL	A	408	1/1	0.92	0.16	-	46,46,46,46	0
2	NAG	C	401	14/15	0.87	0.24	-	70,79,84,87	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
2	NAG	D	402	14/15	0.69	0.27	-	78,93,101,107	0
5	CA	D	404	1/1	0.58	0.20	-	106,106,106,106	0
3	FUC	C	403	10/11	0.90	0.22	-	65,68,75,76	0
2	NAG	D	401	14/15	0.69	0.24	-	88,98,109,112	0
2	NAG	B	402	14/15	0.93	0.17	-	36,49,62,62	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.