



# wwPDB X-ray Structure Validation Summary Report ⓘ

Jun 16, 2020 – 08:07 pm BST

PDB ID : 3IWM  
Title : The octameric SARS-CoV main protease  
Authors : Zhong, N.; Zhang, S.; Xue, F.; Lou, Z.; Rao, Z.; Xia, B.  
Deposited on : 2009-09-02  
Resolution : 3.20 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

<https://www.wwpdb.org/validation/2017/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 : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.11  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.11

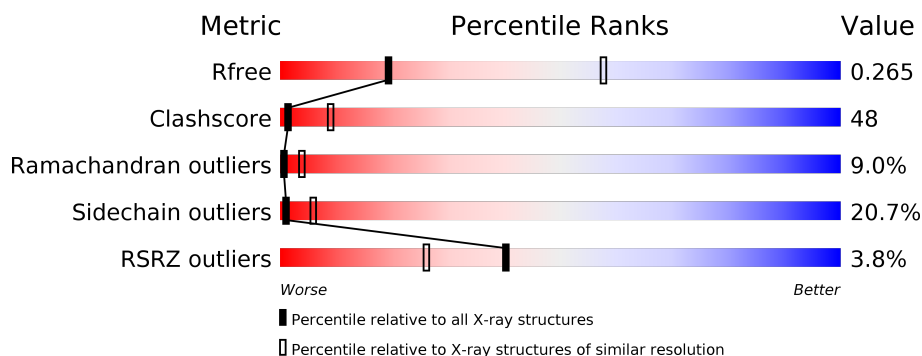
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.20 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))
$R_{free}$	130704	1133 (3.20-3.20)
Clashscore	141614	1253 (3.20-3.20)
Ramachandran outliers	138981	1234 (3.20-3.20)
Sidechain outliers	138945	1233 (3.20-3.20)
RSRZ outliers	127900	1095 (3.20-3.20)

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 respectively. 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	306	<div> <div>2%</div> <div> <div>34%</div> <div>50%</div> <div>12%</div> <div>• •</div> </div> </div>
1	B	306	<div> <div>2%</div> <div> <div>36%</div> <div>46%</div> <div>14%</div> <div>• •</div> </div> </div>
1	C	306	<div> <div>0%</div> <div> <div>34%</div> <div>47%</div> <div>14%</div> <div>• •</div> </div> </div>
1	D	306	<div> <div>11%</div> <div> <div>31%</div> <div>47%</div> <div>19%</div> <div>• •</div> </div> </div>
2	E	6	<div> <div>17%</div> <div> <div>17%</div> <div>33%</div> <div>17%</div> <div>33%</div> </div> </div>
2	F	6	<div> <div>50%</div> <div> <div>33%</div> <div>17%</div> </div> </div>

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Mol	Chain	Length	Quality of chain
2	G	6	
2	H	6	

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	02J	E	1	-	-	-	X
2	PJE	E	5	X	X	X	-
2	PJE	F	5	-	-	X	-
2	PJE	G	5	X	-	-	-
2	02J	H	1	-	-	-	X
2	PJE	H	5	X	-	X	-

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 9512 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 3C-like proteinase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	301	Total	C	N	O	S	0	0	0
			2332	1474	399	437	22			
1	B	301	Total	C	N	O	S	0	0	0
			2332	1474	399	437	22			
1	C	300	Total	C	N	O	S	0	0	0
			2326	1471	398	435	22			
1	D	300	Total	C	N	O	S	0	0	0
			2326	1471	398	435	22			

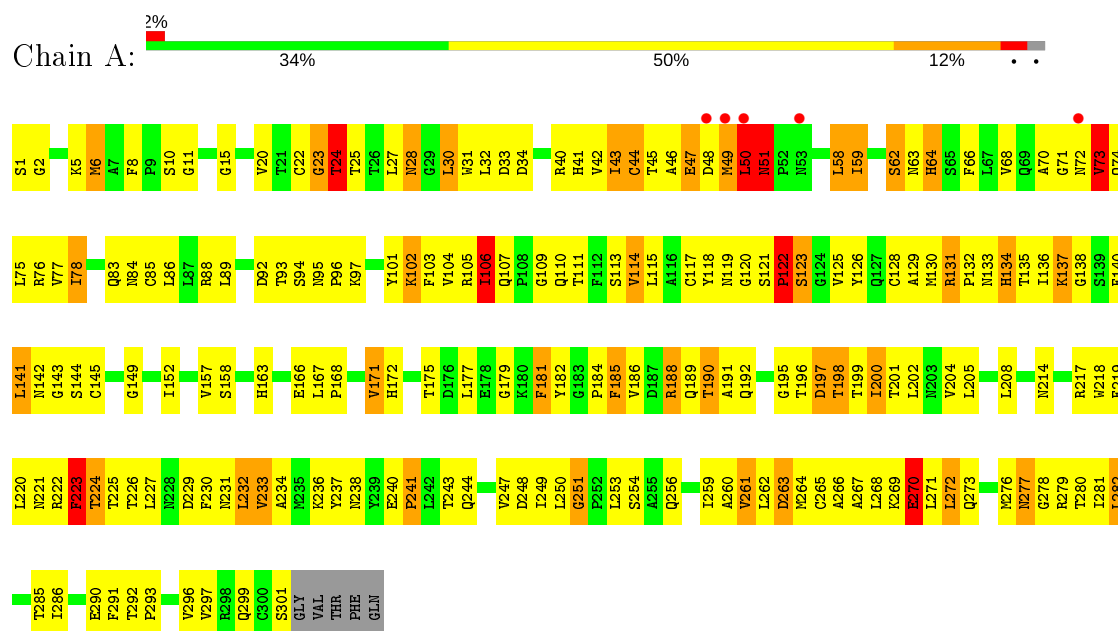
- Molecule 2 is a protein called N-[(5-METHYLISOXAZOL-3-YL)CARBONYL]ALANYL-L-VALYL-N 1 -((1R,2Z)-4-(BENZYLOXY)-4-OXO-1-[(3R)-2-OXOPYRROLIDIN-3-YL]METHYL}BUT-2-ENYL)-L-LEUCINAMIDE.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	H	6	Total	C	N	O	0	0	0
			49	35	6	8			
2	F	6	Total	C	N	O	0	0	0
			49	35	6	8			
2	G	6	Total	C	N	O	0	0	0
			49	35	6	8			
2	E	6	Total	C	N	O	0	0	0
			49	35	6	8			

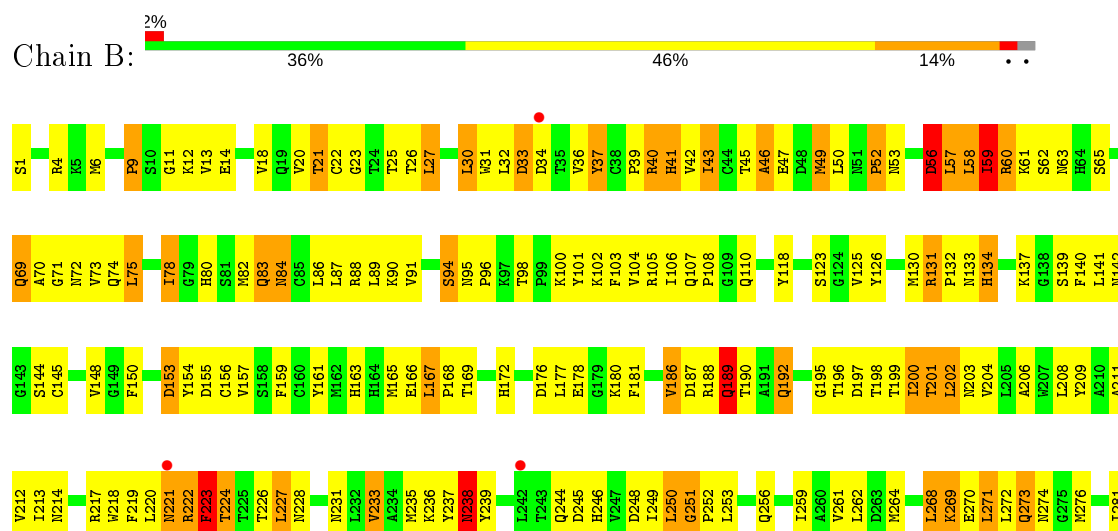
### 3 Residue-property plots

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: 3C-like proteinase

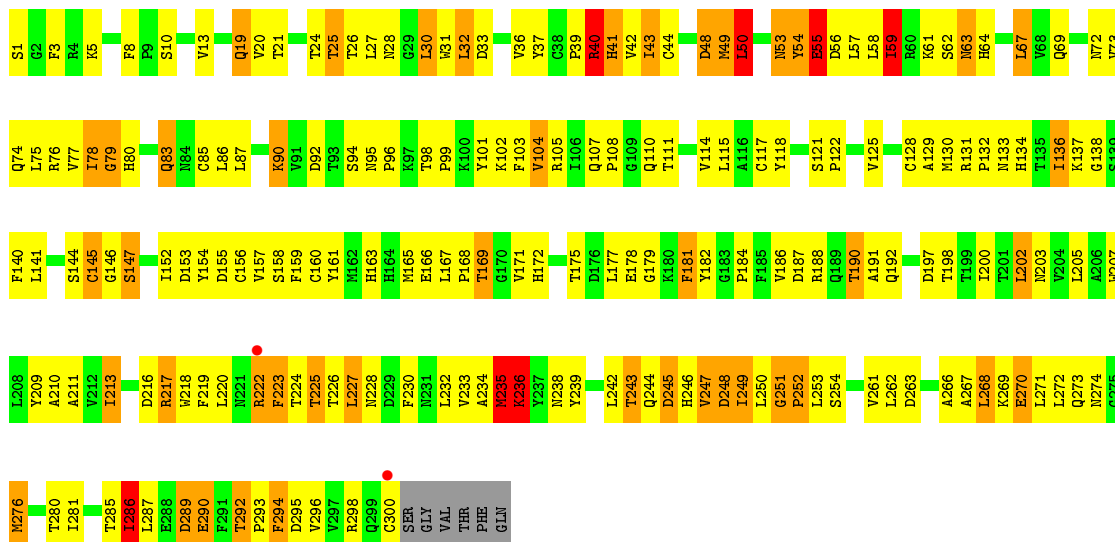


#### • Molecule 1: 3C-like proteinase

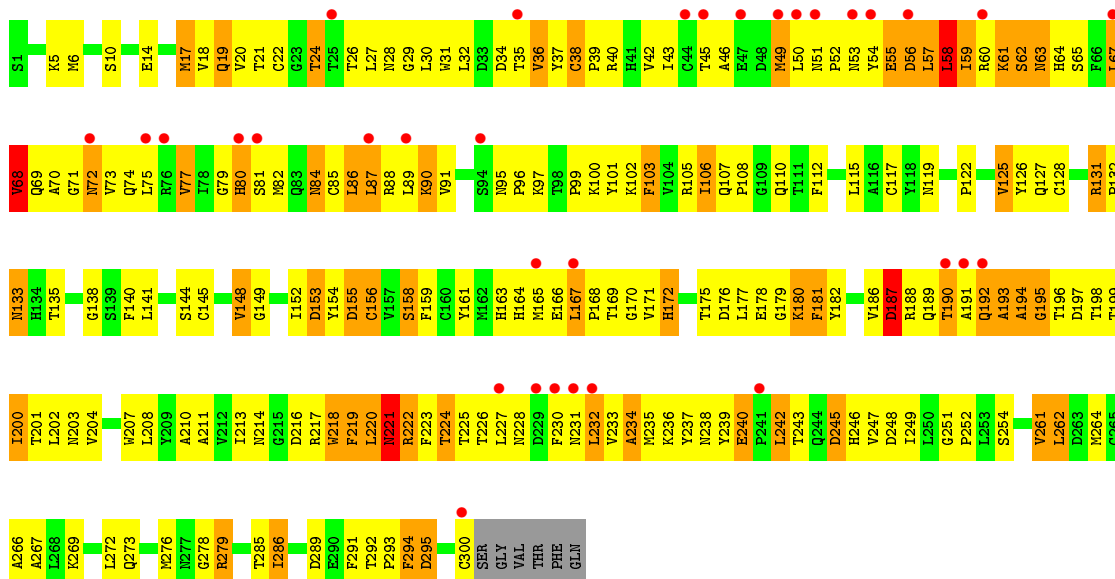




• Molecule 1: 3C-like proteinase

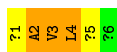


• Molecule 1: 3C-like proteinase

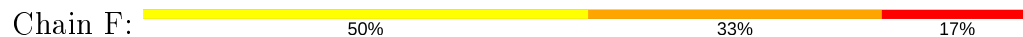


• Molecule 2: N-[(5-METHYLISOXAZOL-3-YL)CARBONYL]ALANYL-L-VALYL-N 1 -((1R,2Z)-4-(BENZYLOXY)-4-OXO-1-[(3R)-2-OXOPYRROLIDIN-3-YL]METHYL}BUT-2-ENYL)-L-L EUCINAMIDE





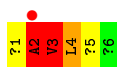
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## 4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	161.93Å 161.93Å 166.44Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.94 – 3.20 48.94 – 2.99	Depositor EDS
% Data completeness (in resolution range)	94.1 (48.94-3.20) 80.8 (48.94-2.99)	Depositor EDS
$R_{merge}$	0.15	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.07 (at 3.01Å)	Xtriage
Refinement program	PHENIX (phenix.refine)	Depositor
R, $R_{free}$	0.220 , 0.272 0.214 , 0.265	Depositor DCC
$R_{free}$ test set	1849 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	99.6	Xtriage
Anisotropy	0.167	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 77.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.013 for -h,l,k 0.006 for -l,-k,-h	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	9512	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	86.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.07% 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: 010, PJE, 02J

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	0.47	0/2384	0.70	0/3239
1	B	0.46	0/2384	0.72	0/3239
1	C	0.50	1/2378 (0.0%)	0.71	1/3231 (0.0%)
1	D	0.42	0/2378	0.69	1/3231 (0.0%)
2	E	2.21	2/19 (10.5%)	2.17	0/25
2	F	2.10	2/19 (10.5%)	1.85	0/25
2	G	2.19	2/19 (10.5%)	1.62	0/25
2	H	2.13	2/19 (10.5%)	1.83	0/25
All	All	0.50	9/9600 (0.1%)	0.72	2/13040 (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	A	0	2
1	B	0	2
1	C	0	2
1	D	0	1
2	E	1	1
2	F	0	2
2	G	1	1
2	H	1	1
All	All	3	12

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	G	3	VAL	C-N	6.08	1.48	1.34
2	E	3	VAL	C-N	5.94	1.47	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	2	ALA	C-N	5.87	1.47	1.34
2	F	2	ALA	C-N	5.73	1.47	1.34
2	G	2	ALA	C-N	5.66	1.47	1.34

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	59	ILE	N-CA-C	-6.30	94.00	111.00
1	C	217	ARG	N-CA-C	5.09	124.73	111.00

All (3) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	H	5	PJE	C26
2	G	5	PJE	C19
2	E	5	PJE	C19

5 of 12 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	223	PHE	Peptide
1	A	71	GLY	Peptide
1	B	222	ARG	Peptide
1	B	59	ILE	Peptide
1	C	50	LEU	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	2332	0	2286	264	0
1	B	2332	0	2286	238	0
1	C	2326	0	2281	226	0
1	D	2326	0	2281	259	0
2	E	49	0	47	12	0
2	F	49	0	45	16	0
2	G	49	0	45	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	H	49	0	46	17	0
All	All	9512	0	9317	898	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 48.

The worst 5 of 898 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:D:191:ALA:HA	2:E:2:ALA:HB3	1.26	1.14
1:D:106:ILE:HD11	1:D:110:GLN:HB2	1.31	1.09
1:B:83:GLN:HG3	1:B:88:ARG:HH12	0.93	1.07
1:D:50:LEU:HA	1:D:189:GLN:HB3	1.37	1.05
1:A:270:GLU:HA	1:A:273:GLN:H	1.27	1.00

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	299/306 (98%)	238 (80%)	32 (11%)	29 (10%)	0	3
1	B	299/306 (98%)	230 (77%)	43 (14%)	26 (9%)	1	4
1	C	298/306 (97%)	230 (77%)	43 (14%)	25 (8%)	1	5
1	D	298/306 (97%)	223 (75%)	47 (16%)	28 (9%)	0	3
2	E	1/6 (17%)	1 (100%)	0	0	100	100
2	F	1/6 (17%)	0	1 (100%)	0	100	100
2	G	1/6 (17%)	1 (100%)	0	0	100	100
2	H	1/6 (17%)	0	1 (100%)	0	100	100
All	All	1198/1248 (96%)	923 (77%)	167 (14%)	108 (9%)	1	4

5 of 108 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	24	THR
1	A	51	ASN
1	A	106	ILE
1	A	122	PRO
1	A	123	SER

### 5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	259/263 (98%)	211 (82%)	48 (18%)	1	8
1	B	259/263 (98%)	210 (81%)	49 (19%)	1	8
1	C	258/263 (98%)	204 (79%)	54 (21%)	1	6
1	D	258/263 (98%)	199 (77%)	59 (23%)	1	4
2	E	2/2 (100%)	0	2 (100%)	0	0
2	F	2/2 (100%)	1 (50%)	1 (50%)	0	0
2	G	2/2 (100%)	0	2 (100%)	0	0
2	H	2/2 (100%)	1 (50%)	1 (50%)	0	0
All	All	1042/1060 (98%)	826 (79%)	216 (21%)	1	6

5 of 216 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	1	SER
1	C	158	SER
1	D	242	LEU
1	C	25	THR
1	C	67	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 38 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	134	HIS
1	C	53	ASN
1	D	228	ASN
1	B	274	ASN
1	C	63	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

8 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	02J	G	1	2	6,8,9	2.98	3 (50%)	4,10,12	3.52	1 (25%)
2	02J	E	1	2	6,8,9	3.55	4 (66%)	4,10,12	3.03	1 (25%)
2	02J	H	1	2	6,8,9	3.38	4 (66%)	4,10,12	4.79	2 (50%)
2	PJE	E	5	2	12,13,14	6.69	6 (50%)	12,16,18	3.08	10 (83%)
2	PJE	F	5	2	12,13,14	7.43	7 (58%)	12,16,18	4.27	7 (58%)
2	02J	F	1	2	6,8,9	2.78	4 (66%)	4,10,12	4.27	1 (25%)
2	PJE	G	5	2	12,13,14	6.62	6 (50%)	12,16,18	4.34	6 (50%)
2	PJE	H	5	2	12,13,14	6.23	6 (50%)	12,16,18	2.41	4 (33%)

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	02J	G	1	2	-	0/0/2/4	0/1/1/1
2	02J	E	1	2	-	0/0/2/4	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	02J	H	1	2	-	0/0/2/4	0/1/1/1
2	PJE	E	5	2	1/1/3/7	4/7/18/19	0/1/1/1
2	PJE	F	5	2	-	3/7/18/19	0/1/1/1
2	02J	F	1	2	-	0/0/2/4	0/1/1/1
2	PJE	G	5	2	1/1/3/7	4/7/18/19	0/1/1/1
2	PJE	H	5	2	1/1/3/7	5/7/18/19	0/1/1/1

The worst 5 of 40 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	5	PJE	C29-N6	22.03	1.57	1.33
2	H	5	PJE	C29-N6	19.61	1.54	1.33
2	E	5	PJE	C29-N6	19.60	1.54	1.33
2	G	5	PJE	C29-N6	19.56	1.54	1.33
2	F	5	PJE	O8-C29	8.46	1.40	1.23

The worst 5 of 32 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	5	PJE	O8-C29-N6	-10.55	110.90	125.54
2	G	5	PJE	C19-C20-C21	-9.49	110.85	124.41
2	H	1	02J	O42-C41-C3	-9.12	115.58	124.22
2	F	1	02J	O42-C41-C3	-8.39	116.27	124.22
2	G	5	PJE	O8-C29-C26	-7.89	116.95	126.23

All (3) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	E	5	PJE	C19
2	G	5	PJE	C19
2	H	5	PJE	C26

5 of 16 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	E	5	PJE	C25-C19-C20-C21
2	E	5	PJE	C20-C19-C25-C26
2	E	5	PJE	N5-C19-C25-C26
2	E	5	PJE	C20-C21-C22-O7
2	F	5	PJE	C20-C21-C22-O7

There are no ring outliers.

7 monomers are involved in 33 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	E	1	02J	2	0
2	H	1	02J	3	0
2	E	5	PJE	6	0
2	F	5	PJE	7	0
2	F	1	02J	2	0
2	G	5	PJE	5	0
2	H	5	PJE	8	0

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 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 [i](#)

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	301/306 (98%)	0.17	5 (1%) 70 57	58, 78, 102, 127	0
1	B	301/306 (98%)	0.19	5 (1%) 70 57	55, 84, 112, 134	0
1	C	300/306 (98%)	0.15	2 (0%) 87 81	57, 75, 102, 122	0
1	D	300/306 (98%)	0.60	33 (11%) 5 3	67, 96, 147, 159	0
2	E	3/6 (50%)	2.20	1 (33%) 0 0	127, 127, 130, 140	0
2	F	3/6 (50%)	0.22	0 100 100	104, 104, 106, 112	0
2	G	3/6 (50%)	0.93	0 100 100	81, 81, 87, 95	0
2	H	3/6 (50%)	0.97	0 100 100	101, 101, 103, 114	0
All	All	1214/1248 (97%)	0.28	46 (3%) 40 26	55, 83, 123, 159	0

The worst 5 of 46 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	50	LEU	7.7
1	B	301	SER	4.4
1	D	56	ASP	4.2
1	A	72	ASN	3.8
2	E	2	ALA	3.7

### 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. 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	B-factors(Å <sup>2</sup> )	Q<0.9
2	02J	E	1	8/9	0.22	0.98	148,151,152,152	0

*Continued on next page...*



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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	02J	H	1	8/9	0.73	0.51	119,124,125,126	0
2	02J	F	1	8/9	0.81	0.47	115,119,120,120	0
2	02J	G	1	8/9	0.83	0.50	103,106,108,108	0
2	PJE	F	5	13/14	0.85	0.35	103,104,109,110	0
2	PJE	H	5	13/14	0.90	0.33	102,103,115,116	0
2	PJE	E	5	13/14	0.93	0.25	123,125,129,129	0
2	PJE	G	5	13/14	0.94	0.26	77,79,83,85	0

### 6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

### 6.4 Ligands [i](#)

There are no ligands in this entry.

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

There are no such residues in this entry.