



# Full wwPDB X-ray Structure Validation Report ⓘ

Oct 15, 2023 – 05:42 AM EDT

PDB ID : 8EAW  
Title : An asymmetric disk assembly formed by tandem dimers of the tobacco mosaic viral capsid protein (TMV)  
Authors : Dai, J.; Pereira, J.H.; Adams, P.D.; Francis, M.B.  
Deposited on : 2022-08-29  
Resolution : 2.80 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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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  
Xtrriage (Phenix) : 1.13  
EDS : **FAILED**  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.36

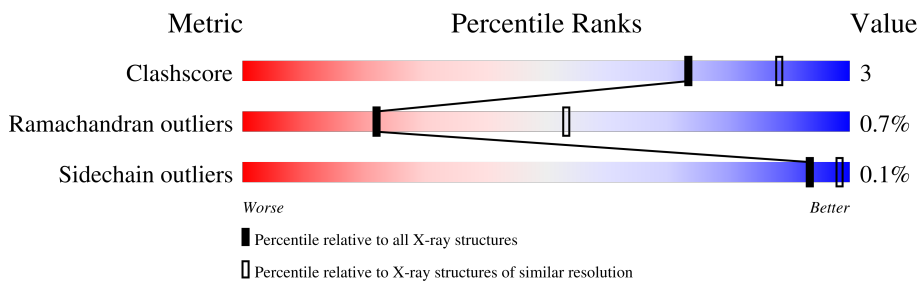
# 1 Overall quality at a glance

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))
Clashscore	141614	3569 (2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (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 of 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  $\leq 5\%$ .

Note EDS failed to run properly.

Mol	Chain	Length	Quality of chain
1	a	323	
1	b	323	
1	c	323	
1	d	323	
1	e	323	
1	f	323	
1	g	323	
1	h	323	

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Mol	Chain	Length	Quality of chain
1	i	323	 88% • 11%
1	j	323	 88% • 11%
1	k	323	 88% • 11%
1	l	323	 88% • 11%
1	m	323	 88% • 11%
1	n	323	 88% • 11%
1	o	323	 88% • 11%
1	p	323	 87% • 11%
1	q	323	 88% • 11%

## 2 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 38318 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 Capsid protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	a	287	2254	1422	392	436	4	0	0	0
1	b	287	2254	1422	392	436	4	0	0	0
1	c	287	2254	1422	392	436	4	0	0	0
1	d	287	2254	1422	392	436	4	0	0	0
1	e	287	2254	1422	392	436	4	0	0	0
1	f	287	2254	1422	392	436	4	0	0	0
1	g	287	2254	1422	392	436	4	0	0	0
1	h	287	2254	1422	392	436	4	0	0	0
1	i	287	2254	1422	392	436	4	0	0	0
1	j	287	2254	1422	392	436	4	0	0	0
1	k	287	2254	1422	392	436	4	0	0	0
1	l	287	2254	1422	392	436	4	0	0	0
1	m	287	2254	1422	392	436	4	0	0	0
1	n	287	2254	1422	392	436	4	0	0	0
1	o	287	2254	1422	392	436	4	0	0	0
1	p	287	2254	1422	392	436	4	0	0	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	q	287	2254	1422	392	436	4	0	0	0

There are 153 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
a	123	CYS	SER	engineered mutation	UNP P69687
a	159	GLY	-	linker	UNP P69687
a	160	GLY	-	linker	UNP P69687
a	161	GLY	-	linker	UNP P69687
a	162	GLU	-	linker	UNP P69687
a	163	GLY	-	linker	UNP P69687
a	164	GLY	-	linker	UNP P69687
a	165	GLY	-	linker	UNP P69687
a	288	CYS	SER	engineered mutation	UNP P69687
b	123	CYS	SER	engineered mutation	UNP P69687
b	159	GLY	-	linker	UNP P69687
b	160	GLY	-	linker	UNP P69687
b	161	GLY	-	linker	UNP P69687
b	162	GLU	-	linker	UNP P69687
b	163	GLY	-	linker	UNP P69687
b	164	GLY	-	linker	UNP P69687
b	165	GLY	-	linker	UNP P69687
b	288	CYS	SER	engineered mutation	UNP P69687
c	123	CYS	SER	engineered mutation	UNP P69687
c	159	GLY	-	linker	UNP P69687
c	160	GLY	-	linker	UNP P69687
c	161	GLY	-	linker	UNP P69687
c	162	GLU	-	linker	UNP P69687
c	163	GLY	-	linker	UNP P69687
c	164	GLY	-	linker	UNP P69687
c	165	GLY	-	linker	UNP P69687
c	288	CYS	SER	engineered mutation	UNP P69687
d	123	CYS	SER	engineered mutation	UNP P69687
d	159	GLY	-	linker	UNP P69687
d	160	GLY	-	linker	UNP P69687
d	161	GLY	-	linker	UNP P69687
d	162	GLU	-	linker	UNP P69687
d	163	GLY	-	linker	UNP P69687
d	164	GLY	-	linker	UNP P69687
d	165	GLY	-	linker	UNP P69687
d	288	CYS	SER	engineered mutation	UNP P69687

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Chain	Residue	Modelled	Actual	Comment	Reference
e	123	CYS	SER	engineered mutation	UNP P69687
e	159	GLY	-	linker	UNP P69687
e	160	GLY	-	linker	UNP P69687
e	161	GLY	-	linker	UNP P69687
e	162	GLU	-	linker	UNP P69687
e	163	GLY	-	linker	UNP P69687
e	164	GLY	-	linker	UNP P69687
e	165	GLY	-	linker	UNP P69687
e	288	CYS	SER	engineered mutation	UNP P69687
f	123	CYS	SER	engineered mutation	UNP P69687
f	159	GLY	-	linker	UNP P69687
f	160	GLY	-	linker	UNP P69687
f	161	GLY	-	linker	UNP P69687
f	162	GLU	-	linker	UNP P69687
f	163	GLY	-	linker	UNP P69687
f	164	GLY	-	linker	UNP P69687
f	165	GLY	-	linker	UNP P69687
f	288	CYS	SER	engineered mutation	UNP P69687
g	123	CYS	SER	engineered mutation	UNP P69687
g	159	GLY	-	linker	UNP P69687
g	160	GLY	-	linker	UNP P69687
g	161	GLY	-	linker	UNP P69687
g	162	GLU	-	linker	UNP P69687
g	163	GLY	-	linker	UNP P69687
g	164	GLY	-	linker	UNP P69687
g	165	GLY	-	linker	UNP P69687
g	288	CYS	SER	engineered mutation	UNP P69687
h	123	CYS	SER	engineered mutation	UNP P69687
h	159	GLY	-	linker	UNP P69687
h	160	GLY	-	linker	UNP P69687
h	161	GLY	-	linker	UNP P69687
h	162	GLU	-	linker	UNP P69687
h	163	GLY	-	linker	UNP P69687
h	164	GLY	-	linker	UNP P69687
h	165	GLY	-	linker	UNP P69687
h	288	CYS	SER	engineered mutation	UNP P69687
i	123	CYS	SER	engineered mutation	UNP P69687
i	159	GLY	-	linker	UNP P69687
i	160	GLY	-	linker	UNP P69687
i	161	GLY	-	linker	UNP P69687
i	162	GLU	-	linker	UNP P69687
i	163	GLY	-	linker	UNP P69687

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Chain	Residue	Modelled	Actual	Comment	Reference
i	164	GLY	-	linker	UNP P69687
i	165	GLY	-	linker	UNP P69687
i	288	CYS	SER	engineered mutation	UNP P69687
j	123	CYS	SER	engineered mutation	UNP P69687
j	159	GLY	-	linker	UNP P69687
j	160	GLY	-	linker	UNP P69687
j	161	GLY	-	linker	UNP P69687
j	162	GLU	-	linker	UNP P69687
j	163	GLY	-	linker	UNP P69687
j	164	GLY	-	linker	UNP P69687
j	165	GLY	-	linker	UNP P69687
j	288	CYS	SER	engineered mutation	UNP P69687
k	123	CYS	SER	engineered mutation	UNP P69687
k	159	GLY	-	linker	UNP P69687
k	160	GLY	-	linker	UNP P69687
k	161	GLY	-	linker	UNP P69687
k	162	GLU	-	linker	UNP P69687
k	163	GLY	-	linker	UNP P69687
k	164	GLY	-	linker	UNP P69687
k	165	GLY	-	linker	UNP P69687
k	288	CYS	SER	engineered mutation	UNP P69687
l	123	CYS	SER	engineered mutation	UNP P69687
l	159	GLY	-	linker	UNP P69687
l	160	GLY	-	linker	UNP P69687
l	161	GLY	-	linker	UNP P69687
l	162	GLU	-	linker	UNP P69687
l	163	GLY	-	linker	UNP P69687
l	164	GLY	-	linker	UNP P69687
l	165	GLY	-	linker	UNP P69687
l	288	CYS	SER	engineered mutation	UNP P69687
m	123	CYS	SER	engineered mutation	UNP P69687
m	159	GLY	-	linker	UNP P69687
m	160	GLY	-	linker	UNP P69687
m	161	GLY	-	linker	UNP P69687
m	162	GLU	-	linker	UNP P69687
m	163	GLY	-	linker	UNP P69687
m	164	GLY	-	linker	UNP P69687
m	165	GLY	-	linker	UNP P69687
m	288	CYS	SER	engineered mutation	UNP P69687
n	123	CYS	SER	engineered mutation	UNP P69687
n	159	GLY	-	linker	UNP P69687
n	160	GLY	-	linker	UNP P69687

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Chain	Residue	Modelled	Actual	Comment	Reference
n	161	GLY	-	linker	UNP P69687
n	162	GLU	-	linker	UNP P69687
n	163	GLY	-	linker	UNP P69687
n	164	GLY	-	linker	UNP P69687
n	165	GLY	-	linker	UNP P69687
n	288	CYS	SER	engineered mutation	UNP P69687
o	123	CYS	SER	engineered mutation	UNP P69687
o	159	GLY	-	linker	UNP P69687
o	160	GLY	-	linker	UNP P69687
o	161	GLY	-	linker	UNP P69687
o	162	GLU	-	linker	UNP P69687
o	163	GLY	-	linker	UNP P69687
o	164	GLY	-	linker	UNP P69687
o	165	GLY	-	linker	UNP P69687
o	288	CYS	SER	engineered mutation	UNP P69687
p	123	CYS	SER	engineered mutation	UNP P69687
p	159	GLY	-	linker	UNP P69687
p	160	GLY	-	linker	UNP P69687
p	161	GLY	-	linker	UNP P69687
p	162	GLU	-	linker	UNP P69687
p	163	GLY	-	linker	UNP P69687
p	164	GLY	-	linker	UNP P69687
p	165	GLY	-	linker	UNP P69687
p	288	CYS	SER	engineered mutation	UNP P69687
q	123	CYS	SER	engineered mutation	UNP P69687
q	159	GLY	-	linker	UNP P69687
q	160	GLY	-	linker	UNP P69687
q	161	GLY	-	linker	UNP P69687
q	162	GLU	-	linker	UNP P69687
q	163	GLY	-	linker	UNP P69687
q	164	GLY	-	linker	UNP P69687
q	165	GLY	-	linker	UNP P69687
q	288	CYS	SER	engineered mutation	UNP P69687




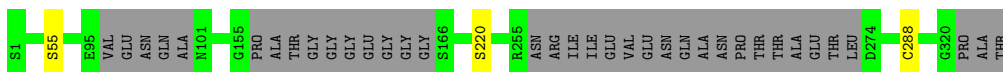
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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. 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. 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.


Note EDS failed to run properly.

- Molecule 1: Capsid protein

Chain a:  88% 11%




- Molecule 1: Capsid protein

Chain b:  88% 11%




- Molecule 1: Capsid protein

Chain c:  88% 11%




- Molecule 1: Capsid protein

Chain d:  88% 11%




- Molecule 1: Capsid protein

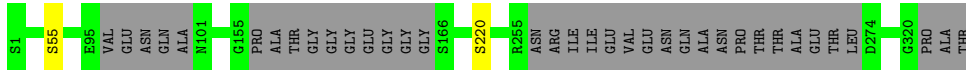
Chain e:  88% 11%




- Molecule 1: Capsid protein

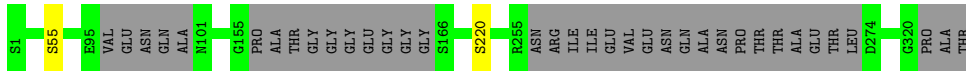


Chain m:  88% • 11%




• Molecule 1: Capsid protein

Chain n:  88% • 11%




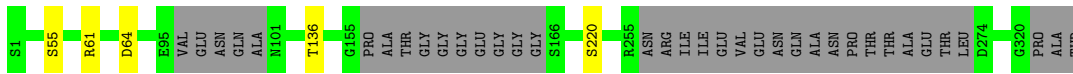
• Molecule 1: Capsid protein

Chain o:  88% • 11%




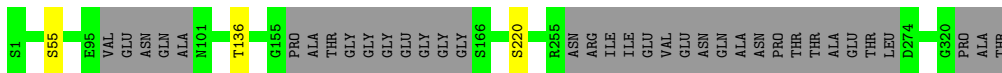
• Molecule 1: Capsid protein

Chain p:  87% • 11%



• Molecule 1: Capsid protein

Chain q:  88% • 11%



## 4 Data and refinement statistics

EDS failed to run properly - this section is therefore incomplete.

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	208.51Å 255.50Å 260.85Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	81.44 – 2.80	Depositor
% Data completeness (in resolution range)	99.7 (81.44-2.80)	Depositor
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.34 (at 2.82Å)	Xtrriage
Refinement program	PHENIX 1.18.2_3874	Depositor
R, $R_{free}$	0.196 , 0.234	Depositor
Wilson B-factor (Å <sup>2</sup> )	58.8	Xtrriage
Anisotropy	0.275	Xtrriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.51$ , $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
Total number of atoms	38318	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	62.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.95% 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](#)

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	0.26	0/2299	0.41	0/3136
1	b	0.26	0/2299	0.41	0/3136
1	c	0.25	0/2299	0.41	0/3136
1	d	0.25	0/2299	0.41	0/3136
1	e	0.25	0/2299	0.40	0/3136
1	f	0.25	0/2299	0.41	0/3136
1	g	0.25	0/2299	0.41	0/3136
1	h	0.25	0/2299	0.41	0/3136
1	i	0.25	0/2299	0.40	0/3136
1	j	0.25	0/2299	0.40	0/3136
1	k	0.25	0/2299	0.40	0/3136
1	l	0.25	0/2299	0.41	0/3136
1	m	0.25	0/2299	0.41	0/3136
1	n	0.25	0/2299	0.41	0/3136
1	o	0.25	0/2299	0.41	0/3136
1	p	0.25	0/2299	0.41	0/3136
1	q	0.26	0/2299	0.41	0/3136
All	All	0.25	0/39083	0.41	0/53312

There are no bond length outliers.

There are no bond angle outliers.

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	2254	0	2212	0	0
1	b	2254	0	2212	0	0
1	c	2254	0	2212	0	0
1	d	2254	0	2212	0	0
1	e	2254	0	2212	0	0
1	f	2254	0	2212	0	0
1	g	2254	0	2212	0	0
1	h	2254	0	2212	0	0
1	i	2254	0	2212	0	0
1	j	2254	0	2212	0	0
1	k	2254	0	2212	0	0
1	l	2254	0	2212	0	0
1	m	2254	0	2212	0	0
1	n	2254	0	2212	0	0
1	o	2254	0	2212	0	0
1	p	2254	0	2212	0	1
1	q	2254	0	2212	0	0
All	All	38318	0	37604	0	1

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 3.

There are no clashes within the asymmetric unit.

All (1) 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:p:61:ARG:NH1	1:p:64:ASP:OD1[4_565]	2.11	0.09

## 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	279/323 (86%)	270 (97%)	7 (2%)	2 (1%)	22 53

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	b	279/323 (86%)	268 (96%)	9 (3%)	2 (1%)	22	53
1	c	279/323 (86%)	269 (96%)	8 (3%)	2 (1%)	22	53
1	d	279/323 (86%)	269 (96%)	8 (3%)	2 (1%)	22	53
1	e	279/323 (86%)	268 (96%)	9 (3%)	2 (1%)	22	53
1	f	279/323 (86%)	266 (95%)	11 (4%)	2 (1%)	22	53
1	g	279/323 (86%)	269 (96%)	8 (3%)	2 (1%)	22	53
1	h	279/323 (86%)	270 (97%)	7 (2%)	2 (1%)	22	53
1	i	279/323 (86%)	269 (96%)	8 (3%)	2 (1%)	22	53
1	j	279/323 (86%)	271 (97%)	6 (2%)	2 (1%)	22	53
1	k	279/323 (86%)	267 (96%)	9 (3%)	3 (1%)	14	41
1	l	279/323 (86%)	269 (96%)	8 (3%)	2 (1%)	22	53
1	m	279/323 (86%)	269 (96%)	8 (3%)	2 (1%)	22	53
1	n	279/323 (86%)	271 (97%)	6 (2%)	2 (1%)	22	53
1	o	279/323 (86%)	270 (97%)	7 (2%)	2 (1%)	22	53
1	p	279/323 (86%)	269 (96%)	8 (3%)	2 (1%)	22	53
1	q	279/323 (86%)	269 (96%)	8 (3%)	2 (1%)	22	53
All	All	4743/5491 (86%)	4573 (96%)	135 (3%)	35 (1%)	22	53

All (35) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	k	58	VAL
1	a	55	SER
1	a	220	SER
1	b	220	SER
1	c	55	SER
1	c	220	SER
1	d	55	SER
1	d	220	SER
1	e	220	SER
1	f	55	SER
1	f	220	SER
1	g	220	SER
1	h	220	SER
1	i	55	SER
1	i	220	SER

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Mol	Chain	Res	Type
1	j	220	SER
1	k	220	SER
1	l	55	SER
1	l	220	SER
1	m	55	SER
1	m	220	SER
1	n	55	SER
1	n	220	SER
1	o	55	SER
1	o	220	SER
1	p	55	SER
1	p	220	SER
1	q	55	SER
1	q	220	SER
1	b	55	SER
1	e	55	SER
1	g	55	SER
1	h	55	SER
1	j	55	SER
1	k	55	SER

### 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	252/277 (91%)	251 (100%)	1 (0%)	91	97
1	b	252/277 (91%)	252 (100%)	0	100	100
1	c	252/277 (91%)	252 (100%)	0	100	100
1	d	252/277 (91%)	252 (100%)	0	100	100
1	e	252/277 (91%)	252 (100%)	0	100	100
1	f	252/277 (91%)	252 (100%)	0	100	100
1	g	252/277 (91%)	252 (100%)	0	100	100
1	h	252/277 (91%)	252 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	i	252/277 (91%)	251 (100%)	1 (0%)	91	97
1	j	252/277 (91%)	252 (100%)	0	100	100
1	k	252/277 (91%)	252 (100%)	0	100	100
1	l	252/277 (91%)	252 (100%)	0	100	100
1	m	252/277 (91%)	252 (100%)	0	100	100
1	n	252/277 (91%)	252 (100%)	0	100	100
1	o	252/277 (91%)	252 (100%)	0	100	100
1	p	252/277 (91%)	251 (100%)	1 (0%)	91	97
1	q	252/277 (91%)	251 (100%)	1 (0%)	91	97
All	All	4284/4709 (91%)	4280 (100%)	4 (0%)	93	98

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	a	288	CYS
1	i	39	GLN
1	p	136	THR
1	q	136	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 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 monosaccharides 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](#)

EDS failed to run properly - this section is therefore empty.

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

EDS failed to run properly - this section is therefore empty.

### 6.3 Carbohydrates [i](#)

EDS failed to run properly - this section is therefore empty.

### 6.4 Ligands [i](#)

EDS failed to run properly - this section is therefore empty.

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

EDS failed to run properly - this section is therefore empty.