



# wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 24, 2022 – 01:00 PM JST

PDB ID : 7YDG  
Title : Crystal structure of human SARS2 catalytic domain with a disease related mutation  
Authors : Wu, S.; Li, P.; Zhou, X.L.; Fang, P.  
Deposited on : 2022-07-04  
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.

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
Xtriage (Phenix)	:	1.13
EDS	:	2.31.2
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)	:	2.31.2

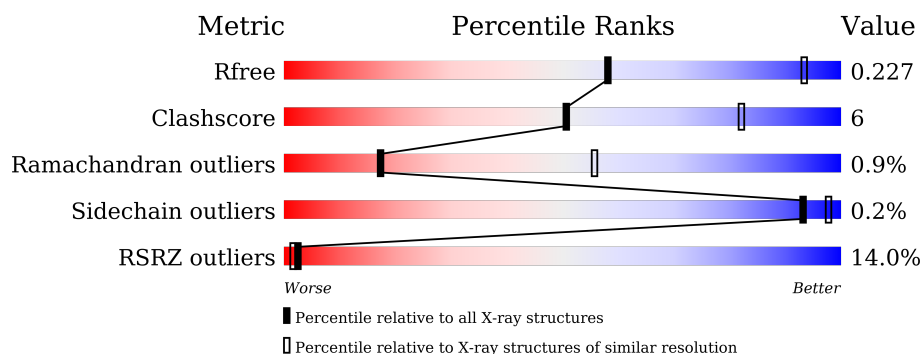
# 1 Overall quality at a glance

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 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  $\leq 5\%$ . 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	355	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, green 1%, yellow 8%, grey 91%);"></div> <div style="display: flex; justify-content: space-between; padding: 0 5px;"> <span>%</span> <span>63%</span> <span>8%</span> <span>•</span> <span>29%</span> </div> </div>
1	B	355	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, green 1%, yellow 8%, grey 91%);"></div> <div style="display: flex; justify-content: space-between; padding: 0 5px;"> <span>%</span> <span>62%</span> <span>8%</span> <span>•</span> <span>29%</span> </div> </div>
1	C	355	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 10%, green 1%, yellow 10%, grey 79%);"></div> <div style="display: flex; justify-content: space-between; padding: 0 5px;"> <span>10%</span> <span>61%</span> <span>10%</span> <span></span> <span>29%</span> </div> </div>
1	D	355	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 27%, green 1%, yellow 11%, grey 61%);"></div> <div style="display: flex; justify-content: space-between; padding: 0 5px;"> <span>27%</span> <span>59%</span> <span>11%</span> <span>•</span> <span>29%</span> </div> </div>

## 2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 7952 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 Serine-tRNA ligase, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	252	Total	C	N	O	S	0	0	0
			1988	1268	350	357	13			
1	B	252	Total	C	N	O	S	0	0	0
			1988	1268	350	357	13			
1	C	252	Total	C	N	O	S	0	0	0
			1988	1268	350	357	13			
1	D	252	Total	C	N	O	S	0	0	0
			1988	1268	350	357	13			

There are 72 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	168	MET	-	initiating methionine	UNP Q9NP81
A	169	GLY	-	expression tag	UNP Q9NP81
A	170	SER	-	expression tag	UNP Q9NP81
A	171	SER	-	expression tag	UNP Q9NP81
A	172	HIS	-	expression tag	UNP Q9NP81
A	173	HIS	-	expression tag	UNP Q9NP81
A	174	HIS	-	expression tag	UNP Q9NP81
A	175	HIS	-	expression tag	UNP Q9NP81
A	176	HIS	-	expression tag	UNP Q9NP81
A	177	HIS	-	expression tag	UNP Q9NP81
A	178	SER	-	expression tag	UNP Q9NP81
A	179	SER	-	expression tag	UNP Q9NP81
A	180	GLY	-	expression tag	UNP Q9NP81
A	218	ASN	-	insertion	UNP Q9NP81
A	219	LEU	-	insertion	UNP Q9NP81
A	220	SER	-	insertion	UNP Q9NP81
A	221	PRO	-	insertion	UNP Q9NP81
A	222	ARG	LYS	engineered mutation	UNP Q9NP81
B	168	MET	-	initiating methionine	UNP Q9NP81
B	169	GLY	-	expression tag	UNP Q9NP81
B	170	SER	-	expression tag	UNP Q9NP81

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Chain	Residue	Modelled	Actual	Comment	Reference
B	171	SER	-	expression tag	UNP Q9NP81
B	172	HIS	-	expression tag	UNP Q9NP81
B	173	HIS	-	expression tag	UNP Q9NP81
B	174	HIS	-	expression tag	UNP Q9NP81
B	175	HIS	-	expression tag	UNP Q9NP81
B	176	HIS	-	expression tag	UNP Q9NP81
B	177	HIS	-	expression tag	UNP Q9NP81
B	178	SER	-	expression tag	UNP Q9NP81
B	179	SER	-	expression tag	UNP Q9NP81
B	180	GLY	-	expression tag	UNP Q9NP81
B	218	ASN	-	insertion	UNP Q9NP81
B	219	LEU	-	insertion	UNP Q9NP81
B	220	SER	-	insertion	UNP Q9NP81
B	221	PRO	-	insertion	UNP Q9NP81
B	222	ARG	LYS	engineered mutation	UNP Q9NP81
C	168	MET	-	initiating methionine	UNP Q9NP81
C	169	GLY	-	expression tag	UNP Q9NP81
C	170	SER	-	expression tag	UNP Q9NP81
C	171	SER	-	expression tag	UNP Q9NP81
C	172	HIS	-	expression tag	UNP Q9NP81
C	173	HIS	-	expression tag	UNP Q9NP81
C	174	HIS	-	expression tag	UNP Q9NP81
C	175	HIS	-	expression tag	UNP Q9NP81
C	176	HIS	-	expression tag	UNP Q9NP81
C	177	HIS	-	expression tag	UNP Q9NP81
C	178	SER	-	expression tag	UNP Q9NP81
C	179	SER	-	expression tag	UNP Q9NP81
C	180	GLY	-	expression tag	UNP Q9NP81
C	218	ASN	-	insertion	UNP Q9NP81
C	219	LEU	-	insertion	UNP Q9NP81
C	220	SER	-	insertion	UNP Q9NP81
C	221	PRO	-	insertion	UNP Q9NP81
C	222	ARG	LYS	engineered mutation	UNP Q9NP81
D	168	MET	-	initiating methionine	UNP Q9NP81
D	169	GLY	-	expression tag	UNP Q9NP81
D	170	SER	-	expression tag	UNP Q9NP81
D	171	SER	-	expression tag	UNP Q9NP81
D	172	HIS	-	expression tag	UNP Q9NP81
D	173	HIS	-	expression tag	UNP Q9NP81
D	174	HIS	-	expression tag	UNP Q9NP81
D	175	HIS	-	expression tag	UNP Q9NP81
D	176	HIS	-	expression tag	UNP Q9NP81

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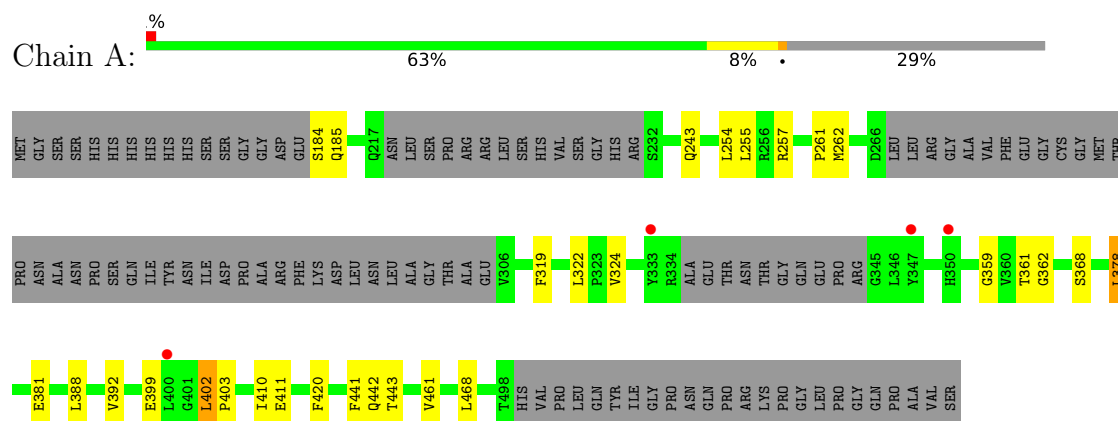
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Chain	Residue	Modelled	Actual	Comment	Reference
D	177	HIS	-	expression tag	UNP Q9NP81
D	178	SER	-	expression tag	UNP Q9NP81
D	179	SER	-	expression tag	UNP Q9NP81
D	180	GLY	-	expression tag	UNP Q9NP81
D	218	ASN	-	insertion	UNP Q9NP81
D	219	LEU	-	insertion	UNP Q9NP81
D	220	SER	-	insertion	UNP Q9NP81
D	221	PRO	-	insertion	UNP Q9NP81
D	222	ARG	LYS	engineered mutation	UNP Q9NP81

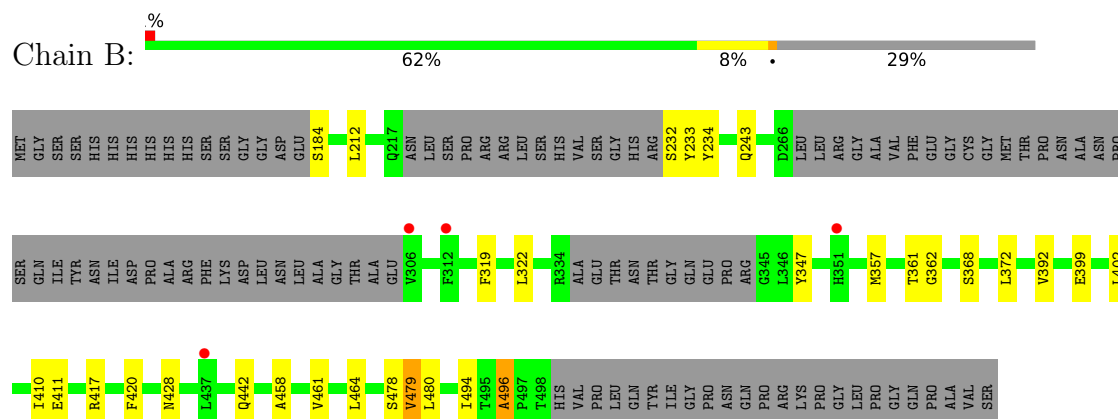
### 3 Residue-property plots

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 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.

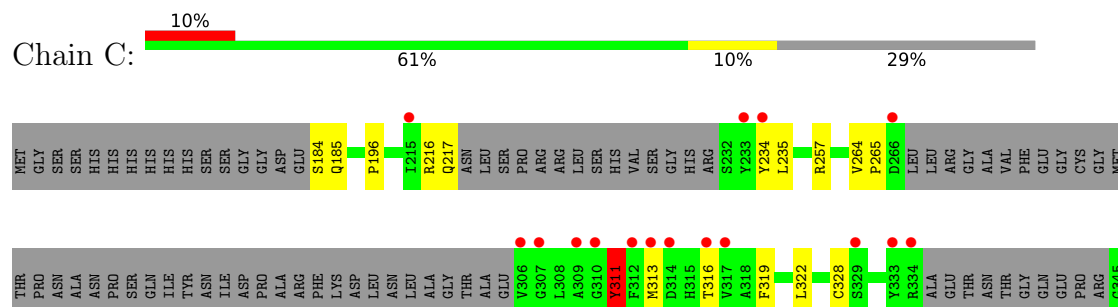
#### • Molecule 1: Serine-tRNA ligase, mitochondrial

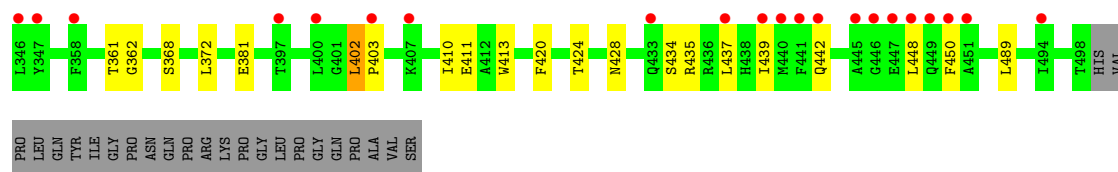


#### • Molecule 1: Serine-tRNA ligase, mitochondrial

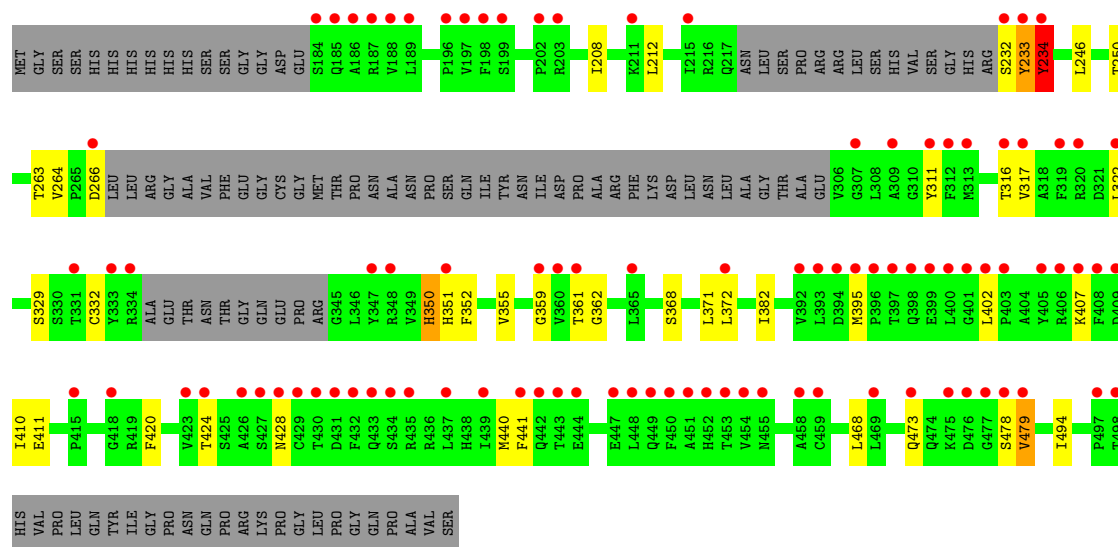


#### • Molecule 1: Serine-tRNA ligase, mitochondrial





- Molecule 1: Serine-tRNA ligase, mitochondrial



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	144.18Å 144.18Å 245.47Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	25.45 – 3.20 49.91 – 3.20	Depositor EDS
% Data completeness (in resolution range)	85.6 (25.45-3.20) 85.6 (49.91-3.20)	Depositor EDS
$R_{merge}$	0.27	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.91 (at 3.19Å)	Xtriage
Refinement program	PHENIX 1.13	Depositor
R, $R_{free}$	0.203 , 0.228 0.205 , 0.227	Depositor DCC
$R_{free}$ test set	2000 reflections (5.39%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	100.7	Xtriage
Anisotropy	0.037	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 81.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.46$ , $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	7952	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	122.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.31% 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

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	0.39	0/2031	0.69	1/2744 (0.0%)
1	B	0.36	0/2031	0.71	0/2744
1	C	0.36	1/2031 (0.0%)	0.65	2/2744 (0.1%)
1	D	0.31	0/2031	0.68	5/2744 (0.2%)
All	All	0.35	1/8124 (0.0%)	0.68	8/10976 (0.1%)

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	D	0	2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	311	TYR	CB-CG	-5.65	1.43	1.51

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	234	TYR	CA-CB-CG	11.28	134.84	113.40
1	D	234	TYR	CB-CG-CD2	-8.50	115.90	121.00
1	D	234	TYR	CB-CG-CD1	8.22	125.93	121.00
1	A	378	LEU	CB-CG-CD2	-6.87	99.32	111.00
1	D	234	TYR	N-CA-CB	-6.51	98.88	110.60

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	D	233	TYR	Peptide
1	D	234	TYR	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	1988	0	1980	23	0
1	B	1988	0	1980	23	0
1	C	1988	0	1980	29	0
1	D	1988	0	1980	30	0
All	All	7952	0	7920	90	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 6.

The worst 5 of 90 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:264:VAL:HG12	1:D:234:TYR:HE1	1.39	0.86
1:A:262:MET:HG3	1:B:234:TYR:HE1	1.49	0.78
1:A:262:MET:SD	1:B:234:TYR:CE1	2.79	0.76
1:A:262:MET:CG	1:B:234:TYR:HE1	1.99	0.74
1:C:322:LEU:HD13	1:C:362:GLY:HA2	1.71	0.72

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	244/355 (69%)	238 (98%)	5 (2%)	1 (0%)	34	69
1	B	244/355 (69%)	233 (96%)	8 (3%)	3 (1%)	13	49
1	C	244/355 (69%)	238 (98%)	5 (2%)	1 (0%)	34	69
1	D	244/355 (69%)	231 (95%)	9 (4%)	4 (2%)	9	43
All	All	976/1420 (69%)	940 (96%)	27 (3%)	9 (1%)	17	56

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	402	LEU
1	B	402	LEU
1	C	402	LEU
1	D	402	LEU
1	D	234	TYR

### 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	215/299 (72%)	215 (100%)	0	100	100
1	B	215/299 (72%)	215 (100%)	0	100	100
1	C	215/299 (72%)	214 (100%)	1 (0%)	88	95
1	D	215/299 (72%)	214 (100%)	1 (0%)	88	95
All	All	860/1196 (72%)	858 (100%)	2 (0%)	93	98

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	311	TYR
1	D	234	TYR

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](#)

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	252/355 (70%)	0.28	4 (1%) 72 59	46, 75, 148, 209	0
1	B	252/355 (70%)	0.34	4 (1%) 72 59	50, 86, 152, 203	0
1	C	252/355 (70%)	0.81	37 (14%) 2 1	75, 115, 198, 291	0
1	D	252/355 (70%)	1.68	96 (38%) 0 0	112, 183, 243, 290	0
All	All	1008/1420 (70%)	0.78	141 (13%) 2 1	46, 108, 218, 291	0

The worst 5 of 141 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	403	PRO	9.4
1	D	408	PHE	9.3
1	D	426	ALA	8.4
1	D	184	SER	8.3
1	D	347	TYR	8.3

### 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 monosaccharides 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.