



# Full wwPDB X-ray Structure Validation Report ⓘ

May 14, 2020 – 12:03 pm BST

PDB ID : 5OJ3  
Title : YCF48 from Cyanidioschyzon merolae  
Authors : Michoux, F.; Murray, J.W.; Nixon, P.J.  
Deposited on : 2017-07-20  
Resolution : 2.98 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.

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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 : 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

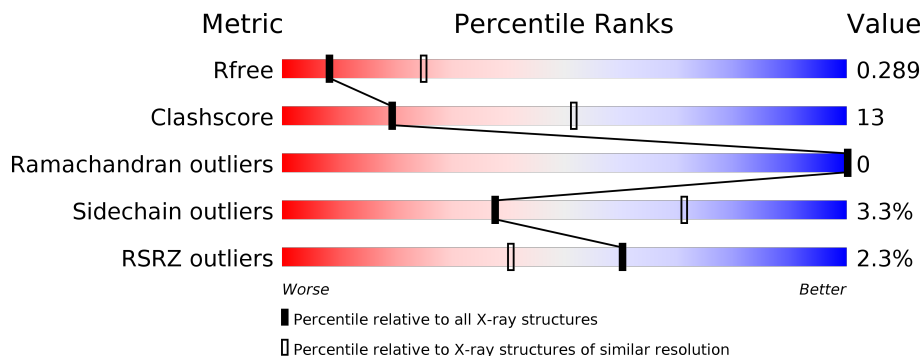
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.98 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	2754 (3.00-2.96)
Clashscore	141614	3103 (3.00-2.96)
Ramachandran outliers	138981	2993 (3.00-2.96)
Sidechain outliers	138945	2996 (3.00-2.96)
RSRZ outliers	127900	2644 (3.00-2.96)

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	437	 2% 55% 18% 26%
1	B	437	 2% 54% 18% 26%

## 2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 4939 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.

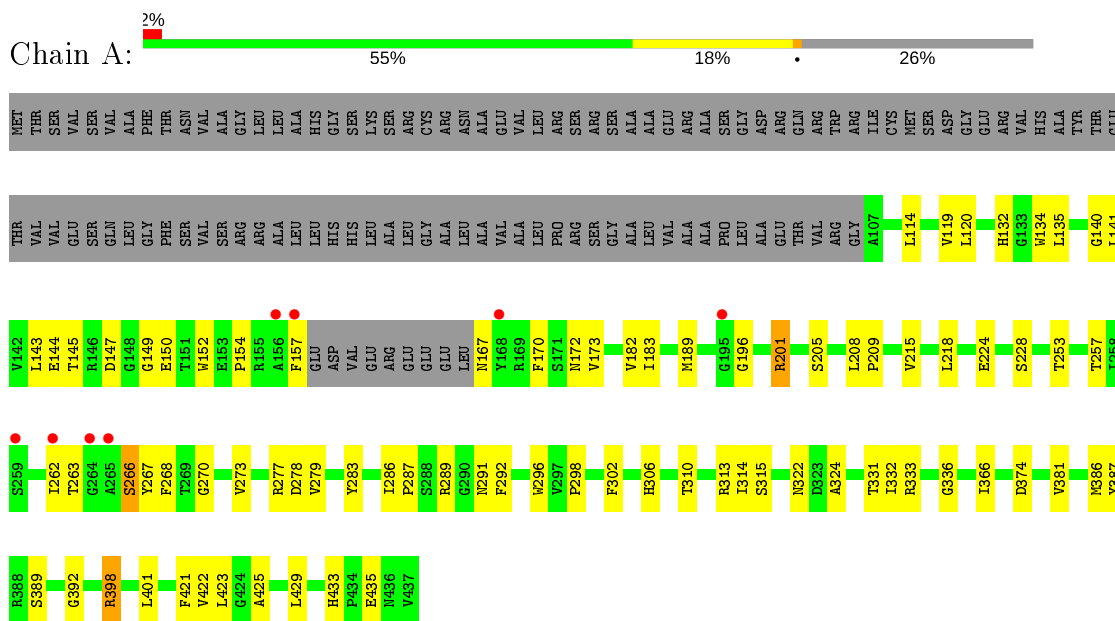
- Molecule 1 is a protein called Photosystem II stability/assembly factor HCF136.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	322	Total 2463	C 1570	N 428	O 460	S 5	0	0	0
1	B	322	Total 2476	C 1572	N 434	O 465	S 5	0	0	0

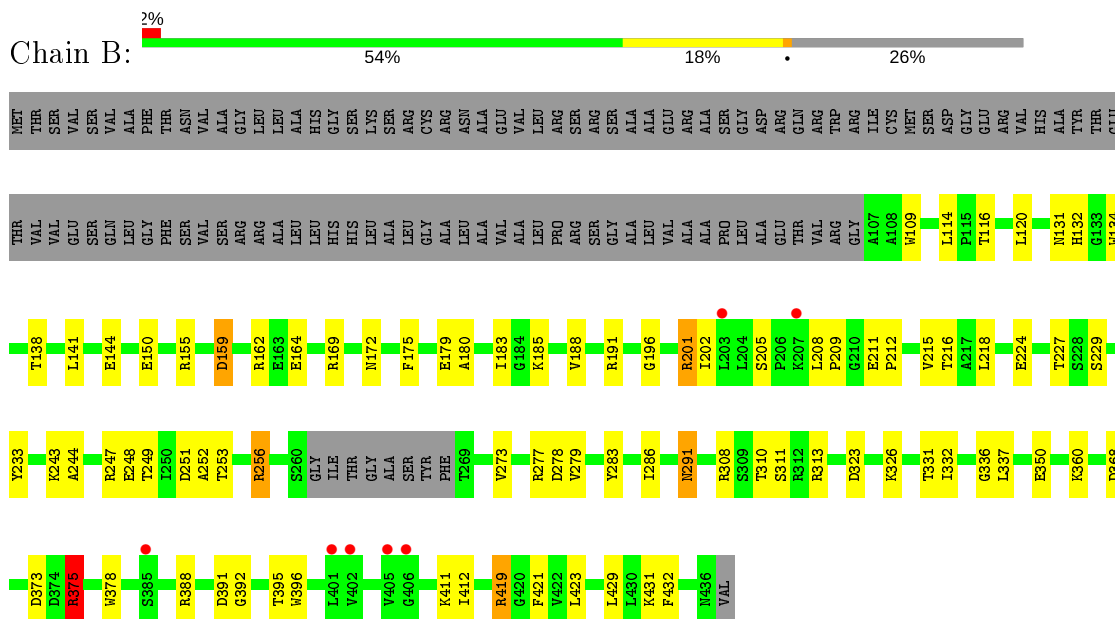
### 3 Residue-property plots

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: Photosystem II stability/assembly factor HCF136



- Molecule 1: Photosystem II stability/assembly factor HCF136



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	60.81Å 97.12Å 110.62Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	37.69 – 2.98 37.71 – 2.98	Depositor EDS
% Data completeness (in resolution range)	99.3 (37.69-2.98) 99.4 (37.71-2.98)	Depositor EDS
$R_{merge}$	0.13	Depositor
$R_{sym}$	0.07	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.84 (at 3.01Å)	Xtrriage
Refinement program	PHENIX (1.12_2829: ???)	Depositor
R, $R_{free}$	0.223 , 0.280 0.231 , 0.289	Depositor DCC
$R_{free}$ test set	640 reflections (4.63%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	63.6	Xtrriage
Anisotropy	0.110	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.28 , 33.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	4939	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	67.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.56% 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	0.30	0/2528	0.57	0/3439
1	B	0.31	0/2539	0.71	3/3452 (0.1%)
All	All	0.30	0/5067	0.65	3/6891 (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	B	0	1

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	B	375	ARG	NE-CZ-NH2	-15.27	112.67	120.30
1	B	375	ARG	NE-CZ-NH1	12.88	126.74	120.30
1	B	375	ARG	CG-CD-NE	-11.53	87.58	111.80

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	350	GLU	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	2463	0	2388	60	0
1	B	2476	0	2397	66	0
All	All	4939	0	4785	124	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 13.

All (124) 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:A:145:THR:HG21	1:A:149:GLY:H	1.17	1.04
1:B:188:VAL:HG23	1:B:201:ARG:NH1	1.72	1.02
1:B:248:GLU:OE1	1:B:256:ARG:NH2	2.00	0.95
1:B:227:THR:HG22	1:B:229:SER:H	1.32	0.91
1:B:188:VAL:HG23	1:B:201:ARG:HH12	1.34	0.89
1:B:172:ASN:HD21	1:B:215:VAL:H	1.24	0.85
1:B:248:GLU:OE1	1:B:256:ARG:CZ	2.28	0.80
1:A:145:THR:HG21	1:A:149:GLY:N	1.99	0.76
1:A:183:ILE:HG22	1:A:189:MET:HG3	1.69	0.74
1:A:286:ILE:HD11	1:A:314:ILE:HB	1.69	0.73
1:B:179:GLU:OE1	1:B:191:ARG:NH1	2.21	0.72
1:B:248:GLU:OE1	1:B:256:ARG:NH1	2.24	0.71
1:B:201:ARG:HH11	1:B:201:ARG:HG3	1.56	0.70
1:A:268:PHE:HE1	1:A:287:PRO:HB3	1.57	0.69
1:A:205:SER:HB3	1:A:208:LEU:HD13	1.76	0.68
1:A:262:ILE:HB	1:A:292:PHE:HE1	1.60	0.66
1:A:262:ILE:HB	1:A:292:PHE:CE1	2.30	0.65
1:B:138:THR:HA	1:B:169:ARG:HG2	1.76	0.65
1:A:421:PHE:HD2	1:A:429:LEU:HD11	1.62	0.64
1:B:360:LYS:NZ	1:B:396:TRP:O	2.32	0.63
1:B:308:ARG:NH1	1:B:310:THR:O	2.32	0.63
1:A:218:LEU:HD11	1:A:224:GLU:HG3	1.81	0.62
1:B:218:LEU:HD11	1:B:224:GLU:HG3	1.81	0.62
1:B:331:THR:HG22	1:B:337:LEU:HD13	1.83	0.61
1:B:131:ASN:OD1	1:B:419:ARG:NH1	2.33	0.61
1:B:243:LYS:NZ	1:B:247:ARG:HH21	1.99	0.60
1:B:248:GLU:HG2	1:B:253:THR:HG22	1.81	0.60
1:B:172:ASN:ND2	1:B:215:VAL:H	1.96	0.59
1:B:391:ASP:OD2	1:B:395:THR:HB	2.02	0.59
1:B:243:LYS:HZ2	1:B:244:ALA:H	1.51	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:243:LYS:HZ3	1:B:247:ARG:HH21	1.52	0.58
1:B:277:ARG:HD2	1:B:283:TYR:CZ	2.39	0.58
1:A:277:ARG:HD2	1:A:283:TYR:CZ	2.38	0.57
1:B:252:ALA:O	1:B:256:ARG:HB2	2.05	0.57
1:A:145:THR:OG1	1:A:152:TRP:CD2	2.58	0.57
1:A:278:ASP:OD1	1:A:324:ALA:N	2.38	0.57
1:A:120:LEU:HB2	1:A:423:LEU:HB3	1.87	0.56
1:A:140:GLY:HA3	1:A:167:ASN:HB2	1.88	0.56
1:B:191:ARG:HB2	1:B:202:ILE:HD11	1.88	0.56
1:B:229:SER:OG	1:B:249:THR:HG22	2.05	0.56
1:B:411:LYS:HG2	1:B:423:LEU:HD12	1.87	0.55
1:A:172:ASN:HD21	1:A:215:VAL:H	1.53	0.55
1:B:375:ARG:HG3	1:B:391:ASP:HA	1.89	0.55
1:B:191:ARG:HB2	1:B:202:ILE:CD1	2.37	0.55
1:A:279:VAL:HG22	1:B:279:VAL:HB	1.89	0.55
1:A:143:LEU:HD23	1:A:154:PRO:HA	1.88	0.54
1:A:310:THR:HG21	1:A:332:ILE:HG13	1.90	0.54
1:B:216:THR:HG21	1:B:277:ARG:HD3	1.88	0.54
1:A:173:VAL:HG23	1:A:182:VAL:HG22	1.89	0.54
1:B:243:LYS:NZ	1:B:244:ALA:H	2.05	0.53
1:B:332:ILE:HB	1:B:336:GLY:HA3	1.89	0.53
1:B:323:ASP:HB3	1:B:326:LYS:HD2	1.90	0.53
1:A:132:HIS:HE1	1:A:144:GLU:OE2	1.92	0.53
1:B:205:SER:HB3	1:B:208:LEU:HG	1.90	0.52
1:A:332:ILE:HB	1:A:336:GLY:HA3	1.91	0.52
1:A:289:ARG:HB2	1:A:291:ASN:HD21	1.74	0.52
1:A:145:THR:OG1	1:A:152:TRP:CE3	2.63	0.51
1:A:262:ILE:HG21	1:A:268:PHE:HB2	1.91	0.51
1:A:119:VAL:HG23	1:A:425:ALA:HA	1.92	0.51
1:A:268:PHE:CE2	1:A:270:GLY:HA2	2.45	0.51
1:B:248:GLU:HG2	1:B:253:THR:CG2	2.41	0.51
1:A:135:LEU:HD23	1:A:152:TRP:CZ2	2.47	0.50
1:B:375:ARG:HG3	1:B:392:GLY:H	1.76	0.50
1:B:114:LEU:CD1	1:B:116:THR:HG22	2.42	0.50
1:A:386:MET:HE1	1:A:422:VAL:HG11	1.95	0.49
1:B:273:VAL:O	1:B:286:ILE:HG22	2.13	0.49
1:B:209:PRO:O	1:B:227:THR:HG21	2.13	0.48
1:A:253:THR:HG21	1:A:302:PHE:HB2	1.94	0.48
1:B:132:HIS:NE2	1:B:144:GLU:OE2	2.26	0.48
1:A:262:ILE:HD13	1:A:268:PHE:HA	1.95	0.48
1:A:114:LEU:HD22	1:A:143:LEU:CD1	2.43	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:150:GLU:HG2	1:B:431:LYS:HE3	1.94	0.48
1:B:134:TRP:CZ2	1:B:196:GLY:HA3	2.49	0.47
1:B:256:ARG:HG3	1:B:256:ARG:HH11	1.79	0.47
1:B:233:TYR:CE1	1:B:244:ALA:HB2	2.50	0.47
1:A:315:SER:OG	1:A:333:ARG:HG2	2.14	0.47
1:A:315:SER:OG	1:A:333:ARG:CG	2.62	0.47
1:B:375:ARG:NE	1:B:391:ASP:HA	2.30	0.47
1:B:391:ASP:OD1	1:B:391:ASP:N	2.48	0.46
1:A:145:THR:CG2	1:A:149:GLY:H	2.07	0.46
1:A:201:ARG:H	1:A:201:ARG:HG2	1.57	0.46
1:B:421:PHE:HB3	1:B:429:LEU:HD11	1.97	0.45
1:A:134:TRP:CZ2	1:A:196:GLY:HA3	2.51	0.45
1:A:433:HIS:HB3	1:A:435:GLU:OE2	2.16	0.45
1:B:249:THR:O	1:B:253:THR:HG23	2.16	0.45
1:A:291:ASN:OD1	1:A:313:ARG:NH1	2.49	0.45
1:A:366:ILE:HD13	1:A:381:VAL:HG22	1.99	0.45
1:A:331:THR:HG21	1:A:366:ILE:O	2.17	0.44
1:B:175:PHE:CE1	1:B:180:ALA:HB2	2.52	0.44
1:B:248:GLU:CD	1:B:256:ARG:HH12	2.21	0.44
1:B:172:ASN:OD1	1:B:172:ASN:N	2.50	0.44
1:A:279:VAL:HB	1:A:322:ASN:O	2.17	0.44
1:B:368:ASP:OD2	1:B:412:ILE:N	2.36	0.44
1:B:162:ARG:C	1:B:164:GLU:H	2.22	0.43
1:A:387:TYR:CZ	1:A:398:ARG:HB2	2.54	0.43
1:A:120:LEU:CD1	1:A:429:LEU:HB2	2.48	0.43
1:B:120:LEU:HB2	1:B:423:LEU:HB3	1.99	0.43
1:B:211:GLU:N	1:B:227:THR:HG23	2.34	0.43
1:B:183:ILE:HD12	1:B:212:PRO:HB2	2.01	0.43
1:A:253:THR:O	1:A:257:THR:HG23	2.19	0.43
1:A:292:PHE:HB2	1:A:306:HIS:O	2.19	0.43
1:A:389:SER:OG	1:A:392:GLY:O	2.30	0.43
1:A:263:THR:HG23	1:A:263:THR:H	1.54	0.42
1:B:116:THR:HG21	1:B:141:LEU:CD1	2.48	0.42
1:A:157:PHE:HE2	1:A:170:PHE:CZ	2.37	0.42
1:A:296:TRP:CH2	1:A:298:PRO:HA	2.54	0.42
1:A:134:TRP:HZ2	1:A:196:GLY:HA3	1.84	0.42
1:A:135:LEU:HD23	1:A:152:TRP:CH2	2.55	0.42
1:B:378:TRP:CZ3	1:B:388:ARG:HB3	2.54	0.42
1:A:208:LEU:HA	1:A:209:PRO:HD3	1.93	0.41
1:B:201:ARG:HH11	1:B:201:ARG:CG	2.29	0.41
1:A:273:VAL:O	1:A:286:ILE:HG22	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:114:LEU:CD2	1:A:143:LEU:CD1	2.98	0.41
1:B:159:ASP:HB3	1:B:201:ARG:HB2	2.03	0.41
1:A:374:ASP:OD2	1:B:373:ASP:HB2	2.20	0.41
1:B:109:TRP:CZ3	1:B:432:PHE:HB2	2.56	0.41
1:A:141:LEU:HD11	1:A:143:LEU:HG	2.03	0.41
1:A:145:THR:HG23	1:A:147:ASP:OD1	2.21	0.41
1:B:138:THR:HG22	1:B:169:ARG:CG	2.51	0.41
1:A:147:ASP:OD2	1:A:150:GLU:HB2	2.21	0.40
1:B:114:LEU:HD12	1:B:116:THR:HG22	2.02	0.40
1:B:291:ASN:HB2	1:B:313:ARG:HH21	1.86	0.40
1:B:277:ARG:HD2	1:B:283:TYR:OH	2.21	0.40
1:A:262:ILE:HG12	1:A:266:SER:O	2.22	0.40

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	318/437 (73%)	305 (96%)	13 (4%)	0	100	100
1	B	318/437 (73%)	306 (96%)	12 (4%)	0	100	100
All	All	636/874 (73%)	611 (96%)	25 (4%)	0	100	100

There are no Ramachandran outliers to report.

### 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	259/353 (73%)	253 (98%)	6 (2%)	50	79
1	B	261/353 (74%)	250 (96%)	11 (4%)	30	64
All	All	520/706 (74%)	503 (97%)	17 (3%)	38	71

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	201	ARG
1	A	228	SER
1	A	266	SER
1	A	267	TYR
1	A	398	ARG
1	A	401	LEU
1	B	155	ARG
1	B	159	ASP
1	B	185	LYS
1	B	201	ARG
1	B	251	ASP
1	B	256	ARG
1	B	278	ASP
1	B	291	ASN
1	B	311	SER
1	B	375	ARG
1	B	419	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	291	ASN

### 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](#)

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	322/437 (73%)	0.07	8 (2%) 57 38	30, 63, 110, 196	0
1	B	322/437 (73%)	0.09	7 (2%) 62 42	35, 64, 111, 157	0
All	All	644/874 (73%)	0.08	15 (2%) 60 40	30, 63, 111, 196	0

All (15) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	207	LYS	5.6
1	B	405	VAL	5.1
1	A	262	ILE	5.0
1	B	406	GLY	4.8
1	A	265	ALA	4.6
1	A	168	TYR	3.4
1	B	401	LEU	3.0
1	B	203	LEU	2.9
1	B	402	VAL	2.8
1	A	157	PHE	2.7
1	A	264	GLY	2.7
1	A	259	SER	2.6
1	B	385	SER	2.5
1	A	195	GLY	2.0
1	A	156	ALA	2.0

### 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

There are no ligands in this entry.

## 6.5 Other polymers

There are no such residues in this entry.