



# Full wwPDB X-ray Structure Validation Report ⓘ

Dec 21, 2017 – 02:37 PM EST

PDB ID : 5OQN  
Title : Crystal structure of the *S. cerevisiae* condensin Ycg1-Brn1 subcomplex bound to DNA (short kleisin loop)  
Authors : Kschonsak, M.; Hassler, M.; Haering, C.H.  
Deposited on : 2017-08-14  
Resolution : 3.15 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

<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
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20030736
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-20030736

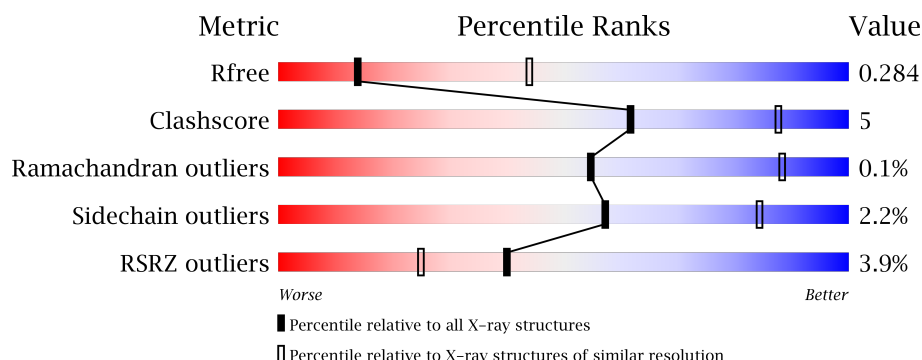
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.15 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	1259 (3.20-3.12)
Clashscore	112137	1397 (3.20-3.12)
Ramachandran outliers	110173	1368 (3.20-3.12)
Sidechain outliers	110143	1367 (3.20-3.12)
RSRZ outliers	101464	1264 (3.20-3.12)

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	871	
2	B	125	
3	C	18	
3	D	18	

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 15999 atoms, of which 7887 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 Condensin complex subunit 3.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	813	Total	C	H	N	O	S	0	0	0
			13213	4180	6663	1110	1231	29			

There are 58 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	5	MET	-	initiating methionine	UNP Q06680
A	?	-	GLN	deletion	UNP Q06680
A	?	-	GLU	deletion	UNP Q06680
A	?	-	GLU	deletion	UNP Q06680
A	?	-	LYS	deletion	UNP Q06680
A	?	-	ILE	deletion	UNP Q06680
A	?	-	LYS	deletion	UNP Q06680
A	?	-	SER	deletion	UNP Q06680
A	?	-	LYS	deletion	UNP Q06680
A	?	-	ILE	deletion	UNP Q06680
A	?	-	ASN	deletion	UNP Q06680
A	?	-	ARG	deletion	UNP Q06680
A	?	-	ARG	deletion	UNP Q06680
A	?	-	ASN	deletion	UNP Q06680
A	?	-	GLU	deletion	UNP Q06680
A	?	-	THR	deletion	UNP Q06680
A	?	-	SER	deletion	UNP Q06680
A	?	-	VAL	deletion	UNP Q06680
A	?	-	ASP	deletion	UNP Q06680
A	?	-	GLU	deletion	UNP Q06680
A	?	-	GLU	deletion	UNP Q06680
A	?	-	ASP	deletion	UNP Q06680
A	?	-	GLU	deletion	UNP Q06680
A	?	-	ASN	deletion	UNP Q06680
A	?	-	GLY	deletion	UNP Q06680
A	?	-	THR	deletion	UNP Q06680

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Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	HIS	deletion	UNP Q06680
A	?	-	ASN	deletion	UNP Q06680
A	?	-	ASP	deletion	UNP Q06680
A	?	-	GLU	deletion	UNP Q06680
A	?	-	VAL	deletion	UNP Q06680
A	?	-	ASN	deletion	UNP Q06680
A	?	-	GLU	deletion	UNP Q06680
A	?	-	ASP	deletion	UNP Q06680
A	?	-	GLU	deletion	UNP Q06680
A	?	-	GLU	deletion	UNP Q06680
A	?	-	ASP	deletion	UNP Q06680
A	?	-	ASP	deletion	UNP Q06680
A	?	-	ASN	deletion	UNP Q06680
A	?	-	ILE	deletion	UNP Q06680
A	?	-	SER	deletion	UNP Q06680
A	?	-	SER	deletion	UNP Q06680
A	?	-	PHE	deletion	UNP Q06680
A	?	-	HIS	deletion	UNP Q06680
A	?	-	SER	deletion	UNP Q06680
A	?	-	ALA	deletion	UNP Q06680
A	?	-	VAL	deletion	UNP Q06680
A	?	-	GLU	deletion	UNP Q06680
A	?	-	ASN	deletion	UNP Q06680
A	?	-	LEU	deletion	UNP Q06680
A	?	-	VAL	deletion	UNP Q06680
A	?	-	GLN	deletion	UNP Q06680
A	?	-	GLY	deletion	UNP Q06680
A	?	-	ASN	deletion	UNP Q06680
A	?	-	GLY	deletion	UNP Q06680
A	?	-	ASN	deletion	UNP Q06680
A	?	-	VAL	deletion	UNP Q06680

- Molecule 2 is a protein called Condensin complex subunit 2.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	B	97	Total	C	H	N	O	S	0	0	0
			1647	534	817	144	148	4			

There are 33 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	378	GLY	-	expression tag	UNP P38170

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Chain	Residue	Modelled	Actual	Comment	Reference
B	379	PRO	-	expression tag	UNP P38170
B	380	LEU	-	expression tag	UNP P38170
B	381	GLY	-	expression tag	UNP P38170
B	382	HIS	-	expression tag	UNP P38170
B	383	MET	-	expression tag	UNP P38170
B	?	-	LEU	deletion	UNP P38170
B	?	-	VAL	deletion	UNP P38170
B	?	-	ASN	deletion	UNP P38170
B	?	-	LYS	deletion	UNP P38170
B	?	-	GLU	deletion	UNP P38170
B	?	-	SER	deletion	UNP P38170
B	?	-	ASP	deletion	UNP P38170
B	?	-	LEU	deletion	UNP P38170
B	?	-	LEU	deletion	UNP P38170
B	?	-	GLU	deletion	UNP P38170
B	?	-	GLU	deletion	UNP P38170
B	?	-	THR	deletion	UNP P38170
B	?	-	ARG	deletion	UNP P38170
B	?	-	THR	deletion	UNP P38170
B	?	-	THR	deletion	UNP P38170
B	?	-	ILE	deletion	UNP P38170
B	?	-	GLY	deletion	UNP P38170
B	?	-	ASP	deletion	UNP P38170
B	?	-	THR	deletion	UNP P38170
B	?	-	THR	deletion	UNP P38170
B	?	-	ASP	deletion	UNP P38170
B	?	-	LYS	deletion	UNP P38170
B	?	-	ASN	deletion	UNP P38170
B	?	-	THR	deletion	UNP P38170
B	?	-	THR	deletion	UNP P38170
B	?	-	ASP	deletion	UNP P38170
B	?	-	ASP	deletion	UNP P38170

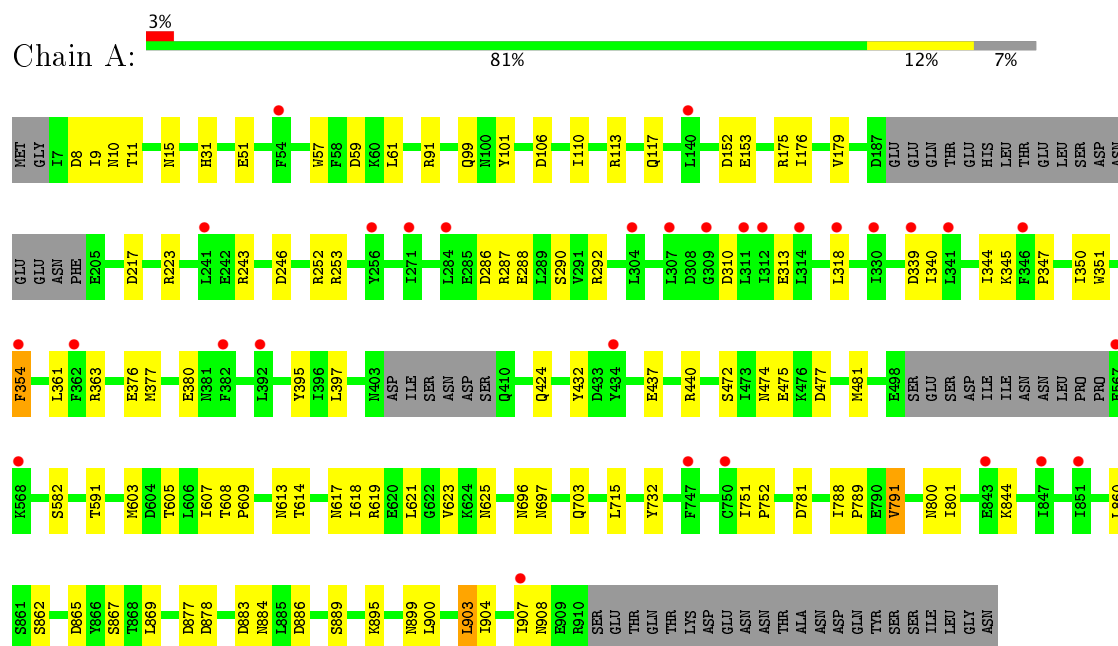
- Molecule 3 is a DNA chain called DNA (5'-D(\*GP\*AP\*TP\*GP\*TP\*GP\*TP\*AP\*GP\*CP\*TP\*AP\*CP\*AP\*CP\*AP\*TP\*C)-3').

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
3	C	18	Total 569	C 176	H 203	N 67	O 106	P 17	0	0	0
3	D	18	Total 570	C 176	H 204	N 67	O 106	P 17	0	0	0

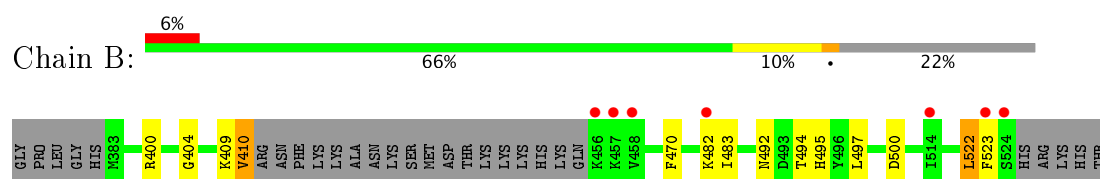
### 3 Residue-property plots [i](#)

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.

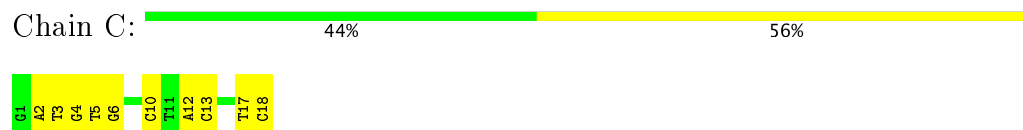
#### • Molecule 1: Condensin complex subunit 3



#### • Molecule 2: Condensin complex subunit 2

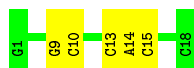


#### • Molecule 3: DNA (5'-D(\*GP\*AP\*TP\*GP\*TP\*GP\*TP\*AP\*GP\*CP\*TP\*AP\*CP\*AP\*CP\*AP\*TP\*C)-3')



#### • Molecule 3: DNA (5'-D(\*GP\*AP\*TP\*GP\*TP\*GP\*TP\*AP\*GP\*CP\*TP\*AP\*CP\*AP\*CP\*AP\*TP\*C)-3')

Chain D:  72% 28%



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	89.15Å 116.22Å 155.52Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.34 – 3.15 47.34 – 3.15	Depositor EDS
% Data completeness (in resolution range)	99.9 (47.34-3.15) 98.0 (47.34-3.15)	Depositor EDS
$R_{merge}$	0.20	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.76 (at 3.12Å)	Xtriage
Refinement program	PHENIX (1.10.1 _2155: ???)	Depositor
R, $R_{free}$	0.249 , 0.281 0.251 , 0.284	Depositor DCC
$R_{free}$ test set	1959 reflections (6.99%)	DCC
Wilson B-factor (Å <sup>2</sup> )	76.5	Xtriage
Anisotropy	0.254	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.29 , -7.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.37$ , $\langle L^2 \rangle = 0.20$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.91	EDS
Total number of atoms	15999	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	76.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.96% 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	0.24	0/6651	0.40	0/8992
2	B	0.24	0/850	0.45	0/1135
3	C	0.59	0/410	1.06	0/631
3	D	0.57	0/410	1.01	0/631
All	All	0.29	0/8321	0.52	0/11389

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	6550	6663	6674	59	0
2	B	830	817	817	11	0
3	C	366	203	205	9	0
3	D	366	204	205	5	0
All	All	8112	7887	7901	78	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 5.

All (78) 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:437:GLU:OE2	1:A:440:ARG:NH1	1.99	0.95
3:C:6:DG:N2	3:D:13:DC:O2	2.05	0.89
1:A:252:ARG:NH1	1:A:286:ASP:OD1	2.05	0.89
3:C:4:DG:N2	3:D:15:DC:O2	2.09	0.86
3:C:10:DC:O2	3:D:9:DG:N2	2.09	0.84
1:A:288:GLU:OE2	2:B:400:ARG:NH1	2.13	0.82
1:A:900:LEU:O	1:A:903:LEU:N	2.17	0.77
1:A:51:GLU:OE1	1:A:113:ARG:NH1	2.20	0.75
1:A:732:TYR:OH	2:B:404:GLY:O	2.05	0.74
2:B:492:ASN:OD1	2:B:494:THR:OG1	2.05	0.73
1:A:877:ASP:OD1	1:A:878:ASP:N	2.23	0.71
1:A:286:ASP:O	1:A:292:ARG:NH1	2.25	0.70
1:A:339:ASP:OD2	1:A:340:ILE:N	2.26	0.67
1:A:696:ASN:O	1:A:703:GLN:NE2	2.27	0.67
1:A:904:ILE:O	1:A:908:ASN:HB2	1.95	0.66
1:A:613:ASN:OD1	1:A:614:THR:N	2.29	0.65
1:A:152:ASP:OD1	1:A:153:GLU:N	2.31	0.63
1:A:175:ARG:NH1	1:A:217:ASP:OD1	2.32	0.62
1:A:11:THR:O	1:A:15:ASN:ND2	2.30	0.62
1:A:363:ARG:NE	1:A:424:GLN:OE1	2.34	0.60
1:A:99:GLN:OE1	1:A:99:GLN:N	2.36	0.59
1:A:883:ASP:OD2	1:A:884:ASN:N	2.36	0.58
1:A:886:ASP:O	1:A:889:SER:N	2.36	0.58
1:A:223:ARG:NH2	1:A:246:ASP:OD2	2.38	0.56
3:C:3:DT:H2'	3:C:4:DG:C8	2.42	0.55
1:A:243:ARG:NH2	1:A:246:ASP:OD1	2.38	0.55
1:A:475:GLU:OE1	1:A:591:THR:OG1	2.24	0.54
1:A:59:ASP:OD2	1:A:117:GLN:NE2	2.41	0.54
1:A:621:LEU:O	1:A:625:ASN:ND2	2.40	0.54
1:A:223:ARG:HH21	1:A:246:ASP:CG	2.10	0.54
1:A:472:SER:OG	1:A:474:ASN:O	2.26	0.53
1:A:895:LYS:O	1:A:899:ASN:ND2	2.39	0.53
3:C:17:DT:H2''	3:C:18:DC:OP2	2.09	0.52
1:A:8:ASP:OD1	1:A:9:ILE:N	2.44	0.51
3:C:2:DA:H2''	3:C:3:DT:O5'	2.10	0.51
1:A:243:ARG:NH1	2:B:497:LEU:HD21	2.26	0.51
2:B:409:LYS:O	2:B:410:VAL:HG13	2.12	0.50
1:A:617:ASN:OD1	1:A:618:ILE:N	2.44	0.49
1:A:310:ASP:OD1	1:A:313:GLU:N	2.24	0.49
1:A:781:ASP:OD2	1:A:844:LYS:NZ	2.31	0.48
1:A:380:GLU:OE1	1:A:380:GLU:N	2.47	0.47
1:A:347:PRO:HB2	1:A:350:ILE:HG12	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:522:LEU:HD22	2:B:523:PHE:CD2	2.51	0.46
1:A:10:ASN:OD1	1:A:57:TRP:NE1	2.40	0.46
1:A:608:THR:HB	1:A:609:PRO:HD3	1.97	0.46
1:A:788:ILE:CG2	1:A:789:PRO:HD2	2.45	0.46
1:A:800:ASN:OD1	1:A:801:ILE:N	2.49	0.45
1:A:862:SER:HA	1:A:903:LEU:HD11	1.98	0.45
1:A:865:ASP:O	1:A:869:LEU:HD13	2.18	0.44
3:C:12:DA:H2''	3:C:13:DC:O4'	2.18	0.44
3:C:5:DT:H2''	3:C:6:DG:H8	1.82	0.43
1:A:788:ILE:O	1:A:791:VAL:HG13	2.18	0.43
1:A:106:ASP:OD2	1:A:113:ARG:NH2	2.51	0.43
1:A:865:ASP:OD2	1:A:867:SER:N	2.51	0.43
1:A:477:ASP:O	1:A:481:MET:HG3	2.18	0.43
1:A:603:MET:HA	1:A:607:ILE:HB	2.01	0.43
3:C:17:DT:C2'	3:C:18:DC:OP2	2.66	0.43
1:A:351:TRP:CD1	1:A:351:TRP:N	2.86	0.43
1:A:345:LYS:O	1:A:347:PRO:HD3	2.19	0.43
1:A:582:SER:OG	1:A:625:ASN:OD1	2.32	0.43
2:B:483:ILE:O	2:B:483:ILE:HD12	2.19	0.42
3:D:9:DG:H2'	3:D:10:DC:O4'	2.20	0.42
2:B:522:LEU:CD1	2:B:522:LEU:H	2.33	0.41
2:B:522:LEU:O	2:B:523:PHE:HB2	2.20	0.41
1:A:176:ILE:O	1:A:179:VAL:HG22	2.20	0.41
1:A:751:ILE:HB	1:A:752:PRO:HD3	2.01	0.41
1:A:788:ILE:HG23	1:A:789:PRO:HD2	2.02	0.41
1:A:253:ARG:NH1	1:A:290:SER:OG	2.53	0.41
1:A:354:PHE:HB2	1:A:395:TYR:OH	2.19	0.41
1:A:110:ILE:HA	1:A:113:ARG:NH1	2.36	0.41
1:A:344:ILE:HG13	1:A:377:MET:HE1	2.03	0.41
3:D:14:DA:H2'	3:D:15:DC:O4'	2.21	0.41
2:B:482:LYS:O	2:B:483:ILE:HG13	2.20	0.41
1:A:286:ASP:OD2	1:A:287:ARG:N	2.54	0.41
1:A:605:THR:O	1:A:609:PRO:HG2	2.21	0.41
1:A:619:ARG:O	1:A:623:VAL:HG23	2.22	0.40
1:A:697:ASN:HA	1:A:703:GLN:NE2	2.36	0.40
2:B:495:HIS:HB2	2:B:497:LEU:HD23	2.03	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	805/871 (92%)	775 (96%)	29 (4%)	1 (0%)	55	88
2	B	93/125 (74%)	80 (86%)	13 (14%)	0	100	100
All	All	898/996 (90%)	855 (95%)	42 (5%)	1 (0%)	55	88

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	318	LEU

### 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	739/794 (93%)	725 (98%)	14 (2%)	62	86
2	B	92/117 (79%)	88 (96%)	4 (4%)	33	70
All	All	831/911 (91%)	813 (98%)	18 (2%)	57	84

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	31	HIS
1	A	61	LEU
1	A	91	ARG
1	A	101	TYR
1	A	354	PHE

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Mol	Chain	Res	Type
1	A	361	LEU
1	A	376	GLU
1	A	397	LEU
1	A	432	TYR
1	A	715	LEU
1	A	791	VAL
1	A	860	LEU
1	A	903	LEU
1	A	907	ILE
2	B	410	VAL
2	B	470	PHE
2	B	500	ASP
2	B	522	LEU

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

Mol	Chain	Res	Type
1	A	908	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

There are no ligands in this entry.

## 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 ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

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	813/871 (93%)	0.29	30 (3%) 42 26	30, 65, 99, 127	0
2	B	97/125 (77%)	0.31	7 (7%) 16 9	37, 68, 103, 114	0
3	C	18/18 (100%)	-0.65	0 100 100	92, 110, 123, 125	0
3	D	18/18 (100%)	-0.63	0 100 100	71, 115, 130, 131	0
All	All	946/1032 (91%)	0.25	37 (3%) 40 25	30, 66, 104, 131	0

All (37) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	567	GLU	4.7
2	B	458	VAL	3.7
1	A	341	LEU	3.5
1	A	346	PHE	3.3
1	A	339	ASP	3.3
1	A	311	LEU	3.3
1	A	318	LEU	3.2
2	B	524	SER	3.2
2	B	456	LYS	3.2
1	A	309	GLY	3.0
2	B	457	LYS	2.9
1	A	907	ILE	2.8
1	A	434	TYR	2.8
1	A	382	PHE	2.8
1	A	330	ILE	2.8
1	A	314	LEU	2.8
1	A	312	ILE	2.7
1	A	284	LEU	2.5
1	A	307	LEU	2.5
1	A	362	PHE	2.5
1	A	140	LEU	2.4

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Mol	Chain	Res	Type	RSRZ
2	B	514	ILE	2.3
2	B	523	PHE	2.3
1	A	392	LEU	2.3
1	A	354	PHE	2.3
1	A	304	LEU	2.3
1	A	568	LYS	2.3
1	A	271	ILE	2.2
1	A	750	CYS	2.2
1	A	256	TYR	2.1
1	A	851	ILE	2.1
1	A	54	PHE	2.1
1	A	847	ILE	2.1
2	B	482	LYS	2.1
1	A	241	LEU	2.1
1	A	843	GLU	2.0
1	A	747	PHE	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 [i](#)

There are no ligands in this entry.

## 6.5 Other polymers [i](#)

There are no such residues in this entry.