



# Full wwPDB X-ray Structure Validation Report ⓘ

Jan 11, 2018 – 07:54 AM EST

PDB ID : 6F4A  
Title : Yeast mitochondrial RNA degradosome complex mtEXO  
Authors : Razew, M.; Nowak, E.; Nowotny, M.  
Deposited on : 2017-11-29  
Resolution : 3.55 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.

---

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

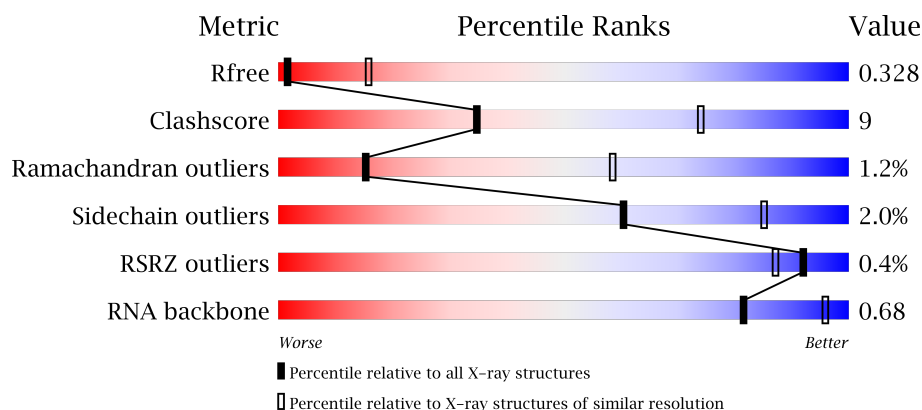
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.55 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	1072 (3.70-3.42)
Clashscore	112137	1003 (3.66-3.46)
Ramachandran outliers	110173	1153 (3.70-3.42)
Sidechain outliers	110143	1153 (3.70-3.42)
RSRZ outliers	101464	1098 (3.70-3.42)
RNA backbone	2435	1004 (4.22-2.88)

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	832	<div> <div>62%</div> <div>15%</div> <div>•</div> <div>23%</div> </div>
2	B	644	<div> <div>72%</div> <div>11%</div> <div>17%</div> </div>
3	C	6	<div> <div>33%</div> <div>67%</div> </div>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 7574 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 Exoribonuclease II, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	644	Total	C	N	O	S	0	0	0
			4154	2598	730	813	13			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	69	MET	-	initiating methionine	UNP A0A0W0CXR7
A	477	ASN	ASP	conflict	UNP A0A0W0CXR7
A	882	VAL	ILE	conflict	UNP A0A0W0CXR7

- Molecule 2 is a protein called Suv3 helicase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	534	Total	C	N	O	S	0	0	0
			3301	2067	586	633	15			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	42	MET	-	initiating methionine	UNP Q6FKD7

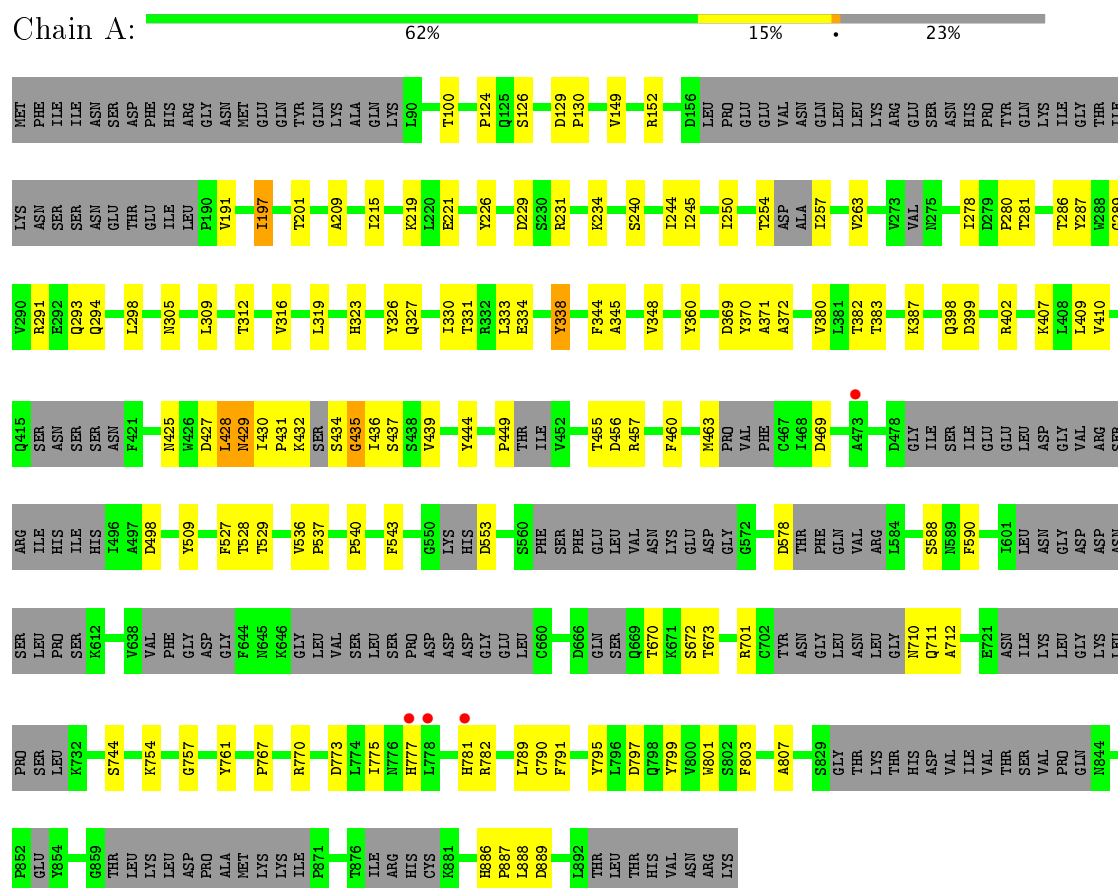
- Molecule 3 is a RNA chain called RNA (5'-R(P\*AP\*GP\*AP\*UP\*AP\*C)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	6	Total	C	N	O	P	0	0	0
			119	53	20	40	6			

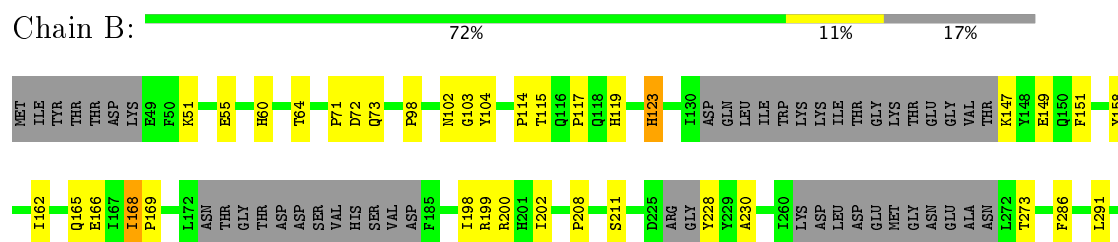
### 3 Residue-property plots

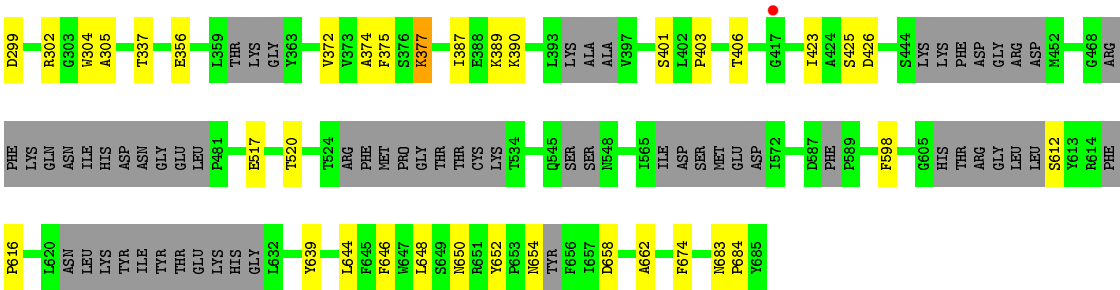
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are 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: Exoribonuclease II, mitochondrial

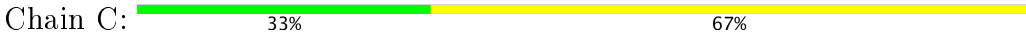


- Molecule 2: Suv3 helicase





● Molecule 3: RNA (5'-R(P\*AP\*GP\*AP\*UP\*AP\*C)-3')



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	104.55Å 151.24Å 284.22Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.06 – 3.55 49.06 – 3.55	Depositor EDS
% Data completeness (in resolution range)	95.4 (49.06-3.55) 95.5 (49.06-3.55)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	5.92 (at 3.57Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, $R_{free}$	0.296 , 0.328 0.295 , 0.328	Depositor DCC
$R_{free}$ test set	1316 reflections (4.99%)	DCC
Wilson B-factor (Å <sup>2</sup> )	139.5	Xtriage
Anisotropy	0.552	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.28 , 214.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.89	EDS
Total number of atoms	7574	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	153.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.85% 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	0.33	0/4215	0.64	0/5792
2	B	0.36	0/3351	0.70	3/4609 (0.1%)
3	C	0.23	0/132	0.80	0/203
All	All	0.34	0/7698	0.67	3/10604 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	377	LYS	N-CA-C	-6.27	94.07	111.00
2	B	123	HIS	CB-CA-C	6.13	122.65	110.40
2	B	123	HIS	N-CA-CB	-5.78	100.20	110.60

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	4154	0	3132	86	0
2	B	3301	0	2356	36	0
3	C	119	0	61	3	0
All	All	7574	0	5549	123	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 9.

All (123) 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:209:ALA:HA	1:A:281:THR:HG23	1.69	0.75
1:A:770:ARG:NH1	1:A:773:ASP:OD1	2.22	0.73
1:A:553:ASP:N	1:A:588:SER:O	2.23	0.72
1:A:528:THR:HG23	1:A:537:PRO:HA	1.72	0.71
1:A:245:ILE:HD12	1:A:286:THR:HG23	1.73	0.70
2:B:652:TYR:O	2:B:654:ASN:N	2.22	0.69
1:A:527:PHE:HD2	1:A:770:ARG:HG2	1.62	0.64
1:A:326:TYR:OH	1:A:369:ASP:OD2	2.15	0.63
1:A:670:THR:HG1	1:A:672:SER:HG	1.46	0.63
1:A:100:THR:OG1	1:A:152:ARG:NH2	2.32	0.62
1:A:670:THR:H	1:A:673:THR:HB	1.64	0.62
1:A:371:ALA:HA	1:A:402:ARG:HG3	1.82	0.61
1:A:229:ASP:OD1	1:A:231:ARG:HD3	2.01	0.61
1:A:509:TYR:HA	1:A:782:ARG:HH12	1.65	0.61
1:A:527:PHE:CE1	1:A:807:ALA:HB2	2.36	0.61
1:A:498:ASP:OD1	1:A:781:HIS:NE2	2.34	0.60
2:B:119:HIS:ND1	2:B:119:HIS:O	2.34	0.59
1:A:215:ILE:HG22	1:A:219:LYS:HE3	1.85	0.59
2:B:612:SER:N	2:B:658:ASP:OD2	2.36	0.59
2:B:403:PRO:HB3	2:B:639:TYR:CZ	2.38	0.58
1:A:226:TYR:HD2	1:A:263:VAL:HG11	1.69	0.58
2:B:158:TYR:O	2:B:162:ILE:HG12	2.03	0.58
2:B:200:ARG:HH11	2:B:337:THR:HG21	1.69	0.58
1:A:327:GLN:O	1:A:331:THR:HG23	2.04	0.57
1:A:434:SER:O	1:A:436:ILE:N	2.38	0.57
1:A:529:THR:HB	1:A:536:VAL:HB	1.84	0.57
1:A:371:ALA:O	1:A:402:ARG:HD3	2.05	0.56
1:A:254:THR:O	1:A:257:ILE:N	2.39	0.56
1:A:209:ALA:CA	1:A:281:THR:HG23	2.36	0.55
2:B:200:ARG:NH2	2:B:202:ILE:HD11	2.22	0.55
1:A:797:ASP:O	1:A:801:TRP:HD1	1.90	0.55
1:A:428:LEU:O	1:A:430:ILE:N	2.34	0.54
1:A:402:ARG:N	1:A:889:ASP:OD2	2.31	0.54
1:A:234:LYS:O	1:A:316:VAL:HG22	2.06	0.54
2:B:646:PHE:O	2:B:650:ASN:ND2	2.31	0.54
1:A:372:ALA:O	1:A:425:ASN:ND2	2.35	0.54
1:A:372:ALA:HB1	1:A:425:ASN:HA	1.89	0.53
1:A:434:SER:O	1:A:437:SER:N	2.42	0.52
1:A:432:LYS:O	1:A:434:SER:OG	2.27	0.52
1:A:338:TYR:HE2	1:A:387:LYS:HE3	1.73	0.52

*Continued on next page...*



*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:299:ASP:OD2	2:B:302:ARG:N	2.41	0.52
1:A:219:LYS:HG2	1:A:250:ILE:HD11	1.93	0.51
2:B:658:ASP:HB3	2:B:662:ALA:HB2	1.93	0.51
2:B:147:LYS:N	2:B:149:GLU:OE1	2.43	0.51
1:A:338:TYR:N	1:A:338:TYR:CD1	2.78	0.51
1:A:455:THR:C	1:A:457:ARG:H	2.14	0.51
1:A:444:TYR:CZ	1:A:540:PRO:HD3	2.47	0.50
1:A:407:LYS:O	1:A:410:VAL:HG22	2.11	0.50
1:A:334:GLU:HA	1:A:338:TYR:CD1	2.47	0.50
1:A:449:PRO:HB3	1:A:543:PHE:CE2	2.47	0.50
2:B:117:PRO:HA	2:B:158:TYR:HE2	1.77	0.49
2:B:375:PHE:O	2:B:377:LYS:N	2.45	0.49
2:B:200:ARG:HH22	2:B:202:ILE:HD11	1.78	0.49
2:B:598:PHE:HE2	2:B:644:LEU:HD23	1.78	0.49
1:A:124:PRO:O	1:A:710:ASN:ND2	2.45	0.49
1:A:509:TYR:HA	1:A:782:ARG:NH1	2.28	0.49
2:B:374:ALA:O	2:B:425:SER:HA	2.14	0.48
1:A:460:PHE:O	1:A:463:MET:HG3	2.13	0.48
1:A:370:TYR:HE1	1:A:382:THR:HG22	1.77	0.48
1:A:197:ILE:O	1:A:201:THR:HG23	2.14	0.47
1:A:319:LEU:HD12	1:A:323:HIS:HB3	1.96	0.47
1:A:670:THR:OG1	1:A:672:SER:OG	2.23	0.47
1:A:553:ASP:N	1:A:590:PHE:H	2.12	0.47
1:A:293:GLN:HB3	1:A:298:LEU:HD12	1.96	0.47
1:A:338:TYR:HD1	1:A:338:TYR:N	2.12	0.47
1:A:701:ARG:O	1:A:761:TYR:HB3	2.14	0.47
1:A:333:LEU:O	1:A:338:TYR:HA	2.15	0.47
2:B:648:LEU:O	2:B:652:TYR:N	2.48	0.47
1:A:744:SER:OG	3:C:2:A:OP1	2.25	0.47
2:B:51:LYS:O	2:B:55:GLU:HG2	2.15	0.46
1:A:435:GLY:O	1:A:439:VAL:HG23	2.15	0.46
1:A:402:ARG:HD2	1:A:888:LEU:O	2.14	0.46
2:B:304:TRP:CD1	2:B:305:ALA:N	2.84	0.46
1:A:754:LYS:HA	1:A:757:GLY:O	2.16	0.46
2:B:228:TYR:HA	2:B:273:THR:O	2.15	0.46
2:B:406:THR:HG22	2:B:674:PHE:HB2	1.97	0.46
1:A:278:ILE:O	1:A:280:PRO:HD3	2.16	0.45
1:A:345:ALA:HA	1:A:348:VAL:HG12	1.98	0.45
2:B:208:PRO:O	2:B:211:SER:OG	2.31	0.45
1:A:767:PRO:HA	1:A:773:ASP:HB2	1.98	0.45
2:B:372:VAL:O	2:B:423:ILE:HG23	2.16	0.45

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:782:ARG:HH21	1:A:789:LEU:C	2.20	0.45
1:A:126:SER:C	1:A:712:ALA:HB2	2.36	0.45
2:B:166:GLU:O	2:B:169:PRO:HD2	2.17	0.45
1:A:344:PHE:HD1	1:A:360:TYR:CD2	2.34	0.44
1:A:149:VAL:HB	1:A:309:LEU:HD23	1.99	0.44
1:A:469:ASP:OD1	3:C:5:C:H5'	2.18	0.44
1:A:886:HIS:HA	1:A:887:PRO:HD2	1.73	0.43
1:A:291:ARG:O	1:A:294:GLN:HB2	2.18	0.43
1:A:240:SER:O	1:A:244:ILE:HG13	2.18	0.43
1:A:380:VAL:HA	1:A:383:THR:HG22	2.01	0.43
1:A:767:PRO:HG3	1:A:777:HIS:CE1	2.53	0.43
1:A:775:ILE:HG12	1:A:791:PHE:HE2	1.84	0.43
2:B:517:GLU:O	2:B:520:THR:OG1	2.37	0.43
2:B:102:ASN:O	2:B:104:TYR:N	2.50	0.43
2:B:230:ALA:HB3	2:B:291:LEU:HD23	2.01	0.43
2:B:683:ASN:HA	2:B:684:PRO:HD2	1.81	0.43
1:A:782:ARG:NH2	1:A:790:CYS:HA	2.34	0.42
1:A:795:TYR:O	1:A:799:TYR:HD1	2.03	0.42
2:B:60:HIS:O	2:B:64:THR:HG23	2.19	0.42
1:A:129:ASP:HA	1:A:130:PRO:HD3	1.63	0.42
1:A:527:PHE:CD2	1:A:770:ARG:HG2	2.50	0.42
2:B:168:ILE:H	2:B:169:PRO:HD2	1.84	0.42
1:A:330:ILE:O	1:A:334:GLU:HG2	2.20	0.42
2:B:387:ILE:HA	2:B:390:LYS:HE3	2.01	0.42
1:A:427:ASP:O	1:A:429:ASN:N	2.53	0.41
1:A:775:ILE:HD12	1:A:803:PHE:CE2	2.55	0.41
1:A:409:LEU:HA	1:A:409:LEU:HD23	1.79	0.41
2:B:198:ILE:HG23	2:B:199:ARG:O	2.20	0.41
1:A:398:GLN:HG3	1:A:399:ASP:N	2.35	0.41
2:B:165:GLN:O	2:B:169:PRO:HD3	2.20	0.41
2:B:403:PRO:O	2:B:406:THR:OG1	2.37	0.41
1:A:287:TYR:OH	1:A:291:ARG:NH1	2.52	0.41
1:A:289:GLY:O	1:A:293:GLN:HG3	2.21	0.41
1:A:305:ASN:HB2	1:A:312:THR:HG21	2.03	0.41
1:A:331:THR:HA	1:A:334:GLU:HG2	2.02	0.41
1:A:372:ALA:HB1	1:A:425:ASN:CA	2.51	0.41
1:A:431:PRO:HA	1:A:434:SER:HB2	2.03	0.40
1:A:770:ARG:NH2	1:A:773:ASP:OD2	2.55	0.40
2:B:426:ASP:OD1	2:B:426:ASP:N	2.53	0.40
3:C:0:A:O2'	3:C:1:G:H8	2.04	0.40
1:A:345:ALA:O	1:A:348:VAL:HG12	2.22	0.40

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:71:PRO:O	2:B:73:GLN:N	2.54	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	600/832 (72%)	571 (95%)	23 (4%)	6 (1%)	18	62
2	B	500/644 (78%)	446 (89%)	47 (9%)	7 (1%)	13	55
All	All	1100/1476 (74%)	1017 (92%)	70 (6%)	13 (1%)	15	58

All (13) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	429	ASN
1	A	435	GLY
1	A	456	ASP
2	B	168	ILE
2	B	356	GLU
2	B	72	ASP
2	B	114	PRO
2	B	115	THR
1	A	428	LEU
2	B	98	PRO
2	B	103	GLY
1	A	191	VAL
1	A	197	ILE

### 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	294/759 (39%)	290 (99%)	4 (1%)	71	89
2	B	194/568 (34%)	188 (97%)	6 (3%)	45	78
All	All	488/1327 (37%)	478 (98%)	10 (2%)	60	85

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	221	GLU
1	A	338	TYR
1	A	578	ASP
1	A	711	GLN
2	B	123	HIS
2	B	151	PHE
2	B	286	PHE
2	B	389	LYS
2	B	401	SER
2	B	616	PRO

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

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
3	C	5/6 (83%)	0	0

There are no RNA backbone outliers to report.

There are no RNA pucker outliers to report.

## 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 [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	644/832 (77%)	-0.52	4 (0%) 89 82	75, 152, 237, 307	0
2	B	534/644 (82%)	-0.58	1 (0%) 94 91	86, 152, 221, 287	0
3	C	6/6 (100%)	-0.01	0 100 100	149, 168, 179, 203	0
All	All	1184/1482 (79%)	-0.54	5 (0%) 92 87	75, 152, 231, 307	0

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	777	HIS	2.6
2	B	417	GLY	2.4
1	A	781	HIS	2.3
1	A	778	LEU	2.1
1	A	473	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 [i](#)

There are no ligands in this entry.

## 6.5 Other polymers

There are no such residues in this entry.