



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 12, 2026 – 08:10 PM UTC

PDB ID : 4XGT / pdb_00004xgt
Title : Structure of RNA Helicase FRH a Critical Component of the Neurospora Crassa Circadian Clock
Authors : Conrad, K.S.; Crane, B.C.
Deposited on : 2015-01-02
Resolution : 3.09 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

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>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

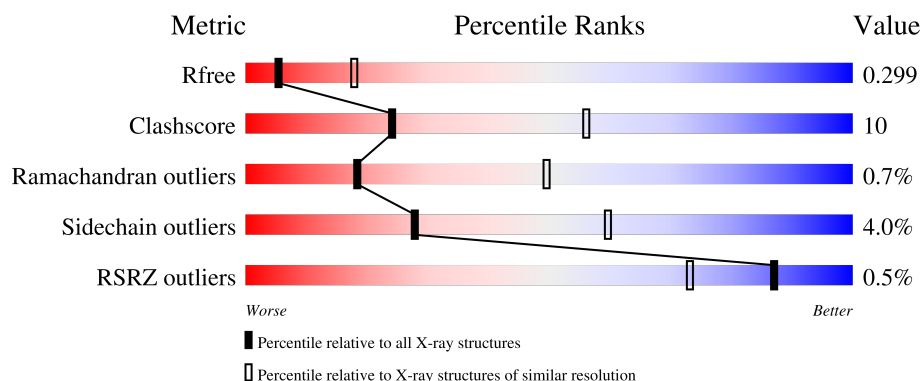
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.09 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}	180053	1456 (3.10-3.10)
Clashscore	190562	1539 (3.10-3.10)
Ramachandran outliers	187476	1467 (3.10-3.10)
Sidechain outliers	187428	1467 (3.10-3.10)
RSRZ outliers	180081	1456 (3.10-3.10)

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 ≥ 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	993	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 7699 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 FRQ-interacting RNA helicase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	961	Total	C	N	O	S	0	0	0
			7681	4897	1321	1421	42			

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	18	Total	O	0	0
			18	18		

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	78.84Å 113.46Å 143.63Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	69.11 – 3.09 69.11 – 3.09	Depositor EDS
% Data completeness (in resolution range)	99.9 (69.11-3.09) 93.1 (69.11-3.09)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.11 (at 3.07Å)	Xtriage
Refinement program	PHENIX (phenix.refine: dev_1819)	Depositor
R, R_{free}	0.232 , 0.295 0.237 , 0.299	Depositor DCC
R_{free} test set	1237 reflections (5.10%)	wwPDB-VP
Wilson B-factor (Å ²)	90.6	Xtriage
Anisotropy	0.320	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 66.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	7699	wwPDB-VP
Average B, all atoms (Å ²)	95.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.20% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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	0.34	0/7829	0.82	9/10572 (0.1%)

There are no bond length outliers.

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1022	TYR	N-CA-C	-9.07	102.21	113.28
1	A	959	ASN	N-CA-C	-6.63	105.17	113.20
1	A	544	ASN	N-CA-C	5.65	119.80	113.02
1	A	652	VAL	CA-C-N	-5.29	113.09	118.85
1	A	652	VAL	C-N-CA	-5.29	113.09	118.85
1	A	700	HIS	CA-C-N	5.19	125.49	119.47
1	A	700	HIS	C-N-CA	5.19	125.49	119.47
1	A	169	PRO	CA-C-N	5.05	124.77	119.82
1	A	169	PRO	C-N-CA	5.05	124.77	119.82

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	7681	0	7776	154	0
2	A	18	0	0	5	0
All	All	7699	0	7776	154	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 10.

All (154) 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:1037:TRP:O	1:A:1096:ARG:NH1	2.11	0.83
1:A:237:ASN:O	2:A:1201:HOH:O	2.05	0.75
1:A:435:ILE:HG23	1:A:440:PHE:HB2	1.69	0.75
1:A:764:ASN:HD21	1:A:766:LYS:HE2	1.52	0.73
1:A:475:ASN:OD1	1:A:503:ARG:NH1	2.23	0.70
1:A:526:GLN:HG2	1:A:545:MET:HG2	1.75	0.69
1:A:715:HIS:NE2	1:A:723:ASP:OD1	2.23	0.69
1:A:553:THR:HG22	1:A:554:GLN:HG2	1.75	0.69
1:A:253:MET:HG2	1:A:258:THR:HG23	1.75	0.69
1:A:274:ARG:HD2	1:A:306:VAL:HG13	1.75	0.68
1:A:928:ASN:HD22	1:A:934:GLN:HG2	1.58	0.68
1:A:493:PRO:O	2:A:1202:HOH:O	2.13	0.66
1:A:804:GLN:HA	1:A:840:LEU:HD13	1.78	0.66
1:A:664:GLN:O	1:A:668:ALA:N	2.24	0.65
1:A:597:LEU:HD22	1:A:601:THR:HG21	1.79	0.64
1:A:239:LYS:HZ3	1:A:543:LEU:HD21	1.64	0.63
1:A:551:VAL:HG22	1:A:590:ILE:HB	1.85	0.59
1:A:447:ASN:HD21	1:A:453:CYS:HA	1.68	0.59
1:A:627:LEU:HD13	1:A:635:PRO:HA	1.85	0.57
1:A:761:GLY:HA3	1:A:763:PHE:CD2	2.39	0.57
1:A:990:GLU:HA	1:A:993:ALA:HB3	1.87	0.57
1:A:1042:PRO:HG2	1:A:1045:GLU:HG3	1.85	0.57
1:A:241:ARG:HA	1:A:244:GLN:HB3	1.87	0.56
1:A:561:GLN:HE21	1:A:561:GLN:HA	1.71	0.56
1:A:718:SER:HB2	1:A:773:MET:HE3	1.87	0.56
1:A:761:GLY:HA3	1:A:763:PHE:HD2	1.71	0.55
1:A:831:ARG:HE	1:A:832:ARG:HH21	1.53	0.55
1:A:992:LEU:HD11	1:A:1035:LEU:HD22	1.88	0.55
1:A:270:THR:HG21	1:A:307:TRP:CH2	2.42	0.55
1:A:353:ARG:HH12	1:A:576:GLY:HA2	1.72	0.55
1:A:639:LEU:HD11	1:A:910:GLN:HB3	1.89	0.54
1:A:676:ILE:HD13	1:A:872:LEU:HD11	1.89	0.54
1:A:713:LEU:HD11	1:A:829:ILE:HD13	1.90	0.54
1:A:139:GLU:OE2	1:A:582:GLY:HA2	2.07	0.54
1:A:228:TYR:OH	1:A:293:ASP:OD2	2.25	0.54
1:A:382:ASN:OD1	1:A:383:ASN:N	2.41	0.54
1:A:190:ALA:O	2:A:1203:HOH:O	2.18	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:364:ALA:HB3	1:A:391:ILE:HG23	1.90	0.54
1:A:232:ILE:HG22	1:A:234:ALA:H	1.71	0.53
1:A:312:ILE:HD11	1:A:642:CYS:HA	1.91	0.53
1:A:663:GLN:HG2	1:A:895:ILE:HD11	1.92	0.52
1:A:634:SER:HB2	1:A:636:GLU:OE1	2.09	0.52
1:A:427:ASP:HA	1:A:430:LYS:HG3	1.91	0.52
1:A:340:ILE:HG13	1:A:641:ARG:HD3	1.92	0.51
1:A:633:ILE:HG12	1:A:637:TYR:CD2	2.45	0.51
1:A:939:VAL:HG13	1:A:1074:ALA:HB1	1.92	0.51
1:A:302:ILE:HG13	1:A:303:ARG:HG3	1.91	0.51
1:A:831:ARG:HE	1:A:832:ARG:NH2	2.09	0.51
1:A:1046:ILE:HA	1:A:1049:MET:HB2	1.92	0.51
1:A:671:ILE:HG12	1:A:884:GLN:HB3	1.93	0.51
1:A:768:ARG:NH2	2:A:1205:HOH:O	2.43	0.50
1:A:974:LEU:HD21	1:A:1071:MET:HE2	1.93	0.50
1:A:1050:THR:OG1	1:A:1051:ASN:N	2.43	0.50
1:A:522:GLU:O	1:A:526:GLN:HG3	2.13	0.49
1:A:604:ALA:HA	1:A:608:GLY:HA3	1.94	0.49
1:A:312:ILE:HG21	1:A:638:MET:HG3	1.95	0.48
1:A:1037:TRP:HB2	1:A:1046:ILE:HD13	1.94	0.48
1:A:652:VAL:HA	1:A:655:LEU:HD12	1.95	0.48
1:A:444:ILE:HG13	1:A:547:ALA:HB2	1.95	0.48
1:A:713:LEU:HB2	1:A:803:GLY:HA3	1.95	0.48
1:A:295:ILE:HG22	1:A:324:SER:HB2	1.96	0.48
1:A:655:LEU:HB3	1:A:902:ILE:HG12	1.95	0.48
1:A:249:ASP:O	1:A:263:ALA:HB1	2.13	0.47
1:A:231:PRO:HB3	1:A:307:TRP:HZ2	1.79	0.47
1:A:336:TRP:O	1:A:340:ILE:HG22	2.14	0.47
1:A:362:PHE:HB2	1:A:369:ILE:HG22	1.96	0.47
1:A:232:ILE:HD12	1:A:232:ILE:H	1.80	0.47
1:A:707:PHE:CZ	1:A:846:MET:HA	2.49	0.47
1:A:311:ILE:O	1:A:341:HIS:NE2	2.39	0.47
1:A:1030:LEU:O	1:A:1034:VAL:HG12	2.15	0.47
1:A:1062:ARG:HA	1:A:1065:GLU:HG2	1.95	0.47
1:A:435:ILE:HG21	1:A:443:VAL:HG21	1.97	0.47
1:A:314:LEU:HD13	1:A:320:TYR:HE1	1.79	0.46
1:A:627:LEU:HD21	1:A:638:MET:HE3	1.96	0.46
1:A:966:SER:HB3	1:A:969:ILE:HD12	1.97	0.46
1:A:665:GLU:HA	1:A:668:ALA:HB3	1.98	0.46
1:A:760:SER:N	1:A:779:PRO:HD3	2.30	0.46
1:A:428:ILE:O	1:A:432:ILE:HD12	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:254:THR:HG22	1:A:269:THR:HG23	1.97	0.46
1:A:565:PRO:HB3	1:A:605:ILE:HD11	1.98	0.46
1:A:815:SER:HB3	1:A:818:GLU:CD	2.41	0.46
1:A:216:ILE:O	1:A:220:LEU:HG	2.17	0.45
1:A:168:LYS:HA	1:A:169:PRO:HD3	1.81	0.45
1:A:253:MET:HE2	1:A:266:LEU:HD22	1.98	0.45
1:A:449:SER:HB3	1:A:452:GLU:HG2	1.98	0.45
1:A:235:LEU:HD13	1:A:543:LEU:HB2	1.99	0.45
1:A:773:MET:HE2	1:A:798:CYS:SG	2.57	0.45
1:A:1009:VAL:O	1:A:1012:GLU:HG2	2.17	0.45
1:A:499:LEU:HG	1:A:503:ARG:HH22	1.80	0.44
1:A:1078:MET:HE2	1:A:1078:MET:HB3	1.88	0.44
1:A:566:LEU:O	1:A:605:ILE:HG12	2.17	0.44
1:A:663:GLN:HG2	1:A:895:ILE:CD1	2.47	0.44
1:A:340:ILE:HD12	1:A:641:ARG:HB3	1.99	0.44
1:A:898:LYS:O	1:A:902:ILE:HG13	2.17	0.44
1:A:1027:LYS:HB3	1:A:1029:GLN:OE1	2.18	0.44
1:A:463:MET:H	1:A:463:MET:HG3	1.63	0.44
1:A:240:TYR:CD1	1:A:252:LEU:HB2	2.53	0.44
1:A:315:PRO:O	1:A:318:VAL:HG22	2.18	0.43
1:A:712:ARG:NH1	1:A:804:GLN:O	2.46	0.43
1:A:231:PRO:HA	1:A:303:ARG:HH22	1.83	0.43
1:A:1021:GLU:HA	1:A:1023:VAL:HG22	2.00	0.43
1:A:982:LYS:HE2	1:A:1027:LYS:HE3	1.99	0.43
1:A:1044:SER:OG	2:A:1204:HOH:O	2.21	0.43
1:A:760:SER:HB3	1:A:777:ILE:HG13	2.00	0.43
1:A:963:ASN:O	1:A:1086:LYS:NZ	2.43	0.43
1:A:1008:LYS:HB3	1:A:1019:GLU:HG3	1.99	0.43
1:A:1028:TRP:HA	1:A:1031:MET:HG3	2.01	0.43
1:A:870:ASN:HA	1:A:871:PRO:HD3	1.89	0.43
1:A:443:VAL:HG22	1:A:549:THR:HB	2.01	0.43
1:A:1001:ALA:O	1:A:1005:ILE:HG13	2.19	0.43
1:A:258:THR:HG22	1:A:261:PRO:HG3	2.01	0.43
1:A:1003:ALA:HB3	1:A:1023:VAL:HG12	2.00	0.43
1:A:285:ARG:O	1:A:317:LYS:NZ	2.51	0.43
1:A:634:SER:O	1:A:637:TYR:HB3	2.19	0.42
1:A:913:GLU:OE2	1:A:917:ARG:NH2	2.34	0.42
1:A:936:LYS:HZ2	1:A:958:PHE:HD2	1.65	0.42
1:A:225:ARG:NH2	1:A:266:LEU:HD11	2.34	0.42
1:A:314:LEU:HD13	1:A:320:TYR:CE1	2.53	0.42
1:A:972:CYS:HA	1:A:1034:VAL:CG1	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:304:GLY:HA3	1:A:616:ALA:HB3	2.00	0.42
1:A:511:SER:HB3	1:A:1059:ARG:NH2	2.34	0.42
1:A:978:ILE:HG13	1:A:979:PHE:N	2.35	0.42
1:A:983:ILE:O	1:A:1029:GLN:HG2	2.20	0.42
1:A:133:PHE:O	1:A:585:ASP:N	2.53	0.42
1:A:445:VAL:HG22	1:A:551:VAL:HB	2.01	0.42
1:A:329:ASN:HB2	1:A:332:GLN:HB3	2.02	0.42
1:A:517:LEU:HD23	1:A:517:LEU:HA	1.86	0.42
1:A:760:SER:HA	1:A:786:ASN:O	2.20	0.42
1:A:442:PRO:HG2	1:A:547:ALA:HA	2.02	0.41
1:A:499:LEU:HG	1:A:503:ARG:NH2	2.35	0.41
1:A:778:MET:HE3	1:A:778:MET:HB2	1.91	0.41
1:A:561:GLN:HE21	1:A:561:GLN:CA	2.33	0.41
1:A:1067:LEU:O	1:A:1071:MET:HG2	2.20	0.41
1:A:790:GLU:OE1	1:A:819:LYS:NZ	2.52	0.41
1:A:1004:ARG:O	1:A:1008:LYS:HG2	2.21	0.41
1:A:180:LYS:HD3	1:A:180:LYS:HA	1.77	0.41
1:A:336:TRP:CG	1:A:643:PHE:HD1	2.39	0.41
1:A:929:ASP:C	1:A:931:GLU:H	2.27	0.41
1:A:207:GLY:O	1:A:210:VAL:HG12	2.20	0.41
1:A:1056:SER:O	1:A:1060:LEU:HG	2.20	0.41
1:A:452:GLU:O	1:A:456:MET:HG3	2.21	0.41
1:A:763:PHE:HB3	1:A:775:GLU:O	2.21	0.41
1:A:947:GLU:OE1	1:A:1025:SER:HB3	2.21	0.41
1:A:303:ARG:O	1:A:307:TRP:HD1	2.04	0.41
1:A:569:SER:O	1:A:572:ILE:HG13	2.21	0.40
1:A:431:ILE:O	1:A:435:ILE:HG13	2.21	0.40
1:A:709:GLN:HB3	1:A:806:ARG:CZ	2.51	0.40
1:A:157:LEU:HA	1:A:157:LEU:HD12	1.72	0.40
1:A:900:LYS:HA	1:A:900:LYS:HD2	1.81	0.40
1:A:676:ILE:H	1:A:676:ILE:HG13	1.62	0.40
1:A:855:LYS:HG3	1:A:859:LYS:NZ	2.36	0.40
1:A:441:GLN:HG2	1:A:531:LYS:HB3	2.04	0.40
1:A:516:ILE:O	1:A:520:THR:OG1	2.24	0.40
1:A:989:LYS:O	1:A:993:ALA:N	2.55	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	957/993 (96%)	898 (94%)	52 (5%)	7 (1%)	18	49

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	167	HIS
1	A	743	PRO
1	A	294	GLU
1	A	785	LYS
1	A	1097	ASP
1	A	1102	ASN
1	A	606	VAL

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	843/867 (97%)	809 (96%)	34 (4%)	28	60

All (34) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	127	VAL
1	A	128	THR
1	A	166	GLU
1	A	189	VAL

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Mol	Chain	Res	Type
1	A	198	VAL
1	A	233	LYS
1	A	271	GLU
1	A	287	VAL
1	A	372	ILE
1	A	451	ARG
1	A	463	MET
1	A	508	VAL
1	A	541	ILE
1	A	556	THR
1	A	561	GLN
1	A	600	GLU
1	A	612	LYS
1	A	630	ILE
1	A	633	ILE
1	A	659	LEU
1	A	676	ILE
1	A	691	ASN
1	A	755	VAL
1	A	813	LEU
1	A	844	GLU
1	A	850	ASP
1	A	860	ILE
1	A	874	ASN
1	A	897	GLU
1	A	932	VAL
1	A	946	THR
1	A	981	GLU
1	A	1048	LYS
1	A	1058	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	150	GLN
1	A	244	GLN
1	A	385	ASN
1	A	554	GLN
1	A	561	GLN
1	A	702	GLN
1	A	764	ASN
1	A	873	HIS

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Mol	Chain	Res	Type
1	A	928	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 oligosaccharides 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, 95th 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 ²)	Q<0.9
1	A	961/993 (96%)	-0.18	5 (0%) 87 73	59, 94, 132, 168	0

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1061	PHE	3.6
1	A	1106	LEU	2.6
1	A	114	ILE	2.5
1	A	116	THR	2.2
1	A	115	MET	2.2

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 oligosaccharides 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.