



Full wwPDB X-ray Structure Validation Report ⓘ

May 28, 2020 – 08:35 pm BST

PDB ID : 1U0B
Title : Crystal structure of cysteinyl-tRNA synthetase binary complex with tRNACys
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Deposited on : 2004-07-13
Resolution : 2.30 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 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	:	2.11
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

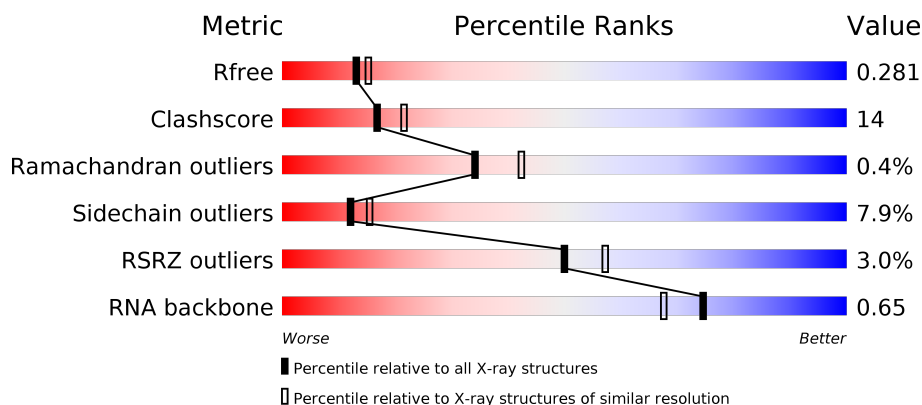
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)
RNA backbone	3102	1090 (2.70-1.90)

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 ≥ 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	74	<div> <div>4%</div> <div> <div></div> <div>55%</div> <div>22%</div> <div>22%</div> </div> <div>.</div> </div>
2	B	461	<div> <div>3%</div> <div> <div></div> <div>73%</div> <div>23%</div> </div> <div>.</div> </div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 5199 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 RNA chain called CysteinyI-tRNA synthetase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	74	Total	C	N	O	P	0	0	0
			1576	703	280	519	74			

- Molecule 2 is a protein called cysteinyl tRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	461	Total	C	N	O	S	0	0	0
			3518	2215	619	658	26			

- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total	Zn	0	0
			1	1		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	22	Total	O	0	0
			22	22		
4	B	82	Total	O	0	0
			82	82		

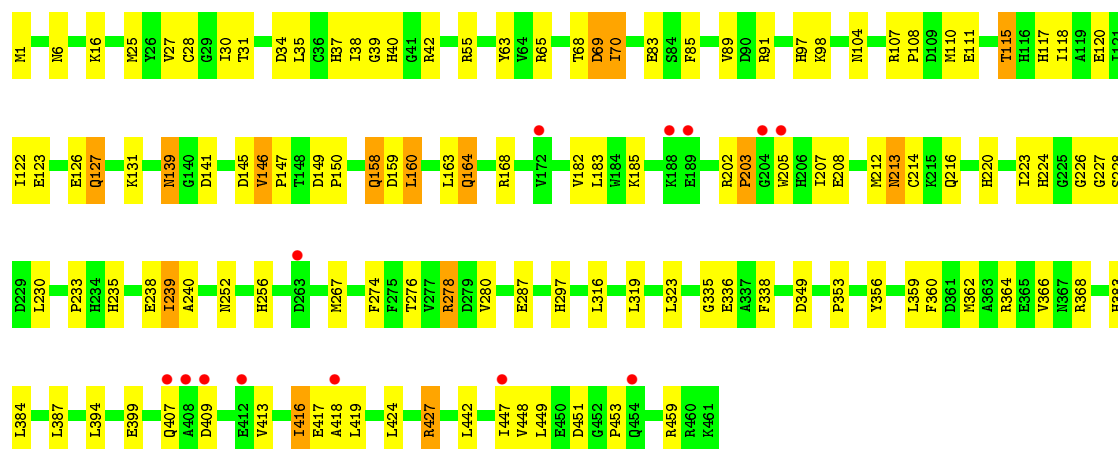
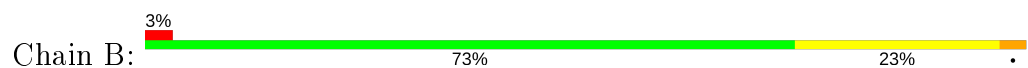
3 Residue-property plots

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: Cysteinyl-tRNA synthetase



• Molecule 2: cysteinyl tRNA



4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	129.49 Å 129.49 Å 91.02 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	24.91 – 2.30 48.86 – 2.30	Depositor EDS
% Data completeness (in resolution range)	90.2 (24.91-2.30) 90.2 (48.86-2.30)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	7.01 (at 2.29 Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.233 , 0.277 0.236 , 0.281	Depositor DCC
R_{free} test set	1578 reflections (4.57%)	wwPDB-VP
Wilson B-factor (Å ²)	37.0	Xtriage
Anisotropy	0.445	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 45.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	5199	wwPDB-VP
Average B, all atoms (Å ²)	42.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.37% 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](#)

Bond lengths and bond angles in the following residue types are not validated in this section: ZN

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	0.51	1/1760 (0.1%)	0.72	0/2739
2	B	0.44	0/3596	0.61	0/4876
All	All	0.46	1/5356 (0.0%)	0.65	0/7615

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	A	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1	G	OP3-P	-7.46	1.52	1.61

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	60	U	Sidechain

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	1576	0	799	42	0
2	B	3518	0	3276	96	0
3	B	1	0	0	0	0
4	A	22	0	0	0	0
4	B	82	0	0	6	0
All	All	5199	0	4075	129	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 14.

All (129) 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:44:C:H2'	1:A:45:U:H5''	1.44	0.95
2:B:287:GLU:HG2	2:B:316:LEU:HD21	1.54	0.86
1:A:44:C:C2'	1:A:45:U:H5''	2.05	0.85
2:B:38:ILE:HD11	2:B:280:VAL:HG21	1.62	0.82
2:B:65:ARG:HG2	2:B:65:ARG:HH11	1.51	0.76
1:A:75:C:O2'	1:A:76:A:OP1	2.06	0.73
2:B:69:ASP:OD2	2:B:115:THR:HB	1.91	0.70
2:B:213:ASN:HD22	2:B:214:CYS:N	1.89	0.70
2:B:159:ASP:O	2:B:163:LEU:HB2	1.92	0.70
1:A:76:A:O3'	2:B:230:LEU:HD11	1.92	0.69
1:A:45:U:H6	1:A:45:U:H5'	1.57	0.69
1:A:76:A:H5'	2:B:30:ILE:HG22	1.73	0.69
1:A:60:U:O2'	1:A:61:C:OP1	2.10	0.68
1:A:18:G:H2'	1:A:57:G:N2	2.09	0.67
2:B:205:TRP:O	4:B:463:HOH:O	2.13	0.66
2:B:37:HIS:HD2	2:B:39:GLY:H	1.45	0.65
2:B:239:ILE:HG13	2:B:240:ALA:N	2.11	0.65
2:B:28:CYS:SG	2:B:235:HIS:HE1	2.21	0.63
2:B:267:MET:HG3	2:B:274:PHE:HA	1.80	0.63
1:A:58:A:O2'	1:A:59:C:O5'	2.15	0.62
2:B:83:GLU:CD	2:B:91:ARG:HH22	2.03	0.61
1:A:18:G:H2'	1:A:57:G:H22	1.64	0.60
1:A:73:U:H1'	2:B:168:ARG:NH2	2.17	0.60
2:B:323:LEU:HD11	2:B:394:LEU:HD13	1.85	0.58
1:A:36:A:N6	2:B:451:ASP:HB2	2.19	0.57
2:B:37:HIS:HD2	2:B:39:GLY:N	2.03	0.57
2:B:37:HIS:H	2:B:40:HIS:HD2	1.53	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:235:HIS:HD2	2:B:256:HIS:NE2	2.03	0.56
2:B:37:HIS:H	2:B:40:HIS:CD2	2.24	0.55
2:B:97:HIS:HB3	2:B:107:ARG:NH2	2.21	0.55
2:B:407:GLN:C	2:B:409:ASP:H	2.09	0.55
2:B:65:ARG:HG2	2:B:65:ARG:NH1	2.21	0.55
1:A:53:G:H2'	1:A:54:U:C6	2.42	0.55
2:B:297:HIS:HE1	2:B:349:ASP:O	1.90	0.54
2:B:416:ILE:C	2:B:418:ALA:H	2.11	0.54
1:A:58:A:HO2'	1:A:59:C:P	2.31	0.54
2:B:335:GLY:H	2:B:383:HIS:CD2	2.26	0.53
2:B:419:LEU:HB2	2:B:442:LEU:HD21	1.90	0.53
2:B:183:LEU:O	2:B:203:PRO:O	2.27	0.53
2:B:442:LEU:HB3	2:B:447:ILE:HG23	1.91	0.53
1:A:55:U:H2'	1:A:57:G:OP2	2.08	0.52
2:B:158:GLN:HB3	2:B:163:LEU:HD13	1.91	0.52
2:B:224:HIS:HE1	2:B:238:GLU:OE1	1.93	0.52
1:A:58:A:O2'	1:A:59:C:P	2.67	0.52
2:B:427:ARG:HH21	2:B:427:ARG:HG2	1.74	0.51
1:A:36:A:H61	2:B:451:ASP:HB2	1.75	0.51
2:B:83:GLU:OE1	2:B:91:ARG:NH2	2.42	0.51
2:B:267:MET:CG	2:B:274:PHE:HA	2.40	0.51
2:B:416:ILE:O	2:B:419:LEU:HG	2.10	0.51
2:B:37:HIS:HA	2:B:276:THR:HA	1.91	0.51
2:B:139:ASN:HD21	2:B:141:ASP:HB2	1.75	0.51
1:A:58:A:H2'	1:A:60:U:OP2	2.11	0.51
1:A:75:C:HO2'	1:A:76:A:P	2.30	0.51
1:A:18:G:O2'	1:A:19:G:P	2.69	0.51
1:A:65:A:H2'	1:A:66:A:C8	2.46	0.51
2:B:419:LEU:HD12	2:B:442:LEU:CD2	2.41	0.50
2:B:213:ASN:C	2:B:213:ASN:HD22	2.14	0.50
2:B:208:GLU:O	2:B:212:MET:HE2	2.11	0.50
2:B:362:MET:HE1	2:B:387:LEU:HD12	1.93	0.50
2:B:182:VAL:HG11	2:B:185:LYS:HB2	1.92	0.49
1:A:58:A:H4'	1:A:59:C:OP1	2.12	0.49
2:B:146:VAL:N	2:B:147:PRO:CD	2.75	0.49
2:B:413:VAL:O	2:B:417:GLU:HG2	2.12	0.49
2:B:65:ARG:O	2:B:111:GLU:HA	2.13	0.49
2:B:145:ASP:OD1	2:B:147:PRO:HD2	2.13	0.49
2:B:319:LEU:HG	2:B:360:PHE:CE2	2.48	0.48
1:A:30:G:O2'	1:A:31:A:H5'	2.14	0.48
2:B:122:ILE:HG13	2:B:123:GLU:N	2.27	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:122:ILE:O	2:B:126:GLU:HG3	2.13	0.48
1:A:19:G:N2	1:A:56:C:N3	2.62	0.48
2:B:427:ARG:HG2	2:B:427:ARG:NH2	2.29	0.48
2:B:207:ILE:HG23	2:B:208:GLU:N	2.29	0.47
2:B:448:VAL:HG11	2:B:459:ARG:CZ	2.44	0.47
1:A:76:A:O3'	2:B:230:LEU:CD1	2.62	0.47
1:A:18:G:O2'	1:A:19:G:OP1	2.32	0.47
1:A:73:U:H1'	2:B:168:ARG:CZ	2.44	0.46
1:A:34:G:N7	2:B:427:ARG:NH2	2.64	0.46
1:A:44:C:C3'	1:A:45:U:H5''	2.44	0.46
2:B:117:HIS:HB3	2:B:120:GLU:HG2	1.98	0.46
2:B:97:HIS:HB3	2:B:107:ARG:HH21	1.80	0.46
1:A:53:G:H2'	1:A:54:U:H6	1.79	0.46
2:B:160:LEU:O	2:B:164:GLN:HB2	2.15	0.46
2:B:226:GLY:O	2:B:256:HIS:HA	2.16	0.46
2:B:362:MET:HE2	2:B:362:MET:HB2	1.70	0.46
2:B:34:ASP:CG	2:B:35:LEU:H	2.19	0.46
1:A:48:G:O2'	1:A:49:U:P	2.74	0.46
2:B:30:ILE:HG13	4:B:515:HOH:O	2.15	0.46
2:B:55:ARG:NE	4:B:499:HOH:O	2.29	0.45
1:A:7:U:C4'	1:A:8:U:OP2	2.64	0.45
2:B:108:PRO:HD3	4:B:525:HOH:O	2.16	0.45
2:B:139:ASN:ND2	2:B:141:ASP:H	2.13	0.45
2:B:70:ILE:HD12	4:B:537:HOH:O	2.18	0.44
2:B:139:ASN:N	2:B:139:ASN:HD22	2.15	0.44
2:B:220:HIS:HE1	2:B:252:ASN:ND2	2.16	0.44
1:A:19:G:H5''	1:A:20:U:OP2	2.18	0.44
1:A:7:U:H4'	1:A:8:U:OP2	2.18	0.44
2:B:413:VAL:O	2:B:416:ILE:HG13	2.18	0.43
2:B:85:PHE:O	2:B:89:VAL:HG13	2.17	0.43
2:B:25:MET:HA	2:B:223:ILE:O	2.18	0.43
2:B:117:HIS:HB3	2:B:120:GLU:CG	2.48	0.43
1:A:8:U:O2	1:A:46:A:H2	2.01	0.43
1:A:65:A:H2'	1:A:66:A:H8	1.83	0.43
2:B:419:LEU:HD12	2:B:442:LEU:HD23	2.00	0.43
2:B:448:VAL:HG22	2:B:449:LEU:N	2.33	0.43
2:B:98:LYS:HD3	2:B:278:ARG:NH1	2.34	0.42
2:B:202:ARG:HB2	2:B:203:PRO:HD2	2.00	0.42
2:B:362:MET:O	2:B:366:VAL:HG23	2.20	0.42
2:B:118:ILE:O	2:B:122:ILE:HG23	2.19	0.42
2:B:127:GLN:O	2:B:131:LYS:HG3	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:30:G:C2'	1:A:31:A:H5'	2.50	0.42
1:A:58:A:O2'	1:A:60:U:H5	2.03	0.42
1:A:9:A:O2'	1:A:45:U:H2'	2.20	0.42
2:B:336:GLU:H	2:B:336:GLU:CD	2.22	0.42
2:B:362:MET:CE	2:B:387:LEU:HD12	2.50	0.42
2:B:448:VAL:HG23	4:B:471:HOH:O	2.18	0.42
2:B:353:PRO:O	2:B:356:TYR:HB2	2.20	0.41
2:B:117:HIS:O	2:B:120:GLU:HG2	2.20	0.41
2:B:419:LEU:HD12	2:B:442:LEU:HD21	2.03	0.41
2:B:31:THR:HA	2:B:68:THR:HB	2.02	0.41
2:B:235:HIS:O	2:B:239:ILE:HG23	2.21	0.41
1:A:18:G:H4'	1:A:19:G:OP1	2.20	0.41
1:A:20:U:C6	1:A:20:U:H3'	2.56	0.41
2:B:27:VAL:HG13	2:B:63:TYR:HE1	1.85	0.41
2:B:70:ILE:HG23	2:B:85:PHE:CE1	2.55	0.41
2:B:110:MET:SD	2:B:216:GLN:CD	2.99	0.41
1:A:76:A:H2'	2:B:227:GLY:HA3	2.02	0.41
2:B:407:GLN:C	2:B:409:ASP:N	2.72	0.40
2:B:149:ASP:HA	2:B:150:PRO:HD3	1.90	0.40
2:B:338:PHE:HB3	2:B:362:MET:CE	2.51	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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
2	B	459/461 (100%)	435 (95%)	22 (5%)	2 (0%)	34 42

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	453	PRO

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Mol	Chain	Res	Type
2	B	203	PRO

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	
2	B	340/381 (89%)	313 (92%)	27 (8%)	12	15

All (27) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	1	MET
2	B	6	ASN
2	B	16	LYS
2	B	42	ARG
2	B	69	ASP
2	B	70	ILE
2	B	104	ASN
2	B	115	THR
2	B	127	GLN
2	B	139	ASN
2	B	146	VAL
2	B	158	GLN
2	B	160	LEU
2	B	164	GLN
2	B	213	ASN
2	B	228	SER
2	B	233	PRO
2	B	239	ILE
2	B	278	ARG
2	B	359	LEU
2	B	364	ARG
2	B	368	ARG
2	B	384	LEU
2	B	399	GLU
2	B	416	ILE

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Mol	Chain	Res	Type
2	B	424	LEU
2	B	427	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	6	ASN
2	B	37	HIS
2	B	40	HIS
2	B	81	ASN
2	B	104	ASN
2	B	116	HIS
2	B	139	ASN
2	B	213	ASN
2	B	220	HIS
2	B	224	HIS
2	B	235	HIS
2	B	252	ASN
2	B	297	HIS
2	B	383	HIS
2	B	396	GLN
2	B	403	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	73/74 (98%)	15 (20%)	8 (10%)

All (15) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	7	U
1	A	8	U
1	A	9	A
1	A	10	A
1	A	18	G
1	A	19	G
1	A	20	U
1	A	22	A
1	A	45	U

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Mol	Chain	Res	Type
1	A	46	A
1	A	49	U
1	A	59	C
1	A	61	C
1	A	74	C
1	A	76	A

All (8) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	7	U
1	A	9	A
1	A	18	G
1	A	48	G
1	A	58	A
1	A	60	U
1	A	73	U
1	A	75	C

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](#)

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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 [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	74/74 (100%)	0.42	3 (4%) 37 44	36, 52, 78, 86	0
2	B	461/461 (100%)	0.33	13 (2%) 53 60	23, 35, 58, 76	0
All	All	535/535 (100%)	0.34	16 (2%) 50 57	23, 37, 67, 86	0

All (16) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	408	ALA	9.2
2	B	407	GLN	4.9
2	B	172	VAL	3.3
2	B	189	GLU	3.2
1	A	21	U	2.9
2	B	412	GLU	2.7
2	B	454	GLN	2.7
2	B	205	TRP	2.7
1	A	20	U	2.4
1	A	63	G	2.3
2	B	263	ASP	2.3
2	B	447	ILE	2.3
2	B	188	LYS	2.2
2	B	409	ASP	2.2
2	B	204	GLY	2.2
2	B	418	ALA	2.1

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](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	ZN	B	462	1/1	0.99	0.15	33,33,33,33	0

6.5 Other polymers [i](#)

There are no such residues in this entry.