



Full wwPDB X-ray Structure Validation Report

Feb 28, 2014 – 05:43 AM GMT

PDB ID : 2PY9
Title : Protein-RNA Interaction involving KH1 domain from Human Poly(C)-Binding Protein-2
Authors : James, T.L.; Du, Z.; Lee, J.K.
Deposited on : 2007-05-15
Resolution : 2.56 Å(reported)

This is a full wwPDB validation report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

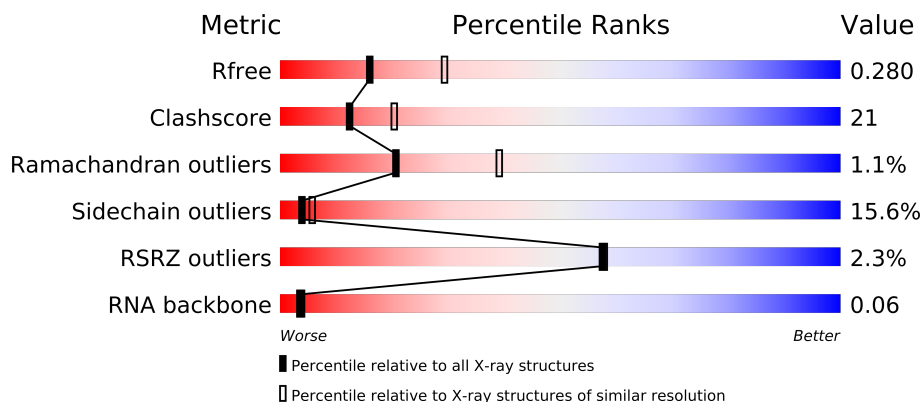
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 2.56 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}	66092	2347 (2.60-2.52)
Clashscore	79885	2876 (2.60-2.52)
Ramachandran outliers	78287	2826 (2.60-2.52)
Sidechain outliers	78261	2826 (2.60-2.52)
RSRZ outliers	66119	2347 (2.60-2.52)
RNA backbone	1838	1008 (3.10-2.02)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	E	12	
1	F	12	
2	A	73	
2	B	73	
2	C	73	
2	D	73	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 2669 atoms, of which 0 are hydrogen and 0 are deuterium.

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 12-mer C-rich strand of human telomeric RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	E	12	Total	C	N	O	P	0	0	0
			245	112	42	80	11			
1	F	12	Total	C	N	O	P	0	0	0
			245	112	42	80	11			

- Molecule 2 is a protein called Poly(rC)-binding protein 2.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	A	72	Total	C	N	O	S	Se	0	0	0
			550	346	98	102	1	3			
2	B	69	Total	C	N	O	S	Se	0	0	0
			526	331	93	98	1	3			
2	C	69	Total	C	N	O	S	Se	0	0	0
			526	331	93	98	1	3			
2	D	69	Total	C	N	O	S	Se	0	0	0
			526	331	93	98	1	3			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	10	LYS	-	CLONING ARTIFACT	UNP Q15366
A	20	MSE	MET	MODIFIED RESIDUE	UNP Q15366
A	39	MSE	MET	MODIFIED RESIDUE	UNP Q15366
A	74	MSE	MET	MODIFIED RESIDUE	UNP Q15366
B	10	LYS	-	CLONING ARTIFACT	UNP Q15366
B	20	MSE	MET	MODIFIED RESIDUE	UNP Q15366
B	39	MSE	MET	MODIFIED RESIDUE	UNP Q15366
B	74	MSE	MET	MODIFIED RESIDUE	UNP Q15366
C	10	LYS	-	CLONING ARTIFACT	UNP Q15366
C	20	MSE	MET	MODIFIED RESIDUE	UNP Q15366
C	39	MSE	MET	MODIFIED RESIDUE	UNP Q15366
C	74	MSE	MET	MODIFIED RESIDUE	UNP Q15366
D	10	LYS	-	CLONING ARTIFACT	UNP Q15366

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Chain	Residue	Modelled	Actual	Comment	Reference
D	20	MSE	MET	MODIFIED RESIDUE	UNP Q15366
D	39	MSE	MET	MODIFIED RESIDUE	UNP Q15366
D	74	MSE	MET	MODIFIED RESIDUE	UNP Q15366

- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	9	Total O 9 9	0	0
3	B	14	Total O 14 14	0	0
3	C	11	Total O 11 11	0	0
3	D	10	Total O 10 10	0	0
3	E	3	Total O 3 3	0	0
3	F	4	Total O 4 4	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 errors 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.

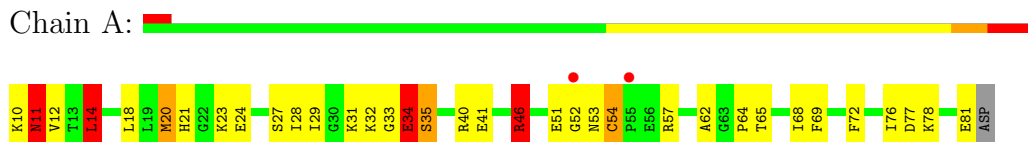
- Molecule 1: 12-mer C-rich strand of human telomeric RNA



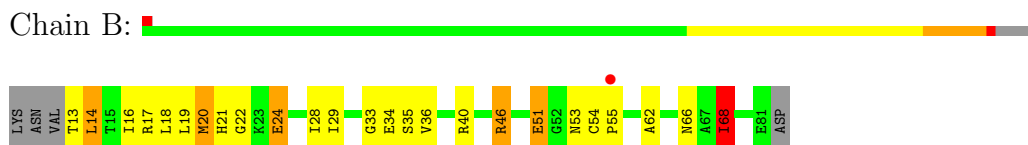
- Molecule 1: 12-mer C-rich strand of human telomeric RNA



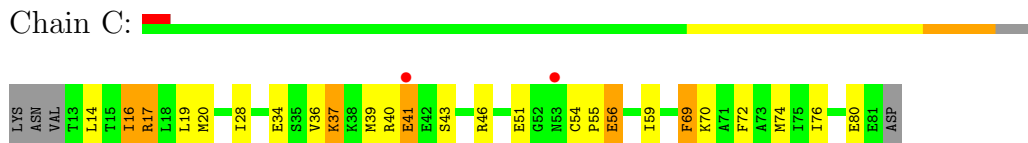
- Molecule 2: Poly(rC)-binding protein 2



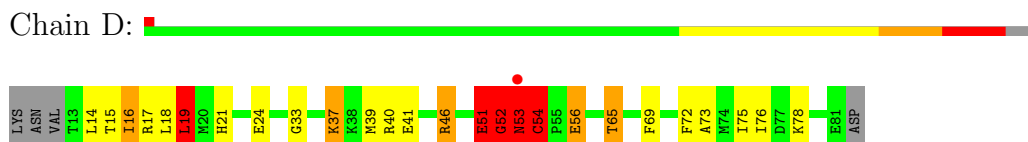
- Molecule 2: Poly(rC)-binding protein 2



- Molecule 2: Poly(rC)-binding protein 2



- Molecule 2: Poly(rC)-binding protein 2



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	92.01Å 58.70Å 71.50Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.00 – 2.56 71.50 – 2.56	Depositor EDS
% Data completeness (in resolution range)	94.2 (40.00-2.56) 94.2 (71.50-2.56)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.11 (at 2.55Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.218 , 0.269 0.238 , 0.280	Depositor DCC
R_{free} test set	591 reflections (5.07%)	DCC
Wilson B-factor (Å ²)	52.1	Xtriage
Anisotropy	0.279	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 17.3	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 12252 reflections	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	2669	wwPDB-VP
Average B, all atoms (Å ²)	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 15.59% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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	E	2.45	12/272 (4.4%)	4.09	88/420 (21.0%)
1	F	2.48	17/272 (6.2%)	3.83	72/420 (17.1%)
2	A	1.66	8/551 (1.5%)	1.46	10/729 (1.4%)
2	B	1.48	3/527 (0.6%)	1.53	6/697 (0.9%)
2	C	1.41	5/527 (0.9%)	1.49	8/697 (1.1%)
2	D	1.52	6/527 (1.1%)	1.49	7/697 (1.0%)
All	All	1.75	51/2676 (1.9%)	2.31	191/3660 (5.2%)

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
2	D	0	2

All (51) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	54	CYS	CB-SG	-10.44	1.64	1.82
2	D	51	GLU	CB-CG	-9.70	1.33	1.52
1	F	8	A	N9-C4	9.40	1.43	1.37
2	A	41	GLU	CG-CD	8.82	1.65	1.51
1	E	2	A	P-O5'	8.63	1.68	1.59
2	B	54	CYS	CB-SG	-8.25	1.68	1.82
1	E	9	C	C3'-O3'	8.08	1.53	1.42
2	D	54	CYS	CB-SG	-8.00	1.68	1.82
1	F	8	A	C6-N1	7.65	1.41	1.35
1	F	9	C	N1-C2	7.34	1.47	1.40
1	F	6	U	C2-N3	7.24	1.42	1.37
2	C	56	GLU	CB-CG	-6.67	1.39	1.52
2	B	46	ARG	CB-CG	-6.56	1.34	1.52
2	A	46	ARG	CZ-NH2	-6.56	1.24	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	51	GLU	CG-CD	-6.38	1.42	1.51
2	C	34	GLU	CG-CD	6.33	1.61	1.51
2	C	51	GLU	CB-CG	-6.26	1.40	1.52
1	E	9	C	P-O5'	6.24	1.66	1.59
1	E	8	A	O5'-C5'	6.21	1.54	1.44
2	B	46	ARG	CZ-NH2	-6.20	1.25	1.33
1	F	7	A	C8-N7	6.07	1.35	1.31
1	E	7	A	C8-N7	5.99	1.35	1.31
1	F	10	C	C1'-N1	5.97	1.57	1.48
1	F	8	A	C8-N7	5.93	1.35	1.31
1	E	11	C	P-O5'	5.91	1.65	1.59
1	F	2	A	N3-C4	-5.87	1.31	1.34
1	F	7	A	C6-N1	5.84	1.39	1.35
2	A	35	SER	CB-OG	-5.82	1.34	1.42
1	E	9	C	C2-O2	5.76	1.29	1.24
1	E	6	U	C2-O2	5.70	1.27	1.22
1	F	5	C	N1-C6	5.67	1.40	1.37
2	A	81	GLU	CG-CD	5.67	1.60	1.51
1	E	10	C	C3'-O3'	5.60	1.50	1.42
1	F	11	C	P-O5'	5.59	1.65	1.59
2	A	69	PHE	CB-CG	-5.56	1.42	1.51
1	E	2	A	O5'-C5'	5.52	1.53	1.44
2	D	37	LYS	CB-CG	-5.44	1.37	1.52
1	F	9	C	N3-C4	5.43	1.37	1.33
2	D	72	PHE	CD1-CE1	5.41	1.50	1.39
1	E	3	C	C3'-O3'	-5.40	1.34	1.42
1	F	7	A	O4'-C1'	5.40	1.48	1.41
2	A	69	PHE	CE2-CZ	5.27	1.47	1.37
2	D	16	ILE	CA-CB	5.25	1.67	1.54
1	F	3	C	N3-C4	5.23	1.37	1.33
1	E	7	A	N9-C8	5.20	1.42	1.37
1	F	10	C	C2-N3	5.19	1.40	1.35
1	F	10	C	N3-C4	5.19	1.37	1.33
2	A	34	GLU	CB-CG	-5.16	1.42	1.52
1	F	4	C	N1-C6	5.14	1.40	1.37
2	D	72	PHE	CE2-CZ	5.13	1.47	1.37
2	C	41	GLU	CG-CD	5.05	1.59	1.51

All (191) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	10	C	O5'-P-OP2	-18.63	88.34	110.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	4	C	O4'-C1'-N1	15.28	120.42	108.20
1	E	10	C	O4'-C1'-C2'	-14.44	91.36	105.80
2	B	46	ARG	NE-CZ-NH1	13.51	127.05	120.30
1	F	11	C	O4'-C1'-N1	13.32	118.86	108.20
1	E	2	A	O4'-C1'-N9	12.87	118.50	108.20
1	E	2	A	C3'-C2'-C1'	-12.16	91.78	101.50
1	F	11	C	OP1-P-OP2	11.82	137.33	119.60
1	E	4	C	N1-C2-O2	11.65	125.89	118.90
1	F	7	A	C5'-C4'-O4'	11.45	122.84	109.10
1	F	4	C	C4'-C3'-C2'	-11.26	91.34	102.60
1	F	10	C	C5-C6-N1	11.21	126.60	121.00
1	F	8	A	N1-C2-N3	-11.05	123.77	129.30
1	E	11	C	C4'-C3'-C2'	-10.76	91.84	102.60
1	E	1	A	C3'-C2'-C1'	-10.72	92.92	101.50
1	E	5	C	C3'-C2'-C1'	10.66	110.03	101.50
1	F	6	U	C5-C6-N1	10.63	128.01	122.70
1	F	12	U	C5-C6-N1	10.43	127.92	122.70
1	E	5	C	N1-C2-O2	10.37	125.12	118.90
1	E	9	C	O5'-P-OP2	10.33	123.10	110.70
2	C	46	ARG	NE-CZ-NH1	-10.24	115.18	120.30
1	E	12	U	O4'-C1'-N1	10.17	116.33	108.20
2	C	46	ARG	NE-CZ-NH2	10.06	125.33	120.30
1	F	9	C	N3-C4-C5	9.65	125.76	121.90
1	F	6	U	O4'-C1'-N1	9.49	115.80	108.20
2	A	46	ARG	NE-CZ-NH2	9.45	125.03	120.30
1	F	4	C	O4'-C1'-C2'	-9.38	96.42	105.80
1	F	2	A	O4'-C1'-N9	9.28	115.62	108.20
1	F	11	C	N1-C1'-C2'	-9.13	101.96	112.00
1	F	3	C	N1-C2-O2	-9.01	113.50	118.90
1	E	11	C	N1-C2-O2	8.87	124.22	118.90
1	F	9	C	N1-C2-O2	8.77	124.16	118.90
1	E	11	C	O4'-C1'-N1	8.75	115.20	108.20
1	F	3	C	C5-C4-N4	-8.74	114.08	120.20
1	E	1	A	P-O3'-C3'	8.73	130.17	119.70
1	F	9	C	C5-C4-N4	-8.68	114.12	120.20
2	C	69	PHE	CB-CG-CD2	-8.66	114.73	120.80
1	E	9	C	N1-C2-N3	-8.57	113.20	119.20
1	E	10	C	C2-N1-C1'	8.40	128.04	118.80
1	E	5	C	N3-C2-O2	-8.23	116.14	121.90
1	E	11	C	N1-C1'-C2'	8.21	124.67	114.00
2	C	69	PHE	CB-CG-CD1	8.16	126.51	120.80
2	D	69	PHE	CB-CG-CD1	-8.12	115.12	120.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	6	U	C4-C5-C6	-8.09	114.85	119.70
1	E	3	C	O4'-C1'-N1	8.08	114.67	108.20
1	E	1	A	N9-C1'-C2'	8.03	124.43	114.00
1	F	6	U	N3-C2-O2	7.96	127.77	122.20
1	F	8	A	P-O3'-C3'	7.94	129.23	119.70
1	F	9	C	C3'-C2'-C1'	7.86	107.79	101.50
2	B	46	ARG	NE-CZ-NH2	-7.84	116.38	120.30
1	E	3	C	N1-C2-O2	7.80	123.58	118.90
1	E	10	C	C5'-C4'-O4'	-7.68	99.89	109.10
1	E	2	A	P-O5'-C5'	7.67	133.17	120.90
1	F	9	C	C6-N1-C1'	-7.67	111.60	120.80
1	E	8	A	O4'-C1'-N9	7.66	114.33	108.20
2	A	78	LYS	CD-CE-NZ	-7.65	94.10	111.70
1	E	3	C	C5-C6-N1	7.64	124.82	121.00
2	A	40	ARG	NE-CZ-NH1	7.57	124.08	120.30
1	F	12	U	C5'-C4'-O4'	7.55	118.16	109.10
1	E	9	C	C5'-C4'-O4'	7.48	118.08	109.10
1	F	12	U	C4-C5-C6	-7.48	115.21	119.70
1	E	10	C	OP1-P-OP2	7.47	130.81	119.60
1	F	11	C	C3'-C2'-C1'	7.44	107.45	101.50
1	F	6	U	C5-C4-O4	-7.43	121.44	125.90
1	E	10	C	C1'-O4'-C4'	7.35	115.78	109.90
1	E	9	C	N1-C2-O2	7.32	123.29	118.90
1	F	8	A	N1-C6-N6	7.32	122.99	118.60
1	F	11	C	C4-C5-C6	7.31	121.06	117.40
1	F	3	C	O4'-C1'-N1	7.31	114.05	108.20
1	E	9	C	C4'-C3'-C2'	-7.26	95.34	102.60
1	E	8	A	O5'-P-OP1	-7.22	99.20	105.70
1	E	12	U	C5'-C4'-O4'	7.16	117.69	109.10
1	F	3	C	N3-C4-C5	7.12	124.75	121.90
1	E	4	C	C6-N1-C2	7.08	123.13	120.30
1	F	3	C	C4-C5-C6	-7.06	113.87	117.40
1	E	6	U	C5-C6-N1	7.05	126.23	122.70
2	D	19	LEU	CB-CG-CD1	-7.03	99.04	111.00
1	F	3	C	N3-C2-O2	6.98	126.79	121.90
1	E	2	A	N1-C6-N6	6.97	122.78	118.60
1	E	3	C	C4-C5-C6	-6.95	113.93	117.40
1	F	6	U	C3'-C2'-C1'	6.94	107.05	101.50
2	D	56	GLU	CA-CB-CG	-6.87	98.30	113.40
1	F	9	C	O4'-C1'-C2'	-6.86	98.94	105.80
1	E	11	C	OP1-P-OP2	6.82	129.84	119.60
1	F	12	U	P-O5'-C5'	6.75	131.69	120.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	6	U	N3-C4-O4	6.69	124.08	119.40
1	F	10	C	O5'-P-OP2	-6.66	99.71	105.70
1	E	10	C	O4'-C1'-N1	-6.66	102.87	108.20
1	E	11	C	C2-N3-C4	6.53	123.17	119.90
2	B	68	ILE	CG1-CB-CG2	-6.52	97.06	111.40
2	B	34	GLU	OE1-CD-OE2	-6.50	115.50	123.30
2	D	37	LYS	CD-CE-NZ	-6.50	96.76	111.70
2	D	69	PHE	CB-CG-CD2	6.48	125.34	120.80
1	E	12	U	O5'-P-OP2	-6.44	99.90	105.70
1	E	5	C	O4'-C1'-N1	6.44	113.35	108.20
1	F	9	C	C2-N1-C1'	6.42	125.86	118.80
2	B	46	ARG	CB-CG-CD	-6.41	94.92	111.60
1	F	6	U	OP1-P-OP2	6.37	129.16	119.60
1	E	10	C	C6-N1-C1'	-6.33	113.20	120.80
1	E	8	A	N1-C6-N6	-6.32	114.81	118.60
1	E	11	C	O4'-C1'-C2'	-6.32	99.48	105.80
1	F	1	A	O4'-C1'-N9	6.30	113.24	108.20
1	E	7	A	C3'-C2'-C1'	6.30	106.54	101.50
1	E	9	C	C2-N3-C4	6.30	123.05	119.90
1	E	5	C	P-O3'-C3'	6.29	127.25	119.70
1	E	5	C	C5'-C4'-C3'	-6.28	105.94	116.00
1	F	10	C	C6-N1-C2	-6.27	117.79	120.30
2	C	40	ARG	NE-CZ-NH1	6.26	123.43	120.30
1	F	5	C	O3'-P-O5'	6.25	115.88	104.00
1	F	8	A	C2-N3-C4	6.24	113.72	110.60
1	F	3	C	C5'-C4'-O4'	6.21	116.56	109.10
1	E	12	U	C3'-C2'-C1'	6.20	106.46	101.50
1	E	6	U	O5'-P-OP2	-6.16	100.16	105.70
1	F	11	C	C5'-C4'-O4'	6.14	116.47	109.10
1	E	7	A	C6-N1-C2	-6.14	114.92	118.60
1	F	6	U	C1'-C2'-O2'	-6.12	92.25	110.60
1	E	11	C	C6-N1-C2	-6.10	117.86	120.30
2	D	18	LEU	CB-CG-CD1	-6.10	100.63	111.00
1	F	6	U	C4-C5-C6	-6.09	116.04	119.70
1	E	2	A	O5'-P-OP2	6.03	117.94	110.70
1	E	9	C	C5-C6-N1	6.03	124.01	121.00
1	E	7	A	O4'-C1'-C2'	-6.00	99.80	105.80
2	A	77	ASP	CB-CG-OD2	6.00	123.70	118.30
1	F	3	C	C3'-C2'-C1'	5.94	106.25	101.50
1	E	11	C	O5'-C5'-C4'	-5.93	100.44	111.70
1	E	10	C	C5-C6-N1	5.90	123.95	121.00
1	E	12	U	C5-C6-N1	5.88	125.64	122.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	6	U	O5'-P-OP2	-5.87	100.42	105.70
1	E	9	C	O4'-C1'-N1	5.83	112.86	108.20
2	A	46	ARG	NH1-CZ-NH2	-5.81	113.01	119.40
1	E	9	C	C6-N1-C1'	-5.80	113.84	120.80
1	F	2	A	P-O3'-C3'	-5.80	112.74	119.70
2	A	35	SER	CB-CA-C	-5.78	99.11	110.10
1	E	9	C	C5-C4-N4	-5.78	116.15	120.20
1	E	7	A	C1'-O4'-C4'	5.77	114.52	109.90
1	E	10	C	O5'-P-OP1	5.77	117.62	110.70
2	C	56	GLU	N-CA-CB	-5.71	100.32	110.60
1	F	8	A	O4'-C1'-N9	5.68	112.74	108.20
1	F	12	U	C1'-O4'-C4'	5.66	114.43	109.90
2	A	69	PHE	CB-CG-CD1	-5.66	116.84	120.80
1	F	4	C	O5'-P-OP1	-5.66	100.61	105.70
1	E	10	C	C2-N3-C4	5.65	122.73	119.90
2	B	46	ARG	CB-CA-C	-5.65	99.10	110.40
1	E	2	A	C5-N7-C8	-5.64	101.08	103.90
1	E	4	C	N1-C2-N3	-5.63	115.26	119.20
1	E	10	C	N3-C4-N4	5.57	121.90	118.00
1	E	3	C	C5'-C4'-O4'	5.57	115.78	109.10
1	E	3	C	O5'-P-OP2	5.51	117.31	110.70
2	A	77	ASP	N-CA-CB	-5.50	100.71	110.60
1	E	7	A	C5'-C4'-O4'	5.49	115.69	109.10
1	F	9	C	C6-N1-C2	5.49	122.50	120.30
1	E	11	C	C5-C4-N4	5.47	124.03	120.20
1	F	10	C	OP1-P-OP2	5.47	127.81	119.60
1	F	9	C	C1'-C2'-O2'	-5.46	94.20	110.60
1	E	5	C	N3-C4-N4	-5.46	114.18	118.00
1	F	10	C	OP2-P-O3'	-5.46	93.19	105.20
2	A	14	LEU	CA-CB-CG	5.46	127.85	115.30
1	F	10	C	N3-C4-N4	5.45	121.81	118.00
1	E	8	A	N1-C2-N3	-5.43	126.58	129.30
1	F	12	U	OP1-P-OP2	5.43	127.75	119.60
1	F	12	U	O4'-C1'-C2'	-5.38	100.42	105.80
1	F	10	C	C4-C5-C6	-5.38	114.71	117.40
2	C	40	ARG	NE-CZ-NH2	-5.37	117.61	120.30
1	F	7	A	P-O3'-C3'	5.36	126.13	119.70
1	F	2	A	O4'-C1'-C2'	-5.33	100.47	105.80
1	E	1	A	C4'-C3'-C2'	-5.33	97.27	102.60
1	E	1	A	C5'-C4'-O4'	5.33	115.49	109.10
1	F	10	C	C1'-O4'-C4'	5.31	114.15	109.90
1	F	6	U	C1'-O4'-C4'	5.30	114.14	109.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	5	C	C6-N1-C2	-5.29	118.18	120.30
1	F	4	C	C5'-C4'-C3'	-5.25	107.59	116.00
1	F	3	C	C2-N3-C4	-5.25	117.27	119.90
1	E	10	C	N3-C4-C5	-5.24	119.81	121.90
1	F	5	C	C5-C6-N1	5.21	123.60	121.00
1	E	3	C	O4'-C1'-C2'	-5.20	100.60	105.80
2	C	34	GLU	OE1-CD-OE2	-5.20	117.06	123.30
1	E	4	C	OP1-P-OP2	5.19	127.39	119.60
2	D	65	THR	CA-CB-CG2	-5.17	105.16	112.40
1	E	8	A	N3-C4-N9	-5.17	123.27	127.40
1	E	7	A	N9-C4-C5	5.16	107.87	105.80
1	E	9	C	O3'-P-O5'	5.14	113.76	104.00
1	E	2	A	O5'-P-OP1	-5.12	101.09	105.70
1	E	8	A	C6-C5-N7	5.10	135.87	132.30
1	F	12	U	C6-N1-C2	-5.10	117.94	121.00
1	E	6	U	O4'-C1'-C2'	-5.07	100.73	105.80
1	E	7	A	C8-N9-C4	-5.06	103.78	105.80
2	A	77	ASP	CB-CG-OD1	-5.05	113.75	118.30
1	E	11	C	C5-C6-N1	5.04	123.52	121.00
1	F	10	C	O4'-C1'-N1	5.03	112.22	108.20
1	F	11	C	N3-C4-C5	-5.01	119.89	121.90
1	F	10	C	O4'-C1'-C2'	-5.01	100.79	105.80

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	D	52	GLY	Peptide
2	D	53	ASN	Peptide

5.2 Close contacts ⓘ

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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	E	245	0	132	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	F	245	0	132	9	0
2	A	550	0	588	30	0
2	B	526	0	560	21	0
2	C	526	0	560	27	0
2	D	526	0	560	24	0
3	A	9	0	0	3	0
3	B	14	0	0	1	0
3	C	11	0	0	3	0
3	D	10	0	0	2	0
3	E	3	0	0	0	0
3	F	4	0	0	0	0
All	All	2669	0	2532	109	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 21.

All (109) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:A:46:ARG:CG	2:A:46:ARG:HH11	1.64	1.10
2:A:46:ARG:HG2	2:A:46:ARG:HH11	0.87	1.03
2:C:56:GLU:HB3	3:C:86:HOH:O	1.57	1.02
2:A:46:ARG:HG2	2:A:46:ARG:NH1	1.65	1.00
2:A:18:LEU:HD23	2:B:18:LEU:HD23	1.45	0.97
2:D:46:ARG:HH11	2:D:46:ARG:HG2	1.30	0.96
2:A:46:ARG:CG	2:A:46:ARG:NH1	2.26	0.86
2:D:39:MSE:HE1	2:D:75:ILE:HG12	1.60	0.82
2:D:39:MSE:CE	2:D:75:ILE:HG13	2.09	0.82
2:D:39:MSE:HE3	2:D:75:ILE:HG13	1.63	0.81
2:A:18:LEU:CD2	2:B:18:LEU:HD23	2.13	0.77
2:D:39:MSE:HE1	2:D:75:ILE:CG1	2.14	0.77
1:F:4:C:O5'	1:F:4:C:H2'	1.86	0.75
2:D:56:GLU:O	2:D:56:GLU:HG3	1.86	0.74
2:D:39:MSE:CE	2:D:75:ILE:CG1	2.65	0.74
2:B:51:GLU:HA	2:B:51:GLU:OE2	1.85	0.73
1:F:11:C:H2'	1:F:12:U:C6	2.25	0.72
1:E:6:U:O2'	1:E:7:A:C8	2.43	0.71
2:A:20:MSE:HA	3:A:87:HOH:O	1.92	0.69
2:B:29:ILE:HG23	2:B:33:GLY:HA2	1.74	0.69
2:A:11:ASN:HB3	3:A:83:HOH:O	1.93	0.69
1:F:4:C:H4'	1:F:5:C:H5'	1.77	0.67
2:C:76:ILE:CG2	2:D:65:THR:HG23	2.24	0.67
2:D:46:ARG:HH11	2:D:46:ARG:CG	2.04	0.66

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:C:20:MSE:HE2	2:C:28:ILE:CD1	2.25	0.66
2:C:55:PRO:HD2	3:C:86:HOH:O	1.96	0.65
1:E:3:C:OP1	1:E:3:C:H2'	1.97	0.65
2:B:29:ILE:CG2	2:B:33:GLY:HA2	2.27	0.65
1:E:7:A:O2'	1:E:8:A:C8	2.48	0.64
1:E:8:A:H1'	1:E:9:C:H5'	1.79	0.63
2:A:53:ASN:N	3:A:90:HOH:O	2.31	0.63
2:C:43:SER:HB3	2:C:74:MSE:CE	2.30	0.62
2:A:10:LYS:O	2:A:10:LYS:HG3	2.00	0.61
2:B:20:MSE:HE1	2:B:28:ILE:CD1	2.31	0.61
2:B:17:ARG:HD2	3:B:92:HOH:O	2.00	0.61
2:C:36:VAL:HG23	2:C:39:MSE:HE2	1.82	0.60
2:C:20:MSE:HG3	2:C:59:ILE:HG13	1.83	0.60
2:A:21:HIS:HB2	2:A:24:GLU:HG3	1.84	0.60
2:D:40:ARG:HG2	3:D:84:HOH:O	2.02	0.60
2:C:16:ILE:HD12	2:C:17:ARG:N	2.18	0.59
2:C:54:CYS:C	2:C:56:GLU:H	2.05	0.59
2:B:21:HIS:HB2	2:B:24:GLU:HG3	1.85	0.58
2:A:46:ARG:CB	2:A:46:ARG:NH1	2.66	0.58
2:C:72:PHE:CE1	2:C:76:ILE:CD1	2.86	0.58
1:E:11:C:H2'	1:E:12:U:H5'	1.85	0.58
2:C:19:LEU:HB2	2:D:19:LEU:HD12	1.85	0.57
2:C:72:PHE:CZ	2:C:76:ILE:CD1	2.88	0.56
2:A:46:ARG:CZ	2:A:46:ARG:CB	2.80	0.56
1:E:5:C:O2'	1:E:6:U:H5'	2.06	0.55
2:C:72:PHE:CZ	2:C:76:ILE:HD11	2.42	0.55
2:A:18:LEU:HD23	2:B:18:LEU:CD2	2.30	0.54
2:A:29:ILE:HG22	2:A:33:GLY:HA2	1.89	0.54
2:B:51:GLU:OE2	2:B:51:GLU:CA	2.50	0.54
2:D:78:LYS:HE2	3:D:92:HOH:O	2.08	0.54
2:D:53:ASN:HB3	2:D:54:CYS:HA	1.89	0.54
2:B:19:LEU:C	2:B:20:MSE:HG2	2.30	0.53
2:C:76:ILE:CG2	2:D:65:THR:CG2	2.88	0.51
1:F:1:A:N3	1:F:1:A:H5'	2.26	0.51
2:C:76:ILE:HG23	2:D:65:THR:HG23	1.93	0.50
1:E:11:C:C2'	1:E:12:U:H5'	2.42	0.50
2:A:18:LEU:CD2	2:B:18:LEU:CD2	2.87	0.49
2:A:20:MSE:HE3	2:A:24:GLU:HB2	1.95	0.48
1:F:1:A:O2'	1:F:2:A:P	2.71	0.48
1:F:10:C:N3	2:A:57:ARG:NH1	2.59	0.48
2:A:46:ARG:HB3	2:A:46:ARG:NH1	2.29	0.47
1:E:8:A:C2	1:E:9:C:C2	3.02	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:C:20:MSE:HE2	2:C:28:ILE:HD12	1.97	0.47
2:A:31:LYS:O	2:A:34:GLU:HG2	2.14	0.46
2:B:22:GLY:N	2:B:55:PRO:O	2.48	0.46
1:F:2:A:C3'	1:F:3:C:H5''	2.45	0.46
2:D:51:GLU:O	2:D:52:GLY:O	2.32	0.46
2:D:33:GLY:O	2:D:37:LYS:HB2	2.16	0.46
2:A:52:GLY:C	2:A:54:CYS:H	2.19	0.46
2:D:65:THR:HG22	2:D:65:THR:O	2.16	0.46
2:C:20:MSE:CE	2:C:28:ILE:HD11	2.46	0.45
2:B:14:LEU:O	2:B:62:ALA:HA	2.15	0.45
2:C:43:SER:HB3	2:C:74:MSE:HE1	1.98	0.45
1:E:4:C:H4'	1:E:5:C:H5'	1.98	0.45
2:C:69:PHE:HZ	2:D:73:ALA:HA	1.82	0.45
2:C:20:MSE:HE2	2:C:28:ILE:HD11	1.97	0.45
2:A:28:ILE:O	2:A:35:SER:CB	2.65	0.45
2:D:51:GLU:O	2:D:52:GLY:C	2.55	0.44
2:A:51:GLU:HG3	2:A:51:GLU:O	2.16	0.44
2:B:24:GLU:O	2:B:28:ILE:HD12	2.17	0.44
1:F:4:C:O5'	1:F:4:C:C2'	2.63	0.44
2:B:36:VAL:O	2:B:40:ARG:HG3	2.17	0.44
2:A:72:PHE:CE2	2:B:16:ILE:HD13	2.54	0.43
2:A:20:MSE:HE3	2:A:20:MSE:HB3	1.59	0.43
2:B:14:LEU:HB2	2:B:68:ILE:HD11	2.00	0.43
2:C:16:ILE:C	2:C:16:ILE:HD12	2.39	0.43
2:D:52:GLY:O	2:D:54:CYS:HB2	2.19	0.42
2:C:43:SER:HB3	2:C:74:MSE:HE3	1.99	0.42
2:A:29:ILE:CG2	2:A:33:GLY:HA2	2.50	0.42
2:C:56:GLU:CB	3:C:86:HOH:O	2.37	0.42
2:A:12:VAL:O	2:A:64:PRO:HA	2.19	0.42
2:C:37:LYS:HE2	2:C:37:LYS:HB2	1.52	0.42
2:D:54:CYS:C	2:D:56:GLU:H	2.22	0.42
2:D:53:ASN:N	2:D:54:CYS:HB2	2.35	0.42
2:A:20:MSE:HE1	2:A:28:ILE:HD12	2.03	0.41
2:B:20:MSE:HE3	2:B:24:GLU:HB2	2.03	0.41
2:C:54:CYS:C	2:C:56:GLU:N	2.68	0.41
2:D:21:HIS:N	2:D:24:GLU:OE2	2.51	0.41
2:A:14:LEU:O	2:A:62:ALA:HA	2.20	0.41
2:C:14:LEU:HD12	2:C:14:LEU:HA	1.93	0.41
2:C:72:PHE:CE1	2:C:76:ILE:HD12	2.56	0.40
2:B:20:MSE:HE3	2:B:20:MSE:HB3	1.61	0.40
1:F:9:C:N4	2:A:27:SER:HB3	2.37	0.40
1:E:5:C:O2'	1:E:6:U:C5'	2.68	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:B:21:HIS:O	2:B:24:GLU:HG3	2.22	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	A	70/73 (96%)	63 (90%)	5 (7%)	2 (3%)	7	10
2	B	67/73 (92%)	64 (96%)	3 (4%)	0	100	100
2	C	67/73 (92%)	63 (94%)	4 (6%)	0	100	100
2	D	67/73 (92%)	60 (90%)	6 (9%)	1 (2%)	15	28
All	All	271/292 (93%)	250 (92%)	18 (7%)	3 (1%)	21	39

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	D	52	GLY
2	A	11	ASN
2	A	65	THR

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	A	60/58 (103%)	51 (85%)	9 (15%)	4	6
2	B	57/58 (98%)	47 (82%)	10 (18%)	3	4
2	C	57/58 (98%)	51 (90%)	6 (10%)	10	17

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	D	57/58 (98%)	46 (81%)	11 (19%)	2	3
All	All	231/232 (100%)	195 (84%)	36 (16%)	4	6

All (36) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	A	11	ASN
2	A	14	LEU
2	A	20	MSE
2	A	23	LYS
2	A	32	LYS
2	A	34	GLU
2	A	46	ARG
2	A	68	ILE
2	A	76	ILE
2	B	13	THR
2	B	14	LEU
2	B	20	MSE
2	B	24	GLU
2	B	35	SER
2	B	46	ARG
2	B	51	GLU
2	B	53	ASN
2	B	66	ASN
2	B	68	ILE
2	C	16	ILE
2	C	17	ARG
2	C	37	LYS
2	C	41	GLU
2	C	70	LYS
2	C	80	GLU
2	D	14	LEU
2	D	15	THR
2	D	16	ILE
2	D	17	ARG
2	D	19	LEU
2	D	41	GLU
2	D	46	ARG
2	D	51	GLU
2	D	53	ASN
2	D	54	CYS
2	D	76	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
2	A	11	ASN
2	B	53	ASN
2	B	66	ASN
2	D	53	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	E	12/12 (100%)	8 (66%)	3 (25%)
1	F	12/12 (100%)	5 (41%)	2 (16%)
All	All	24/24 (100%)	13 (54%)	5 (20%)

All (13) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	E	2	A
1	E	3	C
1	E	4	C
1	E	5	C
1	E	7	A
1	E	8	A
1	E	9	C
1	E	10	C
1	F	2	A
1	F	4	C
1	F	7	A
1	F	8	A
1	F	9	C

All (5) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	E	1	A
1	E	2	A
1	E	3	C
1	F	1	A
1	F	9	C

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, 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	E	12/12 (100%)	0.53	1 (8%) 11 10	39, 52, 76, 81	0
1	F	12/12 (100%)	0.29	0 100 100	44, 48, 63, 82	0
2	A	72/73 (98%)	0.08	2 (2%) 50 51	18, 31, 51, 56	0
2	B	69/73 (94%)	0.00	1 (1%) 72 74	19, 31, 46, 60	0
2	C	69/73 (94%)	0.09	2 (2%) 49 49	21, 33, 49, 57	0
2	D	69/73 (94%)	0.13	1 (1%) 72 74	23, 34, 49, 63	0
All	All	303/316 (95%)	0.10	7 (2%) 57 58	18, 33, 53, 82	0

All (7) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	53	ASN	6.4
1	E	1	A	3.2
2	C	53	ASN	2.8
2	B	55	PRO	2.3
2	C	41	GLU	2.2
2	A	52	GLY	2.1
2	A	55	PRO	2.0

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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

6.3 Carbohydrates ⓘ

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.