



# Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 09:43 PM GMT

PDB ID : 1QAJ  
Title : CRYSTAL STRUCTURES OF THE N-TERMINAL FRAGMENT FROM  
MOLONEY MURINE LEUKEMIA VIRUS REVERSE TRANSCRIPTASE  
COMPLEXED WITH NUCLEIC ACID: FUNCTIONAL IMPLICATIONS  
FOR TEMPLATE-PRIMER BINDING TO THE FINGERS DOMAIN  
Authors : Najmudin, S.; Cote, M.; Sun, D.; Yohannan, S.; Montano, S.P.; Gu, J.; Geor-  
giadis, M.M.  
Deposited on : 1999-03-18  
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](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  
Mogul : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
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) : trunk26865

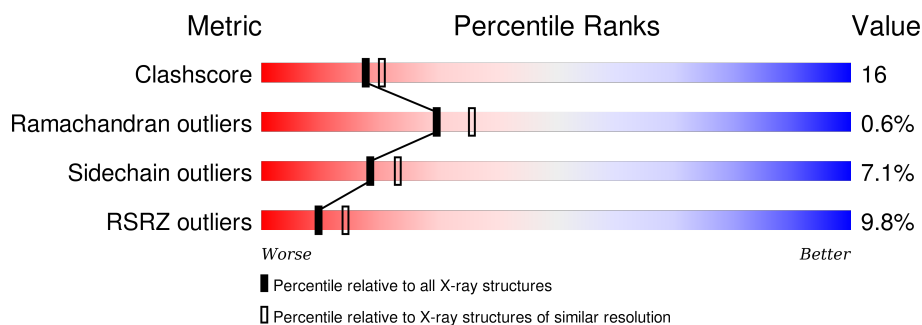
# 1 Overall quality at a glance

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))
Clashscore	102246	4452 (2.30-2.30)
Ramachandran outliers	100387	4410 (2.30-2.30)
Sidechain outliers	100360	4409 (2.30-2.30)
RSRZ outliers	91569	3857 (2.30-2.30)

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	C	8	<div> <div>25%</div> <div>75%</div> </div>
1	D	8	<div> <div>100%</div> </div>
2	A	259	<div> <div>4%</div> <div>73%</div> <div>25%</div> <div>.</div> </div>
2	B	259	<div> <div>16%</div> <div>68%</div> <div>25%</div> <div>5%</div> <div>..</div> </div>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4856 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 DNA chain called DNA (5'-D(\*CP\*AP\*TP\*GP\*CP\*AP\*TP\*G)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	C	8	Total	C	N	O	P	0	0	0
			161	78	30	46	7			
1	D	8	Total	C	N	O	P	0	0	0
			161	78	30	46	7			

- Molecule 2 is a protein called REVERSE TRANSCRIPTASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	A	259	Total	C	N	O	S	0	0	0
			2069	1327	362	372	8			
2	B	257	Total	C	N	O	S	0	0	0
			2059	1322	360	369	8			

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	238	Total	O	0	0
			238	238		
3	B	146	Total	O	0	0
			146	146		
3	C	12	Total	O	0	0
			12	12		
3	D	10	Total	O	0	0
			10	10		

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

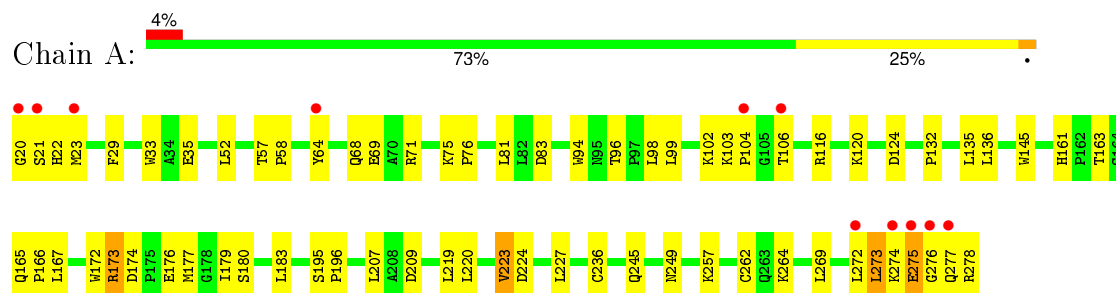


- Molecule 1: DNA (5'-D(\*CP\*AP\*TP\*GP\*CP\*AP\*TP\*G)-3')

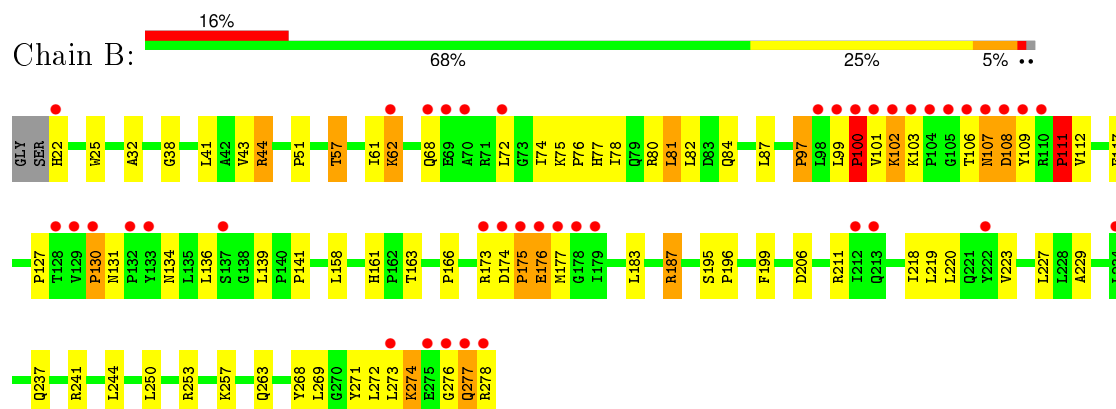


There are no outlier residues recorded for this chain.

- Molecule 2: REVERSE TRANSCRIPTASE



- Molecule 2: REVERSE TRANSCRIPTASE



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	65.87Å 63.59Å 73.40Å 90.00° 102.91° 90.00°	Depositor
Resolution (Å)	20.00 – 2.30 19.84 – 2.30	Depositor EDS
% Data completeness (in resolution range)	98.7 (20.00-2.30) 98.7 (19.84-2.30)	Depositor EDS
$R_{merge}$	0.05	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	5.43 (at 2.30Å)	Xtriage
Refinement program	CNS	Depositor
R, $R_{free}$	0.200 , 0.259 0.209 , (Not available)	Depositor DCC
$R_{free}$ test set	No test flags present.	DCC
Wilson B-factor (Å <sup>2</sup> )	30.7	Xtriage
Anisotropy	0.271	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 57.4	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 26109 reflections	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	4856	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	35.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.13% 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, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

## 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	C	0.25	0/180	0.68	0/276
1	D	0.26	0/180	0.73	0/276
2	A	0.44	1/2126 (0.0%)	0.74	0/2896
2	B	0.48	0/2116	0.80	6/2883 (0.2%)
All	All	0.44	1/4602 (0.0%)	0.77	6/6331 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	22	HIS	CB-CG	5.18	1.59	1.50

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	100	PRO	CA-N-CD	-8.26	99.94	111.50
2	B	111	PRO	CA-N-CD	-8.07	100.20	111.50
2	B	97	PRO	CA-N-CD	-6.72	102.09	111.50
2	B	175	PRO	CA-N-CD	-5.77	103.42	111.50
2	B	127	PRO	CA-N-CD	-5.44	103.89	111.50
2	B	130	PRO	CA-N-CD	-5.27	104.12	111.50

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-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 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	C	161	0	92	5	0
1	D	161	0	92	0	0
2	A	2069	0	2080	60	0
2	B	2059	0	2072	76	0
3	A	238	0	0	7	0
3	B	146	0	0	7	0
3	C	12	0	0	0	0
3	D	10	0	0	0	0
All	All	4856	0	4336	140	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 16.

All (140) 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)
2:A:173:ARG:HB3	2:A:173:ARG:HH11	1.39	0.87
2:B:272:LEU:HD23	2:B:278:ARG:HD2	1.59	0.85
2:A:272:LEU:HD21	2:A:274:LYS:HE2	1.57	0.83
2:B:161:HIS:HD2	2:B:163:THR:H	1.25	0.80
2:A:71:ARG:NH2	2:A:173:ARG:H	1.79	0.79
2:A:173:ARG:HH11	2:A:173:ARG:CB	1.97	0.79
2:B:274:LYS:H	2:B:274:LYS:HD2	1.48	0.78
2:B:78:ILE:O	2:B:82:LEU:HD23	1.84	0.78
1:C:3:DT:H1'	1:C:4:DG:N7	2.00	0.77
2:A:173:ARG:CG	2:A:173:ARG:HH11	1.99	0.74
2:B:43:VAL:HG23	2:B:44:ARG:HE	1.50	0.74
2:B:75:LYS:NZ	2:B:176:GLU:HG3	2.02	0.73
2:B:101:VAL:HG12	2:B:102:LYS:N	2.04	0.72
2:B:62:LYS:HD2	2:B:62:LYS:H	1.55	0.72
2:A:173:ARG:NH1	2:A:173:ARG:HB3	2.05	0.72
2:B:61:ILE:HD11	2:B:117:GLU:HG3	1.70	0.72
2:B:174:ASP:OD1	2:B:176:GLU:HG2	1.91	0.70
2:A:135:LEU:HG	2:A:220:LEU:HG	1.73	0.70
2:B:62:LYS:HD2	2:B:62:LYS:N	2.06	0.70
2:A:71:ARG:HH22	2:A:173:ARG:H	1.43	0.66
2:A:64:TYR:CE2	2:A:99:LEU:HD11	2.30	0.66
2:B:102:LYS:O	2:B:103:LYS:HG2	1.96	0.66
2:A:172:TRP:O	2:A:173:ARG:HD2	1.97	0.65
2:B:272:LEU:HG	2:B:274:LYS:HE3	1.77	0.65
2:A:273:LEU:N	2:A:273:LEU:HD23	2.12	0.64
2:A:145:TRP:NE1	2:A:264:LYS:HE3	2.13	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:274:LYS:HD2	2:B:274:LYS:N	2.14	0.62
2:A:245:GLN:HE21	2:A:249:ASN:HD21	1.48	0.60
2:A:174:ASP:OD1	2:A:176:GLU:HB3	2.01	0.60
2:A:173:ARG:HG2	3:A:449:HOH:O	2.01	0.60
2:B:101:VAL:CG1	2:B:102:LYS:H	2.15	0.60
2:A:272:LEU:O	2:A:278:ARG:N	2.32	0.60
2:A:173:ARG:HH11	2:A:173:ARG:HG3	1.67	0.60
2:A:83:ASP:OD1	2:B:161:HIS:HE1	1.85	0.59
2:A:132:PRO:O	2:A:136:LEU:HD13	2.01	0.59
2:B:161:HIS:CD2	2:B:163:THR:H	2.15	0.59
2:B:101:VAL:HG12	2:B:102:LYS:H	1.67	0.59
2:B:101:VAL:CG1	2:B:102:LYS:N	2.64	0.59
2:B:57:THR:HG22	3:B:289:HOH:O	2.04	0.58
2:B:237:GLN:O	2:B:241:ARG:HG3	2.03	0.58
2:B:82:LEU:HD22	2:B:87:LEU:HB2	1.84	0.58
1:C:6:DA:H4'	1:C:7:DT:OP1	2.03	0.58
1:C:1:DC:H2''	1:C:2:DA:C8	2.40	0.57
2:B:74:ILE:HG23	2:B:111:PRO:HG3	1.87	0.57
2:B:272:LEU:CG	2:B:274:LYS:HE3	2.35	0.56
2:A:161:HIS:HD2	2:A:163:THR:H	1.53	0.56
2:B:75:LYS:N	2:B:76:PRO:HD2	2.22	0.55
2:A:207:LEU:HD13	2:A:219:LEU:HD21	1.88	0.55
2:A:179:ILE:HD12	2:A:183:LEU:HD21	1.87	0.54
2:B:176:GLU:HB2	3:B:396:HOH:O	2.06	0.54
2:A:64:TYR:HE2	2:A:99:LEU:HD11	1.71	0.54
2:B:82:LEU:HD21	2:B:183:LEU:HD13	1.88	0.54
2:B:131:ASN:HB3	2:B:134:ASN:HD22	1.72	0.54
2:B:187:ARG:NH1	3:B:372:HOH:O	2.41	0.54
2:B:101:VAL:HG21	2:B:112:VAL:HG21	1.90	0.53
2:B:62:LYS:CD	2:B:62:LYS:H	2.16	0.53
2:A:277:GLN:O	2:A:278:ARG:OXT	2.27	0.53
2:B:22:HIS:HB3	2:B:25:TRP:CD1	2.43	0.53
2:A:161:HIS:CD2	2:A:163:THR:HG23	2.44	0.53
2:B:74:ILE:HD11	2:B:100:PRO:HA	1.91	0.53
2:B:80:ARG:O	2:B:84:GLN:HG3	2.09	0.53
2:A:245:GLN:HE21	2:A:249:ASN:ND2	2.07	0.53
2:A:145:TRP:CE2	2:A:264:LYS:HE3	2.44	0.52
2:A:75:LYS:HB3	2:A:76:PRO:HD3	1.91	0.52
2:A:120:LYS:HG3	3:A:318:HOH:O	2.10	0.52
1:C:3:DT:H1'	1:C:4:DG:C8	2.44	0.52
2:A:273:LEU:HD23	2:A:273:LEU:H	1.73	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:274:LYS:C	2:A:276:GLY:H	2.15	0.51
2:A:35:GLU:OE2	2:A:257:LYS:HG3	2.10	0.51
2:B:273:LEU:HB2	3:B:418:HOH:O	2.10	0.50
2:B:195:SER:HB2	2:B:196:PRO:HD3	1.93	0.50
2:A:161:HIS:CD2	2:A:163:THR:H	2.29	0.49
2:A:274:LYS:O	2:A:276:GLY:N	2.45	0.49
2:A:103:LYS:HB3	2:A:106:THR:OG1	2.13	0.49
2:A:173:ARG:NH1	3:A:450:HOH:O	2.45	0.49
2:A:57:THR:HG23	2:A:58:PRO:HD2	1.94	0.48
2:B:273:LEU:HB3	2:B:277:GLN:OE1	2.12	0.48
2:A:94:TRP:CE2	2:A:167:LEU:HD23	2.49	0.48
2:B:268:TYR:CE1	2:B:269:LEU:HD13	2.49	0.48
2:B:43:VAL:CG2	2:B:44:ARG:HE	2.22	0.48
2:B:227:LEU:C	2:B:227:LEU:HD23	2.34	0.47
2:A:272:LEU:CD2	2:A:274:LYS:HE2	2.36	0.47
2:B:174:ASP:CG	2:B:176:GLU:HG2	2.34	0.47
2:A:71:ARG:NH2	2:A:173:ARG:N	2.54	0.47
2:B:102:LYS:HG2	2:B:103:LYS:N	2.29	0.47
2:B:68:GLN:O	2:B:72:LEU:HG	2.15	0.47
2:B:51:PRO:HD2	3:B:324:HOH:O	2.14	0.46
2:B:99:LEU:N	2:B:99:LEU:HD22	2.29	0.46
2:B:131:ASN:HB3	2:B:134:ASN:ND2	2.29	0.46
2:B:176:GLU:N	2:B:176:GLU:OE1	2.49	0.45
2:A:245:GLN:NE2	2:A:249:ASN:HD21	2.14	0.45
2:B:101:VAL:O	2:B:109:TYR:HD1	1.99	0.45
2:B:61:ILE:HD11	2:B:117:GLU:CG	2.42	0.45
2:B:273:LEU:N	2:B:273:LEU:HD23	2.31	0.45
2:B:106:THR:HG23	2:B:107:ASN:N	2.32	0.45
2:A:98:LEU:HD12	2:A:98:LEU:HA	1.84	0.45
2:A:166:PRO:HG3	3:A:302:HOH:O	2.16	0.45
2:B:75:LYS:HZ1	2:B:176:GLU:HG3	1.80	0.45
2:A:236:CYS:SG	2:A:262:CYS:HA	2.55	0.45
2:B:62:LYS:CD	2:B:62:LYS:N	2.72	0.45
2:B:32:ALA:HB2	2:B:244:LEU:O	2.17	0.45
2:B:211:ARG:NH1	2:B:219:LEU:HB3	2.33	0.44
2:A:272:LEU:HD21	2:A:274:LYS:CE	2.37	0.44
2:B:80:ARG:HB2	2:B:80:ARG:CZ	2.47	0.44
2:B:158:LEU:HD11	2:B:199:PHE:HA	1.98	0.44
2:B:136:LEU:HD12	2:B:271:TYR:CD2	2.53	0.44
2:A:173:ARG:NH1	2:A:173:ARG:CG	2.69	0.44
2:A:52:LEU:HD21	2:A:167:LEU:HD21	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:74:ILE:HG12	2:B:111:PRO:HD3	2.00	0.44
2:B:187:ARG:HH11	2:B:187:ARG:HG2	1.82	0.44
2:B:187:ARG:HH11	2:B:187:ARG:CG	2.31	0.44
2:B:139:LEU:O	2:B:141:PRO:HD3	2.18	0.44
2:B:106:THR:HG23	2:B:107:ASN:H	1.83	0.43
2:A:165:GLN:N	2:A:166:PRO:CD	2.81	0.43
2:B:257:LYS:HD3	3:B:295:HOH:O	2.18	0.43
2:B:41:LEU:C	2:B:41:LEU:HD23	2.39	0.43
2:A:227:LEU:C	2:A:227:LEU:HD23	2.38	0.43
2:B:274:LYS:C	2:B:276:GLY:H	2.22	0.43
2:B:177:MET:HE1	3:B:398:HOH:O	2.17	0.43
2:A:272:LEU:CD2	2:A:274:LYS:CE	2.97	0.43
2:A:223:VAL:HG12	2:A:224:ASP:N	2.34	0.43
2:B:77:HIS:O	2:B:81:LEU:HD22	2.19	0.42
2:B:206:ASP:HB3	2:B:250:LEU:HD13	2.01	0.42
2:A:173:ARG:NH1	2:A:173:ARG:HG3	2.32	0.42
2:B:75:LYS:HZ3	2:B:176:GLU:HG3	1.81	0.42
2:B:273:LEU:H	2:B:273:LEU:HD23	1.85	0.42
2:A:57:THR:HG22	3:A:281:HOH:O	2.19	0.42
2:B:272:LEU:CD2	2:B:274:LYS:HE3	2.50	0.42
2:A:103:LYS:HA	2:A:104:PRO:HD3	1.89	0.42
2:A:29:PHE:O	2:A:33:TRP:CD1	2.73	0.42
2:B:218:ILE:HB	2:B:229:ALA:HB3	2.01	0.41
2:B:175:PRO:HB2	2:B:176:GLU:OE1	2.19	0.41
2:B:38:GLY:O	2:B:253:ARG:HG3	2.20	0.41
2:A:173:ARG:HE	2:A:180:SER:C	2.22	0.41
2:A:69:GLU:H	2:A:69:GLU:CD	2.24	0.41
2:A:20:GLY:N	3:A:438:HOH:O	2.54	0.40
2:B:103:LYS:HB2	2:B:108:ASP:HB2	2.04	0.40
2:A:195:SER:HB2	2:A:196:PRO:HD3	2.03	0.40
1:C:3:DT:H4'	1:C:4:DG:OP1	2.22	0.40
2:A:177:MET:HG3	3:A:344:HOH:O	2.21	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	257/259 (99%)	248 (96%)	7 (3%)	2 (1%)	24	27
2	B	255/259 (98%)	237 (93%)	17 (7%)	1 (0%)	39	48
All	All	512/518 (99%)	485 (95%)	24 (5%)	3 (1%)	30	36

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	A	275	GLU
2	B	223	VAL
2	A	223	VAL

### 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	227/227 (100%)	214 (94%)	13 (6%)	25	34
2	B	226/227 (100%)	207 (92%)	19 (8%)	14	16
All	All	453/454 (100%)	421 (93%)	32 (7%)	18	23

All (32) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	A	21	SER
2	A	23	MET
2	A	68	GLN
2	A	81	LEU
2	A	96	THR
2	A	102	LYS
2	A	116	ARG
2	A	124	ASP
2	A	173	ARG

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Mol	Chain	Res	Type
2	A	209	ASP
2	A	269	LEU
2	A	273	LEU
2	A	275	GLU
2	B	44	ARG
2	B	57	THR
2	B	62	LYS
2	B	81	LEU
2	B	97	PRO
2	B	100	PRO
2	B	102	LYS
2	B	107	ASN
2	B	108	ASP
2	B	111	PRO
2	B	130	PRO
2	B	166	PRO
2	B	173	ARG
2	B	176	GLU
2	B	187	ARG
2	B	220	LEU
2	B	263	GLN
2	B	274	LYS
2	B	277	GLN

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

Mol	Chain	Res	Type
2	A	68	GLN
2	A	84	GLN
2	A	134	ASN
2	A	161	HIS
2	A	213	GLN
2	A	249	ASN
2	B	68	GLN
2	B	84	GLN
2	B	107	ASN
2	B	134	ASN
2	B	161	HIS
2	B	190	GLN
2	B	204	HIS
2	B	245	GLN
2	B	249	ASN

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Mol	Chain	Res	Type
2	B	265	GLN

### 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 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 ⓘ

### 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	C	8/8 (100%)	0.62	0 100 100	39, 53, 64, 77	0
1	D	8/8 (100%)	-0.25	0 100 100	31, 45, 46, 52	0
2	A	259/259 (100%)	0.03	11 (4%) 40 49	13, 24, 52, 72	0
2	B	257/259 (99%)	0.71	41 (15%) 3 4	15, 34, 74, 96	0
All	All	532/534 (99%)	0.36	52 (9%) 10 14	13, 30, 67, 96	0

All (52) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	276	GLY	8.4
2	B	106	THR	8.2
2	B	109	TYR	7.2
2	A	20	GLY	6.5
2	B	104	PRO	5.4
2	B	102	LYS	5.4
2	B	107	ASN	5.4
2	B	103	LYS	4.9
2	B	133	TYR	4.7
2	B	175	PRO	4.4
2	A	21	SER	4.3
2	B	178	GLY	4.2
2	B	177	MET	4.2
2	A	276	GLY	4.0
2	B	72	LEU	3.4
2	B	22	HIS	3.4
2	B	277	GLN	3.2
2	B	108	ASP	3.2
2	A	64	TYR	3.1
2	B	99	LEU	3.1
2	B	278	ARG	3.0

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Mol	Chain	Res	Type	RSRZ
2	A	104	PRO	2.9
2	B	101	VAL	2.8
2	B	176	GLU	2.8
2	B	179	ILE	2.7
2	B	173	ARG	2.7
2	B	213	GLN	2.6
2	A	106	THR	2.5
2	B	130	PRO	2.5
2	B	275	GLU	2.5
2	B	69	GLU	2.5
2	B	137	SER	2.4
2	B	98	LEU	2.4
2	B	174	ASP	2.4
2	A	274	LYS	2.4
2	B	110	ARG	2.3
2	B	68	GLN	2.3
2	B	128	THR	2.3
2	A	277	GLN	2.3
2	A	275	GLU	2.3
2	B	273	LEU	2.3
2	B	105	GLY	2.2
2	B	234	LEU	2.2
2	B	129	VAL	2.2
2	B	70	ALA	2.2
2	B	62	LYS	2.1
2	A	23	MET	2.1
2	B	212	ILE	2.1
2	A	272	LEU	2.0
2	B	222	TYR	2.0
2	B	100	PRO	2.0
2	B	132	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 [i](#)

There are no ligands in this entry.

## 6.5 Other polymers [i](#)

There are no such residues in this entry.