



# Full wwPDB X-ray Structure Validation Report ⓘ

Sep 25, 2017 – 10:54 AM EDT

PDB ID : 5DMQ  
Title : Crystal structure of mouse eRF1 in complex with Reverse Transcriptase (RT) of Moloney Murine Leukemia Virus  
Authors : Tang, T.; Song, H.  
Deposited on : unknown  
Resolution : 4.00 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
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20030345
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-20030345

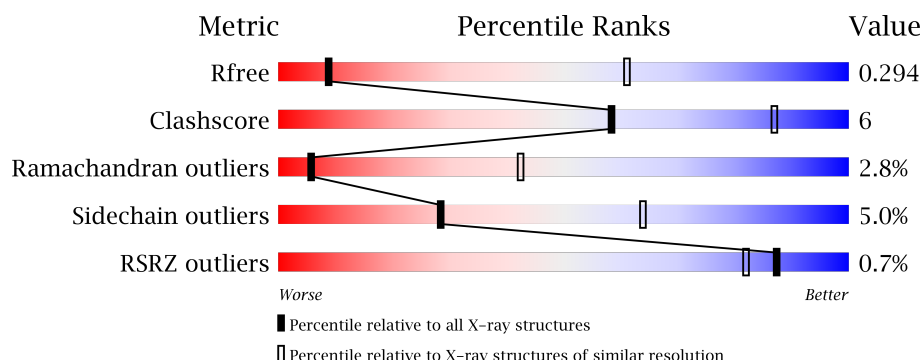
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 4.00 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	1088 (4.40-3.60)
Clashscore	112137	1187 (4.40-3.60)
Ramachandran outliers	110173	1139 (4.40-3.60)
Sidechain outliers	110143	1126 (4.40-3.60)
RSRZ outliers	101464	1099 (4.40-3.60)

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	648	
2	B	437	

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 7877 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 Reverse transcriptase/ribonuclease H p80.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	609	Total	C	N	O	S	0	0	0
			4773	3067	834	855	17			

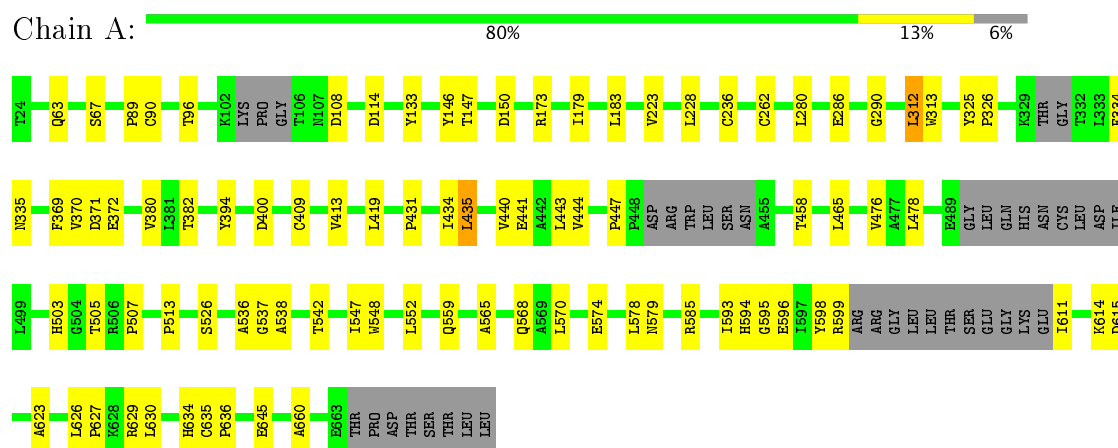
- Molecule 2 is a protein called Eukaryotic peptide chain release factor subunit 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	395	Total	C	N	O	S	0	0	0
			3104	1981	529	583	11			

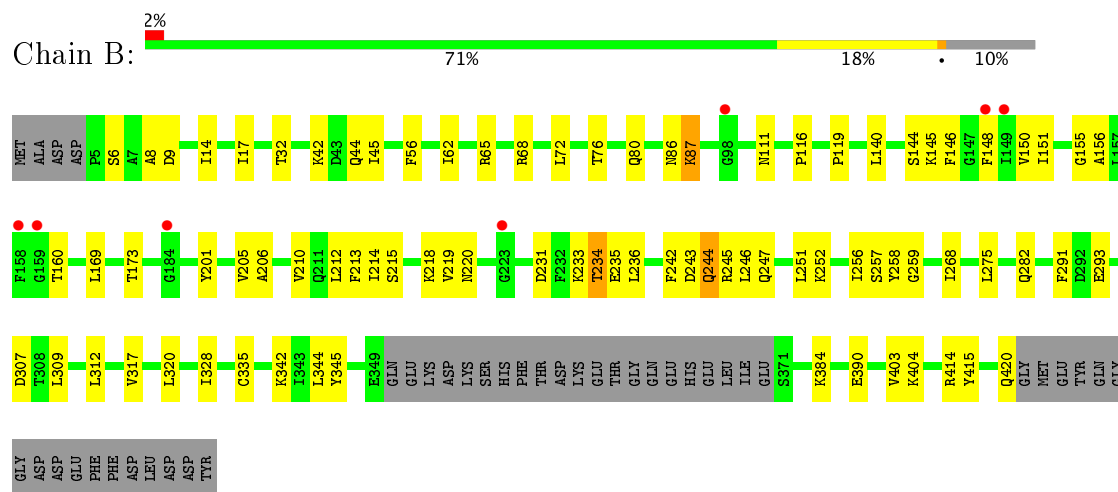
### 3 Residue-property plots

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: Reverse transcriptase/ribonuclease H p80



- Molecule 2: Eukaryotic peptide chain release factor subunit 1



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	92.65Å 92.65Å 289.95Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	96.65 – 4.00 48.32 – 4.00	Depositor EDS
% Data completeness (in resolution range)	99.8 (96.65-4.00) 99.9 (48.32-4.00)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.67 (at 4.00Å)	Xtriage
Refinement program	REFMAC 5.8.0131	Depositor
R, $R_{free}$	0.241 , 0.295 0.244 , 0.294	Depositor DCC
$R_{free}$ test set	637 reflections (5.22%)	DCC
Wilson B-factor (Å <sup>2</sup> )	192.8	Xtriage
Anisotropy	0.189	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.28 , 190.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.46$ , $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	0.058 for -h,-k,l	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	7877	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	228.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.88% 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	0.45	2/4893 (0.0%)	0.66	0/6662
2	B	0.48	0/3154	0.68	0/4242
All	All	0.46	2/8047 (0.0%)	0.67	0/10904

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	435	LEU	CG-CD2	5.41	1.71	1.51
1	A	435	LEU	CB-CG	5.40	1.68	1.52

There are no bond angle outliers.

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	4773	0	4846	53	0
2	B	3104	0	3166	37	0
All	All	7877	0	8012	88	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 6.

All (88) 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:B:312:LEU:HD21	2:B:320:LEU:HD21	1.12	1.09
1:A:634:HIS:CE1	1:A:636:PRO:HG3	2.06	0.90
1:A:147:THR:HG23	1:A:236:CYS:SG	2.11	0.90
2:B:414:ARG:O	2:B:415:TYR:CD1	2.25	0.89
1:A:147:THR:CG2	1:A:236:CYS:SG	2.61	0.88
1:A:147:THR:HG22	1:A:262:CYS:H	1.40	0.87
2:B:312:LEU:CD2	2:B:320:LEU:HD21	2.02	0.86
2:B:312:LEU:HD21	2:B:320:LEU:CD2	2.04	0.83
1:A:634:HIS:CE1	1:A:636:PRO:CG	2.65	0.78
1:A:634:HIS:CE1	1:A:636:PRO:CD	2.70	0.74
1:A:434:ILE:O	1:A:435:LEU:HD12	1.89	0.72
1:A:441:GLU:O	1:A:444:VAL:HG22	1.90	0.71
1:A:440:VAL:HG22	1:A:443:LEU:HB2	1.76	0.67
1:A:147:THR:OG1	1:A:228:LEU:HB3	1.94	0.67
1:A:147:THR:HG21	1:A:236:CYS:SG	2.35	0.67
1:A:440:VAL:CG2	1:A:443:LEU:HD12	2.25	0.66
1:A:434:ILE:C	1:A:435:LEU:HD12	2.24	0.58
2:B:317:VAL:CG2	2:B:320:LEU:HD12	2.33	0.58
1:A:611:ILE:HG23	1:A:614:LYS:HE2	1.86	0.56
1:A:369:PHE:CE1	1:A:435:LEU:HD22	2.40	0.56
2:B:414:ARG:O	2:B:415:TYR:CG	2.58	0.55
2:B:317:VAL:HG21	2:B:320:LEU:CD1	2.38	0.54
2:B:214:ILE:HD13	2:B:219:VAL:HG23	1.90	0.53
1:A:370:VAL:HG13	1:A:419:LEU:HD12	1.91	0.53
2:B:317:VAL:HG21	2:B:320:LEU:HD12	1.91	0.53
2:B:210:VAL:HG21	2:B:244:GLN:OE1	2.09	0.52
1:A:634:HIS:HE1	1:A:636:PRO:HG3	1.70	0.52
1:A:634:HIS:CE1	1:A:636:PRO:HD3	2.43	0.52
1:A:286:GLU:O	1:A:290:GLY:N	2.41	0.52
1:A:537:GLY:HA3	1:A:660:ALA:HB1	1.92	0.51
1:A:133:TYR:CG	1:A:312:LEU:HD23	2.45	0.51
2:B:146:PHE:CG	2:B:275:LEU:HD22	2.45	0.51
2:B:151:ILE:HD11	2:B:205:VAL:HG11	1.93	0.51
2:B:150:VAL:HG13	2:B:256:ILE:HD11	1.93	0.50
1:A:444:VAL:HB	1:A:465:LEU:HD11	1.92	0.50
2:B:151:ILE:HD12	2:B:236:LEU:HD11	1.93	0.50
1:A:146:TYR:O	1:A:147:THR:HG23	2.11	0.50
2:B:62:ILE:HB	2:B:68:ARG:HG3	1.94	0.50
2:B:309:LEU:HA	2:B:312:LEU:HD12	1.93	0.49
2:B:156:ALA:HB2	2:B:201:TYR:OH	2.13	0.49
2:B:148:PHE:CZ	2:B:268:ILE:HG22	2.48	0.49
2:B:17:ILE:HG21	2:B:140:LEU:HD11	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:380:VAL:HG12	1:A:394:TYR:CD2	2.48	0.48
1:A:280:LEU:HD11	1:A:313:TRP:CG	2.48	0.48
2:B:169:LEU:HD13	2:B:212:LEU:HD21	1.94	0.48
2:B:145:LYS:HE2	2:B:160:THR:HG21	1.96	0.48
2:B:169:LEU:HD13	2:B:212:LEU:CD2	2.43	0.48
1:A:634:HIS:ND1	1:A:636:PRO:CD	2.78	0.47
2:B:312:LEU:HD23	2:B:317:VAL:HG11	1.96	0.47
1:A:369:PHE:HE1	1:A:435:LEU:HD22	1.78	0.46
1:A:594:HIS:HB3	1:A:595:GLY:HA3	1.96	0.46
2:B:155:GLY:HA3	2:B:173:THR:HG22	1.97	0.46
2:B:317:VAL:HG22	2:B:320:LEU:HD12	1.96	0.46
1:A:89:PRO:HA	1:A:183:LEU:HD23	1.98	0.45
1:A:634:HIS:HE1	1:A:636:PRO:CG	2.26	0.45
1:A:444:VAL:HG11	1:A:465:LEU:HD21	1.99	0.45
2:B:76:THR:O	2:B:80:GLN:HG2	2.17	0.45
2:B:243:ASP:HA	2:B:247:GLN:HB2	2.00	0.44
1:A:440:VAL:HG23	1:A:443:LEU:HD12	1.99	0.44
1:A:623:ALA:O	1:A:626:LEU:HD23	2.18	0.44
1:A:536:ALA:HB1	1:A:552:LEU:HB2	2.00	0.44
1:A:593:ILE:HD11	2:B:291:PHE:HA	2.00	0.44
1:A:133:TYR:CD1	1:A:312:LEU:HD23	2.53	0.43
1:A:147:THR:HG22	1:A:262:CYS:N	2.20	0.43
2:B:14:ILE:HA	2:B:17:ILE:HD12	2.01	0.43
1:A:626:LEU:HB2	1:A:627:PRO:HD3	2.00	0.43
1:A:369:PHE:HB3	1:A:478:LEU:HD21	2.00	0.43
2:B:206:ALA:O	2:B:210:VAL:HG23	2.19	0.43
2:B:213:PHE:O	2:B:220:ASN:HB3	2.18	0.43
1:A:435:LEU:HD23	1:A:476:VAL:HG11	2.01	0.43
2:B:233:LYS:O	2:B:234:THR:HG23	2.19	0.43
1:A:548:TRP:CH2	1:A:568:GLN:HG2	2.55	0.42
2:B:231:ASP:O	2:B:235:GLU:N	2.50	0.42
1:A:146:TYR:O	1:A:147:THR:CG2	2.68	0.42
2:B:328:ILE:HD11	2:B:344:LEU:HB3	2.01	0.42
1:A:409:CYS:O	1:A:413:VAL:HG23	2.20	0.41
1:A:538:ALA:HB1	1:A:565:ALA:HB2	2.01	0.41
2:B:257:SER:O	2:B:259:GLY:N	2.54	0.41
2:B:56:PHE:CZ	2:B:72:LEU:HD22	2.55	0.41
1:A:443:LEU:HD23	1:A:443:LEU:HA	1.89	0.41
1:A:371:ASP:OD1	1:A:372:GLU:N	2.53	0.41
1:A:585:ARG:NH1	2:B:307:ASP:OD2	2.54	0.41
1:A:280:LEU:HD12	1:A:280:LEU:N	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:280:LEU:HD11	1:A:313:TRP:CD2	2.55	0.41
1:A:325:TYR:N	1:A:326:PRO:HD2	2.37	0.40
1:A:635:CYS:SG	1:A:635:CYS:O	2.79	0.40
1:A:173:ARG:HA	1:A:179:ILE:O	2.21	0.40
1:A:593:ILE:HG23	1:A:593:ILE:O	2.20	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	597/648 (92%)	518 (87%)	66 (11%)	13 (2%)	8	47
2	B	391/437 (90%)	336 (86%)	40 (10%)	15 (4%)	4	35
All	All	988/1085 (91%)	854 (86%)	106 (11%)	28 (3%)	6	42

All (28) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	65	ARG
2	B	87	LYS
2	B	218	LYS
1	A	507	PRO
1	A	645	GLU
2	B	8	ALA
2	B	32	THR
2	B	116	PRO
2	B	258	TYR
1	A	223	VAL
1	A	335	ASN
1	A	447	PRO
1	A	578	LEU

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Mol	Chain	Res	Type
1	A	615	ASP
1	A	629	ARG
2	B	119	PRO
2	B	244	GLN
1	A	505	THR
2	B	251	LEU
2	B	384	LYS
1	A	114	ASP
1	A	574	GLU
2	B	111	ASN
2	B	245	ARG
2	B	403	VAL
1	A	513	PRO
1	A	547	ILE
2	B	234	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	
1	A	504/540 (93%)	482 (96%)	22 (4%)	33	67
2	B	339/376 (90%)	319 (94%)	20 (6%)	23	59
All	All	843/916 (92%)	801 (95%)	42 (5%)	28	64

All (42) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	63	GLN
1	A	67	SER
1	A	90	CYS
1	A	96	THR
1	A	108	ASP
1	A	150	ASP
1	A	312	LEU
1	A	334	PHE

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Mol	Chain	Res	Type
1	A	382	THR
1	A	400	ASP
1	A	431	PRO
1	A	458	THR
1	A	503	HIS
1	A	526	SER
1	A	542	THR
1	A	559	GLN
1	A	570	LEU
1	A	579	ASN
1	A	596	GLU
1	A	598	TYR
1	A	599	ARG
1	A	630	LEU
2	B	6	SER
2	B	9	ASP
2	B	42	LYS
2	B	44	GLN
2	B	45	ILE
2	B	86	ASN
2	B	87	LYS
2	B	144	SER
2	B	215	SER
2	B	242	PHE
2	B	246	LEU
2	B	252	LYS
2	B	282	GLN
2	B	293	GLU
2	B	335	CYS
2	B	342	LYS
2	B	345	TYR
2	B	390	GLU
2	B	404	LYS
2	B	420	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	131	ASN
1	A	134	ASN
1	A	299	GLN
1	A	430	GLN

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Mol	Chain	Res	Type
1	A	592	HIS
1	A	594	HIS
1	A	634	HIS
1	A	638	HIS
1	A	649	ASN
2	B	80	GLN
2	B	200	ASN
2	B	265	ASN
2	B	401	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 [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	609/648 (93%)	-0.41	0	100 100	101, 214, 269, 289	0
2	B	395/437 (90%)	-0.15	7 (1%)	69 60	178, 249, 284, 289	0
All	All	1004/1085 (92%)	-0.31	7 (0%)	87 82	101, 229, 280, 289	0

All (7) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	98	GLY	3.9
2	B	159	GLY	3.0
2	B	158	PHE	2.6
2	B	148	PHE	2.6
2	B	184	GLY	2.5
2	B	223	GLY	2.4
2	B	149	ILE	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](#)

There are no ligands in this entry.

## 6.5 Other polymers [i](#)

There are no such residues in this entry.