



Full wwPDB X-ray Structure Validation Report ⓘ

Jul 14, 2016 – 08:28 PM EDT

PDB ID : 4WN4
Title : Crystal structure of designed cPPR-polyA protein
Authors : Coquille, S.C.; Filipovska, A.; Chia, T.S.; Rajappa, L.; Lingford, J.P.; Razif, M.F.M.; Thore, S.; Rackham, O.
Deposited on : 2014-10-10
Resolution : 3.85 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
<http://wwpdb.org/validation/2016/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
Mogul : unknown
Xtriage (Phenix) : 1.9-1692
EDS : rb-20027790
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) : rb-20027790

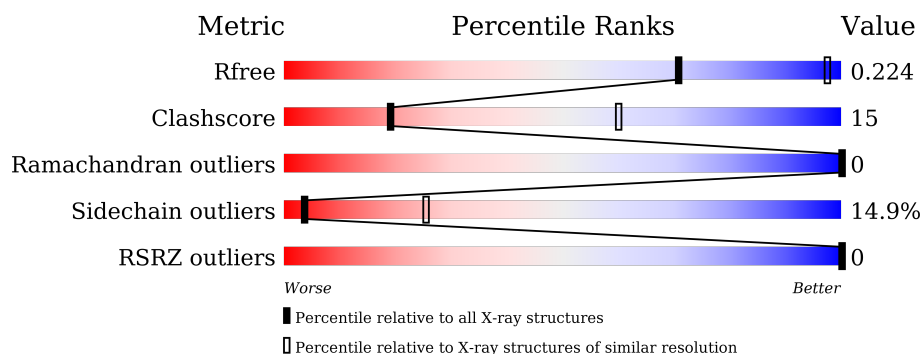
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.85 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}	91344	1000 (4.20-3.52)
Clashscore	102246	1090 (4.20-3.52)
Ramachandran outliers	100387	1046 (4.20-3.52)
Sidechain outliers	100360	1038 (4.20-3.52)
RSRZ outliers	91569	1004 (4.20-3.52)

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. 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	303	<div> <div>44%</div> <div>23%</div> <div>.</div> <div>31%</div> </div>
1	B	303	<div> <div>45%</div> <div>20%</div> <div>5%</div> <div>31%</div> </div>

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 3216 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.

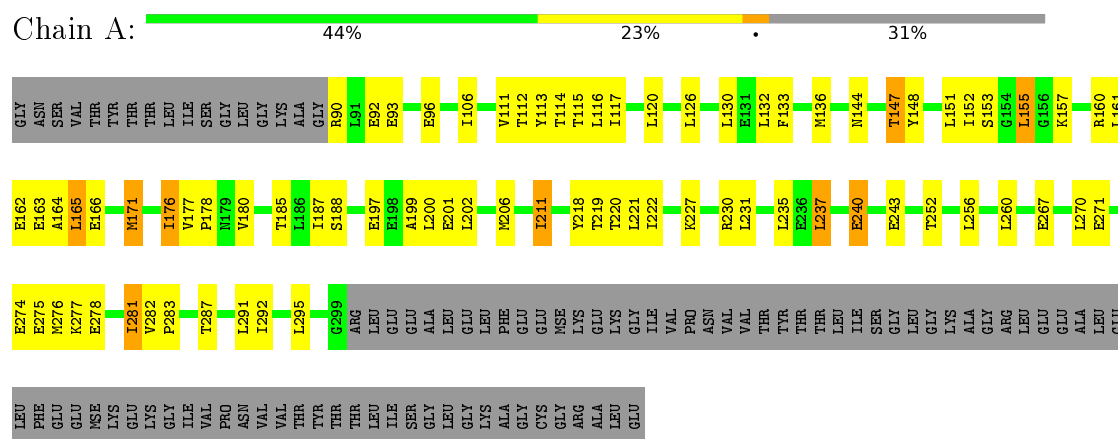
- Molecule 1 is a protein called Pentatricopeptide repeat protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	210	Total	C	N	O	Se	0	0	0
			1608	1032	252	318	6			
1	B	210	Total	C	N	O	Se	0	0	0
			1608	1032	252	318	6			

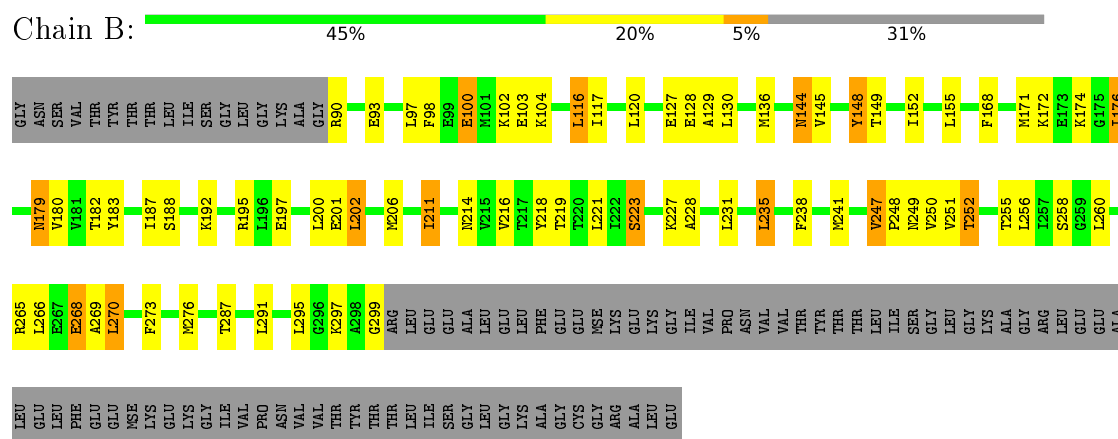
3 Residue-property plots

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: Pentatricopeptide repeat protein



• Molecule 1: Pentatricopeptide repeat protein



4 Data and refinement statistics

Property	Value	Source
Space group	F 2 3	Depositor
Cell constants a, b, c, α , β , γ	204.72Å 204.72Å 204.72Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.79 – 3.85 46.97 – 3.85	Depositor EDS
% Data completeness (in resolution range)	99.9 (19.79-3.85) 100.0 (46.97-3.85)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.82 (at 3.88Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.1_1168)	Depositor
R, R_{free}	0.179 , 0.230 0.179 , 0.224	Depositor DCC
R_{free} test set	678 reflections (9.90%)	DCC
Wilson B-factor (Å ²)	179.9	Xtriage
Anisotropy	0.000	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 156.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.049 for k,h,-l	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	3216	wwPDB-VP
Average B, all atoms (Å ²)	192.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.49% 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	0.51	0/1619	0.67	0/2169
1	B	0.55	1/1619 (0.1%)	0.71	1/2169 (0.0%)
All	All	0.53	1/3238 (0.0%)	0.69	1/4338 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	248	PRO	N-CD	5.25	1.55	1.47

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	247	VAL	C-N-CD	5.71	140.40	128.40

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	1608	0	1679	41	2
1	B	1608	0	1679	60	2
All	All	3216	0	3358	100	2

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 15.

All (100) 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:B:219:THR:HG22	1:B:252:THR:CG2	1.81	1.10
1:B:219:THR:HG22	1:B:252:THR:HG23	1.14	1.10
1:B:249:ASN:HD21	1:B:251:VAL:HB	1.22	1.02
1:B:249:ASN:O	1:B:252:THR:OG1	1.88	0.92
1:B:249:ASN:ND2	1:B:251:VAL:HB	1.89	0.88
1:B:179:ASN:HD22	1:B:179:ASN:H	1.31	0.79
1:A:231:LEU:HD21	1:A:260:LEU:HD23	1.65	0.79
1:A:276:MSE:HE3	1:A:281:ILE:HD12	1.65	0.79
1:B:249:ASN:OD1	1:B:252:THR:N	2.17	0.77
1:B:231:LEU:HD21	1:B:260:LEU:HD23	1.66	0.76
1:A:187:ILE:HG23	1:A:199:ALA:HB1	1.68	0.75
1:B:223:SER:HA	1:B:255:THR:HG21	1.74	0.69
1:B:144:ASN:N	1:B:144:ASN:OD1	2.29	0.66
1:A:90:ARG:HG2	1:A:93:GLU:HG3	1.80	0.64
1:B:149:THR:HG21	1:B:179:ASN:HD21	1.63	0.64
1:B:265:ARG:HB3	1:B:268:GLU:HG3	1.79	0.64
1:A:188:SER:HA	1:A:220:THR:HG21	1.81	0.63
1:A:153:SER:HA	1:A:185:THR:HG21	1.83	0.60
1:B:260:LEU:HD13	1:B:268:GLU:HB2	1.83	0.59
1:B:219:THR:HG21	1:B:249:ASN:CG	2.23	0.59
1:B:174:LYS:HB2	1:B:176:ILE:HD11	1.86	0.58
1:B:238:PHE:HA	1:B:241:MSE:HE2	1.83	0.58
1:B:127:GLU:O	1:B:130:LEU:HB2	2.04	0.57
1:B:168:PHE:CE2	1:B:172:LYS:HD2	2.39	0.57
1:A:219:THR:HG22	1:A:252:THR:OG1	2.06	0.56
1:B:148:TYR:HE2	1:B:176:ILE:HD12	1.70	0.56
1:B:214:ASN:N	1:B:214:ASN:OD1	2.39	0.56
1:B:250:VAL:HG13	1:B:251:VAL:N	2.20	0.55
1:B:149:THR:HG21	1:B:179:ASN:ND2	2.22	0.55
1:B:265:ARG:NE	1:B:268:GLU:OE1	2.40	0.54
1:B:249:ASN:OD1	1:B:252:THR:HG23	2.07	0.54
1:B:273:PHE:O	1:B:276:MSE:HB3	2.09	0.53
1:B:247:VAL:O	1:B:247:VAL:HG13	2.09	0.52
1:A:148:TYR:CD2	1:A:171:MSE:HB2	2.44	0.52
1:B:249:ASN:OD1	1:B:252:THR:OG1	2.18	0.52
1:A:275:GLU:HA	1:A:278:GLU:HG3	1.92	0.52
1:B:148:TYR:O	1:B:152:ILE:HG13	2.10	0.51
1:B:206:MSE:HG3	1:B:211:ILE:HB	1.91	0.51
1:A:197:GLU:O	1:A:201:GLU:HG3	2.10	0.51
1:B:179:ASN:HD22	1:B:179:ASN:N	2.06	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:92:GLU:O	1:A:96:GLU:HG3	2.12	0.50
1:A:206:MSE:HG3	1:A:211:ILE:HB	1.94	0.50
1:A:111:VAL:HA	1:A:114:THR:HG22	1.93	0.50
1:A:153:SER:O	1:A:157:LYS:HG2	2.11	0.50
1:B:197:GLU:O	1:B:201:GLU:HG3	2.12	0.50
1:B:219:THR:CG2	1:B:252:THR:HG23	2.09	0.49
1:A:117:ILE:HD11	1:A:132:LEU:HB3	1.94	0.48
1:B:120:LEU:HB3	1:B:129:ALA:HB2	1.96	0.48
1:A:155:LEU:HB3	1:A:164:ALA:HB2	1.95	0.48
1:B:266:LEU:HD11	1:B:295:LEU:HA	1.96	0.48
1:A:291:LEU:O	1:A:295:LEU:HB2	2.14	0.47
1:A:147:THR:O	1:A:151:LEU:HG	2.14	0.47
1:A:206:MSE:O	1:A:211:ILE:HG12	2.14	0.47
1:A:130:LEU:HA	1:A:130:LEU:HD23	1.67	0.47
1:A:180:VAL:HG22	1:A:211:ILE:HG22	1.97	0.46
1:B:100:GLU:O	1:B:104:LYS:HG3	2.15	0.46
1:A:230:ARG:HG3	1:B:228:ALA:HB1	1.97	0.46
1:B:200:LEU:HA	1:B:200:LEU:HD23	1.79	0.46
1:B:270:LEU:HA	1:B:270:LEU:HD12	1.68	0.46
1:A:171:MSE:HG3	1:A:176:ILE:HB	1.98	0.45
1:B:219:THR:HG22	1:B:252:THR:HG21	1.86	0.45
1:B:171:MSE:O	1:B:176:ILE:HG13	2.17	0.45
1:B:179:ASN:H	1:B:179:ASN:ND2	2.08	0.45
1:B:200:LEU:HD23	1:B:221:LEU:HD22	1.99	0.44
1:A:165:LEU:HA	1:A:165:LEU:HD22	1.81	0.44
1:A:282:VAL:HA	1:A:283:PRO:HD3	1.72	0.44
1:B:235:LEU:HD13	1:B:235:LEU:HA	1.82	0.44
1:A:111:VAL:O	1:A:115:THR:HG23	2.18	0.44
1:A:148:TYR:O	1:A:152:ILE:HG13	2.18	0.44
1:B:148:TYR:CE2	1:B:176:ILE:HD12	2.51	0.44
1:B:249:ASN:ND2	1:B:251:VAL:CB	2.73	0.44
1:B:291:LEU:HD23	1:B:291:LEU:HA	1.82	0.43
1:A:116:LEU:HA	1:A:116:LEU:HD23	1.71	0.43
1:B:116:LEU:HA	1:B:116:LEU:HD22	1.84	0.43
1:B:120:LEU:HA	1:B:120:LEU:HD23	1.75	0.43
1:B:183:TYR:O	1:B:187:ILE:HG12	2.19	0.43
1:B:97:LEU:HD12	1:B:97:LEU:HA	1.83	0.43
1:B:174:LYS:HB2	1:B:176:ILE:CG1	2.49	0.42
1:A:240:GLU:HA	1:A:243:GLU:HB2	2.02	0.42
1:A:256:LEU:HA	1:A:256:LEU:HD23	1.86	0.42
1:B:260:LEU:HB2	1:B:269:ALA:HB2	2.01	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:223:SER:O	1:B:227:LYS:HB2	2.20	0.42
1:A:113:TYR:HE2	1:A:136:MSE:HA	1.84	0.42
1:A:113:TYR:HD2	1:A:136:MSE:HG3	1.85	0.41
1:A:160:ARG:HG2	1:A:163:GLU:HG3	2.01	0.41
1:B:98:PHE:CE2	1:B:102:LYS:HD2	2.55	0.41
1:B:260:LEU:HD12	1:B:269:ALA:HA	2.02	0.41
1:A:120:LEU:HD23	1:A:120:LEU:HA	1.81	0.41
1:A:222:ILE:HG12	1:A:237:LEU:HD22	2.03	0.41
1:B:100:GLU:HA	1:B:103:GLU:HB3	2.01	0.41
1:A:155:LEU:HD22	1:A:155:LEU:HA	1.90	0.41
1:B:155:LEU:HD23	1:B:155:LEU:HA	1.87	0.41
1:A:162:GLU:O	1:A:166:GLU:HG3	2.20	0.41
1:B:174:LYS:HE2	1:B:174:LYS:HB3	1.84	0.41
1:B:297:LYS:HE3	1:B:297:LYS:HB2	1.79	0.41
1:B:202:LEU:HD23	1:B:202:LEU:HA	1.85	0.41
1:A:274:GLU:O	1:A:278:GLU:HG2	2.21	0.40
1:A:133:PHE:CD1	1:A:151:LEU:HD11	2.56	0.40
1:A:177:VAL:HA	1:A:178:PRO:HD3	1.74	0.40
1:A:267:GLU:O	1:A:270:LEU:HB2	2.21	0.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:277:LYS:NZ	1:B:100:GLU:OE2[18_544]	2.06	0.14
1:A:90:ARG:N	1:B:299:GLY:O[10_555]	2.15	0.05

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	208/303 (69%)	207 (100%)	1 (0%)	0	100 100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	208/303 (69%)	200 (96%)	8 (4%)	0	100	100
All	All	416/606 (69%)	407 (98%)	9 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	174/240 (72%)	151 (87%)	23 (13%)	5	30
1	B	174/240 (72%)	145 (83%)	29 (17%)	3	21
All	All	348/480 (72%)	296 (85%)	52 (15%)	4	25

All (52) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	106	ILE
1	A	112	THR
1	A	126	LEU
1	A	144	ASN
1	A	147	THR
1	A	155	LEU
1	A	161	LEU
1	A	165	LEU
1	A	171	MSE
1	A	176	ILE
1	A	200	LEU
1	A	202	LEU
1	A	211	ILE
1	A	218	TYR
1	A	221	LEU
1	A	227	LYS
1	A	235	LEU
1	A	237	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	240	GLU
1	A	271	GLU
1	A	281	ILE
1	A	287	THR
1	A	292	ILE
1	B	90	ARG
1	B	93	GLU
1	B	100	GLU
1	B	116	LEU
1	B	117	ILE
1	B	128	GLU
1	B	136	MSE
1	B	144	ASN
1	B	145	VAL
1	B	148	TYR
1	B	176	ILE
1	B	179	ASN
1	B	180	VAL
1	B	182	THR
1	B	188	SER
1	B	192	LYS
1	B	195	ARG
1	B	202	LEU
1	B	211	ILE
1	B	216	VAL
1	B	218	TYR
1	B	223	SER
1	B	235	LEU
1	B	252	THR
1	B	256	LEU
1	B	258	SER
1	B	268	GLU
1	B	270	LEU
1	B	287	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	179	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 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, 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	204/303 (67%)	-0.29	0 100 100	169, 195, 211, 222	0
1	B	204/303 (67%)	-0.20	0 100 100	166, 190, 207, 223	0
All	All	408/606 (67%)	-0.24	0 100 100	166, 192, 210, 223	0

There are no RSRZ outliers to report.

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.