



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 12:34 PM UTC

PDB ID : 5CQR / pdb_00005cqr
Title : Dimerization of Elp1 is essential for Elongator complex assembly
Authors : Lin, Z.; Xu, H.; Li, F.; Diao, W.; Long, J.; Shen, Y.
Deposited on : 2015-07-22
Resolution : 3.02 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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

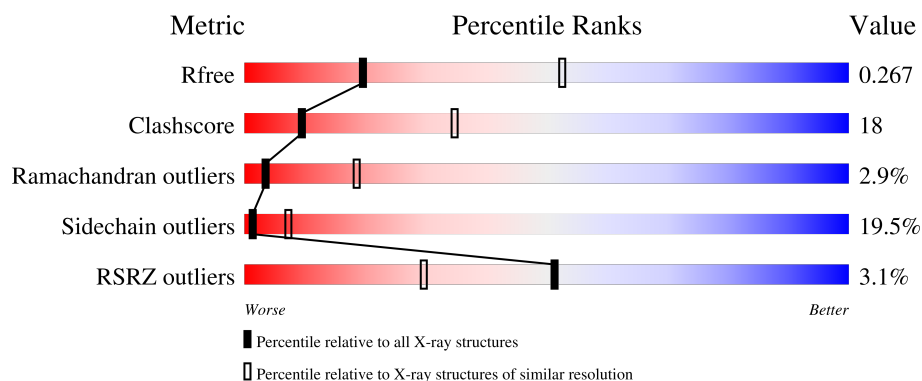
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.02 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}	180053	3131 (3.04-3.00)
Clashscore	190562	3444 (3.04-3.00)
Ramachandran outliers	187476	3319 (3.04-3.00)
Sidechain outliers	187428	3322 (3.04-3.00)
RSRZ outliers	180081	3130 (3.04-3.00)

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 of 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	622	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 3600 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 Elongator complex protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	455	Total	C	N	O	S	0	0	0
			3595	2310	598	665	22			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	711	GLY	-	expression tag	UNP O95163
A	712	PRO	-	expression tag	UNP O95163
A	713	GLY	-	expression tag	UNP O95163
A	714	SER	-	expression tag	UNP O95163

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	5	Total	O	0	0
			5	5		

4 Data and refinement statistics

Property	Value	Source
Space group	P 61 2 2	Depositor
Cell constants a, b, c, α , β , γ	73.02Å 73.02Å 479.51Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	46.47 – 3.02 46.47 – 3.02	Depositor EDS
% Data completeness (in resolution range)	86.8 (46.47-3.02) 86.7 (46.47-3.02)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.32 (at 3.01Å)	Xtriage
Refinement program	PHENIX 1.6.4_486	Depositor
R, R_{free}	0.221 , 0.270 0.218 , 0.267	Depositor DCC
R_{free} test set	1398 reflections (9.84%)	wwPDB-VP
Wilson B-factor (Å ²)	50.3	Xtriage
Anisotropy	0.323	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 61.0	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	0.91	EDS
Total number of atoms	3600	wwPDB-VP
Average B, all atoms (Å ²)	58.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.39% 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	0.58	0/3664	0.93	8/4957 (0.2%)

There are no bond length outliers.

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1072	CYS	N-CA-C	6.94	118.92	111.36
1	A	917	TYR	N-CA-C	-6.04	105.45	114.64
1	A	765	GLY	N-CA-C	-5.49	107.44	114.85
1	A	1232	LEU	N-CA-C	-5.21	107.09	112.93
1	A	954	GLY	CA-C-N	5.11	125.94	120.47
1	A	954	GLY	C-N-CA	5.11	125.94	120.47
1	A	774	ILE	CB-CA-C	-5.06	102.99	111.29
1	A	830	ILE	N-CA-C	5.01	117.31	111.05

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	3595	0	3506	127	0
2	A	5	0	0	1	0
All	All	3600	0	3506	127	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 18.

All (127) 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:1090:GLU:HG3	1:A:1238:HIS:HE1	1.37	0.87
1:A:776:SER:O	1:A:780:ILE:HG22	1.74	0.87
1:A:855:LEU:HD13	1:A:893:HIS:HB3	1.58	0.86
1:A:722:ARG:CG	1:A:722:ARG:HH11	1.89	0.85
1:A:791:ASP:OD1	1:A:793:THR:HB	1.81	0.81
1:A:1121:MET:HE1	1:A:1258:ALA:CB	2.12	0.80
1:A:1090:GLU:HG3	1:A:1238:HIS:CE1	2.17	0.79
1:A:996:LEU:HB3	1:A:1005:ALA:HB2	1.63	0.78
1:A:918:LEU:N	1:A:919:PRO:HD2	1.97	0.78
1:A:722:ARG:HH11	1:A:722:ARG:HG2	1.47	0.77
1:A:830:ILE:O	1:A:831:ASN:HB2	1.87	0.73
1:A:1121:MET:HE1	1:A:1258:ALA:HB1	1.76	0.64
1:A:1121:MET:HA	1:A:1121:MET:HE2	1.78	0.64
1:A:1227:GLN:HG3	1:A:1229:THR:HG23	1.80	0.64
1:A:1235:GLU:O	1:A:1239:ILE:HG22	1.98	0.63
1:A:824:ARG:HG3	1:A:839:ILE:HG23	1.80	0.62
1:A:958:PHE:N	1:A:959:PRO:HD2	2.15	0.61
1:A:975:LEU:HD21	1:A:988:ILE:HG22	1.82	0.61
1:A:950:LEU:HD13	1:A:961:CYS:HB2	1.83	0.61
1:A:1023:LEU:CD2	1:A:1052:LEU:HD23	2.30	0.60
1:A:1264:GLN:C	1:A:1266:MET:H	2.08	0.60
1:A:780:ILE:HD11	1:A:827:MET:SD	2.41	0.60
1:A:928:GLU:OE1	1:A:930:ASN:HB2	2.01	0.60
1:A:1103:ASP:O	1:A:1107:THR:HG23	2.02	0.59
1:A:919:PRO:O	1:A:923:THR:HG23	2.01	0.59
1:A:1046:VAL:HG22	1:A:1073:ALA:HA	1.85	0.59
1:A:749:ARG:CZ	1:A:749:ARG:HB2	2.32	0.58
1:A:904:LEU:O	1:A:908:GLU:HG2	2.03	0.58
1:A:1121:MET:HE1	1:A:1258:ALA:HB3	1.85	0.58
1:A:928:GLU:HG2	1:A:929:THR:N	2.17	0.58
1:A:794:LYS:HE3	1:A:794:LYS:HA	1.86	0.58
1:A:835:TYR:O	1:A:839:ILE:HG13	2.05	0.57
1:A:769:THR:O	1:A:773:GLN:HG3	2.06	0.56
1:A:1261:ASP:C	1:A:1263:LEU:H	2.13	0.56
1:A:917:TYR:CE1	1:A:918:LEU:HD22	2.41	0.56
1:A:918:LEU:N	1:A:919:PRO:CD	2.68	0.56
1:A:1023:LEU:HD23	1:A:1052:LEU:HD23	1.87	0.56
1:A:722:ARG:HG2	1:A:722:ARG:NH1	2.14	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1330:LEU:O	1:A:1331:LEU:HD23	2.07	0.55
1:A:761:LYS:HE3	1:A:811:PRO:N	2.22	0.55
1:A:1002:TYR:CE1	1:A:1024:THR:HG21	2.42	0.55
1:A:924:LEU:O	1:A:927:MET:HG3	2.07	0.54
1:A:743:GLU:HA	1:A:743:GLU:OE1	2.07	0.54
1:A:745:MET:SD	1:A:755:ILE:HG22	2.48	0.54
1:A:1063:ILE:HD12	1:A:1088:ALA:HB2	1.89	0.54
1:A:1003:GLU:HB3	1:A:1004:PRO:HD3	1.90	0.54
1:A:742:PHE:C	1:A:742:PHE:CD2	2.85	0.53
1:A:814:ASN:O	1:A:818:LEU:HG	2.08	0.53
1:A:1050:ARG:HH12	1:A:1075:ASP:CG	2.16	0.53
1:A:824:ARG:O	1:A:828:GLU:HG2	2.08	0.53
1:A:868:ASP:C	1:A:870:ASP:H	2.16	0.53
1:A:927:MET:HB2	1:A:932:GLN:HB2	1.90	0.53
1:A:978:TYR:CD1	1:A:978:TYR:N	2.76	0.53
1:A:1328:LEU:C	1:A:1330:LEU:N	2.66	0.53
1:A:1015:HIS:HB2	1:A:1038:LEU:HD21	1.91	0.52
1:A:774:ILE:O	1:A:775:ASP:C	2.50	0.52
1:A:1129:ALA:C	1:A:1131:PHE:H	2.17	0.52
1:A:756:TYR:C	1:A:756:TYR:CD2	2.87	0.52
1:A:812:ASP:OD1	1:A:812:ASP:C	2.52	0.52
1:A:1264:GLN:C	1:A:1266:MET:N	2.67	0.52
1:A:978:TYR:N	1:A:978:TYR:HD1	2.08	0.52
1:A:745:MET:HE1	1:A:755:ILE:HG22	1.92	0.52
1:A:997:MET:HE1	1:A:1021:ALA:HB2	1.92	0.52
1:A:771:ILE:CD1	1:A:780:ILE:HD12	2.40	0.51
1:A:722:ARG:HH11	1:A:722:ARG:HG3	1.75	0.51
1:A:855:LEU:HD13	1:A:893:HIS:CB	2.34	0.51
1:A:950:LEU:HD22	1:A:957:TYR:HB3	1.94	0.50
1:A:1028:TRP:CE3	1:A:1068:VAL:HG22	2.47	0.50
1:A:1256:GLN:HE22	1:A:1328:LEU:H	1.60	0.49
1:A:729:ILE:CG2	1:A:745:MET:HE2	2.42	0.49
1:A:763:PHE:C	1:A:763:PHE:CD2	2.90	0.49
1:A:780:ILE:O	1:A:780:ILE:HG12	2.11	0.49
1:A:903:VAL:O	1:A:906:VAL:HG22	2.13	0.49
1:A:729:ILE:HG23	1:A:745:MET:HE2	1.94	0.49
1:A:943:TYR:O	1:A:947:ILE:HG12	2.12	0.49
1:A:776:SER:O	1:A:780:ILE:CG2	2.56	0.48
1:A:944:GLU:HG3	1:A:973:GLU:HG3	1.95	0.47
1:A:1232:LEU:HG	1:A:1232:LEU:O	2.15	0.47
1:A:1050:ARG:NH1	1:A:1075:ASP:OD2	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:843:HIS:HB3	1:A:854:VAL:HG23	1.95	0.47
1:A:1328:LEU:C	1:A:1330:LEU:H	2.23	0.46
1:A:958:PHE:N	1:A:959:PRO:CD	2.79	0.46
1:A:1259:PHE:O	1:A:1263:LEU:HB2	2.15	0.46
1:A:1261:ASP:C	1:A:1263:LEU:N	2.73	0.46
1:A:1328:LEU:HD22	1:A:1328:LEU:HA	1.75	0.46
1:A:953:CYS:O	1:A:957:TYR:HD2	1.98	0.46
1:A:1234:ASP:O	1:A:1237:TYR:HB3	2.15	0.46
1:A:1244:PHE:CD2	1:A:1244:PHE:C	2.94	0.46
1:A:1117:GLN:HG3	1:A:1118:LYS:N	2.31	0.45
1:A:1053:ALA:HB2	1:A:1069:LEU:HD13	1.98	0.45
1:A:728:GLN:CA	1:A:728:GLN:NE2	2.80	0.45
1:A:768:GLU:HA	1:A:826:VAL:HG11	1.99	0.45
1:A:1098:LYS:O	1:A:1098:LYS:HG2	2.16	0.44
1:A:1232:LEU:O	1:A:1236:VAL:HG23	2.17	0.44
1:A:980:PRO:O	1:A:981:SER:CB	2.66	0.44
1:A:1028:TRP:HA	1:A:1031:ALA:HB3	2.00	0.44
1:A:975:LEU:CD2	1:A:988:ILE:HG22	2.47	0.44
1:A:868:ASP:C	1:A:870:ASP:N	2.76	0.44
1:A:780:ILE:O	1:A:780:ILE:CG1	2.66	0.43
1:A:749:ARG:HB2	1:A:749:ARG:NH1	2.33	0.43
1:A:917:TYR:C	1:A:917:TYR:CD1	2.96	0.43
1:A:1261:ASP:O	1:A:1265:LEU:HB2	2.18	0.43
1:A:858:VAL:O	1:A:858:VAL:CG1	2.66	0.43
1:A:1067:MET:O	1:A:1071:GLU:HG2	2.18	0.43
1:A:1256:GLN:HE22	1:A:1327:LYS:HA	1.83	0.43
1:A:776:SER:HB3	1:A:779:HIS:HB2	2.00	0.43
1:A:1251:GLN:CD	1:A:1251:GLN:H	2.26	0.43
1:A:861:LEU:HD23	1:A:861:LEU:HA	1.81	0.43
1:A:905:MET:HE3	1:A:905:MET:HB2	1.86	0.43
1:A:1075:ASP:O	1:A:1076:TYR:C	2.62	0.42
1:A:788:LYS:NZ	1:A:788:LYS:HB2	2.34	0.42
1:A:1028:TRP:CB	1:A:1052:LEU:HD13	2.49	0.42
1:A:780:ILE:HD13	1:A:780:ILE:HG21	1.76	0.42
1:A:852:GLU:HB2	2:A:1402:HOH:O	2.20	0.42
1:A:1055:LYS:NZ	1:A:1055:LYS:HB3	2.35	0.42
1:A:908:GLU:C	1:A:910:SER:H	2.28	0.42
1:A:996:LEU:HD12	1:A:996:LEU:HA	1.68	0.41
1:A:1264:GLN:O	1:A:1266:MET:N	2.53	0.41
1:A:1028:TRP:HB2	1:A:1052:LEU:HD13	2.02	0.41
1:A:1262:THR:HG22	1:A:1262:THR:O	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:993:GLY:HA3	1:A:1009:PHE:CZ	2.55	0.41
1:A:1235:GLU:H	1:A:1235:GLU:HG3	1.68	0.41
1:A:852:GLU:O	1:A:856:GLN:HG2	2.20	0.41
1:A:721:HIS:CD2	1:A:721:HIS:H	2.38	0.41
1:A:1083:LEU:HD12	1:A:1092:ALA:HA	2.03	0.40
1:A:1232:LEU:C	1:A:1232:LEU:HD23	2.46	0.40
1:A:755:ILE:HG21	1:A:755:ILE:HD13	1.66	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	445/622 (72%)	389 (87%)	43 (10%)	13 (3%)	3	18

All (13) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1122	ALA
1	A	1126	SER
1	A	776	SER
1	A	831	ASN
1	A	895	LEU
1	A	1265	LEU
1	A	1130	THR
1	A	910	SER
1	A	1076	TYR
1	A	950	LEU
1	A	1262	THR
1	A	869	PRO
1	A	868	ASP

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	374/555 (67%)	301 (80%)	73 (20%)	1 7

All (73) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	722	ARG
1	A	724	LEU
1	A	728	GLN
1	A	735	LYS
1	A	740	GLU
1	A	744	CYS
1	A	749	ARG
1	A	754	LEU
1	A	755	ILE
1	A	761	LYS
1	A	768	GLU
1	A	769	THR
1	A	774	ILE
1	A	775	ASP
1	A	780	ILE
1	A	782	LEU
1	A	788	LYS
1	A	793	THR
1	A	794	LYS
1	A	812	ASP
1	A	838	SER
1	A	844	VAL
1	A	852	GLU
1	A	855	LEU
1	A	858	VAL
1	A	870	ASP
1	A	875	GLU
1	A	878	LEU
1	A	882	LEU
1	A	890	LEU

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Mol	Chain	Res	Type
1	A	918	LEU
1	A	923	THR
1	A	928	GLU
1	A	936	ILE
1	A	941	LYS
1	A	964	LEU
1	A	968	LYS
1	A	973	GLU
1	A	978	TYR
1	A	989	SER
1	A	994	GLU
1	A	996	LEU
1	A	1001	MET
1	A	1003	GLU
1	A	1017	LYS
1	A	1023	LEU
1	A	1046	VAL
1	A	1048	LEU
1	A	1055	LYS
1	A	1057	VAL
1	A	1069	LEU
1	A	1075	ASP
1	A	1078	GLU
1	A	1085	GLU
1	A	1093	LEU
1	A	1105	ILE
1	A	1108	ASN
1	A	1117	GLN
1	A	1121	MET
1	A	1125	ASP
1	A	1227	GLN
1	A	1232	LEU
1	A	1234	ASP
1	A	1239	ILE
1	A	1247	GLU
1	A	1251	GLN
1	A	1255	LEU
1	A	1263	LEU
1	A	1264	GLN
1	A	1265	LEU
1	A	1324	THR
1	A	1325	GLN

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Mol	Chain	Res	Type
1	A	1328	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	721	HIS
1	A	728	GLN
1	A	893	HIS
1	A	922	ASN
1	A	949	HIS
1	A	963	ASN
1	A	986	GLN
1	A	1037	GLN
1	A	1039	ASN
1	A	1044	GLN
1	A	1117	GLN
1	A	1227	GLN
1	A	1238	HIS
1	A	1256	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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 oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

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	455/622 (73%)	-0.21	14 (3%)	51 30	23, 53, 109, 158	0

All (14) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	911	GLN	5.2
1	A	811	PRO	5.0
1	A	800	PRO	3.4
1	A	812	ASP	3.0
1	A	1225	VAL	2.8
1	A	865	ALA	2.8
1	A	1331	LEU	2.7
1	A	1229	THR	2.5
1	A	868	ASP	2.4
1	A	869	PRO	2.4
1	A	1321	ASN	2.3
1	A	866	PRO	2.2
1	A	1126	SER	2.1
1	A	1265	LEU	2.0

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 oligosaccharides 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.