



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 11:49 AM UTC

PDB ID : 6H02 / pdb_00006h02
Title : Crystal structure of human Mediator subunit MED23
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Deposited on : 2018-07-06
Resolution : 2.80 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

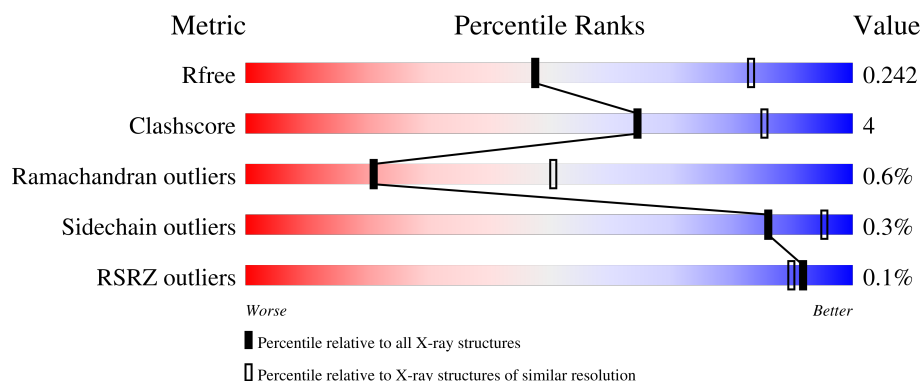
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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	3866 (2.80-2.80)
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (2.80-2.80)

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	1382	 86% 10% .
2	B	134	 75% 17% 8%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 11714 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 Mediator of RNA polymerase II transcription subunit 23.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1334	Total	C	N	O	S	0	0	0
			10774	6967	1827	1909	71			

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1369	ASP	-	expression tag	UNP Q9ULK4
A	1370	VAL	-	expression tag	UNP Q9ULK4
A	1371	LEU	-	expression tag	UNP Q9ULK4
A	1372	PHE	-	expression tag	UNP Q9ULK4
A	1373	GLN	-	expression tag	UNP Q9ULK4
A	1374	GLY	-	expression tag	UNP Q9ULK4
A	1375	PRO	-	expression tag	UNP Q9ULK4
A	1376	GLY	-	expression tag	UNP Q9ULK4
A	1377	HIS	-	expression tag	UNP Q9ULK4
A	1378	HIS	-	expression tag	UNP Q9ULK4
A	1379	HIS	-	expression tag	UNP Q9ULK4
A	1380	HIS	-	expression tag	UNP Q9ULK4
A	1381	HIS	-	expression tag	UNP Q9ULK4
A	1382	HIS	-	expression tag	UNP Q9ULK4

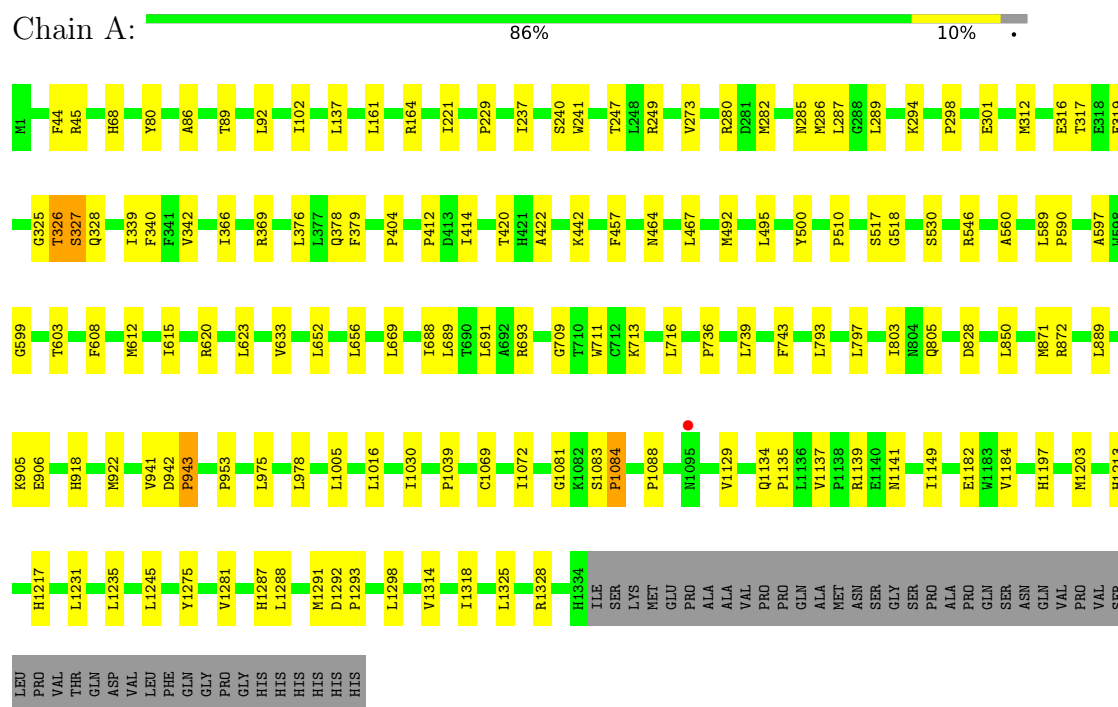
- Molecule 2 is a protein called LAMA nanobody NB106.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	123	Total	C	N	O	S	0	0	0
			940	588	165	181	6			

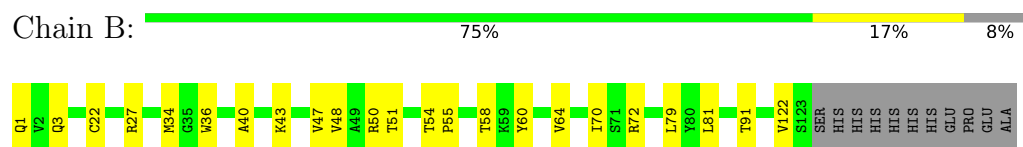
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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: Mediator of RNA polymerase II transcription subunit 23



• Molecule 2: LAMA nanobody NB106



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	75.65Å 137.18Å 90.11Å 90.00° 110.98° 90.00°	Depositor
Resolution (Å)	15.00 – 2.80 15.00 – 2.80	Depositor EDS
% Data completeness (in resolution range)	99.9 (15.00-2.80) 99.3 (15.00-2.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.30 (at 2.81Å)	Xtriage
Refinement program	PHENIX 1.13_2998, PHENIX 1.13_2998	Depositor
R, R_{free}	0.199 , 0.240 0.202 , 0.242	Depositor DCC
R_{free} test set	2010 reflections (4.75%)	wwPDB-VP
Wilson B-factor (Å ²)	75.8	Xtriage
Anisotropy	0.590	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 61.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	11714	wwPDB-VP
Average B, all atoms (Å ²)	91.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.22% 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	0.10	0/11056	0.28	1/15023 (0.0%)
2	B	0.10	0/959	0.31	0/1301
All	All	0.10	0/12015	0.29	1/16324 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	518	GLY	N-CA-C	6.32	120.31	112.73

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	10774	0	10838	79	0
2	B	940	0	913	12	0
All	All	11714	0	11751	91	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 4.

All (91) 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:510:PRO:HD3	1:A:922:MET:HE1	1.64	0.80
1:A:273:VAL:HG21	1:A:286:MET:HE1	1.65	0.78
2:B:47:VAL:HG21	2:B:50:ARG:HH11	1.55	0.72
1:A:45:ARG:HH22	1:A:89:THR:HG21	1.55	0.71
1:A:623:LEU:HD23	1:A:652:LEU:HD11	1.72	0.71
2:B:91:THR:HG22	2:B:122:VAL:H	1.54	0.70
1:A:517:SER:HB2	1:A:560:ALA:HB2	1.78	0.66
1:A:793:LEU:HD22	1:A:803:ILE:HD13	1.79	0.64
1:A:615:ILE:O	1:A:620:ARG:NH1	2.33	0.62
1:A:86:ALA:HB1	1:A:92:LEU:HD13	1.82	0.61
1:A:44:PHE:HE2	1:A:92:LEU:HD11	1.66	0.60
2:B:1:GLN:OE1	2:B:3:GLN:NE2	2.34	0.60
1:A:669:LEU:HD21	1:A:711:TRP:HA	1.83	0.59
2:B:1:GLN:H3	2:B:27:ARG:HD3	1.68	0.58
1:A:736:PRO:HD2	1:A:739:LEU:HD12	1.86	0.58
1:A:1072:ILE:HD13	1:A:1149:ILE:HG12	1.85	0.58
1:A:312:MET:HE1	1:A:366:ILE:HG23	1.87	0.56
1:A:1197:HIS:ND1	1:A:1203:MET:SD	2.79	0.56
1:A:339:ILE:HD11	1:A:378:GLN:HB3	1.87	0.56
1:A:1231:LEU:HD23	1:A:1235:LEU:HD12	1.88	0.55
1:A:850:LEU:HG	1:A:889:LEU:HD21	1.88	0.55
2:B:22:CYS:HB3	2:B:79:LEU:HB3	1.89	0.54
1:A:597:ALA:O	1:A:599:GLY:N	2.41	0.54
1:A:369:ARG:HH12	1:A:404:PRO:HD3	1.74	0.53
1:A:805:GLN:HG3	1:A:943:PRO:HG2	1.91	0.52
2:B:34:MET:HG2	2:B:79:LEU:HD22	1.92	0.52
2:B:40:ALA:HB3	2:B:43:LYS:HB2	1.92	0.51
1:A:942:ASP:HB3	1:A:943:PRO:HD3	1.92	0.51
1:A:500:TYR:HE2	1:A:546:ARG:HB3	1.75	0.51
1:A:1291:MET:HE2	1:A:1328:ARG:HD2	1.93	0.51
1:A:709:GLY:H	1:A:713:LYS:HD3	1.76	0.51
1:A:608:PHE:HA	1:A:612:MET:HG2	1.93	0.50
1:A:905:LYS:NZ	1:A:906:GLU:OE2	2.44	0.49
1:A:342:VAL:HG11	1:A:379:PHE:CD1	2.46	0.49
1:A:1139:ARG:C	1:A:1141:ASN:H	2.21	0.48
1:A:247:THR:HB	1:A:249:ARG:HD3	1.94	0.48
1:A:1135:PRO:C	1:A:1137:VAL:H	2.21	0.48
1:A:282:MET:HG2	1:A:286:MET:HE3	1.95	0.48
1:A:237:ILE:HG21	1:A:285:ASN:HB3	1.97	0.47
1:A:599:GLY:O	1:A:603:THR:HG23	2.14	0.47
2:B:54:THR:OG1	2:B:55:PRO:HD3	2.14	0.47
1:A:326:THR:HG22	1:A:327:SER:H	1.80	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:48:VAL:HG13	2:B:64:VAL:HG21	1.97	0.46
1:A:688:ILE:HD13	1:A:743:PHE:HZ	1.81	0.46
1:A:420:THR:HG21	1:A:530:SER:HB3	1.98	0.46
1:A:793:LEU:O	1:A:797:LEU:HG	2.16	0.46
1:A:918:HIS:NE2	1:A:922:MET:HE3	2.31	0.45
1:A:221:ILE:HG23	1:A:1213:HIS:HB3	1.98	0.45
1:A:280:ARG:HD2	1:A:340:PHE:CD1	2.52	0.45
1:A:376:LEU:HA	1:A:379:PHE:CD2	2.51	0.45
1:A:603:THR:HG22	1:A:953:PRO:HB2	1.98	0.45
1:A:102:ILE:HD12	1:A:137:LEU:HD22	1.98	0.45
1:A:240:SER:HB3	1:A:1217:HIS:CE1	2.52	0.45
1:A:978:LEU:H	1:A:978:LEU:HD22	1.82	0.45
1:A:656:LEU:O	1:A:693:ARG:NH2	2.34	0.45
2:B:36:TRP:CD1	2:B:81:LEU:HD13	2.52	0.45
1:A:1314:VAL:O	1:A:1318:ILE:HG12	2.18	0.44
1:A:492:MET:HE3	1:A:495:LEU:HD21	1.99	0.44
1:A:1292:ASP:HB2	1:A:1293:PRO:HD3	1.98	0.44
2:B:60:TYR:CE1	2:B:70:ILE:HG22	2.53	0.44
1:A:298:PRO:HA	1:A:301:GLU:HB3	1.99	0.44
1:A:44:PHE:CE2	1:A:92:LEU:HD11	2.51	0.44
2:B:51:THR:HG22	2:B:58:THR:HG22	2.00	0.44
1:A:1245:LEU:HB2	1:A:1281:VAL:HG21	2.00	0.44
1:A:589:LEU:HB3	1:A:590:PRO:HD3	2.00	0.43
1:A:975:LEU:HD22	1:A:1016:LEU:HD21	1.99	0.43
1:A:366:ILE:HG22	1:A:369:ARG:HB3	2.01	0.43
1:A:1182:GLU:OE2	1:A:1287:HIS:NE2	2.49	0.43
1:A:161:LEU:HD22	1:A:164:ARG:HD2	2.00	0.43
1:A:287:LEU:HB2	1:A:289:LEU:HG	2.00	0.43
1:A:326:THR:O	1:A:328:GLN:N	2.51	0.43
1:A:316:GLU:HG2	1:A:317:THR:H	1.84	0.43
1:A:1072:ILE:HD12	1:A:1129:VAL:HG21	2.01	0.43
1:A:229:PRO:HB3	1:A:241:TRP:CE2	2.54	0.43
1:A:68:HIS:NE2	1:A:80:TYR:OH	2.52	0.42
1:A:689:LEU:HD11	1:A:871:MET:HE1	2.01	0.42
1:A:237:ILE:HD11	1:A:282:MET:HE3	2.02	0.42
1:A:805:GLN:HA	1:A:941:VAL:HG21	2.01	0.42
1:A:1039:PRO:HB2	1:A:1088:PRO:HG3	2.02	0.42
1:A:1288:LEU:HD12	1:A:1325:LEU:HD11	2.00	0.42
1:A:828:ASP:OD1	1:A:872:ARG:HD3	2.19	0.42
1:A:691:LEU:HD12	1:A:716:LEU:HD21	2.02	0.41
1:A:412:PRO:HG3	1:A:422:ALA:HB3	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1069:CYS:SG	1:A:1134:GLN:HG2	2.60	0.41
1:A:464:ASN:HB3	1:A:467:LEU:HD21	2.03	0.41
1:A:369:ARG:NH1	1:A:404:PRO:HD3	2.35	0.40
1:A:414:ILE:HD13	1:A:457:PHE:HZ	1.87	0.40
1:A:376:LEU:HA	1:A:379:PHE:HD2	1.86	0.40
1:A:1083:SER:HB2	1:A:1084:PRO:HD3	2.04	0.40
1:A:1005:LEU:HD21	1:A:1030:ILE:HD12	2.03	0.40
1:A:1275:TYR:CE1	1:A:1298:LEU:HD13	2.56	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	
1	A	1332/1382 (96%)	1257 (94%)	67 (5%)	8 (1%)	21	51
2	B	121/134 (90%)	117 (97%)	4 (3%)	0	100	100
All	All	1453/1516 (96%)	1374 (95%)	71 (5%)	8 (1%)	21	51

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	327	SER
1	A	325	GLY
1	A	294	LYS
1	A	442	LYS
1	A	943	PRO
1	A	633	VAL
1	A	1081	GLY
1	A	1084	PRO

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	1203/1244 (97%)	1200 (100%)	3 (0%)	87	96
2	B	96/106 (91%)	95 (99%)	1 (1%)	68	88
All	All	1299/1350 (96%)	1295 (100%)	4 (0%)	86	95

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	319	GLU
1	A	326	THR
1	A	1184	VAL
2	B	72	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	239	ASN
1	A	290	ASN
1	A	357	HIS
1	A	385	GLN
1	A	468	GLN
1	A	628	HIS
1	A	637	ASN
1	A	717	GLN
1	A	746	ASN
1	A	923	ASN

5.3.3 RNA ⓘ

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 oligosaccharides 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	1334/1382 (96%)	-0.61	1 (0%) 92 90	55, 84, 144, 273	0
2	B	123/134 (91%)	-0.62	0 100 100	57, 82, 111, 128	0
All	All	1457/1516 (96%)	-0.61	1 (0%) 92 90	55, 84, 143, 273	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1095	ASN	2.3

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.