



Full wwPDB X-ray Structure Validation Report ⓘ

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PDB ID : 6N31 / pdb_00006n31
Title : WD repeats of human WDR12
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Deposited on : 2018-11-14
Resolution : 2.60 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

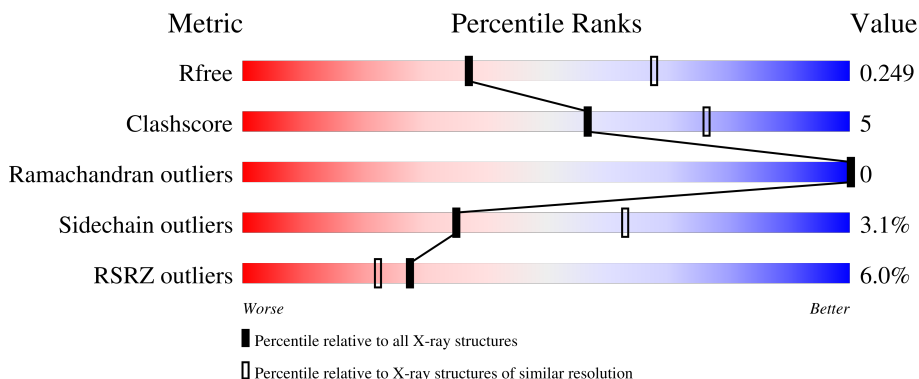
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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	4008 (2.60-2.60)
Clashscore	190562	4347 (2.60-2.60)
Ramachandran outliers	187476	4277 (2.60-2.60)
Sidechain outliers	187428	4277 (2.60-2.60)
RSRZ outliers	180081	4008 (2.60-2.60)

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 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	351	
1	B	351	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 4743 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 Ribosome biogenesis protein WDR12.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	308	Total	C	N	O	S	0	3	1
			2339	1485	395	444	15			
1	B	312	Total	C	N	O	S	0	2	0
			2368	1506	400	446	16			

There are 38 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	72	MET	-	initiating methionine	UNP Q9GZL7
A	73	HIS	-	expression tag	UNP Q9GZL7
A	74	HIS	-	expression tag	UNP Q9GZL7
A	75	HIS	-	expression tag	UNP Q9GZL7
A	76	HIS	-	expression tag	UNP Q9GZL7
A	77	HIS	-	expression tag	UNP Q9GZL7
A	78	HIS	-	expression tag	UNP Q9GZL7
A	79	SER	-	expression tag	UNP Q9GZL7
A	80	SER	-	expression tag	UNP Q9GZL7
A	81	GLY	-	expression tag	UNP Q9GZL7
A	82	ARG	-	expression tag	UNP Q9GZL7
A	83	GLU	-	expression tag	UNP Q9GZL7
A	84	ASN	-	expression tag	UNP Q9GZL7
A	85	LEU	-	expression tag	UNP Q9GZL7
A	86	TYR	-	expression tag	UNP Q9GZL7
A	87	PHE	-	expression tag	UNP Q9GZL7
A	88	GLN	-	expression tag	UNP Q9GZL7
A	89	GLY	-	expression tag	UNP Q9GZL7
A	286	GLY	GLU	conflict	UNP Q9GZL7
B	72	MET	-	initiating methionine	UNP Q9GZL7
B	73	HIS	-	expression tag	UNP Q9GZL7
B	74	HIS	-	expression tag	UNP Q9GZL7
B	75	HIS	-	expression tag	UNP Q9GZL7
B	76	HIS	-	expression tag	UNP Q9GZL7
B	77	HIS	-	expression tag	UNP Q9GZL7

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Chain	Residue	Modelled	Actual	Comment	Reference
B	78	HIS	-	expression tag	UNP Q9GZL7
B	79	SER	-	expression tag	UNP Q9GZL7
B	80	SER	-	expression tag	UNP Q9GZL7
B	81	GLY	-	expression tag	UNP Q9GZL7
B	82	ARG	-	expression tag	UNP Q9GZL7
B	83	GLU	-	expression tag	UNP Q9GZL7
B	84	ASN	-	expression tag	UNP Q9GZL7
B	85	LEU	-	expression tag	UNP Q9GZL7
B	86	TYR	-	expression tag	UNP Q9GZL7
B	87	PHE	-	expression tag	UNP Q9GZL7
B	88	GLN	-	expression tag	UNP Q9GZL7
B	89	GLY	-	expression tag	UNP Q9GZL7
B	286	GLY	GLU	conflict	UNP Q9GZL7

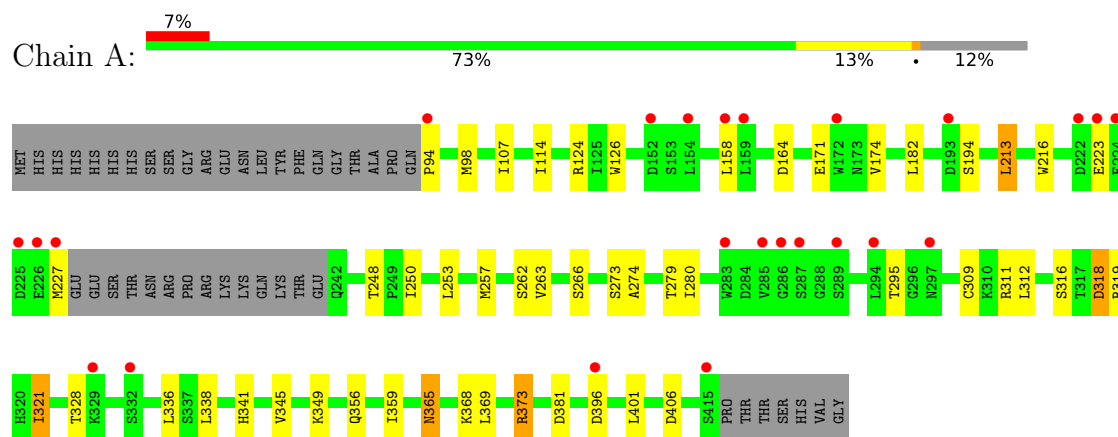
- Molecule 2 is UNKNOWN ATOM OR ION (CCD ID: UNX) (formula: X).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	14	Total X 14 14	0	0
2	B	22	Total X 22 22	0	0

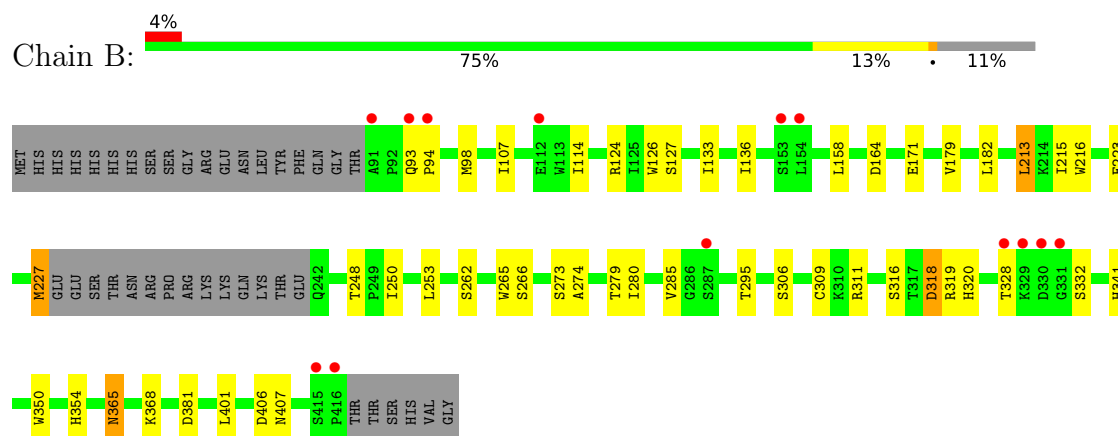
3 Residue-property plots [i](#)

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: Ribosome biogenesis protein WDR12



• Molecule 1: Ribosome biogenesis protein WDR12



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	52.74Å 87.05Å 155.87Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	76.00 – 2.60 76.00 – 2.60	Depositor EDS
% Data completeness (in resolution range)	95.9 (76.00-2.60) 95.8 (76.00-2.60)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.70 (at 2.61Å)	Xtrriage
Refinement program	BUSTER 2.10.2	Depositor
R, R_{free}	0.203 , 0.233 0.214 , 0.249	Depositor DCC
R_{free} test set	1046 reflections (4.58%)	wwPDB-VP
Wilson B-factor (Å ²)	47.3	Xtrriage
Anisotropy	0.315	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 65.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	4743	wwPDB-VP
Average B, all atoms (Å ²)	49.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 21.06 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 7.6059e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: UNX

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	0.85	0/2404	1.31	14/3279 (0.4%)
1	B	0.90	1/2432 (0.0%)	1.33	12/3318 (0.4%)
All	All	0.87	1/4836 (0.0%)	1.32	26/6597 (0.4%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	93	GLN	CA-C	5.21	1.58	1.52

All (26) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	318	ASP	CA-CB-CG	8.50	121.10	112.60
1	A	318	ASP	CA-CB-CG	8.12	120.72	112.60
1	B	250	ILE	N-CA-C	-7.07	103.96	110.82
1	B	94	PRO	CA-C-N	6.97	130.11	120.63
1	B	94	PRO	C-N-CA	6.97	130.11	120.63
1	A	94	PRO	CA-C-N	6.84	129.94	120.63
1	A	94	PRO	C-N-CA	6.84	129.94	120.63
1	A	250	ILE	N-CA-C	-6.71	104.32	110.82
1	A	365	ASN	CA-CB-CG	6.40	119.00	112.60
1	B	365	ASN	CA-CB-CG	6.18	118.78	112.60
1	A	396	ASP	CA-CB-CG	5.72	118.32	112.60
1	B	406	ASP	CA-CB-CG	5.69	118.29	112.60
1	B	223	GLU	CA-C-N	5.67	129.53	121.42
1	B	223	GLU	C-N-CA	5.67	129.53	121.42
1	B	164	ASP	CA-CB-CG	5.65	118.25	112.60
1	A	406	ASP	CA-CB-CG	5.58	118.18	112.60
1	A	164	ASP	CA-CB-CG	5.43	118.03	112.60
1	A	373	ARG	N-CA-C	-5.38	106.85	113.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	321	ILE	N-CA-C	-5.33	100.20	107.99
1	A	223	GLU	CA-C-N	5.25	128.93	121.42
1	A	223	GLU	C-N-CA	5.25	128.93	121.42
1	B	354	HIS	CA-C-N	5.19	127.18	120.44
1	B	354	HIS	C-N-CA	5.19	127.18	120.44
1	A	174	VAL	CA-C-N	5.18	127.49	120.65
1	A	174	VAL	C-N-CA	5.18	127.49	120.65
1	B	320	HIS	N-CA-C	5.15	118.00	109.46

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	A	2339	0	2213	20	0
1	B	2368	0	2253	22	0
2	A	14	0	0	0	0
2	B	22	0	0	0	0
All	All	4743	0	4466	42	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 5.

All (42) 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:171:GLU:HB2	1:B:182:LEU:HD11	1.81	0.61
1:B:215:ILE:HD13	1:B:285:VAL:HG13	1.82	0.61
1:A:171:GLU:HB2	1:A:182:LEU:HD11	1.83	0.60
1:B:319:ARG:HB2	1:B:341:HIS:O	2.04	0.57
1:B:279:THR:HG22	1:B:295:THR:HG22	1.89	0.54
1:A:319:ARG:HB2	1:A:341:HIS:O	2.10	0.52
1:B:306:SER:HB2	1:B:350:TRP:CG	2.44	0.52
1:A:279:THR:HG22	1:A:295:THR:HG22	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:227:MET:HE3	1:B:248:THR:HG22	1.93	0.51
1:A:257:MET:HA	1:A:257:MET:HE2	1.95	0.48
1:A:280:ILE:HG21	1:A:312:LEU:HD21	1.96	0.48
1:A:213:LEU:HB3	1:A:253:LEU:HB2	1.95	0.48
1:B:213:LEU:HB3	1:B:253:LEU:HB2	1.95	0.47
1:B:341:HIS:CE1	1:B:368:LYS:HD2	2.50	0.46
1:B:316:SER:C	1:B:318:ASP:H	2.23	0.46
1:A:309:CYS:SG	1:A:311:ARG:HD2	2.56	0.46
1:B:328:THR:O	1:B:332:SER:HB3	2.15	0.46
1:B:368:LYS:HG2	1:B:381:ASP:OD1	2.16	0.45
1:B:265:TRP:CZ3	1:B:285:VAL:HG21	2.51	0.45
1:A:316:SER:C	1:A:318:ASP:H	2.24	0.45
1:B:124[B]:ARG:HG2	1:B:126:TRP:CE2	2.52	0.44
1:A:262:SER:HB3	1:A:274:ALA:HB3	1.99	0.44
1:A:273:SER:O	1:A:280:ILE:HA	2.18	0.44
1:A:107:ILE:HG21	1:A:401:LEU:HB3	2.00	0.44
1:A:356:GLN:HG2	1:A:373:ARG:HG3	2.00	0.44
1:B:262:SER:HB3	1:B:274:ALA:HB3	1.99	0.44
1:B:273:SER:O	1:B:280:ILE:HA	2.18	0.43
1:A:349:LYS:O	1:A:359[A]:ILE:HG22	2.18	0.43
1:B:136:ILE:HG23	1:B:179:VAL:HG21	2.00	0.43
1:B:127:SER:HB3	1:B:133:ILE:HD11	2.01	0.43
1:A:227:MET:HE3	1:A:248:THR:HG22	2.01	0.43
1:A:124[B]:ARG:HG2	1:A:126:TRP:CE2	2.54	0.42
1:B:107:ILE:HG21	1:B:401:LEU:HB3	2.01	0.42
1:A:321:ILE:HG13	1:A:345:VAL:HG21	2.01	0.42
1:A:194:SER:HB3	1:A:263[B]:VAL:HG23	2.01	0.42
1:B:309:CYS:SG	1:B:311:ARG:HB2	2.60	0.42
1:A:368:LYS:HG2	1:A:381:ASP:OD1	2.20	0.42
1:A:98:MET:HE1	1:A:114:ILE:HD12	2.01	0.41
1:A:321:ILE:HB	1:A:338:LEU:HB2	2.02	0.41
1:B:213:LEU:HD22	1:B:253:LEU:HD12	2.01	0.41
1:B:98:MET:HE1	1:B:114:ILE:HD12	2.02	0.40
1:B:306:SER:HB2	1:B:350:TRP:CD2	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	307/351 (88%)	295 (96%)	12 (4%)	0	100	100
1	B	310/351 (88%)	298 (96%)	12 (4%)	0	100	100
All	All	617/702 (88%)	593 (96%)	24 (4%)	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	247/312 (79%)	239 (97%)	8 (3%)	34	62
1	B	249/312 (80%)	242 (97%)	7 (3%)	38	66
All	All	496/624 (80%)	481 (97%)	15 (3%)	35	64

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	158	LEU
1	A	213	LEU
1	A	216	TRP
1	A	266	SER
1	A	328	THR
1	A	336	LEU
1	A	365	ASN
1	A	369	LEU

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Mol	Chain	Res	Type
1	B	158	LEU
1	B	213	LEU
1	B	216	TRP
1	B	227	MET
1	B	266	SER
1	B	365	ASN
1	B	407	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	357	GLN
1	A	365	ASN

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 ⓘ

Of 36 ligands modelled in this entry, 36 are unknown - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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, 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	308/351 (87%)	0.43	24 (7%) 19 15	24, 53, 78, 109	3 (0%)
1	B	312/351 (88%)	0.15	13 (4%) 40 35	29, 43, 68, 92	2 (0%)
All	All	620/702 (88%)	0.29	37 (5%) 27 22	24, 47, 75, 109	5 (0%)

All (37) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	415	SER	6.3
1	A	289	SER	4.6
1	B	331	GLY	4.1
1	B	93	GLN	4.0
1	A	154	LEU	3.9
1	A	152	ASP	3.3
1	A	226	GLU	3.3
1	B	328	THR	3.2
1	B	154	LEU	3.1
1	B	91	ALA	3.1
1	A	159	LEU	3.0
1	B	94	PRO	3.0
1	B	329	LYS	2.9
1	B	330	ASP	2.8
1	A	286	GLY	2.8
1	A	225	ASP	2.7
1	B	416	PRO	2.6
1	A	283	TRP	2.5
1	A	294	LEU	2.5
1	A	223	GLU	2.5
1	A	287	SER	2.4
1	B	112	GLU	2.3
1	A	285	VAL	2.3
1	A	227	MET	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	329	LYS	2.2
1	A	297	ASN	2.2
1	A	193	ASP	2.2
1	A	94	PRO	2.2
1	A	396	ASP	2.2
1	B	287	SER	2.2
1	B	415	SER	2.1
1	A	172	TRP	2.1
1	A	224	GLU	2.1
1	A	332	SER	2.0
1	A	222	ASP	2.0
1	B	153	SER	2.0
1	A	158	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](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	UNX	B	505	1/1	0.72	0.26	67,67,67,67	0
2	UNX	B	511	1/1	0.73	0.16	44,44,44,44	0
2	UNX	B	508	1/1	0.80	0.31	47,47,47,47	0
2	UNX	A	514	1/1	0.81	0.11	31,31,31,31	0
2	UNX	B	517	1/1	0.81	0.21	33,33,33,33	0
2	UNX	A	504	1/1	0.84	0.18	35,35,35,35	0
2	UNX	A	501	1/1	0.84	0.20	47,47,47,47	0
2	UNX	A	502	1/1	0.84	0.27	50,50,50,50	0
2	UNX	A	509	1/1	0.87	0.14	40,40,40,40	0
2	UNX	B	516	1/1	0.87	0.13	42,42,42,42	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	UNX	B	502	1/1	0.87	0.22	43,43,43,43	0
2	UNX	B	522	1/1	0.87	0.17	52,52,52,52	0
2	UNX	A	505	1/1	0.88	0.14	30,30,30,30	0
2	UNX	A	513	1/1	0.89	0.16	33,33,33,33	0
2	UNX	B	509	1/1	0.90	0.19	45,45,45,45	0
2	UNX	A	512	1/1	0.90	0.11	30,30,30,30	0
2	UNX	A	503	1/1	0.90	0.19	31,31,31,31	0
2	UNX	B	506	1/1	0.90	0.16	36,36,36,36	0
2	UNX	A	511	1/1	0.90	0.15	33,33,33,33	0
2	UNX	B	513	1/1	0.91	0.18	42,42,42,42	0
2	UNX	A	510	1/1	0.91	0.07	20,20,20,20	0
2	UNX	A	508	1/1	0.91	0.16	35,35,35,35	0
2	UNX	B	507	1/1	0.91	0.20	54,54,54,54	0
2	UNX	B	514	1/1	0.92	0.07	25,25,25,25	0
2	UNX	B	521	1/1	0.92	0.13	31,31,31,31	0
2	UNX	A	506	1/1	0.92	0.12	43,43,43,43	0
2	UNX	B	504	1/1	0.94	0.12	38,38,38,38	0
2	UNX	B	520	1/1	0.94	0.06	19,19,19,19	0
2	UNX	B	515	1/1	0.95	0.11	31,31,31,31	0
2	UNX	B	512	1/1	0.96	0.14	35,35,35,35	0
2	UNX	B	510	1/1	0.96	0.07	16,16,16,16	0
2	UNX	B	503	1/1	0.96	0.13	28,28,28,28	0
2	UNX	A	507	1/1	0.97	0.04	18,18,18,18	0
2	UNX	B	518	1/1	0.97	0.04	18,18,18,18	0
2	UNX	B	519	1/1	0.97	0.05	13,13,13,13	0
2	UNX	B	501	1/1	0.98	0.09	15,15,15,15	0

6.5 Other polymers [i](#)

There are no such residues in this entry.