



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 20, 2026 – 03:15 PM UTC

PDB ID : 1UQ5 / pdb_00001uq5
Title : RICIN A-CHAIN (RECOMBINANT) N122A MUTANT
Authors : Marsden, C.J.; Fulop, V.
Deposited on : 2003-10-15
Resolution : 1.40 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
Mogul : 2022.3.0, CSD as543be (2022)
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

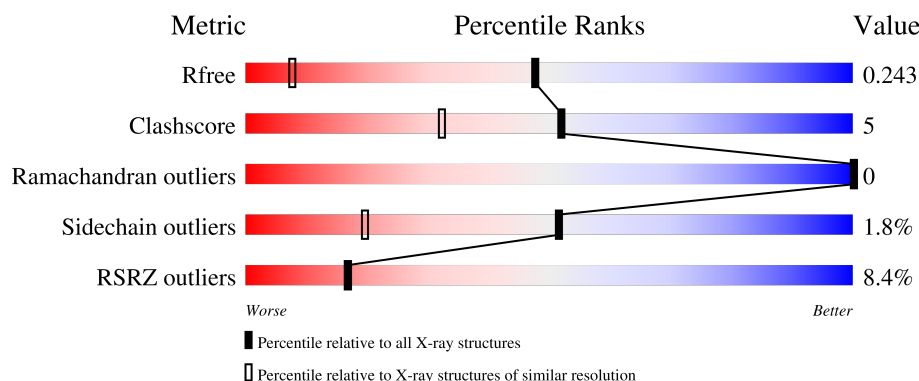
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.40 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	2563 (1.40-1.40)
Clashscore	190562	2660 (1.40-1.40)
Ramachandran outliers	187476	2611 (1.40-1.40)
Sidechain outliers	187428	2610 (1.40-1.40)
RSRZ outliers	180081	2561 (1.40-1.40)

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	263	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	ACT	A	1268	-	-	X	-

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 2596 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.

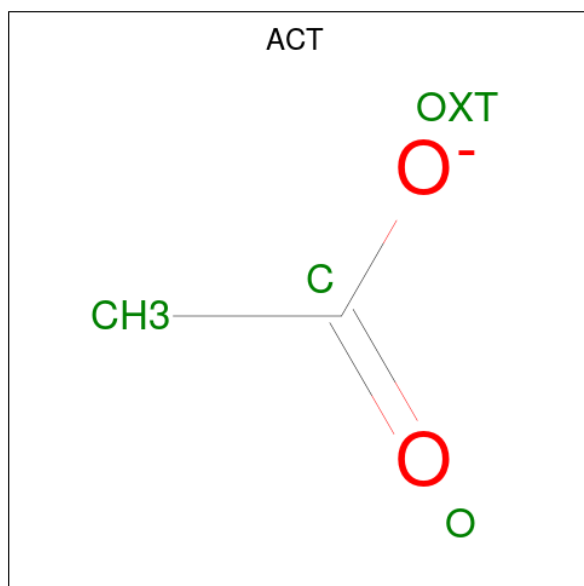
- Molecule 1 is a protein called RICIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	263	2076	1315	366	390	5	0	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	118	ALA	ASN	engineered mutation	UNP P02879

- Molecule 2 is ACETATE ION (CCD ID: ACT) (formula: $C_2H_3O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
2	A	1	4	2	2	0	0

- Molecule 3 is SULFATE ION (CCD ID: SO4) (formula: O_4S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	S	0	0
			5	4	1		
3	A	1	Total	O	S	0	0
			5	4	1		

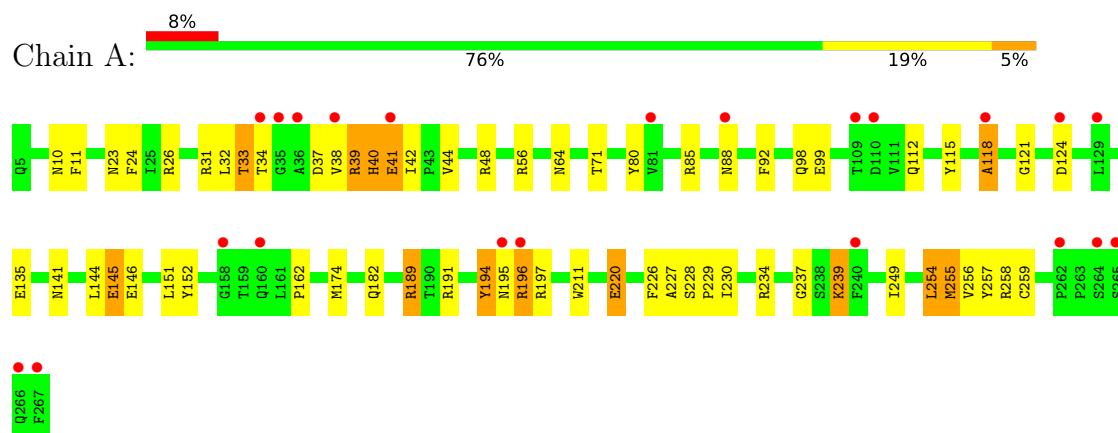
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	506	Total	O	0	0
			506	506		

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: RICIN



4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	67.50Å 67.50Å 140.60Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.00 – 1.40 46.00 – 1.40	Depositor EDS
% Data completeness (in resolution range)	93.9 (46.00-1.40) 93.9 (46.00-1.40)	Depositor EDS
R_{merge}	0.03	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.20 (at 1.40Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.177 , 0.214 (Not available) , 0.243	Depositor DCC
R_{free} test set	2448 reflections (4.02%)	wwPDB-VP
Wilson B-factor (Å ²)	14.3	Xtriage
Anisotropy	0.361	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 44.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	2596	wwPDB-VP
Average B, all atoms (Å ²)	19.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.18% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: SO4, ACT

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	2.03	47/2122 (2.2%)	1.72	32/2887 (1.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	3

All (47) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	249	ILE	CA-CB	9.71	1.60	1.53
1	A	39	ARG	CG-CD	-9.41	1.24	1.52
1	A	39	ARG	CB-CG	9.20	1.80	1.52
1	A	34	THR	CA-C	-9.07	1.40	1.52
1	A	37	ASP	CA-C	-8.58	1.42	1.52
1	A	33	THR	CB-CG2	-7.99	1.26	1.52
1	A	259	CYS	CA-C	-7.19	1.44	1.52
1	A	38	VAL	CA-CB	7.04	1.63	1.54
1	A	92	PHE	CA-C	-6.89	1.44	1.52
1	A	259	CYS	C-O	6.87	1.31	1.23
1	A	228	SER	CB-OG	-6.80	1.28	1.42
1	A	33	THR	CA-C	-6.66	1.44	1.52
1	A	196	ARG	CD-NE	6.62	1.55	1.46
1	A	42	ILE	N-CA	6.60	1.52	1.46
1	A	194	TYR	C-O	6.55	1.33	1.24
1	A	145	GLU	CD-OE2	6.47	1.37	1.25
1	A	10	ASN	CG-OD1	-6.39	1.11	1.23
1	A	85	ARG	NE-CZ	6.38	1.40	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	121	GLY	C-O	-6.18	1.20	1.24
1	A	33	THR	N-CA	6.12	1.53	1.45
1	A	118	ALA	CA-C	-6.10	1.44	1.52
1	A	196	ARG	C-O	6.04	1.31	1.23
1	A	42	ILE	C-O	-5.85	1.17	1.24
1	A	23	ASN	CG-OD1	5.81	1.34	1.23
1	A	195	ASN	CG-OD1	5.79	1.34	1.23
1	A	162	PRO	N-CD	5.76	1.55	1.47
1	A	151	LEU	CG-CD1	-5.75	1.33	1.52
1	A	41	GLU	C-N	5.62	1.38	1.33
1	A	32	LEU	CA-CB	5.61	1.62	1.53
1	A	145	GLU	N-CA	5.59	1.53	1.46
1	A	33	THR	CA-CB	5.53	1.68	1.54
1	A	31	ARG	CA-C	-5.52	1.45	1.52
1	A	258	ARG	CD-NE	-5.48	1.38	1.46
1	A	182	GLN	CA-CB	5.45	1.62	1.53
1	A	197	ARG	NE-CZ	5.45	1.39	1.33
1	A	220	GLU	CA-C	-5.43	1.44	1.52
1	A	229	PRO	C-O	5.35	1.30	1.23
1	A	182	GLN	CA-C	-5.32	1.45	1.52
1	A	194	TYR	CA-C	-5.30	1.45	1.52
1	A	228	SER	CA-C	5.22	1.58	1.52
1	A	98	GLN	CA-C	-5.21	1.46	1.52
1	A	237	GLY	C-O	-5.20	1.16	1.24
1	A	257	TYR	CZ-OH	5.20	1.49	1.38
1	A	254	LEU	CG-CD1	-5.10	1.35	1.52
1	A	71	THR	CA-CB	-5.05	1.46	1.53
1	A	115	TYR	C-O	5.04	1.30	1.23
1	A	144	LEU	CA-CB	5.03	1.61	1.53

All (32) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	254	LEU	CB-CG-CD1	-14.72	66.55	110.70
1	A	39	ARG	CA-CB-CG	11.88	137.86	114.10
1	A	228	SER	CB-CA-C	11.32	126.19	109.20
1	A	189	ARG	CD-NE-CZ	8.32	136.05	124.40
1	A	26	ARG	CD-NE-CZ	7.09	134.33	124.40
1	A	26	ARG	CG-CD-NE	-6.84	96.95	112.00
1	A	34	THR	CB-CA-C	-6.58	98.49	109.55
1	A	226	PHE	CA-C-O	6.49	128.93	121.47
1	A	80	TYR	CA-C-O	6.47	128.92	121.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	42	ILE	O-C-N	6.42	127.09	121.12
1	A	220	GLU	CB-CG-CD	6.32	123.34	112.60
1	A	152	TYR	CA-C-O	-6.25	113.80	120.42
1	A	254	LEU	CB-CG-CD2	6.15	129.15	110.70
1	A	56	ARG	NE-CZ-NH2	-6.04	113.77	119.20
1	A	194	TYR	CA-C-O	-6.01	112.50	119.59
1	A	39	ARG	NE-CZ-NH2	-5.93	113.86	119.20
1	A	196	ARG	CG-CD-NE	5.86	124.89	112.00
1	A	228	SER	CA-CB-OG	-5.84	99.41	111.10
1	A	40	HIS	CB-CG-CD2	5.79	138.72	131.20
1	A	194	TYR	CA-C-N	5.66	130.16	122.07
1	A	194	TYR	C-N-CA	5.66	130.16	122.07
1	A	124	ASP	N-CA-C	-5.63	105.05	111.07
1	A	26	ARG	NE-CZ-NH2	-5.55	114.21	119.20
1	A	34	THR	CA-C-N	-5.49	114.84	122.86
1	A	34	THR	C-N-CA	-5.49	114.84	122.86
1	A	249	ILE	O-C-N	5.48	123.96	120.07
1	A	32	LEU	CA-C-O	-5.34	114.32	120.24
1	A	255	MET	O-C-N	-5.30	116.72	123.24
1	A	40	HIS	N-CA-C	5.25	118.68	111.54
1	A	230	ILE	O-C-N	-5.23	117.69	123.18
1	A	254	LEU	CB-CA-C	5.05	121.32	110.45
1	A	146	GLU	CG-CD-OE1	5.02	129.95	118.40

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	118	ALA	Mainchain
1	A	220	GLU	Sidechain
1	A	33	THR	Mainchain

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	2076	0	2040	21	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	4	0	3	2	0
3	A	10	0	0	0	0
4	A	506	0	0	7	0
All	All	2596	0	2043	21	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 (21) 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:39:ARG:CB	1:A:39:ARG:CG	1.80	1.59
1:A:39:ARG:CB	1:A:39:ARG:CD	2.56	0.79
1:A:239:LYS:HD2	4:A:2454:HOH:O	1.86	0.76
1:A:239:LYS:HB3	4:A:2453:HOH:O	1.96	0.66
1:A:174:MET:HE2	2:A:1268:ACT:H3	1.78	0.66
1:A:64:ASN:HB2	1:A:145:GLU:CD	2.21	0.66
1:A:99:GLU:HG3	4:A:2270:HOH:O	1.97	0.64
1:A:40:HIS:O	1:A:41:GLU:HB2	2.02	0.60
1:A:39:ARG:CG	1:A:39:ARG:HB2	2.22	0.51
1:A:189:ARG:NE	4:A:2399:HOH:O	2.46	0.49
1:A:48:ARG:HD2	4:A:2160:HOH:O	2.13	0.48
1:A:44:VAL:HG22	1:A:255:MET:HE3	1.99	0.45
1:A:191:ARG:HG3	1:A:196:ARG:HH21	1.83	0.43
1:A:11:PHE:HB2	1:A:24:PHE:CD1	2.54	0.42
1:A:88:ASN:CG	1:A:112:GLN:HB2	2.44	0.42
1:A:39:ARG:CG	1:A:39:ARG:HB3	2.22	0.42
1:A:227:ALA:HB2	4:A:2436:HOH:O	2.20	0.41
1:A:141:ASN:OD1	2:A:1268:ACT:OXT	2.39	0.41
1:A:194:TYR:HB2	1:A:196:ARG:HG3	2.03	0.41
1:A:211:TRP:CH2	1:A:256:VAL:HB	2.56	0.41
1:A:239:LYS:CD	4:A:2454:HOH:O	2.59	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	261/263 (99%)	258 (99%)	3 (1%)	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	221/221 (100%)	217 (98%)	4 (2%)	51	20

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

Mol	Chain	Res	Type
1	A	135	GLU
1	A	234	ARG
1	A	239	LYS
1	A	254	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	98	GLN
1	A	141	ASN
1	A	173	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 ⓘ

3 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	SO4	A	1269	-	4,4,4	0.21	0	6,6,6	0.79	0
3	SO4	A	1270	-	4,4,4	1.10	0	6,6,6	1.48	1 (16%)
2	ACT	A	1268	-	3,3,3	0.74	0	3,3,3	1.16	0

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1270	SO4	O4-S-O1	-2.49	96.53	109.56

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1268	ACT	2	0

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	263/263 (100%)	0.63	22 (8%) 17 17	8, 14, 26, 36	0

All (22) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	267	PHE	4.4
1	A	36	ALA	3.3
1	A	265	SER	3.2
1	A	196	ARG	3.1
1	A	88	ASN	2.9
1	A	262	PRO	2.8
1	A	38	VAL	2.7
1	A	118	ALA	2.7
1	A	34	THR	2.6
1	A	35	GLY	2.5
1	A	195	ASN	2.4
1	A	240	PHE	2.4
1	A	160	GLN	2.4
1	A	158	GLY	2.4
1	A	110	ASP	2.3
1	A	41	GLU	2.2
1	A	266	GLN	2.2
1	A	124	ASP	2.1
1	A	81	VAL	2.1
1	A	109	THR	2.1
1	A	129	LEU	2.0
1	A	264	SER	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
3	SO4	A	1269	5/5	0.89	0.10	40,49,51,51	0
3	SO4	A	1270	5/5	0.96	0.09	16,22,26,29	0
2	ACT	A	1268	4/4	0.97	0.09	14,17,18,19	0

6.5 Other polymers [i](#)

There are no such residues in this entry.