



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 12:08 AM GMT

PDB ID : 1ZR4  
Title : Structure of a Synaptic gamma-delta Resolvase Tetramer Covalently linked to two Cleaved DNAs  
Authors : Li, W.; Kamtekar, S.; Xiong, Y.; Sarkis, G.J.; Grindley, N.D.; Steitz, T.A.  
Deposited on : 2005-05-19  
Resolution : 3.40 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.  
We welcome your comments at [validation@mail.wwpdb.org](mailto: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.

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

MolProbity : 4.02b-467  
Mogul : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
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) : trunk26865

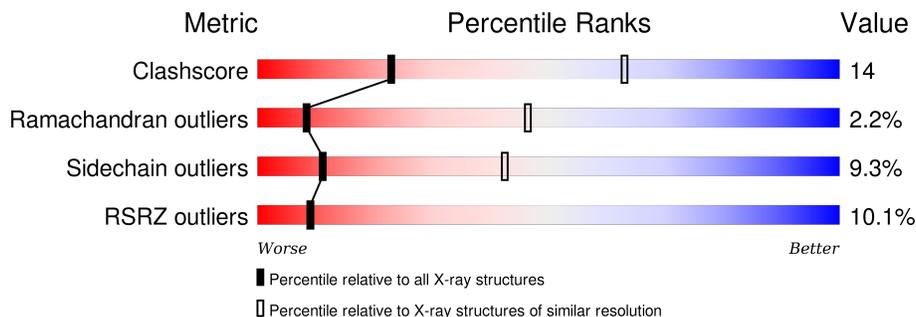
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.40 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))
Clashscore	102246	1611 (3.50-3.30)
Ramachandran outliers	100387	1571 (3.50-3.30)
Sidechain outliers	100360	1571 (3.50-3.30)
RSRZ outliers	91569	1485 (3.50-3.30)

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  $\geq 3$ , 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	J	19	
1	M	19	
1	U	19	
1	X	19	
2	I	3	
2	O	3	
2	W	3	

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Mol	Chain	Length	Quality of chain
2	Z	3	
3	K	13	
3	N	13	
3	V	13	
3	Y	13	
4	A	183	
4	B	183	
4	D	183	
4	E	183	

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 8516 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 DNA chain called TCAGTGTCCGATAATTTAT.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
1	X	19	Total 385	C 187	N 65	O 115	P 18	0	0	0
1	J	19	Total 385	C 187	N 65	O 115	P 18	0	0	0
1	U	19	Total 385	C 187	N 65	O 115	P 18	0	0	0
1	M	19	Total 385	C 187	N 65	O 115	P 18	0	0	0

- Molecule 2 is a DNA chain called AAA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
2	Z	3	Total 63	C 30	N 15	O 15	P 3	0	0	0
2	I	3	Total 63	C 30	N 15	O 15	P 3	0	0	0
2	W	3	Total 63	C 30	N 15	O 15	P 3	0	0	0
2	O	3	Total 63	C 30	N 15	O 15	P 3	0	0	0

- Molecule 3 is a DNA chain called TTATCGGACACTG.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
3	Y	13	Total 263	C 127	N 47	O 77	P 12	0	0	0
3	K	13	Total 263	C 127	N 47	O 77	P 12	0	0	0
3	V	13	Total 263	C 127	N 47	O 77	P 12	0	0	0
3	N	13	Total 263	C 127	N 47	O 77	P 12	0	0	0

- Molecule 4 is a protein called Transposon gamma-delta resolvase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
4	A	183	1422	881	266	268	7	0	0	0
4	B	182	1414	876	265	267	6	0	0	0
4	E	183	1422	881	266	268	7	0	0	0
4	D	182	1414	876	265	267	6	0	0	0

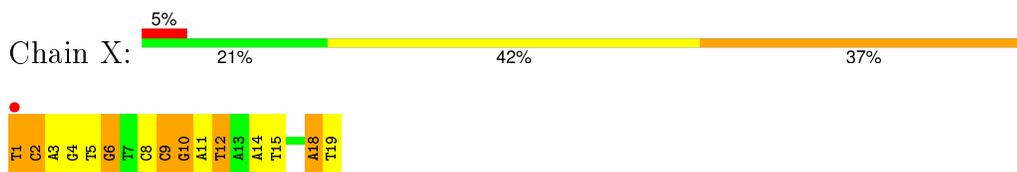
There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	2	ALA	ARG	ENGINEERED	UNP P03012
A	56	LYS	GLU	ENGINEERED	UNP P03012
A	101	SER	GLY	ENGINEERED	UNP P03012
A	102	TYR	GLU	ENGINEERED	UNP P03012
A	103	ILE	MET	ENGINEERED	UNP P03012
A	124	GLN	GLU	ENGINEERED	UNP P03012
B	2	ALA	ARG	ENGINEERED	UNP P03012
B	56	LYS	GLU	ENGINEERED	UNP P03012
B	101	SER	GLY	ENGINEERED	UNP P03012
B	102	TYR	GLU	ENGINEERED	UNP P03012
B	103	ILE	MET	ENGINEERED	UNP P03012
B	124	GLN	GLU	ENGINEERED	UNP P03012
E	2	ALA	ARG	ENGINEERED	UNP P03012
E	56	LYS	GLU	ENGINEERED	UNP P03012
E	101	SER	GLY	ENGINEERED	UNP P03012
E	102	TYR	GLU	ENGINEERED	UNP P03012
E	103	ILE	MET	ENGINEERED	UNP P03012
E	124	GLN	GLU	ENGINEERED	UNP P03012
D	2	ALA	ARG	ENGINEERED	UNP P03012
D	56	LYS	GLU	ENGINEERED	UNP P03012
D	101	SER	GLY	ENGINEERED	UNP P03012
D	102	TYR	GLU	ENGINEERED	UNP P03012
D	103	ILE	MET	ENGINEERED	UNP P03012
D	124	GLN	GLU	ENGINEERED	UNP P03012

### 3 Residue-property plots [i](#)

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.

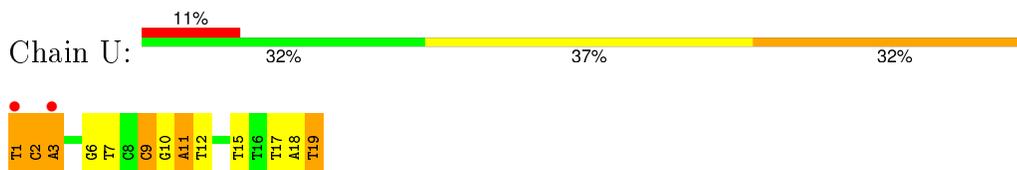
- Molecule 1: TCAGTGTCCGATAATTTAT



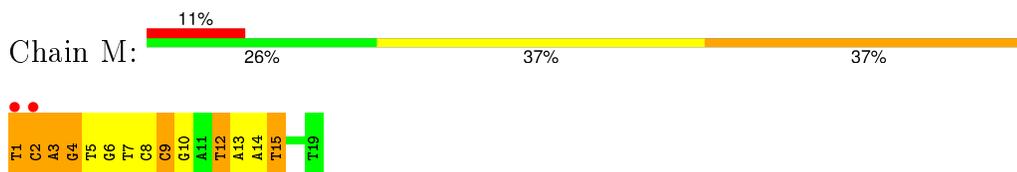
- Molecule 1: TCAGTGTCCGATAATTTAT



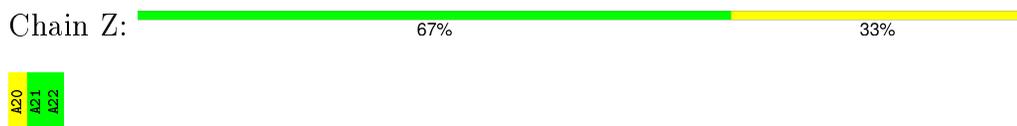
- Molecule 1: TCAGTGTCCGATAATTTAT



- Molecule 1: TCAGTGTCCGATAATTTAT



- Molecule 2: AAA



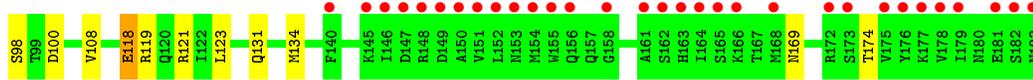
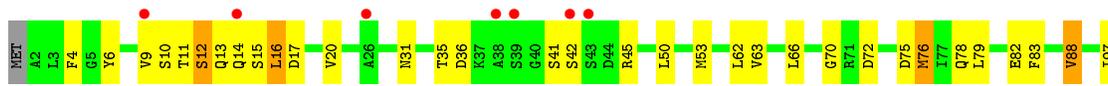
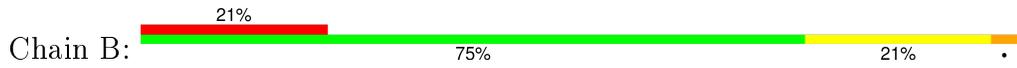
- Molecule 2: AAA



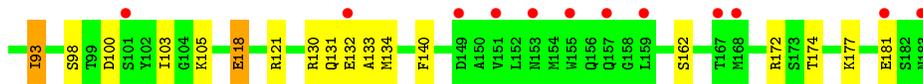
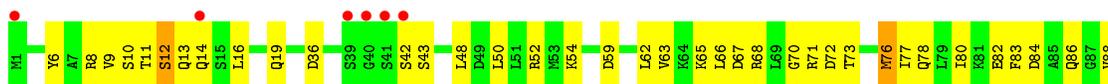




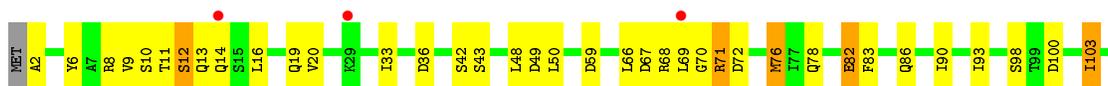
- Molecule 4: Transposon gamma-delta resolvase



- Molecule 4: Transposon gamma-delta resolvase



- Molecule 4: Transposon gamma-delta resolvase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	119.16Å 127.29Å 140.42Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 3.40 43.57 – 3.28	Depositor EDS
% Data completeness (in resolution range)	99.7 (50.00-3.40) 99.4 (43.57-3.28)	Depositor EDS
$R_{merge}$	0.05	Depositor
$R_{sym}$	0.05	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.38 (at 3.25Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, $R_{free}$	0.264 , 0.295 0.264 , (Not available)	Depositor DCC
$R_{free}$ test set	No test flags present.	DCC
Wilson B-factor (Å <sup>2</sup> )	82.3	Xtriage
Anisotropy	0.086	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.23 , 77.6	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 33091 reflections	Xtriage
$F_o, F_c$ correlation	0.89	EDS
Total number of atoms	8516	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	111.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.76% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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	J	0.78	0/430	1.43	5/662 (0.8%)
1	M	1.06	1/430 (0.2%)	1.82	12/662 (1.8%)
1	U	0.83	0/430	1.64	10/662 (1.5%)
1	X	0.93	0/430	2.01	15/662 (2.3%)
2	I	0.53	0/71	1.09	0/107
2	O	0.90	0/71	1.25	0/107
2	W	0.64	0/71	1.13	0/107
2	Z	0.68	0/71	1.02	0/107
3	K	0.69	0/294	1.28	0/452
3	N	1.04	1/294 (0.3%)	1.91	11/452 (2.4%)
3	V	0.68	0/294	1.53	4/452 (0.9%)
3	Y	0.81	0/294	1.77	7/452 (1.5%)
4	A	0.49	0/1432	0.66	0/1914
4	B	0.46	0/1424	0.61	0/1904
4	D	0.46	0/1424	0.67	1/1902 (0.1%)
4	E	0.47	0/1432	0.61	0/1914
All	All	0.64	2/8892 (0.0%)	1.15	65/12518 (0.5%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	N	34	DT	C1'-N1	5.96	1.56	1.49
1	M	1	DT	C1'-N1	5.10	1.55	1.49

The worst 5 of 65 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	X	2	DC	O4'-C1'-N1	15.64	118.95	108.00
1	X	1	DT	O4'-C1'-N1	12.22	116.56	108.00
3	N	26	DT	C6-C5-C7	-9.86	116.99	122.90
3	Y	24	DT	C6-C5-C7	-9.82	117.01	122.90
1	X	1	DT	C1'-O4'-C4'	-9.01	101.09	110.10

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	J	385	0	219	3	0
1	M	385	0	219	11	0
1	U	385	0	219	10	0
1	X	385	0	219	20	0
2	I	63	0	34	1	0
2	O	63	0	34	1	0
2	W	63	0	34	2	0
2	Z	63	0	34	1	0
3	K	263	0	149	4	0
3	N	263	0	149	12	0
3	V	263	0	149	13	0
3	Y	263	0	149	16	0
4	A	1422	0	1483	44	0
4	B	1414	0	1471	20	0
4	D	1414	0	1471	34	0
4	E	1422	0	1483	37	0
All	All	8516	0	7516	216	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 14.

The worst 5 of 216 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)
3:Y:30:DA:H2''	3:Y:31:DC:H5''	1.27	1.15
3:N:28:DG:H2''	3:N:29:DG:H5''	1.29	1.12
3:Y:25:DA:H2''	3:Y:26:DT:H5''	1.34	1.07
1:X:2:DC:H2''	1:X:3:DA:OP2	1.52	1.05
3:N:30:DA:H2''	3:N:31:DC:H5''	1.46	0.95

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	
4	A	181/183 (99%)	159 (88%)	16 (9%)	6 (3%)	5	37
4	B	180/183 (98%)	154 (86%)	23 (13%)	3 (2%)	11	51
4	D	180/183 (98%)	155 (86%)	22 (12%)	3 (2%)	11	51
4	E	181/183 (99%)	153 (84%)	24 (13%)	4 (2%)	8	46
All	All	722/732 (99%)	621 (86%)	85 (12%)	16 (2%)	8	46

5 of 16 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	B	31	ASN
4	E	42	SER
4	A	31	ASN
4	A	39	SER
4	A	99	THR

### 5.3.2 Protein sidechains [i](#)

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	
4	A	153/153 (100%)	139 (91%)	14 (9%)	11	43
4	B	152/153 (99%)	135 (89%)	17 (11%)	7	32
4	D	152/153 (99%)	137 (90%)	15 (10%)	10	39
4	E	153/153 (100%)	142 (93%)	11 (7%)	18	56
All	All	610/612 (100%)	553 (91%)	57 (9%)	11	42

5 of 57 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	B	97	ILE
4	E	12	SER
4	D	119	ARG
4	B	118	GLU
4	B	123	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
4	E	120	GLN
4	D	169	ASN
4	E	163	HIS
4	B	183	ASN
4	E	127	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

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q < 0.9
1	J	19/19 (100%)	1.50	6 (31%) 1 1	116, 121, 156, 175	0
1	M	19/19 (100%)	0.57	2 (10%) 8 8	107, 121, 166, 180	0
1	U	19/19 (100%)	0.82	2 (10%) 8 8	116, 121, 159, 177	0
1	X	19/19 (100%)	-0.26	1 (5%) 30 27	108, 113, 133, 151	0
2	I	3/3 (100%)	0.20	0 100 100	86, 86, 105, 119	0
2	O	3/3 (100%)	-0.42	0 100 100	85, 85, 105, 120	0
2	W	3/3 (100%)	-0.57	0 100 100	86, 86, 105, 120	0
2	Z	3/3 (100%)	-0.41	0 100 100	86, 86, 104, 119	0
3	K	13/13 (100%)	2.18	4 (30%) 1 1	116, 119, 121, 122	0
3	N	13/13 (100%)	0.41	1 (7%) 16 16	112, 119, 130, 137	0
3	V	13/13 (100%)	-0.04	0 100 100	115, 120, 123, 135	0
3	Y	13/13 (100%)	-0.38	0 100 100	100, 111, 117, 117	0
4	A	183/183 (100%)	0.37	6 (3%) 50 45	67, 100, 137, 221	0
4	B	182/183 (99%)	1.06	38 (20%) 1 1	68, 106, 141, 221	0
4	D	182/183 (99%)	0.29	10 (5%) 29 26	68, 106, 135, 221	0
4	E	183/183 (100%)	0.52	18 (9%) 10 10	68, 106, 140, 221	0
All	All	870/872 (99%)	0.56	88 (10%) 9 9	67, 108, 140, 221	0

The worst 5 of 88 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	U	1	DT	15.5
4	B	151	VAL	10.1
3	K	33	DC	8.6
4	B	146	ILE	8.5
3	K	32	DA	8.4

## 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.