



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 19, 2026 – 11:58 PM UTC

PDB ID : 1FT8 / pdb_00001ft8
Title : CRYSTAL STRUCTURE OF THE RNA-BINDING DOMAIN OF THE MRNA EXPORT FACTOR TAP
Authors : Liker, E.; Fernandez, E.; Izaurralde, E.; Conti, E.
Deposited on : 2000-09-12
Resolution : 3.15 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

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
Xtrriage (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

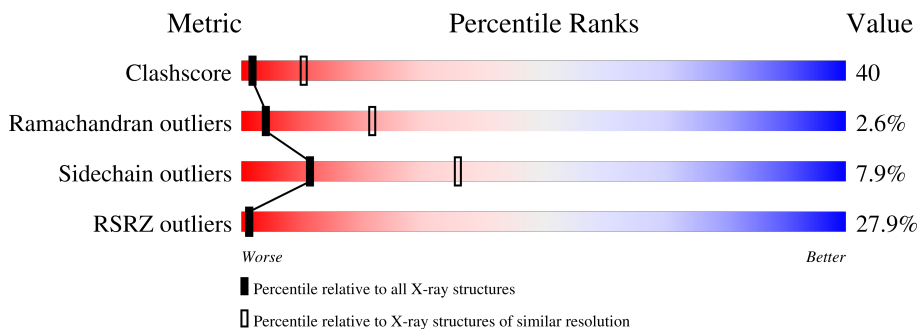
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.15 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	190562	2486 (3.20-3.12)
Ramachandran outliers	187476	2405 (3.20-3.12)
Sidechain outliers	187428	2404 (3.20-3.12)
RSRZ outliers	180081	2361 (3.20-3.12)

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	271	
1	B	271	
1	C	271	
1	D	271	
1	E	271	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 6913 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 TIP ASSOCIATING PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	242	Total 1961	C 1245	N 343	O 366	S 7	0	0	0
1	B	165	Total 1323	C 831	N 232	O 255	S 5	0	0	0
1	C	244	Total 1973	C 1253	N 346	O 367	S 7	0	0	0
1	D	162	Total 1302	C 818	N 229	O 250	S 5	0	0	0
1	E	44	Total 354	C 236	N 54	O 62	S 2	0	0	0

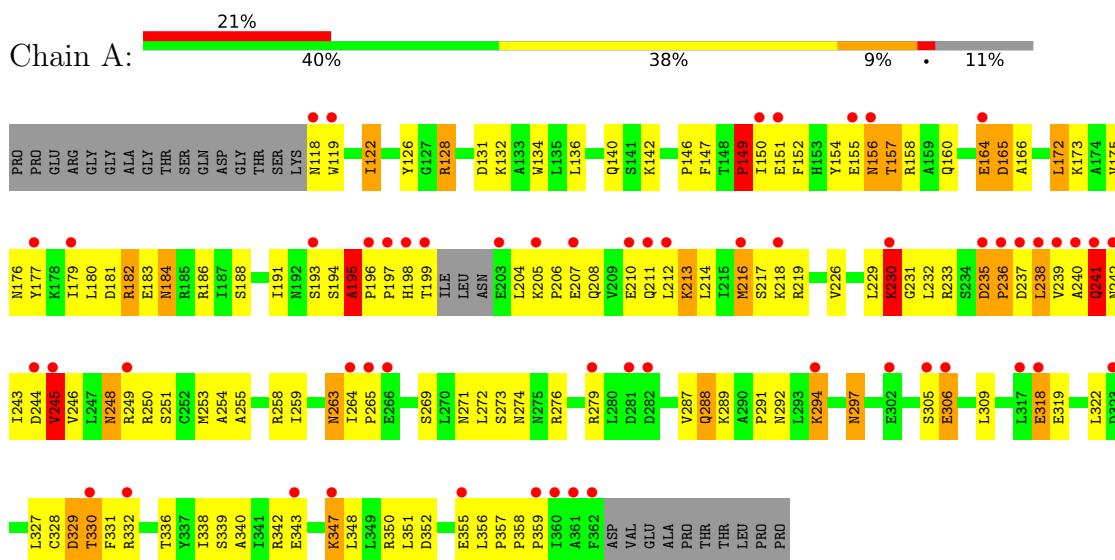
There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	119	TRP	CYS	engineered mutation	UNP Q9UBU9
A	226	VAL	ALA	engineered mutation	UNP Q9UBU9
B	119	TRP	CYS	engineered mutation	UNP Q9UBU9
B	226	VAL	ALA	engineered mutation	UNP Q9UBU9
C	119	TRP	CYS	engineered mutation	UNP Q9UBU9
C	226	VAL	ALA	engineered mutation	UNP Q9UBU9
D	119	TRP	CYS	engineered mutation	UNP Q9UBU9
D	226	VAL	ALA	engineered mutation	UNP Q9UBU9
E	119	TRP	CYS	engineered mutation	UNP Q9UBU9
E	226	VAL	ALA	engineered mutation	UNP Q9UBU9

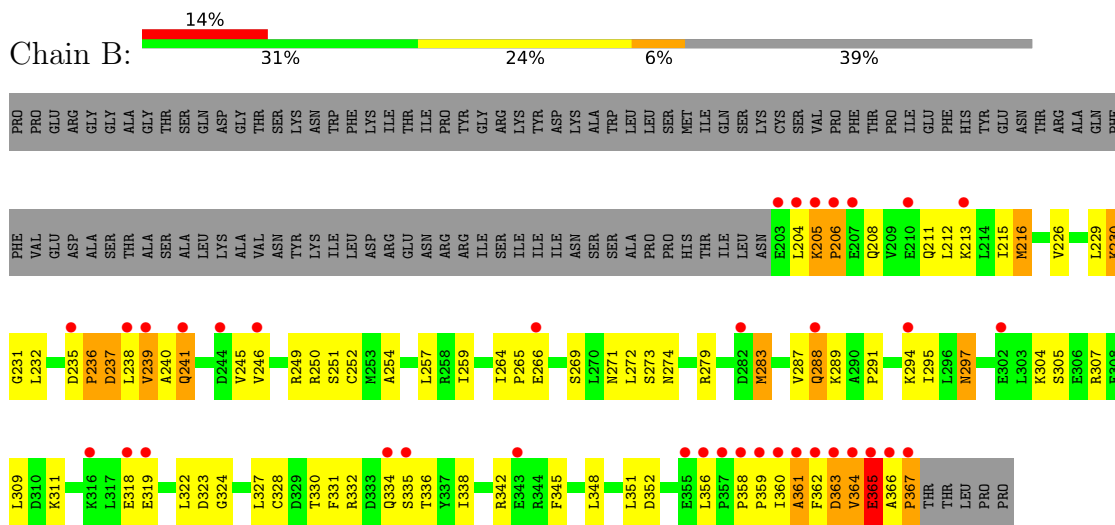
3 Residue-property plots i

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: TIP ASSOCIATING PROTEIN

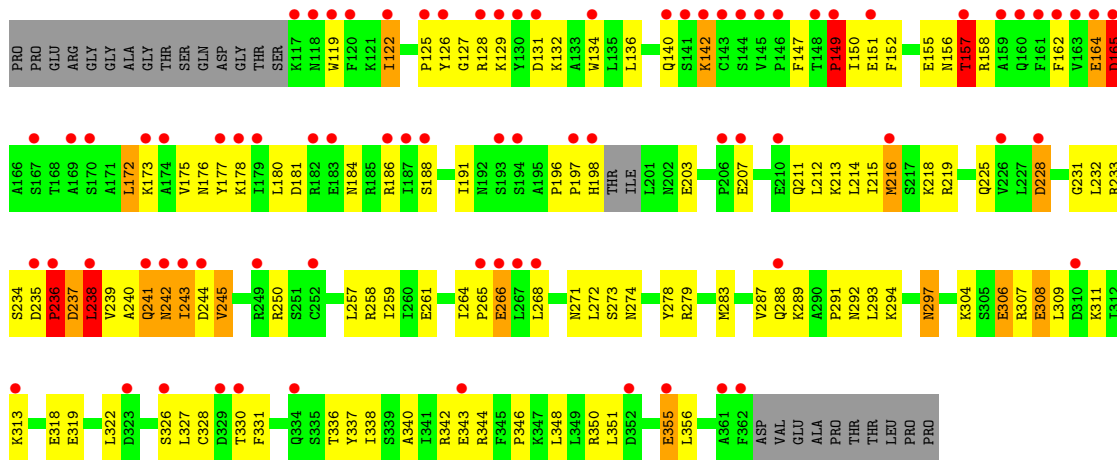


• Molecule 1: TIP ASSOCIATING PROTEIN

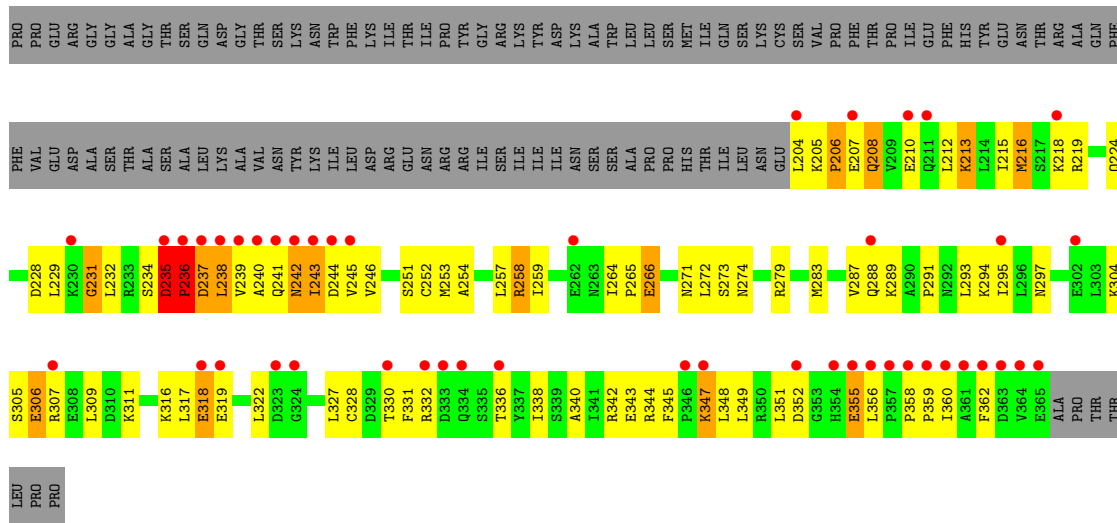
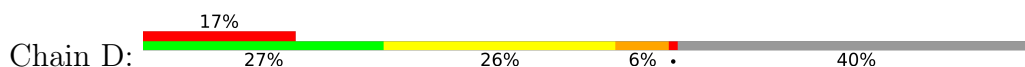


• Molecule 1: TIP ASSOCIATING PROTEIN

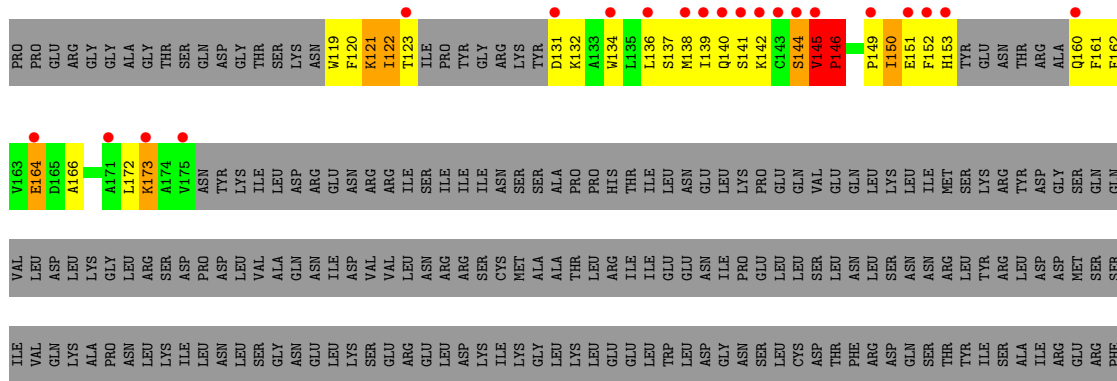




• Molecule 1: TIP ASSOCIATING PROTEIN



• Molecule 1: TIP ASSOCIATING PROTEIN



PRO
LYS
LEU
LEU
ARG
LEU
ASP
GLY
HIS
GLU
LEU
PRO
PRO
PRO
PRO
ILE
ALA
PHE
ASP
VAL
GLU
ALA
PRO
THR
THR
LEU
PRO
PRO

4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	139.92Å 139.92Å 206.70Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 3.15 30.00 – 3.15	Depositor EDS
% Data completeness (in resolution range)	(Not available) (30.00-3.15) 99.4 (30.00-3.15)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	6.10 (at 3.18Å)	Xtrriage
Refinement program	CNS	Depositor
R, R_{free}	0.303 , 0.303 0.296 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	80.0	Xtrriage
Anisotropy	0.046	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 28.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.86	EDS
Total number of atoms	6913	wwPDB-VP
Average B, all atoms (Å ²)	72.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.48% 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	0.83	5/1996 (0.3%)	1.27	21/2696 (0.8%)
1	B	0.75	2/1340 (0.1%)	1.17	10/1808 (0.6%)
1	C	0.90	11/2008 (0.5%)	1.17	18/2711 (0.7%)
1	D	0.77	2/1318 (0.2%)	1.22	14/1777 (0.8%)
1	E	0.84	0/363	1.44	7/489 (1.4%)
All	All	0.83	20/7025 (0.3%)	1.22	70/9481 (0.7%)

The worst 5 of 20 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	242	ASN	CA-C	-10.81	1.38	1.52
1	A	165	ASP	CB-CG	-9.84	1.27	1.52
1	C	242	ASN	CA-CB	9.48	1.69	1.53
1	C	228	ASP	CB-CG	-8.67	1.30	1.52
1	C	165	ASP	CB-CG	-7.71	1.32	1.52

The worst 5 of 70 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	195	ALA	CA-C-N	17.35	138.25	120.38
1	A	195	ALA	C-N-CA	17.35	138.25	120.38
1	E	144	SER	CA-C-N	-10.01	103.62	122.13
1	E	144	SER	C-N-CA	-10.01	103.62	122.13
1	A	235	ASP	N-CA-C	9.88	122.52	110.07

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	1961	0	2003	175	0
1	B	1323	0	1363	112	0
1	C	1973	0	2013	137	0
1	D	1302	0	1345	120	0
1	E	354	0	349	51	1
All	All	6913	0	7073	555	1

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 40.

The worst 5 of 555 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:230:LYS:HD2	1:A:273:SER:OG	1.29	1.32
1:B:323:ASP:HB2	1:C:177:TYR:CE2	1.78	1.19
1:C:119:TRP:HZ3	1:C:150:ILE:CD1	1.56	1.19
1:E:144:SER:O	1:E:145:VAL:HG23	1.39	1.19
1:E:145:VAL:HG22	1:E:146:PRO:CD	1.73	1.17

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:142:LYS:NZ	1:E:142:LYS:NZ[8_665]	1.44	0.76

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.

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	238/271 (88%)	213 (90%)	20 (8%)	5 (2%)	5	26
1	B	163/271 (60%)	149 (91%)	10 (6%)	4 (2%)	4	22
1	C	240/271 (89%)	216 (90%)	17 (7%)	7 (3%)	3	20
1	D	160/271 (59%)	139 (87%)	16 (10%)	5 (3%)	3	18
1	E	38/271 (14%)	35 (92%)	2 (5%)	1 (3%)	4	21
All	All	839/1355 (62%)	752 (90%)	65 (8%)	22 (3%)	4	21

5 of 22 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	236	PRO
1	C	157	THR
1	C	236	PRO
1	C	238	LEU
1	C	308	GLU

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	
1	A	222/245 (91%)	201 (90%)	21 (10%)	8	29
1	B	152/245 (62%)	142 (93%)	10 (7%)	15	42
1	C	222/245 (91%)	207 (93%)	15 (7%)	14	41
1	D	150/245 (61%)	141 (94%)	9 (6%)	17	45
1	E	39/245 (16%)	32 (82%)	7 (18%)	2	8
All	All	785/1225 (64%)	723 (92%)	62 (8%)	11	36

5 of 62 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	364	VAL
1	E	121	LYS
1	C	165	ASP
1	D	355	GLU
1	E	150	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 21 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	156	ASN
1	C	334	GLN
1	E	160	GLN
1	D	208	GLN
1	C	297	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 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	242/271 (89%)	1.37	56 (23%) 2 2	55, 66, 89, 109	0
1	B	165/271 (60%)	1.32	37 (22%) 2 2	49, 63, 82, 97	0
1	C	244/271 (90%)	1.62	79 (32%) 1 1	55, 74, 106, 106	0
1	D	162/271 (59%)	1.46	46 (28%) 1 1	52, 65, 85, 100	0
1	E	44/271 (16%)	2.23	21 (47%) 0 1	89, 94, 94, 94	0
All	All	857/1355 (63%)	1.49	239 (27%) 1 1	49, 68, 106, 109	0

The worst 5 of 239 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	319	GLU	7.7
1	A	211	GLN	6.0
1	B	210	GLU	5.7
1	B	318	GLU	5.4
1	C	228	ASP	5.1

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.