



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 01:43 PM UTC

PDB ID : 3TU3 / pdb_00003tu3
Title : 1.92 Angstrom resolution crystal structure of the full-length SpcU in complex with full-length ExoU from the type III secretion system of *Pseudomonas aeruginosa*
Authors : Halavaty, A.S.; Borek, D.; Otwinowski, Z.; Minasov, G.; Veesenmeyer, J.L.; Tyson, G.; Shuvalova, L.; Hauser, A.R.; Anderson, W.F.; Center for Structural Genomics of Infectious Diseases (CSGID)
Deposited on : 2011-09-15
Resolution : 1.92 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

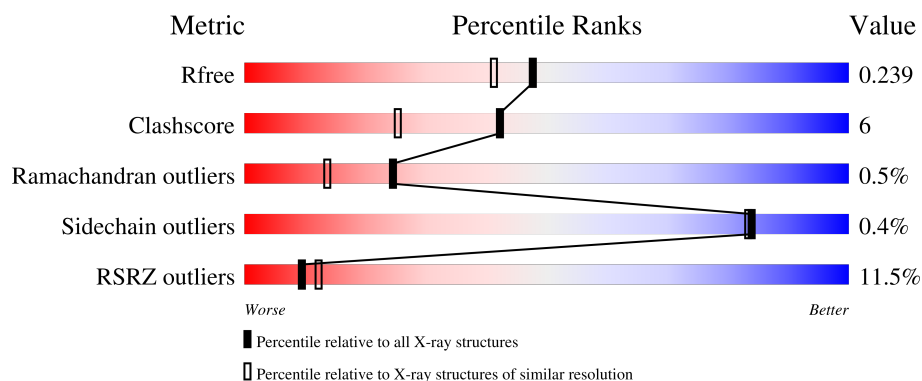
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.92 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	1188 (1.92-1.92)
Clashscore	190562	1209 (1.92-1.92)
Ramachandran outliers	187476	1195 (1.92-1.92)
Sidechain outliers	187428	1195 (1.92-1.92)
RSRZ outliers	180081	1188 (1.92-1.92)

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	161	7% 61% 12% • 26%
2	B	711	9% 65% 9% 26%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 5674 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 ExoU chaperone.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	119	Total	C	N	O	S	0	4	0
			958	610	169	177	2			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-23	MET	-	expression tag	UNP O66100
A	-22	HIS	-	expression tag	UNP O66100
A	-21	HIS	-	expression tag	UNP O66100
A	-20	HIS	-	expression tag	UNP O66100
A	-19	HIS	-	expression tag	UNP O66100
A	-18	HIS	-	expression tag	UNP O66100
A	-17	HIS	-	expression tag	UNP O66100
A	-16	SER	-	expression tag	UNP O66100
A	-15	SER	-	expression tag	UNP O66100
A	-14	GLY	-	expression tag	UNP O66100
A	-13	VAL	-	expression tag	UNP O66100
A	-12	ASP	-	expression tag	UNP O66100
A	-11	LEU	-	expression tag	UNP O66100
A	-10	GLY	-	expression tag	UNP O66100
A	-9	THR	-	expression tag	UNP O66100
A	-8	GLU	-	expression tag	UNP O66100
A	-7	ASN	-	expression tag	UNP O66100
A	-6	LEU	-	expression tag	UNP O66100
A	-5	TYR	-	expression tag	UNP O66100
A	-4	PHE	-	expression tag	UNP O66100
A	-3	GLN	-	expression tag	UNP O66100
A	-2	SER	-	expression tag	UNP O66100
A	-1	ASN	-	expression tag	UNP O66100
A	0	ALA	-	expression tag	UNP O66100

- Molecule 2 is a protein called ExoU.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	526	Total	C	N	O	S	0	24	0
			4215	2610	767	826	12			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-23	MET	-	expression tag	UNP O34208
B	-22	HIS	-	expression tag	UNP O34208
B	-21	HIS	-	expression tag	UNP O34208
B	-20	HIS	-	expression tag	UNP O34208
B	-19	HIS	-	expression tag	UNP O34208
B	-18	HIS	-	expression tag	UNP O34208
B	-17	HIS	-	expression tag	UNP O34208
B	-16	SER	-	expression tag	UNP O34208
B	-15	SER	-	expression tag	UNP O34208
B	-14	GLY	-	expression tag	UNP O34208
B	-13	VAL	-	expression tag	UNP O34208
B	-12	ASP	-	expression tag	UNP O34208
B	-11	LEU	-	expression tag	UNP O34208
B	-10	GLY	-	expression tag	UNP O34208
B	-9	THR	-	expression tag	UNP O34208
B	-8	GLU	-	expression tag	UNP O34208
B	-7	ASN	-	expression tag	UNP O34208
B	-6	LEU	-	expression tag	UNP O34208
B	-5	TYR	-	expression tag	UNP O34208
B	-4	PHE	-	expression tag	UNP O34208
B	-3	GLN	-	expression tag	UNP O34208
B	-2	SER	-	expression tag	UNP O34208
B	-1	ASN	-	expression tag	UNP O34208
B	0	ALA	-	expression tag	UNP O34208

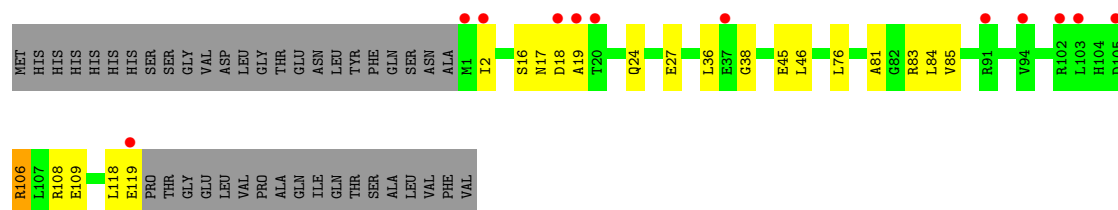
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	54	Total	O	0	3
			56	56		
3	B	436	Total	O	0	18
			445	445		

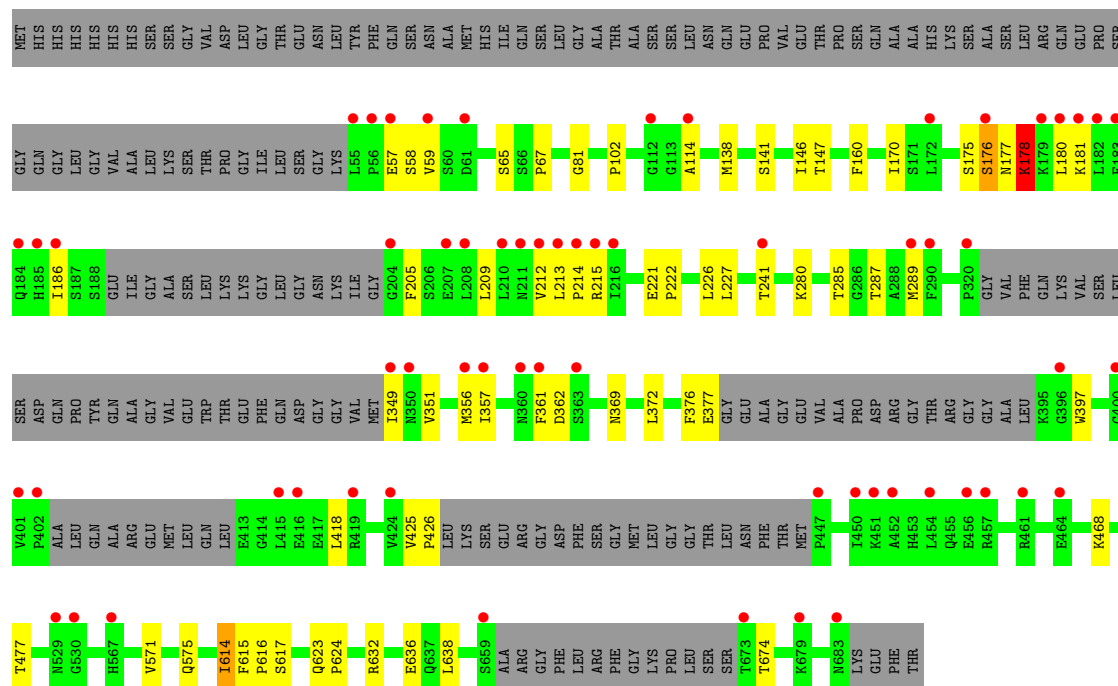
3 Residue-property plots [i](#)

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: ExoU chaperone



• Molecule 2: ExoU



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	154.14Å 52.58Å 119.54Å 90.00° 126.59° 90.00°	Depositor
Resolution (Å)	29.17 – 1.92 29.17 – 1.92	Depositor EDS
% Data completeness (in resolution range)	99.8 (29.17-1.92) 99.8 (29.17-1.92)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.78 (at 1.92Å)	Xtriage
Refinement program	REFMAC 5.5.0102	Depositor
R, R_{free}	0.191 , 0.225 0.210 , 0.239	Depositor DCC
R_{free} test set	2975 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	28.5	Xtriage
Anisotropy	0.020	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 38.8	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	5674	wwPDB-VP
Average B, all atoms (Å ²)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.09% 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	0.51	0/977	0.94	1/1332 (0.1%)
2	B	0.54	0/4272	0.87	5/5776 (0.1%)
All	All	0.53	0/5249	0.89	6/7108 (0.1%)

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	81	GLY	CA-C-N	6.78	126.74	119.28
2	B	81	GLY	C-N-CA	6.78	126.74	119.28
2	B	614	ILE	N-CA-C	6.41	116.56	110.53
1	A	2	ILE	N-CA-C	6.28	117.03	110.62
2	B	181	LYS	N-CA-C	-6.17	104.67	111.82
2	B	372	LEU	N-CA-C	-5.25	98.84	108.02

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	958	0	969	20	0
2	B	4215	0	4206	51	0
3	A	56	0	0	0	0
3	B	445	0	0	4	0
All	All	5674	0	5175	65	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 6.

All (65) 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:76:LEU:HD11	1:A:84[B]:LEU:HD21	1.36	1.06
1:A:76:LEU:HD11	1:A:84[B]:LEU:CD2	1.94	0.97
2:B:287:THR:HG23	2:B:351:VAL:HG22	1.75	0.68
2:B:209:LEU:C	2:B:209:LEU:HD23	2.21	0.65
2:B:186:ILE:O	2:B:186:ILE:HG22	1.94	0.65
2:B:175:SER:O	2:B:176:SER:C	2.41	0.64
1:A:16:SER:O	1:A:18:ASP:N	2.34	0.60
1:A:45:GLU:CG	1:A:83:ARG:HD3	2.33	0.59
1:A:118:LEU:O	1:A:119:GLU:C	2.47	0.58
2:B:425:VAL:HG13	2:B:426:PRO:HD2	1.86	0.57
1:A:76:LEU:CD1	1:A:84[B]:LEU:CD2	2.75	0.56
2:B:59:VAL:HG22	2:B:59:VAL:O	2.04	0.56
2:B:186:ILE:O	2:B:186:ILE:CG2	2.56	0.53
2:B:175:SER:O	2:B:177:ASN:N	2.42	0.53
2:B:376:PHE:O	2:B:377:GLU:HB2	2.09	0.53
2:B:146:ILE:HG23	2:B:227:LEU:HD21	1.92	0.52
2:B:361:PHE:O	2:B:362[B]:ASP:OD2	2.28	0.52
1:A:45:GLU:HG3	1:A:83:ARG:HD3	1.90	0.52
2:B:571:VAL:O	2:B:575[A]:GLN:HG3	2.10	0.52
2:B:632[A]:ARG:NH1	3:B:1118[A]:HOH:O	2.42	0.51
1:A:24:GLN:HB2	2:B:65:SER:HB3	1.93	0.51
1:A:106[A]:ARG:NH1	1:A:109[A]:GLU:HG2	2.26	0.51
2:B:67:PRO:HB2	2:B:477:THR:HG22	1.92	0.50
2:B:241[B]:THR:O	2:B:241[B]:THR:HG22	2.11	0.50
2:B:289:MET:HG2	2:B:349:ILE:CD1	2.42	0.50
1:A:108:ARG:HH11	2:B:58:SER:CB	2.25	0.49
1:A:108:ARG:HH11	2:B:58:SER:HB2	1.77	0.49
2:B:177:ASN:OD1	2:B:178:LYS:HE3	2.13	0.49
2:B:617[A]:SER:OG	2:B:674:THR:OG1	2.24	0.49
1:A:108:ARG:NH1	2:B:58:SER:HB2	2.27	0.49
2:B:614:ILE:HD12	2:B:638:LEU:HD12	1.95	0.48
2:B:138:MET:HE2	2:B:280:LYS:HG3	1.95	0.48
2:B:212:VAL:HG12	2:B:215:ARG:NH1	2.28	0.48
2:B:180:LEU:HD12	2:B:180:LEU:N	2.29	0.48
2:B:362[A]:ASP:OD2	3:B:1051:HOH:O	2.20	0.47
2:B:141:SER:HB3	2:B:356:MET:SD	2.54	0.47
2:B:376:PHE:O	2:B:377:GLU:CB	2.62	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:102:PRO:HB2	2:B:369:ASN:HA	1.96	0.47
2:B:362[A]:ASP:OD2	3:B:935:HOH:O	2.21	0.46
1:A:106[A]:ARG:NE	1:A:106[A]:ARG:HA	2.30	0.46
2:B:357:ILE:CD1	2:B:418:LEU:HD22	2.46	0.46
1:A:76:LEU:CD1	1:A:84[B]:LEU:HD21	2.25	0.46
2:B:114:ALA:HB2	2:B:170:ILE:HG12	1.98	0.45
2:B:186:ILE:HD13	2:B:205:PHE:CE1	2.53	0.44
2:B:623:GLN:OE1	2:B:624:PRO:HD2	2.18	0.44
1:A:18:ASP:OD1	1:A:19:ALA:N	2.51	0.44
2:B:209:LEU:O	2:B:212:VAL:HG22	2.17	0.44
2:B:209:LEU:HD23	2:B:209:LEU:O	2.17	0.43
2:B:615:PHE:HB3	2:B:616:PRO:HD3	2.00	0.43
1:A:85:VAL:HG21	2:B:397:TRP:CH2	2.54	0.43
2:B:57:GLU:CD	2:B:57:GLU:C	2.87	0.42
1:A:27[A]:GLU:OE1	1:A:27[A]:GLU:C	2.63	0.42
2:B:147:THR:HG23	2:B:160:PHE:CZ	2.55	0.42
2:B:221:GLU:CD	2:B:222:PRO:HD2	2.45	0.42
2:B:289:MET:CG	2:B:349:ILE:HD13	2.50	0.42
2:B:209:LEU:C	2:B:209:LEU:CD2	2.91	0.41
2:B:468:LYS:HE3	2:B:468:LYS:HB2	1.86	0.41
1:A:46:LEU:HD12	1:A:84[B]:LEU:HD22	2.02	0.41
2:B:357:ILE:CD1	2:B:418:LEU:CD2	2.99	0.41
1:A:36:LEU:O	1:A:38:GLY:N	2.54	0.41
2:B:213:LEU:N	2:B:214:PRO:CD	2.85	0.40
2:B:425:VAL:CG1	2:B:426:PRO:HD2	2.50	0.40
1:A:81:ALA:HB1	2:B:636:GLU:HB2	2.03	0.40
2:B:141:SER:HA	2:B:285:THR:O	2.22	0.40
2:B:226:LEU:CD1	3:B:1020:HOH:O	2.68	0.40

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	
1	A	121/161 (75%)	118 (98%)	2 (2%)	1 (1%)	16	6
2	B	536/711 (75%)	526 (98%)	8 (2%)	2 (0%)	30	19
All	All	657/872 (75%)	644 (98%)	10 (2%)	3 (0%)	24	14

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	17	ASN
2	B	176	SER
2	B	178	LYS

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	103/135 (76%)	101 (98%)	2 (2%)	50	37
2	B	456/575 (79%)	455 (100%)	1 (0%)	87	87
All	All	559/710 (79%)	556 (100%)	3 (0%)	84	80

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	106[A]	ARG
1	A	106[B]	ARG
2	B	178	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	295	GLN
2	B	311	GLN
2	B	350	ASN
2	B	500	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 ⓘ

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	119/161 (73%)	0.72	12 (10%)	12	16	15, 37, 63, 68	4 (3%)
2	B	526/711 (73%)	0.58	62 (11%)	9	12	12, 31, 67, 94	24 (4%)
All	All	645/872 (73%)	0.61	74 (11%)	9	12	12, 32, 66, 94	28 (4%)

All (74) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	182	LEU	9.9
2	B	529	ASN	5.6
2	B	180	LEU	4.8
2	B	424	VAL	4.6
2	B	216	ILE	4.6
2	B	55	LEU	4.4
2	B	183	PHE	4.3
2	B	114	ALA	4.1
1	A	19	ALA	4.0
2	B	415	LEU	3.9
2	B	186	ILE	3.9
2	B	401	VAL	3.8
2	B	56	PRO	3.7
2	B	357	ILE	3.6
2	B	210	LEU	3.6
2	B	447	PRO	3.5
2	B	530	GLY	3.5
2	B	402	PRO	3.5
2	B	659	SER	3.4
2	B	181	LYS	3.4
1	A	119	GLU	3.4
2	B	349	ILE	3.4
2	B	213	LEU	3.3
2	B	350	ASN	3.3

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Mol	Chain	Res	Type	RSRZ
2	B	57	GLU	3.3
2	B	112	GLY	3.3
2	B	59	VAL	3.3
2	B	179	LYS	3.2
1	A	18	ASP	3.0
2	B	457	ARG	3.0
1	A	105	ASP	2.9
2	B	400	GLY	2.9
2	B	452	ALA	2.9
1	A	37	GLU	2.9
2	B	215	ARG	2.8
2	B	212	VAL	2.8
2	B	567[A]	HIS	2.7
2	B	176	SER	2.7
1	A	94	VAL	2.7
2	B	464[A]	GLU	2.7
2	B	185	HIS	2.6
1	A	1	MET	2.6
2	B	289	MET	2.5
2	B	361	PHE	2.5
2	B	416	GLU	2.5
2	B	172	LEU	2.5
2	B	320	PRO	2.5
1	A	20	THR	2.5
2	B	214	PRO	2.4
2	B	184	GLN	2.4
2	B	356	MET	2.4
2	B	241[A]	THR	2.4
2	B	61	ASP	2.4
2	B	461	ARG	2.3
1	A	2	ILE	2.3
2	B	363	SER	2.3
1	A	91	ARG	2.2
2	B	204	GLY	2.2
2	B	450	ILE	2.2
1	A	102	ARG	2.2
2	B	290	PHE	2.2
2	B	454	LEU	2.2
2	B	451	LYS	2.2
2	B	211	ASN	2.1
2	B	208	LEU	2.1
1	A	103	LEU	2.1

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Mol	Chain	Res	Type	RSRZ
2	B	456	GLU	2.1
2	B	673	THR	2.1
2	B	207	GLU	2.0
2	B	360	ASN	2.0
2	B	419	ARG	2.0
2	B	679	LYS	2.0
2	B	396	GLY	2.0
2	B	683	ASN	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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.