



wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 18, 2023 – 06:24 pm GMT

PDB ID : 8AF9
Title : Structure of a T4SS effector from Brucella sp.
Authors : Gueguen-Chaignon, V.; Salcedo, S.P.; Terradot, L.
Deposited on : 2022-07-16
Resolution : 2.50 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 : 4.02b-467
Xtriage (Phenix) : 1.13
EDS : 2.31.3
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.3

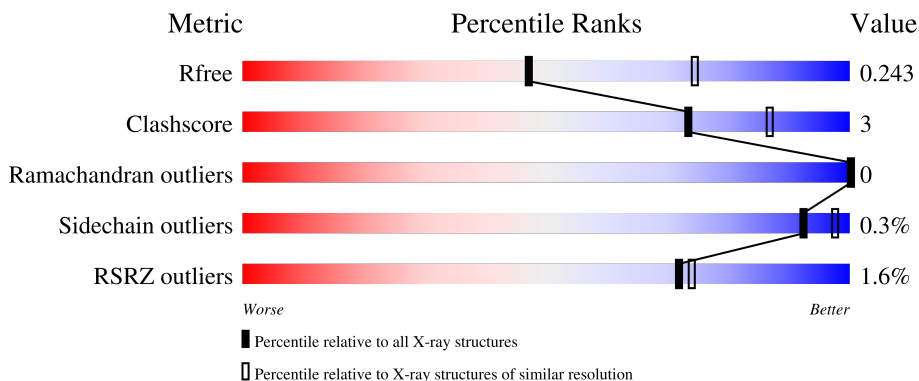
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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}	130704	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (2.50-2.50)

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	134	 2% 78% 10% 13%
1	B	134	 % 84% 12%
1	C	134	 % 81% 7% 12%
1	D	134	 % 75% 13% 12%
1	E	134	 % 81% 6% 13%

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Mol	Chain	Length	Quality of chain
1	F	134	<p>% 76% 10% 13%</p>
1	G	134	<p>4% 83% 13%</p>
1	H	134	<p>% 74% 13% 13%</p>
1	I	134	<p>% 80% 8% 12%</p>
1	J	134	<p>78% 8% 13%</p>
1	K	134	<p>% 84% 13%</p>
1	L	134	<p>% 81% 7% 12%</p>

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 22005 atoms, of which 10440 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 NyxB, T4SS effector protein from Brucella.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
			Total	C	H	N	O				S
1	A	117	1766	588	854	147	172	5	32	0	0
1	B	118	1822	604	885	149	179	5	28	0	0
1	C	118	1840	606	897	151	180	6	28	1	0
1	D	118	1788	594	871	146	172	5	32	0	0
1	E	116	1756	581	858	144	168	5	33	0	0
1	F	116	1770	585	864	145	171	5	31	0	0
1	G	117	1781	588	868	148	173	4	32	0	0
1	H	117	1757	592	839	148	173	5	28	0	0
1	I	118	1844	608	899	153	179	5	26	0	0
1	J	116	1770	589	857	145	175	4	29	0	0
1	K	116	1763	584	857	145	173	4	30	0	0
1	L	118	1829	605	891	150	178	5	28	0	0

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	27	Total	O	0	0
			27	27		
2	B	74	Total	O	0	0
			74	74		

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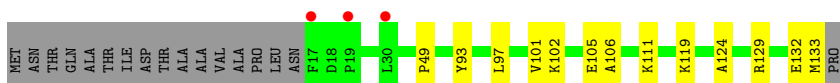
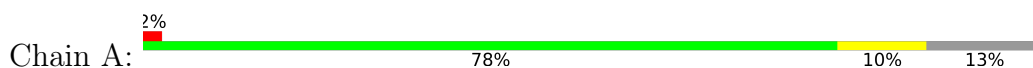
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	C	75	Total 75	O 75	0	0
2	D	50	Total 50	O 50	0	0
2	E	26	Total 26	O 26	0	0
2	F	11	Total 11	O 11	0	0
2	G	31	Total 31	O 31	0	0
2	H	28	Total 28	O 28	0	0
2	I	47	Total 47	O 47	0	0
2	J	48	Total 48	O 48	0	0
2	K	43	Total 43	O 43	0	0
2	L	59	Total 59	O 59	0	0

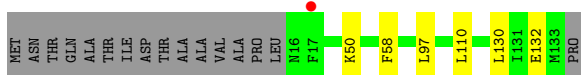
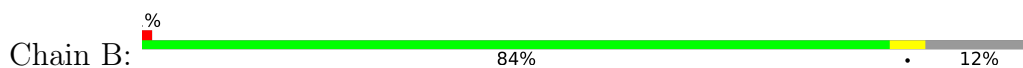
3 Residue-property plots [i](#)

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.

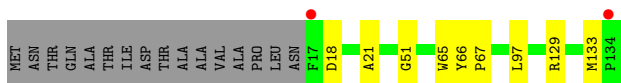
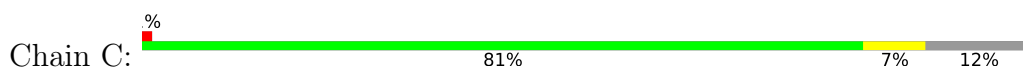
- Molecule 1: NyxB, T4SS effector protein from Brucella



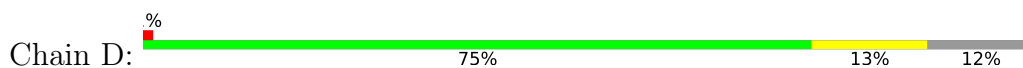
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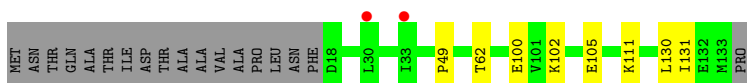
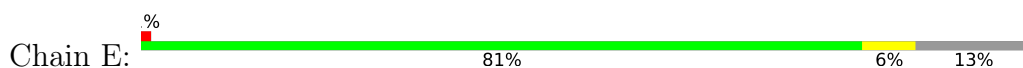
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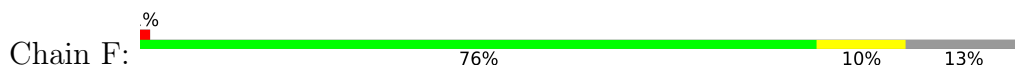
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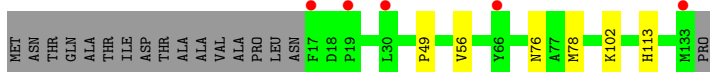
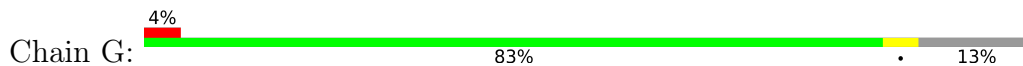
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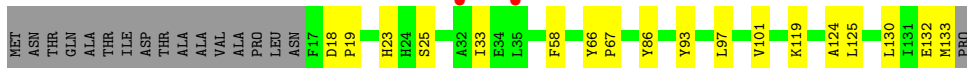
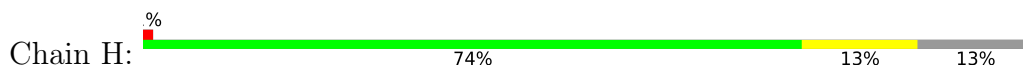
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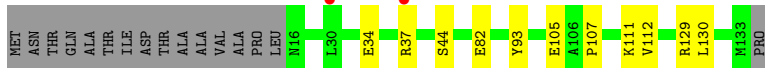
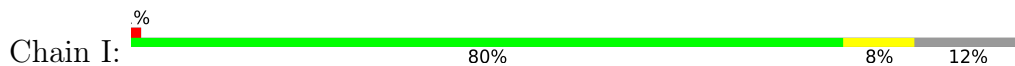
- Molecule 1: NyxB, T4SS effector protein from Brucella



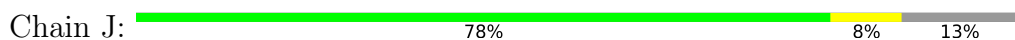
- Molecule 1: NyxB, T4SS effector protein from Brucella



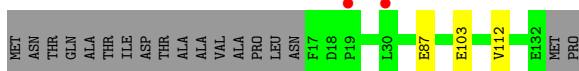
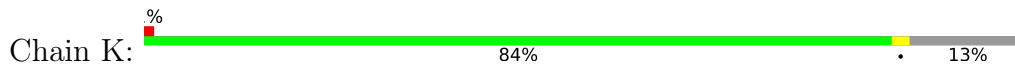
- Molecule 1: NyxB, T4SS effector protein from Brucella



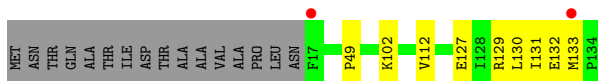
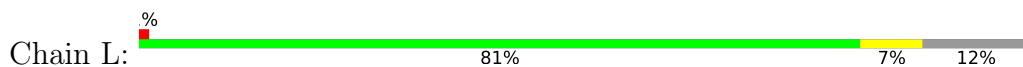
- Molecule 1: NyxB, T4SS effector protein from Brucella



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- Molecule 1: NyxB, T4SS effector protein from Brucella



4 Data and refinement statistics

Property	Value	Source
Space group	P 61 2 2	Depositor
Cell constants a, b, c, α , β , γ	133.91Å 133.91Å 389.51Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	46.61 – 2.50 46.61 – 2.50	Depositor EDS
% Data completeness (in resolution range)	99.6 (46.61-2.50) 100.0 (46.61-2.50)	Depositor EDS
R_{merge}	0.18	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.94 (at 2.51Å)	Xtrriage
Refinement program	PHENIX 1.20_4459	Depositor
R, R_{free}	0.216 , 0.245 0.215 , 0.243	Depositor DCC
R_{free} test set	3613 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	45.0	Xtrriage
Anisotropy	0.602	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 36.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	22005	wwPDB-VP
Average B, all atoms (Å ²)	56.0	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 34.00 % 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 7.3188e-04. 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 [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	0.56	0/940	0.71	0/1283
1	B	0.71	0/965	0.82	1/1314 (0.1%)
1	C	0.68	0/971	0.80	0/1322
1	D	0.68	1/945 (0.1%)	0.84	3/1289 (0.2%)
1	E	0.57	0/925	0.68	0/1262
1	F	0.62	0/933	0.70	0/1272
1	G	0.62	0/940	0.74	0/1282
1	H	0.63	0/946	0.72	1/1287 (0.1%)
1	I	0.67	1/973 (0.1%)	0.77	0/1323
1	J	0.64	1/941 (0.1%)	0.77	1/1283 (0.1%)
1	K	0.64	0/933	0.75	0/1273
1	L	0.64	0/967	0.79	1/1316 (0.1%)
All	All	0.64	3/11379 (0.0%)	0.76	7/15506 (0.0%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	I	82	GLU	CG-CD	5.88	1.60	1.51
1	D	44	SER	C-N	-5.29	1.21	1.34
1	J	44	SER	C-N	-5.10	1.22	1.34

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	110	LEU	CB-CG-CD2	6.33	121.77	111.00
1	L	130	LEU	CB-CG-CD1	5.91	121.04	111.00
1	D	30	LEU	CB-CG-CD2	-5.63	101.43	111.00
1	J	27	MET	CG-SD-CE	5.50	108.99	100.20
1	D	27	MET	CG-SD-CE	5.42	108.88	100.20

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	912	854	838	10	0
1	B	937	885	874	6	0
1	C	943	897	887	8	0
1	D	917	871	852	10	0
1	E	898	858	839	7	0
1	F	906	864	849	7	0
1	G	913	868	851	4	0
1	H	918	839	849	13	0
1	I	945	899	892	6	1
1	J	913	857	846	8	0
1	K	906	857	844	1	0
1	L	938	891	882	5	1
2	A	27	0	0	0	0
2	B	74	0	0	0	0
2	C	75	0	0	0	0
2	D	50	0	0	1	0
2	E	26	0	0	0	0
2	F	11	0	0	0	0
2	G	31	0	0	0	0
2	H	28	0	0	0	0
2	I	47	0	0	1	0
2	J	48	0	0	0	0
2	K	43	0	0	0	0
2	L	59	0	0	0	0
All	All	11565	10440	10303	71	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 3.

The worst 5 of 71 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:F:33:ILE:HD13	1:F:67:PRO:HG2	1.61	0.82
1:L:49:PRO:HG2	1:L:102:LYS:HD3	1.64	0.79
1:A:49:PRO:HG2	1:A:102:LYS:HD3	1.63	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:132:GLU:OE2	1:D:93:TYR:OH	2.01	0.77
1:E:49:PRO:HG2	1:E:102:LYS:HD3	1.67	0.75

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:I:93:TYR:OH	1:L:132:GLU:OE2[5_554]	2.18	0.02

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	115/134 (86%)	113 (98%)	2 (2%)	0	100	100
1	B	116/134 (87%)	115 (99%)	1 (1%)	0	100	100
1	C	117/134 (87%)	115 (98%)	2 (2%)	0	100	100
1	D	116/134 (87%)	114 (98%)	2 (2%)	0	100	100
1	E	114/134 (85%)	112 (98%)	2 (2%)	0	100	100
1	F	114/134 (85%)	113 (99%)	1 (1%)	0	100	100
1	G	115/134 (86%)	114 (99%)	1 (1%)	0	100	100
1	H	115/134 (86%)	114 (99%)	1 (1%)	0	100	100
1	I	116/134 (87%)	114 (98%)	2 (2%)	0	100	100
1	J	114/134 (85%)	112 (98%)	2 (2%)	0	100	100
1	K	114/134 (85%)	113 (99%)	1 (1%)	0	100	100
1	L	116/134 (87%)	114 (98%)	2 (2%)	0	100	100
All	All	1382/1608 (86%)	1363 (99%)	19 (1%)	0	100	100

There are no Ramachandran outliers to report.

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	90/110 (82%)	90 (100%)	0	100	100
1	B	95/110 (86%)	95 (100%)	0	100	100
1	C	97/110 (88%)	97 (100%)	0	100	100
1	D	91/110 (83%)	91 (100%)	0	100	100
1	E	89/110 (81%)	89 (100%)	0	100	100
1	F	91/110 (83%)	90 (99%)	1 (1%)	73	89
1	G	91/110 (83%)	91 (100%)	0	100	100
1	H	90/110 (82%)	90 (100%)	0	100	100
1	I	97/110 (88%)	97 (100%)	0	100	100
1	J	92/110 (84%)	92 (100%)	0	100	100
1	K	91/110 (83%)	89 (98%)	2 (2%)	52	77
1	L	96/110 (87%)	96 (100%)	0	100	100
All	All	1110/1320 (84%)	1107 (100%)	3 (0%)	92	97

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

Mol	Chain	Res	Type
1	F	20	ASN
1	K	87	GLU
1	K	103	GLU

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

Mol	Chain	Res	Type
1	B	113	HIS
1	H	23	HIS

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 monosaccharides 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	117/134 (87%)	0.20	3 (2%) 56 59	44, 56, 74, 82	0
1	B	118/134 (88%)	0.17	1 (0%) 86 87	31, 40, 56, 74	0
1	C	118/134 (88%)	0.23	2 (1%) 70 72	33, 45, 59, 84	2 (1%)
1	D	118/134 (88%)	0.16	1 (0%) 86 87	31, 45, 60, 82	1 (0%)
1	E	116/134 (86%)	0.26	2 (1%) 70 72	46, 63, 79, 89	0
1	F	116/134 (86%)	0.12	1 (0%) 84 86	46, 58, 80, 86	0
1	G	117/134 (87%)	0.32	5 (4%) 35 38	40, 52, 79, 98	0
1	H	117/134 (87%)	0.31	2 (1%) 70 72	42, 58, 86, 96	2 (1%)
1	I	118/134 (88%)	0.19	2 (1%) 70 72	37, 49, 65, 80	0
1	J	116/134 (86%)	0.23	0 100 100	37, 48, 62, 80	0
1	K	116/134 (86%)	0.14	2 (1%) 70 72	36, 47, 61, 77	0
1	L	118/134 (88%)	0.19	2 (1%) 70 72	33, 44, 57, 76	2 (1%)
All	All	1405/1608 (87%)	0.21	23 (1%) 72 74	31, 50, 73, 98	7 (0%)

The worst 5 of 23 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	17	PHE	5.1
1	K	30	LEU	4.3
1	G	133	MET	4.1
1	L	17	PHE	3.8
1	G	17	PHE	3.8

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 monosaccharides 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.