



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 18, 2026 – 07:07 AM UTC

PDB ID : 6N40 / pdb_00006n40
Title : Crystal structure of MmpL3 from Mycobacterium smegmatis
Authors : Su, C.-C.
Deposited on : 2018-11-16
Resolution : 3.31 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

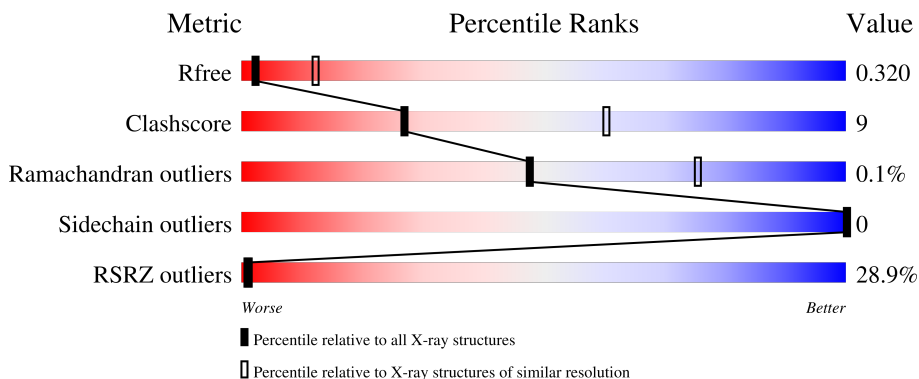
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.31 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	1169 (3.32-3.28)
Clashscore	190562	1209 (3.32-3.28)
Ramachandran outliers	187476	1188 (3.32-3.28)
Sidechain outliers	187428	1187 (3.32-3.28)
RSRZ outliers	180081	1169 (3.32-3.28)

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	779	27% 74% 19% 7%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 5535 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 Membrane protein, MmpL family protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	726	5535	3583	919	1005	28	0	0	0

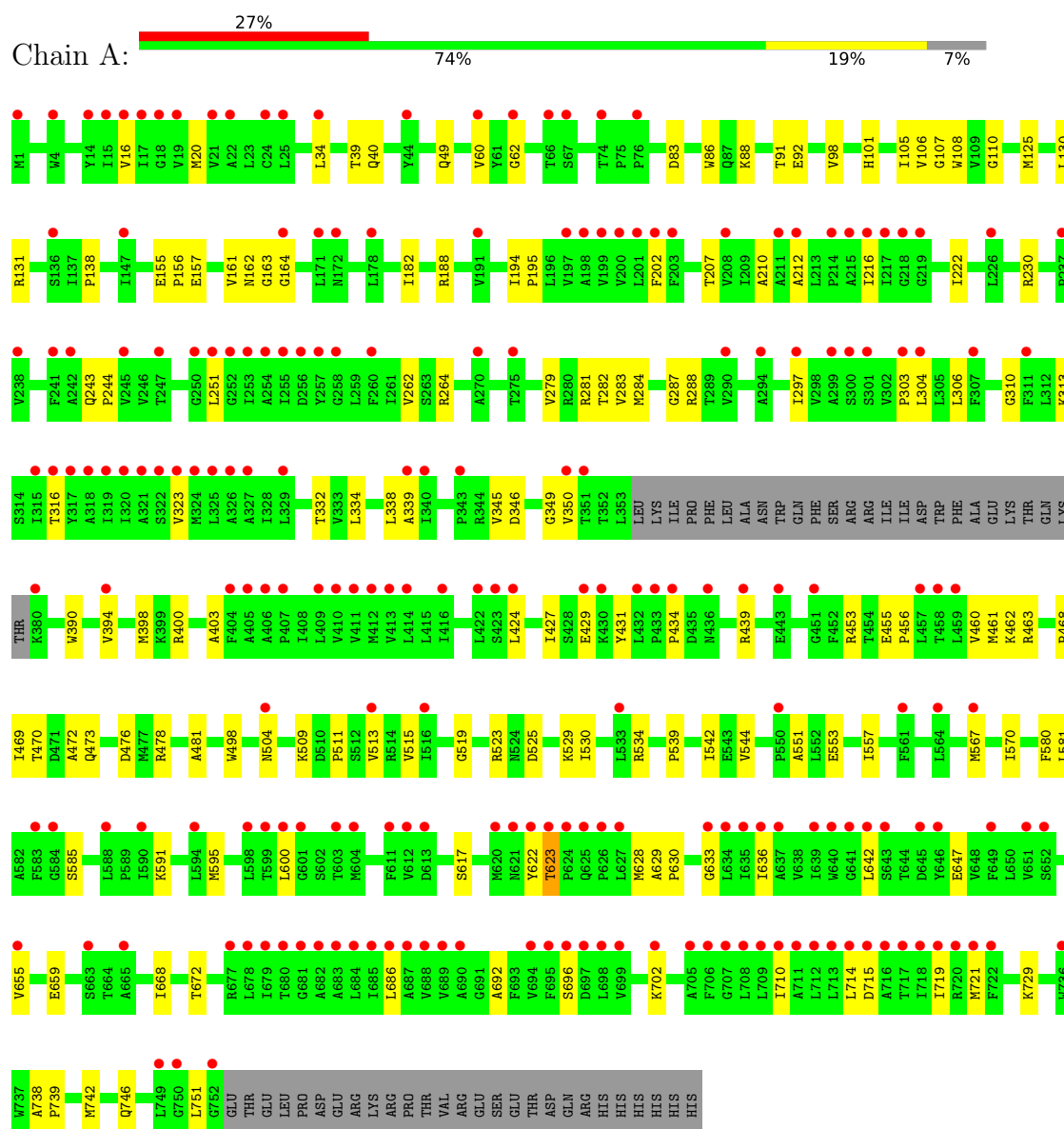
There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	774	HIS	-	expression tag	UNP A0QP27
A	775	HIS	-	expression tag	UNP A0QP27
A	776	HIS	-	expression tag	UNP A0QP27
A	777	HIS	-	expression tag	UNP A0QP27
A	778	HIS	-	expression tag	UNP A0QP27
A	779	HIS	-	expression tag	UNP A0QP27

3 Residue-property plots

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: Membrane protein, MmpL family protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	84.24Å 130.92Å 155.63Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	100.19 – 3.31 100.19 – 3.31	Depositor EDS
% Data completeness (in resolution range)	98.9 (100.19-3.31) 99.2 (100.19-3.31)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.47 (at 3.33Å)	Xtriage
Refinement program	PHENIX (1.14rc1_3177: ???)	Depositor
R, R_{free}	0.266 , 0.315 0.275 , 0.320	Depositor DCC
R_{free} test set	1306 reflections (3.14%)	wwPDB-VP
Wilson B-factor (Å ²)	118.3	Xtriage
Anisotropy	0.601	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 79.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.78	EDS
Total number of atoms	5535	wwPDB-VP
Average B, all atoms (Å ²)	126.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.38% 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	0.20	1/5645 (0.0%)	0.36	0/7681

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	623	THR	C-O	-5.35	1.19	1.24

There are no bond angle outliers.

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	5535	0	5705	103	0
All	All	5535	0	5705	103	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 9.

All (103) 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:696:SER:O	1:A:702:LYS:HE3	1.68	0.94
1:A:105:ILE:HG22	1:A:107:GLY:H	1.51	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:264:ARG:HG3	1:A:282:THR:HG22	1.75	0.69
1:A:628:MET:HG2	1:A:630:PRO:HD2	1.75	0.68
1:A:739:PRO:HD2	1:A:742:MET:HE2	1.75	0.67
1:A:62:GLY:HA3	1:A:504:ASN:HB2	1.76	0.67
1:A:746:GLN:NE2	1:A:751:LEU:O	2.27	0.67
1:A:455:GLU:OE1	1:A:523:ARG:NH1	2.29	0.66
1:A:617:SER:HA	1:A:622:TYR:CE2	2.32	0.64
1:A:281:ARG:HA	1:A:284:MET:HE2	1.81	0.62
1:A:523:ARG:NH2	1:A:553:GLU:OE1	2.33	0.61
1:A:283:VAL:HA	1:A:287:GLY:HA3	1.81	0.60
1:A:262:VAL:HG23	1:A:334:LEU:HD21	1.82	0.60
1:A:429:GLU:OE2	1:A:453:ARG:NH1	2.35	0.60
1:A:222:ILE:HD11	1:A:251:LEU:HB2	1.83	0.59
1:A:207:THR:HG21	1:A:346:ASP:HA	1.85	0.58
1:A:434:PRO:HG3	1:A:623:THR:OG1	2.04	0.58
1:A:182:ILE:HG23	1:A:244:PRO:HG3	1.86	0.58
1:A:525:ASP:HB3	1:A:529:LYS:HD3	1.86	0.57
1:A:539:PRO:HD2	1:A:542:ILE:HD11	1.88	0.55
1:A:194:ILE:HG22	1:A:195:PRO:HD3	1.88	0.55
1:A:461:MET:HB2	1:A:542:ILE:HD12	1.87	0.55
1:A:210:ALA:HB2	1:A:345:VAL:HG12	1.88	0.55
1:A:83:ASP:OD1	1:A:86:TRP:N	2.35	0.54
1:A:303:PRO:HB2	1:A:567:MET:HG3	1.90	0.54
1:A:463:ARG:HD3	1:A:469:ILE:HG12	1.88	0.54
1:A:310:GLY:HA2	1:A:313:LYS:HE3	1.91	0.53
1:A:460:VAL:HA	1:A:515:VAL:HG12	1.91	0.52
1:A:580:PHE:CZ	1:A:742:MET:HB3	2.45	0.52
1:A:297:ILE:HG21	1:A:323:VAL:HG21	1.92	0.51
1:A:60:VAL:HG21	1:A:513:VAL:HB	1.93	0.51
1:A:306:LEU:HD11	1:A:570:ILE:HD12	1.93	0.50
1:A:60:VAL:HG13	1:A:509:LYS:HA	1.94	0.50
1:A:642:LEU:HD11	1:A:686:LEU:HD21	1.93	0.50
1:A:91:THR:HG23	1:A:108:TRP:HZ2	1.77	0.49
1:A:462:LYS:HB2	1:A:513:VAL:HG22	1.94	0.49
1:A:668:ILE:O	1:A:672:THR:HG22	2.13	0.49
1:A:207:THR:HG23	1:A:349:GLY:H	1.77	0.49
1:A:591:LYS:NZ	1:A:647:GLU:OE1	2.45	0.49
1:A:304:LEU:HB2	1:A:316:THR:HG21	1.95	0.49
1:A:20:MET:HE3	1:A:332:THR:HG21	1.95	0.49
1:A:161:VAL:HG23	1:A:162:ASN:H	1.76	0.49
1:A:202:PHE:HE1	1:A:350:VAL:HG22	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:394:VAL:HG21	1:A:672:THR:HG21	1.95	0.49
1:A:655:VAL:O	1:A:659:GLU:HG2	2.13	0.48
1:A:463:ARG:HH11	1:A:469:ILE:HA	1.79	0.48
1:A:262:VAL:HA	1:A:338:LEU:HD11	1.95	0.48
1:A:472:ALA:O	1:A:476:ASP:N	2.47	0.48
1:A:390:TRP:HZ3	1:A:721:MET:HG2	1.79	0.48
1:A:394:VAL:HG12	1:A:398:MET:HE2	1.95	0.48
1:A:715:ASP:HA	1:A:719:ILE:HB	1.96	0.47
1:A:49:GLN:HB3	1:A:534:ARG:HH12	1.80	0.47
1:A:530:ILE:HD13	1:A:551:ALA:HA	1.97	0.47
1:A:91:THR:HG23	1:A:108:TRP:CZ2	2.50	0.46
1:A:182:ILE:HD12	1:A:244:PRO:HG2	1.97	0.46
1:A:107:GLY:O	1:A:138:PRO:HD2	2.15	0.46
1:A:557:ILE:HG12	1:A:629:ALA:HB2	1.97	0.46
1:A:424:LEU:HD12	1:A:557:ILE:HG23	1.97	0.46
1:A:585:SER:HA	1:A:738:ALA:HB2	1.97	0.46
1:A:110:GLY:HA2	1:A:125:MET:HE1	1.97	0.46
1:A:202:PHE:CE1	1:A:350:VAL:HG22	2.51	0.46
1:A:595:MET:HG2	1:A:719:ILE:HD12	1.99	0.45
1:A:88:LYS:O	1:A:92:GLU:HB2	2.17	0.45
1:A:478:ARG:HG3	1:A:498:TRP:HB2	2.00	0.44
1:A:394:VAL:HG21	1:A:672:THR:CG2	2.47	0.44
1:A:461:MET:HB3	1:A:544:VAL:HG22	1.99	0.44
1:A:101:HIS:NE2	1:A:157:GLU:OE1	2.41	0.44
1:A:212:ALA:O	1:A:216:ILE:HG12	2.18	0.44
1:A:98:VAL:HG11	1:A:107:GLY:HA2	2.00	0.44
1:A:696:SER:O	1:A:702:LYS:CE	2.55	0.43
1:A:39:THR:OG1	1:A:40:GLN:N	2.50	0.43
1:A:279:VAL:HG21	1:A:339:ALA:HB2	2.00	0.43
1:A:439:ARG:HH12	1:A:623:THR:HG21	1.83	0.43
1:A:463:ARG:NH1	1:A:473:GLN:OE1	2.52	0.42
1:A:473:GLN:HA	1:A:476:ASP:HB3	2.02	0.42
1:A:98:VAL:HG21	1:A:108:TRP:HD1	1.84	0.42
1:A:600:LEU:HD11	1:A:636:ILE:HG23	2.01	0.42
1:A:468:PRO:HA	1:A:511:PRO:O	2.19	0.41
1:A:427:ILE:HD12	1:A:431:TYR:CE2	2.55	0.41
1:A:595:MET:HE3	1:A:595:MET:HB2	1.97	0.41
1:A:106:VAL:CG2	1:A:138:PRO:HB2	2.50	0.41
1:A:155:GLU:N	1:A:156:PRO:HD2	2.35	0.41
1:A:710:ILE:O	1:A:714:LEU:HB2	2.20	0.41
1:A:130:LEU:O	1:A:131:ARG:HB2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:243:GLN:HB2	1:A:244:PRO:HD3	2.01	0.41
1:A:288:ARG:NH2	1:A:581:LEU:O	2.54	0.41
1:A:481:ALA:HB1	1:A:498:TRP:CE2	2.55	0.41
1:A:400:ARG:HG3	1:A:403:ALA:HB3	2.01	0.41
1:A:161:VAL:C	1:A:163:GLY:H	2.29	0.41
1:A:264:ARG:HA	1:A:264:ARG:HD3	1.96	0.41
1:A:390:TRP:CZ3	1:A:721:MET:HG2	2.55	0.41
1:A:463:ARG:CG	1:A:542:ILE:HG22	2.50	0.41
1:A:207:THR:CG2	1:A:349:GLY:H	2.34	0.41
1:A:188:ARG:HD2	1:A:692:ALA:O	2.21	0.40
1:A:16:VAL:HG13	1:A:332:THR:HG23	2.03	0.40
1:A:456:PRO:HA	1:A:519:GLY:HA2	2.03	0.40
1:A:34:LEU:HD13	1:A:230:ARG:HA	2.04	0.40
1:A:470:THR:HB	1:A:473:GLN:HG3	2.02	0.40
1:A:304:LEU:HD21	1:A:633:GLY:O	2.22	0.40
1:A:530:ILE:HG22	1:A:534:ARG:HE	1.86	0.40
1:A:591:LYS:HE3	1:A:591:LYS:HB3	1.92	0.40
1:A:398:MET:HG2	1:A:729:LYS:HB2	2.03	0.40
1:A:617:SER:HA	1:A:622:TYR:CZ	2.56	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	722/779 (93%)	684 (95%)	37 (5%)	1 (0%)	48 75

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	164	GLY

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	590/643 (92%)	590 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

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	172	ASN
1	A	243	GLN
1	A	436	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 ⓘ

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	726/779 (93%)	1.49	210 (28%) 1 1	93, 122, 160, 190	0

All (210) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	715	ASP	15.1
1	A	716	ALA	13.0
1	A	713	LEU	10.6
1	A	203	PHE	10.5
1	A	684	LEU	10.4
1	A	410	VAL	10.4
1	A	681	GLY	9.8
1	A	685	ILE	9.7
1	A	683	ALA	9.6
1	A	254	ALA	9.6
1	A	717	THR	9.2
1	A	712	LEU	9.2
1	A	18	GLY	8.8
1	A	686	LEU	8.0
1	A	682	ALA	7.6
1	A	679	ILE	7.4
1	A	643	SER	7.4
1	A	707	GLY	7.3
1	A	680	THR	7.2
1	A	257	TYR	7.2
1	A	646	TYR	6.8
1	A	216	ILE	6.6
1	A	711	ALA	6.6
1	A	351	THR	6.6
1	A	252	GLY	6.4
1	A	326	ALA	6.3
1	A	256	ASP	6.2

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Mol	Chain	Res	Type	RSRZ
1	A	255	ILE	6.0
1	A	721	MET	5.9
1	A	687	ALA	5.6
1	A	324	MET	5.5
1	A	322	SER	5.5
1	A	258	GLY	5.5
1	A	22	ALA	5.4
1	A	699	VAL	5.2
1	A	323	VAL	5.2
1	A	321	ALA	5.2
1	A	623	THR	5.2
1	A	251	LEU	5.1
1	A	212	ALA	5.0
1	A	17	ILE	5.0
1	A	211	ALA	5.0
1	A	697	ASP	4.9
1	A	432	LEU	4.9
1	A	413	VAL	4.8
1	A	202	PHE	4.8
1	A	218	GLY	4.7
1	A	635	ILE	4.7
1	A	642	LEU	4.7
1	A	637	ALA	4.6
1	A	429	GLU	4.6
1	A	219	GLY	4.6
1	A	688	VAL	4.6
1	A	457	LEU	4.5
1	A	612	VAL	4.5
1	A	406	ALA	4.4
1	A	594	LEU	4.4
1	A	430	LYS	4.4
1	A	567	MET	4.3
1	A	649	PHE	4.3
1	A	245	VAL	4.3
1	A	199	VAL	4.2
1	A	601	GLY	4.2
1	A	640	TRP	4.1
1	A	304	LEU	4.1
1	A	749	LEU	4.1
1	A	215	ALA	4.1
1	A	320	ILE	4.1
1	A	714	LEU	4.1

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Mol	Chain	Res	Type	RSRZ
1	A	584	GLY	4.1
1	A	217	ILE	4.0
1	A	599	THR	4.0
1	A	307	PHE	4.0
1	A	750	GLY	3.9
1	A	423	SER	3.9
1	A	200	VAL	3.9
1	A	407	PRO	3.9
1	A	641	GLY	3.8
1	A	710	ILE	3.8
1	A	241	PHE	3.8
1	A	294	ALA	3.7
1	A	405	ALA	3.7
1	A	636	ILE	3.7
1	A	624	PRO	3.7
1	A	311	PHE	3.7
1	A	639	ILE	3.6
1	A	722	PHE	3.6
1	A	752	GLY	3.6
1	A	325	LEU	3.6
1	A	603	THR	3.6
1	A	16	VAL	3.6
1	A	60	VAL	3.6
1	A	208	VAL	3.6
1	A	327	ALA	3.6
1	A	164	GLY	3.5
1	A	459	LEU	3.5
1	A	622	TYR	3.5
1	A	424	LEU	3.5
1	A	690	ALA	3.4
1	A	708	LEU	3.4
1	A	709	LEU	3.4
1	A	247	THR	3.4
1	A	600	LEU	3.4
1	A	275	THR	3.4
1	A	433	PRO	3.3
1	A	720	ARG	3.3
1	A	409	LEU	3.3
1	A	698	LEU	3.3
1	A	19	VAL	3.2
1	A	15	ILE	3.2
1	A	633	GLY	3.2

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Mol	Chain	Res	Type	RSRZ
1	A	634	LEU	3.2
1	A	655	VAL	3.2
1	A	443	GLU	3.2
1	A	689	VAL	3.1
1	A	319	ILE	3.1
1	A	696	SER	3.1
1	A	34	LEU	3.0
1	A	67	SER	3.0
1	A	136	SER	3.0
1	A	1	MET	3.0
1	A	678	LEU	3.0
1	A	416	ILE	3.0
1	A	702	LYS	3.0
1	A	561	PHE	3.0
1	A	14	TYR	3.0
1	A	315	ILE	2.9
1	A	718	ILE	2.9
1	A	214	PRO	2.9
1	A	705	ALA	2.9
1	A	665	ALA	2.9
1	A	303	PRO	2.8
1	A	300	SER	2.8
1	A	21	VAL	2.8
1	A	317	TYR	2.8
1	A	613	ASP	2.8
1	A	719	ILE	2.8
1	A	588	LEU	2.7
1	A	414	LEU	2.7
1	A	652	SER	2.7
1	A	238	VAL	2.7
1	A	350	VAL	2.7
1	A	694	VAL	2.7
1	A	439	ARG	2.7
1	A	172	ASN	2.7
1	A	147	ILE	2.6
1	A	516	ILE	2.6
1	A	250	GLY	2.6
1	A	736	TRP	2.6
1	A	25	LEU	2.6
1	A	651	VAL	2.6
1	A	318	ALA	2.6
1	A	76	PRO	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	44	TYR	2.6
1	A	404	PHE	2.6
1	A	411	VAL	2.6
1	A	583	PHE	2.5
1	A	611	PHE	2.5
1	A	434	PRO	2.5
1	A	550	PRO	2.5
1	A	270	ALA	2.5
1	A	590	ILE	2.5
1	A	422	LEU	2.5
1	A	339	ALA	2.5
1	A	260	PHE	2.5
1	A	237	PRO	2.5
1	A	677	ARG	2.5
1	A	626	PRO	2.5
1	A	604	MET	2.4
1	A	66	THR	2.4
1	A	645	ASP	2.4
1	A	343	PRO	2.4
1	A	290	VAL	2.4
1	A	329	LEU	2.4
1	A	451	GLY	2.4
1	A	178	LEU	2.4
1	A	627	LEU	2.4
1	A	316	THR	2.3
1	A	226	LEU	2.3
1	A	598	LEU	2.3
1	A	513	VAL	2.3
1	A	380	LYS	2.3
1	A	297	ILE	2.3
1	A	198	ALA	2.3
1	A	412	MET	2.3
1	A	301	SER	2.3
1	A	74	THR	2.3
1	A	24	CYS	2.3
1	A	533	LEU	2.2
1	A	706	PHE	2.2
1	A	394	VAL	2.2
1	A	436	ASN	2.2
1	A	621	ASN	2.2
1	A	625	GLN	2.2
1	A	253	ILE	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	62	GLY	2.2
1	A	620	MET	2.2
1	A	458	THR	2.2
1	A	695	PHE	2.1
1	A	201	LEU	2.1
1	A	171	LEU	2.1
1	A	663	SER	2.0
1	A	340	ILE	2.0
1	A	4	TRP	2.0
1	A	242	ALA	2.0
1	A	299	ALA	2.0
1	A	504	ASN	2.0
1	A	191	VAL	2.0
1	A	197	VAL	2.0
1	A	564	LEU	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.