



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 08:08 AM UTC

PDB ID : 8A9X / pdb_00008a9x
Title : Crystal structure of PulM C-ter domain
Authors : Dazzoni, R.; Li, Y.; Lopez-Castilla, A.; Brier, S.; Mechaly, A.; Cordier, F.;
Haouz, A.; Nilges, M.; Francetic, O.; Bardiaux, B.; Izadi-Pruneyre, N.
Deposited on : 2022-06-29
Resolution : 1.52 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

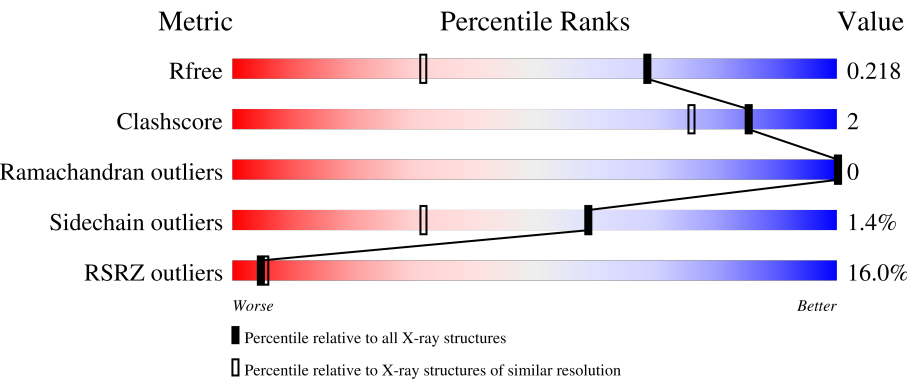
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.52 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	5890 (1.54-1.50)
Clashscore	190562	6116 (1.54-1.50)
Ramachandran outliers	187476	6002 (1.54-1.50)
Sidechain outliers	187428	5999 (1.54-1.50)
RSRZ outliers	180081	5891 (1.54-1.50)

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	80	6% 91% 9%
1	B	80	11% 82% 14% .
1	C	80	12% 89% 9% .
1	D	80	15% 94% 5% .
1	E	80	6% 91% 8% .

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Mol	Chain	Length	Quality of chain
1	F	80	12% 92% • • •
1	G	80	46% 92% 5% •

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 4680 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 Type II secretion system protein M.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	80	Total	C	N	O	S	0	0	0
			600	375	107	115	3			
1	B	77	Total	C	N	O	S	0	0	0
			578	364	104	107	3			
1	C	78	Total	C	N	O	S	0	0	0
			587	369	105	110	3			
1	D	79	Total	C	N	O	S	0	0	0
			593	372	106	112	3			
1	E	79	Total	C	N	O	S	0	0	0
			594	372	106	113	3			
1	F	78	Total	C	N	O	S	0	0	0
			587	369	105	110	3			
1	G	78	Total	C	N	O	S	0	0	0
			585	367	105	110	3			

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	79	SER	-	expression tag	UNP A0A8B2TA77
B	79	SER	-	expression tag	UNP A0A8B2TA77
C	79	SER	-	expression tag	UNP A0A8B2TA77
D	79	SER	-	expression tag	UNP A0A8B2TA77
E	79	SER	-	expression tag	UNP A0A8B2TA77
F	79	SER	-	expression tag	UNP A0A8B2TA77
G	79	SER	-	expression tag	UNP A0A8B2TA77

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	115	Total	O	0	0
			115	115		
2	B	76	Total	O	0	0
			76	76		

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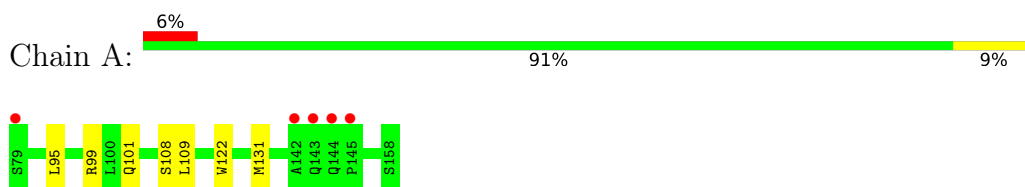
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	C	67	Total 67	O 67	0	0
2	D	79	Total 79	O 79	0	0
2	E	99	Total 99	O 99	0	0
2	F	73	Total 73	O 73	0	0
2	G	47	Total 47	O 47	0	0

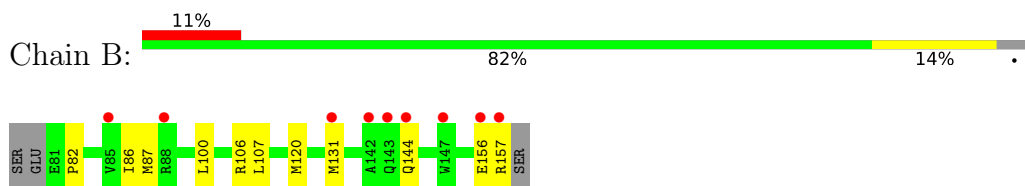
3 Residue-property plots [i](#)

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.

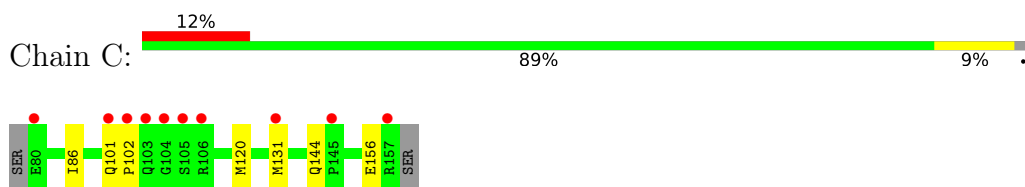
- Molecule 1: Type II secretion system protein M



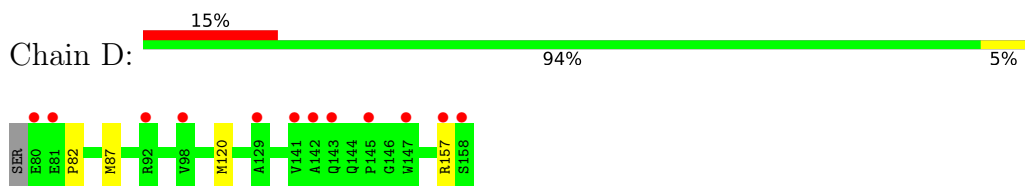
- Molecule 1: Type II secretion system protein M



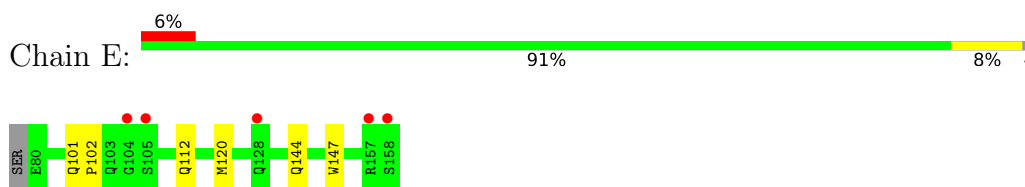
- Molecule 1: Type II secretion system protein M



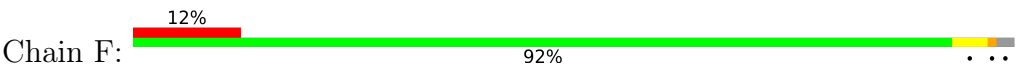
- Molecule 1: Type II secretion system protein M



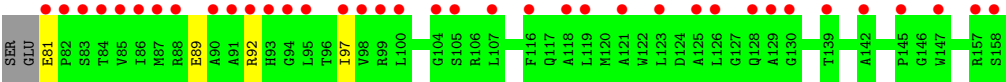
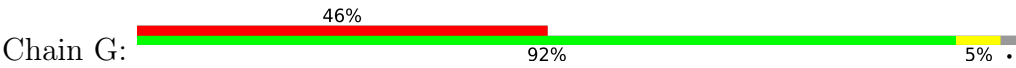
- Molecule 1: Type II secretion system protein M



- Molecule 1: Type II secretion system protein M



● Molecule 1: Type II secretion system protein M



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	80.85Å 135.53Å 109.41Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	67.76 – 1.52 67.76 – 1.52	Depositor EDS
% Data completeness (in resolution range)	100.0 (67.76-1.52) 100.0 (67.76-1.52)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.34 (at 1.52Å)	Xtriage
Refinement program	BUSTER 2.10.4 (8-JUN-2022)	Depositor
R, R_{free}	0.217 , 0.231 0.206 , 0.218	Depositor DCC
R_{free} test set	4685 reflections (5.11%)	wwPDB-VP
Wilson B-factor (Å ²)	25.0	Xtriage
Anisotropy	0.355	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 39.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.008 for 1/2*h-1/2*k,-3/2*h-1/2*k,-l 0.015 for 1/2*h+1/2*k,3/2*h-1/2*k,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	4680	wwPDB-VP
Average B, all atoms (Å ²)	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.72% 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	0.93	1/609 (0.2%)	0.88	0/831
1	B	0.80	1/587 (0.2%)	0.88	0/803
1	C	0.85	1/596 (0.2%)	0.84	0/815
1	D	0.88	2/602 (0.3%)	0.85	0/823
1	E	1.00	1/603 (0.2%)	0.91	0/823
1	F	0.71	1/596 (0.2%)	0.85	0/815
1	G	0.71	0/594	0.92	0/811
All	All	0.85	7/4187 (0.2%)	0.88	0/5721

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	120	MET	SD-CE	-13.12	1.46	1.79
1	D	120	MET	SD-CE	-11.25	1.51	1.79
1	C	120	MET	SD-CE	-9.95	1.54	1.79
1	A	131	MET	SD-CE	-9.73	1.55	1.79
1	F	120	MET	SD-CE	-7.13	1.61	1.79
1	B	120	MET	SD-CE	-5.46	1.65	1.79
1	D	87	MET	SD-CE	-5.24	1.66	1.79

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	600	0	611	5	0
1	B	578	0	595	6	0
1	C	587	0	601	2	0
1	D	593	0	606	1	0
1	E	594	0	606	2	0
1	F	587	0	601	1	0
1	G	585	0	600	2	0
2	A	115	0	0	0	0
2	B	76	0	0	1	0
2	C	67	0	0	0	0
2	D	79	0	0	0	0
2	E	99	0	0	0	0
2	F	73	0	0	0	0
2	G	47	0	0	0	0
All	All	4680	0	4220	18	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 2.

All (18) 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:B:86:ILE:HD11	1:B:131:MET:HE1	1.72	0.69
1:A:99:ARG:HD3	1:A:101:GLN:OE1	1.94	0.67
1:C:86:ILE:HD11	1:C:131:MET:HE1	1.81	0.62
1:B:82:PRO:HG2	1:B:157:ARG:HE	1.66	0.60
1:A:95:LEU:HD12	1:A:122:TRP:CD2	2.40	0.56
1:A:95:LEU:CD1	1:A:122:TRP:CE3	2.91	0.54
1:B:100:LEU:HD21	1:B:107:LEU:HD22	1.90	0.53
1:F:105:SER:O	1:F:157:ARG:HD2	2.11	0.51
1:B:144:GLN:HG3	2:B:268:HOH:O	2.10	0.50
1:G:89:GLU:CD	1:G:92:ARG:HH21	2.22	0.47
1:B:106:ARG:HG2	1:B:156:GLU:HG2	1.96	0.47
1:A:95:LEU:CD1	1:A:122:TRP:CD2	2.98	0.46
1:E:101:GLN:HA	1:E:102:PRO:HD3	1.93	0.42
1:C:101:GLN:HA	1:C:102:PRO:HD3	1.85	0.41
1:A:108:SER:C	1:A:109:LEU:HD12	2.46	0.41
1:B:87:MET:SD	1:G:97:ILE:O	2.79	0.41
1:D:82:PRO:HG2	1:D:157:ARG:HD2	2.03	0.40
1:E:144:GLN:HE21	1:E:147:TRP:CG	2.40	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	78/80 (98%)	78 (100%)	0	0	100	100
1	B	75/80 (94%)	74 (99%)	1 (1%)	0	100	100
1	C	76/80 (95%)	75 (99%)	1 (1%)	0	100	100
1	D	77/80 (96%)	76 (99%)	1 (1%)	0	100	100
1	E	77/80 (96%)	76 (99%)	1 (1%)	0	100	100
1	F	76/80 (95%)	75 (99%)	1 (1%)	0	100	100
1	G	76/80 (95%)	75 (99%)	1 (1%)	0	100	100
All	All	535/560 (96%)	529 (99%)	6 (1%)	0	100	100

There are no Ramachandran outliers to report.

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	64/64 (100%)	64 (100%)	0	100	100
1	B	61/64 (95%)	61 (100%)	0	100	100
1	C	62/64 (97%)	60 (97%)	2 (3%)	34	8
1	D	63/64 (98%)	63 (100%)	0	100	100
1	E	63/64 (98%)	62 (98%)	1 (2%)	55	27
1	F	62/64 (97%)	60 (97%)	2 (3%)	34	8
1	G	62/64 (97%)	61 (98%)	1 (2%)	55	27

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	437/448 (98%)	431 (99%)	6 (1%)	59 31

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	144	GLN
1	C	156	GLU
1	E	112	GLN
1	F	106	ARG
1	F	157	ARG
1	G	81	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	112	GLN
1	C	93	HIS
1	C	144	GLN
1	D	93	HIS
1	D	103	GLN
1	E	93	HIS
1	E	101	GLN
1	E	112	GLN
1	F	93	HIS
1	F	128	GLN
1	F	144	GLN
1	G	143	GLN
1	G	151	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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	80/80 (100%)	0.51	5 (6%) 26 31	21, 24, 37, 46	0
1	B	77/80 (96%)	0.86	9 (11%) 9 11	21, 27, 45, 54	0
1	C	78/80 (97%)	0.92	10 (12%) 7 9	20, 26, 52, 63	0
1	D	79/80 (98%)	1.09	12 (15%) 5 6	22, 28, 47, 62	0
1	E	79/80 (98%)	0.54	5 (6%) 26 31	20, 24, 38, 54	0
1	F	78/80 (97%)	1.13	10 (12%) 7 9	21, 33, 48, 67	0
1	G	78/80 (97%)	2.20	37 (47%) 0 0	31, 43, 64, 81	0
All	All	549/560 (98%)	1.03	88 (16%) 5 5	20, 28, 53, 81	0

All (88) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	102	PRO	5.8
1	G	86	ILE	4.9
1	G	84	THR	4.8
1	G	81	GLU	4.6
1	C	103	GLN	4.6
1	B	147	TRP	4.5
1	E	158	SER	4.4
1	G	85	VAL	4.4
1	G	82	PRO	4.2
1	G	91	ALA	4.2
1	G	98	VAL	4.0
1	G	100	LEU	4.0
1	D	158	SER	4.0
1	G	83	SER	3.9
1	G	158	SER	3.9
1	G	107	LEU	3.8
1	G	87	MET	3.8

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Mol	Chain	Res	Type	RSRZ
1	F	157	ARG	3.7
1	G	97	ILE	3.7
1	F	143	GLN	3.7
1	G	142	ALA	3.6
1	C	104	GLY	3.5
1	B	142	ALA	3.5
1	G	145	PRO	3.5
1	B	157	ARG	3.4
1	A	145	PRO	3.4
1	C	145	PRO	3.4
1	A	79	SER	3.4
1	D	80	GLU	3.3
1	G	129	ALA	3.2
1	G	95	LEU	3.2
1	B	88	ARG	3.1
1	G	139	THR	3.1
1	A	143	GLN	3.1
1	A	144	GLN	3.1
1	C	101	GLN	3.0
1	B	143	GLN	3.0
1	B	131	MET	2.9
1	E	104	GLY	2.9
1	D	142	ALA	2.8
1	D	92	ARG	2.8
1	G	119	LEU	2.8
1	D	147	TRP	2.7
1	B	144	GLN	2.7
1	G	147	TRP	2.6
1	F	82	PRO	2.6
1	G	157	ARG	2.6
1	G	94	GLY	2.6
1	G	90	ALA	2.5
1	F	81	GLU	2.5
1	G	126	LEU	2.5
1	G	88	ARG	2.5
1	G	104	GLY	2.5
1	G	130	GLY	2.5
1	F	105	SER	2.5
1	G	125	ALA	2.5
1	G	105	SER	2.5
1	C	131	MET	2.5
1	B	156	GLU	2.5

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Mol	Chain	Res	Type	RSRZ
1	D	129	ALA	2.4
1	G	121	ALA	2.4
1	G	92	ARG	2.4
1	D	141	VAL	2.4
1	C	80	GLU	2.4
1	G	128	GLN	2.4
1	G	93	HIS	2.3
1	B	85	VAL	2.3
1	C	105	SER	2.2
1	E	105	SER	2.2
1	E	157	ARG	2.2
1	D	81	GLU	2.2
1	A	142	ALA	2.2
1	F	142	ALA	2.2
1	F	102	PRO	2.2
1	G	118	ALA	2.1
1	D	143	GLN	2.1
1	G	116	PHE	2.1
1	F	104	GLY	2.1
1	C	157	ARG	2.1
1	G	123	LEU	2.1
1	E	128	GLN	2.1
1	D	145	PRO	2.1
1	F	98	VAL	2.0
1	C	106	ARG	2.0
1	F	92	ARG	2.0
1	D	157	ARG	2.0
1	G	99	ARG	2.0
1	D	98	VAL	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.