



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 07:41 AM UTC

PDB ID : 5VAW / pdb_00005vaw
Title : Fusion of Maltose-binding Protein and PilA from *Acinetobacter baumannii* AB5075
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Deposited on : 2017-03-28
Resolution : 1.69 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

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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
Mogul	:	2022.3.0, CSD as543be (2022)
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

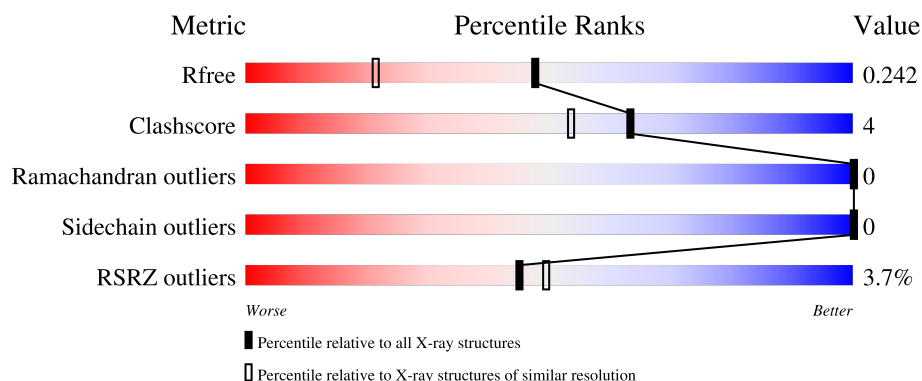
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.69 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	5551 (1.70-1.70)
Clashscore	190562	5924 (1.70-1.70)
Ramachandran outliers	187476	5846 (1.70-1.70)
Sidechain outliers	187428	5846 (1.70-1.70)
RSRZ outliers	180081	5554 (1.70-1.70)

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	508	

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 3966 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.

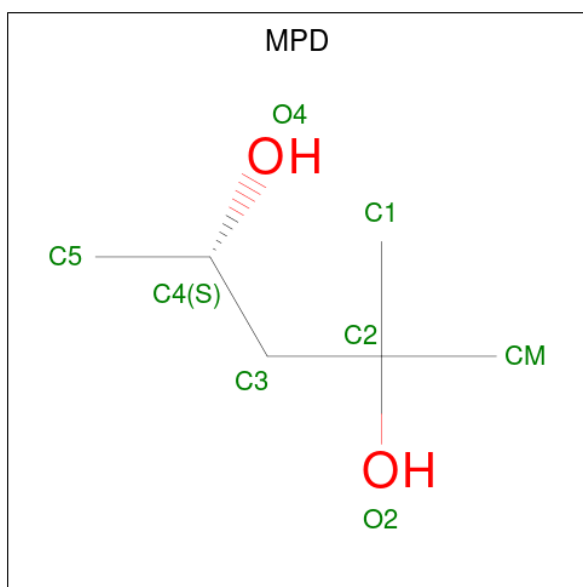
- Molecule 1 is a protein called Maltose-binding periplasmic protein, Type IV pilin PilA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	484	3633	2310	590	723	10	0	11	0

There are 21 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	MET	-	initiating methionine	UNP D8A942
A	82	ALA	ASP	engineered mutation	UNP D8A942
A	83	ALA	LYS	engineered mutation	UNP D8A942
A	87	ALA	ASP	engineered mutation	UNP D8A942
A	88	ALA	LYS	engineered mutation	UNP D8A942
A	172	ALA	GLU	engineered mutation	UNP D8A942
A	173	ALA	ASN	engineered mutation	UNP D8A942
A	239	ALA	LYS	engineered mutation	UNP D8A942
A	362	ALA	LYS	engineered mutation	UNP D8A942
A	363	ALA	ASP	engineered mutation	UNP D8A942
A	367	ASN	-	linker	UNP D8A942
A	369	ALA	ILE	engineered mutation	UNP A0A0D5YCX7
A	370	ALA	PRO	engineered mutation	UNP A0A0D5YCX7
A	1152	LEU	-	expression tag	UNP A0A0D5YCX7
A	1153	GLU	-	expression tag	UNP A0A0D5YCX7
A	1154	HIS	-	expression tag	UNP A0A0D5YCX7
A	1155	HIS	-	expression tag	UNP A0A0D5YCX7
A	1156	HIS	-	expression tag	UNP A0A0D5YCX7
A	1157	HIS	-	expression tag	UNP A0A0D5YCX7
A	1158	HIS	-	expression tag	UNP A0A0D5YCX7
A	1159	HIS	-	expression tag	UNP A0A0D5YCX7

- Molecule 2 is (4S)-2-METHYL-2,4-PENTANEDIOL (CCD ID: MPD) (formula: C₆H₁₄O₂).

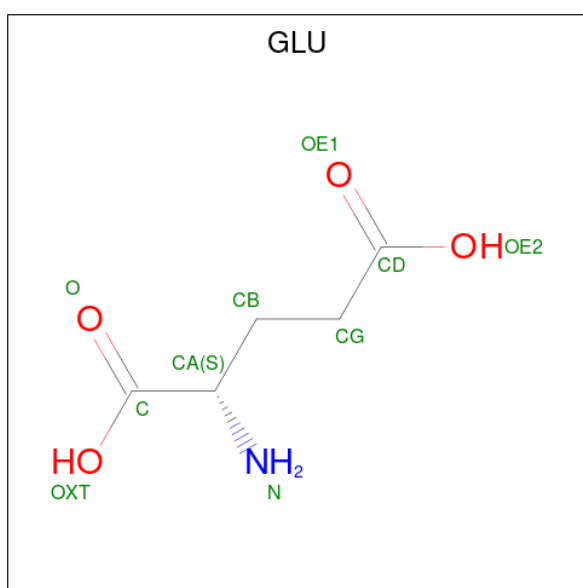


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			8	6	2		

- Molecule 3 is SODIUM ION (CCD ID: NA) (formula: Na).

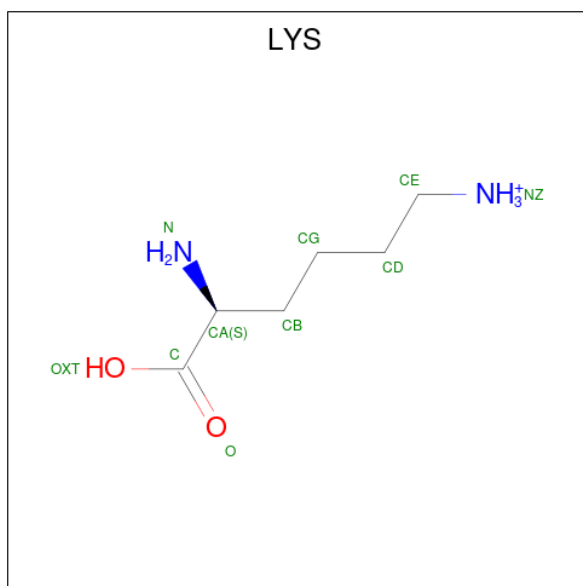
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Na	0	0
			1	1		

- Molecule 4 is GLUTAMIC ACID (CCD ID: GLU) (formula: C₅H₉NO₄).



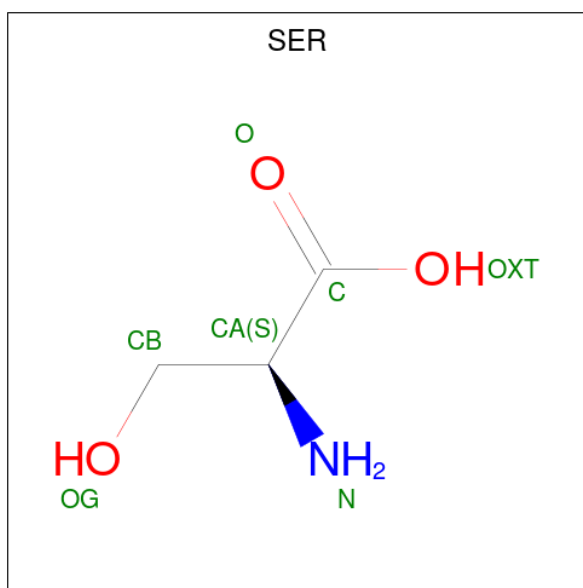
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			10	5	1	4		

- Molecule 5 is LYSINE (CCD ID: LYS) (formula: $C_6H_{15}N_2O_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	N	O	0	0
			10	6	2	2		

- Molecule 6 is SERINE (CCD ID: SER) (formula: $C_3H_7NO_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	A	1	Total	C	N	O	0	0
			7	3	1	3		

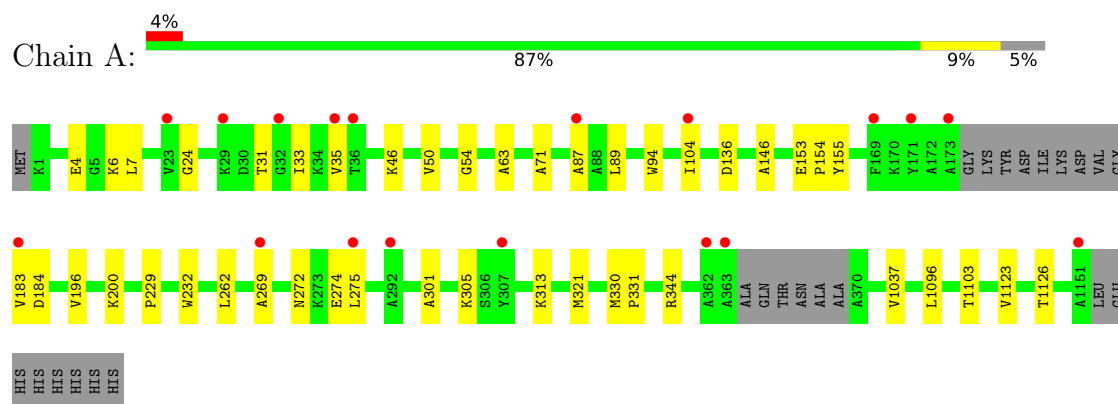
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	297	Total	O	0	0
			297	297		

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: Maltose-binding periplasmic protein, Type IV pilin PilA



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	39.56Å 103.04Å 56.20Å 90.00° 98.95° 90.00°	Depositor
Resolution (Å)	29.21 – 1.69 29.21 – 1.69	Depositor EDS
% Data completeness (in resolution range)	91.5 (29.21-1.69) 79.4 (29.21-1.69)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.16 (at 1.69Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.209 , 0.242 0.209 , 0.242	Depositor DCC
R_{free} test set	2000 reflections (4.03%)	wwPDB-VP
Wilson B-factor (Å ²)	21.7	Xtriage
Anisotropy	0.488	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 43.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	3966	wwPDB-VP
Average B, all atoms (Å ²)	42.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.48% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MPD, NA

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	0.16	0/3743	0.34	0/5108

There are no bond length outliers.

There are no bond angle outliers.

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	3633	0	3537	29	0
2	A	8	0	14	0	0
3	A	1	0	0	0	0
4	A	10	0	5	0	0
5	A	10	0	12	1	0
6	A	7	0	4	3	0
7	A	297	0	0	1	0
All	All	3966	0	3572	29	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 4.

All (29) 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:1096:LEU:H	5:A:1204:LYS:N	1.76	0.83
1:A:196:VAL:HG12	1:A:200:LYS:HD2	1.73	0.71
1:A:24:GLY:HA3	1:A:35:VAL:HG21	1.76	0.67
1:A:63:ALA:H	6:A:1205:SER:N	2.04	0.55
1:A:31:THR:HB	1:A:33:ILE:HG12	1.89	0.54
1:A:262:LEU:HD13	6:A:1205:SER:HB2	1.90	0.53
1:A:274[B]:GLU:HG2	1:A:275:LEU:HD22	1.91	0.53
1:A:4:GLU:HA	1:A:272:ASN:HD21	1.73	0.53
1:A:71:ALA:HB2	1:A:104:ILE:HG12	1.91	0.51
1:A:154:PRO:HG2	1:A:344:ARG:HG3	1.93	0.51
1:A:153[A]:GLU:HG3	1:A:155:TYR:HB3	1.93	0.50
1:A:87:ALA:O	1:A:305:LYS:NZ	2.28	0.49
1:A:46:LYS:O	1:A:50:VAL:HG22	2.14	0.48
1:A:183:VAL:N	7:A:1313:HOH:O	2.47	0.48
1:A:1103:THR:HG22	1:A:1126[A]:THR:HG22	1.95	0.48
1:A:136:ASP:HA	1:A:146:ALA:HB2	1.97	0.47
1:A:54:GLY:HA2	1:A:269:ALA:HB1	1.98	0.46
1:A:24:GLY:CA	1:A:35:VAL:HG21	2.46	0.45
1:A:330:MET:HG3	1:A:331:PRO:HD2	1.98	0.44
1:A:301:ALA:HB1	1:A:321:MET:HE2	1.99	0.44
1:A:6:LYS:HG2	1:A:7:LEU:N	2.33	0.43
1:A:229:PRO:HA	1:A:232:TRP:CE2	2.55	0.41
1:A:89:LEU:HD22	1:A:94:TRP:CZ2	2.55	0.41
1:A:184:ASP:OD1	1:A:184:ASP:N	2.48	0.40
1:A:272:ASN:HB3	1:A:275:LEU:HB2	2.02	0.40
1:A:1037:VAL:HG22	1:A:1123:VAL:HG11	2.04	0.40
1:A:63:ALA:N	6:A:1205:SER:N	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	489/508 (96%)	481 (98%)	8 (2%)	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	369/388 (95%)	369 (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 (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	282	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](#)

Of 5 ligands modelled in this entry, 1 is monoatomic - leaving 4 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
2	MPD	A	1201	-	7,7,7	0.29	0	9,10,10	0.55	0
5	LYS	A	1204	-	8,9,9	0.85	1 (12%)	7,10,10	0.90	1 (14%)
4	GLU	A	1203	-	8,9,9	1.10	1 (12%)	8,11,11	1.15	1 (12%)
6	SER	A	1205	-	4,6,6	1.16	1 (25%)	2,7,7	1.43	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	MPD	A	1201	-	-	5/5/5/5	-
5	LYS	A	1204	-	-	2/9/9/9	-
4	GLU	A	1203	-	-	6/9/9/9	-
6	SER	A	1205	-	-	1/6/6/6	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1203	GLU	OXT-C	-2.17	1.23	1.30
6	A	1205	SER	OXT-C	-2.16	1.23	1.30
5	A	1204	LYS	OXT-C	-2.12	1.23	1.30

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1203	GLU	OXT-C-O	-2.53	118.34	124.08
5	A	1204	LYS	OXT-C-O	-2.21	119.06	124.08

There are no chirality outliers.

All (14) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1201	MPD	C1-C2-C3-C4
2	A	1201	MPD	C2-C3-C4-O4
2	A	1201	MPD	C2-C3-C4-C5
4	A	1203	GLU	OXT-C-CA-N
5	A	1204	LYS	CE-CD-CG-CB
4	A	1203	GLU	O-C-CA-N
4	A	1203	GLU	O-C-CA-CB
4	A	1203	GLU	OXT-C-CA-CB
2	A	1201	MPD	O2-C2-C3-C4
2	A	1201	MPD	CM-C2-C3-C4
4	A	1203	GLU	OE1-CD-CG-CB
4	A	1203	GLU	OE2-CD-CG-CB
5	A	1204	LYS	OXT-C-CA-N
6	A	1205	SER	OXT-C-CA-N

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	1204	LYS	1	0
6	A	1205	SER	3	0

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	484/508 (95%)	0.36	18 (3%) 45 49	17, 38, 68, 101	11 (2%)

All (18) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	183	VAL	3.9
1	A	169	PHE	3.8
1	A	363	ALA	3.7
1	A	87	ALA	2.8
1	A	362	ALA	2.7
1	A	173	ALA	2.6
1	A	171	TYR	2.3
1	A	292	ALA	2.3
1	A	275	LEU	2.3
1	A	29	LYS	2.3
1	A	307	TYR	2.2
1	A	23	VAL	2.1
1	A	36	THR	2.1
1	A	104	ILE	2.1
1	A	269	ALA	2.1
1	A	1151	ALA	2.1
1	A	32	GLY	2.0
1	A	35	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](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	MPD	A	1201	8/8	0.73	0.20	53,53,54,55	0
5	LYS	A	1204	10/10	0.76	0.17	55,57,59,62	0
4	GLU	A	1203	10/10	0.81	0.14	96,98,100,100	0
6	SER	A	1205	7/7	0.90	0.17	58,88,109,119	0
3	NA	A	1202	1/1	0.95	0.07	45,45,45,45	0

6.5 Other polymers [i](#)

There are no such residues in this entry.