



Full wwPDB X-ray Structure Validation Report ⓘ

May 13, 2020 – 02:32 am BST

PDB ID : 3RZA
Title : Crystal structure of a tripeptidase (SAV1512) from staphylococcus aureus subsp. aureus mu50 at 2.10 Å resolution
Authors : Joint Center for Structural Genomics (JCSG)
Deposited on : 2011-05-11
Resolution : 2.10 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.11
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) : 2.11

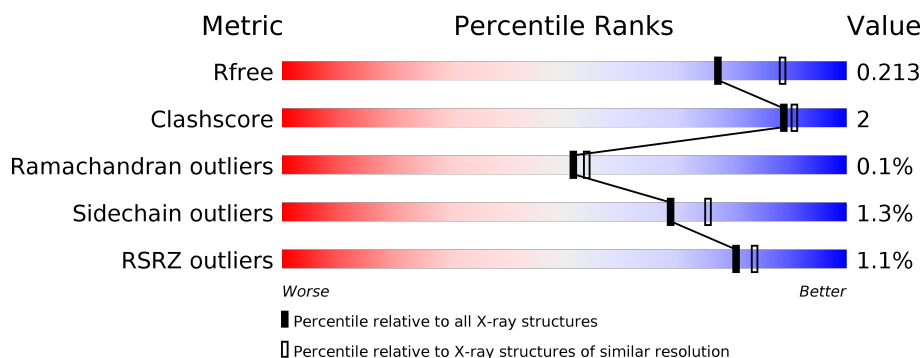
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION



The reported resolution of this entry is 2.10 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	5197 (2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)
RSRZ outliers	127900	5083 (2.10-2.10)

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 on 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	396	
1	B	396	

2 Entry composition [i](#)

There are 9 unique types of molecules in this entry. The entry contains 6117 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 tripeptidase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	373	Total	C	N	O	S	Se	0	11	0
			2821	1783	468	561	1	8			
1	B	373	Total	C	N	O	S	Se	0	4	0
			2788	1759	466	554	1	8			

There are 38 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-18	MSE	-	leader sequence	UNP Q99TY1
A	-17	GLY	-	leader sequence	UNP Q99TY1
A	-16	SER	-	leader sequence	UNP Q99TY1
A	-15	ASP	-	leader sequence	UNP Q99TY1
A	-14	LYS	-	leader sequence	UNP Q99TY1
A	-13	ILE	-	leader sequence	UNP Q99TY1
A	-12	HIS	-	leader sequence	UNP Q99TY1
A	-11	HIS	-	leader sequence	UNP Q99TY1
A	-10	HIS	-	leader sequence	UNP Q99TY1
A	-9	HIS	-	leader sequence	UNP Q99TY1
A	-8	HIS	-	leader sequence	UNP Q99TY1
A	-7	HIS	-	leader sequence	UNP Q99TY1
A	-6	GLU	-	leader sequence	UNP Q99TY1
A	-5	ASN	-	leader sequence	UNP Q99TY1
A	-4	LEU	-	leader sequence	UNP Q99TY1
A	-3	TYR	-	leader sequence	UNP Q99TY1
A	-2	PHE	-	leader sequence	UNP Q99TY1
A	-1	GLN	-	leader sequence	UNP Q99TY1
A	0	GLY	-	leader sequence	UNP Q99TY1
B	-18	MSE	-	leader sequence	UNP Q99TY1
B	-17	GLY	-	leader sequence	UNP Q99TY1
B	-16	SER	-	leader sequence	UNP Q99TY1
B	-15	ASP	-	leader sequence	UNP Q99TY1
B	-14	LYS	-	leader sequence	UNP Q99TY1
B	-13	ILE	-	leader sequence	UNP Q99TY1

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-12	HIS	-	leader sequence	UNP Q99TY1
B	-11	HIS	-	leader sequence	UNP Q99TY1
B	-10	HIS	-	leader sequence	UNP Q99TY1
B	-9	HIS	-	leader sequence	UNP Q99TY1
B	-8	HIS	-	leader sequence	UNP Q99TY1
B	-7	HIS	-	leader sequence	UNP Q99TY1
B	-6	GLU	-	leader sequence	UNP Q99TY1
B	-5	ASN	-	leader sequence	UNP Q99TY1
B	-4	LEU	-	leader sequence	UNP Q99TY1
B	-3	TYR	-	leader sequence	UNP Q99TY1
B	-2	PHE	-	leader sequence	UNP Q99TY1
B	-1	GLN	-	leader sequence	UNP Q99TY1
B	0	GLY	-	leader sequence	UNP Q99TY1

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total	Zn	0	0
			1	1		
2	A	1	Total	Zn	0	0
			1	1		

- Molecule 3 is CALCIUM ION (three-letter code: CA) (formula: Ca).

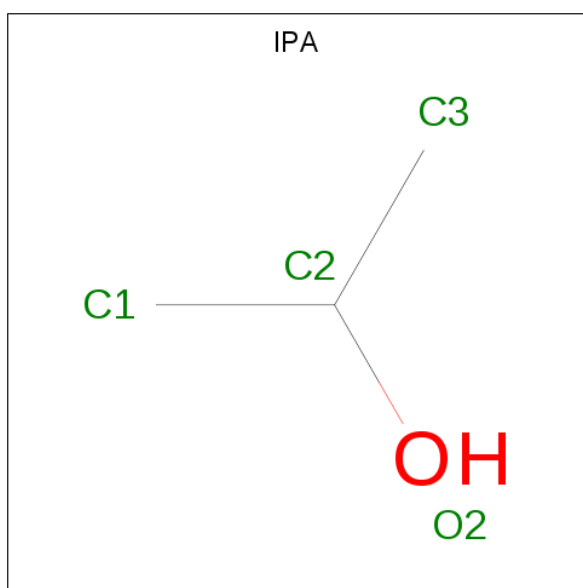
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	3	Total	Ca	0	0
			3	3		
3	A	2	Total	Ca	0	0
			2	2		

- Molecule 4 is CITRIC ACID (three-letter code: CIT) (formula: C₆H₈O₇).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			13	6	7		
4	A	1	Total	C	O	0	0
			13	6	7		

- Molecule 5 is ISOPROPYL ALCOHOL (three-letter code: IPA) (formula: C_3H_8O).



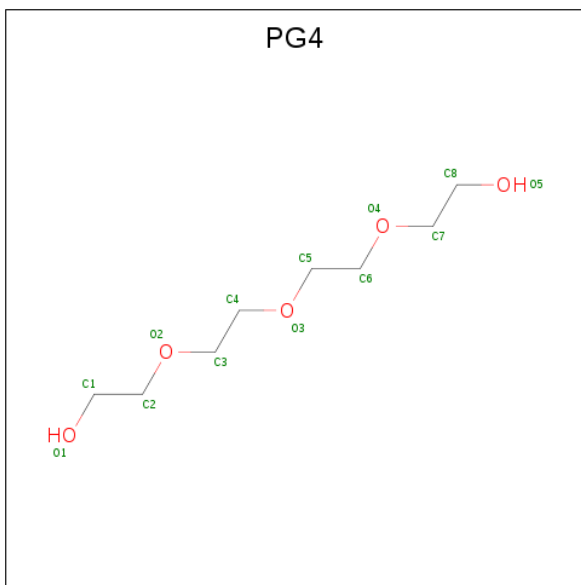
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			4	3	1		

- Molecule 6 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: $C_4H_{10}O_3$).



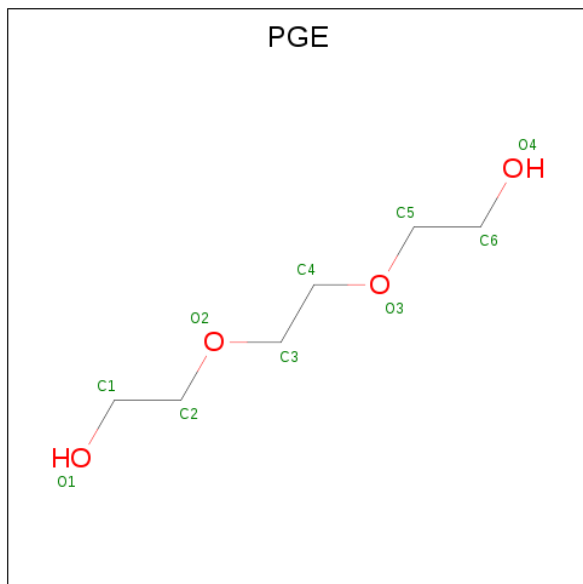
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			7	4	3		
6	A	1	Total	C	O	0	0
			5	3	2		
6	A	1	Total	C	O	0	0
			7	4	3		
6	B	1	Total	C	O	0	0
			7	4	3		

- Molecule 7 is TETRAETHYLENE GLYCOL (three-letter code: PG4) (formula: $C_8H_{18}O_5$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	C	O	0	0
			13	8	5		
7	B	1	Total	C	O	0	0
			13	8	5		
7	B	1	Total	C	O	0	0
			12	8	4		

- Molecule 8 is TRIETHYLENE GLYCOL (three-letter code: PGE) (formula: C₆H₁₄O₄).

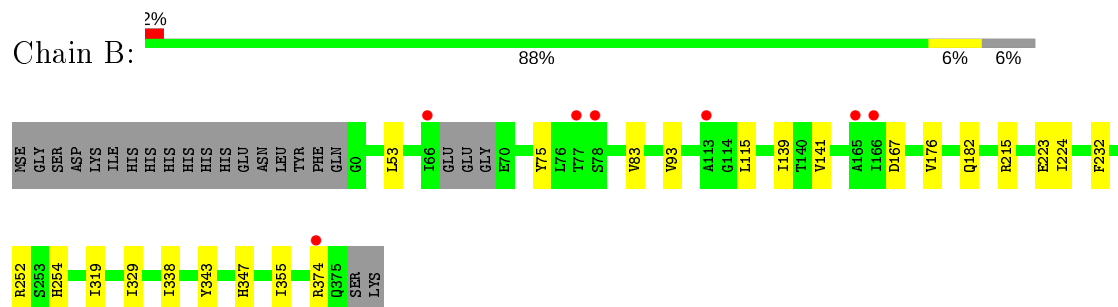
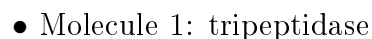


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	B	1	Total	C	O	0	0
			10	6	4		

- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	216	Total	O	0	2
			216	216		
9	B	181	Total	O	0	0
			181	181		

- Molecule 1: tripeptidase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	47.00 Å 57.80 Å 79.86 Å 89.67° 73.38° 72.36°	Depositor
Resolution (Å)	29.52 – 2.10 29.52 – 2.10	Depositor EDS
% Data completeness (in resolution range)	96.4 (29.52-2.10) 96.4 (29.52-2.10)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.86 (at 2.10 Å)	Xtriage
Refinement program	REFMAC 5.5.0110	Depositor
R, R_{free}	0.167 , 0.212 0.170 , 0.213	Depositor DCC
R_{free} test set	2176 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	23.6	Xtriage
Anisotropy	0.293	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 45.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	6117	wwPDB-VP
Average B, all atoms (Å ²)	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.26% 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: ZN, PGE, CA, PG4, IPA, CIT, PEG

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	0.74	0/2879	0.69	2/3889 (0.1%)
1	B	0.72	0/2826	0.69	4/3819 (0.1%)
All	All	0.73	0/5705	0.69	6/7708 (0.1%)

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	252	ARG	NE-CZ-NH1	5.62	123.11	120.30
1	A	222	ASP	CB-CG-OD1	5.49	123.24	118.30
1	B	215	ARG	NE-CZ-NH2	5.33	122.96	120.30
1	A	309	ARG	NE-CZ-NH1	5.03	122.81	120.30
1	B	374[A]	ARG	NE-CZ-NH1	5.02	122.81	120.30
1	B	374[B]	ARG	NE-CZ-NH1	5.02	122.81	120.30

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	2821	0	2895	14	0
1	B	2788	0	2820	8	0
2	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	1	0	0	0	0
3	A	2	0	0	0	0
3	B	3	0	0	0	0
4	A	26	0	10	0	0
5	A	4	0	8	0	0
6	A	19	0	25	0	0
6	B	7	0	10	0	0
7	A	13	0	18	0	0
7	B	25	0	33	0	0
8	B	10	0	14	0	0
9	A	216	0	0	0	0
9	B	181	0	0	0	0
All	All	6117	0	5833	22	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 (22) 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:185[A]:ILE:HG23	1:A:249:ALA:HB3	1.75	0.67
1:A:80:MSE:HE2	1:A:139:ILE:HG22	1.77	0.67
1:A:254[B]:HIS:CE1	1:A:319:ILE:CG2	2.90	0.55
1:A:66:ILE:HD13	1:A:71:VAL:HG11	1.92	0.50
1:A:245:VAL:HG12	1:A:247[A]:LEU:HD22	1.95	0.49
1:B:223:GLU:HG3	1:B:224:ILE:HG23	1.94	0.48
1:B:53:LEU:HD22	1:B:141:VAL:HG23	1.95	0.48
1:A:75:TYR:CZ	1:A:329:ILE:HG21	2.50	0.46
1:B:176:VAL:HB	1:B:338:ILE:HB	1.98	0.45
1:A:188:LYS:HE2	1:A:190:ILE:HD11	1.98	0.44
1:A:188:LYS:CE	1:A:190:ILE:HD11	2.48	0.44
1:B:75:TYR:CZ	1:B:329[B]:ILE:HG21	2.53	0.44
1:B:254[B]:HIS:CE1	1:B:319:ILE:CG2	3.02	0.43
1:A:40:LEU:HD11	1:A:122:LEU:HD22	1.99	0.43
1:A:80:MSE:HE2	1:A:139:ILE:CG2	2.47	0.42
1:B:83:VAL:HG21	1:B:347:HIS:HA	2.01	0.42
1:B:115:LEU:HD21	1:B:139:ILE:HG23	2.01	0.42
1:A:78:SER:N	1:A:118:MSE:HE1	2.34	0.42
1:A:86:ALA:HB2	1:A:106:ILE:HG12	2.02	0.42
1:A:118:MSE:HE3	1:A:166:ILE:HD12	2.01	0.41
1:A:193[A]:THR:HG23	1:A:243:ASP:OD2	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:93:VAL:HG13	1:B:355:ILE:HD11	2.03	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	380/396 (96%)	370 (97%)	10 (3%)	0	100	100
1	B	373/396 (94%)	363 (97%)	9 (2%)	1 (0%)	41	41
All	All	753/792 (95%)	733 (97%)	19 (2%)	1 (0%)	51	54

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	167	ASP

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	310/318 (98%)	305 (98%)	5 (2%)	62	69
1	B	299/318 (94%)	296 (99%)	3 (1%)	76	82
All	All	609/636 (96%)	601 (99%)	8 (1%)	69	75

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MSE
1	A	182	GLN
1	A	232	PHE
1	A	256	PRO
1	A	343	TYR
1	B	182	GLN
1	B	232	PHE
1	B	343	TYR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	5	GLN

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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 18 ligands modelled in this entry, 7 are monoatomic - leaving 11 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
6	PEG	A	411	-	4,4,6	0.58	0	3,3,5	0.26	0
7	PG4	A	416	-	12,12,12	0.54	0	11,11,11	0.23	0
6	PEG	A	409	-	6,6,6	0.48	0	5,5,5	0.45	0
4	CIT	A	406	-	3,12,12	1.10	0	3,17,17	0.99	0
4	CIT	A	407	-	3,12,12	1.26	0	3,17,17	2.03	2 (66%)
6	PEG	B	410	-	6,6,6	0.46	0	5,5,5	0.54	0
8	PGE	B	413	-	9,9,9	0.64	0	8,8,8	0.52	0
7	PG4	B	415	3	11,11,12	0.80	0	10,10,11	0.34	0
7	PG4	B	414	-	12,12,12	0.42	0	11,11,11	0.27	0
6	PEG	A	412	-	6,6,6	0.48	0	5,5,5	0.50	0
5	IPA	A	408	-	3,3,3	0.52	0	3,3,3	0.38	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
6	PEG	A	411	-	-	2/2/2/4	-
7	PG4	A	416	-	-	1/10/10/10	-
6	PEG	A	409	-	-	3/4/4/4	-
4	CIT	A	406	-	-	0/6/16/16	-
4	CIT	A	407	-	-	0/6/16/16	-
6	PEG	B	410	-	-	2/4/4/4	-
8	PGE	B	413	-	-	4/7/7/7	-
7	PG4	B	415	3	-	3/9/9/10	-
7	PG4	B	414	-	-	0/10/10/10	-
6	PEG	A	412	-	-	3/4/4/4	-

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	407	CIT	C3-C4-C5	-2.66	110.72	114.98
4	A	407	CIT	C4-C3-C2	2.06	114.84	109.33

There are no chirality outliers.

All (18) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	A	412	PEG	O2-C3-C4-O4
6	A	411	PEG	O1-C1-C2-O2
6	A	409	PEG	O1-C1-C2-O2
6	B	410	PEG	O1-C1-C2-O2
8	B	413	PGE	O1-C1-C2-O2
6	A	409	PEG	O2-C3-C4-O4
8	B	413	PGE	O3-C5-C6-O4
6	B	410	PEG	C1-C2-O2-C3
7	B	415	PG4	C8-C7-O4-C6
6	A	412	PEG	O1-C1-C2-O2
8	B	413	PGE	C6-C5-O3-C4
6	A	411	PEG	C1-C2-O2-C3
6	A	412	PEG	C1-C2-O2-C3
7	A	416	PG4	C6-C5-O3-C4
6	A	409	PEG	C1-C2-O2-C3
8	B	413	PGE	O2-C3-C4-O3
7	B	415	PG4	O1-C1-C2-O2
7	B	415	PG4	O3-C5-C6-O4

There are no ring outliers.

No monomer is involved in short contacts.

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	365/396 (92%)	-0.43	1 (0%) 94 94	14, 21, 34, 55	0
1	B	365/396 (92%)	-0.26	7 (1%) 66 71	15, 24, 38, 62	0
All	All	730/792 (92%)	-0.35	8 (1%) 80 84	14, 22, 37, 62	0

All (8) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	166	ILE	3.4
1	B	78	SER	2.4
1	B	77	THR	2.3
1	B	374[A]	ARG	2.2
1	B	66	ILE	2.1
1	A	66	ILE	2.1
1	B	113	ALA	2.1
1	B	165	ALA	2.1

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 carbohydrates 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(Å ²)	Q<0.9
4	CIT	A	407	13/13	0.81	0.16	48,55,61,62	0
6	PEG	B	410	7/7	0.82	0.14	49,49,54,54	0
8	PGE	B	413	10/10	0.82	0.20	50,53,56,58	0
6	PEG	A	411	5/7	0.83	0.12	43,46,48,51	0
4	CIT	A	406	13/13	0.86	0.17	50,60,62,64	0
6	PEG	A	412	7/7	0.86	0.20	56,58,65,68	0
6	PEG	A	409	7/7	0.87	0.23	51,52,54,55	0
7	PG4	B	415	12/13	0.88	0.18	40,44,49,50	0
3	CA	A	405	1/1	0.90	0.17	59,59,59,59	0
5	IPA	A	408	4/4	0.90	0.15	34,37,37,37	0
3	CA	B	404	1/1	0.91	0.20	65,65,65,65	0
3	CA	B	403	1/1	0.92	0.24	61,61,61,61	0
3	CA	B	402	1/1	0.95	0.07	38,38,38,38	0
7	PG4	B	414	13/13	0.95	0.10	26,29,35,37	0
7	PG4	A	416	13/13	0.95	0.11	27,31,35,35	0
3	CA	A	402	1/1	0.98	0.06	32,32,32,32	0
2	ZN	A	401	1/1	1.00	0.05	26,26,26,26	0
2	ZN	B	401	1/1	1.00	0.07	35,35,35,35	0

6.5 Other polymers

There are no such residues in this entry.