



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 20, 2026 – 08:34 AM UTC

PDB ID : 4Q1V / pdb_00004q1v
Title : Crystal structure of a putative dipeptidyl aminopeptidase IV (BA-COVA_01349) from Bacteroides ovatus ATCC 8483 at 2.48 Å resolution
Authors : Joint Center for Structural Genomics (JCSG)
Deposited on : 2014-04-04
Resolution : 2.48 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
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

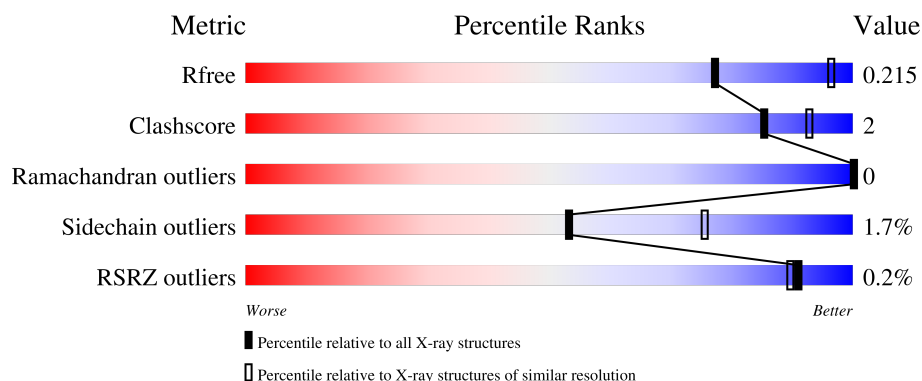
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.48 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	7589 (2.50-2.46)
Clashscore	190562	8295 (2.50-2.46)
Ramachandran outliers	187476	8164 (2.50-2.46)
Sidechain outliers	187428	8166 (2.50-2.46)
RSRZ outliers	180081	7593 (2.50-2.46)

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	710	 90% 9%
1	B	710	 91% 9%

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 12075 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.

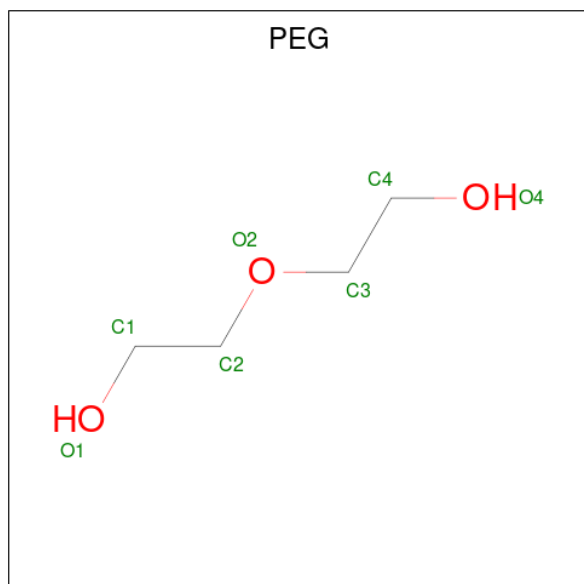
- Molecule 1 is a protein called putative dipeptidyl aminopeptidase IV.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	707	Total	C	N	O	S	Se	0	13	0
			5726	3646	971	1081	10	18			
1	B	707	Total	C	N	O	S	Se	0	9	0
			5685	3620	964	1073	10	18			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	GLY	-	expression tag	UNP A7LU53
B	0	GLY	-	expression tag	UNP A7LU53

- Molecule 2 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: C₄H₁₀O₃).



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

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

- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total Mg 1 1	0	0
3	B	1	Total Mg 1 1	0	0

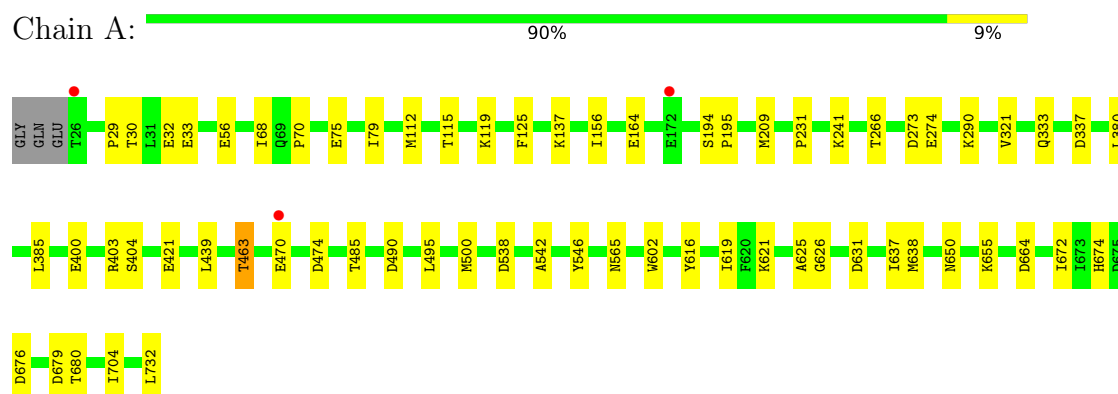
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	341	Total O 341 341	0	0
4	B	300	Total O 300 300	0	0

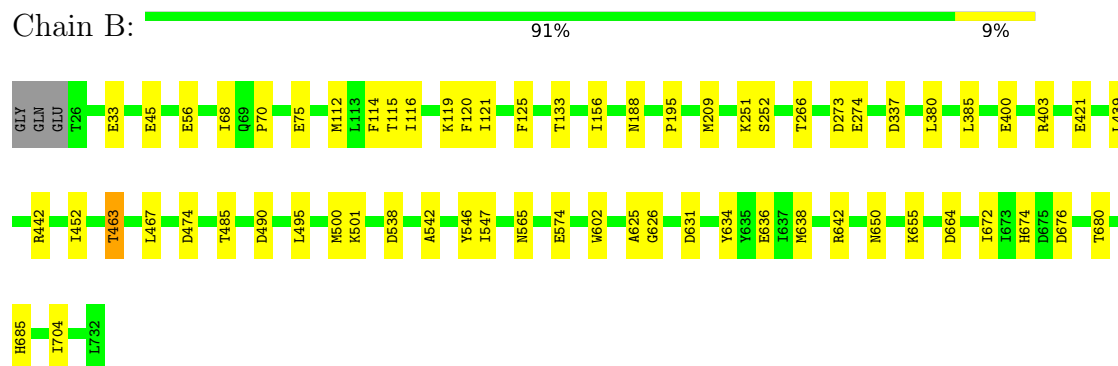
3 Residue-property plots

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: putative dipeptidyl aminopeptidase IV



- Molecule 1: putative dipeptidyl aminopeptidase IV



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	92.49Å 133.70Å 159.13Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.30 – 2.48 49.30 – 2.48	Depositor EDS
% Data completeness (in resolution range)	100.0 (49.30-2.48) 99.9 (49.30-2.48)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.56 (at 2.48Å)	Xtriage
Refinement program	BUSTER-TNT 2.10.0, BUSTER 2.10.0	Depositor
R, R_{free}	0.171 , 0.207 0.180 , 0.215	Depositor DCC
R_{free} test set	3561 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å ²)	35.6	Xtriage
Anisotropy	0.240	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 45.0	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	0.96	EDS
Total number of atoms	12075	wwPDB-VP
Average B, all atoms (Å ²)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 49.15 % 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 7.7713e-05. 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

5.1 Standard geometry

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

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	0.84	0/5880	1.16	13/7946 (0.2%)
1	B	0.84	0/5837	1.17	16/7884 (0.2%)
All	All	0.84	0/11717	1.17	29/15830 (0.2%)

There are no bond length outliers.

All (29) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	676	ASP	CA-CB-CG	7.46	120.06	112.60
1	A	490	ASP	CA-CB-CG	7.10	119.70	112.60
1	B	490	ASP	CA-CB-CG	7.08	119.68	112.60
1	A	676	ASP	CA-CB-CG	6.88	119.48	112.60
1	A	164	GLU	CB-CG-CD	6.63	123.88	112.60
1	B	664	ASP	CA-CB-CG	6.38	118.98	112.60
1	A	650	ASN	CA-CB-CG	6.25	118.85	112.60
1	A	664	ASP	CA-CB-CG	6.24	118.84	112.60
1	B	631	ASP	CA-CB-CG	6.12	118.72	112.60
1	B	650	ASN	CA-CB-CG	6.10	118.70	112.60
1	A	631	ASP	CA-CB-CG	6.09	118.69	112.60
1	B	565	ASN	CA-CB-CG	6.07	118.67	112.60
1	B	680	THR	N-CA-C	-6.03	103.46	111.96
1	A	680	THR	N-CA-C	-5.94	103.58	111.96
1	A	565	ASN	CA-CB-CG	5.65	118.25	112.60
1	B	337	ASP	CA-CB-CG	5.54	118.14	112.60
1	B	636	GLU	CA-C-N	5.54	127.54	120.56
1	B	636	GLU	C-N-CA	5.54	127.54	120.56
1	B	273	ASP	CA-CB-CG	5.52	118.12	112.60
1	A	337	ASP	CA-CB-CG	5.51	118.11	112.60
1	B	655	LYS	CA-C-N	5.41	127.53	120.28
1	B	655	LYS	C-N-CA	5.41	127.53	120.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	679	ASP	CA-CB-CG	5.24	117.84	112.60
1	A	273	ASP	CA-CB-CG	5.22	117.82	112.60
1	A	655	LYS	CA-C-N	5.21	127.27	120.28
1	A	655	LYS	C-N-CA	5.21	127.27	120.28
1	B	114	PHE	CA-CB-CG	5.03	118.83	113.80
1	B	574	GLU	CA-C-N	5.03	126.98	120.44
1	B	574	GLU	C-N-CA	5.03	126.98	120.44

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	5726	0	5540	27	0
1	B	5685	0	5519	23	0
2	A	14	0	20	1	0
2	B	7	0	10	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	341	0	0	2	0
4	B	300	0	0	1	0
All	All	12075	0	11089	50	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 (50) 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:68:ILE:HG12	1:B:75:GLU:HG2	1.75	0.67
1:A:385:LEU:HD13	1:A:439[B]:LEU:HD11	1.78	0.65
1:B:385:LEU:HD13	1:B:439[B]:LEU:HD11	1.85	0.59
1:B:112:MSE:HE3	1:B:125:PHE:CD1	2.38	0.58
1:A:621:LYS:HD3	1:A:732:LEU:HD12	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:79:ILE:HG21	1:A:112:MSE:HE1	1.87	0.57
1:B:209:MSE:H	1:B:209:MSE:SE	2.39	0.56
1:A:30[A]:THR:HG22	1:A:32:GLU:H	1.71	0.54
1:A:195:PRO:HD2	1:A:274:GLU:HG2	1.90	0.53
1:A:290:LYS:CD	1:A:290:LYS:NZ	2.72	0.52
1:A:70:PRO:O	1:A:463:THR:CG2	2.58	0.52
1:B:542:ALA:HA	1:B:546:TYR:O	2.10	0.52
1:A:542:ALA:HA	1:A:546:TYR:O	2.11	0.51
1:B:70:PRO:O	1:B:463:THR:CG2	2.59	0.51
1:B:195:PRO:HD2	1:B:274:GLU:HG2	1.91	0.51
1:B:602:TRP:CE3	1:B:626:GLY:HA3	2.45	0.50
1:A:602:TRP:CE3	1:A:626:GLY:HA3	2.47	0.50
1:A:70:PRO:O	1:A:463:THR:HG23	2.13	0.49
1:B:70:PRO:O	1:B:463:THR:HG23	2.14	0.48
1:B:642:ARG:HD3	4:B:1046:HOH:O	2.14	0.48
1:A:209:MSE:SE	1:A:209:MSE:H	2.47	0.47
1:A:68:ILE:HG12	1:A:75:GLU:HG2	1.98	0.45
1:A:241:LYS:HD2	2:A:802:PEG:H42	1.99	0.45
1:A:674:HIS:O	1:A:704:ILE:HA	2.17	0.45
1:B:674:HIS:O	1:B:704:ILE:HA	2.17	0.45
1:B:485:THR:HA	1:B:495:LEU:O	2.17	0.45
1:B:116:ILE:HD12	1:B:121:ILE:HD13	1.98	0.44
1:B:400:GLU:OE1	1:B:403[A]:ARG:NH2	2.47	0.44
1:A:485:THR:HA	1:A:495:LEU:O	2.17	0.44
1:B:120:PHE:O	1:B:133:THR:HA	2.17	0.44
1:B:500:MSE:SE	1:B:538:ASP:HB3	2.68	0.44
1:A:112:MSE:HE3	1:A:125:PHE:CD2	2.53	0.44
1:A:29:PRO:HD2	4:A:984:HOH:O	2.16	0.43
1:A:137:LYS:HB2	1:A:156[B]:ILE:HD11	2.00	0.43
1:A:400:GLU:OE1	1:A:403[A]:ARG:NH2	2.46	0.43
1:A:500:MSE:SE	1:A:538:ASP:HB3	2.69	0.43
1:B:625:ALA:HB3	1:B:672:ILE:HD13	2.01	0.43
1:A:333:GLN:HG3	4:A:904:HOH:O	2.18	0.42
1:A:616:TYR:HB3	1:A:619:ILE:HD12	2.01	0.42
1:B:442:ARG:HG2	1:B:452:ILE:HG12	2.02	0.42
1:A:194[A]:SER:HB3	1:A:274:GLU:OE2	2.20	0.42
1:B:501:LYS:HG2	1:B:547[A]:ILE:HD12	2.01	0.42
1:A:403[B]:ARG:NH2	1:A:421:GLU:O	2.53	0.41
1:A:625:ALA:HB3	1:A:672:ILE:HD13	2.02	0.41
1:B:115:THR:HA	1:B:119:LYS:O	2.20	0.41
1:B:403[B]:ARG:NH2	1:B:421:GLU:O	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:115:THR:HA	1:A:119:LYS:O	2.20	0.41
1:A:231:PRO:HB2	1:A:637:ILE:HD12	2.02	0.40
1:B:45:GLU:HG3	1:B:467:LEU:HD11	2.04	0.40
1:B:634:TYR:HB2	1:B:685:HIS:CE1	2.57	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	718/710 (101%)	697 (97%)	21 (3%)	0	100	100
1	B	714/710 (101%)	694 (97%)	20 (3%)	0	100	100
All	All	1432/1420 (101%)	1391 (97%)	41 (3%)	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	616/590 (104%)	605 (98%)	11 (2%)	51	74
1	B	613/590 (104%)	602 (98%)	11 (2%)	51	74
All	All	1229/1180 (104%)	1207 (98%)	22 (2%)	53	74

All (22) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	33	GLU
1	A	56	GLU
1	A	266	THR
1	A	321[A]	VAL
1	A	321[B]	VAL
1	A	380	LEU
1	A	404	SER
1	A	463	THR
1	A	470	GLU
1	A	474	ASP
1	A	638	MSE
1	B	33	GLU
1	B	56	GLU
1	B	156	ILE
1	B	188	ASN
1	B	251	LYS
1	B	252	SER
1	B	266	THR
1	B	380	LEU
1	B	463	THR
1	B	474	ASP
1	B	638	MSE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	83	GLN
1	A	129	GLN
1	A	188	ASN
1	A	198	ASN
1	A	418	GLN
1	A	422	ASN
1	A	465	ASN
1	A	496	HIS
1	A	558	ASN
1	B	129	GLN
1	B	198	ASN
1	B	418	GLN
1	B	422	ASN
1	B	465	ASN
1	B	558	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 ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 5 ligands modelled in this entry, 2 are monoatomic - leaving 3 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	PEG	A	802	-	6,6,6	0.31	0	5,5,5	0.26	0
2	PEG	A	801	-	6,6,6	0.31	0	5,5,5	0.11	0
2	PEG	B	801	-	6,6,6	0.26	0	5,5,5	0.17	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	PEG	A	802	-	-	2/4/4/4	-
2	PEG	A	801	-	-	2/4/4/4	-
2	PEG	B	801	-	-	2/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	802	PEG	O1-C1-C2-O2
2	A	802	PEG	O2-C3-C4-O4
2	B	801	PEG	O2-C3-C4-O4
2	A	801	PEG	O1-C1-C2-O2
2	A	801	PEG	O2-C3-C4-O4
2	B	801	PEG	C4-C3-O2-C2

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	802	PEG	1	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	689/710 (97%)	-0.46	3 (0%) 88 87	15, 34, 55, 69	13 (1%)
1	B	689/710 (97%)	-0.47	0 100 100	16, 34, 57, 75	9 (1%)
All	All	1378/1420 (97%)	-0.47	3 (0%) 91 90	15, 34, 56, 75	22 (1%)

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	26	THR	2.8
1	A	172[A]	GLU	2.7
1	A	470	GLU	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 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(Å ²)	Q<0.9
2	PEG	B	801	7/7	0.72	0.24	67,68,70,70	0
2	PEG	A	801	7/7	0.88	0.15	55,57,59,60	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	PEG	A	802	7/7	0.91	0.13	57,58,60,60	0
3	MG	A	803	1/1	0.99	0.02	19,19,19,19	0
3	MG	B	802	1/1	0.99	0.03	18,18,18,18	0

6.5 Other polymers [i](#)

There are no such residues in this entry.