Full wwPDB X-ray Structure Validation Report ⓘ

Sep 16, 2023 – 02:12 PM EDT

PDB ID	:	4P2X
Title	:	Swapped Dimer of Mycobacterial Adenylyl cyclase Rv1625c: Form 2
Authors	:	Barathy, D.V.; Mattoo, R.; Visweswariah, S.S.; Suguna, K.
Deposited on	:	2014-03-05
Resolution	:	2.40 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:

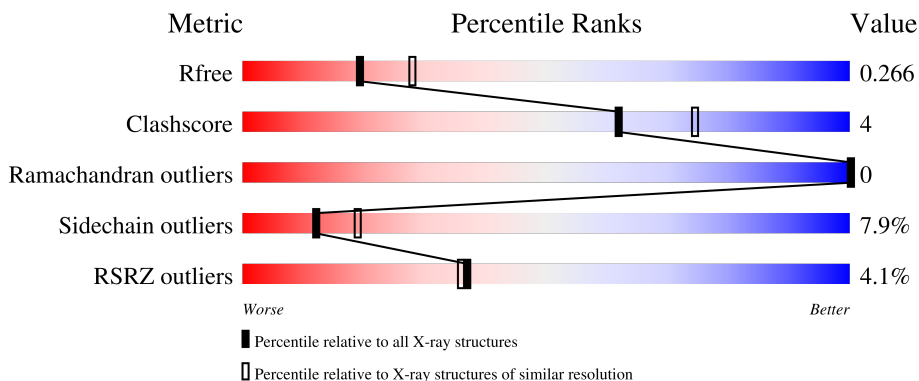|		
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35.1

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 2.40 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	Percentile Ranks	Value
Rfree		0.266
Clashscore		4
Ramachandran outliers		0
Sidechain outliers		7.9%
RSRZ outliers		4.1%

Worse — *Better*

▮ Percentile relative to all X-ray structures
▯ Percentile relative to X-ray structures of similar resolution

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	3907 (2.40-2.40)
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)
RSRZ outliers	127900	3811 (2.40-2.40)

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 <=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	257	3% / 55% / 9% · / 35%
1	B	257	3% / 60% / 5% · / 33%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	CL	B	503	-	-	X	-

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 2636 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 Adenylate cyclase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	167	Total	C	N	O	S	0	1	0
			1267	806	215	241	5			
1	B	172	Total	C	N	O	S	0	1	0
			1281	815	223	239	4			

There are 50 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	187	MET	-	expression tag	UNP P0A4Y0
A	188	SER	-	expression tag	UNP P0A4Y0
A	189	TYR	-	expression tag	UNP P0A4Y0
A	190	TYR	-	expression tag	UNP P0A4Y0
A	191	HIS	-	expression tag	UNP P0A4Y0
A	192	HIS	-	expression tag	UNP P0A4Y0
A	193	HIS	-	expression tag	UNP P0A4Y0
A	194	HIS	-	expression tag	UNP P0A4Y0
A	195	HIS	-	expression tag	UNP P0A4Y0
A	196	HIS	-	expression tag	UNP P0A4Y0
A	197	ASP	-	expression tag	UNP P0A4Y0
A	198	TYR	-	expression tag	UNP P0A4Y0
A	199	ASP	-	expression tag	UNP P0A4Y0
A	200	ILE	-	expression tag	UNP P0A4Y0
A	201	PRO	-	expression tag	UNP P0A4Y0
A	202	THR	-	expression tag	UNP P0A4Y0
A	203	THR	-	expression tag	UNP P0A4Y0
A	204	GLU	-	expression tag	UNP P0A4Y0
A	205	ASN	-	expression tag	UNP P0A4Y0
A	206	LEU	-	expression tag	UNP P0A4Y0
A	207	TYR	-	expression tag	UNP P0A4Y0
A	208	PHE	-	expression tag	UNP P0A4Y0
A	209	GLN	-	expression tag	UNP P0A4Y0
A	210	GLY	-	expression tag	UNP P0A4Y0
A	211	ALA	-	expression tag	UNP P0A4Y0

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Chain	Residue	Modelled	Actual	Comment	Reference
B	187	MET	-	expression tag	UNP P0A4Y0
B	188	SER	-	expression tag	UNP P0A4Y0
B	189	TYR	-	expression tag	UNP P0A4Y0
B	190	TYR	-	expression tag	UNP P0A4Y0
B	191	HIS	-	expression tag	UNP P0A4Y0
B	192	HIS	-	expression tag	UNP P0A4Y0
B	193	HIS	-	expression tag	UNP P0A4Y0
B	194	HIS	-	expression tag	UNP P0A4Y0
B	195	HIS	-	expression tag	UNP P0A4Y0
B	196	HIS	-	expression tag	UNP P0A4Y0
B	197	ASP	-	expression tag	UNP P0A4Y0
B	198	TYR	-	expression tag	UNP P0A4Y0
B	199	ASP	-	expression tag	UNP P0A4Y0
B	200	ILE	-	expression tag	UNP P0A4Y0
B	201	PRO	-	expression tag	UNP P0A4Y0
B	202	THR	-	expression tag	UNP P0A4Y0
B	203	THR	-	expression tag	UNP P0A4Y0
B	204	GLU	-	expression tag	UNP P0A4Y0
B	205	ASN	-	expression tag	UNP P0A4Y0
B	206	LEU	-	expression tag	UNP P0A4Y0
B	207	TYR	-	expression tag	UNP P0A4Y0
B	208	PHE	-	expression tag	UNP P0A4Y0
B	209	GLN	-	expression tag	UNP P0A4Y0
B	210	GLY	-	expression tag	UNP P0A4Y0
B	211	ALA	-	expression tag	UNP P0A4Y0

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O_4S).
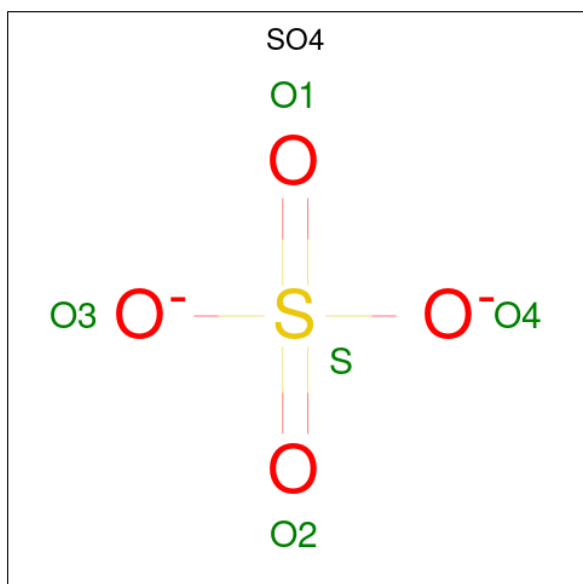
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total 5	O 4	S 1	0	0

- Molecule 3 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: $C_4H_{10}O_3$).
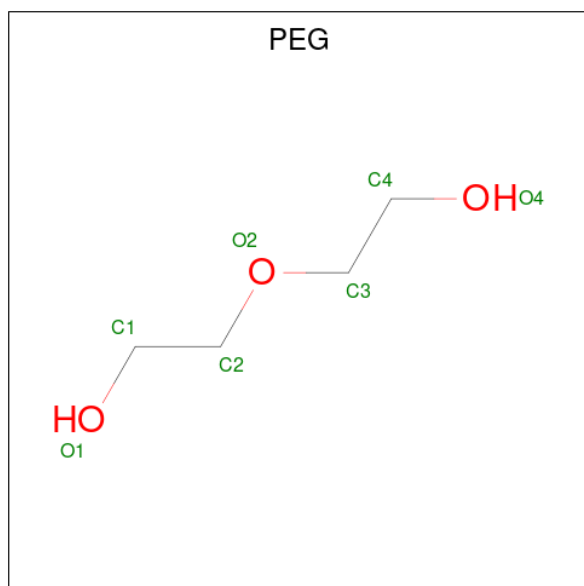
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total 7	C 4	O 3	0	0
3	A	1	Total 7	C 4	O 3	0	0
3	B	1	Total 7	C 4	O 3	0	0
3	B	1	Total 7	C 4	O 3	0	0

- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total 1	Mg 1	0	0

- Molecule 5 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

| Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	1	Total 1	Cl 1	0	0

• Molecule 6 is water.

| Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	30	Total O 30 30		0	0
6	B	23	Total O 23 23		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: Adenylate cyclase
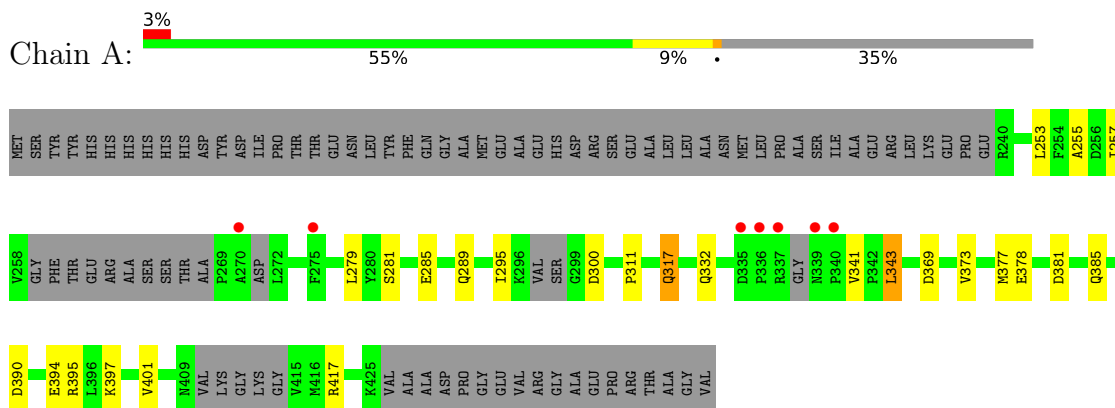
- Molecule 1: Adenylate cyclase
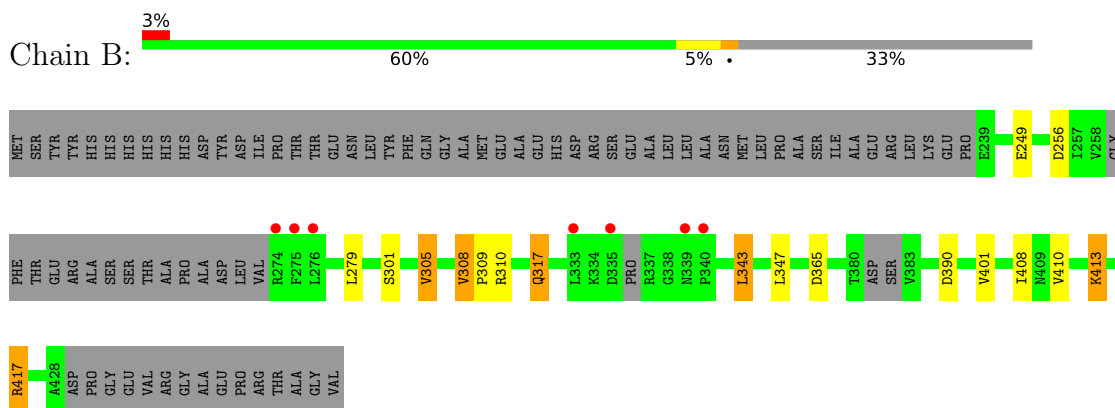
4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 65	Depositor
Cell constants a, b, c, α, β, γ	75.57Å 75.57Å 133.17Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	36.76 – 2.40 36.74 – 2.40	Depositor EDS
% Data completeness (in resolution range)	99.8 (36.76-2.40) 99.8 (36.74-2.40)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.92 (at 2.39Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, R_{free}	0.196 , 0.260 0.206 , 0.266	Depositor DCC
R_{free} test set	849 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å^2)	37.1	Xtriage
Anisotropy	0.023	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 38.2	EDS
L-test for twinning[2]	$< |L| > = 0.49, < L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.067 for h,-h-k,-l	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	2636	wwPDB-VP
Average B, all atoms (Å^2)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.66% of the height of the origin peak. No significant pseudotranslation is detected.*

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[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ 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, SO4, MG, CL

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	0.40	0/1293	0.58	0/1756
1	B	0.38	0/1304	0.59	0/1774
All	All	0.39	0/2597	0.59	0/3530

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	1267	0	1191	13	0
1	B	1281	0	1207	11	0
2	A	5	0	0	0	0
3	A	14	0	20	1	0
3	B	14	0	20	2	0
4	A	1	0	0	0	0
5	B	1	0	0	2	0
6	A	30	0	0	1	0
6	B	23	0	0	0	0
All	All	2636	0	2438	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 4.

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:B:317:GLN:NE2	5:B:503:CL:CL	2.46	0.86
1:A:395:ARG:NH1	5:B:503:CL:CL	2.71	0.60
1:B:410:VAL:HG13	1:B:413:LYS:HB3	1.83	0.59
1:B:305:VAL:HG13	1:B:308:VAL:HG13	1.87	0.56
1:A:317:GLN:NE2	6:A:615:HOH:O	2.40	0.54
1:A:373:VAL:O	1:A:377:MET:HG2	2.11	0.50
1:A:390:ASP:OD1	1:A:417:ARG:HD2	2.11	0.50
1:A:285:GLU:O	1:A:289:GLN:HG3	2.13	0.48
1:A:253:LEU:HD23	1:A:253:LEU:C	2.35	0.46
1:B:310:ARG:HB3	3:B:501:PEG:H42	1.98	0.46
1:A:381:ASP:OD2	1:A:385:GLN:O	2.35	0.45
1:A:311:PRO:HA	3:A:503:PEG:H22	1.99	0.45
1:B:256:ASP:O	1:B:343:LEU:HD23	2.16	0.45
1:B:408:ILE:C	1:B:408:ILE:HD12	2.37	0.44
1:B:309:PRO:HD2	3:B:501:PEG:H41	2.00	0.44
1:A:295:ILE:HG23	1:B:365:ASP:HA	2.00	0.43
1:A:394:GLU:OE1	1:A:397:LYS:HE3	2.19	0.42
1:A:255:ALA:HB1	1:A:343:LEU:HD21	2.02	0.42
1:B:390:ASP:OD2	1:B:417:ARG:NH1	2.53	0.42
1:A:341:VAL:O	1:A:341:VAL:HG23	2.20	0.40
1:B:317:GLN:HE21	1:B:317:GLN:HB2	1.68	0.40
1:A:395:ARG:NH2	1:B:249:GLU:OE1	2.55	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	156/257 (61%)	154 (99%)	2 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	165/257 (64%)	161 (98%)	4 (2%)	0	100	100
All	All	321/514 (62%)	315 (98%)	6 (2%)	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	129/212 (61%)	119 (92%)	10 (8%)	12	19
1	B	126/212 (59%)	116 (92%)	10 (8%)	12	19
All	All	255/424 (60%)	235 (92%)	20 (8%)	12	19

All (20) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	257	ILE
1	A	279	LEU
1	A	281	SER
1	A	300	ASP
1	A	317	GLN
1	A	332	GLN
1	A	343	LEU
1	A	369	ASP
1	A	378	GLU
1	A	401	VAL
1	B	279	LEU
1	B	301	SER
1	B	305	VAL
1	B	308	VAL
1	B	317	GLN
1	B	343	LEU
1	B	347	LEU
1	B	401	VAL

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Mol	Chain	Res	Type
1	B	413	LYS
1	B	417	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	317	GLN
1	A	372	ASN
1	B	317	GLN
1	B	387	GLN

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 monosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 7 ligands modelled in this entry, 2 are monoatomic - leaving 5 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	#$|Z| > 2$
3	PEG	B	502	-	6,6,6	0.38	0	5,5,5	0.33	0
2	SO4	A	501	-	4,4,4	0.36	0	6,6,6	0.49	0
3	PEG	B	501	-	6,6,6	0.59	0	5,5,5	0.42	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	#|Z| > 2	Counts	RMSZ	#|Z| > 2
3	PEG	A	503	-	6,6,6	0.45	0	5,5,5	0.57	0
3	PEG	A	502	-	6,6,6	0.54	0	5,5,5	0.52	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
3	PEG	A	503	-	-	1/4/4/4	-
3	PEG	A	502	-	-	2/4/4/4	-
3	PEG	B	502	-	-	2/4/4/4	-
3	PEG	B	501	-	-	4/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	502	PEG	C1-C2-O2-C3
3	B	501	PEG	O2-C3-C4-O4
3	A	502	PEG	O2-C3-C4-O4
3	B	502	PEG	O1-C1-C2-O2
3	A	503	PEG	O2-C3-C4-O4
3	B	501	PEG	O1-C1-C2-O2
3	B	501	PEG	C1-C2-O2-C3
3	B	502	PEG	O2-C3-C4-O4
3	B	501	PEG	C4-C3-O2-C2

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	501	PEG	2	0
3	A	503	PEG	1	0

5.7 Other polymers ⓘ

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	167/257 (64%)	-0.10	7 (4%)	36	35	23, 35, 75, 106	0
1	B	172/257 (66%)	-0.10	7 (4%)	37	36	22, 38, 64, 82	0
All	All	339/514 (65%)	-0.10	14 (4%)	37	36	22, 37, 67, 106	0

All (14) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	275	PHE	4.2
1	A	340	PRO	4.0
1	A	337	ARG	3.8
1	B	340	PRO	3.7
1	A	270	ALA	3.7
1	A	336	PRO	3.6
1	A	339	ASN	3.2
1	A	275	PHE	3.1
1	B	276	LEU	2.7
1	A	335	ASP	2.3
1	B	333	LEU	2.3
1	B	339	ASN	2.3
1	B	274	ARG	2.1
1	B	335	ASP	2.0

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

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates ⓘ

There are no monosaccharides in this entry.

6.4 Ligands ⓘ

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
3	PEG	A	502	7/7	0.64	0.24	75,79,82,83	0
3	PEG	A	503	7/7	0.76	0.39	49,58,66,69	0
3	PEG	B	501	7/7	0.82	0.34	42,46,57,59	0
3	PEG	B	502	7/7	0.88	0.22	57,60,68,71	0
4	MG	A	504	1/1	0.97	0.09	30,30,30,30	0
2	SO4	A	501	5/5	0.99	0.10	36,38,38,39	0
5	CL	B	503	1/1	0.99	0.13	47,47,47,47	0

6.5 Other polymers ⓘ

There are no such residues in this entry.