



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 28, 2026 – 09:59 PM UTC

PDB ID : 6MOI / pdb_00006moi
Title : Dimeric DARPin C_angle_R5 complex with EpoR
Authors : Jude, K.M.; Mohan, K.; Garcia, K.C.; Guo, Y.
Deposited on : 2018-10-04
Resolution : 2.06 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

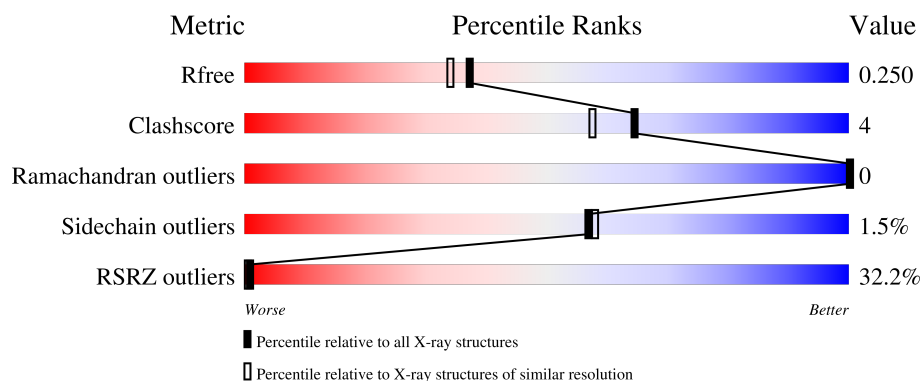
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.06 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	3774 (2.08-2.04)
Clashscore	190562	3883 (2.08-2.04)
Ramachandran outliers	187476	3860 (2.08-2.04)
Sidechain outliers	187428	3860 (2.08-2.04)
RSRZ outliers	180081	3775 (2.08-2.04)

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	231	
2	B	229	

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	MG	A	308	-	-	-	X

2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 3390 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 Dimeric DARPing CCR5 (C_angle_R5).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	222	Total	C	N	O	S	0	0	0
			1629	1025	286	313	5			

- Molecule 2 is a protein called Erythropoietin receptor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	210	Total	C	N	O	S	0	2	0
			1645	1046	288	304	7			

There are 13 discrepancies between the modelled and reference sequences:

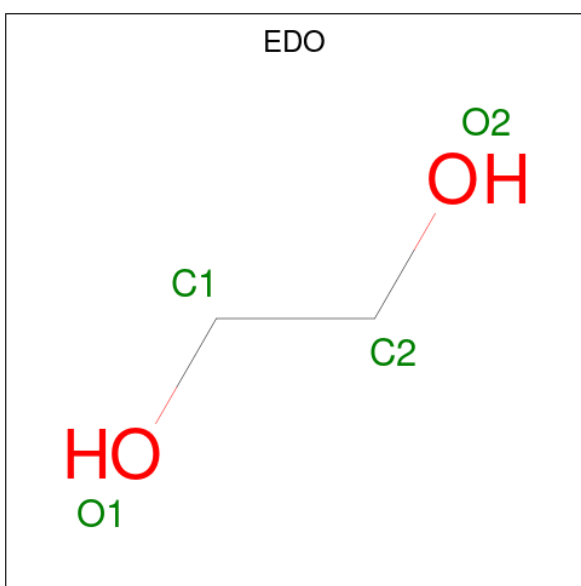
Chain	Residue	Modelled	Actual	Comment	Reference
B	3	PHE	-	expression tag	UNP P19235
B	4	ALA	-	expression tag	UNP P19235
B	5	GLY	-	expression tag	UNP P19235
B	6	SER	-	expression tag	UNP P19235
B	7	ALA	-	expression tag	UNP P19235
B	52	GLN	ASN	conflict	UNP P19235
B	164	GLN	ASN	conflict	UNP P19235
B	226	LYS	-	expression tag	UNP P19235
B	227	GLU	-	expression tag	UNP P19235
B	228	LYS	-	expression tag	UNP P19235
B	229	ALA	-	expression tag	UNP P19235
B	230	ALA	-	expression tag	UNP P19235
B	231	ALA	-	expression tag	UNP P19235

- Molecule 3 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



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

- Molecule 4 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



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

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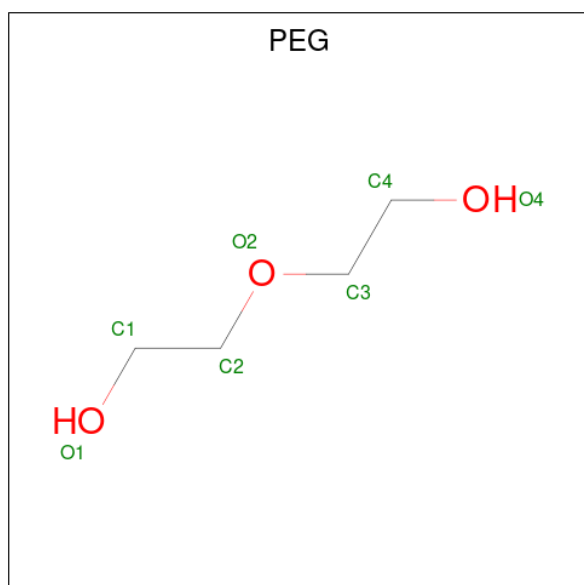
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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 4 2 2	0	0
4	A	1	Total C O 4 2 2	0	0
4	A	1	Total C O 4 2 2	0	0
4	A	1	Total C O 4 2 2	0	0
4	B	1	Total C O 4 2 2	0	0
4	B	1	Total C O 4 2 2	0	0
4	B	1	Total C O 4 2 2	0	0
4	B	1	Total C O 4 2 2	0	0

- Molecule 5 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

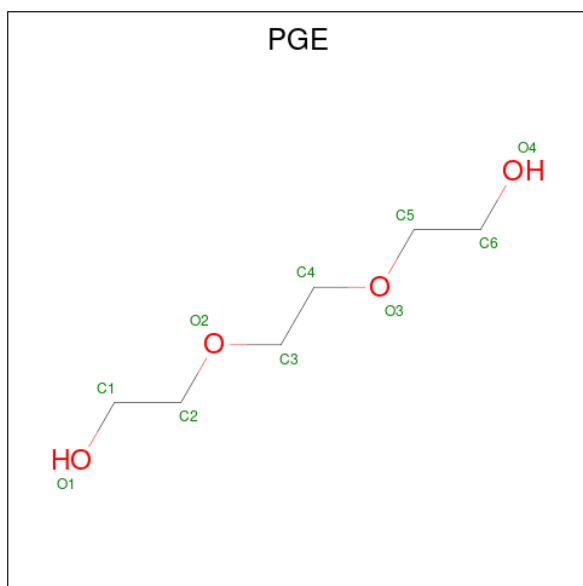
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total Mg 1 1	0	0
5	B	1	Total Mg 1 1	0	0

- Molecule 6 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: C₄H₁₀O₃).



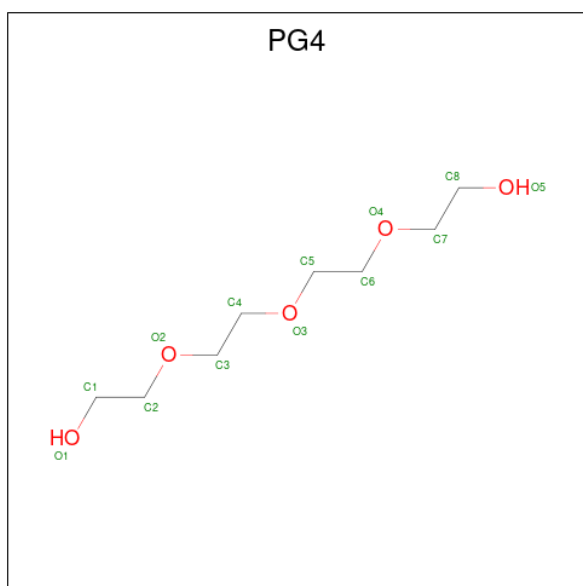
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			7	4	3		

- Molecule 7 is TRIETHYLENE GLYCOL (CCD ID: PGE) (formula: $C_6H_{14}O_4$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	C	O	0	0
			10	6	4		

- Molecule 8 is TETRAETHYLENE GLYCOL (CCD ID: PG4) (formula: $C_8H_{18}O_5$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	A	1	Total	C	O	0	0
			13	8	5		

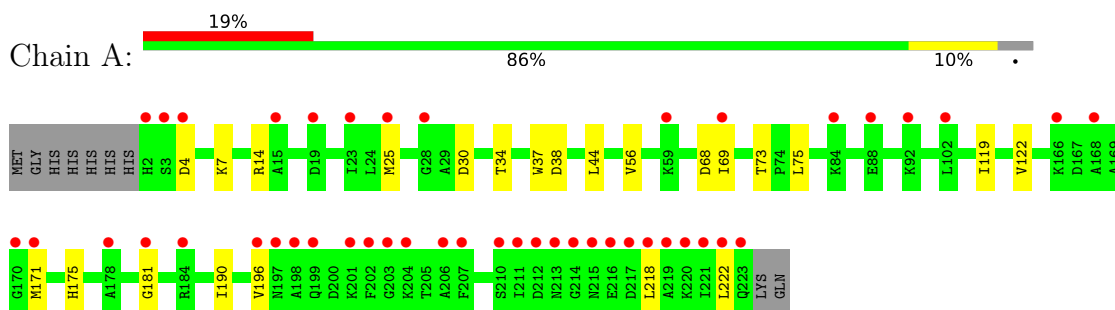
- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	15	Total	O	0	0
			15	15		
9	B	19	Total	O	0	0
			19	19		

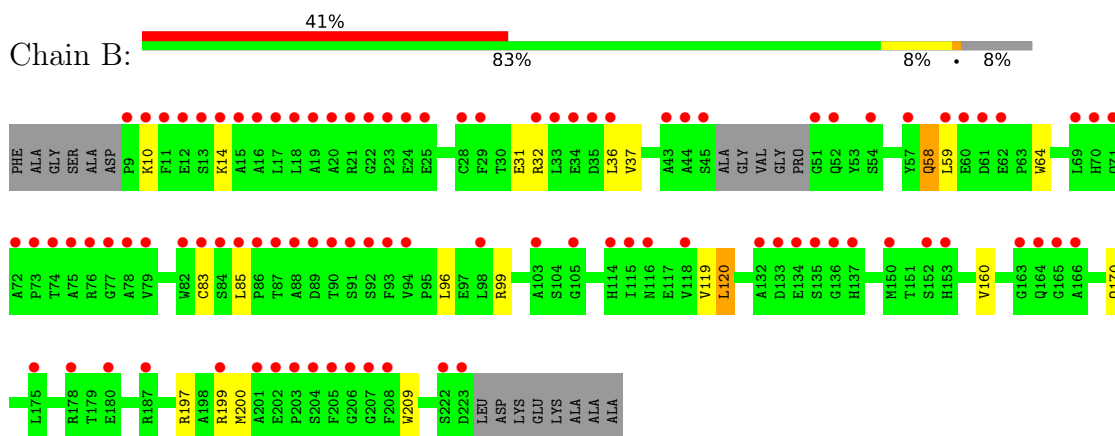
3 Residue-property plots [i](#)

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: Dimeric DARPing CCR5 (C_angle_R5)



- Molecule 2: Erythropoietin receptor



4 Data and refinement statistics

Property	Value	Source
Space group	P 65 2 2	Depositor
Cell constants a, b, c, α , β , γ	112.75Å 112.75Å 280.79Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	48.82 – 2.06 48.82 – 2.06	Depositor EDS
% Data completeness (in resolution range)	45.0 (48.82-2.06) 41.4 (48.82-2.06)	Depositor EDS
R_{merge}	0.47	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.77 (at 2.07Å)	Xtriage
Refinement program	PHENIX (1.13_2998: ???)	Depositor
R, R_{free}	0.214 , 0.251 0.216 , 0.250	Depositor DCC
R_{free} test set	1573 reflections (3.96%)	wwPDB-VP
Wilson B-factor (Å ²)	40.0	Xtriage
Anisotropy	0.026	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 42.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.36	EDS
Total number of atoms	3390	wwPDB-VP
Average B, all atoms (Å ²)	58.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.51% 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](#)

Bond lengths and bond angles in the following residue types are not validated in this section: SO4, MG, EDO, PGE, PG4, 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	0.09	0/1651	0.24	0/2246
2	B	0.10	0/1689	0.32	0/2302
All	All	0.10	0/3340	0.28	0/4548

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 [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	1629	0	1650	14	0
2	B	1645	0	1595	13	0
3	A	5	0	0	0	0
3	B	5	0	0	0	0
4	A	24	0	36	2	0
4	B	16	0	24	2	0
5	A	1	0	0	0	0
5	B	1	0	0	0	0
6	A	7	0	10	0	0
7	A	10	0	14	1	0
8	A	13	0	18	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
9	A	15	0	0	0	0
9	B	19	0	0	0	0
All	All	3390	0	3347	26	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 (26) 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:171:MET:HE2	1:A:175:HIS:HB3	1.75	0.67
2:B:31:GLU:H	4:B:303:EDO:H21	1.59	0.67
2:B:36:LEU:HD23	2:B:85:LEU:HD13	1.84	0.60
2:B:10:LYS:HE2	2:B:32:ARG:HH22	1.68	0.58
2:B:31:GLU:N	4:B:303:EDO:H21	2.20	0.56
2:B:59:LEU:HB2	2:B:96:LEU:HD12	1.89	0.55
2:B:197:ARG:HD2	2:B:209:TRP:HB3	1.90	0.53
2:B:58:GLN:HB2	2:B:64:TRP:CE2	2.45	0.51
1:A:34:THR:HB	1:A:38:ASP:HA	1.94	0.50
1:A:25:MET:HE1	1:A:56:VAL:HG12	1.93	0.50
1:A:75:LEU:HB3	4:A:302:EDO:H22	1.95	0.49
1:A:37:TRP:O	1:A:68:ASP:HB2	2.14	0.48
1:A:14:ARG:HB2	1:A:44:LEU:HD13	1.97	0.47
1:A:30:ASP:OD1	7:A:310:PGE:H42	2.14	0.47
1:A:119:ILE:HA	1:A:122:VAL:HG12	1.97	0.47
2:B:119:VAL:HG11	2:B:200[B]:MET:HG3	1.97	0.47
1:A:181:GLY:HA2	1:A:218:LEU:HD11	1.96	0.47
1:A:73:THR:HB	4:A:302:EDO:H11	1.97	0.45
2:B:14:LYS:HB3	2:B:120:LEU:HD13	1.99	0.45
1:A:38:ASP:HB2	1:A:69:ILE:HG23	2.00	0.44
1:A:190:ILE:HD11	1:A:222:LEU:HD23	1.98	0.44
2:B:160:VAL:HB	2:B:170:GLN:HB2	1.99	0.43
2:B:199:ARG:HB2	2:B:209:TRP:CE3	2.54	0.43
1:A:37:TRP:CE2	2:B:99:ARG:HD3	2.55	0.41
1:A:4:ASP:HA	1:A:7:LYS:HE3	2.02	0.40
2:B:58:GLN:HB2	2:B:64:TRP:CD2	2.57	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	220/231 (95%)	217 (99%)	3 (1%)	0	100	100
2	B	207/229 (90%)	200 (97%)	7 (3%)	0	100	100
All	All	427/460 (93%)	417 (98%)	10 (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	164/172 (95%)	163 (99%)	1 (1%)	78	82
2	B	174/185 (94%)	170 (98%)	4 (2%)	44	41
All	All	338/357 (95%)	333 (98%)	5 (2%)	57	58

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	196	VAL
2	B	37	VAL
2	B	58	GLN
2	B	83	CYS
2	B	120	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	60	ASN
2	B	70	HIS

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 17 ligands modelled in this entry, 2 are monoatomic - leaving 15 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	$\# Z > 2$
4	EDO	B	303	-	3,3,3	0.43	0	2,2,2	0.35	0
4	EDO	B	304	-	3,3,3	0.42	0	2,2,2	0.38	0
3	SO4	B	301	5	4,4,4	0.24	0	6,6,6	0.07	0
3	SO4	A	301	-	4,4,4	0.24	0	6,6,6	0.07	0
6	PEG	A	309	-	6,6,6	0.43	0	5,5,5	0.54	0
4	EDO	A	305	-	3,3,3	0.41	0	2,2,2	0.40	0
4	EDO	A	306	-	3,3,3	0.42	0	2,2,2	0.41	0
4	EDO	B	305	-	3,3,3	0.43	0	2,2,2	0.39	0
4	EDO	B	302	-	3,3,3	0.43	0	2,2,2	0.36	0
7	PGE	A	310	-	9,9,9	0.32	0	8,8,8	0.24	0
4	EDO	A	304	-	3,3,3	0.42	0	2,2,2	0.40	0
4	EDO	A	303	-	3,3,3	0.41	0	2,2,2	0.34	0
4	EDO	A	307	-	3,3,3	0.42	0	2,2,2	0.42	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
8	PG4	A	311	-	12,12,12	0.46	0	11,11,11	0.46	0
4	EDO	A	302	-	3,3,3	0.41	0	2,2,2	0.29	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
4	EDO	B	303	-	-	0/1/1/1	-
4	EDO	B	304	-	-	1/1/1/1	-
6	PEG	A	309	-	-	1/4/4/4	-
4	EDO	A	306	-	-	1/1/1/1	-
4	EDO	A	305	-	-	0/1/1/1	-
4	EDO	B	305	-	-	0/1/1/1	-
4	EDO	B	302	-	-	0/1/1/1	-
7	PGE	A	310	-	-	2/7/7/7	-
4	EDO	A	304	-	-	1/1/1/1	-
4	EDO	A	303	-	-	0/1/1/1	-
4	EDO	A	307	-	-	0/1/1/1	-
8	PG4	A	311	-	-	5/10/10/10	-
4	EDO	A	302	-	-	0/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (11) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	A	310	PGE	C1-C2-O2-C3
8	A	311	PG4	O1-C1-C2-O2
4	B	304	EDO	O1-C1-C2-O2
8	A	311	PG4	O3-C5-C6-O4
7	A	310	PGE	O2-C3-C4-O3
8	A	311	PG4	C6-C5-O3-C4
8	A	311	PG4	C3-C4-O3-C5
6	A	309	PEG	C4-C3-O2-C2
4	A	306	EDO	O1-C1-C2-O2
4	A	304	EDO	O1-C1-C2-O2
8	A	311	PG4	O2-C3-C4-O3

There are no ring outliers.

3 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	303	EDO	2	0
7	A	310	PGE	1	0
4	A	302	EDO	2	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

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	222/231 (96%)	1.44	45 (20%)	3 2	32, 48, 84, 115	0
2	B	210/229 (91%)	2.49	94 (44%)	0 0	23, 56, 111, 133	1 (0%)
All	All	432/460 (93%)	1.95	139 (32%)	1 0	23, 51, 100, 133	1 (0%)

All (139) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	88	ALA	12.1
2	B	9	PRO	9.7
2	B	135	SER	9.2
2	B	75	ALA	9.1
2	B	87	THR	8.6
1	A	2	HIS	8.2
2	B	115	ILE	7.7
2	B	76	ARG	7.6
2	B	10	LYS	7.4
2	B	208	PHE	7.3
2	B	77	GLY	7.3
2	B	93	PHE	7.2
2	B	51	GLY	7.0
2	B	78	ALA	7.0
2	B	11	PHE	6.8
2	B	207	GLY	6.8
2	B	45	SER	6.8
1	A	202	PHE	6.7
2	B	23	PRO	6.5
2	B	164	GLN	6.5
2	B	44	ALA	6.4
2	B	204	SER	6.0
2	B	136	GLY	6.0
2	B	74	THR	5.9

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Mol	Chain	Res	Type	RSRZ
2	B	90	THR	5.9
2	B	91	SER	5.8
2	B	85	LEU	5.4
2	B	203	PRO	5.3
2	B	72	ALA	5.3
1	A	203	GLY	5.1
2	B	92	SER	5.1
2	B	43	ALA	5.0
1	A	3	SER	4.9
2	B	165	GLY	4.9
1	A	223	GLN	4.8
2	B	223	ASP	4.6
2	B	133	ASP	4.6
2	B	52	GLN	4.6
2	B	86	PRO	4.5
2	B	22	GLY	4.5
2	B	163	GLY	4.5
2	B	166	ALA	4.5
2	B	61	ASP	4.4
2	B	21	ARG	4.4
2	B	16	ALA	4.3
2	B	89	ASP	4.2
2	B	205	PHE	4.2
1	A	4	ASP	4.1
2	B	222	SER	4.1
1	A	201	LYS	4.1
2	B	17	LEU	4.1
2	B	73	PRO	4.1
2	B	20	ALA	4.0
1	A	213	ASN	3.9
1	A	216	GLU	3.9
2	B	12	GLU	3.9
2	B	79	VAL	3.8
1	A	207	PHE	3.7
2	B	13	SER	3.7
2	B	202	GLU	3.6
2	B	24	GLU	3.6
2	B	35	ASP	3.5
1	A	222	LEU	3.5
1	A	168	ALA	3.4
2	B	137	HIS	3.4
2	B	116	ASN	3.4

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Mol	Chain	Res	Type	RSRZ
2	B	118	VAL	3.4
2	B	19	ALA	3.3
1	A	199	GLN	3.3
2	B	132	ALA	3.3
2	B	59	LEU	3.3
2	B	71	GLN	3.3
1	A	184	ARG	3.2
1	A	25	MET	3.2
1	A	219	ALA	3.2
1	A	178	ALA	3.1
1	A	221	ILE	3.1
2	B	62	GLU	3.1
1	A	220	LYS	3.1
1	A	214	GLY	3.1
2	B	32	ARG	3.1
2	B	15	ALA	3.0
1	A	166	LYS	3.0
2	B	34	GLU	3.0
2	B	18	LEU	3.0
2	B	153	HIS	3.0
2	B	178	ARG	2.9
2	B	134	GLU	2.9
1	A	204	LYS	2.9
2	B	103	ALA	2.8
1	A	211	ILE	2.8
1	A	59	LYS	2.8
1	A	212	ASP	2.7
1	A	28	GLY	2.7
1	A	170	GLY	2.7
2	B	175	LEU	2.7
2	B	187[A]	ARG	2.7
2	B	94	VAL	2.7
1	A	23	ILE	2.7
2	B	114	HIS	2.7
1	A	88	GLU	2.6
2	B	83	CYS	2.6
2	B	150	MET	2.5
1	A	197	ASN	2.5
1	A	92	LYS	2.5
2	B	206	GLY	2.5
1	A	217	ASP	2.5
2	B	60	GLU	2.4

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Mol	Chain	Res	Type	RSRZ
2	B	105	GLY	2.4
2	B	29	PHE	2.4
1	A	198	ALA	2.4
1	A	196	VAL	2.3
2	B	36	LEU	2.3
1	A	84	LYS	2.3
2	B	152	SER	2.3
2	B	70	HIS	2.3
1	A	181	GLY	2.3
2	B	82	TRP	2.3
2	B	14	LYS	2.2
1	A	206	ALA	2.2
1	A	210	SER	2.2
2	B	54	SER	2.2
1	A	215	ASN	2.2
2	B	28	CYS	2.2
2	B	98	LEU	2.2
1	A	19	ASP	2.2
2	B	33	LEU	2.2
1	A	171	MET	2.2
2	B	180	GLU	2.1
1	A	102	LEU	2.1
1	A	218	LEU	2.1
2	B	199	ARG	2.1
2	B	25	GLU	2.1
1	A	69	ILE	2.1
1	A	15	ALA	2.1
2	B	84	SER	2.1
2	B	57	TYR	2.1
2	B	201	ALA	2.1
2	B	69	LEU	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 ⓘ

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
5	MG	A	308	1/1	0.19	0.65	167,167,167,167	0
4	EDO	A	306	4/4	0.64	0.33	69,72,81,90	0
4	EDO	A	307	4/4	0.74	0.35	77,85,87,88	0
7	PGE	A	310	10/10	0.74	0.33	57,75,99,99	0
3	SO4	A	301	5/5	0.76	0.18	86,91,101,101	0
3	SO4	B	301	5/5	0.77	0.16	84,86,94,98	0
4	EDO	A	304	4/4	0.79	0.24	50,55,57,76	0
4	EDO	A	305	4/4	0.81	0.28	66,69,70,78	0
4	EDO	B	303	4/4	0.82	0.20	48,52,53,58	0
6	PEG	A	309	7/7	0.82	0.28	56,78,86,90	0
4	EDO	B	305	4/4	0.82	0.23	57,58,67,68	0
8	PG4	A	311	13/13	0.82	0.32	56,89,101,108	0
4	EDO	A	302	4/4	0.83	0.31	61,70,72,76	0
4	EDO	A	303	4/4	0.84	0.33	75,90,95,103	0
5	MG	B	306	1/1	0.85	0.16	63,63,63,63	0
4	EDO	B	302	4/4	0.85	0.23	59,68,77,78	0
4	EDO	B	304	4/4	0.93	0.12	47,47,47,47	4

6.5 Other polymers ⓘ

There are no such residues in this entry.