



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 08:12 AM UTC

PDB ID : 2RCC / pdb_00002rcc
Title : Crystal structure of putative class I ribonucleotide reductase (NP_241368.1) from *Bacillus halodurans* at 1.90 Å resolution
Authors : Joint Center for Structural Genomics (JCSG)
Deposited on : 2007-09-19
Resolution : 1.90 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

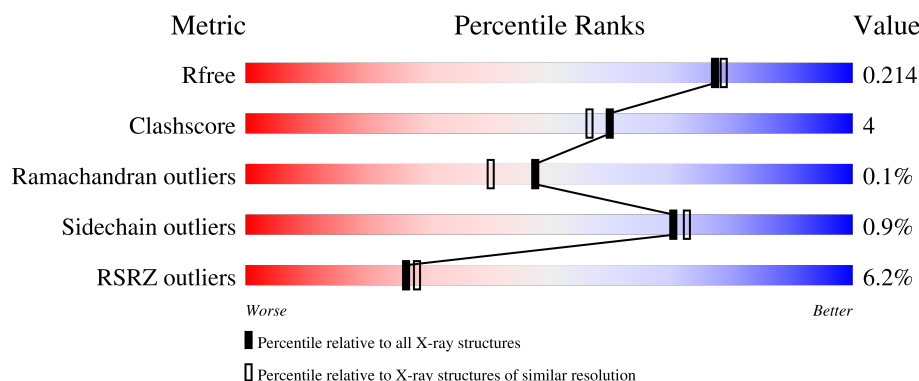
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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	7789 (1.90-1.90)
Clashscore	190562	8410 (1.90-1.90)
Ramachandran outliers	187476	8333 (1.90-1.90)
Sidechain outliers	187428	8333 (1.90-1.90)
RSRZ outliers	180081	7790 (1.90-1.90)

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	346	5% 81% 9% 10%
1	B	346	% 79% 19%
1	C	346	10% 79% 10% 10%

2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 7885 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.

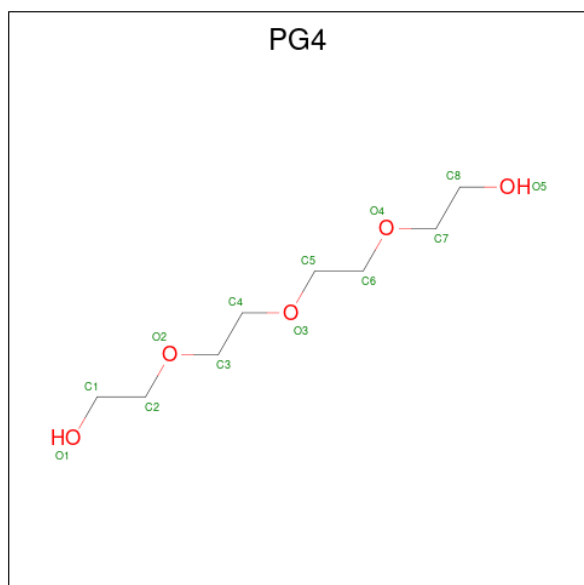
- Molecule 1 is a protein called Ribonucleoside-diphosphate reductase subunit beta.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	313	Total	C	N	O	Se	0	14	0
			2596	1698	399	487	12			
1	B	280	Total	C	N	O	Se	0	5	0
			2322	1526	350	434	12			
1	C	311	Total	C	N	O	Se	0	7	0
			2547	1656	397	484	10			

There are 3 discrepancies between the modelled and reference sequences:

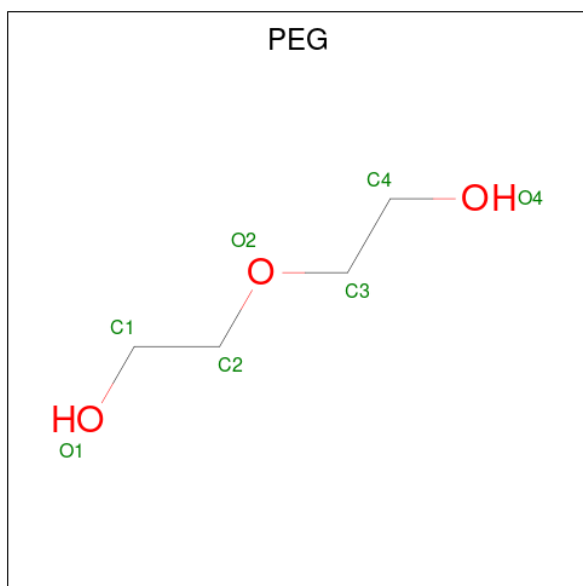
Chain	Residue	Modelled	Actual	Comment	Reference
A	0	GLY	-	expression tag	UNP Q9KFH7
B	0	GLY	-	expression tag	UNP Q9KFH7
C	0	GLY	-	expression tag	UNP Q9KFH7

- Molecule 2 is TETRAETHYLENE GLYCOL (CCD ID: PG4) (formula: $C_8H_{18}O_5$).



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

- Molecule 3 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: $C_4H_{10}O_3$).

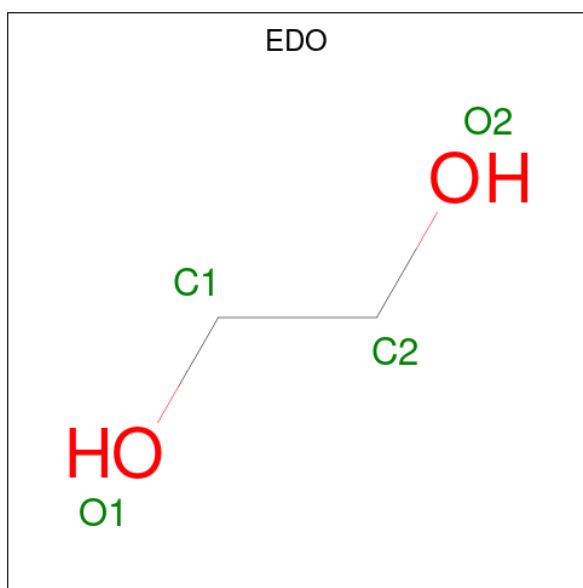


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			7	4	3		
3	B	1	Total	C	O	0	0
			6	4	2		
3	B	1	Total	C	O	0	0
			4	2	2		
3	C	1	Total	C	O	0	0
			5	3	2		
3	C	1	Total	C	O	0	0
			5	3	2		
3	C	1	Total	C	O	0	0
			4	2	2		

- Molecule 4 is ZINC ION (CCD ID: ZN) (formula: Zn).

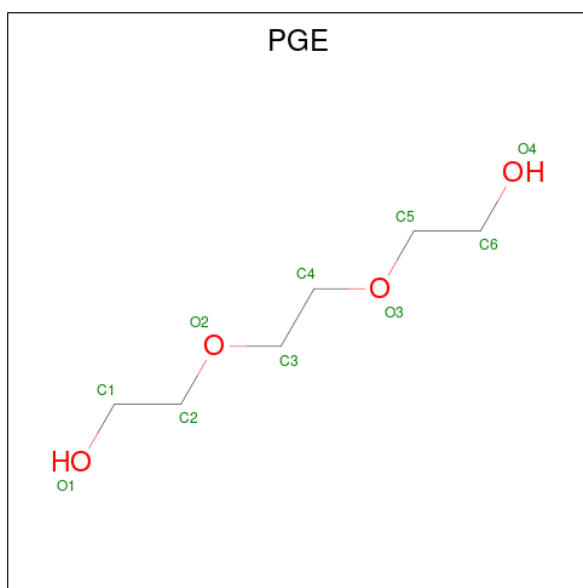
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	2	Total	Zn	0	0
			2	2		
4	C	2	Total	Zn	0	0
			2	2		

- Molecule 5 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: $C_2H_6O_2$).



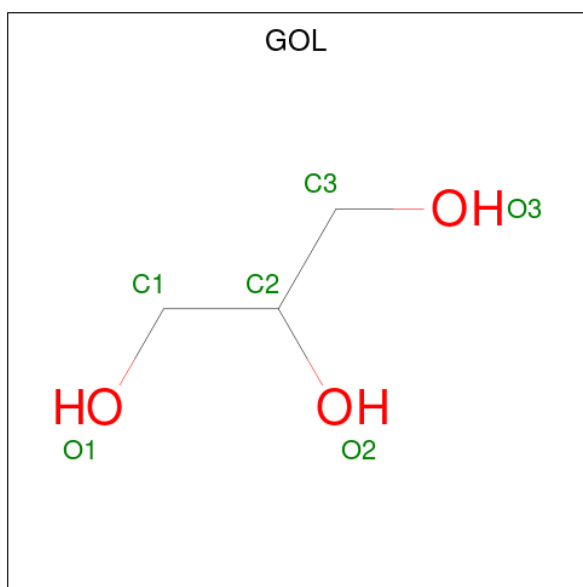
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	B	1	Total	C	O	0	0
			4	2	2		

- Molecule 6 is TRIETHYLENE GLYCOL (CCD ID: PGE) (formula: $C_6H_{14}O_4$).



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

- Molecule 7 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



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

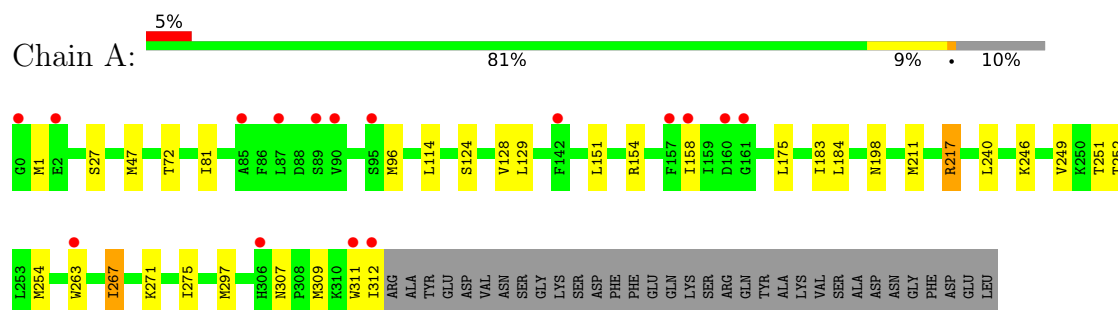
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	126	Total	O	0	0
			126	126		
8	B	104	Total	O	0	0
			104	104		
8	C	110	Total	O	0	0
			110	110		

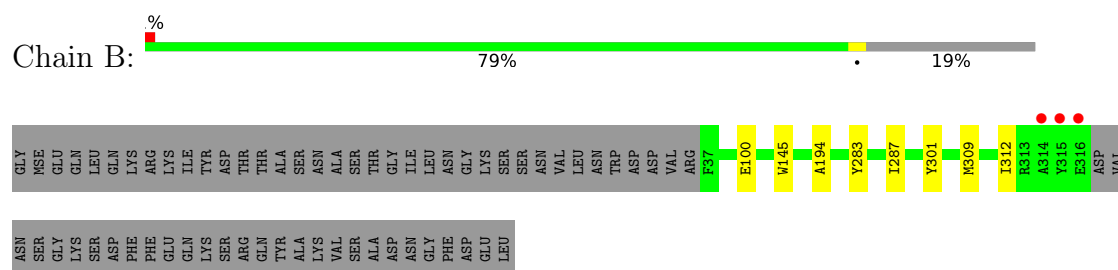
3 Residue-property plots [i](#)

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.

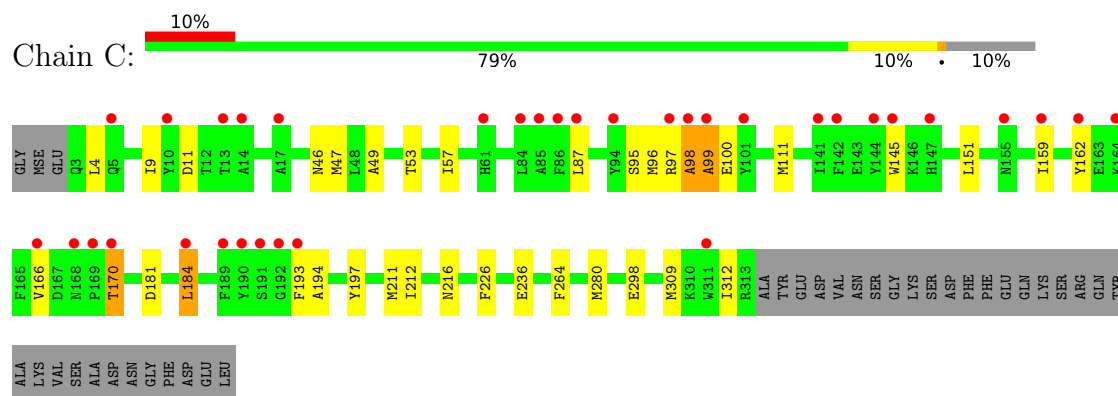
- Molecule 1: Ribonucleoside-diphosphate reductase subunit beta



- Molecule 1: Ribonucleoside-diphosphate reductase subunit beta



- Molecule 1: Ribonucleoside-diphosphate reductase subunit beta



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	175.26Å 72.78Å 111.77Å 90.00° 124.90° 90.00°	Depositor
Resolution (Å)	28.50 – 1.90 28.50 – 1.90	Depositor EDS
% Data completeness (in resolution range)	99.5 (28.50-1.90) 99.5 (28.50-1.90)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.13 (at 1.91Å)	Xtriage
Refinement program	REFMAC 5.3.0040, PHENIX	Depositor
R, R_{free}	0.183 , 0.215 0.187 , 0.214	Depositor DCC
R_{free} test set	4538 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	28.8	Xtriage
Anisotropy	0.123	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 51.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	7885	wwPDB-VP
Average B, all atoms (Å ²)	24.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.78% 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: PEG, ZN, PG4, GOL, EDO, PGE

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	0.89	0/2690	1.02	4/3638 (0.1%)
1	B	0.93	0/2391	1.00	2/3231 (0.1%)
1	C	1.06	4/2621 (0.2%)	1.12	4/3549 (0.1%)
All	All	0.96	4/7702 (0.1%)	1.05	10/10418 (0.1%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	95	SER	C-O	-7.01	1.15	1.24
1	C	47	MSE	SE-CE	-6.23	1.76	1.95
1	C	159	ILE	CA-CB	5.40	1.61	1.54
1	C	170	THR	CA-C	5.22	1.59	1.52

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	98	ALA	N-CA-C	-7.24	99.32	110.10
1	A	217	ARG	CG-CD-NE	6.47	126.24	112.00
1	A	267	ILE	N-CA-C	5.79	116.79	111.81
1	A	217	ARG	CD-NE-CZ	5.63	132.29	124.40
1	C	236	GLU	N-CA-C	5.58	117.44	111.36
1	C	100	GLU	N-CA-CB	5.43	119.67	110.49
1	C	96	MSE	N-CA-C	-5.42	105.45	111.36
1	B	301	TYR	CA-C-N	5.18	124.98	119.28
1	B	301	TYR	C-N-CA	5.18	124.98	119.28
1	A	217	ARG	NE-CZ-NH1	5.00	126.50	121.50

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	2596	0	2505	36	0
1	B	2322	0	2234	5	0
1	C	2547	0	2428	24	0
2	A	13	0	18	0	0
3	A	7	0	10	0	0
3	B	10	0	12	3	0
3	C	14	0	15	1	0
4	B	2	0	0	0	0
4	C	2	0	0	0	0
5	B	4	0	6	0	0
6	B	10	0	14	0	0
7	B	12	0	16	0	0
7	C	6	0	8	1	0
8	A	126	0	0	1	0
8	B	104	0	0	0	0
8	C	110	0	0	0	0
All	All	7885	0	7266	64	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 (64) 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:154[A]:ARG:HD2	1:A:263[A]:TRP:NE1	1.46	1.28
1:A:154[A]:ARG:HD2	1:A:263[A]:TRP:CE2	1.87	1.09
1:A:128:VAL:HG23	1:A:211:MSE:HE1	1.48	0.96
1:C:87:LEU:HB3	1:C:184:LEU:HD11	1.53	0.90
1:A:154[A]:ARG:CD	1:A:263[A]:TRP:NE1	2.36	0.87
1:A:47:MSE:HE1	1:A:114:LEU:HD12	1.61	0.82
1:C:11:ASP:OD2	3:C:403:PEG:C3	2.37	0.72
1:A:96:MSE:HE2	3:B:406:PEG:C4	2.19	0.72
1:C:98:ALA:O	1:C:99:ALA:HB3	1.90	0.71
1:C:98:ALA:O	1:C:99:ALA:CB	2.41	0.69
1:A:72[A]:THR:HG21	1:A:271:LYS:HB3	1.75	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:309:MSE:HE2	1:B:312:ILE:HD11	1.74	0.68
1:A:124[A]:SER:HB3	1:A:211:MSE:HE3	1.76	0.68
1:A:154[A]:ARG:HD2	1:A:263[A]:TRP:CD1	2.30	0.66
1:C:87:LEU:HD22	1:C:184:LEU:HD13	1.76	0.65
1:C:309:MSE:HE2	1:C:312:ILE:HD11	1.78	0.65
1:A:128:VAL:HG23	1:A:211:MSE:CE	2.26	0.65
1:A:128:VAL:CG2	1:A:211:MSE:HE1	2.26	0.63
1:A:309:MSE:HE2	1:A:312[A]:ILE:HG13	1.80	0.63
1:A:263[B]:TRP:CZ2	1:A:267:ILE:HD12	2.35	0.61
1:A:154[A]:ARG:HD2	1:A:263[A]:TRP:HE1	1.57	0.61
1:C:4:LEU:HG	1:C:170:THR:HA	1.82	0.60
1:C:309:MSE:CE	1:C:312:ILE:HD11	2.33	0.58
1:A:309:MSE:HE3	1:A:311:TRP:CZ2	2.39	0.57
1:A:251:THR:HA	1:A:254:MSE:HE2	1.87	0.56
1:C:49:ALA:HB2	7:C:402:GOL:H2	1.87	0.56
1:A:124[B]:SER:HB2	1:A:211:MSE:HE3	1.88	0.56
1:C:87:LEU:HD22	1:C:184:LEU:CD1	2.36	0.55
1:A:307:ASN:HD21	1:A:312[B]:ILE:CG2	2.20	0.55
1:B:194:ALA:HB1	1:B:309:MSE:HE1	1.88	0.55
1:A:263[B]:TRP:CE2	1:A:267:ILE:HD12	2.41	0.54
1:C:193:PHE:CD1	1:C:212:ILE:HG23	2.43	0.54
1:A:81:ILE:HG23	1:A:129:LEU:HD13	1.89	0.53
1:C:309:MSE:HE2	1:C:312:ILE:CD1	2.37	0.53
1:A:96:MSE:CE	3:B:406:PEG:C4	2.90	0.49
1:C:97[B]:ARG:HD3	1:C:166:VAL:HG22	1.93	0.49
1:A:158:ILE:HD12	1:A:184:LEU:HD21	1.95	0.48
1:B:283:TYR:CE2	1:B:287[B]:ILE:HD11	2.48	0.48
1:C:162:TYR:O	1:C:166:VAL:HG23	2.13	0.48
1:A:128:VAL:CG2	1:A:211:MSE:CE	2.90	0.48
1:A:249:VAL:HG11	1:A:297[B]:MSE:HG3	1.95	0.47
1:C:145:TRP:HA	1:C:151:LEU:HD23	1.96	0.46
1:C:111:MSE:HE1	1:C:226:PHE:CE1	2.50	0.46
1:C:216:ASN:C	1:C:216:ASN:HD22	2.23	0.45
1:A:307:ASN:HD21	1:A:312[B]:ILE:HG21	1.81	0.45
1:C:57:ILE:HD12	1:C:211:MSE:HE2	1.99	0.45
1:A:198:ASN:HB2	1:A:275[A]:ILE:HD11	1.98	0.44
1:A:249:VAL:HG11	1:A:297[A]:MSE:HG3	2.01	0.43
1:C:264:PHE:CE1	1:C:280:MSE:HE3	2.54	0.43
1:A:175:LEU:HD22	1:A:240:LEU:HD13	2.01	0.42
1:C:97[B]:ARG:CD	1:C:166:VAL:HG13	2.49	0.42
1:A:47:MSE:HE3	8:A:352:HOH:O	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:154[A]:ARG:CD	1:A:263[A]:TRP:HE1	2.25	0.42
1:A:27:SER:HB2	1:B:145:TRP:CZ2	2.54	0.42
1:C:194:ALA:HB1	1:C:309:MSE:HE1	2.02	0.42
1:C:193:PHE:HB3	1:C:197:TYR:CE2	2.55	0.41
1:A:309:MSE:O	1:A:312[B]:ILE:HG22	2.21	0.41
1:B:100:GLU:HG2	3:B:406:PEG:C4	2.50	0.41
1:C:87:LEU:CB	1:C:184:LEU:HD11	2.37	0.41
1:C:181:ASP:OD1	1:C:181:ASP:C	2.63	0.41
1:A:246:LYS:HG2	1:A:297[A]:MSE:SE	2.70	0.41
1:A:151:LEU:HA	1:A:263[A]:TRP:CZ2	2.56	0.41
1:A:183:ILE:CD1	1:A:252:THR:HG22	2.51	0.40
1:A:309:MSE:HE2	1:A:312[A]:ILE:CG1	2.49	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	324/346 (94%)	318 (98%)	6 (2%)	0	100	100
1	B	283/346 (82%)	280 (99%)	3 (1%)	0	100	100
1	C	316/346 (91%)	306 (97%)	9 (3%)	1 (0%)	36	29
All	All	923/1038 (89%)	904 (98%)	18 (2%)	1 (0%)	48	40

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	99	ALA

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	280/302 (93%)	278 (99%)	2 (1%)	76	78
1	B	249/302 (82%)	249 (100%)	0	100	100
1	C	272/302 (90%)	267 (98%)	5 (2%)	51	50
All	All	801/906 (88%)	794 (99%)	7 (1%)	70	73

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MSE
1	A	217	ARG
1	C	9	ILE
1	C	46	ASN
1	C	53	THR
1	C	184	LEU
1	C	298	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	307	ASN
1	B	213	ASN
1	C	122	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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 16 ligands modelled in this entry, 4 are monoatomic - leaving 12 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	$\# Z > 2$
7	GOL	B	405	-	5,5,5	0.53	0	5,5,5	0.40	0
3	PEG	A	347	-	6,6,6	0.55	0	5,5,5	0.38	0
3	PEG	C	405	-	3,3,6	0.30	0	2,2,5	0.44	0
3	PEG	C	403	-	4,4,6	0.17	0	3,3,5	0.57	0
2	PG4	A	346	-	12,12,12	0.48	0	11,11,11	0.45	0
5	EDO	B	402	-	3,3,3	0.38	0	2,2,2	1.06	0
7	GOL	B	404	-	5,5,5	0.55	0	5,5,5	0.56	0
3	PEG	B	406	-	5,5,6	0.63	0	4,4,5	0.41	0
3	PEG	C	404	-	4,4,6	0.44	0	3,3,5	0.23	0
6	PGE	B	403	-	9,9,9	0.43	0	8,8,8	0.45	0
7	GOL	C	402	-	5,5,5	0.81	0	5,5,5	1.22	0
3	PEG	B	407	-	3,3,6	0.28	0	2,2,5	0.54	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
7	GOL	B	405	-	-	0/4/4/4	-
3	PEG	A	347	-	-	2/4/4/4	-
3	PEG	C	405	-	-	1/1/1/4	-
3	PEG	C	403	-	-	0/2/2/4	-
2	PG4	A	346	-	-	1/10/10/10	-
5	EDO	B	402	-	-	0/1/1/1	-
7	GOL	B	404	-	-	2/4/4/4	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	PEG	B	406	-	-	2/3/3/4	-
3	PEG	C	404	-	-	1/2/2/4	-
6	PGE	B	403	-	-	2/7/7/7	-
7	GOL	C	402	-	-	2/4/4/4	-
3	PEG	B	407	-	-	1/1/1/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (14) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	B	404	GOL	O1-C1-C2-C3
7	C	402	GOL	O1-C1-C2-C3
2	A	346	PG4	O4-C7-C8-O5
6	B	403	PGE	O3-C5-C6-O4
3	A	347	PEG	O2-C3-C4-O4
3	C	404	PEG	O1-C1-C2-O2
7	B	404	GOL	O1-C1-C2-O2
7	C	402	GOL	O1-C1-C2-O2
3	B	406	PEG	O1-C1-C2-O2
6	B	403	PGE	O1-C1-C2-O2
3	B	407	PEG	O1-C1-C2-O2
3	A	347	PEG	C4-C3-O2-C2
3	C	405	PEG	O1-C1-C2-O2
3	B	406	PEG	C1-C2-O2-C3

There are no ring outliers.

3 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	403	PEG	1	0
3	B	406	PEG	3	0
7	C	402	GOL	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	302/346 (87%)	0.14	16 (5%) 32 34	10, 21, 41, 62	13 (4%)
1	B	270/346 (78%)	-0.25	3 (1%) 78 80	10, 19, 32, 59	3 (1%)
1	C	301/346 (86%)	0.61	35 (11%) 9 10	5, 24, 37, 53	7 (2%)
All	All	873/1038 (84%)	0.18	54 (6%) 26 28	5, 21, 38, 62	23 (2%)

All (54) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	99	ALA	6.7
1	A	85	ALA	5.4
1	C	98	ALA	4.7
1	C	166	VAL	4.6
1	A	0	GLY	4.5
1	C	193	PHE	4.5
1	C	159	ILE	4.4
1	C	144	TYR	4.2
1	C	190	TYR	3.8
1	C	170	THR	3.8
1	A	90	VAL	3.7
1	C	189	PHE	3.4
1	A	95	SER	3.4
1	C	87	LEU	3.4
1	A	87	LEU	3.3
1	C	17	ALA	3.2
1	C	101	TYR	3.1
1	C	191	SER	3.1
1	B	314	ALA	3.1
1	C	94	TYR	2.9
1	C	192	GLY	2.9
1	A	157	PHE	2.8
1	C	141	ILE	2.8

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Mol	Chain	Res	Type	RSRZ
1	C	311	TRP	2.8
1	A	89	SER	2.7
1	B	316	GLU	2.7
1	C	145	TRP	2.7
1	C	162	TYR	2.7
1	C	85	ALA	2.6
1	A	263[A]	TRP	2.6
1	C	155	ASN	2.6
1	A	160	ASP	2.5
1	A	158	ILE	2.5
1	B	315	TYR	2.5
1	C	142	PHE	2.4
1	C	5	GLN	2.4
1	C	10	TYR	2.4
1	C	61[A]	HIS	2.4
1	C	147	HIS	2.4
1	A	306	HIS	2.3
1	C	97[A]	ARG	2.2
1	C	169	PRO	2.2
1	C	84	LEU	2.2
1	C	164	LYS	2.2
1	C	184	LEU	2.2
1	A	312[A]	ILE	2.2
1	C	14	ALA	2.2
1	A	142	PHE	2.1
1	C	168	ASN	2.1
1	A	161	GLY	2.1
1	A	2	GLU	2.1
1	A	311	TRP	2.1
1	C	86	PHE	2.0
1	C	13	THR	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
3	PEG	C	404	5/7	0.74	0.27	52,52,59,60	5
6	PGE	B	403	10/10	0.79	0.22	43,70,77,79	0
3	PEG	A	347	7/7	0.80	0.20	47,58,63,68	0
7	GOL	B	404	6/6	0.82	0.18	52,64,66,71	0
3	PEG	C	403	5/7	0.83	0.17	47,54,57,59	0
3	PEG	B	407	4/7	0.86	0.13	45,45,55,55	0
7	GOL	B	405	6/6	0.86	0.15	35,51,52,55	0
7	GOL	C	402	6/6	0.88	0.12	30,44,48,60	0
3	PEG	C	405	4/7	0.89	0.14	54,54,55,62	0
2	PG4	A	346	13/13	0.90	0.12	39,47,59,60	0
3	PEG	B	406	6/7	0.91	0.26	20,29,51,56	0
5	EDO	B	402	4/4	0.94	0.11	26,32,35,40	0
4	ZN	C	400	1/1	0.97	0.11	52,52,52,52	1
4	ZN	C	401	1/1	0.99	0.12	40,40,40,40	1
4	ZN	B	401	1/1	0.99	0.05	27,27,27,27	1
4	ZN	B	400	1/1	1.00	0.08	38,38,38,38	1

6.5 Other polymers

There are no such residues in this entry.