



# Full wwPDB X-ray Structure Validation Report ⓘ

Dec 15, 2024 – 06:26 PM EST

PDB ID : 5DC2  
Title : X-RAY CRYSTAL STRUCTURE OF A ENZYMATICALLY DEGRADED  
BIAPENEM-ADDUCT OF L,D-TRANSPEPTIDASE 2 FROM MYCOBAC-  
TERIUM TUBERCULOSIS  
Authors : Pan, Y.; Basta, L.; Lamichhane, G.; Bianchet, M.A.  
Deposited on : 2015-08-23  
Resolution : 2.18 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](mailto: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>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.21
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.004 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.40

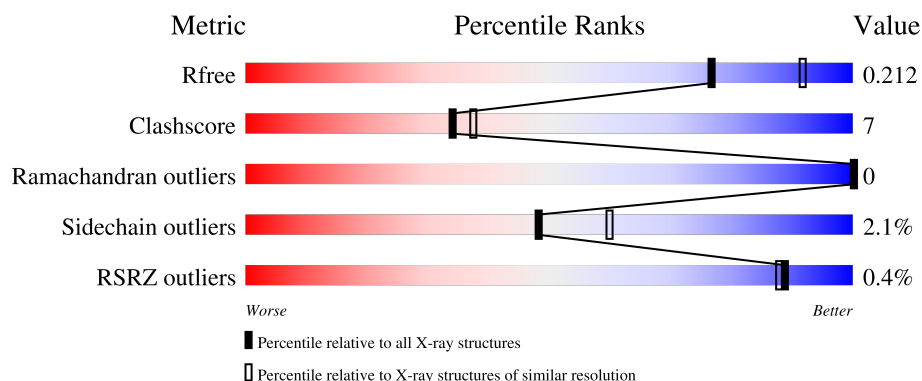
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*



The reported resolution of this entry is 2.18 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))
$R_{free}$	164625	8336 (2.20-2.16)
Clashscore	180529	9404 (2.20-2.16)
Ramachandran outliers	177936	9297 (2.20-2.16)
Sidechain outliers	177891	9297 (2.20-2.16)
RSRZ outliers	164620	8337 (2.20-2.16)

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  $\geq 3$ , 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	353	 88% 11% .
1	B	353	 88% 11% .

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
3	SO4	B	506	-	-	X	-
4	PEG	A	509	-	-	X	-

## 2 Entry composition [i](#)

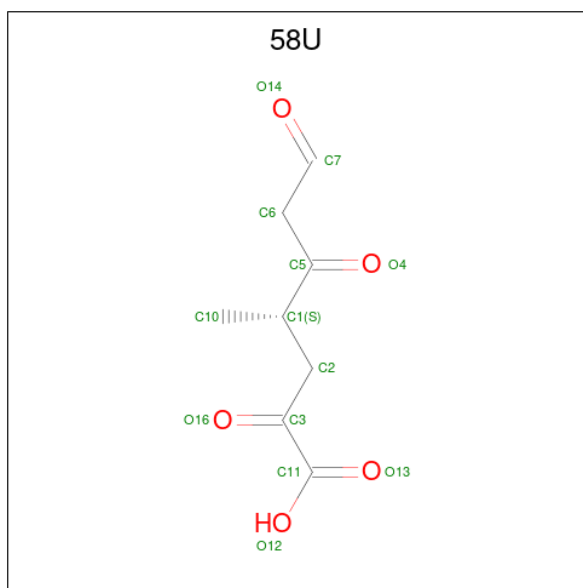
There are 8 unique types of molecules in this entry. The entry contains 6265 atoms, of which 58 are hydrogens and 0 are deuteriums.

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 L,D-transpeptidase 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	352	Total	C	N	O	S	0	3	0
			2687	1685	473	521	8			
1	B	353	Total	C	N	O	S	0	7	0
			2717	1699	480	529	9			

- Molecule 2 is (4S)-4-methyl-2,5,7-trioxoheptanoic acid (three-letter code: 58U) (formula: C<sub>8</sub>H<sub>10</sub>O<sub>5</sub>).



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

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



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

- Molecule 4 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: C<sub>4</sub>H<sub>10</sub>O<sub>3</sub>).



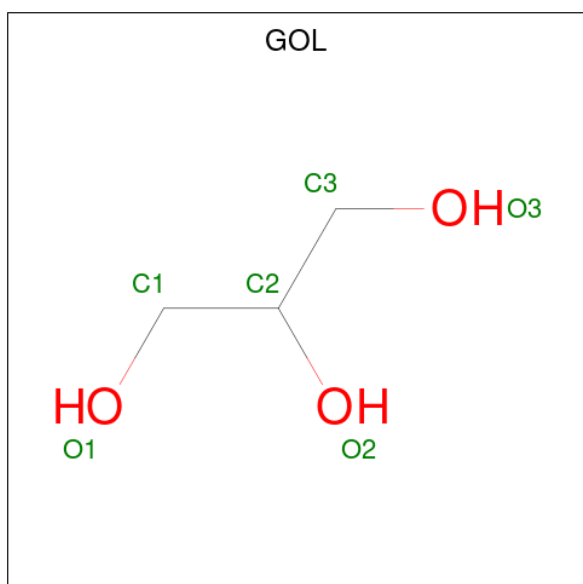
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			4	2	2		
4	A	1	Total	C	O	0	0
			4	2	2		
4	A	1	Total	C	O	0	0
			4	2	2		
4	A	1	Total	C	O	0	0
			7	4	3		
4	B	1	Total	C	O	0	0
			4	2	2		
4	B	1	Total	C	O	0	0
			4	2	2		
4	B	1	Total	C	O	0	0
			4	2	2		
4	B	1	Total	C	O	0	0
			4	2	2		

- Molecule 5 is TRIETHYLENE GLYCOL (three-letter code: PGE) (formula: C<sub>6</sub>H<sub>14</sub>O<sub>4</sub>).



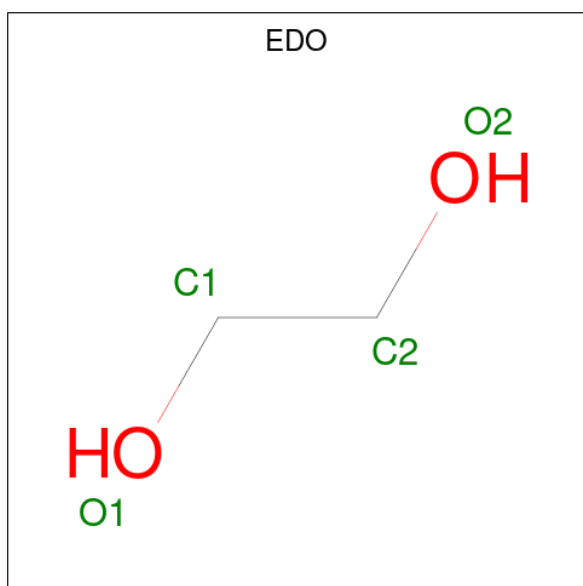
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C O 10 6 4	0	0
5	A	1	Total C H O 24 6 14 4	0	0
5	B	1	Total C O 10 6 4	0	0
5	B	1	Total C H O 24 6 14 4	0	0
5	B	1	Total C H O 24 6 14 4	0	0

- Molecule 6 is GLYCEROL (three-letter code: GOL) (formula:  $C_3H_8O_3$ ).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total C O 6 3 3	0	0
6	A	1	Total C O 6 3 3	0	0
6	A	1	Total C H O 14 3 8 3	0	0
6	B	1	Total C O 6 3 3	0	0
6	B	1	Total C H O 14 3 8 3	0	0

- Molecule 7 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula:  $C_2H_6O_2$ ).



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

- Molecule 8 is water.

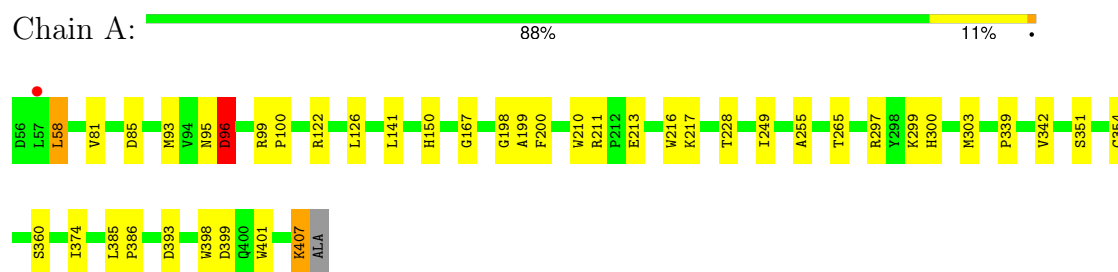
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	A	300	Total O 300 300	0	0
8	B	302	Total O 302 302	0	0



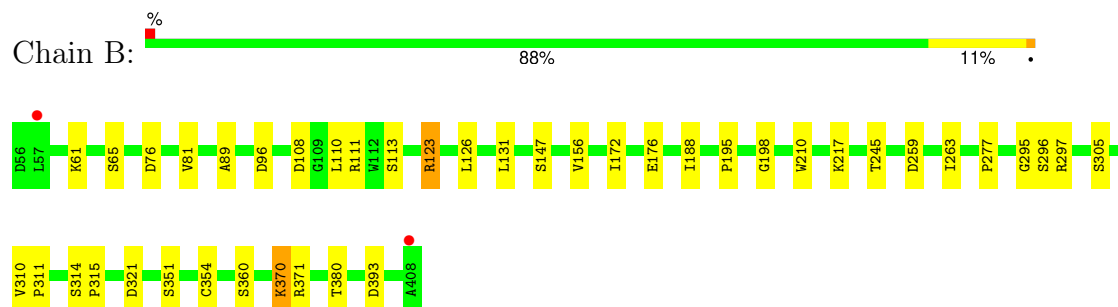
### 3 Residue-property plots

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: L,D-transpeptidase 2



- Molecule 1: L,D-transpeptidase 2



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	60.82Å 93.35Å 75.24Å 90.00° 92.61° 90.00°	Depositor
Resolution (Å)	37.02 – 2.18 37.02 – 2.18	Depositor EDS
% Data completeness (in resolution range)	96.6 (37.02-2.18) 96.6 (37.02-2.18)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.06	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.63 (at 2.05Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, $R_{free}$	0.160 , 0.208 0.163 , 0.212	Depositor DCC
$R_{free}$ test set	2108 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	28.2	Xtriage
Anisotropy	0.176	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 51.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.095 for h,-k,-l	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	6265	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.83% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: EDO, GOL, PGE, 58U, PEG, SO4

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	0.43	0/2754	0.56	1/3770 (0.0%)
1	B	0.42	0/2795	0.57	1/3822 (0.0%)
All	All	0.43	0/5549	0.56	2/7592 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	123	ARG	NE-CZ-NH1	-6.39	117.11	120.30
1	A	96	ASP	CB-CG-OD2	6.19	123.87	118.30

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	2687	0	2586	41	1
1	B	2717	0	2603	38	5
2	A	13	0	0	4	0
2	B	13	0	0	3	0
3	A	25	0	0	1	0
3	B	25	0	0	3	4
4	A	19	0	25	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	20	0	25	1	0
5	A	20	14	28	1	0
5	B	30	28	42	6	0
6	A	18	8	24	1	0
6	B	12	8	16	0	0
7	A	3	0	3	0	0
7	B	3	0	3	0	0
8	A	300	0	0	8	2
8	B	302	0	0	8	2
All	All	6207	58	5355	82	7

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 7.

All (82) 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:111[B]:ARG:CA	1:B:111[B]:ARG:N	1.80	1.44
1:A:199:ALA:HB1	4:A:509:PEG:H41	1.41	1.02
1:A:200:PHE:H	4:A:509:PEG:H32	1.24	1.01
1:B:297[B]:ARG:NH2	8:B:602:HOH:O	1.92	1.01
1:B:76:ASP:OD2	8:B:601:HOH:O	1.87	0.92
5:B:512:PGE:O4	8:B:603:HOH:O	1.95	0.83
1:B:176[A]:GLU:OE1	8:B:604:HOH:O	1.96	0.82
1:A:210:TRP:HE1	4:A:510:PEG:H22	1.44	0.81
1:A:200:PHE:H	4:A:509:PEG:C3	2.00	0.75
1:B:172:ILE:HD13	1:B:188:ILE:HD13	1.69	0.74
3:A:502:SO4:O3	8:A:601:HOH:O	2.04	0.74
1:B:351:SER:HB2	2:B:501:58U:C2	2.19	0.73
1:A:217:LYS:NZ	8:A:602:HOH:O	2.15	0.73
1:A:93:MET:HE3	1:A:126[A]:LEU:HD21	1.70	0.72
1:A:200:PHE:N	4:A:509:PEG:H32	2.04	0.72
1:B:111[B]:ARG:N	1:B:111[B]:ARG:CB	2.57	0.67
1:A:81:VAL:CG2	1:A:126[B]:LEU:HD21	2.24	0.67
1:B:108:ASP:OD2	1:B:111[A]:ARG:NH2	2.29	0.66
6:A:513:GOL:O2	8:A:603:HOH:O	2.15	0.65
1:A:95:ASN:HD21	1:A:99:ARG:HB3	1.61	0.65
1:A:385:LEU:HD12	1:A:386:PRO:HD2	1.83	0.61
1:A:95:ASN:ND2	8:A:604:HOH:O	2.24	0.61
1:B:198:GLY:HA3	1:B:210:TRP:CH2	2.37	0.59
1:A:210:TRP:HE1	4:A:510:PEG:C2	2.13	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:122:ARG:NH2	8:A:601:HOH:O	2.35	0.58
1:B:198:GLY:HA3	1:B:210:TRP:CZ2	2.38	0.57
1:A:58:LEU:HD13	1:A:85:ASP:HB3	1.86	0.57
3:B:506:SO4:O2	8:B:605:HOH:O	2.18	0.56
1:A:81:VAL:HG21	1:A:126[B]:LEU:HD21	1.89	0.53
1:A:213:GLU:HB2	1:A:398:TRP:CE2	2.44	0.53
1:A:198:GLY:HA3	1:A:210:TRP:CH2	2.44	0.52
1:B:176[A]:GLU:OE1	8:B:606:HOH:O	2.19	0.52
1:A:198:GLY:HA3	1:A:210:TRP:CZ2	2.44	0.52
1:A:351:SER:HB2	2:A:501:58U:C2	2.40	0.52
1:A:141:LEU:HD12	1:A:141:LEU:N	2.24	0.51
1:B:311:PRO:HB2	1:B:314:SER:OG	2.10	0.51
1:B:354:CYS:HB2	2:B:501:58U:C1	2.40	0.51
1:A:58:LEU:HD12	1:A:58:LEU:H	1.76	0.50
1:B:360[A]:SER:HB3	3:B:506:SO4:O3	2.14	0.48
1:A:96:ASP:OD2	1:A:96:ASP:N	2.40	0.48
1:A:303:MET:HE3	2:A:501:58U:C10	2.43	0.48
1:B:370:LYS:HE3	8:B:611:HOH:O	2.14	0.48
1:A:399:ASP:HB3	1:B:65:SER:HA	1.95	0.47
1:B:314:SER:HB3	1:B:315:PRO:HD2	1.95	0.47
1:A:354:CYS:HB2	2:A:501:58U:C1	2.44	0.47
1:B:371:ARG:NE	3:B:502:SO4:O4	2.42	0.47
1:B:156:VAL:HG11	1:B:245:THR:CG2	2.45	0.47
1:B:156:VAL:HG11	1:B:245:THR:HG22	1.97	0.46
1:A:216:TRP:HB3	1:A:249:ILE:HG13	1.97	0.46
5:A:511:PGE:H42	8:A:638:HOH:O	2.16	0.46
1:A:167:GLY:HA3	1:A:374:ILE:HD11	1.96	0.46
1:A:399:ASP:CB	1:B:65:SER:HA	2.45	0.46
1:B:111[B]:ARG:NH2	1:B:113:SER:HB2	2.31	0.46
1:A:339:PRO:O	1:A:342:VAL:HG22	2.16	0.46
1:B:354:CYS:HB2	2:B:501:58U:C5	2.46	0.45
1:A:213:GLU:HA	1:A:398:TRP:CE3	2.52	0.45
1:B:297[B]:ARG:HH11	1:B:297[B]:ARG:HG3	1.81	0.45
1:A:407:LYS:NZ	1:B:61:LYS:HE2	2.31	0.45
1:A:93:MET:HE3	1:A:126[A]:LEU:CD2	2.45	0.44
1:B:259:ASP:HB2	1:B:380:THR:HG22	1.99	0.44
1:A:255:ALA:HA	1:A:265:THR:O	2.17	0.44
1:A:93:MET:HE2	1:A:126[A]:LEU:HG	2.00	0.44
1:B:296:SER:H	5:B:513:PGE:H12	1.83	0.43
1:A:213:GLU:HG3	1:A:398:TRP:CG	2.54	0.43
1:B:110:LEU:C	1:B:111[B]:ARG:CA	2.75	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:300:HIS:ND1	8:A:610:HOH:O	2.35	0.42
1:A:211:ARG:HG2	1:A:401:TRP:CZ2	2.55	0.42
1:A:299:LYS:NZ	8:A:620:HOH:O	2.50	0.42
1:B:89:ALA:HB2	1:B:131:LEU:HG	2.01	0.42
1:A:99:ARG:HA	1:A:100:PRO:HD3	1.91	0.42
1:B:156:VAL:CG1	1:B:245:THR:HG21	2.50	0.42
1:B:295:GLY:HA3	5:B:513:PGE:C1	2.50	0.42
4:B:510:PEG:H42	5:B:514:PGE:O4	2.20	0.41
1:A:93:MET:HB2	1:A:126[A]:LEU:HD23	2.02	0.41
1:B:263:ILE:HD13	1:B:277:PRO:HA	2.03	0.41
1:B:305:SER:HB2	1:B:310:VAL:HB	2.03	0.41
1:A:354:CYS:HB2	2:A:501:58U:C5	2.51	0.41
1:B:195:PRO:HD2	8:B:764:HOH:O	2.21	0.40
1:B:296:SER:H	5:B:513:PGE:C1	2.34	0.40
1:B:81:VAL:CG2	1:B:126:LEU:HD21	2.51	0.40
1:B:296:SER:N	5:B:513:PGE:H12	2.36	0.40

All (7) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:123:ARG:NH2	3:B:506:SO4:O1[1_556]	0.92	1.28
1:B:123:ARG:NH2	3:B:506:SO4:S[1_556]	1.69	0.51
8:A:827:HOH:O	8:B:654:HOH:O[2_557]	1.87	0.33
1:B:123:ARG:NH2	3:B:506:SO4:O3[1_556]	2.00	0.20
8:A:842:HOH:O	8:B:793:HOH:O[2_557]	2.03	0.17
1:B:123:ARG:CZ	3:B:506:SO4:O1[1_556]	2.07	0.13
1:A:150[A]:HIS:ND1	1:B:321:ASP:OD2[1_656]	2.17	0.03

## 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	353/353 (100%)	346 (98%)	7 (2%)	0	100	100
1	B	358/353 (101%)	347 (97%)	11 (3%)	0	100	100
All	All	711/706 (101%)	693 (98%)	18 (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	286/283 (101%)	279 (98%)	7 (2%)	44	54
1	B	290/283 (102%)	285 (98%)	5 (2%)	56	68
All	All	576/566 (102%)	564 (98%)	12 (2%)	48	60

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	58	LEU
1	A	96	ASP
1	A	228	THR
1	A	297	ARG
1	A	360	SER
1	A	393	ASP
1	A	407	LYS
1	B	96	ASP
1	B	147	SER
1	B	217	LYS
1	B	370	LYS
1	B	393	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 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 ⓘ

33 ligands are modelled in this entry.

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	PEG	B	510	-	3,3,6	0.40	0	2,2,5	0.36	0
5	PGE	B	512	-	9,9,9	0.43	0	8,8,8	0.39	0
5	PGE	A	512	-	9,9,9	0.49	0	8,8,8	0.23	0
4	PEG	A	507	-	3,3,6	0.44	0	2,2,5	0.27	0
3	SO4	A	505	-	4,4,4	0.23	0	6,6,6	0.12	0
3	SO4	A	502	-	4,4,4	0.25	0	6,6,6	0.24	0
3	SO4	A	503	-	4,4,4	0.25	0	6,6,6	0.14	0
5	PGE	B	513	-	9,9,9	0.48	0	8,8,8	0.40	0
4	PEG	A	509	-	3,3,6	0.40	0	2,2,5	0.25	0
3	SO4	B	505	-	4,4,4	0.24	0	6,6,6	0.11	0
3	SO4	B	503	-	4,4,4	0.23	0	6,6,6	0.15	0
4	PEG	B	509	-	3,3,6	0.41	0	2,2,5	0.45	0
6	GOL	A	515	-	5,5,5	0.29	0	5,5,5	0.33	0
7	EDO	B	517	-	2,2,3	0.82	0	1,1,2	0.57	0
4	PEG	A	510	-	6,6,6	0.40	0	5,5,5	0.52	0
2	58U	B	501	1	10,12,12	1.88	1 (10%)	10,15,15	1.69	3 (30%)
5	PGE	B	514	-	9,9,9	0.52	0	8,8,8	0.20	0



Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	SO4	B	506	-	4,4,4	0.23	0	6,6,6	0.20	0
4	PEG	B	511	-	3,3,6	0.46	0	2,2,5	0.38	0
3	SO4	A	504	-	4,4,4	0.24	0	6,6,6	0.07	0
6	GOL	A	513	-	5,5,5	0.43	0	5,5,5	0.61	0
4	PEG	B	507	-	3,3,6	0.35	0	2,2,5	0.60	0
5	PGE	A	511	-	9,9,9	0.54	0	8,8,8	0.46	0
3	SO4	B	504	-	4,4,4	0.25	0	6,6,6	0.08	0
4	PEG	A	508	-	3,3,6	0.42	0	2,2,5	0.40	0
2	58U	A	501	1	10,12,12	1.90	1 (10%)	10,15,15	1.66	3 (30%)
3	SO4	B	502	-	4,4,4	0.26	0	6,6,6	0.11	0
4	PEG	B	508	-	3,3,6	0.50	0	2,2,5	0.27	0
3	SO4	A	506	-	4,4,4	0.24	0	6,6,6	0.16	0
6	GOL	B	516	-	5,5,5	0.39	0	5,5,5	0.28	0
6	GOL	A	514	-	5,5,5	0.35	0	5,5,5	0.34	0
7	EDO	A	516	-	2,2,3	0.83	0	1,1,2	0.60	0
6	GOL	B	515	-	5,5,5	0.41	0	5,5,5	0.49	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	PEG	B	510	-	-	0/1/1/4	-
5	PGE	B	512	-	-	2/7/7/7	-
5	PGE	A	512	-	-	5/7/7/7	-
4	PEG	A	507	-	-	0/1/1/4	-
5	PGE	B	513	-	-	3/7/7/7	-
4	PEG	A	509	-	-	0/1/1/4	-
4	PEG	B	509	-	-	0/1/1/4	-
6	GOL	A	515	-	-	1/4/4/4	-
4	PEG	A	510	-	-	1/4/4/4	-
2	58U	B	501	1	-	4/15/15/15	-
5	PGE	B	514	-	-	3/7/7/7	-
4	PEG	B	511	-	-	0/1/1/4	-
6	GOL	A	513	-	-	2/4/4/4	-
4	PEG	B	507	-	-	0/1/1/4	-
5	PGE	A	511	-	-	5/7/7/7	-
4	PEG	A	508	-	-	1/1/1/4	-
2	58U	A	501	1	-	3/15/15/15	-
4	PEG	B	508	-	-	1/1/1/4	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	GOL	B	516	-	-	2/4/4/4	-
6	GOL	A	514	-	-	2/4/4/4	-
6	GOL	B	515	-	-	2/4/4/4	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	501	58U	C3-C11	-5.11	1.45	1.53
2	B	501	58U	C3-C11	-5.06	1.45	1.53

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	501	58U	O14-C7-C6	-2.69	118.01	126.34
2	B	501	58U	O13-C11-C3	-2.58	118.61	121.81
2	B	501	58U	O12-C11-C3	2.58	120.73	113.59
2	B	501	58U	O14-C7-C6	-2.42	118.84	126.34
2	A	501	58U	O12-C11-C3	2.29	119.93	113.59
2	A	501	58U	C2-C3-C11	2.01	119.47	115.89

There are no chirality outliers.

All (37) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	501	58U	C5-C6-C7-O14
2	B	501	58U	C10-C1-C2-C3
6	B	515	GOL	O1-C1-C2-C3
6	B	516	GOL	C1-C2-C3-O3
6	B	516	GOL	O2-C2-C3-O3
5	A	511	PGE	O2-C3-C4-O3
5	B	513	PGE	O2-C3-C4-O3
5	A	512	PGE	O3-C5-C6-O4
5	B	514	PGE	O3-C5-C6-O4
6	A	513	GOL	O1-C1-C2-C3
6	A	514	GOL	O1-C1-C2-C3
6	A	514	GOL	O1-C1-C2-O2
6	B	515	GOL	O1-C1-C2-O2
2	B	501	58U	C10-C1-C5-O4
2	B	501	58U	C10-C1-C5-C6
4	A	508	PEG	O2-C3-C4-O4

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Mol	Chain	Res	Type	Atoms
4	B	508	PEG	O2-C3-C4-O4
5	B	512	PGE	O2-C3-C4-O3
6	A	515	GOL	O1-C1-C2-O2
5	A	511	PGE	C4-C3-O2-C2
4	A	510	PEG	C1-C2-O2-C3
5	A	511	PGE	C1-C2-O2-C3
5	B	513	PGE	C1-C2-O2-C3
5	A	511	PGE	C6-C5-O3-C4
5	A	511	PGE	C3-C4-O3-C5
5	B	513	PGE	O3-C5-C6-O4
2	A	501	58U	C10-C1-C5-O4
2	A	501	58U	C10-C1-C5-C6
5	B	514	PGE	O1-C1-C2-O2
6	A	513	GOL	O1-C1-C2-O2
5	B	514	PGE	C4-C3-O2-C2
5	B	512	PGE	O3-C5-C6-O4
5	A	512	PGE	C6-C5-O3-C4
5	A	512	PGE	O1-C1-C2-O2
5	A	512	PGE	C3-C4-O3-C5
2	A	501	58U	C1-C5-C6-C7
5	A	512	PGE	O2-C3-C4-O3

There are no ring outliers.

13 monomers are involved in 29 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	510	PEG	1	0
5	B	512	PGE	1	0
3	A	502	SO4	1	0
5	B	513	PGE	4	0
4	A	509	PEG	4	0
4	A	510	PEG	2	0
2	B	501	58U	3	0
5	B	514	PGE	1	0
3	B	506	SO4	2	4
6	A	513	GOL	1	0
5	A	511	PGE	1	0
2	A	501	58U	4	0
3	B	502	SO4	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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	352/353 (99%)	-0.55	1 (0%) 90 90	13, 29, 45, 100	3 (0%)
1	B	353/353 (100%)	-0.53	2 (0%) 85 84	15, 28, 49, 106	6 (1%)
All	All	705/706 (99%)	-0.54	3 (0%) 89 88	13, 28, 47, 106	9 (1%)

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	408	ALA	3.8
1	B	57	LEU	3.3
1	A	57	LEU	2.3

### 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 monosaccharides 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
3	SO4	B	505	5/5	0.74	0.15	111,111,111,112	0
5	PGE	B	514	10/10	0.75	0.19	65,79,79,79	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
5	PGE	A	512	10/10	0.76	0.20	78,94,95,95	0
5	PGE	B	513	10/10	0.77	0.25	70,85,85,86	0
5	PGE	A	511	10/10	0.77	0.24	57,59,60,60	0
3	SO4	B	506	5/5	0.78	0.15	91,92,92,92	0
3	SO4	A	505	5/5	0.79	0.13	75,75,75,76	5
5	PGE	B	512	10/10	0.79	0.23	83,83,83,83	0
6	GOL	B	516	6/6	0.79	0.18	68,82,82,83	0
7	EDO	B	517	3/4	0.82	0.21	54,54,54,55	0
4	PEG	A	507	4/7	0.83	0.16	56,56,56,57	0
6	GOL	A	514	6/6	0.84	0.15	66,66,66,66	0
4	PEG	A	510	7/7	0.84	0.18	58,58,58,59	0
7	EDO	A	516	3/4	0.84	0.26	56,56,57,57	0
2	58U	B	501	13/13	0.84	0.19	25,41,50,62	13
4	PEG	B	508	4/7	0.86	0.15	43,43,44,44	0
2	58U	A	501	13/13	0.86	0.17	25,39,55,55	13
4	PEG	B	511	4/7	0.87	0.14	54,54,55,55	0
6	GOL	A	513	6/6	0.87	0.17	62,63,64,64	0
6	GOL	A	515	6/6	0.88	0.17	71,85,87,89	0
3	SO4	B	504	5/5	0.89	0.14	89,89,89,89	0
3	SO4	A	506	5/5	0.89	0.14	91,91,91,91	0
3	SO4	B	503	5/5	0.89	0.12	72,72,72,72	0
4	PEG	B	510	4/7	0.89	0.13	60,60,60,60	0
3	SO4	B	502	5/5	0.90	0.11	73,73,74,74	0
6	GOL	B	515	6/6	0.90	0.26	71,72,73,73	0
3	SO4	A	504	5/5	0.90	0.16	104,105,105,105	0
4	PEG	B	509	4/7	0.90	0.14	57,58,58,58	0
4	PEG	A	508	4/7	0.90	0.11	56,56,56,56	0
3	SO4	A	503	5/5	0.92	0.09	67,68,68,69	0
4	PEG	A	509	4/7	0.92	0.14	39,40,40,40	0
3	SO4	A	502	5/5	0.92	0.14	59,59,59,60	0
4	PEG	B	507	4/7	0.92	0.14	35,36,36,36	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.