



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 04:48 AM UTC

PDB ID : 6H2K / pdb_00006h2k
Title : Structure of BlaC from Mycobacterium tuberculosis bound to the trans-
enamine adduct of sulbactam.
Authors : Tassoni, R.; Pannu, N.S.; Ubbink, M.
Deposited on : 2018-07-13
Resolution : 1.90 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

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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

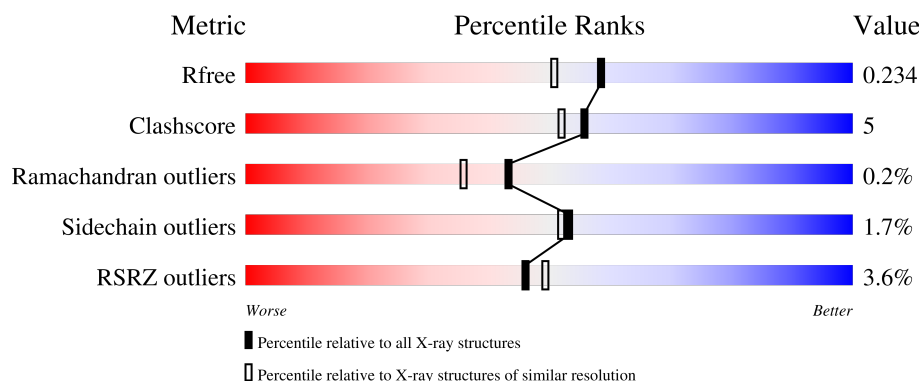
1 Overall quality at a glance

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	274	5% 87% 10% ..
1	B	274	2% 85% 11% ..

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 4490 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.

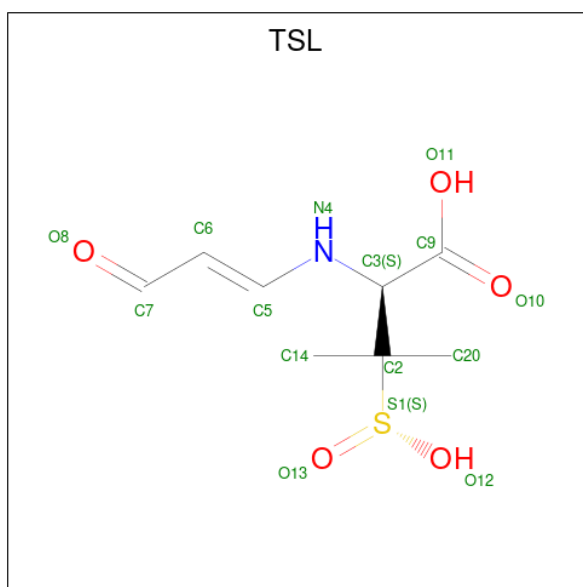
- Molecule 1 is a protein called Beta-lactamase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	269	Total	C	N	O	S	0	2	0
			2040	1276	364	394	6			
1	B	265	Total	C	N	O	S	0	1	0
			1993	1248	352	387	6			

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	28	MET	-	initiating methionine	UNP A0A0T9EA39
A	294	LEU	-	expression tag	UNP A0A0T9EA39
A	295	GLU	-	expression tag	UNP A0A0T9EA39
A	296	HIS	-	expression tag	UNP A0A0T9EA39
A	297	HIS	-	expression tag	UNP A0A0T9EA39
A	298	HIS	-	expression tag	UNP A0A0T9EA39
A	299	HIS	-	expression tag	UNP A0A0T9EA39
A	300	HIS	-	expression tag	UNP A0A0T9EA39
A	301	HIS	-	expression tag	UNP A0A0T9EA39
B	28	MET	-	initiating methionine	UNP A0A0T9EA39
B	294	LEU	-	expression tag	UNP A0A0T9EA39
B	295	GLU	-	expression tag	UNP A0A0T9EA39
B	296	HIS	-	expression tag	UNP A0A0T9EA39
B	297	HIS	-	expression tag	UNP A0A0T9EA39
B	298	HIS	-	expression tag	UNP A0A0T9EA39
B	299	HIS	-	expression tag	UNP A0A0T9EA39
B	300	HIS	-	expression tag	UNP A0A0T9EA39
B	301	HIS	-	expression tag	UNP A0A0T9EA39

- Molecule 2 is TRANS-ENAMINE INTERMEDIATE OF SULBACTAM (CCD ID: TSL) (formula: C₈H₁₃NO₅S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			15	8	1	5	1		
2	B	1	Total	C	N	O	S	0	0
			15	8	1	5	1		

- 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	A	1	Total	C	O	0	0
			7	4	3		

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

- Molecule 4 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



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

- Molecule 5 is ACETATE ION (CCD ID: ACT) (formula: $C_2H_3O_2$).



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

- Molecule 6 is water.

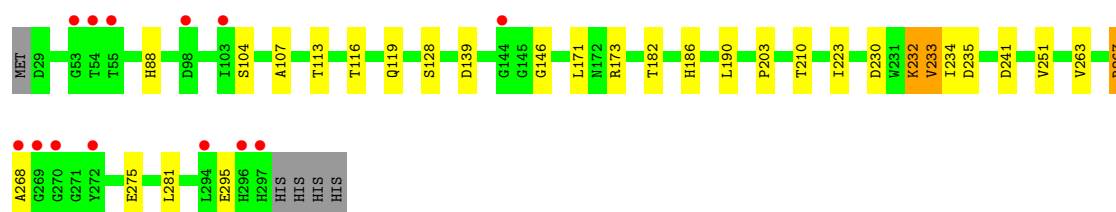
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	171	Total	O	0	0
			171	171		
6	B	176	Total	O	0	0
			176	176		

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.

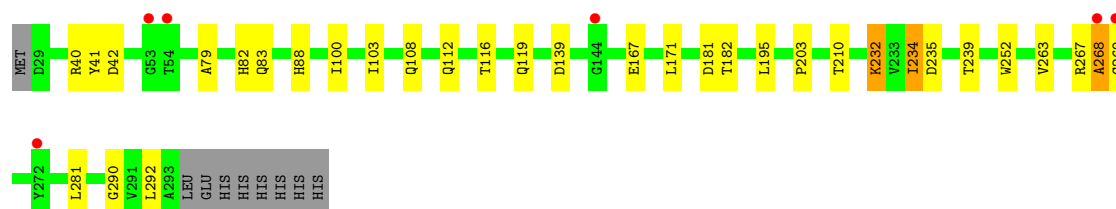
• Molecule 1: Beta-lactamase

Chain A: 



• Molecule 1: Beta-lactamase

Chain B: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	39.71Å 41.95Å 76.93Å 105.10° 89.95° 90.81°	Depositor
Resolution (Å)	40.50 – 1.90 40.50 – 1.90	Depositor EDS
% Data completeness (in resolution range)	85.9 (40.50-1.90) 85.9 (40.50-1.90)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	6.82 (at 1.89Å)	Xtriage
Refinement program	REFMAC 5.8.0189	Depositor
R, R_{free}	0.182 , 0.227 0.192 , 0.234	Depositor DCC
R_{free} test set	1627 reflections (4.31%)	wwPDB-VP
Wilson B-factor (Å ²)	10.7	Xtriage
Anisotropy	0.074	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 34.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.036 for h,-k,-l 0.020 for -h,k,-k-l 0.000 for -h,-k,k+l	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	4490	wwPDB-VP
Average B, all atoms (Å ²)	12.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 19.23% 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: ACT, GOL, PEG, TSL

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	1.25	5/2084 (0.2%)	1.09	1/2844 (0.0%)
1	B	1.23	8/2035 (0.4%)	1.09	2/2778 (0.1%)
All	All	1.24	13/4119 (0.3%)	1.09	3/5622 (0.1%)

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	41	TYR	C-O	-6.08	1.15	1.23
1	B	268	ALA	N-CA	5.66	1.53	1.46
1	A	182	THR	C-O	-5.65	1.16	1.23
1	B	182	THR	C-O	-5.63	1.16	1.23
1	A	233	VAL	C-O	5.55	1.29	1.24
1	B	42	ASP	CG-OD1	-5.52	1.14	1.25
1	A	268	ALA	N-CA	5.47	1.53	1.46
1	A	295	GLU	CD-OE1	-5.30	1.15	1.25
1	B	181	ASP	C-O	-5.22	1.17	1.23
1	A	146	GLY	N-CA	5.17	1.52	1.45
1	B	40	ARG	C-O	-5.17	1.18	1.24
1	B	234	ILE	C-O	-5.16	1.18	1.24
1	B	195	LEU	C-O	-5.13	1.18	1.24

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	267	ARG	NE-CZ-NH1	-6.64	114.86	121.50
1	B	292	LEU	N-CA-C	5.08	117.55	111.71
1	B	267	ARG	NE-CZ-NH2	5.03	123.73	119.20

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	2040	0	2007	20	0
1	B	1993	0	1966	19	0
2	A	15	0	11	0	0
2	B	15	0	11	3	0
3	A	35	0	50	0	0
3	B	7	0	10	2	0
4	A	12	0	16	1	0
4	B	6	0	8	0	0
5	A	12	0	9	0	0
5	B	8	0	6	1	0
6	A	171	0	0	7	0
6	B	176	0	0	3	0
All	All	4490	0	4094	39	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 5.

All (39) 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:116:THR:H	1:B:119:GLN:HE21	1.29	0.80
1:A:116:THR:H	1:A:119:GLN:HE21	1.30	0.75
1:A:263[A]:VAL:HG12	1:A:281:LEU:HD22	1.69	0.74
1:B:263:VAL:HG12	1:B:281:LEU:HD22	1.73	0.71
1:A:230:ASP:OD2	6:A:601:HOH:O	2.11	0.68
1:B:82:HIS:HD2	6:B:712:HOH:O	1.79	0.64
1:B:268:ALA:HB2	6:B:732:HOH:O	1.99	0.63
1:A:232:LYS:HE2	6:A:752:HOH:O	2.02	0.57
1:A:267:ARG:HD3	1:A:275:GLU:O	2.06	0.56
1:A:171:LEU:HD11	6:A:640:HOH:O	2.07	0.54
1:A:233:VAL:O	4:A:507:GOL:H11	2.09	0.53
1:B:112:GLN:HE21	3:B:502:PEG:H42	1.74	0.53
1:A:186:HIS:NE2	1:A:190:LEU:HD11	2.26	0.51
1:B:103:ILE:HD12	2:B:501:TSL:C20	2.42	0.49
1:A:232:LYS:CD	6:A:622:HOH:O	2.60	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:186:HIS:CD2	1:A:190:LEU:HD11	2.48	0.48
1:A:88:HIS:HD2	6:A:756:HOH:O	1.97	0.48
1:B:112:GLN:HE21	3:B:502:PEG:C4	2.27	0.48
1:A:104:SER:HB3	1:A:107:ALA:HB3	1.96	0.47
1:A:263[A]:VAL:CG1	1:A:281:LEU:HD22	2.43	0.47
1:A:88:HIS:HE1	1:A:139:ASP:OD2	1.98	0.47
1:B:82:HIS:ND1	1:B:83:GLN:OE1	2.37	0.46
1:A:232:LYS:CE	6:A:622:HOH:O	2.64	0.46
1:B:239:THR:O	2:B:501:TSL:H5	2.17	0.45
1:A:210:THR:HG23	1:A:234:ILE:HD13	1.99	0.45
1:A:232:LYS:O	1:A:251:VAL:HA	2.16	0.44
1:A:113:THR:HG21	6:A:763:HOH:O	2.18	0.44
1:B:171:LEU:HD11	6:B:622:HOH:O	2.16	0.44
1:B:79:ALA:O	1:B:83:GLN:HG2	2.18	0.44
1:B:232:LYS:HD2	1:B:252:TRP:CE3	2.53	0.43
1:A:223:ILE:HD11	1:A:263[B]:VAL:HG22	2.00	0.43
1:B:263:VAL:CG1	1:B:281:LEU:HD22	2.45	0.43
1:B:88:HIS:HE1	1:B:139:ASP:OD2	2.02	0.43
1:B:210:THR:HG23	1:B:234:ILE:HD13	2.01	0.43
1:B:103:ILE:HD12	2:B:501:TSL:H202	2.01	0.43
1:B:100:ILE:HG21	1:B:108:GLN:NE2	2.33	0.42
1:B:167:GLU:C	1:B:171:LEU:HD23	2.45	0.42
1:A:173:ARG:HG2	1:A:241:ASP:OD2	2.19	0.41
1:B:290:GLY:HA3	5:B:505:ACT:O	2.21	0.41

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	269/274 (98%)	261 (97%)	8 (3%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	264/274 (96%)	256 (97%)	7 (3%)	1 (0%)	30	22
All	All	533/548 (97%)	517 (97%)	15 (3%)	1 (0%)	43	36

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	269	GLY

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	208/211 (99%)	204 (98%)	4 (2%)	50	47
1	B	203/211 (96%)	200 (98%)	3 (2%)	57	56
All	All	411/422 (97%)	404 (98%)	7 (2%)	53	52

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

Mol	Chain	Res	Type
1	A	128	SER
1	A	203	PRO
1	A	232	LYS
1	A	235	ASP
1	B	203	PRO
1	B	232	LYS
1	B	235	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	82	HIS
1	A	88	HIS
1	A	110	HIS

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Mol	Chain	Res	Type
1	A	119	GLN
1	A	194	GLN
1	B	88	HIS
1	B	108	GLN
1	B	112	GLN
1	B	119	GLN
1	B	199	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 ⓘ

16 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	$\# Z > 2$
5	ACT	B	504	-	3,3,3	0.84	0	3,3,3	1.29	0
4	GOL	A	507	-	5,5,5	0.51	0	5,5,5	1.27	1 (20%)
3	PEG	B	502	-	6,6,6	0.43	0	5,5,5	0.63	0
5	ACT	A	511	-	3,3,3	0.72	0	3,3,3	0.91	0
3	PEG	A	506	-	6,6,6	0.62	0	5,5,5	0.61	0
5	ACT	B	505	-	3,3,3	0.61	0	3,3,3	1.36	0
3	PEG	A	503	-	6,6,6	0.68	0	5,5,5	0.44	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	ACT	A	509	-	3,3,3	0.79	0	3,3,3	0.59	0
4	GOL	B	503	-	5,5,5	0.73	0	5,5,5	0.85	0
3	PEG	A	504	-	6,6,6	0.56	0	5,5,5	0.39	0
2	TSL	B	501	1	11,14,14	2.29	1 (9%)	10,19,19	2.14	3 (30%)
2	TSL	A	501	1	11,14,14	1.62	5 (45%)	10,19,19	1.41	2 (20%)
3	PEG	A	502	-	6,6,6	0.95	0	5,5,5	1.55	0
4	GOL	A	508	-	5,5,5	0.92	0	5,5,5	1.67	1 (20%)
5	ACT	A	510	-	3,3,3	0.99	0	3,3,3	0.65	0
3	PEG	A	505	-	6,6,6	0.71	0	5,5,5	0.51	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	GOL	A	507	-	-	2/4/4/4	-
3	PEG	B	502	-	-	4/4/4/4	-
3	PEG	A	506	-	-	4/4/4/4	-
3	PEG	A	503	-	-	2/4/4/4	-
4	GOL	B	503	-	-	2/4/4/4	-
3	PEG	A	504	-	-	3/4/4/4	-
2	TSL	B	501	1	-	1/17/21/21	-
2	TSL	A	501	1	-	3/17/21/21	-
3	PEG	A	502	-	-	2/4/4/4	-
4	GOL	A	508	-	-	3/4/4/4	-
3	PEG	A	505	-	-	3/4/4/4	-

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	501	TSL	O13-S1	6.58	1.53	1.47
2	A	501	TSL	C5-C6	-2.44	1.32	1.37
2	A	501	TSL	O13-S1	2.37	1.49	1.47
2	A	501	TSL	C3-N4	2.34	1.48	1.45
2	A	501	TSL	O10-C9	2.08	1.28	1.22
2	A	501	TSL	O11-C9	-2.07	1.24	1.30

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	501	TSL	C14-C2-S1	4.95	119.12	107.26
2	A	501	TSL	C14-C2-S1	3.12	114.73	107.26
2	B	501	TSL	C6-C5-N4	-2.98	120.44	125.89
4	A	508	GOL	O3-C3-C2	2.66	122.35	110.38
4	A	507	GOL	O1-C1-C2	2.49	121.59	110.38
2	B	501	TSL	C20-C2-C14	-2.08	103.67	109.27
2	A	501	TSL	C20-C2-C14	-2.08	103.67	109.27

There are no chirality outliers.

All (29) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	501	TSL	C14-C2-S1-O13
2	A	501	TSL	C5-C6-C7-O8
2	B	501	TSL	C5-C6-C7-O8
4	A	507	GOL	O2-C2-C3-O3
4	B	503	GOL	C1-C2-C3-O3
3	A	504	PEG	O1-C1-C2-O2
4	A	507	GOL	C1-C2-C3-O3
4	A	508	GOL	O1-C1-C2-C3
3	B	502	PEG	O2-C3-C4-O4
4	A	508	GOL	O1-C1-C2-O2
4	B	503	GOL	O2-C2-C3-O3
3	A	506	PEG	O1-C1-C2-O2
3	A	503	PEG	O2-C3-C4-O4
3	A	505	PEG	O2-C3-C4-O4
3	A	506	PEG	O2-C3-C4-O4
3	A	504	PEG	O2-C3-C4-O4
2	A	501	TSL	C20-C2-S1-O13
4	A	508	GOL	O2-C2-C3-O3
3	A	502	PEG	C4-C3-O2-C2
3	A	503	PEG	C4-C3-O2-C2
3	A	506	PEG	C1-C2-O2-C3
3	A	502	PEG	O1-C1-C2-O2
3	A	505	PEG	C1-C2-O2-C3
3	B	502	PEG	C1-C2-O2-C3
3	B	502	PEG	O1-C1-C2-O2
3	A	506	PEG	C4-C3-O2-C2
3	A	505	PEG	O1-C1-C2-O2
3	A	504	PEG	C1-C2-O2-C3
3	B	502	PEG	C4-C3-O2-C2

There are no ring outliers.

4 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	507	GOL	1	0
3	B	502	PEG	2	0
5	B	505	ACT	1	0
2	B	501	TSL	3	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	269/274 (98%)	0.15	13 (4%) 35 38	3, 9, 26, 49	2 (0%)
1	B	265/274 (96%)	0.08	6 (2%) 61 65	4, 10, 23, 33	1 (0%)
All	All	534/548 (97%)	0.11	19 (3%) 46 49	3, 9, 25, 49	3 (0%)

All (19) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	54	THR	5.6
1	A	53	GLY	5.2
1	B	269	GLY	3.9
1	B	268	ALA	3.2
1	A	269	GLY	3.2
1	A	272	TYR	3.1
1	A	268	ALA	2.9
1	A	103	ILE	2.8
1	A	55	THR	2.8
1	A	297	HIS	2.7
1	A	296	HIS	2.5
1	B	53	GLY	2.3
1	B	272	TYR	2.2
1	B	54	THR	2.2
1	A	98	ASP	2.2
1	A	144	GLY	2.2
1	A	294	LEU	2.2
1	A	270	GLY	2.1
1	B	144	GLY	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 [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($\text{\AA}^2$)	Q<0.9
3	PEG	A	504	7/7	0.75	0.21	33,37,47,47	0
3	PEG	A	505	7/7	0.75	0.19	29,31,35,37	0
3	PEG	A	503	7/7	0.78	0.17	29,30,35,35	0
4	GOL	B	503	6/6	0.80	0.20	32,36,40,42	0
3	PEG	A	502	7/7	0.81	0.14	16,19,21,24	0
5	ACT	A	510	4/4	0.83	0.12	26,27,28,34	0
3	PEG	A	506	7/7	0.84	0.17	33,34,41,43	0
5	ACT	A	511	4/4	0.84	0.13	37,37,39,41	0
3	PEG	B	502	7/7	0.87	0.12	24,27,30,34	0
5	ACT	A	509	4/4	0.88	0.11	15,15,16,16	0
4	GOL	A	507	6/6	0.88	0.16	28,30,34,41	0
2	TSL	A	501	15/15	0.88	0.12	8,24,28,31	0
2	TSL	B	501	15/15	0.89	0.11	8,18,22,23	0
4	GOL	A	508	6/6	0.89	0.12	20,28,29,29	0
5	ACT	B	505	4/4	0.89	0.18	32,43,45,48	0
5	ACT	B	504	4/4	0.92	0.08	17,20,20,20	0

6.5 Other polymers [i](#)

There are no such residues in this entry.