



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 28, 2026 – 10:03 PM UTC

PDB ID : 4C75 / pdb_00004c75
Title : Consensus (ALL-CON) beta-lactamase class A
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Deposited on : 2013-09-19
Resolution : 2.20 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

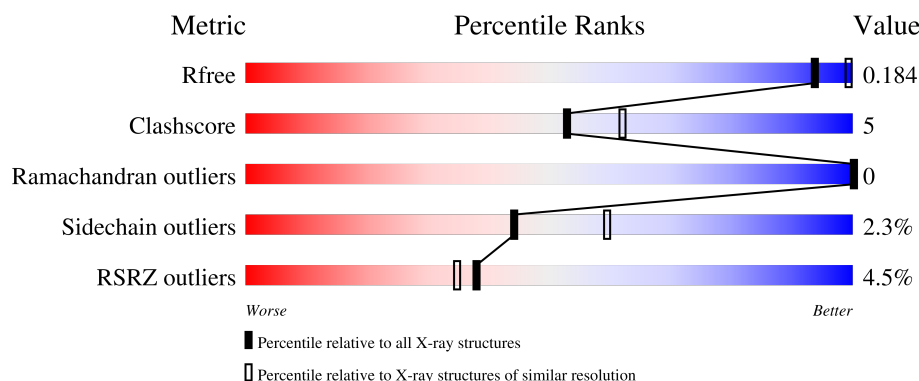
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

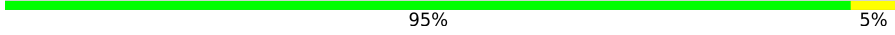
The reported resolution of this entry is 2.20 Å.

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	6164 (2.20-2.20)
Clashscore	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (2.20-2.20)

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	262	 90% 9% .
1	B	262	 88% 12%
1	C	262	 95% 5%
1	D	262	 18% 79% 19% .

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	ACT	B	294	-	-	X	-
4	PEG	B	295	-	-	X	-

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 8718 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	262	Total	C	N	O	S	0	1	0
			1968	1229	344	389	6			
1	B	262	Total	C	N	O	S	0	2	0
			1967	1228	344	389	6			
1	C	262	Total	C	N	O	S	0	5	0
			1989	1240	350	393	6			
1	D	262	Total	C	N	O	S	0	6	0
			1991	1246	342	397	6			

- Molecule 2 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



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

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

- Molecule 3 is ACETATE ION (CCD ID: ACT) (formula: C₂H₃O₂).



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

- Molecule 4 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: C₄H₁₀O₃).



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

- Molecule 5 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total	Na	0	0
			1	1		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	233	Total	O	0	0
			233	233		
6	B	196	Total	O	0	0
			196	196		
6	C	188	Total	O	0	0
			188	188		
6	D	109	Total	O	0	0
			109	109		

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: BETA-LACTAMASE

Chain A: 

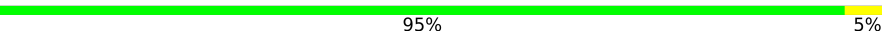


• Molecule 1: BETA-LACTAMASE

Chain B: 



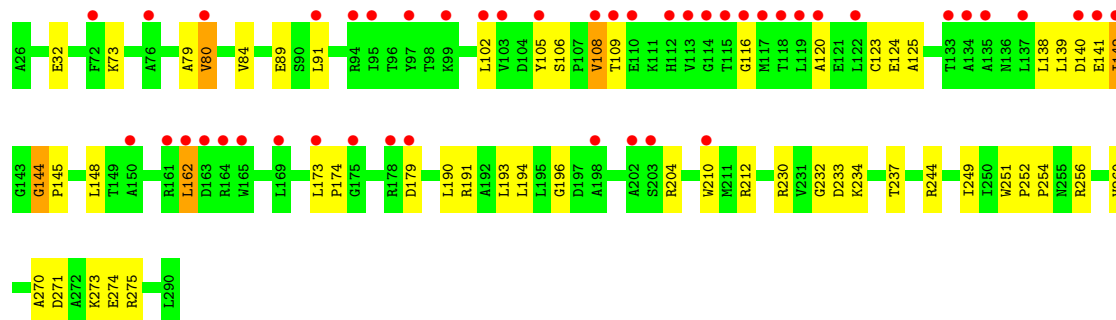
• Molecule 1: BETA-LACTAMASE

Chain C: 



• Molecule 1: BETA-LACTAMASE

Chain D: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	80.72Å 118.83Å 118.94Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.85 – 2.20 47.85 – 2.20	Depositor EDS
% Data completeness (in resolution range)	100.0 (47.85-2.20) 100.0 (47.85-2.20)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.99 (at 1.67Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, R_{free}	0.179 , 0.228 0.182 , 0.184	Depositor DCC
R_{free} test set	5302 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	22.6	Xtriage
Anisotropy	0.540	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 60.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	0.145 for -h,l,k	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	8718	wwPDB-VP
Average B, all atoms (Å ²)	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 19.17% 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: ACT, NA, SO4, 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	0.43	0/2001	0.77	1/2723 (0.0%)
1	B	0.42	0/2002	0.76	0/2725
1	C	0.39	0/2030	0.72	1/2761 (0.0%)
1	D	0.38	0/2030	0.76	2/2765 (0.1%)
All	All	0.40	0/8063	0.76	4/10974 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	144	GLY	CA-C-N	6.80	128.34	119.84
1	D	144	GLY	C-N-CA	6.80	128.34	119.84
1	A	227	ALA	N-CA-C	5.31	116.75	111.07
1	C	227	ALA	N-CA-C	5.08	117.48	111.33

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	1968	0	1955	17	0
1	B	1967	0	1965	22	0
1	C	1989	0	1982	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	1991	0	1974	34	0
2	A	5	0	0	1	0
2	B	5	0	0	0	0
2	C	5	0	0	0	0
2	D	5	0	0	0	0
3	A	4	0	3	0	0
3	B	8	0	6	3	0
3	C	4	0	3	0	0
3	D	12	0	9	0	0
4	A	14	0	18	2	0
4	B	14	0	18	6	0
5	A	1	0	0	0	0
6	A	233	0	0	3	0
6	B	196	0	0	6	1
6	C	188	0	0	3	1
6	D	109	0	0	8	0
All	All	8718	0	7933	80	1

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 (80) 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:D:254:PRO:O	6:D:2091:HOH:O	1.83	0.97
1:D:270:ALA:HB1	1:D:274:GLU:HG3	1.50	0.93
1:B:270:ALA:HB1	1:B:274:GLU:HG3	1.52	0.91
1:A:270:ALA:HB1	1:A:274:GLU:HG3	1.55	0.88
1:B:268[A]:SER:HB2	6:B:2176:HOH:O	1.87	0.73
1:B:191:ARG:NH2	3:B:294:ACT:O	2.18	0.72
1:B:32:GLU:OE2	6:B:2008:HOH:O	2.08	0.71
6:A:2212:HOH:O	1:B:197:ASP:OD1	2.11	0.69
1:D:105[B]:TYR:OH	6:D:2044:HOH:O	2.10	0.68
1:B:93:ARG:NH2	1:B:141:GLU:OE1	2.24	0.67
1:B:100:ASP:OD1	6:B:2084:HOH:O	2.10	0.67
1:A:150:ALA:HA	4:A:293:PEG:H41	1.77	0.67
1:B:271:ASP:OD2	6:B:2184:HOH:O	2.15	0.64
1:A:154:SER:HA	4:A:293:PEG:H11	1.80	0.64
1:D:139:LEU:HB3	1:D:144:GLY:HA2	1.80	0.62
1:D:91:LEU:HB3	1:D:120:ALA:HB2	1.81	0.62
1:D:252:PRO:HG2	1:D:256:ARG:HB2	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:146:LYS:NZ	6:A:2121:HOH:O	2.35	0.59
1:D:32:GLU:OE1	6:D:2004:HOH:O	2.17	0.59
1:C:91:LEU:HB3	1:C:120:ALA:HB2	1.84	0.58
1:D:145:PRO:HA	1:D:162:LEU:HD13	1.87	0.57
1:D:108[A]:VAL:HG11	1:D:125:ALA:HB1	1.86	0.57
1:D:148:LEU:HB3	1:D:162:LEU:HD11	1.86	0.56
1:D:106:SER:HB3	1:D:109:THR:OG1	2.06	0.55
1:B:205:ALA:HB3	4:B:295:PEG:H42	1.89	0.55
1:B:173[B]:LEU:HD12	1:B:174:PRO:HD2	1.88	0.55
1:D:173[A]:LEU:HD12	1:D:174:PRO:HD2	1.89	0.55
1:C:166:GLU:OE2	6:C:2052:HOH:O	2.18	0.55
1:B:212:ARG:NH2	1:B:230:ARG:HH12	2.05	0.54
1:B:26:ALA:HB2	6:B:2029:HOH:O	2.09	0.53
1:D:89:GLU:HG3	1:D:141:GLU:OE2	2.08	0.53
1:D:230:ARG:HB2	1:D:251:TRP:HB2	1.91	0.53
1:A:98:THR:HB	1:A:99:LYS:HE2	1.91	0.52
1:A:80:VAL:HA	1:A:142:ILE:HD11	1.92	0.51
2:A:291:SO4:O2	6:A:2099:HOH:O	2.17	0.51
1:A:119:LEU:HD21	1:A:141:GLU:HG3	1.92	0.51
1:D:116:GLY:HA2	6:D:2041:HOH:O	2.10	0.51
1:C:26:ALA:HB2	6:C:2001:HOH:O	2.12	0.50
1:D:212:ARG:O	6:D:2069:HOH:O	2.19	0.50
1:D:273:LYS:HE2	6:D:2051:HOH:O	2.11	0.50
1:D:162:LEU:HA	1:D:179:ASP:HA	1.93	0.50
1:B:106:SER:HB3	1:B:109:THR:OG1	2.12	0.49
1:B:108:VAL:HG22	4:B:292:PEG:H32	1.96	0.48
1:C:93:ARG:NH1	6:C:2066:HOH:O	2.42	0.48
1:D:140:ASP:OD1	1:D:141:GLU:N	2.47	0.48
1:A:241:TYR:OH	3:B:294:ACT:OXT	2.28	0.48
1:D:271:ASP:OD1	1:D:274:GLU:HG2	2.13	0.48
1:D:124:GLU:HB2	1:D:210:TRP:NE1	2.29	0.47
1:A:80:VAL:HG21	1:A:138:LEU:HD22	1.96	0.47
1:D:237:THR:OG1	1:D:244:ARG:NH1	2.48	0.47
1:A:61:ARG:NH1	4:B:295:PEG:H22	2.30	0.46
1:B:212:ARG:CZ	1:B:230:ARG:HH12	2.29	0.46
1:B:284:LYS:NZ	6:B:2192:HOH:O	2.37	0.46
1:A:194:LEU:HD11	1:A:211:MET:SD	2.56	0.46
1:A:43:ARG:HD2	4:B:295:PEG:H11	1.99	0.45
1:C:106:SER:HB3	1:C:109:THR:OG1	2.17	0.45
1:B:151:PHE:O	1:B:154:SER:OG	2.27	0.44
1:B:50:ASP:HB2	1:B:290:LEU:HD13	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:123:CYS:HA	1:D:138:LEU:HD11	1.99	0.44
1:B:205:ALA:CB	4:B:295:PEG:H42	2.48	0.44
1:D:193:LEU:O	1:D:204:ARG:HG3	2.18	0.44
1:C:168:GLU:O	1:C:171:GLU:HG3	2.17	0.43
1:D:190:LEU:HG	1:D:194:LEU:HD12	1.99	0.43
1:A:174:PRO:HD2	3:B:294:ACT:OXT	2.18	0.43
1:D:191:ARG:HB2	1:D:260:VAL:HG21	2.00	0.43
1:B:111:LYS:NZ	4:B:292:PEG:H31	2.34	0.43
1:D:80:VAL:HG21	1:D:138:LEU:HD22	2.00	0.43
1:D:73:LYS:HB2	1:D:234:LYS:HE3	2.00	0.43
1:D:191:ARG:NH1	6:D:2067:HOH:O	2.31	0.43
1:D:79:ALA:C	1:D:142:ILE:HD11	2.44	0.42
1:D:102:LEU:HD11	1:D:106:SER:HB2	2.02	0.42
1:A:99:LYS:CD	1:A:99:LYS:H	2.31	0.42
1:A:219:LYS:C	1:A:220:LEU:HD12	2.45	0.42
1:D:275:ARG:HD2	6:D:2099:HOH:O	2.19	0.41
1:D:212:ARG:HA	1:D:232:GLY:HA2	2.02	0.41
1:D:196:GLY:O	1:D:204:ARG:NH1	2.53	0.41
1:A:37:GLU:OE1	1:A:60:TYR:OH	2.39	0.41
1:B:37:GLU:OE1	1:B:60:TYR:OH	2.37	0.40
1:B:162:LEU:HD12	1:B:162:LEU:HA	1.95	0.40
1:A:194:LEU:HD21	1:A:207:LEU:HG	2.03	0.40

All (1) 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)
6:B:2119:HOH:O	6:C:2118:HOH:O[4_555]	2.00	0.20

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	261/262 (100%)	255 (98%)	6 (2%)	0	100	100
1	B	262/262 (100%)	259 (99%)	3 (1%)	0	100	100
1	C	265/262 (101%)	263 (99%)	2 (1%)	0	100	100
1	D	266/262 (102%)	259 (97%)	7 (3%)	0	100	100
All	All	1054/1048 (101%)	1036 (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	197/196 (100%)	193 (98%)	4 (2%)	48	64
1	B	198/196 (101%)	192 (97%)	6 (3%)	36	49
1	C	200/196 (102%)	198 (99%)	2 (1%)	68	81
1	D	200/196 (102%)	192 (96%)	8 (4%)	28	38
All	All	795/784 (101%)	775 (98%)	20 (2%)	44	56

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

Mol	Chain	Res	Type
1	A	99	LYS
1	A	142	ILE
1	A	231	VAL
1	A	290	LEU
1	B	103	VAL
1	B	119	LEU
1	B	142	ILE
1	B	219	LYS
1	B	268[A]	SER
1	B	268[B]	SER
1	C	119	LEU
1	C	173	LEU
1	D	80	VAL

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Mol	Chain	Res	Type
1	D	84	VAL
1	D	108[A]	VAL
1	D	108[B]	VAL
1	D	142	ILE
1	D	162	LEU
1	D	233	ASP
1	D	249	ILE

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	170	ASN
1	A	206	GLN
1	B	83	GLN
1	B	170	ASN
1	B	206	GLN
1	C	206	GLN
1	C	214	ASN
1	D	132	ASN
1	D	170	ASN
1	D	214	ASN

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 16 ligands modelled in this entry, 1 is 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
3	ACT	B	293	-	3,3,3	0.80	0	3,3,3	1.41	0
3	ACT	A	292	-	3,3,3	0.79	0	3,3,3	1.50	0
4	PEG	A	293	-	6,6,6	0.61	0	5,5,5	0.33	0
4	PEG	B	292	-	6,6,6	0.59	0	5,5,5	0.37	0
4	PEG	A	295	-	6,6,6	0.59	0	5,5,5	0.29	0
3	ACT	C	292	-	3,3,3	0.77	0	3,3,3	1.39	0
3	ACT	D	292	-	3,3,3	0.82	0	3,3,3	1.44	0
2	SO4	B	291	-	4,4,4	0.16	0	6,6,6	0.16	0
2	SO4	C	291	-	4,4,4	0.23	0	6,6,6	0.29	0
3	ACT	B	294	-	3,3,3	0.83	0	3,3,3	1.80	2 (66%)
3	ACT	D	294	-	3,3,3	0.82	0	3,3,3	1.44	0
3	ACT	D	293	-	3,3,3	0.78	0	3,3,3	1.31	0
2	SO4	A	291	5	4,4,4	0.27	0	6,6,6	0.23	0
2	SO4	D	291	-	4,4,4	0.24	0	6,6,6	0.13	0
4	PEG	B	295	-	6,6,6	0.62	0	5,5,5	0.46	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	A	293	-	-	4/4/4/4	-
4	PEG	B	295	-	-	3/4/4/4	-
4	PEG	B	292	-	-	3/4/4/4	-
4	PEG	A	295	-	-	2/4/4/4	-

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	294	ACT	OXT-C-O	-2.27	113.59	122.03
3	B	294	ACT	OXT-C-CH3	2.13	123.97	115.05

There are no chirality outliers.

All (12) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	295	PEG	O2-C3-C4-O4
4	A	293	PEG	C4-C3-O2-C2
4	B	295	PEG	O1-C1-C2-O2
4	B	295	PEG	O2-C3-C4-O4
4	A	293	PEG	O2-C3-C4-O4
4	B	292	PEG	O2-C3-C4-O4
4	B	292	PEG	O1-C1-C2-O2
4	B	295	PEG	C4-C3-O2-C2
4	A	293	PEG	C1-C2-O2-C3
4	A	293	PEG	O1-C1-C2-O2
4	B	292	PEG	C4-C3-O2-C2
4	A	295	PEG	C1-C2-O2-C3

There are no ring outliers.

5 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	293	PEG	2	0
4	B	292	PEG	2	0
3	B	294	ACT	3	0
2	A	291	SO4	1	0
4	B	295	PEG	4	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	262/262 (100%)	-0.48	1 (0%) 88 87	17, 27, 46, 61	1 (0%)
1	B	262/262 (100%)	-0.40	0 100 100	14, 27, 49, 60	2 (0%)
1	C	262/262 (100%)	-0.36	0 100 100	12, 30, 51, 78	5 (1%)
1	D	262/262 (100%)	0.76	46 (17%) 4 3	23, 50, 93, 112	6 (2%)
All	All	1048/1048 (100%)	-0.12	47 (4%) 38 35	12, 31, 74, 112	14 (1%)

All (47) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	105[A]	TYR	5.7
1	D	114	GLY	4.6
1	D	102	LEU	4.1
1	D	142	ILE	4.0
1	D	72	PHE	3.6
1	D	162	LEU	3.6
1	D	113	VAL	3.2
1	D	108[A]	VAL	3.1
1	D	135	ALA	3.1
1	D	119	LEU	3.1
1	D	95	ILE	3.1
1	D	165	TRP	3.0
1	D	137	LEU	3.0
1	D	115	THR	3.0
1	D	150	ALA	3.0
1	D	173[A]	LEU	2.9
1	D	118	THR	2.9
1	D	97	TYR	2.9
1	D	99	LYS	2.8
1	D	76	ALA	2.8
1	D	163	ASP	2.8

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Mol	Chain	Res	Type	RSRZ
1	D	120	ALA	2.8
1	D	169	LEU	2.7
1	D	210	TRP	2.7
1	D	94	ARG	2.6
1	D	117	MET	2.6
1	D	91	LEU	2.6
1	D	202	ALA	2.6
1	D	80	VAL	2.6
1	D	164	ARG	2.5
1	D	110	GLU	2.4
1	D	133	THR	2.4
1	D	122	LEU	2.4
1	D	112	HIS	2.4
1	D	141	GLU	2.4
1	D	203	SER	2.3
1	D	103	VAL	2.3
1	D	179	ASP	2.2
1	D	178	ARG	2.2
1	D	116	GLY	2.2
1	D	161	ARG	2.2
1	D	109	THR	2.2
1	D	140	ASP	2.2
1	D	134	ALA	2.2
1	A	105[A]	TYR	2.1
1	D	175	GLY	2.1
1	D	198	ALA	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	ACT	A	292	4/4	0.60	0.20	49,52,55,63	0
3	ACT	D	294	4/4	0.72	0.18	54,58,60,62	0
3	ACT	D	292	4/4	0.75	0.15	44,51,54,58	0
4	PEG	A	293	7/7	0.76	0.16	47,56,57,65	0
3	ACT	D	293	4/4	0.80	0.19	54,61,63,70	0
4	PEG	A	295	7/7	0.80	0.15	57,65,77,78	0
3	ACT	B	294	4/4	0.83	0.22	35,47,53,63	0
4	PEG	B	292	7/7	0.83	0.19	55,61,70,75	0
3	ACT	B	293	4/4	0.84	0.13	36,56,58,63	0
4	PEG	B	295	7/7	0.86	0.14	46,48,51,54	0
5	NA	A	294	1/1	0.90	0.17	41,41,41,41	0
3	ACT	C	292	4/4	0.91	0.12	36,47,51,60	0
2	SO4	D	291	5/5	0.92	0.11	48,51,54,57	0
2	SO4	C	291	5/5	0.97	0.07	32,34,37,42	0
2	SO4	A	291	5/5	0.98	0.08	33,38,42,45	0
2	SO4	B	291	5/5	0.98	0.06	32,35,37,43	0

6.5 Other polymers [i](#)

There are no such residues in this entry.