



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 08:18 AM UTC

PDB ID : 4H5G / pdb_00004h5g
Title : Crystal structure of an amino acid ABC transporter substrate-binding protein from *Streptococcus pneumoniae* Canada MDR_19A bound to L-arginine, form 2
Authors : Stogios, P.J.; Wawrzak, Z.; Kudritska, M.; Minasov, G.; Yim, V.; Savchenko, A.; Anderson, W.F.; Center for Structural Genomics of Infectious Diseases (CSGID)
Deposited on : 2012-09-18
Resolution : 1.78 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)

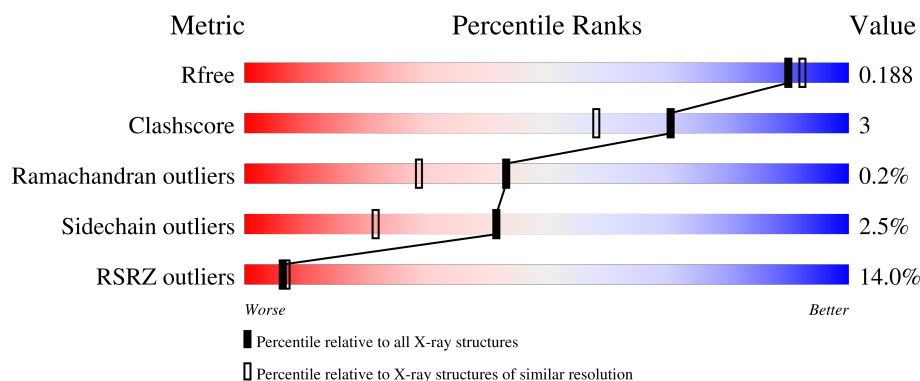
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.78 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	1365 (1.78-1.78)
Clashscore	190562	1395 (1.78-1.78)
Ramachandran outliers	187476	1382 (1.78-1.78)
Sidechain outliers	187428	1382 (1.78-1.78)
RSRZ outliers	180081	1365 (1.78-1.78)

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	243	7% 89% 9%
1	B	243	21% 88% 10%

2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 4262 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.

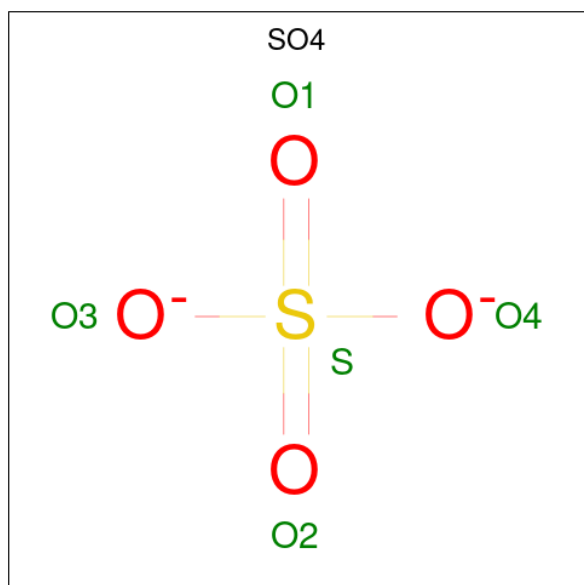
- Molecule 1 is a protein called Amino acid ABC superfamily ATP binding cassette transporter, binding protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	240	Total	C	N	O	S	0	17	0
			1920	1206	313	395	6			
1	B	240	Total	C	N	O	S	0	2	0
			1823	1146	296	375	6			

There are 4 discrepancies between the modelled and reference sequences:

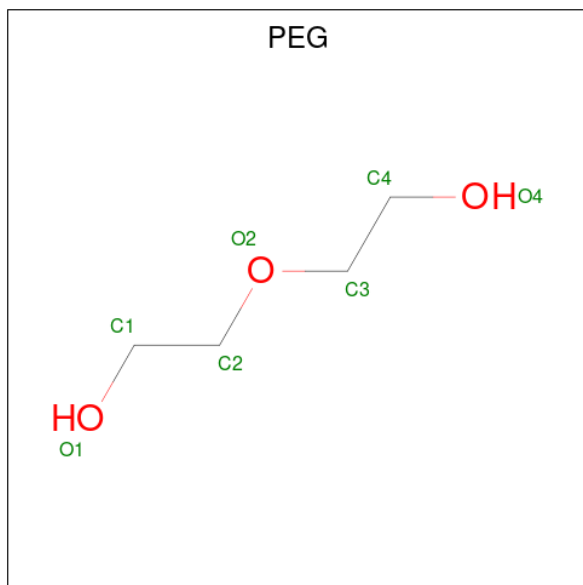
Chain	Residue	Modelled	Actual	Comment	Reference
A	29	GLY	-	expression tag	UNP D6ZRZ2
A	136	HIS	ARG	SEE REMARK 999	UNP D6ZRZ2
B	29	GLY	-	expression tag	UNP D6ZRZ2
B	136	HIS	ARG	SEE REMARK 999	UNP D6ZRZ2

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



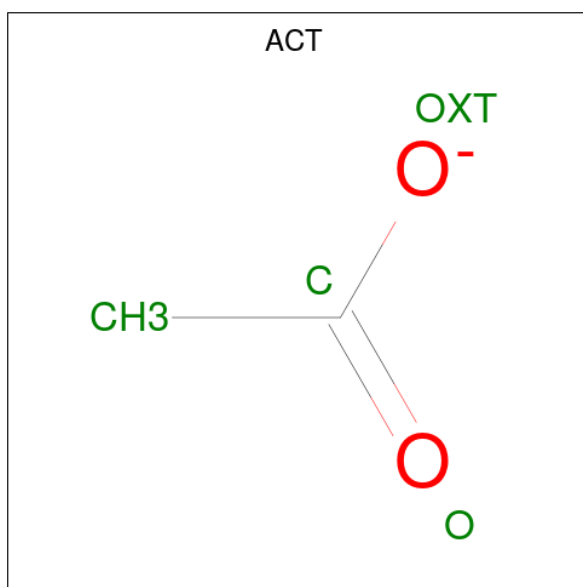
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		

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



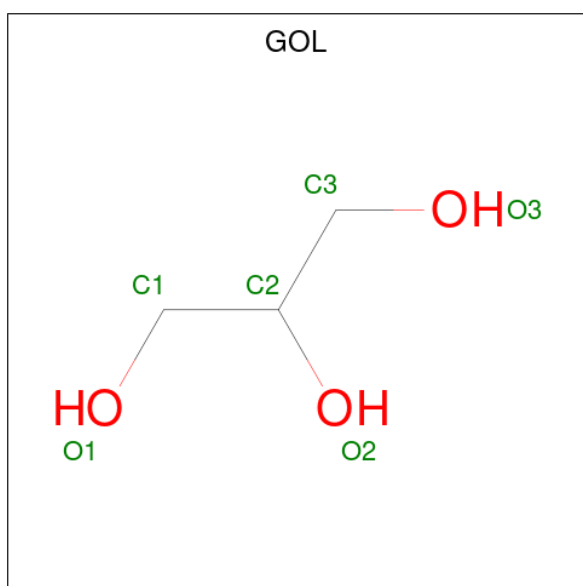
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			7	4	3		
3	A	1	Total	C	O	0	0
			7	4	3		
3	B	1	Total	C	O	0	0
			7	4	3		

- Molecule 4 is ACETATE ION (CCD ID: ACT) (formula: $C_2H_3O_2$).



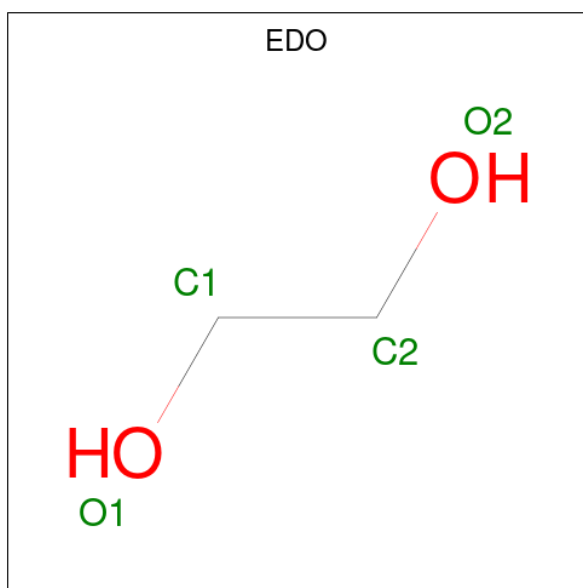
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			4	2	2		
4	A	1	Total	C	O	0	0
			4	2	2		

- Molecule 5 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



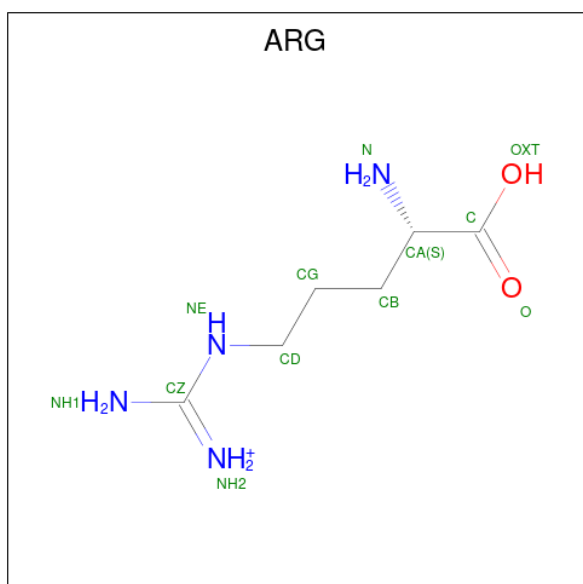
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			6	3	3		
5	B	1	Total	C	O	0	0
			6	3	3		

- Molecule 6 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: $C_2H_6O_2$).



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

- Molecule 7 is ARGinine (CCD ID: ARG) (formula: $C_6H_{15}N_4O_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	A	1	Total	C	N	O	0	0
			12	6	4	2		
7	B	1	Total	C	N	O	0	0
			12	6	4	2		

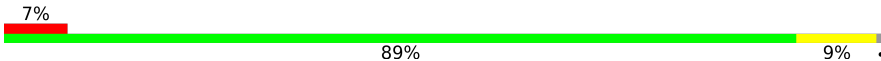
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	245	Total	O	0	5
			250	250		
8	B	174	Total	O	0	4
			178	178		

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.

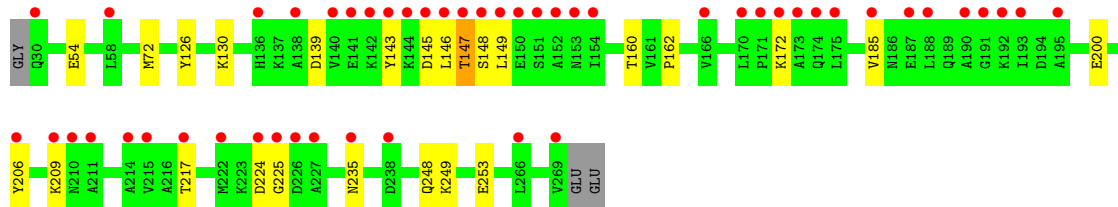
- Molecule 1: Amino acid ABC superfamily ATP binding cassette transporter, binding protein

Chain A: 



- Molecule 1: Amino acid ABC superfamily ATP binding cassette transporter, binding protein

Chain B: 



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	99.60Å 183.94Å 62.02Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	91.97 – 1.78 91.97 – 1.78	Depositor EDS
% Data completeness (in resolution range)	100.0 (91.97-1.78) 96.2 (91.97-1.78)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.25 (at 1.78Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8_1069)	Depositor
R, R_{free}	0.156 , 0.186 0.158 , 0.188	Depositor DCC
R_{free} test set	2789 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å ²)	17.3	Xtriage
Anisotropy	0.397	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 63.7	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	0.96	EDS
Total number of atoms	4262	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 4.69% 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: EDO, SO4, GOL, ACT, 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	0.48	0/1955	0.70	1/2640 (0.0%)
1	B	0.41	0/1846	0.73	0/2494
All	All	0.44	0/3801	0.72	1/5134 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	222	MET	N-CA-C	5.01	117.66	109.59

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	1920	0	1947	14	0
1	B	1823	0	1843	12	0
2	A	5	0	0	0	0
2	B	5	0	0	0	0
3	A	14	0	16	0	0
3	B	7	0	8	0	0
4	A	8	0	6	1	0
5	A	6	0	8	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	B	6	0	8	0	0
6	A	12	0	18	1	0
6	B	4	0	6	0	0
7	A	12	0	12	0	0
7	B	12	0	12	0	0
8	A	250	0	0	1	0
8	B	178	0	0	2	0
All	All	4262	0	3884	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 3.

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:60[A]:ASP:CB	1:A:61[A]:GLY:HA3	2.23	0.69
1:A:60[A]:ASP:HB2	1:A:61[A]:GLY:HA3	1.77	0.67
1:B:146:LEU:O	1:B:149:LEU:N	2.28	0.61
1:A:115:GLU:OE1	1:A:223:LYS:NZ	2.35	0.60
1:B:235:ASN:ND2	8:B:534:HOH:O	2.24	0.57
1:B:145:ASP:O	1:B:148:SER:OG	2.24	0.54
1:A:93:ASN:OD1	1:A:96[B]:THR:OG1	2.25	0.52
1:A:39:LYS:HZ1	1:A:104:ASP:CG	2.17	0.51
1:B:185:VAL:HG21	1:B:206:TYR:CZ	2.50	0.46
1:A:96[B]:THR:HG23	8:A:420:HOH:O	2.14	0.46
1:A:255:THR:HG23	4:A:304:ACT:H3	1.98	0.46
1:A:55:PHE:CD2	1:A:268[B]:GLU:HB3	2.50	0.46
1:B:224:ASP:HA	1:B:225:GLY:HA2	1.74	0.46
1:A:209:LYS:HG2	6:A:307:EDO:H22	1.98	0.45
1:B:139:ASP:HB3	1:B:143:TYR:CE2	2.52	0.45
1:B:249:LYS:HE2	1:B:253:GLU:OE2	2.16	0.45
1:A:222:MET:HE3	1:A:222:MET:HB2	1.77	0.45
1:B:130:LYS:HE2	1:B:200:GLU:OE1	2.17	0.44
1:B:160:THR:HB	1:B:162:PRO:HD2	2.02	0.42
1:A:160:THR:HB	1:A:162:PRO:HD2	2.02	0.42
1:B:72:MET:HE1	1:B:126:TYR:CE2	2.54	0.42
1:A:72:MET:HE1	1:A:126:TYR:CE2	2.55	0.41
1:A:55:PHE:HD2	1:A:268[B]:GLU:HB3	1.85	0.41
1:A:120:PHE:CE2	5:A:306:GOL:H32	2.55	0.41
1:B:248:GLN:OE1	8:B:555:HOH:O	2.21	0.41
1:B:209:LYS:HE2	1:B:209:LYS:HB2	1.86	0.40

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	255/243 (105%)	251 (98%)	4 (2%)	0	100	100
1	B	240/243 (99%)	235 (98%)	4 (2%)	1 (0%)	30	16
All	All	495/486 (102%)	486 (98%)	8 (2%)	1 (0%)	43	29

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	147	THR

5.3.2 Protein sidechains [i](#)

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	211/199 (106%)	204 (97%)	7 (3%)	33	13
1	B	199/199 (100%)	195 (98%)	4 (2%)	48	29
All	All	410/398 (103%)	399 (97%)	11 (3%)	42	19

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	30	GLN
1	A	54	GLU

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Mol	Chain	Res	Type
1	A	58	LEU
1	A	62[A]	LYS
1	A	62[B]	LYS
1	A	144	LYS
1	A	151	SER
1	B	54	GLU
1	B	147	THR
1	B	172	LYS
1	B	217	THR

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	30	GLN
1	A	189	GLN
1	B	74	GLN

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](#)

15 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	GOL	B	303	-	5,5,5	0.36	0	5,5,5	0.21	0
2	SO4	A	301	-	4,4,4	0.22	0	6,6,6	0.15	0
6	EDO	A	307	-	3,3,3	0.43	0	2,2,2	0.34	0
2	SO4	B	301	-	4,4,4	0.23	0	6,6,6	0.11	0
3	PEG	A	302	-	6,6,6	1.01	0	5,5,5	1.74	2 (40%)
5	GOL	A	306	-	5,5,5	0.35	0	5,5,5	0.43	0
3	PEG	B	302	-	6,6,6	1.11	0	5,5,5	3.59	3 (60%)
6	EDO	B	304	-	3,3,3	0.40	0	2,2,2	0.44	0
4	ACT	A	304	-	3,3,3	0.81	0	3,3,3	1.26	0
6	EDO	A	309	-	3,3,3	0.45	0	2,2,2	0.18	0
7	ARG	B	305	-	10,11,11	0.70	0	9,13,13	0.81	1 (11%)
6	EDO	A	308	-	3,3,3	0.41	0	2,2,2	0.37	0
7	ARG	A	310	-	10,11,11	0.80	1 (10%)	9,13,13	0.89	1 (11%)
4	ACT	A	305	-	3,3,3	0.82	0	3,3,3	1.29	0
3	PEG	A	303	-	6,6,6	1.12	0	5,5,5	2.44	3 (60%)

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
5	GOL	B	303	-	-	0/4/4/4	-
6	EDO	A	307	-	-	0/1/1/1	-
3	PEG	A	302	-	-	1/4/4/4	-
5	GOL	A	306	-	-	3/4/4/4	-
3	PEG	B	302	-	-	0/4/4/4	-
6	EDO	B	304	-	-	0/1/1/1	-
7	ARG	B	305	-	-	0/11/11/11	-
6	EDO	A	309	-	-	1/1/1/1	-
6	EDO	A	308	-	-	1/1/1/1	-
7	ARG	A	310	-	-	0/11/11/11	-
3	PEG	A	303	-	-	2/4/4/4	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	A	310	ARG	OXT-C	-2.13	1.23	1.30

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	302	PEG	C3-O2-C2	-5.63	88.60	113.26
3	B	302	PEG	O2-C2-C1	4.06	128.02	110.11
3	B	302	PEG	O2-C3-C4	3.94	127.46	110.11
3	A	303	PEG	O2-C2-C1	3.90	127.29	110.11
7	A	310	ARG	OXT-C-O	-2.48	118.46	124.08
3	A	302	PEG	O2-C3-C4	2.34	120.44	110.11
7	B	305	ARG	OXT-C-O	-2.27	118.93	124.08
3	A	302	PEG	O2-C2-C1	2.26	120.07	110.11
3	A	303	PEG	O1-C1-C2	2.15	124.49	111.82
3	A	303	PEG	C3-O2-C2	2.00	122.03	113.26

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	302	PEG	C1-C2-O2-C3
3	A	303	PEG	C1-C2-O2-C3
3	A	303	PEG	O1-C1-C2-O2
5	A	306	GOL	O1-C1-C2-O2
5	A	306	GOL	O1-C1-C2-C3
5	A	306	GOL	O2-C2-C3-O3
6	A	309	EDO	O1-C1-C2-O2
6	A	308	EDO	O1-C1-C2-O2

There are no ring outliers.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	307	EDO	1	0
5	A	306	GOL	1	0
4	A	304	ACT	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

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	240/243 (98%)	0.01	17 (7%) 22 26	9, 23, 48, 100	17 (7%)
1	B	240/243 (98%)	0.83	50 (20%) 2 2	18, 35, 89, 123	2 (0%)
All	All	480/486 (98%)	0.42	67 (13%) 6 7	9, 28, 81, 123	19 (3%)

All (67) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	138	ALA	5.1
1	B	211	ALA	5.0
1	B	149	LEU	4.4
1	A	225	GLY	4.4
1	B	140	VAL	4.2
1	B	147	THR	4.0
1	B	146	LEU	3.9
1	B	269	VAL	3.8
1	A	31	SER	3.8
1	B	148	SER	3.8
1	A	30	GLN	3.6
1	B	209	LYS	3.6
1	A	223	LYS	3.6
1	B	143	TYR	3.5
1	B	195	ALA	3.4
1	B	193	ILE	3.4
1	A	222	MET	3.4
1	B	172	LYS	3.4
1	A	61[A]	GLY	3.4
1	B	225	GLY	3.2
1	B	235	ASN	3.2
1	B	171	PRO	3.1
1	A	224	ASP	3.1
1	B	150	GLU	3.0

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Mol	Chain	Res	Type	RSRZ
1	A	264	ALA	3.0
1	B	170	LEU	2.9
1	A	60[A]	ASP	2.9
1	A	58	LEU	2.9
1	B	188	LEU	2.9
1	B	190	ALA	2.9
1	B	166	VAL	2.8
1	B	173	ALA	2.8
1	B	222	MET	2.8
1	B	152	ALA	2.8
1	A	269	VAL	2.8
1	B	30	GLN	2.7
1	B	217	THR	2.7
1	B	215	VAL	2.7
1	B	191	GLY	2.6
1	A	226	ASP	2.6
1	B	58	LEU	2.6
1	B	144	LYS	2.6
1	B	151	SER	2.5
1	A	63	ASN	2.5
1	B	192	LYS	2.4
1	A	59[A]	VAL	2.4
1	B	224	ASP	2.4
1	B	142	LYS	2.4
1	A	151	SER	2.3
1	B	214	ALA	2.3
1	B	175	LEU	2.3
1	A	266	LEU	2.3
1	B	238[A]	ASP	2.2
1	B	174	GLN	2.2
1	B	153	ASN	2.2
1	B	206	TYR	2.2
1	B	154	ILE	2.2
1	B	185	VAL	2.1
1	B	266	LEU	2.1
1	B	210	ASN	2.1
1	B	145	ASP	2.1
1	B	227	ALA	2.1
1	B	226	ASP	2.1
1	B	141	GLU	2.0
1	B	187	GLU	2.0
1	A	172	LYS	2.0

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Mol	Chain	Res	Type	RSRZ
1	B	136	HIS	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(Å ²)	Q<0.9
6	EDO	A	307	4/4	0.63	0.26	79,80,81,83	0
4	ACT	A	305	4/4	0.75	0.24	50,57,59,63	0
6	EDO	B	304	4/4	0.75	0.18	65,65,67,75	0
4	ACT	A	304	4/4	0.78	0.21	51,67,70,71	0
3	PEG	A	303	7/7	0.78	0.28	66,69,77,79	0
5	GOL	B	303	6/6	0.81	0.17	80,82,83,84	0
3	PEG	B	302	7/7	0.82	0.22	62,68,77,80	0
6	EDO	A	309	4/4	0.83	0.20	56,60,60,64	0
5	GOL	A	306	6/6	0.83	0.20	65,65,68,69	0
3	PEG	A	302	7/7	0.85	0.17	44,50,68,69	0
6	EDO	A	308	4/4	0.85	0.17	47,47,47,55	0
2	SO4	A	301	5/5	0.91	0.11	40,66,72,73	0
2	SO4	B	301	5/5	0.93	0.10	53,58,60,63	0
7	ARG	B	305	12/12	0.95	0.08	21,25,28,29	0
7	ARG	A	310	12/12	0.99	0.04	15,17,21,24	0

6.5 Other polymers [i](#)

There are no such residues in this entry.