



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 11:07 PM UTC

PDB ID : 3B1C / pdb_00003b1c
Title : Crystal structure of betaC-S lyase from Streptococcus anginosus: Internal aldimine form
Authors : Kezuka, Y.; Yoshida, Y.; Nonaka, T.
Deposited on : 2011-06-29
Resolution : 1.93 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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

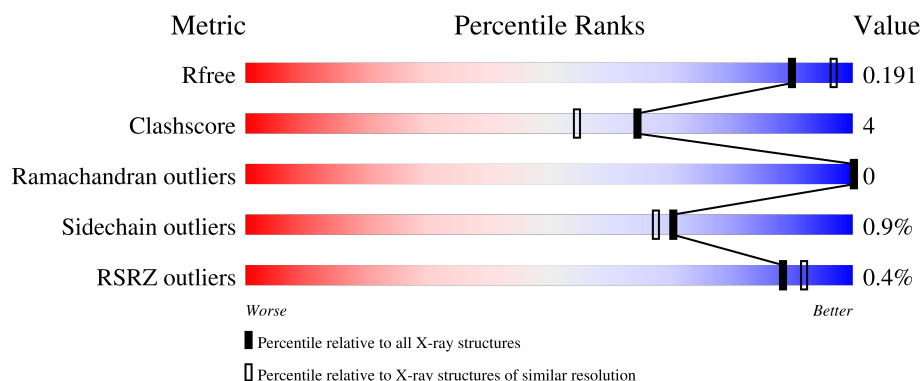
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.93 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	1452 (1.94-1.94)
Clashscore	190562	1494 (1.94-1.94)
Ramachandran outliers	187476	1479 (1.94-1.94)
Sidechain outliers	187428	1479 (1.94-1.94)
RSRZ outliers	180081	1453 (1.94-1.94)

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	392	% 89% 9% ..
1	B	392	88% 10% ..
1	C	392	89% 9% ..
1	D	392	90% 8% .

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
2	PLP	A	401	-	X	-	-
2	PLP	B	401	-	X	-	-
2	PLP	C	401	-	X	-	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 14349 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.

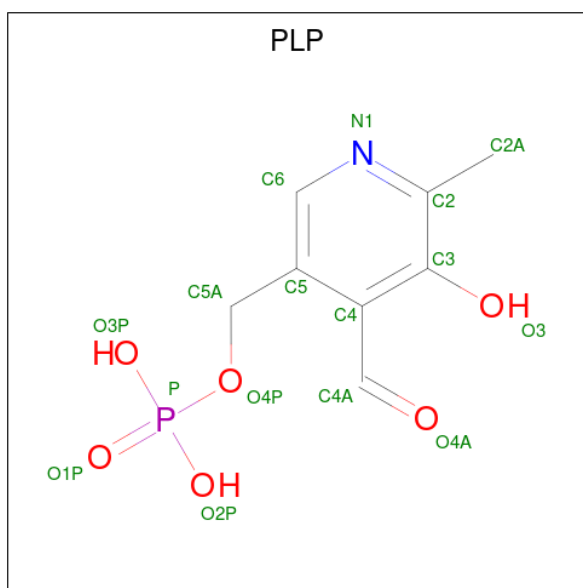
- Molecule 1 is a protein called BetaC-S lyase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	387	Total	C	N	O	S	0	13	0
			3190	2053	527	599	11			
1	B	386	Total	C	N	O	S	0	9	0
			3164	2034	521	598	11			
1	C	387	Total	C	N	O	S	0	12	0
			3191	2052	525	605	9			
1	D	385	Total	C	N	O	S	0	10	0
			3164	2034	525	596	9			

There are 20 discrepancies between the modelled and reference sequences:

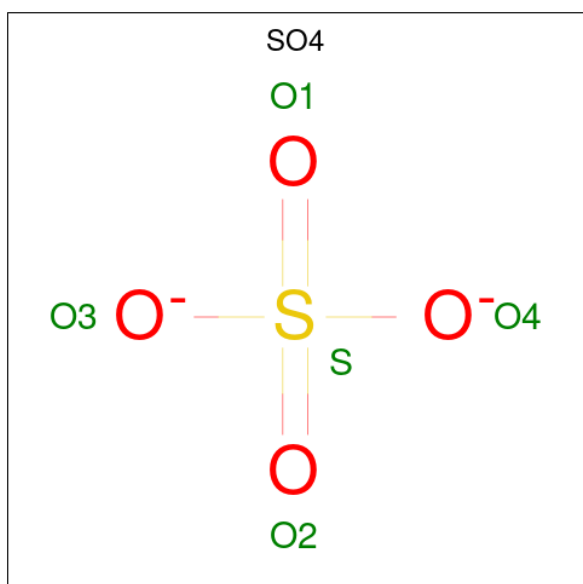
Chain	Residue	Modelled	Actual	Comment	Reference
A	-3	GLY	-	expression tag	UNP A6BMJ3
A	-2	PRO	-	expression tag	UNP A6BMJ3
A	-1	LEU	-	expression tag	UNP A6BMJ3
A	0	GLY	-	expression tag	UNP A6BMJ3
A	1	SER	-	expression tag	UNP A6BMJ3
B	-3	GLY	-	expression tag	UNP A6BMJ3
B	-2	PRO	-	expression tag	UNP A6BMJ3
B	-1	LEU	-	expression tag	UNP A6BMJ3
B	0	GLY	-	expression tag	UNP A6BMJ3
B	1	SER	-	expression tag	UNP A6BMJ3
C	-3	GLY	-	expression tag	UNP A6BMJ3
C	-2	PRO	-	expression tag	UNP A6BMJ3
C	-1	LEU	-	expression tag	UNP A6BMJ3
C	0	GLY	-	expression tag	UNP A6BMJ3
C	1	SER	-	expression tag	UNP A6BMJ3
D	-3	GLY	-	expression tag	UNP A6BMJ3
D	-2	PRO	-	expression tag	UNP A6BMJ3
D	-1	LEU	-	expression tag	UNP A6BMJ3
D	0	GLY	-	expression tag	UNP A6BMJ3
D	1	SER	-	expression tag	UNP A6BMJ3

- Molecule 2 is PYRIDOXAL-5'-PHOSPHATE (CCD ID: PLP) (formula: $C_8H_{10}NO_6P$).



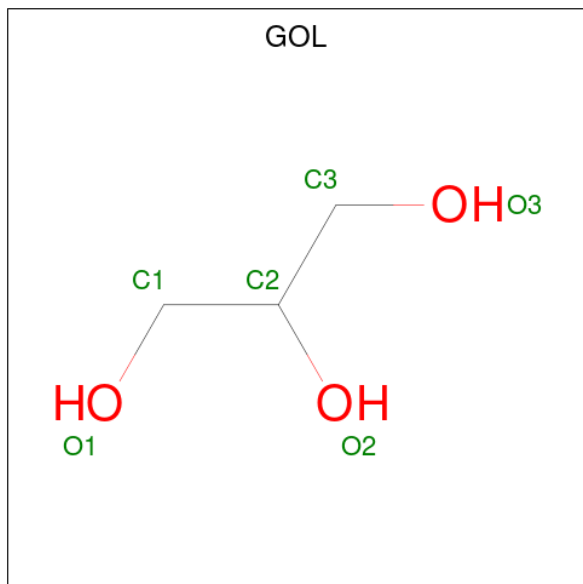
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			15	8	1	5	1		
2	B	1	Total	C	N	O	P	0	0
			15	8	1	5	1		
2	C	1	Total	C	N	O	P	0	0
			15	8	1	5	1		
2	D	1	Total	C	N	O	P	0	0
			15	8	1	5	1		

- Molecule 3 is SULFATE ION (CCD ID: SO4) (formula: O_4S).



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

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



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

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

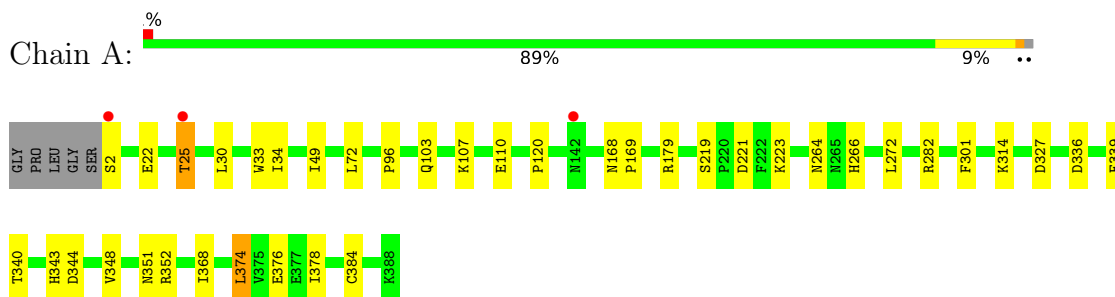
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	372	Total	O	0	6
			372	372		
5	B	394	Total	O	0	9
			394	394		
5	C	364	Total	O	0	6
			364	364		
5	D	336	Total	O	0	1
			336	336		

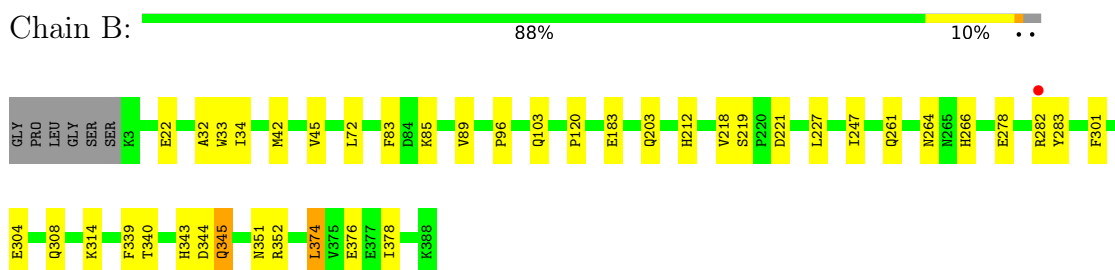
3 Residue-property plots [i](#)

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.

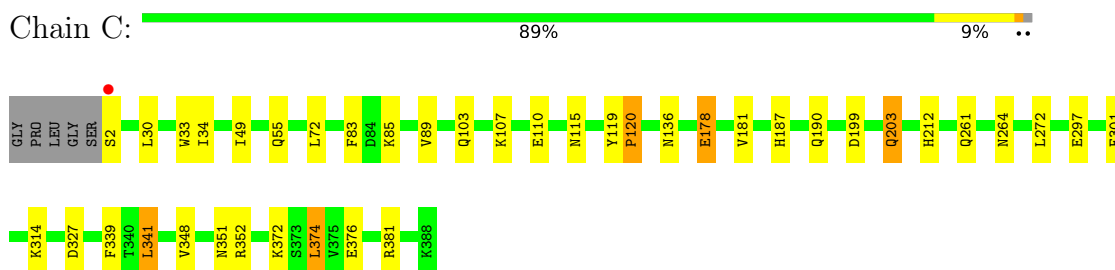
• Molecule 1: BetaC-S lyase



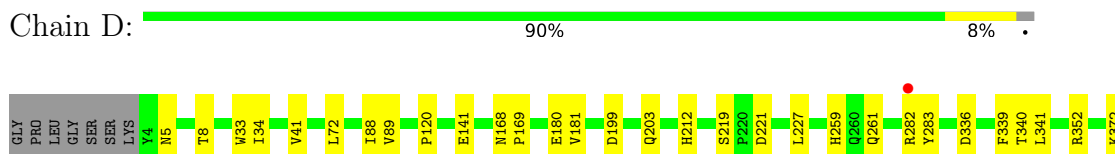
• Molecule 1: BetaC-S lyase



• Molecule 1: BetaC-S lyase



• Molecule 1: BetaC-S lyase



S373	L374	V375	E376	C384	K388
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4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	66.97Å 111.14Å 216.44Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	108.47 – 1.93 108.22 – 1.93	Depositor EDS
% Data completeness (in resolution range)	100.0 (108.47-1.93) 100.0 (108.22-1.93)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	11.04 (at 1.92Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.147 , 0.188 0.153 , 0.191	Depositor DCC
R_{free} test set	6130 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	14.4	Xtriage
Anisotropy	0.577	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 46.2	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	14349	wwPDB-VP
Average B, all atoms (Å ²)	14.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.69% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, SO4, PLP

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	0.84	0/3308	0.84	4/4495 (0.1%)
1	B	0.82	0/3270	0.84	1/4446 (0.0%)
1	C	0.83	0/3306	0.85	2/4491 (0.0%)
1	D	0.82	1/3274 (0.0%)	0.86	2/4454 (0.0%)
All	All	0.82	1/13158 (0.0%)	0.85	9/17886 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	41	VAL	CA-CB	5.92	1.60	1.54

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	120	PRO	N-CA-C	6.44	118.56	110.70
1	C	203	GLN	N-CA-C	5.96	118.57	111.71
1	A	120	PRO	N-CA-C	5.94	117.95	110.70
1	D	384	CYS	N-CA-C	5.62	117.08	111.07
1	C	120	PRO	N-CA-C	5.46	117.36	110.70

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	3190	0	3148	24	0
1	B	3164	0	3100	28	0
1	C	3191	0	3137	28	0
1	D	3164	0	3100	19	0
2	A	15	0	6	0	0
2	B	15	0	6	0	0
2	C	15	0	6	1	0
2	D	15	0	6	1	0
3	A	5	0	0	0	0
3	B	10	0	0	1	0
3	C	5	0	0	1	0
3	D	10	0	0	0	0
4	A	24	0	32	0	0
4	B	18	0	24	3	0
4	C	24	0	32	0	0
4	D	18	0	24	0	0
5	A	372	0	0	3	0
5	B	394	0	0	3	0
5	C	364	0	0	2	0
5	D	336	0	0	1	0
All	All	14349	0	12621	99	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.

The worst 5 of 99 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:103:GLN:HE22	1:B:264:ASN:HD21	1.36	0.73
1:C:30:LEU:HD22	1:C:374:LEU:HD21	1.70	0.71
1:B:103:GLN:NE2	1:B:264:ASN:HD21	1.89	0.71
1:B:72:LEU:HD23	1:B:83:PHE:CE1	2.27	0.69
1:C:103:GLN:HE22	1:C:264:ASN:HD21	1.41	0.69

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	398/392 (102%)	386 (97%)	12 (3%)	0	100	100
1	B	393/392 (100%)	382 (97%)	11 (3%)	0	100	100
1	C	397/392 (101%)	385 (97%)	12 (3%)	0	100	100
1	D	393/392 (100%)	382 (97%)	11 (3%)	0	100	100
All	All	1581/1568 (101%)	1535 (97%)	46 (3%)	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	355/345 (103%)	352 (99%)	3 (1%)	73	71
1	B	350/345 (101%)	346 (99%)	4 (1%)	65	60
1	C	354/345 (103%)	349 (99%)	5 (1%)	59	52
1	D	350/345 (101%)	348 (99%)	2 (1%)	78	78
All	All	1409/1380 (102%)	1395 (99%)	14 (1%)	70	64

5 of 14 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	2	SER
1	C	178[A]	GLU
1	D	374	LEU

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Mol	Chain	Res	Type
1	C	374	LEU
1	D	227	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 33 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	187	HIS
1	D	203	GLN
1	D	264	ASN
1	B	351	ASN
1	B	343	HIS

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](#)

24 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	$\# Z > 2$
3	SO4	B	501	-	4,4,4	0.40	0	6,6,6	1.06	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	PLP	B	401	1	15,15,16	1.78	5 (33%)	21,22,23	2.29	10 (47%)
2	PLP	C	401	1	15,15,16	1.64	5 (33%)	21,22,23	2.49	10 (47%)
4	GOL	D	602	-	5,5,5	0.39	0	5,5,5	0.60	0
4	GOL	D	601	-	5,5,5	0.30	0	5,5,5	0.75	0
3	SO4	C	501	-	4,4,4	0.33	0	6,6,6	1.16	1 (16%)
4	GOL	C	603	-	5,5,5	0.44	0	5,5,5	0.91	0
3	SO4	A	501	-	4,4,4	0.48	0	6,6,6	1.15	1 (16%)
4	GOL	B	603	-	5,5,5	0.32	0	5,5,5	0.87	0
3	SO4	D	502	-	4,4,4	0.24	0	6,6,6	0.35	0
2	PLP	D	401	1	15,15,16	1.67	7 (46%)	21,22,23	2.06	7 (33%)
4	GOL	A	602	-	5,5,5	0.31	0	5,5,5	0.50	0
4	GOL	A	601	-	5,5,5	0.35	0	5,5,5	0.45	0
3	SO4	D	501	-	4,4,4	0.34	0	6,6,6	1.08	1 (16%)
2	PLP	A	401	1	15,15,16	1.63	6 (40%)	21,22,23	2.48	10 (47%)
4	GOL	A	604	-	5,5,5	0.48	0	5,5,5	0.61	0
4	GOL	B	602	-	5,5,5	0.44	0	5,5,5	0.48	0
3	SO4	B	502	-	4,4,4	0.30	0	6,6,6	0.39	0
4	GOL	B	601	-	5,5,5	0.42	0	5,5,5	0.64	0
4	GOL	A	603	-	5,5,5	0.40	0	5,5,5	0.78	0
4	GOL	C	601	-	5,5,5	0.30	0	5,5,5	0.58	0
4	GOL	D	603	-	5,5,5	0.22	0	5,5,5	0.37	0
4	GOL	C	604	-	5,5,5	0.35	0	5,5,5	0.44	0
4	GOL	C	602	-	5,5,5	0.40	0	5,5,5	0.43	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	B	601	-	-	0/4/4/4	-
4	GOL	A	602	-	-	0/4/4/4	-
4	GOL	D	601	-	-	0/4/4/4	-
4	GOL	A	601	-	-	2/4/4/4	-
4	GOL	A	603	-	-	2/4/4/4	-
4	GOL	C	601	-	-	0/4/4/4	-
2	PLP	B	401	1	-	3/6/6/8	0/1/1/1
2	PLP	A	401	1	-	3/6/6/8	0/1/1/1
4	GOL	C	603	-	-	2/4/4/4	-
4	GOL	C	604	-	-	0/4/4/4	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	GOL	B	602	-	-	0/4/4/4	-
4	GOL	B	603	-	-	4/4/4/4	-
4	GOL	A	604	-	-	4/4/4/4	-
4	GOL	D	603	-	-	2/4/4/4	-
2	PLP	C	401	1	-	3/6/6/8	0/1/1/1
4	GOL	C	602	-	-	0/4/4/4	-
2	PLP	D	401	1	-	3/6/6/8	0/1/1/1
4	GOL	D	602	-	-	2/4/4/4	-

The worst 5 of 23 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	401	PLP	C5-C4	-3.45	1.36	1.40
2	C	401	PLP	C5-C4	-3.01	1.37	1.40
2	B	401	PLP	O3-C3	-3.01	1.30	1.36
2	C	401	PLP	C2-N1	2.94	1.39	1.33
2	A	401	PLP	C5-C4	-2.88	1.37	1.40

The worst 5 of 40 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	401	PLP	C4A-C4-C5	-4.60	116.19	120.94
2	C	401	PLP	C6-C5-C4	4.48	121.77	118.10
2	B	401	PLP	O4P-C5A-C5	4.33	117.47	109.36
2	C	401	PLP	O4P-P-O1P	-4.14	95.25	106.44
2	A	401	PLP	C6-C5-C4	4.10	121.46	118.10

There are no chirality outliers.

5 of 30 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	401	PLP	C5A-O4P-P-O2P
2	A	401	PLP	C5A-O4P-P-O3P
2	B	401	PLP	C5A-O4P-P-O2P
2	B	401	PLP	C5A-O4P-P-O3P
2	C	401	PLP	C5A-O4P-P-O1P

There are no ring outliers.

5 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	501	SO4	1	0
2	C	401	PLP	1	0
3	C	501	SO4	1	0
4	B	603	GOL	3	0
2	D	401	PLP	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, 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	387/392 (98%)	-0.58	3 (0%) 82 87	4, 11, 20, 31	13 (3%)
1	B	386/392 (98%)	-0.59	1 (0%) 90 93	6, 11, 19, 28	9 (2%)
1	C	387/392 (98%)	-0.49	1 (0%) 90 93	4, 13, 22, 38	12 (3%)
1	D	385/392 (98%)	-0.43	1 (0%) 90 93	6, 13, 22, 28	10 (2%)
All	All	1545/1568 (98%)	-0.52	6 (0%) 88 92	4, 12, 21, 38	44 (2%)

The worst 5 of 6 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	282	ARG	3.5
1	C	2	SER	2.6
1	B	282	ARG	2.5
1	A	2	SER	2.3
1	A	25	THR	2.1

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	SO4	B	502	5/5	0.77	0.16	19,20,23,24	5
4	GOL	A	603	6/6	0.82	0.19	17,30,32,36	0
4	GOL	C	604	6/6	0.85	0.15	32,38,39,42	0
4	GOL	C	603	6/6	0.87	0.12	35,37,38,40	0
4	GOL	D	603	6/6	0.87	0.15	18,28,32,35	0
4	GOL	B	603	6/6	0.88	0.15	32,37,38,39	0
3	SO4	D	502	5/5	0.88	0.12	21,22,24,24	5
4	GOL	A	602	6/6	0.89	0.12	22,24,25,25	0
3	SO4	B	501	5/5	0.91	0.17	30,30,33,36	0
4	GOL	A	604	6/6	0.91	0.10	33,35,35,36	0
4	GOL	C	602	6/6	0.92	0.08	20,20,21,21	0
4	GOL	D	602	6/6	0.92	0.10	25,29,30,31	0
3	SO4	C	501	5/5	0.92	0.15	30,31,34,35	0
4	GOL	B	601	6/6	0.93	0.13	22,25,26,29	0
4	GOL	B	602	6/6	0.93	0.07	19,21,22,24	0
4	GOL	D	601	6/6	0.93	0.10	25,27,27,28	0
4	GOL	A	601	6/6	0.93	0.09	26,28,29,30	0
3	SO4	D	501	5/5	0.93	0.15	32,34,34,36	0
3	SO4	A	501	5/5	0.94	0.17	24,29,30,31	0
4	GOL	C	601	6/6	0.95	0.07	21,22,24,25	0
2	PLP	C	401	15/16	0.97	0.05	7,10,14,16	0
2	PLP	D	401	15/16	0.98	0.05	9,11,15,16	0
2	PLP	B	401	15/16	0.98	0.04	8,11,15,16	0
2	PLP	A	401	15/16	0.98	0.04	8,10,13,15	0

6.5 Other polymers [i](#)

There are no such residues in this entry.