



# Full wwPDB X-ray Structure Validation Report ⓘ

Aug 22, 2020 – 01:48 PM BST

PDB ID : 3ETT  
Title : Crystal structure of a bacterial arylsulfate sulfotransferase catalytic intermediate with 4-nitrophenol bound in the active site  
Authors : Malojcic, G.; Owen, R.L.; Grimshaw, J.P.; Glockshuber, R.  
Deposited on : 2008-10-08  
Resolution : 2.10 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.

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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 : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.13.1  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.13.1

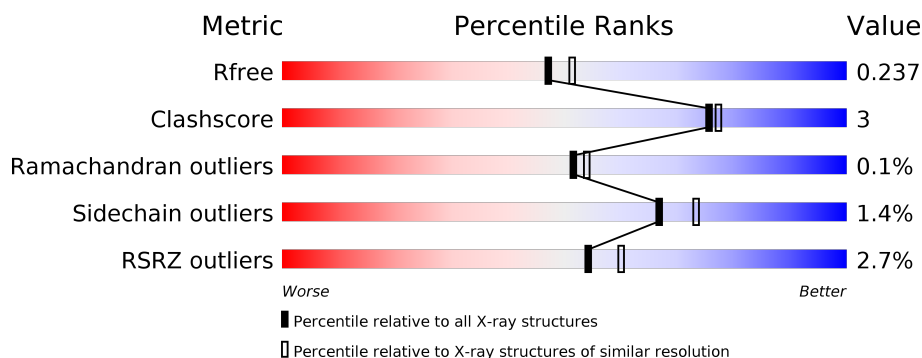
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.10 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))
$R_{free}$	130704	5197 (2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)
RSRZ outliers	127900	5083 (2.10-2.10)

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 on 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	571	<div> <div>4%</div> <div> <div></div> <div>91%</div> <div>8% ..</div> </div> </div>
1	B	571	<div> <div>2%</div> <div> <div></div> <div>93%</div> <div>5% ..</div> </div> </div>

## 2 Entry composition [i](#)

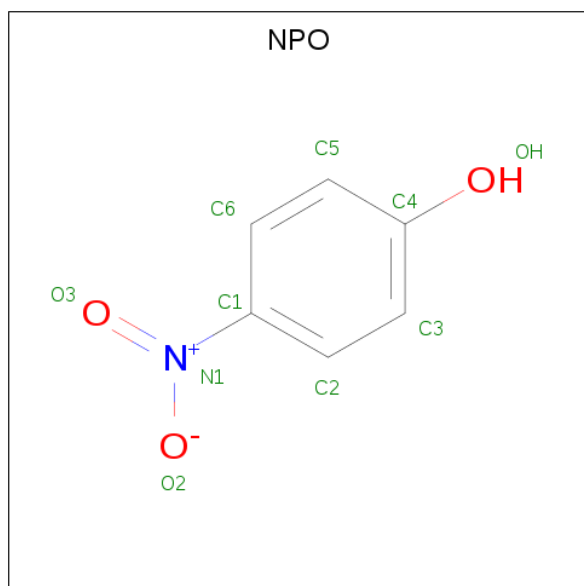
There are 4 unique types of molecules in this entry. The entry contains 9723 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Arylsulfate sulfotransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	565	Total	C	N	O	S	0	2	0
			4461	2833	763	854	11			
1	B	565	Total	C	N	O	S	0	1	0
			4458	2831	763	853	11			

- Molecule 2 is P-NITROPHENOL (three-letter code: NPO) (formula:  $C_6H_5NO_3$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			10	6	1	3		
2	B	1	Total	C	N	O	0	0
			10	6	1	3		

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula:  $O_4S$ ).



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	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		

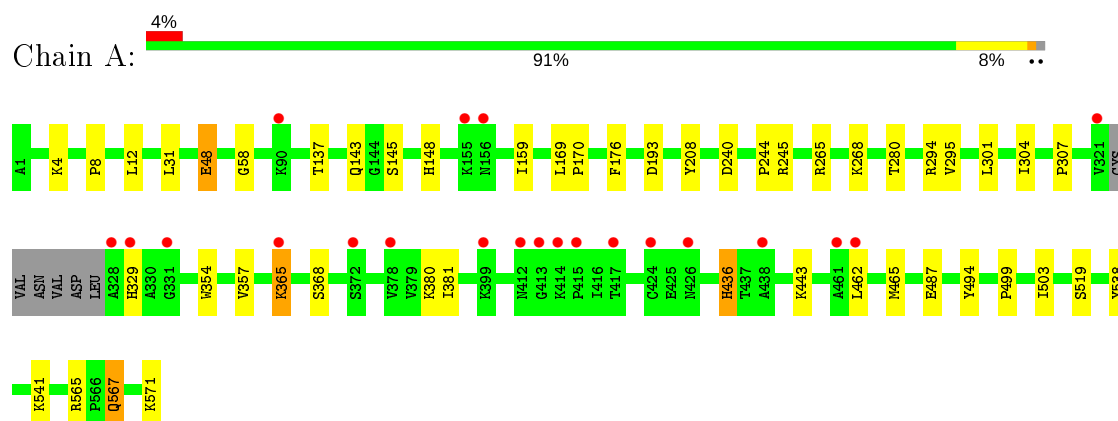
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	373	Total	O	0	0
			373	373		
4	B	381	Total	O	0	0
			381	381		

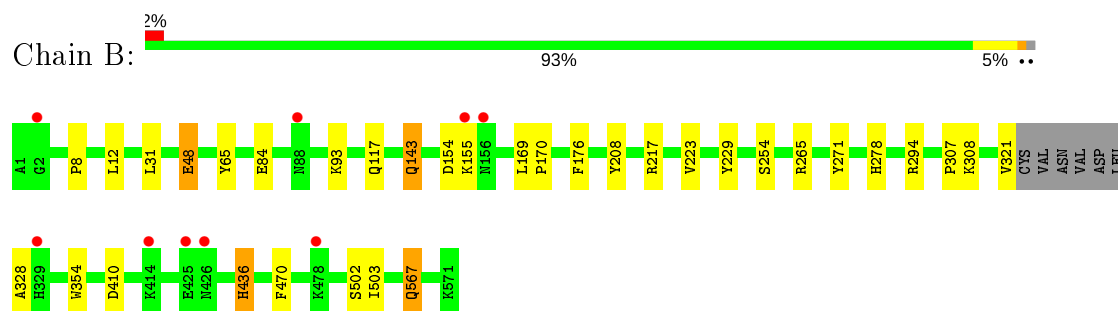
### 3 Residue-property plots [i](#)

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: Arylsulfate sulfotransferase



#### • Molecule 1: Arylsulfate sulfotransferase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 32 1 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	181.50 Å 181.50 Å 99.98 Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	33.98 – 2.10 33.92 – 2.10	Depositor EDS
% Data completeness (in resolution range)	99.6 (33.98-2.10) 99.5 (33.92-2.10)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	0.08	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.47 (at 2.10 Å)	Xtriage
Refinement program	REFMAC 5.3	Depositor
R, $R_{free}$	0.187 , 0.232 0.192 , 0.237	Depositor DCC
$R_{free}$ test set	1778 reflections (1.64%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	29.6	Xtriage
Anisotropy	0.725	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 49.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.027 for -h,-k,l	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	9723	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.59% 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: NPO, HS8, 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	0.98	2/4561 (0.0%)	0.83	1/6188 (0.0%)
1	B	0.98	2/4555 (0.0%)	0.84	3/6181 (0.0%)
All	All	0.98	4/9116 (0.0%)	0.84	4/12369 (0.0%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	365	LYS	CD-CE	12.20	1.81	1.51
1	B	229	TYR	CD2-CE2	6.60	1.49	1.39
1	A	48	GLU	CB-CG	6.13	1.63	1.52
1	B	48	GLU	CG-CD	5.02	1.59	1.51

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	294	ARG	NE-CZ-NH2	7.46	124.03	120.30
1	A	193	ASP	CB-CG-OD1	6.18	123.86	118.30
1	B	217	ARG	NE-CZ-NH2	-6.02	117.29	120.30
1	B	410	ASP	CB-CG-OD1	5.48	123.23	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	4461	0	4302	34	0
1	B	4458	0	4308	21	0
2	A	10	0	4	2	0
2	B	10	0	4	1	0
3	A	15	0	0	0	0
3	B	15	0	0	0	0
4	A	373	0	0	7	0
4	B	381	0	0	7	0
All	All	9723	0	8618	55	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 (55) 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:365:LYS:CE	1:A:365:LYS:CD	1.81	1.54
1:A:436:HS8:NE2	1:A:436:HS8:S	2.08	1.26
1:B:48:GLU:CD	1:B:48:GLU:H	1.94	0.71
2:A:572:NPO:H3	4:A:919:HOH:O	1.94	0.66
1:A:329:HIS:HA	4:A:729:HOH:O	1.97	0.64
1:B:567:GLN:HE21	1:B:567:GLN:H	1.49	0.61
1:A:494:TYR:HD1	4:A:806:HOH:O	1.83	0.60
1:A:565:ARG:HB3	1:A:567:GLN:HE21	1.66	0.60
1:B:84:GLU:HG2	1:B:93:LYS:HG3	1.84	0.59
1:B:436:HS8:S	2:B:572:NPO:OH	2.62	0.58
1:B:169:LEU:N	1:B:170:PRO:CD	2.70	0.54
1:A:567:GLN:HG3	4:A:744:HOH:O	2.08	0.53
1:A:307:PRO:HA	1:A:354:TRP:CE3	2.44	0.53
1:B:154:ASP:OD1	1:B:155:LYS:N	2.42	0.53
1:A:145:SER:HB3	1:A:170:PRO:HB3	1.91	0.52
1:A:48:GLU:CD	1:A:48:GLU:H	2.13	0.52
1:A:567:GLN:NE2	1:A:567:GLN:H	2.09	0.51
1:B:328:ALA:O	4:B:664:HOH:O	2.19	0.50
1:A:169:LEU:N	1:A:170:PRO:CD	2.75	0.50
1:B:321:VAL:HG12	4:B:652:HOH:O	2.12	0.50
1:B:321:VAL:CG1	4:B:652:HOH:O	2.61	0.49
1:A:565:ARG:HB3	1:A:567:GLN:NE2	2.28	0.48
1:A:567:GLN:CG	4:A:744:HOH:O	2.61	0.48
1:A:294:ARG:HD2	4:B:806:HOH:O	2.14	0.47
1:A:301:LEU:CD1	1:A:357:VAL:HG21	2.45	0.47
1:B:567:GLN:NE2	1:B:567:GLN:H	2.11	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:143:GLN:NE2	4:B:710:HOH:O	2.49	0.46
1:B:436:HS8:HE1	4:B:779:HOH:O	2.16	0.46
1:A:567:GLN:HB3	4:A:656:HOH:O	2.16	0.45
1:A:368:SER:OG	1:A:380:LYS:HE2	2.16	0.45
1:B:328:ALA:C	4:B:664:HOH:O	2.54	0.45
1:A:487:GLU:O	1:A:541:LYS:HE3	2.16	0.45
1:A:58:GLY:HA3	1:A:571:LYS:O	2.17	0.44
1:A:31:LEU:HA	1:A:31:LEU:HD12	1.78	0.44
1:A:245:ARG:HD3	1:B:65:TYR:O	2.17	0.44
1:B:307:PRO:HA	1:B:354:TRP:CE3	2.53	0.43
1:B:223:VAL:HG13	1:B:254:SER:HB3	1.99	0.43
1:A:462:LEU:O	1:A:465:MET:HB2	2.18	0.43
1:A:436:HS8:S	2:A:572:NPO:OH	2.77	0.43
1:B:117:GLN:HG3	1:B:176:PHE:CE2	2.54	0.43
1:B:31:LEU:HD12	1:B:31:LEU:HA	1.81	0.42
1:A:365:LYS:CE	1:A:365:LYS:CG	2.86	0.42
1:A:4:LYS:NZ	4:A:864:HOH:O	2.52	0.42
1:A:137:THR:HG23	1:A:176:PHE:HB3	2.00	0.42
1:B:470:PHE:CD1	1:B:470:PHE:N	2.86	0.42
1:A:304:ILE:HG21	1:A:381:ILE:HD13	2.00	0.42
1:A:8:PRO:HB3	1:A:12:LEU:O	2.20	0.41
1:A:443:LYS:HE2	1:A:538:TYR:CZ	2.56	0.41
1:A:240:ASP:C	1:A:240:ASP:OD1	2.59	0.41
1:A:499:PRO:HD2	1:A:519:SER:OG	2.19	0.41
1:B:8:PRO:HB3	1:B:12:LEU:O	2.20	0.41
1:A:268:LYS:O	1:A:280:THR:HA	2.21	0.41
1:A:244:PRO:HG2	1:A:295:VAL:CG2	2.51	0.41
1:B:271:TYR:O	1:B:278:HIS:HA	2.21	0.40
1:A:567:GLN:H	1:A:567:GLN:CD	2.24	0.40

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	562/571 (98%)	541 (96%)	21 (4%)	0	100	100
1	B	561/571 (98%)	535 (95%)	25 (4%)	1 (0%)	47	49
All	All	1123/1142 (98%)	1076 (96%)	46 (4%)	1 (0%)	51	54

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	502	SER

### 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	469/482 (97%)	462 (98%)	7 (2%)	65	71
1	B	469/482 (97%)	463 (99%)	6 (1%)	69	75
All	All	938/964 (97%)	925 (99%)	13 (1%)	67	73

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	143	GLN
1	A	148	HIS
1	A	159	ILE
1	A	208	TYR
1	A	265	ARG
1	A	503	ILE
1	A	567	GLN
1	B	143	GLN
1	B	208	TYR
1	B	265	ARG
1	B	308	LYS
1	B	503	ILE
1	B	567	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such

sidechains are listed below:

Mol	Chain	Res	Type
1	A	567	GLN
1	B	143	GLN
1	B	236	GLN
1	B	567	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

2 non-standard protein/DNA/RNA residues 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	$\# Z  > 2$
1	HS8	A	436	1	10,14,15	0.98	0	4,20,22	1.24	1 (25%)
1	HS8	B	436	1	10,14,15	1.34	1 (10%)	4,20,22	1.47	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
1	HS8	A	436	1	-	0/5/12/14	0/1/1/1
1	HS8	B	436	1	-	0/5/12/14	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	436	HS8	O1-S	3.49	1.48	1.42

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	436	HS8	CB-CG-CD2	2.01	132.09	127.95

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	436	HS8	2	0
1	B	436	HS8	2	0

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

8 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	A	574	-	4,4,4	0.20	0	6,6,6	1.55	2 (33%)
3	SO4	B	574	-	4,4,4	0.31	0	6,6,6	1.09	0
2	NPO	B	572	-	9,10,10	1.82	2 (22%)	11,13,13	1.98	2 (18%)
3	SO4	A	576	-	4,4,4	0.22	0	6,6,6	0.69	0
3	SO4	A	575	-	4,4,4	0.22	0	6,6,6	0.26	0
3	SO4	B	575	-	4,4,4	0.21	0	6,6,6	0.82	0
2	NPO	A	572	-	9,10,10	1.15	1 (11%)	11,13,13	0.69	0
3	SO4	B	576	-	4,4,4	0.35	0	6,6,6	0.34	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
2	NPO	A	572	-	-	0/2/4/4	0/1/1/1
2	NPO	B	572	-	-	0/2/4/4	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	572	NPO	C1-N1	-3.40	1.37	1.45
2	B	572	NPO	OH-C4	-3.25	1.29	1.37
2	A	572	NPO	C1-N1	-2.55	1.39	1.45

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	572	NPO	O3-N1-C1	-4.01	113.13	118.80
2	B	572	NPO	C2-C1-N1	-3.37	116.84	119.38
3	A	574	SO4	O4-S-O2	2.33	121.46	109.31
3	A	574	SO4	O4-S-O3	-2.10	100.08	109.06

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	572	NPO	1	0
2	A	572	NPO	2	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, 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	564/571 (98%)	-0.26	21 (3%) 41 48	23, 34, 55, 85	0
1	B	564/571 (98%)	-0.37	9 (1%) 72 75	24, 34, 55, 88	0
All	All	1128/1142 (98%)	-0.31	30 (2%) 54 60	23, 34, 55, 88	0

All (30) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	155	LYS	5.4
1	A	156[A]	ASN	4.2
1	A	321	VAL	3.8
1	A	462	LEU	3.5
1	B	155	LYS	3.1
1	B	156	ASN	3.1
1	B	425	GLU	3.0
1	A	417	THR	2.9
1	A	412	ASN	2.9
1	A	331	GLY	2.8
1	A	329	HIS	2.7
1	B	2	GLY	2.7
1	A	461	ALA	2.6
1	A	414	LYS	2.6
1	B	88	ASN	2.5
1	A	426	ASN	2.5
1	B	414	LYS	2.4
1	A	399	LYS	2.4
1	A	424	CYS	2.3
1	A	415	PRO	2.3
1	B	426	ASN	2.3
1	B	478	LYS	2.2
1	A	438	ALA	2.2
1	A	413	GLY	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	372	SER	2.2
1	A	378	VAL	2.2
1	A	365	LYS	2.2
1	B	329	HIS	2.0
1	A	90	LYS	2.0
1	A	328	ALA	2.0

## 6.2 Non-standard residues in protein, DNA, RNA chains [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
1	HS8	A	436	14/15	0.98	0.17	29,31,34,36	0
1	HS8	B	436	14/15	0.99	0.14	27,30,33,33	0

## 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
2	NPO	B	572	10/10	0.89	0.23	31,37,40,42	7
2	NPO	A	572	10/10	0.91	0.26	39,45,48,49	7
3	SO4	A	574	5/5	0.95	0.13	46,49,61,64	0
3	SO4	A	576	5/5	0.96	0.14	67,71,74,75	0
3	SO4	B	574	5/5	0.97	0.14	48,54,58,61	0
3	SO4	B	576	5/5	0.97	0.15	66,68,69,70	0
3	SO4	B	575	5/5	0.98	0.13	57,59,65,65	0
3	SO4	A	575	5/5	0.99	0.14	50,50,52,53	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.