



# Full wwPDB X-ray Structure Validation Report ⓘ

Nov 2, 2023 – 12:56 AM EDT

PDB ID : 3L7R  
Title : crystal structure of MetE from streptococcus mutans  
Authors : Fu, T.M.; Liang, Y.H.; Su, X.D.  
Deposited on : 2009-12-29  
Resolution : 2.40 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)

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<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>.

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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 : 2.36  
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) : 2.36

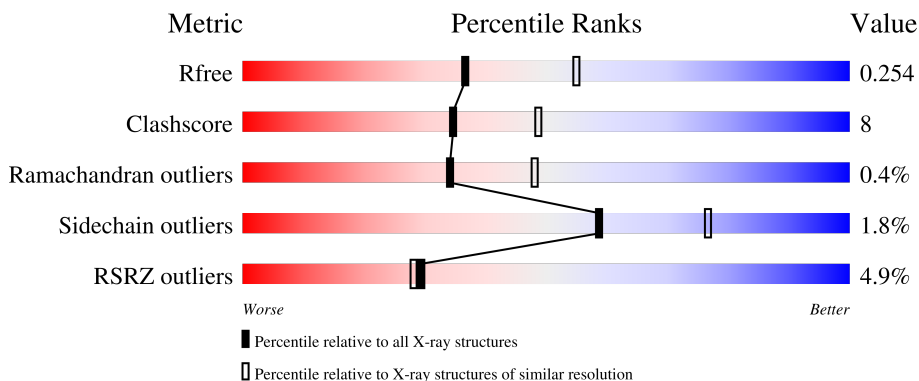
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.40 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	3907 (2.40-2.40)
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)
RSRZ outliers	127900	3811 (2.40-2.40)

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  $\geq 3$ , 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	779	

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 5999 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 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	736	5617	3611	927	1071	8	0	0	0

There are 34 discrepancies between the modelled and reference sequences:

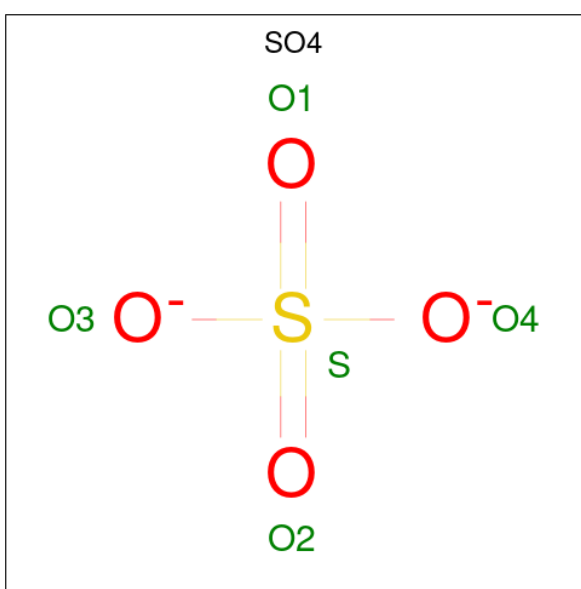
Chain	Residue	Modelled	Actual	Comment	Reference
A	-33	MET	-	expression tag	UNP Q8CWX6
A	-32	GLY	-	expression tag	UNP Q8CWX6
A	-31	SER	-	expression tag	UNP Q8CWX6
A	-30	SER	-	expression tag	UNP Q8CWX6
A	-29	HIS	-	expression tag	UNP Q8CWX6
A	-28	HIS	-	expression tag	UNP Q8CWX6
A	-27	HIS	-	expression tag	UNP Q8CWX6
A	-26	HIS	-	expression tag	UNP Q8CWX6
A	-25	HIS	-	expression tag	UNP Q8CWX6
A	-24	HIS	-	expression tag	UNP Q8CWX6
A	-23	SER	-	expression tag	UNP Q8CWX6
A	-22	SER	-	expression tag	UNP Q8CWX6
A	-21	GLY	-	expression tag	UNP Q8CWX6
A	-20	LEU	-	expression tag	UNP Q8CWX6
A	-19	VAL	-	expression tag	UNP Q8CWX6
A	-18	PRO	-	expression tag	UNP Q8CWX6
A	-17	ARG	-	expression tag	UNP Q8CWX6
A	-16	GLY	-	expression tag	UNP Q8CWX6
A	-15	SER	-	expression tag	UNP Q8CWX6
A	-14	HIS	-	expression tag	UNP Q8CWX6
A	-13	MET	-	expression tag	UNP Q8CWX6
A	-12	ALA	-	expression tag	UNP Q8CWX6
A	-11	SER	-	expression tag	UNP Q8CWX6
A	-10	MET	-	expression tag	UNP Q8CWX6
A	-9	THR	-	expression tag	UNP Q8CWX6
A	-8	GLY	-	expression tag	UNP Q8CWX6

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-7	GLY	-	expression tag	UNP Q8CWX6
A	-6	GLN	-	expression tag	UNP Q8CWX6
A	-5	GLN	-	expression tag	UNP Q8CWX6
A	-4	MET	-	expression tag	UNP Q8CWX6
A	-3	GLY	-	expression tag	UNP Q8CWX6
A	-2	ARG	-	expression tag	UNP Q8CWX6
A	-1	GLY	-	expression tag	UNP Q8CWX6
A	0	SER	-	expression tag	UNP Q8CWX6

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



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

- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	3	Total Zn 3 3	0	0

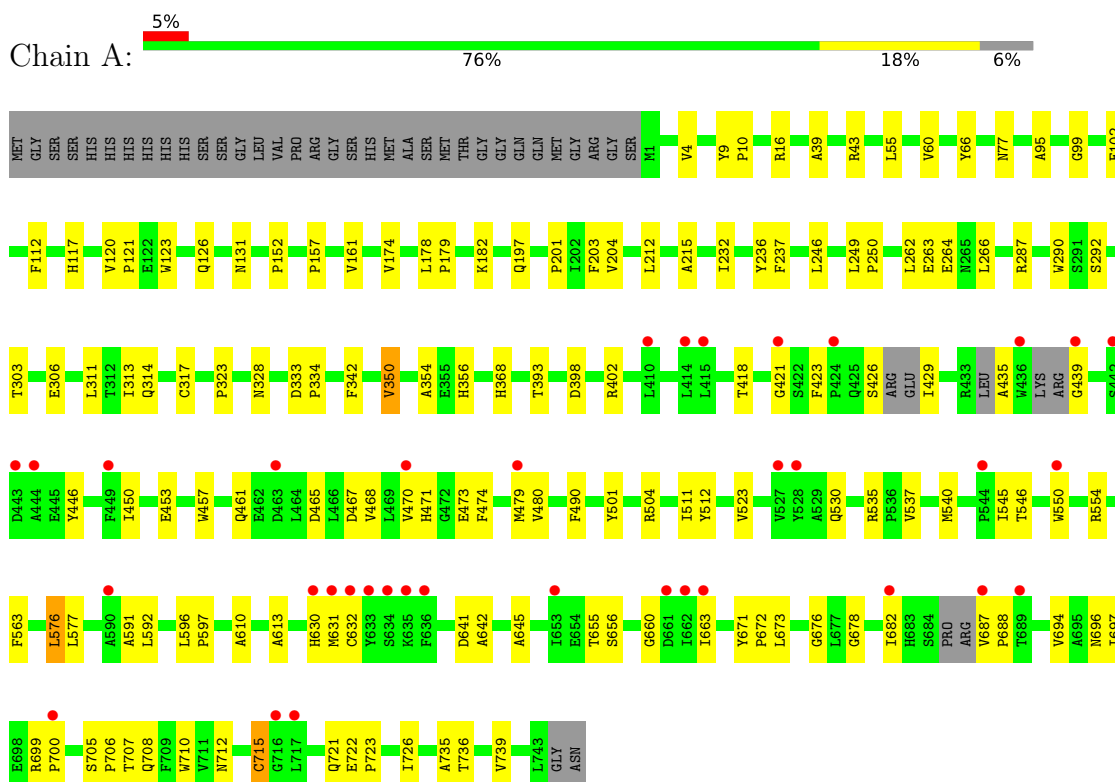
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	364	Total 364	O 364	0	0

### 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: 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	52.91Å 99.36Å 77.45Å 90.00° 94.95° 90.00°	Depositor
Resolution (Å)	45.39 – 2.40 60.94 – 2.40	Depositor EDS
% Data completeness (in resolution range)	92.3 (45.39-2.40) 92.3 (60.94-2.40)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.96 (at 2.40Å)	Xtrriage
Refinement program	PHENIX (phenix.refine)	Depositor
R, $R_{free}$	0.200 , 0.262 0.195 , 0.254	Depositor DCC
$R_{free}$ test set	1449 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	26.0	Xtrriage
Anisotropy	0.514	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 43.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	5999	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	30.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.32% 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: ZN, 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	0.26	0/5737	0.43	0/7817

There are no bond length outliers.

There are no bond angle outliers.

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	5617	0	5339	91	0
2	A	15	0	0	1	0
3	A	3	0	0	0	0
4	A	364	0	0	4	0
All	All	5999	0	5339	91	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 8.

All (91) 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:656:SER:HA	1:A:696:ASN:HD21	1.41	0.85
1:A:123:TRP:HA	1:A:126:GLN:NE2	2.06	0.71
1:A:435:ALA:HA	1:A:439:GLY:HA3	1.77	0.66
1:A:511:ILE:O	1:A:554:ARG:HG3	1.95	0.66
1:A:694:VAL:HG23	1:A:739:VAL:HG12	1.77	0.65
1:A:201:PRO:HG3	1:A:236:TYR:CZ	2.31	0.65
1:A:465:ASP:HA	1:A:535:ARG:HH12	1.60	0.64
1:A:671:TYR:CE2	1:A:673:LEU:HB2	2.32	0.64
1:A:530:GLN:NE2	1:A:537:VAL:H	1.97	0.61
1:A:262:LEU:O	1:A:266:LEU:HB2	2.01	0.61
1:A:736:THR:O	1:A:739:VAL:HG22	1.99	0.61
1:A:592:LEU:HD13	1:A:631:MET:HE1	1.82	0.61
1:A:699:ARG:HB3	1:A:700:PRO:HD3	1.83	0.60
1:A:77:ASN:HD22	1:A:131:ASN:HD21	1.50	0.59
1:A:264:GLU:HG2	4:A:773:HOH:O	2.02	0.58
1:A:501:TYR:CZ	1:A:504:ARG:HG3	2.39	0.57
1:A:314:GLN:HA	1:A:350:VAL:HG21	1.86	0.56
1:A:545:ILE:HD11	1:A:610:ALA:HB1	1.88	0.56
1:A:421:GLY:HA2	1:A:470:VAL:HG11	1.86	0.56
1:A:398:ASP:O	1:A:402:ARG:HG3	2.06	0.56
1:A:530:GLN:HE22	1:A:537:VAL:H	1.53	0.55
1:A:694:VAL:HG23	1:A:739:VAL:CG1	2.36	0.55
1:A:292:SER:O	1:A:368:HIS:HE1	1.90	0.55
1:A:722:GLU:O	1:A:726:ILE:HG12	2.07	0.54
1:A:546:THR:HA	1:A:591:ALA:HB3	1.89	0.54
1:A:157:PRO:O	1:A:161:VAL:HG23	2.08	0.54
1:A:457:TRP:O	1:A:461:GLN:HG3	2.08	0.53
1:A:656:SER:HA	1:A:696:ASN:ND2	2.17	0.53
1:A:4:VAL:HG23	1:A:55:LEU:HA	1.91	0.53
1:A:523:VAL:HG21	1:A:576:LEU:HB3	1.91	0.53
1:A:328:ASN:HB2	4:A:1004:HOH:O	2.10	0.52
1:A:333:ASP:OD1	1:A:334:PRO:HD2	2.10	0.52
1:A:313:ILE:HG22	1:A:350:VAL:HG22	1.90	0.52
1:A:471:HIS:CD2	1:A:473:GLU:H	2.28	0.52
1:A:203:PHE:CZ	1:A:215:ALA:HB2	2.45	0.52
1:A:287:ARG:HG3	1:A:317:CYS:SG	2.51	0.51
1:A:630:HIS:NE2	1:A:632:CYS:SG	2.84	0.51
1:A:480:VAL:HG21	1:A:550:TRP:HB2	1.93	0.50
1:A:697:ILE:O	1:A:700:PRO:HD2	2.12	0.50
1:A:178:LEU:HB2	1:A:179:PRO:HD3	1.94	0.49
1:A:290:TRP:CH2	1:A:512:TYR:HA	2.47	0.49
1:A:77:ASN:ND2	1:A:131:ASN:HD21	2.10	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:490:PHE:CE2	1:A:511:ILE:HG12	2.48	0.49
1:A:117:HIS:HB2	1:A:501:TYR:HB3	1.95	0.49
1:A:4:VAL:CG2	1:A:55:LEU:HA	2.44	0.48
1:A:706:PRO:C	1:A:708:GLN:H	2.17	0.48
1:A:39:ALA:O	1:A:43:ARG:HG3	2.13	0.48
1:A:161:VAL:HG21	1:A:174:VAL:HG22	1.95	0.48
1:A:290:TRP:HH2	1:A:512:TYR:HA	1.79	0.47
1:A:663:ILE:HG13	1:A:663:ILE:O	2.13	0.47
1:A:313:ILE:HD12	1:A:354:ALA:HB2	1.96	0.46
1:A:356:HIS:CE1	4:A:1112:HOH:O	2.68	0.45
1:A:112:PHE:CZ	1:A:201:PRO:HB2	2.51	0.45
1:A:236:TYR:O	1:A:237:PHE:HB2	2.16	0.45
1:A:323:PRO:HB2	1:A:342:PHE:CD2	2.51	0.45
1:A:446:TYR:O	1:A:450:ILE:HG12	2.16	0.45
1:A:479:MET:HG2	1:A:550:TRP:CZ3	2.52	0.45
1:A:655:THR:HB	1:A:660:GLY:HA2	1.98	0.45
1:A:563:PHE:HB3	1:A:613:ALA:HB2	1.99	0.45
1:A:699:ARG:CB	1:A:700:PRO:HD3	2.47	0.45
1:A:457:TRP:CD1	1:A:474:PHE:CZ	3.05	0.44
1:A:201:PRO:O	1:A:204:VAL:HG22	2.17	0.44
1:A:592:LEU:C	1:A:592:LEU:HD23	2.38	0.44
1:A:60:VAL:O	1:A:152:PRO:HA	2.18	0.44
1:A:212:LEU:HD22	1:A:246:LEU:HD21	1.98	0.44
1:A:356:HIS:HE1	4:A:1112:HOH:O	2.01	0.43
1:A:9:TYR:CG	1:A:10:PRO:HD2	2.53	0.43
1:A:249:LEU:HA	1:A:250:PRO:HD3	1.89	0.43
1:A:721:GLN:HB3	1:A:723:PRO:HD2	2.00	0.43
1:A:678:GLY:HA2	1:A:712:ASN:O	2.17	0.43
1:A:418:THR:HB	1:A:468:VAL:HB	2.01	0.43
1:A:642:ALA:O	1:A:645:ALA:HB3	2.19	0.42
1:A:4:VAL:HB	1:A:350:VAL:HG13	2.01	0.42
1:A:423:PHE:HE2	1:A:461:GLN:NE2	2.17	0.42
1:A:457:TRP:CD1	1:A:474:PHE:HZ	2.38	0.42
1:A:676:GLY:HA2	1:A:710:TRP:HB2	2.02	0.42
1:A:705:SER:O	1:A:708:GLN:HB3	2.20	0.42
1:A:303:THR:O	1:A:306:GLU:HG2	2.20	0.42
1:A:426:SER:C	1:A:429:ILE:HA	2.40	0.42
1:A:687:VAL:HA	1:A:688:PRO:HD3	1.82	0.41
1:A:95:ALA:O	1:A:99:GLY:N	2.50	0.41
1:A:120:VAL:HA	1:A:121:PRO:HD3	1.93	0.41
1:A:16:ARG:NH2	2:A:748:SO4:O1	2.47	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:453:GLU:HA	1:A:453:GLU:OE1	2.21	0.41
1:A:596:LEU:HA	1:A:597:PRO:HD3	1.96	0.40
1:A:672:PRO:HG2	1:A:673:LEU:HD13	2.03	0.40
1:A:735:ALA:O	1:A:739:VAL:HG13	2.21	0.40
1:A:161:VAL:HG21	1:A:174:VAL:CG2	2.50	0.40
1:A:523:VAL:HG22	1:A:577:LEU:HD23	2.03	0.40
1:A:197:GLN:HA	1:A:232:ILE:HB	2.04	0.40
1:A:682:ILE:HG21	1:A:715:CYS:H	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	726/779 (93%)	690 (95%)	33 (4%)	3 (0%)	34 48

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	102	GLU
1	A	66	TYR
1	A	707	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	559/668 (84%)	549 (98%)	10 (2%)	59 76

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	182	LYS
1	A	263	GLU
1	A	311	LEU
1	A	350	VAL
1	A	393	THR
1	A	467	ASP
1	A	540	MET
1	A	576	LEU
1	A	641	ASP
1	A	715	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	33	ASN
1	A	50	GLN
1	A	77	ASN
1	A	103	ASN
1	A	248	GLN
1	A	356	HIS
1	A	368	HIS
1	A	530	GLN
1	A	696	ASN
1	A	708	GLN
1	A	721	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 monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 3 are monoatomic - leaving 3 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
2	SO4	A	746	-	4,4,4	0.18	0	6,6,6	0.13	0
2	SO4	A	747	-	4,4,4	0.13	0	6,6,6	0.12	0
2	SO4	A	748	-	4,4,4	0.14	0	6,6,6	0.12	0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	748	SO4	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, 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	736/779 (94%)	0.05	36 (4%) <span style="border: 1px solid red; padding: 2px;">29</span> <span style="border: 1px solid red; padding: 2px;">28</span>	12, 24, 67, 83	0

All (36) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	636	PHE	8.2
1	A	633	TYR	6.3
1	A	634	SER	5.8
1	A	717	LEU	5.2
1	A	700	PRO	4.9
1	A	663	ILE	4.8
1	A	414	LEU	4.3
1	A	682	ILE	4.0
1	A	436	TRP	3.8
1	A	449	PHE	3.3
1	A	716	GLY	3.3
1	A	662	ILE	3.1
1	A	421	GLY	3.0
1	A	479	MET	2.9
1	A	444	ALA	2.9
1	A	443	ASP	2.7
1	A	439	GLY	2.6
1	A	544	PRO	2.5
1	A	442	SER	2.5
1	A	631	MET	2.5
1	A	410	LEU	2.4
1	A	661	ASP	2.4
1	A	424	PRO	2.3
1	A	635	LYS	2.3
1	A	630	HIS	2.3
1	A	687	VAL	2.3
1	A	689	THR	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	463	ASP	2.2
1	A	653	ILE	2.2
1	A	528	TYR	2.1
1	A	590	ALA	2.1
1	A	632	CYS	2.1
1	A	550	TRP	2.1
1	A	415	LEU	2.1
1	A	470	VAL	2.0
1	A	527	VAL	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 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	SO4	A	748	5/5	0.89	0.24	52,55,60,73	0
2	SO4	A	746	5/5	0.93	0.14	30,36,43,51	0
3	ZN	A	750	1/1	0.96	0.10	66,66,66,66	0
3	ZN	A	751	1/1	0.96	0.12	53,53,53,53	0
2	SO4	A	747	5/5	0.97	0.11	32,35,48,51	0
3	ZN	A	749	1/1	0.98	0.07	51,51,51,51	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.