



# Full wwPDB X-ray Structure Validation Report ⓘ

Oct 10, 2021 – 09:31 PM EDT

PDB ID : 3E2X  
Title : H. influenzae beta-carbonic anhydrase, variant V47A  
Authors : Rowlett, R.S.; Lee, J.  
Deposited on : 2008-08-06  
Resolution : 2.55 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 : 2.23.2  
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) : 2.23.2

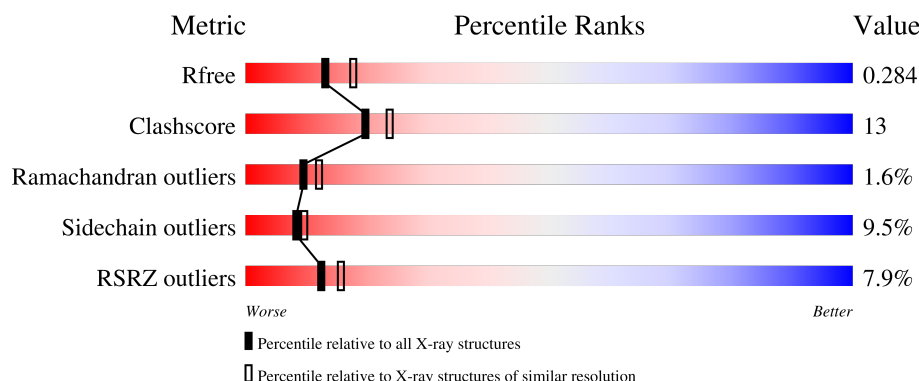
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.55 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	1284 (2.56-2.52)
Clashscore	141614	1332 (2.56-2.52)
Ramachandran outliers	138981	1315 (2.56-2.52)
Sidechain outliers	138945	1315 (2.56-2.52)
RSRZ outliers	127900	1272 (2.56-2.52)

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	229	<div> <div>6%</div> <div>59%</div> <div>18%</div> <div>•</div> <div>21%</div> </div>
1	B	229	<div> <div>7%</div> <div>58%</div> <div>19%</div> <div>•</div> <div>19%</div> </div>

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	SO4	A	231	-	-	X	-
3	SO4	B	234	-	-	X	-

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 2947 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 Carbonic anhydrase 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	182	Total	C	N	O	S	0	0	0
			1443	918	259	259	7			
1	B	186	Total	C	N	O	S	0	0	0
			1477	936	264	270	7			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	47	ALA	VAL	engineered mutation	UNP P45148
B	47	ALA	VAL	engineered mutation	UNP P45148

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Zn	0	0
			1	1		
2	B	1	Total	Zn	0	0
			1	1		

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).

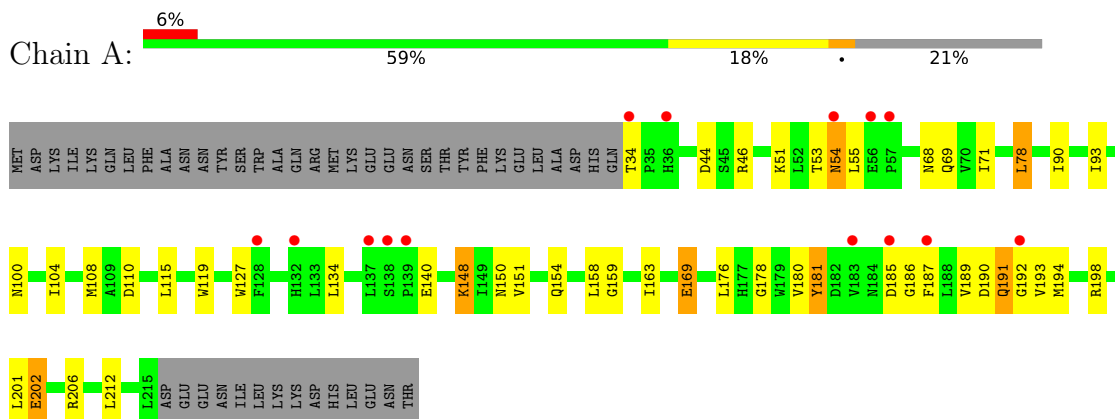


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		

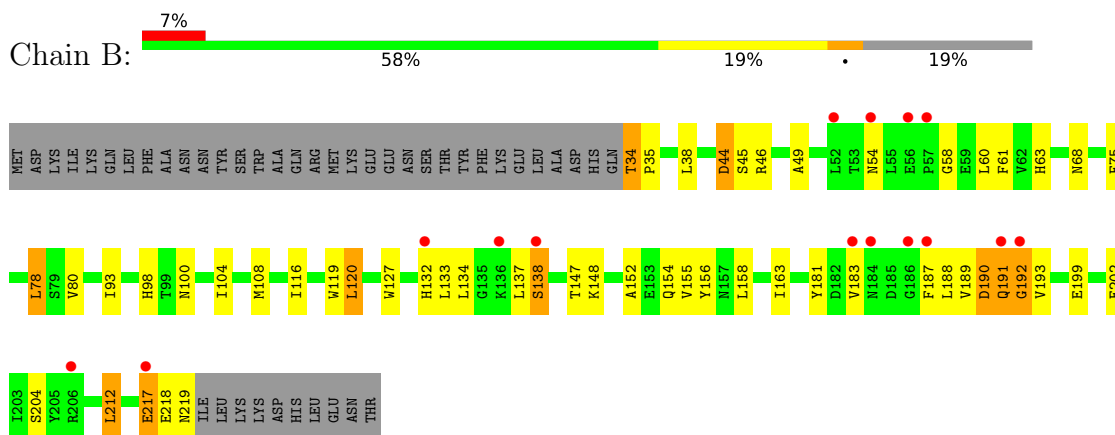
### 3 Residue-property plots [i](#)

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: Carbonic anhydrase 2



- Molecule 1: Carbonic anhydrase 2



## 4 Data and refinement statistics

Property	Value	Source
Space group	I 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	48.14Å 133.32Å 143.89Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	33.98 – 2.55 33.98 – 2.55	Depositor EDS
% Data completeness (in resolution range)	95.2 (33.98-2.55) 95.2 (33.98-2.55)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	0.09	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.05 (at 2.54Å)	Xtriage
Refinement program	REFMAC	Depositor
R, $R_{free}$	0.211 , 0.283 0.218 , 0.284	Depositor DCC
$R_{free}$ test set	743 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	48.8	Xtriage
Anisotropy	0.116	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.39 , 57.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	2947	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	48.0	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.*

<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

### 5.1 Standard geometry

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	0.63	1/1475 (0.1%)	0.69	0/2002
1	B	0.68	1/1509 (0.1%)	0.76	1/2048 (0.0%)
All	All	0.65	2/2984 (0.1%)	0.73	1/4050 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	199	GLU	CB-CG	5.50	1.62	1.52
1	A	169	GLU	CG-CD	5.29	1.59	1.51

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	44	ASP	CB-CA-C	-5.25	99.90	110.40

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	217	GLU	Peptide



## 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	1443	0	1439	34	0
1	B	1477	0	1461	45	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	5	0	0	4	0
3	B	20	0	0	3	0
All	All	2947	0	2900	74	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 13.

All (74) 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:78:LEU:HD13	1:B:163:ILE:CD1	1.85	1.06
1:A:191:GLN:O	1:A:193:VAL:N	1.97	0.97
1:A:189:VAL:HG13	1:A:191:GLN:NE2	1.82	0.94
1:B:78:LEU:HD13	1:B:163:ILE:HD11	1.46	0.94
1:A:181:TYR:OH	3:A:231:SO4:O4	1.87	0.91
1:A:189:VAL:HG13	1:A:191:GLN:HE22	1.36	0.86
1:A:189:VAL:CG1	1:A:191:GLN:HE22	1.91	0.83
1:B:191:GLN:O	1:B:193:VAL:N	2.11	0.81
1:B:46:ARG:HB2	3:B:234:SO4:O1	1.86	0.76
1:B:191:GLN:O	1:B:193:VAL:HG23	1.88	0.73
1:B:78:LEU:HD13	1:B:163:ILE:HD12	1.70	0.71
1:B:93:ILE:HG21	1:B:158:LEU:HD21	1.72	0.71
1:A:53:THR:HB	1:A:55:LEU:HD23	1.73	0.69
1:B:34:THR:HG22	1:B:35:PRO:HD2	1.73	0.69
1:A:44:ASP:HB3	1:B:61:PHE:HE1	1.57	0.69
1:B:78:LEU:CD1	1:B:163:ILE:CD1	2.70	0.66
1:B:78:LEU:CD1	1:B:163:ILE:HD11	2.24	0.63
1:A:44:ASP:HB3	1:B:61:PHE:CE1	2.35	0.62
1:B:34:THR:HG22	1:B:35:PRO:CD	2.30	0.62
1:B:190:ASP:O	1:B:192:GLY:N	2.34	0.60
1:B:156:TYR:OH	1:B:202:GLU:OE2	2.14	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:127:TRP:HD1	1:B:134:LEU:HD13	1.67	0.60
1:B:49:ALA:HB3	1:B:60:LEU:HD13	1.84	0.59
1:B:191:GLN:C	1:B:193:VAL:H	2.05	0.58
1:A:46:ARG:CD	1:B:58:GLY:HA2	2.35	0.57
1:B:188:LEU:O	1:B:189:VAL:HG23	2.06	0.55
1:B:116:ILE:HG13	1:B:120:LEU:HD22	1.87	0.55
1:B:78:LEU:CD1	1:B:163:ILE:HD12	2.37	0.54
1:B:191:GLN:HE22	1:B:212:LEU:HD11	1.73	0.54
1:A:185:ASP:O	1:A:187:PHE:N	2.40	0.54
1:B:181:TYR:CZ	3:B:234:SO4:O3	2.62	0.53
1:A:53:THR:CB	1:A:55:LEU:HD23	2.38	0.53
1:A:93:ILE:HG21	1:A:158:LEU:HD21	1.90	0.53
1:A:46:ARG:HG2	3:A:231:SO4:O3	2.09	0.52
1:A:202:GLU:OE2	1:A:202:GLU:HA	2.09	0.52
1:B:152:ALA:HA	1:B:193:VAL:HG21	1.90	0.52
1:A:159:GLY:HA3	1:A:201:LEU:HD22	1.92	0.51
1:B:127:TRP:CD1	1:B:134:LEU:HD13	2.46	0.51
1:B:181:TYR:HB3	1:B:188:LEU:HD23	1.92	0.51
1:A:151:VAL:HG21	1:A:180:VAL:HG22	1.92	0.51
1:B:98:HIS:O	1:B:147:THR:HG21	2.10	0.51
1:B:63:HIS:HB2	1:B:80:VAL:HG11	1.92	0.51
1:A:71:ILE:HD12	1:A:119:TRP:CH2	2.46	0.51
1:A:78:LEU:HD13	1:A:163:ILE:CD1	2.42	0.49
1:A:115:LEU:HD11	1:B:75:PHE:CZ	2.49	0.48
1:B:44:ASP:O	1:B:45:SER:C	2.50	0.48
1:B:38:LEU:HD12	1:B:61:PHE:O	2.14	0.48
1:A:178:GLY:HA3	1:A:193:VAL:HG23	1.96	0.48
1:A:104:ILE:O	1:A:108:MET:HG3	2.15	0.47
1:A:46:ARG:HD3	1:B:58:GLY:HA2	1.96	0.47
1:B:49:ALA:CB	1:B:60:LEU:HD13	2.46	0.46
1:B:104:ILE:O	1:B:108:MET:HG3	2.16	0.46
1:A:51:LYS:O	1:A:54:ASN:ND2	2.43	0.46
1:A:185:ASP:O	1:A:187:PHE:CG	2.69	0.45
1:B:137:LEU:HD12	1:B:138:SER:H	1.80	0.45
1:A:191:GLN:C	1:A:193:VAL:H	2.20	0.45
1:A:189:VAL:HG11	1:A:191:GLN:HE22	1.79	0.44
1:A:148:LYS:HA	1:A:180:VAL:HG21	1.98	0.44
1:B:191:GLN:O	1:B:191:GLN:HG3	2.19	0.43
1:A:150:ASN:O	1:A:154:GLN:HG2	2.18	0.43
1:B:218:GLU:O	1:B:219:ASN:O	2.36	0.43
1:B:68:ASN:O	1:B:154:GLN:HG3	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:46:ARG:N	3:B:234:SO4:O1	2.40	0.42
1:A:127:TRP:CD1	1:A:134:LEU:HD13	2.53	0.42
1:B:137:LEU:HD12	1:B:219:ASN:C	2.40	0.42
1:B:116:ILE:HD12	1:B:119:TRP:HB3	2.01	0.42
1:B:93:ILE:CG2	1:B:158:LEU:HD21	2.47	0.41
1:A:176:LEU:O	1:A:194:MET:HA	2.20	0.41
1:B:148:LYS:HB3	1:B:191:GLN:NE2	2.35	0.41
1:A:148:LYS:HG3	1:A:180:VAL:HG21	2.02	0.41
1:A:189:VAL:CG1	1:A:191:GLN:NE2	2.60	0.41
1:A:46:ARG:HB2	3:A:231:SO4:O2	2.21	0.41
1:A:46:ARG:N	3:A:231:SO4:O4	2.52	0.40
1:B:155:VAL:HG11	1:B:193:VAL:CG1	2.51	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	180/229 (79%)	172 (96%)	5 (3%)	3 (2%)	9	11
1	B	184/229 (80%)	166 (90%)	15 (8%)	3 (2%)	9	12
All	All	364/458 (80%)	338 (93%)	20 (6%)	6 (2%)	9	12

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	186	GLY
1	A	192	GLY
1	B	191	GLN
1	B	192	GLY
1	A	190	ASP
1	B	190	ASP

### 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	156/200 (78%)	139 (89%)	17 (11%)	6	6
1	B	160/200 (80%)	147 (92%)	13 (8%)	11	14
All	All	316/400 (79%)	286 (90%)	30 (10%)	8	10

All (30) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	34	THR
1	A	54	ASN
1	A	68	ASN
1	A	69	GLN
1	A	78	LEU
1	A	90	ILE
1	A	100	ASN
1	A	110	ASP
1	A	140	GLU
1	A	148	LYS
1	A	169	GLU
1	A	181	TYR
1	A	191	GLN
1	A	198	ARG
1	A	202	GLU
1	A	206	ARG
1	A	212	LEU
1	B	34	THR
1	B	54	ASN
1	B	78	LEU
1	B	100	ASN
1	B	120	LEU
1	B	132	HIS
1	B	133	LEU
1	B	138	SER
1	B	183	VAL
1	B	187	PHE

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Mol	Chain	Res	Type
1	B	204	SER
1	B	212	LEU
1	B	217	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	72	HIS
1	A	100	ASN
1	A	118	ASN
1	A	191	GLN
1	B	54	ASN
1	B	191	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 7 ligands modelled in this entry, 2 are monoatomic - leaving 5 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	SO4	B	234	-	4,4,4	0.21	0	6,6,6	0.43	0
3	SO4	A	231	-	4,4,4	0.28	0	6,6,6	0.59	0
3	SO4	B	233	-	4,4,4	0.22	0	6,6,6	0.46	0
3	SO4	B	232	-	4,4,4	0.20	0	6,6,6	0.30	0
3	SO4	B	231	-	4,4,4	0.15	0	6,6,6	0.27	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.

2 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	234	SO4	3	0
3	A	231	SO4	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, 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	182/229 (79%)	0.50	14 (7%) 13 17	36, 46, 62, 65	0
1	B	186/229 (81%)	0.58	15 (8%) 12 15	35, 46, 64, 67	0
All	All	368/458 (80%)	0.54	29 (7%) 12 16	35, 46, 63, 67	0

All (29) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	184	ASN	4.7
1	A	187	PHE	4.6
1	B	183	VAL	4.5
1	B	217	GLU	4.4
1	B	192	GLY	4.3
1	B	54	ASN	4.2
1	A	183	VAL	3.5
1	A	57	PRO	3.4
1	B	187	PHE	3.2
1	A	36	HIS	3.1
1	A	56	GLU	3.1
1	B	186	GLY	3.0
1	B	52	LEU	2.8
1	A	54	ASN	2.6
1	B	138	SER	2.6
1	A	34	THR	2.6
1	B	57	PRO	2.5
1	A	137	LEU	2.4
1	A	185	ASP	2.3
1	B	136	LYS	2.3
1	B	132	HIS	2.3
1	A	139	PRO	2.2
1	B	191	GLN	2.2
1	B	56	GLU	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	192	GLY	2.2
1	A	138	SER	2.2
1	A	128	PHE	2.1
1	B	206	ARG	2.1
1	A	132	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 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( $\text{\AA}^2$ )	Q<0.9
2	ZN	B	230	1/1	0.94	0.05	46,46,46,46	0
3	SO4	B	234	5/5	0.94	0.24	65,66,67,69	0
3	SO4	B	231	5/5	0.96	0.15	67,69,70,70	0
3	SO4	A	231	5/5	0.96	0.17	63,63,64,65	0
3	SO4	B	233	5/5	0.98	0.11	63,63,64,66	0
3	SO4	B	232	5/5	0.98	0.10	61,61,62,62	0
2	ZN	A	230	1/1	0.99	0.07	43,43,43,43	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.