



# Full wwPDB X-ray Structure Validation Report ⓘ

Jun 16, 2024 – 03:17 AM EDT

PDB ID : 1SQ1  
Title : Crystal Structure of the Chorismate Synthase from *Campylobacter jejuni*, Northeast Structural Genomics Target BR19  
Authors : Forouhar, F.; Lee, I.; Vorobiev, S.M.; Xiao, R.; Acton, T.B.; Montelione, G.T.; Tong, L.; Hunt, J.F.; Northeast Structural Genomics Consortium (NESG)  
Deposited on : 2004-03-17  
Resolution : 2.80 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.

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 : 2022.3.0, CSD as543be (2022)  
Xtriage (Phenix) : 1.20.1  
EDS : 2.37.1  
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) : 2.37.1

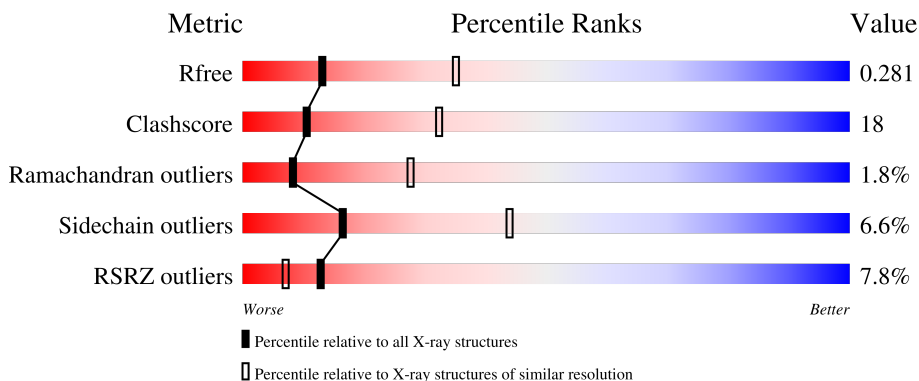
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.80 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	3140 (2.80-2.80)
Clashscore	141614	3569 (2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (2.80-2.80)
RSRZ outliers	127900	3078 (2.80-2.80)

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	370	

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 2168 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 Chorismate synthase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	S	Se			
1	A	288	2151	1359	370	409	6	7	0	0	0

There are 15 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MSE	MET	MODIFIED RESIDUE	UNP Q9PM41
A	28	MSE	MET	MODIFIED RESIDUE	UNP Q9PM41
A	140	MSE	MET	MODIFIED RESIDUE	UNP Q9PM41
A	214	MSE	MET	MODIFIED RESIDUE	UNP Q9PM41
A	235	MSE	MET	MODIFIED RESIDUE	UNP Q9PM41
A	254	MSE	MET	MODIFIED RESIDUE	UNP Q9PM41
A	335	MSE	MET	MODIFIED RESIDUE	UNP Q9PM41
A	363	LEU	-	CLONING ARTIFACT	UNP Q9PM41
A	364	GLU	-	CLONING ARTIFACT	UNP Q9PM41
A	365	HIS	-	CLONING ARTIFACT	UNP Q9PM41
A	366	HIS	-	CLONING ARTIFACT	UNP Q9PM41
A	367	HIS	-	CLONING ARTIFACT	UNP Q9PM41
A	368	HIS	-	CLONING ARTIFACT	UNP Q9PM41
A	369	HIS	-	CLONING ARTIFACT	UNP Q9PM41
A	370	HIS	-	CLONING ARTIFACT	UNP Q9PM41

- 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	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		

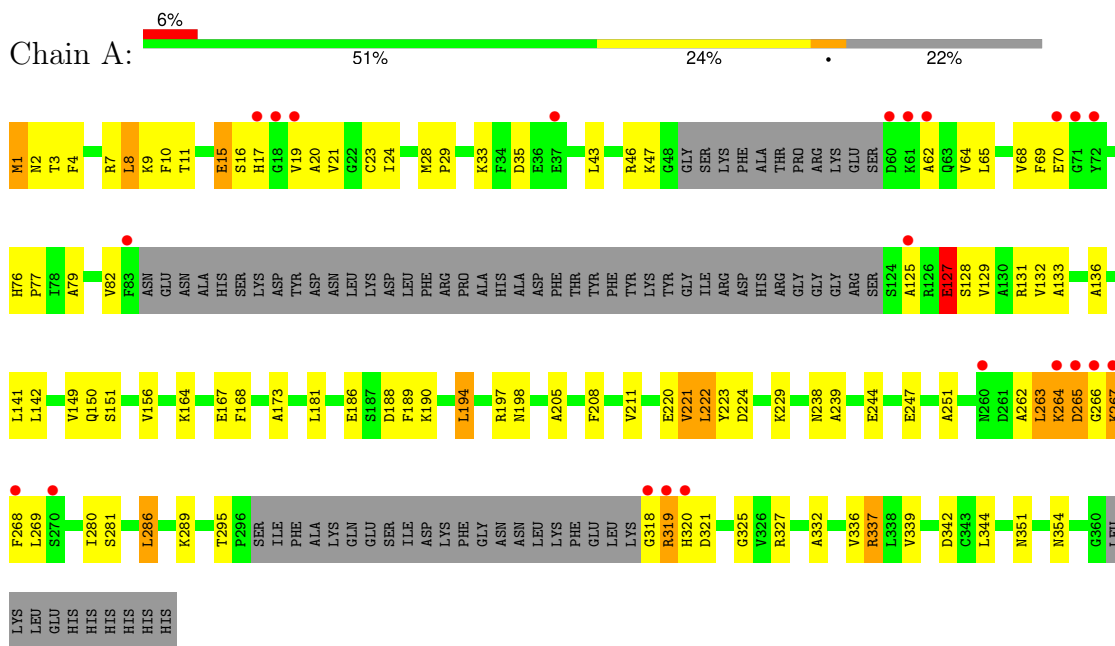
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	7	Total	O	0	0
			7	7		

### 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: Chorismate synthase



## 4 Data and refinement statistics

Property	Value	Source
Space group	I 41 2 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	73.60Å 73.60Å 338.56Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.60 – 2.80 29.60 – 2.80	Depositor EDS
% Data completeness (in resolution range)	9.5 (29.60-2.80) 96.6 (29.60-2.80)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	0.06	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.43 (at 2.80Å)	Xtrriage
Refinement program	CNS	Depositor
R, $R_{free}$	0.224 , 0.279 0.231 , 0.281	Depositor DCC
$R_{free}$ test set	2031 reflections (9.41%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	59.0	Xtrriage
Anisotropy	0.897	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 51.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	2168	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	70.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.36% 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: 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	0.40	0/2174	0.58	0/2908

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	2151	0	2163	80	0
2	A	10	0	0	0	0
3	A	7	0	0	1	0
All	All	2168	0	2163	80	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 18.

All (80) 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:168:PHE:HB3	1:A:181:LEU:HB3	1.58	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:28:MSE:HB2	3:A:403:HOH:O	1.85	0.75
1:A:211:VAL:HB	1:A:286:LEU:HB2	1.70	0.73
1:A:224:ASP:OD1	1:A:229:LYS:HE2	1.89	0.72
1:A:263:LEU:CD1	1:A:264:LYS:H	2.03	0.72
1:A:46:ARG:HH22	1:A:47:LYS:HD3	1.59	0.67
1:A:173:ALA:HB2	1:A:181:LEU:HD23	1.76	0.67
1:A:220:GLU:HB2	1:A:224:ASP:HB3	1.79	0.65
1:A:46:ARG:NH2	1:A:47:LYS:HD3	2.11	0.65
1:A:319:ARG:HD2	1:A:320:HIS:HB2	1.79	0.64
1:A:224:ASP:CG	1:A:229:LYS:HE2	2.18	0.64
1:A:263:LEU:HD13	1:A:264:LYS:H	1.63	0.63
1:A:4:PHE:O	1:A:9:LYS:HA	1.98	0.62
1:A:127:GLU:O	1:A:131:ARG:HG3	1.99	0.62
1:A:127:GLU:OE1	1:A:131:ARG:HD2	1.99	0.62
1:A:221:VAL:O	1:A:222:LEU:HB2	1.98	0.62
1:A:76:HIS:HB3	1:A:77:PRO:HD2	1.80	0.62
1:A:20:ALA:HB1	1:A:82:VAL:O	2.00	0.60
1:A:263:LEU:HA	1:A:269:LEU:HD23	1.84	0.60
1:A:7:ARG:HH21	1:A:7:ARG:HG3	1.69	0.57
1:A:28:MSE:HE2	1:A:29:PRO:HD2	1.87	0.56
1:A:197:ARG:HH11	1:A:318:GLY:HA3	1.70	0.56
1:A:267:LYS:HD2	1:A:268:PHE:H	1.70	0.55
1:A:2:ASN:O	1:A:11:THR:HA	2.07	0.55
1:A:164:LYS:HB2	1:A:167:GLU:HB2	1.88	0.55
1:A:238:ASN:O	1:A:239:ALA:HB3	2.08	0.55
1:A:128:SER:O	1:A:132:VAL:HG23	2.08	0.53
1:A:142:LEU:HD12	1:A:337:ARG:HG3	1.90	0.53
1:A:1:MSE:N	1:A:1:MSE:SE	2.91	0.53
1:A:62:ALA:HA	1:A:82:VAL:HG22	1.91	0.52
1:A:149:VAL:HG22	1:A:211:VAL:HG13	1.90	0.52
1:A:47:LYS:HG3	1:A:327:ARG:CD	2.40	0.52
1:A:263:LEU:H	1:A:263:LEU:HD12	1.75	0.52
1:A:141:LEU:CD1	1:A:344:LEU:HD13	2.40	0.51
1:A:1:MSE:SE	1:A:1:MSE:H3	2.43	0.51
1:A:263:LEU:HB3	1:A:267:LYS:O	2.11	0.51
1:A:320:HIS:CG	1:A:321:ASP:H	2.29	0.51
1:A:127:GLU:CD	1:A:131:ARG:HH21	2.15	0.50
1:A:263:LEU:C	1:A:265:ASP:H	2.14	0.50
1:A:15:GLU:OE2	1:A:19:VAL:HB	2.12	0.49
1:A:280:ILE:HD12	1:A:281:SER:O	2.12	0.49
1:A:16:SER:O	1:A:17:HIS:HB2	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:222:LEU:HD12	1:A:223:TYR:CE2	2.48	0.49
1:A:65:LEU:HB2	1:A:79:ALA:HB3	1.95	0.48
1:A:47:LYS:CD	1:A:327:ARG:HH11	2.26	0.48
1:A:151:SER:HA	1:A:208:PHE:O	2.13	0.48
1:A:263:LEU:HD12	1:A:263:LEU:N	2.28	0.48
1:A:21:VAL:HG21	1:A:129:VAL:HB	1.94	0.48
1:A:7:ARG:HG3	1:A:7:ARG:NH2	2.29	0.47
1:A:194:LEU:HD22	1:A:198:ASN:HD21	1.80	0.47
1:A:263:LEU:HD12	1:A:264:LYS:H	1.77	0.47
1:A:33:LYS:HZ2	1:A:35:ASP:HB2	1.81	0.46
1:A:247:GLU:HB2	1:A:251:ALA:HB2	1.98	0.46
1:A:47:LYS:HG3	1:A:327:ARG:HD2	1.97	0.46
1:A:3:THR:HA	1:A:10:PHE:O	2.16	0.45
1:A:43:LEU:CD1	1:A:62:ALA:HB2	2.47	0.44
1:A:320:HIS:CD2	1:A:321:ASP:H	2.35	0.44
1:A:141:LEU:HD22	1:A:141:LEU:O	2.18	0.44
1:A:47:LYS:HD2	1:A:327:ARG:HH11	1.83	0.43
1:A:262:ALA:O	1:A:269:LEU:HD23	2.18	0.43
1:A:1:MSE:H1	1:A:1:MSE:HE3	1.83	0.43
1:A:156:VAL:HB	1:A:189:PHE:CD1	2.53	0.43
1:A:33:LYS:HZ3	1:A:35:ASP:HA	1.83	0.43
1:A:351:ASN:HB3	1:A:354:ASN:CG	2.39	0.42
1:A:64:VAL:HG11	1:A:68:VAL:HG21	2.00	0.42
1:A:332:ALA:O	1:A:336:VAL:HG23	2.20	0.42
1:A:1:MSE:C	1:A:2:ASN:HD22	2.24	0.41
1:A:4:PHE:N	1:A:10:PHE:O	2.53	0.41
1:A:69:PHE:O	1:A:70:GLU:HB2	2.21	0.41
1:A:244:GLU:HB2	1:A:289:LYS:HB2	2.03	0.41
1:A:186:GLU:OE1	1:A:190:LYS:HE3	2.21	0.41
1:A:247:GLU:CB	1:A:251:ALA:HB2	2.50	0.41
1:A:133:ALA:O	1:A:136:ALA:HB3	2.21	0.41
1:A:339:VAL:O	1:A:342:ASP:HB3	2.21	0.41
1:A:141:LEU:HD13	1:A:344:LEU:HD13	2.02	0.40
1:A:263:LEU:O	1:A:265:ASP:N	2.53	0.40
1:A:23:CYS:O	1:A:24:ILE:HD13	2.21	0.40
1:A:205:ALA:HB3	1:A:325:GLY:HA3	2.04	0.40
1:A:8:LEU:HD21	1:A:28:MSE:HG2	2.04	0.40
1:A:197:ARG:NH1	1:A:318:GLY:HA3	2.34	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	280/370 (76%)	251 (90%)	24 (9%)	5 (2%)	8 28

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	222	LEU
1	A	264	LYS
1	A	127	GLU
1	A	125	ALA
1	A	266	GLY

### 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	229/293 (78%)	214 (93%)	15 (7%)	16 44

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MSE
1	A	8	LEU
1	A	15	GLU
1	A	127	GLU
1	A	150	GLN
1	A	188	ASP

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Mol	Chain	Res	Type
1	A	194	LEU
1	A	221	VAL
1	A	263	LEU
1	A	265	ASP
1	A	267	LYS
1	A	286	LEU
1	A	295	THR
1	A	319	ARG
1	A	337	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	2	ASN
1	A	198	ASN
1	A	250	ASN
1	A	320	HIS
1	A	353	ASN
1	A	354	ASN
1	A	357	ASN

### 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](#)

2 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	$\# Z  > 2$
2	SO4	A	402	-	4,4,4	0.52	0	6,6,6	0.11	0
2	SO4	A	401	-	4,4,4	0.47	0	6,6,6	0.15	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.

No monomer is involved in short contacts.

## 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, 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	281/370 (75%)	0.17	22 (7%) <b>13</b> <b>7</b>	43, 68, 96, 111	0

All (22) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	264	LYS	3.9
1	A	60	ASP	3.8
1	A	265	ASP	3.8
1	A	17	HIS	3.7
1	A	320	HIS	3.7
1	A	318	GLY	3.6
1	A	319	ARG	3.5
1	A	19	VAL	3.3
1	A	125	ALA	3.0
1	A	260	ASN	2.8
1	A	61	LYS	2.7
1	A	266	GLY	2.6
1	A	83	PHE	2.6
1	A	18	GLY	2.5
1	A	70	GLU	2.5
1	A	71	GLY	2.4
1	A	268	PHE	2.4
1	A	72	TYR	2.3
1	A	270	SER	2.2
1	A	267	LYS	2.2
1	A	62	ALA	2.2
1	A	37	GLU	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 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	401	5/5	0.93	0.19	65,69,70,70	0
2	SO4	A	402	5/5	0.95	0.10	87,89,91,91	0

### 6.5 Other polymers [i](#)

There are no such residues in this entry.