



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 12:17 PM UTC

PDB ID : 3GH2 / pdb_00003gh2
Title : Replacement of Val3 in Human Thymidylate Synthase Affects Its Kinetic Properties and Intracellular Stability
Authors : Huang, X.; Gibson, L.M.; Bell, B.J.; Lovelace, L.L.; Lebioda, L.
Deposited on : 2009-03-02
Resolution : 1.75 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

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

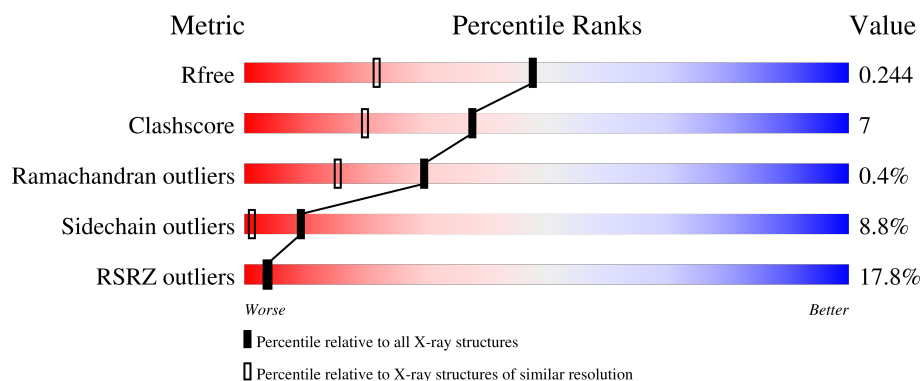
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.75 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	3183 (1.76-1.76)
Clashscore	190562	3299 (1.76-1.76)
Ramachandran outliers	187476	3274 (1.76-1.76)
Sidechain outliers	187428	3274 (1.76-1.76)
RSRZ outliers	180081	3183 (1.76-1.76)

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	X	313	16% 65% 19% • • 12%

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 2350 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 Thymidylate synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	X	276	2234	1429	389	403	13	0	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
X	3	PHE	VAL	engineered mutation	UNP P04818

- Molecule 2 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



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

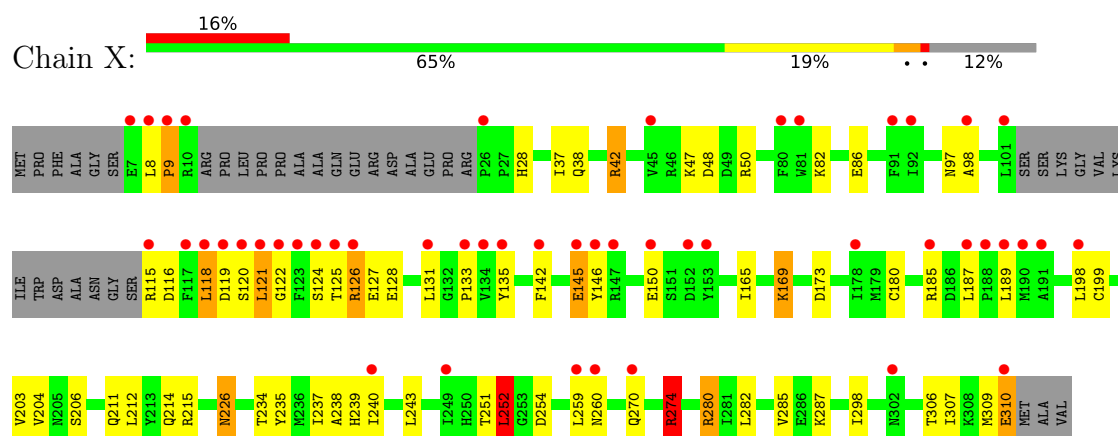
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	X	101	Total 101	O 101	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: Thymidylate synthase



4 Data and refinement statistics

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α , β , γ	96.02Å 96.02Å 80.72Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	50.00 – 1.75 50.00 – 1.75	Depositor EDS
% Data completeness (in resolution range)	85.9 (50.00-1.75) 86.0 (50.00-1.75)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.33 (at 1.75Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.218 , 0.254 0.209 , 0.244	Depositor DCC
R_{free} test set	1885 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	32.8	Xtriage
Anisotropy	0.733	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 48.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.033 for -h,-k,l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	2350	wwPDB-VP
Average B, all atoms (Å ²)	48.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.16% 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: CME, 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	X	1.50	18/2279 (0.8%)	1.37	14/3079 (0.5%)

All (18) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	X	252	LEU	N-CA	-9.77	1.33	1.45
1	X	251	THR	N-CA	7.58	1.54	1.45
1	X	235	TYR	C-O	6.53	1.32	1.24
1	X	212	LEU	CA-CB	-6.34	1.44	1.53
1	X	215	ARG	C-O	6.34	1.32	1.24
1	X	199	CYS	CA-C	6.28	1.60	1.52
1	X	211	GLN	CA-C	6.11	1.59	1.52
1	X	251	THR	C-N	6.09	1.42	1.33
1	X	251	THR	CB-CG2	5.79	1.71	1.52
1	X	234	THR	CA-CB	-5.65	1.44	1.53
1	X	212	LEU	C-O	-5.60	1.17	1.24
1	X	37	ILE	N-CA	5.31	1.52	1.46
1	X	251	THR	CA-C	-5.27	1.46	1.52
1	X	270	GLN	CG-CD	5.21	1.65	1.52
1	X	238	ALA	CA-CB	-5.15	1.45	1.53
1	X	173	ASP	CA-C	-5.14	1.45	1.52
1	X	203	VAL	N-CA	5.10	1.52	1.46
1	X	211	GLN	CA-CB	-5.08	1.45	1.53

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	X	9	PRO	N-CA-CB	9.42	113.14	103.25
1	X	212	LEU	CA-C-O	-7.02	112.60	120.32
1	X	260	ASN	CB-CA-C	-6.71	96.16	110.32

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	X	274	ARG	NE-CZ-NH2	6.65	125.18	119.20
1	X	237	ILE	CB-CA-C	-6.09	102.39	112.26
1	X	226	ASN	N-CA-C	6.04	117.94	111.36
1	X	274	ARG	NE-CZ-NH1	-5.94	115.56	121.50
1	X	252	LEU	N-CA-C	-5.90	100.08	109.23
1	X	199	CYS	N-CA-CB	-5.90	101.29	110.55
1	X	169	LYS	N-CA-C	5.46	119.67	112.89
1	X	270	GLN	CB-CG-CD	5.35	121.69	112.60
1	X	260	ASN	N-CA-C	5.31	118.86	112.38
1	X	135	TYR	N-CA-C	5.14	116.77	108.08
1	X	48	ASP	N-CA-C	5.09	118.25	110.20

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	X	2234	0	2190	31	0
2	X	15	0	0	0	0
3	X	101	0	0	1	0
All	All	2350	0	2190	31	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 7.

All (31) 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:X:239:HIS:HE1	1:X:285:VAL:H	1.21	0.88
1:X:280:ARG:HB2	1:X:280:ARG:HH21	1.41	0.86
1:X:122:GLY:O	1:X:126:ARG:HG3	1.99	0.63
1:X:239:HIS:CE1	1:X:285:VAL:H	2.12	0.60
1:X:145:GLU:H	1:X:145:GLU:CD	2.10	0.60
1:X:309:MET:O	1:X:310:GLU:C	2.46	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:50:ARG:HD2	1:X:185:ARG:CZ	2.37	0.54
1:X:38:GLN:O	1:X:42:ARG:HG3	2.08	0.53
1:X:124:SER:O	1:X:127:GLU:HB2	2.09	0.52
1:X:50:ARG:HD2	1:X:185:ARG:NH2	2.25	0.51
1:X:145:GLU:CD	1:X:145:GLU:N	2.69	0.51
1:X:165:ILE:O	1:X:169:LYS:HG3	2.11	0.51
1:X:97:ASN:HD22	1:X:97:ASN:C	2.20	0.50
1:X:280:ARG:HG2	1:X:282:LEU:HD23	1.95	0.49
1:X:28:HIS:NE2	1:X:274:ARG:O	2.45	0.48
1:X:116:ASP:O	1:X:119:ASP:HB2	2.16	0.46
1:X:125:THR:O	1:X:128:GLU:HG2	2.16	0.46
1:X:133:PRO:HG3	1:X:146:TYR:HB2	1.98	0.46
1:X:214:GLN:HB2	1:X:252:LEU:HD12	1.98	0.46
1:X:118:LEU:HA	1:X:121:LEU:HD22	1.98	0.45
1:X:280:ARG:HH21	1:X:280:ARG:CB	2.23	0.44
1:X:118:LEU:HB3	1:X:126:ARG:NH2	2.33	0.43
1:X:306:THR:HG22	1:X:307:ILE:N	2.32	0.43
1:X:47:LYS:NZ	1:X:254:ASP:OD2	2.48	0.43
1:X:206:SER:HA	1:X:243:LEU:HD22	1.99	0.43
1:X:98:ALA:HB2	1:X:131:LEU:HD11	2.00	0.42
1:X:187:LEU:HD23	1:X:187:LEU:HA	1.78	0.42
1:X:142:PHE:CD2	1:X:142:PHE:C	2.98	0.42
1:X:309:MET:O	3:X:398:HOH:O	2.22	0.41
1:X:118:LEU:HD12	1:X:121:LEU:CD2	2.51	0.41
1:X:8:LEU:HA	1:X:226:ASN:HD21	1.86	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	X	269/313 (86%)	256 (95%)	12 (4%)	1 (0%)	30	15

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	X	9	PRO

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	X	238/270 (88%)	217 (91%)	21 (9%)	9 1

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	X	42	ARG
1	X	82	LYS
1	X	86	GLU
1	X	115	ARG
1	X	118	LEU
1	X	120	SER
1	X	121	LEU
1	X	126	ARG
1	X	145	GLU
1	X	150	GLU
1	X	189	LEU
1	X	198	LEU
1	X	204	VAL
1	X	240	ILE
1	X	252	LEU
1	X	259	LEU
1	X	274	ARG
1	X	280	ARG
1	X	287	LYS
1	X	298	ILE
1	X	310	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	X	97	ASN
1	X	141	HIS
1	X	171	ASN
1	X	226	ASN
1	X	239	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue is 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	CME	X	180	1	8,9,10	0.89	0	6,9,11	1.45	1 (16%)

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	CME	X	180	1	-	2/5/8/10	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	X	180	CME	CB-SG-SD	2.05	109.16	103.86

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	X	180	CME	SD-CE-CZ-OH
1	X	180	CME	CZ-CE-SD-SG

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

3 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	X	317	-	4,4,4	0.55	0	6,6,6	1.08	0
2	SO4	X	315	-	4,4,4	0.42	0	6,6,6	0.78	0
2	SO4	X	318	-	4,4,4	0.33	0	6,6,6	1.14	1 (16%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	X	318	SO4	O3-S-O2	-2.12	98.47	109.56

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 ⓘ

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, 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	X	275/313 (87%)	1.37	49 (17%) 4 4	31, 43, 72, 106	0

All (49) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	X	8	LEU	10.7
1	X	9	PRO	7.1
1	X	10	ARG	5.3
1	X	123	PHE	5.1
1	X	118	LEU	5.0
1	X	121	LEU	4.9
1	X	120	SER	4.7
1	X	7	GLU	4.7
1	X	117	PHE	4.4
1	X	26	PRO	4.0
1	X	133	PRO	3.9
1	X	191	ALA	3.8
1	X	81	TRP	3.6
1	X	115	ARG	3.4
1	X	189	LEU	3.4
1	X	124	SER	3.2
1	X	259	LEU	3.2
1	X	101	LEU	3.0
1	X	142	PHE	3.0
1	X	240	ILE	2.8
1	X	150	GLU	2.8
1	X	135	TYR	2.7
1	X	187	LEU	2.7
1	X	45	VAL	2.7
1	X	146	TYR	2.7
1	X	91	PHE	2.6
1	X	153	TYR	2.6

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Mol	Chain	Res	Type	RSRZ
1	X	131	LEU	2.5
1	X	134	VAL	2.5
1	X	188	PRO	2.5
1	X	122	GLY	2.5
1	X	98	ALA	2.4
1	X	178	ILE	2.4
1	X	147	ARG	2.4
1	X	125	THR	2.4
1	X	119	ASP	2.3
1	X	260	ASN	2.2
1	X	302	ASN	2.2
1	X	190	MET	2.1
1	X	126	ARG	2.1
1	X	185	ARG	2.1
1	X	152	ASP	2.1
1	X	92	ILE	2.1
1	X	80	PHE	2.1
1	X	249	ILE	2.1
1	X	145	GLU	2.0
1	X	270	GLN	2.0
1	X	198	LEU	2.0
1	X	310	GLU	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, 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
1	CME	X	180	10/11	0.94	0.12	40,43,73,75	0

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(Å ²)	Q<0.9
2	SO4	X	315	5/5	0.82	0.12	79,81,82,82	0
2	SO4	X	317	5/5	0.89	0.11	56,60,63,64	0
2	SO4	X	318	5/5	0.96	0.10	53,55,56,58	0

6.5 Other polymers [i](#)

There are no such residues in this entry.