



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 04:16 AM UTC

PDB ID : 3IHI / pdb_00003ihi
Title : Crystal structure of mouse thymidylate synthase
Authors : Dowiercial, A.; Jarmula, A.; Rypniewski, W.R.; Sokolowska, M.; Fraczyk, T.;
Ciesla, J.; Rode, W.
Deposited on : 2009-07-30
Resolution : 1.94 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

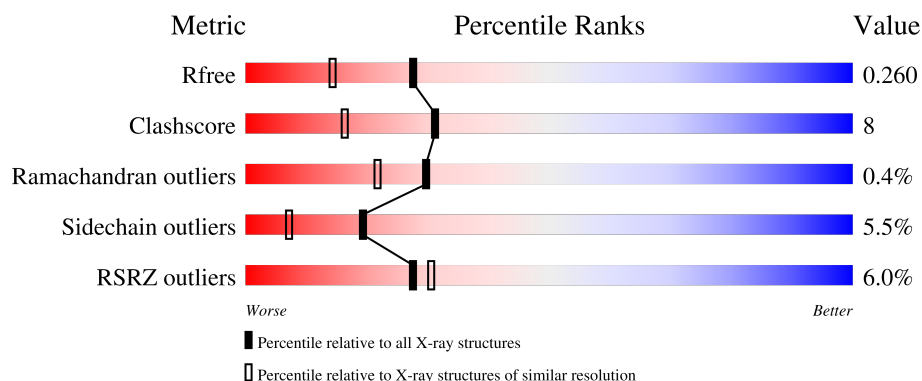
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.94 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	1452 (1.94-1.94)
Clashscore	190562	1494 (1.94-1.94)
Ramachandran outliers	187476	1479 (1.94-1.94)
Sidechain outliers	187428	1479 (1.94-1.94)
RSRZ outliers	180081	1453 (1.94-1.94)

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	A	307	5% 75% 16% • 9%
1	B	307	7% 71% 19% • 8%

2 Entry composition [i](#)

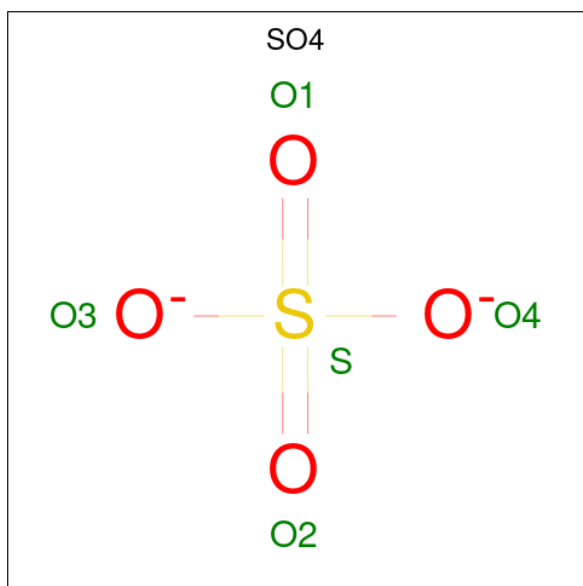
There are 3 unique types of molecules in this entry. The entry contains 4932 atoms, of which 0 are hydrogens and 0 are deuteriums.

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
1	A	280	Total	C	N	O	S	0	0	0
			2264	1450	393	410	11			
1	B	283	Total	C	N	O	S	0	0	0
			2289	1467	397	413	12			

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



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

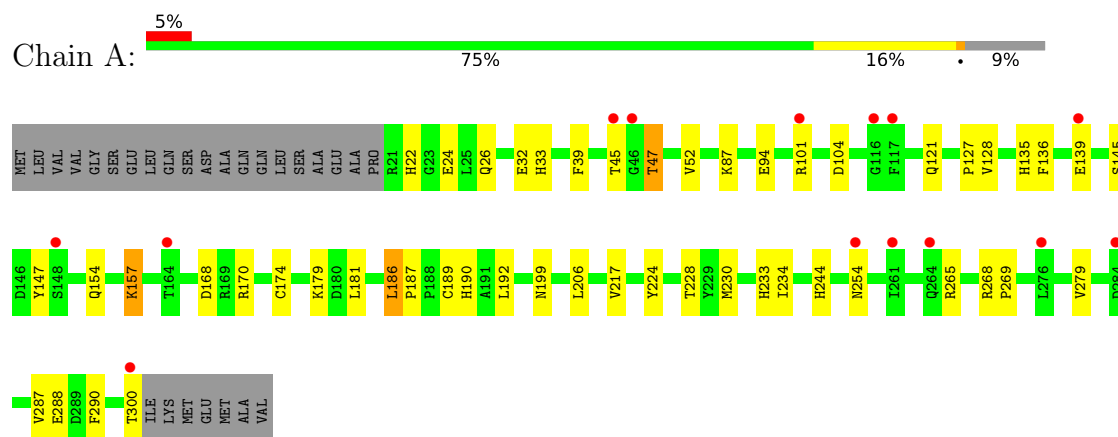
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	205	Total 205	O 205	0	0
3	B	164	Total 164	O 164	0	0

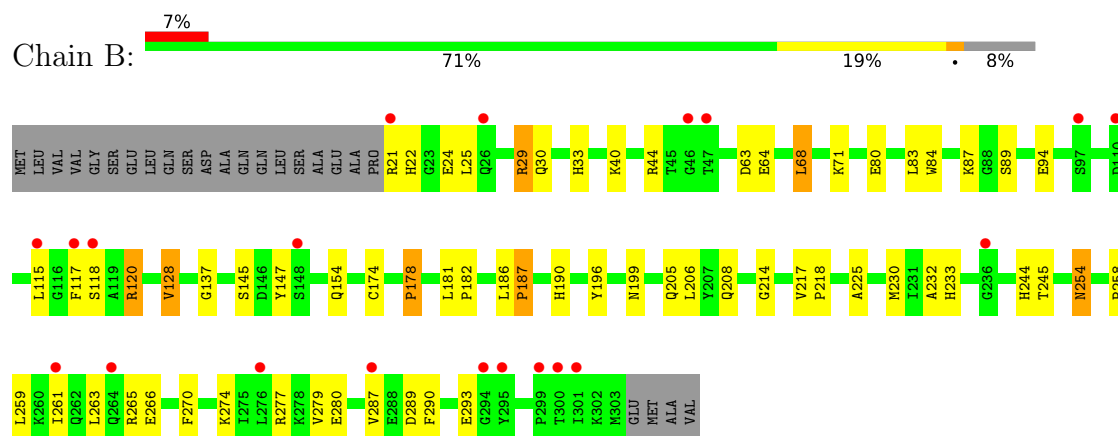
3 Residue-property plots [i](#)

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



• Molecule 1: Thymidylate synthase



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	158.20Å 87.96Å 68.04Å 90.00° 97.43° 90.00°	Depositor
Resolution (Å)	19.48 – 1.94 19.48 – 1.94	Depositor EDS
% Data completeness (in resolution range)	98.5 (19.48-1.94) 98.4 (19.48-1.94)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.12 (at 1.94Å)	Xtriage
Refinement program	REFMAC 5.5.0072	Depositor
R, R_{free}	0.220 , 0.266 0.221 , 0.260	Depositor DCC
R_{free} test set	1366 reflections (2.03%)	wwPDB-VP
Wilson B-factor (Å ²)	35.2	Xtriage
Anisotropy	0.140	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 42.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	4932	wwPDB-VP
Average B, all atoms (Å ²)	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.23% 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 [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	1.44	4/2323 (0.2%)	1.17	3/3142 (0.1%)
1	B	1.38	5/2348 (0.2%)	1.13	4/3174 (0.1%)
All	All	1.41	9/4671 (0.2%)	1.15	7/6316 (0.1%)

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	187	PRO	CA-C	6.50	1.56	1.52
1	A	217	VAL	C-O	-6.11	1.19	1.24
1	A	52	VAL	C-O	-6.06	1.18	1.24
1	A	228	THR	C-O	-5.72	1.17	1.24
1	B	196	TYR	C-O	-5.60	1.17	1.23
1	B	128	VAL	C-O	-5.32	1.17	1.24
1	B	232	ALA	CA-CB	-5.24	1.45	1.53
1	B	225	ALA	C-O	-5.09	1.18	1.24
1	A	127	PRO	CA-C	5.07	1.57	1.52

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	189	CYS	N-CA-C	-5.79	104.94	112.23
1	B	30	GLN	N-CA-C	-5.60	105.26	111.36
1	A	181	LEU	CA-C-N	-5.30	114.15	119.56
1	A	181	LEU	C-N-CA	-5.30	114.15	119.56
1	B	137	GLY	N-CA-C	-5.29	108.33	115.21
1	B	217	VAL	CA-C-N	-5.01	113.48	119.05
1	B	217	VAL	C-N-CA	-5.01	113.48	119.05

There are no chirality outliers.

There are no planarity outliers.

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	2264	0	2228	40	1
1	B	2289	0	2261	36	0
2	A	5	0	0	0	0
2	B	5	0	0	0	0
3	A	205	0	0	12	0
3	B	164	0	0	7	1
All	All	4932	0	4489	74	1

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 (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:199:ASN:HB3	3:B:339:HOH:O	1.37	1.24
1:A:45:THR:OG1	1:A:47:THR:HG22	1.44	1.13
1:B:233:HIS:HE1	1:B:279:VAL:H	1.10	0.95
1:A:22:HIS:HD2	1:A:24:GLU:H	1.19	0.90
1:B:254:ASN:H	1:B:254:ASN:HD22	1.13	0.89
1:A:45:THR:HG1	1:A:47:THR:HG22	1.39	0.87
1:A:45:THR:OG1	1:A:47:THR:CG2	2.25	0.83
1:B:120:ARG:HD2	3:B:424:HOH:O	1.80	0.82
1:B:22:HIS:HD2	1:B:24:GLU:H	1.29	0.81
1:A:233:HIS:HE1	1:A:279:VAL:H	1.30	0.79
1:A:101:ARG:HG3	1:A:104:ASP:OD2	1.85	0.77
1:A:192:LEU:C	1:A:192:LEU:HD12	2.12	0.75
1:A:233:HIS:HD2	3:A:487:HOH:O	1.68	0.75
1:B:94:GLU:OE1	3:B:451:HOH:O	2.07	0.71
1:A:121:GLN:OE1	3:A:378:HOH:O	2.09	0.70
1:B:68:LEU:HD22	1:B:218:PRO:HB3	1.74	0.69
1:A:190:HIS:HD2	3:A:308:HOH:O	1.74	0.68
1:A:22:HIS:HE1	1:A:268:ARG:O	1.77	0.68
1:A:154:GLN:HE22	1:A:174:CYS:H	1.40	0.67
1:A:26:GLN:OE1	3:A:325:HOH:O	2.12	0.67
1:B:154:GLN:HE22	1:B:174:CYS:H	1.42	0.67

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:288:GLU:CG	3:A:311:HOH:O	2.43	0.66
1:B:254:ASN:H	1:B:254:ASN:ND2	1.92	0.65
1:A:87:LYS:HE3	1:A:94:GLU:OE2	1.97	0.65
1:B:274:LYS:HE3	1:B:293:GLU:OE1	1.97	0.63
1:A:154:GLN:NE2	1:A:174:CYS:H	1.98	0.62
1:A:22:HIS:CD2	1:A:24:GLU:H	2.09	0.60
1:A:45:THR:HG1	1:A:47:THR:CG2	2.10	0.60
1:B:233:HIS:CE1	1:B:279:VAL:H	2.03	0.60
1:A:288:GLU:HG3	3:A:311:HOH:O	2.03	0.58
1:B:244:HIS:HD2	3:B:325:HOH:O	1.87	0.57
1:A:244:HIS:HD2	3:A:310:HOH:O	1.88	0.56
1:B:87:LYS:HE3	1:B:94:GLU:OE2	2.05	0.56
1:B:33:HIS:HD2	3:B:461:HOH:O	1.88	0.56
1:B:258:PRO:HA	1:B:261:ILE:HD12	1.89	0.55
1:B:154:GLN:NE2	1:B:174:CYS:H	2.05	0.54
1:B:71:LYS:NZ	1:B:214:GLY:O	2.41	0.53
1:A:192:LEU:C	1:A:192:LEU:CD1	2.83	0.52
1:B:254:ASN:HD22	1:B:254:ASN:N	1.93	0.52
1:A:190:HIS:HB3	1:A:206:LEU:HD11	1.92	0.52
1:B:64:GLU:OE2	1:B:270:PHE:HD2	1.92	0.52
1:A:136:PHE:CZ	1:B:178:PRO:HD2	2.46	0.51
1:A:224:TYR:OH	3:A:499:HOH:O	2.16	0.50
1:B:277:ARG:HH11	1:B:289:ASP:CG	2.19	0.50
1:A:230:MET:HE2	1:A:290:PHE:CZ	2.47	0.49
1:A:233:HIS:CE1	1:A:279:VAL:H	2.21	0.49
1:B:208:GLN:OE1	1:B:244:HIS:HE1	1.96	0.48
1:B:145:SER:HB2	1:B:147:TYR:CZ	2.49	0.48
1:A:145:SER:HB2	1:A:147:TYR:CZ	2.48	0.48
1:A:192:LEU:HD12	1:A:192:LEU:O	2.13	0.48
1:B:181:LEU:HD22	1:B:187:PRO:HB3	1.95	0.47
1:A:288:GLU:OE2	3:A:311:HOH:O	2.21	0.46
1:B:230:MET:HE2	1:B:290:PHE:CZ	2.51	0.46
1:A:186:LEU:HD23	1:A:187:PRO:HD2	1.97	0.45
1:A:288:GLU:CD	3:A:311:HOH:O	2.59	0.45
1:B:33:HIS:HE1	3:B:422:HOH:O	1.98	0.45
1:B:117:PHE:HZ	1:B:182:PRO:O	1.99	0.45
1:B:205:GLN:NE2	1:B:245:THR:OG1	2.46	0.45
1:B:84:TRP:CD1	1:B:89:SER:HB3	2.51	0.44
1:A:168:ASP:OD2	1:A:170:ARG:HB2	2.17	0.44
1:B:190:HIS:HB3	1:B:206:LEU:HD11	2.00	0.44
1:B:80:GLU:OE2	1:B:287:VAL:HG21	2.18	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:157:LYS:HB2	1:A:157:LYS:NZ	2.33	0.43
1:A:233:HIS:HE1	1:A:279:VAL:N	2.07	0.43
1:A:47:THR:CG2	3:A:426:HOH:O	2.66	0.43
1:B:199:ASN:CB	3:B:339:HOH:O	2.20	0.42
1:B:25:LEU:O	1:B:29:ARG:HB2	2.20	0.41
1:A:135:HIS:O	1:A:136:PHE:C	2.61	0.41
1:A:39:PHE:CD2	1:B:199:ASN:ND2	2.77	0.41
1:B:259:LEU:O	1:B:263:LEU:HG	2.20	0.41
1:A:22:HIS:CE1	1:A:268:ARG:O	2.65	0.41
1:B:181:LEU:N	1:B:182:PRO:CD	2.84	0.41
1:A:268:ARG:O	1:A:269:PRO:C	2.63	0.40
1:A:33:HIS:HD2	3:A:485:HOH:O	2.05	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:199:ASN:ND2	3:B:339:HOH:O[4_646]	2.13	0.07

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	278/307 (91%)	270 (97%)	7 (2%)	1 (0%)	30	22
1	B	281/307 (92%)	267 (95%)	13 (5%)	1 (0%)	30	22
All	All	559/614 (91%)	537 (96%)	20 (4%)	2 (0%)	30	22

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	128	VAL

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	128	VAL

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	244/266 (92%)	233 (96%)	11 (4%)	24	11
1	B	247/266 (93%)	231 (94%)	16 (6%)	15	4
All	All	491/532 (92%)	464 (94%)	27 (6%)	19	7

All (27) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	32	GLU
1	A	47	THR
1	A	139	GLU
1	A	157	LYS
1	A	179	LYS
1	A	186	LEU
1	A	234	ILE
1	A	254	ASN
1	A	265	ARG
1	A	287	VAL
1	A	300	THR
1	B	21	ARG
1	B	29	ARG
1	B	40	LYS
1	B	44	ARG
1	B	63	ASP
1	B	68	LEU
1	B	83	LEU
1	B	115	LEU
1	B	118	SER
1	B	120	ARG
1	B	178	PRO

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	186	LEU
1	B	254	ASN
1	B	265	ARG
1	B	266	GLU
1	B	280	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (20) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	22	HIS
1	A	121	GLN
1	A	135	HIS
1	A	154	GLN
1	A	194	GLN
1	A	205	GLN
1	A	233	HIS
1	A	244	HIS
1	B	22	HIS
1	B	56	GLN
1	B	154	GLN
1	B	194	GLN
1	B	205	GLN
1	B	233	HIS
1	B	238	GLN
1	B	244	HIS
1	B	254	ASN
1	B	255	HIS
1	B	264	GLN
1	B	296	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides 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	B	501	-	4,4,4	0.54	0	6,6,6	0.89	0
2	SO4	A	501	-	4,4,4	0.43	0	6,6,6	0.80	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

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	A	280/307 (91%)	0.24	14 (5%) 34 38	24, 37, 55, 64	0
1	B	283/307 (92%)	0.53	20 (7%) 22 25	25, 41, 62, 84	0
All	All	563/614 (91%)	0.38	34 (6%) 27 30	24, 38, 59, 84	0

All (34) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	46	GLY	5.3
1	B	47	THR	4.3
1	A	254	ASN	3.8
1	A	300	THR	3.5
1	B	299	PRO	3.5
1	A	264	GLN	3.1
1	A	148	SER	3.1
1	B	261	ILE	3.0
1	A	45	THR	2.9
1	B	236	GLY	2.9
1	B	110	ASP	2.8
1	B	21	ARG	2.6
1	B	294	GLY	2.5
1	B	148	SER	2.5
1	B	115	LEU	2.5
1	A	261	ILE	2.5
1	B	26	GLN	2.4
1	B	118	SER	2.4
1	B	300	THR	2.3
1	A	164	THR	2.3
1	A	117	PHE	2.3
1	A	46	GLY	2.3
1	B	276	LEU	2.3
1	A	284	ASP	2.2

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	287	VAL	2.2
1	B	97	SER	2.2
1	B	117	PHE	2.2
1	B	301	ILE	2.2
1	A	139	GLU	2.1
1	B	295	TYR	2.1
1	A	276	LEU	2.1
1	A	116	GLY	2.1
1	A	101	ARG	2.1
1	B	264	GLN	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 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($\text{\AA}^2$)	Q<0.9
2	SO4	A	501	5/5	0.95	0.11	47,53,55,58	0
2	SO4	B	501	5/5	0.95	0.11	43,45,55,57	0

6.5 Other polymers [i](#)

There are no such residues in this entry.