



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 10, 2026 – 12:10 AM UTC

PDB ID : 3GG5 / pdb_00003gg5
Title : Replacement of Val3 in Human Thymidylate Synthase Affects Its Kinetic Properties and Intracellular Stability
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Deposited on : 2009-02-27
Resolution : 2.77 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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

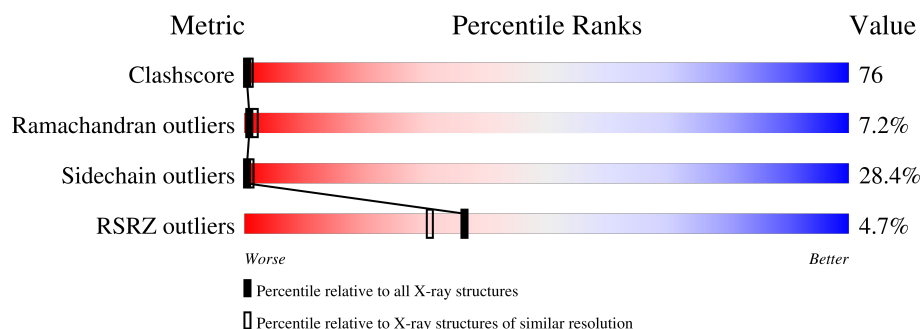
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.77 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))
Clashscore	190562	5693 (2.80-2.76)
Ramachandran outliers	187476	5590 (2.80-2.76)
Sidechain outliers	187428	5592 (2.80-2.76)
RSRZ outliers	180081	5251 (2.80-2.76)

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	A	313	8% 30% 35% 17% 10%
1	B	313	5% 10% 23% 43% 13% 10%
1	C	313	4% 8% 30% 37% 16% 10%
1	D	313	6% 6% 24% 41% 19% 10%

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
2	SO4	A	616	-	X	-	-
3	PO4	B	616	-	X	X	-
3	PO4	D	616	-	-	X	-

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 9174 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	283	Total	C	N	O	S	0	0	0
			2287	1463	400	413	11			
1	B	281	Total	C	N	O	S	0	0	0
			2270	1451	397	411	11			
1	C	283	Total	C	N	O	S	0	0	0
			2287	1463	400	413	11			
1	D	283	Total	C	N	O	S	0	0	0
			2287	1463	400	413	11			

There are 4 discrepancies between the modelled and reference sequences:

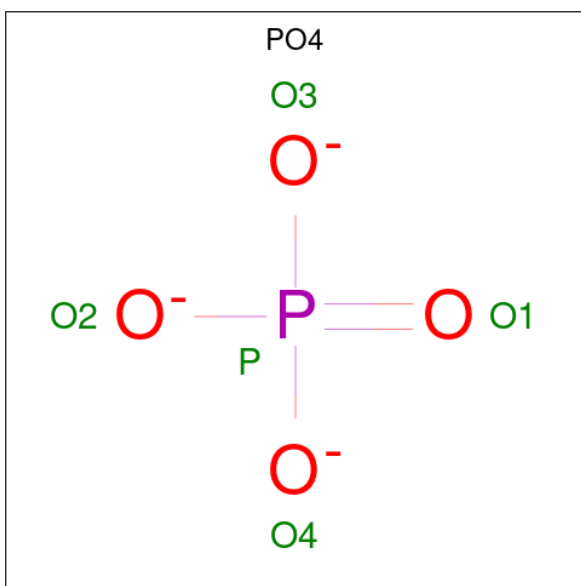
Chain	Residue	Modelled	Actual	Comment	Reference
A	3	TYR	VAL	engineered mutation	UNP P04818
B	3	TYR	VAL	engineered mutation	UNP P04818
C	3	TYR	VAL	engineered mutation	UNP P04818
D	3	TYR	VAL	engineered mutation	UNP P04818

- 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	C	1	Total	O	S	0	0
			5	4	1		

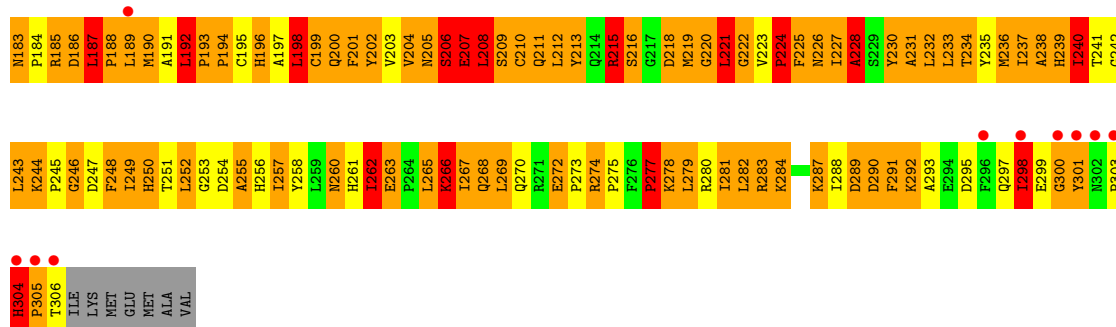
- Molecule 3 is PHOSPHATE ION (CCD ID: PO4) (formula: O_4P).



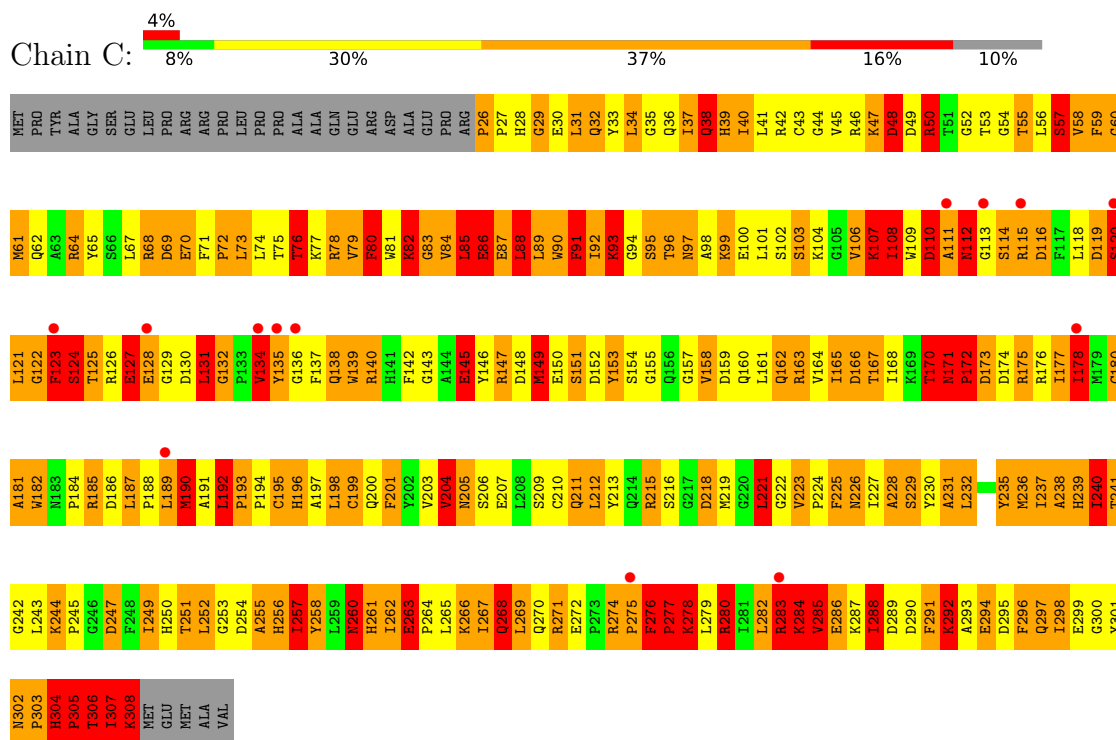
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	B	1	Total	O	P	0	0
			5	4	1		
3	D	1	Total	O	P	0	0
			5	4	1		

- Molecule 4 is water.

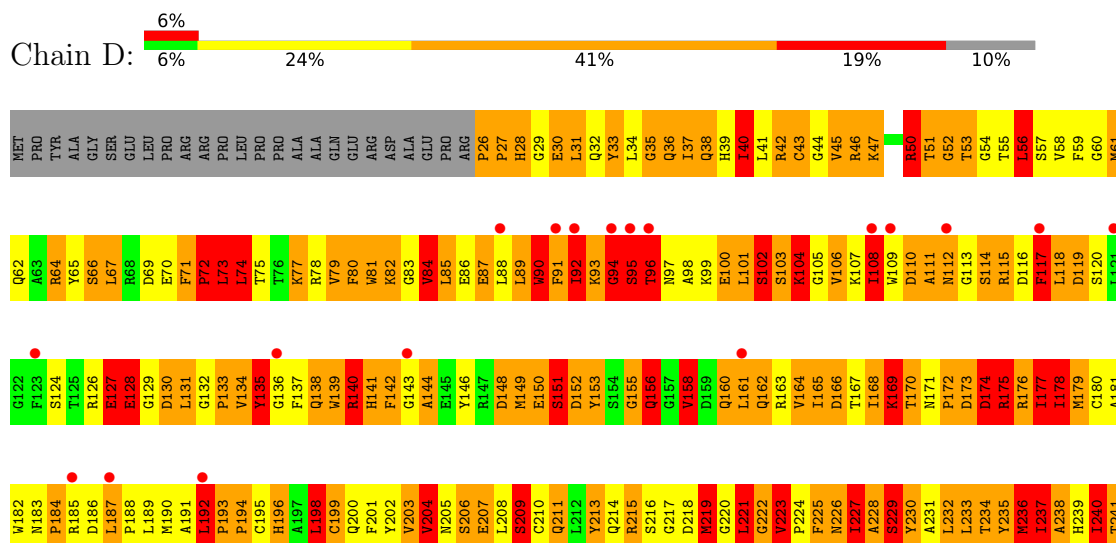
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	6	Total 6	O 6	0	0
4	B	7	Total 7	O 7	0	0
4	C	5	Total 5	O 5	0	0
4	D	5	Total 5	O 5	0	0

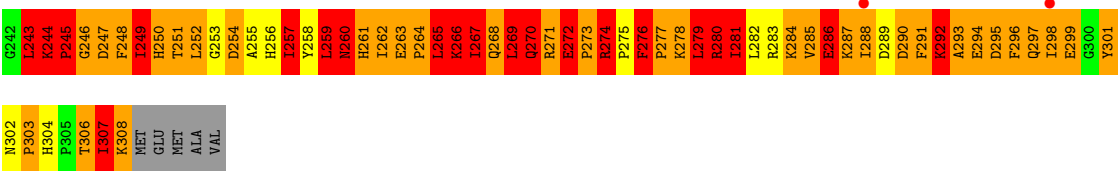


• Molecule 1: Thymidylate synthase



• 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	157.56Å 94.86Å 130.86Å 90.00° 122.43° 90.00°	Depositor
Resolution (Å)	50.00 – 2.77 50.00 – 2.77	Depositor EDS
% Data completeness (in resolution range)	89.3 (50.00-2.77) 80.2 (50.00-2.77)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.20 (at 2.77Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.237 , 0.254 0.248 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	59.0	Xtriage
Anisotropy	0.510	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 56.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	9174	wwPDB-VP
Average B, all atoms (Å ²)	65.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.04% 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: SO4, PO4

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	3.23	239/2347 (10.2%)	2.97	227/3175 (7.1%)
1	B	2.83	179/2330 (7.7%)	2.55	181/3153 (5.7%)
1	C	2.95	212/2347 (9.0%)	2.87	236/3175 (7.4%)
1	D	2.77	187/2347 (8.0%)	2.68	232/3175 (7.3%)
All	All	2.95	817/9371 (8.7%)	2.77	876/12678 (6.9%)

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	A	0	6
1	B	0	6
1	C	0	10
1	D	0	4
All	All	0	26

The worst 5 of 817 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	200	GLN	C-O	29.12	1.60	1.23
1	C	114	SER	CA-C	-22.26	1.23	1.52
1	B	58	VAL	C-O	18.38	1.42	1.24
1	A	185	ARG	CZ-NH2	16.67	1.55	1.33
1	A	185	ARG	NE-CZ	-16.14	1.15	1.33

The worst 5 of 876 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	185	ARG	NE-CZ-NH1	28.98	150.48	121.50
1	A	185	ARG	NE-CZ-NH2	-28.57	93.49	119.20
1	C	123	PHE	O-C-N	23.89	154.36	122.59
1	A	185	ARG	CD-NE-CZ	23.02	156.63	124.40
1	D	281	ILE	N-CA-C	-21.75	76.98	108.53

There are no chirality outliers.

5 of 26 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	188	PRO	Peptide
1	A	200	GLN	Mainchain
1	A	202	TYR	Mainchain
1	A	286	GLU	Peptide
1	A	70	GLU	Peptide,Mainchain

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	2287	0	2258	324	0
1	B	2270	0	2233	369	0
1	C	2287	0	2258	325	0
1	D	2287	0	2259	410	0
2	A	5	0	0	0	0
2	C	5	0	0	0	0
3	B	5	0	0	7	0
3	D	5	0	0	4	0
4	A	6	0	0	0	0
4	B	7	0	0	0	0
4	C	5	0	0	0	0
4	D	5	0	0	0	0
All	All	9174	0	9008	1373	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 76.

The worst 5 of 1373 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:201:PHE:CE2	1:A:201:PHE:CZ	1.74	1.64
1:B:107:LYS:CD	1:B:107:LYS:CE	1.74	1.64
1:B:244:LYS:CG	1:B:244:LYS:CD	1.77	1.62
1:D:266:LYS:CG	1:D:266:LYS:CB	1.75	1.62
1:A:221:LEU:CG	1:A:221:LEU:CD2	1.75	1.62

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	281/313 (90%)	225 (80%)	37 (13%)	19 (7%)	1	2
1	B	279/313 (89%)	205 (74%)	57 (20%)	17 (6%)	1	3
1	C	281/313 (90%)	228 (81%)	41 (15%)	12 (4%)	2	6
1	D	281/313 (90%)	193 (69%)	55 (20%)	33 (12%)	0	0
All	All	1122/1252 (90%)	851 (76%)	190 (17%)	81 (7%)	1	2

5 of 81 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	82	LYS
1	A	116	ASP
1	A	305	PRO
1	B	38	GLN
1	B	76	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	247/271 (91%)	177 (72%)	70 (28%)	0	1
1	B	245/271 (90%)	178 (73%)	67 (27%)	0	1
1	C	247/271 (91%)	179 (72%)	68 (28%)	0	1
1	D	247/271 (91%)	172 (70%)	75 (30%)	0	1
All	All	986/1084 (91%)	706 (72%)	280 (28%)	0	1

5 of 280 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	133	PRO
1	D	158	VAL
1	D	257	ILE
1	B	140	ARG
1	B	116	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 34 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	112	ASN
1	D	160	GLN
1	D	256	HIS
1	B	138	GLN
1	B	97	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 ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

4 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	616	-	4,4,4	1.37	0	6,6,6	3.28	4 (66%)
2	SO4	C	616	-	4,4,4	0.46	0	6,6,6	0.93	0
3	PO4	B	616	-	4,4,4	1.74	2 (50%)	6,6,6	3.92	4 (66%)
3	PO4	D	616	-	4,4,4	0.46	0	6,6,6	2.38	2 (33%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	616	PO4	P-O2	2.09	1.60	1.54
3	B	616	PO4	P-O1	-2.09	1.45	1.50

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	616	PO4	O3-P-O1	-5.62	91.07	110.95
3	B	616	PO4	O3-P-O2	5.39	124.69	107.91
2	A	616	SO4	O4-S-O1	-4.98	83.52	109.56
2	A	616	SO4	O3-S-O1	4.62	133.71	109.56
3	D	616	PO4	O3-P-O1	-4.31	95.71	110.95

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	616	PO4	7	0
3	D	616	PO4	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 [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, 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	283/313 (90%)	0.15	4 (1%) 73 67	26, 53, 94, 116	0
1	B	281/313 (89%)	0.50	16 (5%) 29 24	30, 67, 111, 149	0
1	C	283/313 (90%)	0.31	13 (4%) 37 31	25, 58, 109, 144	0
1	D	283/313 (90%)	0.59	20 (7%) 22 17	29, 71, 115, 130	0
All	All	1130/1252 (90%)	0.38	53 (4%) 36 31	25, 63, 109, 149	0

The worst 5 of 53 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	123	PHE	5.8
1	D	92	ILE	5.7
1	D	95	SER	5.3
1	C	113	GLY	5.3
1	B	304	HIS	4.7

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	C	616	5/5	0.92	0.10	68,69,70,71	0
2	SO4	A	616	5/5	0.93	0.09	61,62,66,67	0
3	PO4	D	616	5/5	0.93	0.07	58,58,63,63	0
3	PO4	B	616	5/5	0.95	0.10	54,58,58,61	0

6.5 Other polymers [i](#)

There are no such residues in this entry.