



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 05:22 AM UTC

PDB ID : 1QPQ / pdb_00001qpq
Title : Structure of Quinolinic Acid Phosphoribosyltransferase from Mycobacterium Tuberculosis: A Potential TB Drug Target
Authors : Sharma, V.; Grubmeyer, C.; Sacchettini, J.C.; TB Structural Genomics Consortium (TBSGC)
Deposited on : 1998-11-20
Resolution : 2.45 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)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

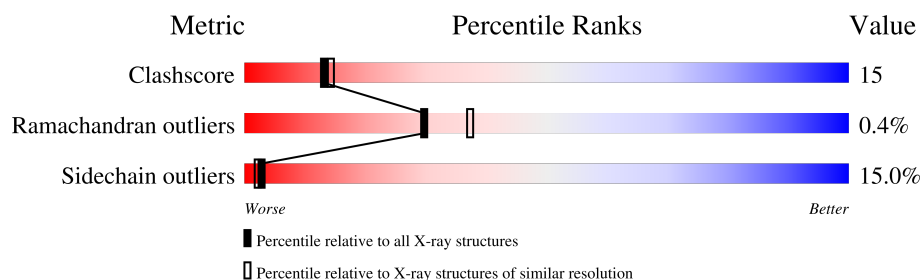
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.45 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	1229 (2.46-2.46)
Ramachandran outliers	187476	1218 (2.46-2.46)
Sidechain outliers	187428	1218 (2.46-2.46)

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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	284	64% 26% 10% .
1	B	284	68% 25% 6% .
1	C	284	63% 29% 6% .
1	D	284	65% 29% 5% .
1	E	284	65% 28% 7% .
1	F	284	63% 29% 8%

2 Entry composition [i](#)

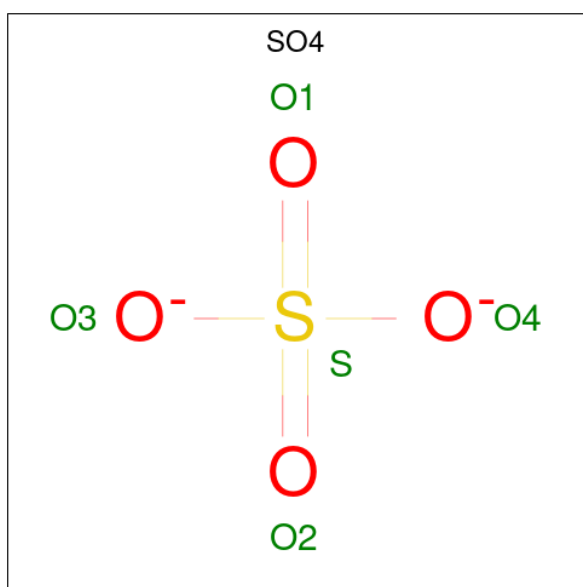
There are 4 unique types of molecules in this entry. The entry contains 12938 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 QUINOLINATE PHOSPHORIBOSYLTRANSFERASE.

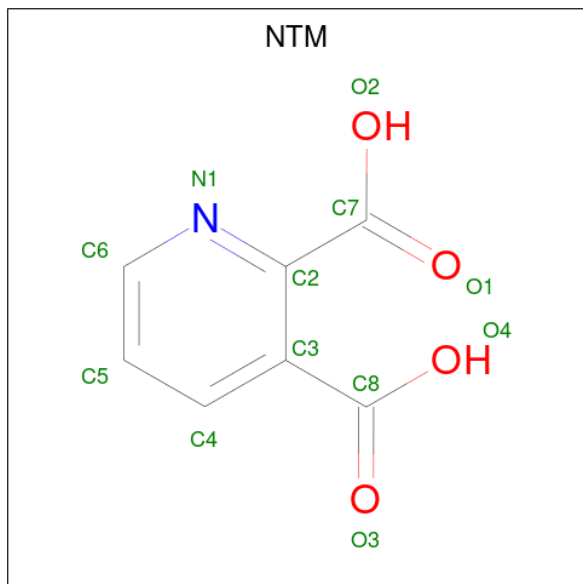
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	284	Total	C	N	O	S	0	0	0
			2095	1301	378	411	5			
1	B	284	Total	C	N	O	S	0	0	0
			2095	1301	378	411	5			
1	C	284	Total	C	N	O	S	0	0	0
			2095	1301	378	411	5			
1	D	284	Total	C	N	O	S	0	0	0
			2095	1301	378	411	5			
1	E	284	Total	C	N	O	S	0	0	0
			2095	1301	378	411	5			
1	F	284	Total	C	N	O	S	0	0	0
			2095	1301	378	411	5			

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



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

- Molecule 3 is QUINOLINIC ACID (CCD ID: NTM) (formula: $C_7H_5NO_4$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C N O 12 7 1 4	0	0
3	B	1	Total C N O 12 7 1 4	0	0
3	C	1	Total C N O 12 7 1 4	0	0
3	D	1	Total C N O 12 7 1 4	0	0
3	E	1	Total C N O 12 7 1 4	0	0
3	F	1	Total C N O 12 7 1 4	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	36	Total 36	O 36	0	0
4	B	47	Total 47	O 47	0	0
4	C	60	Total 60	O 60	0	0
4	D	43	Total 43	O 43	0	0
4	E	47	Total 47	O 47	0	0
4	F	33	Total 33	O 33	0	0

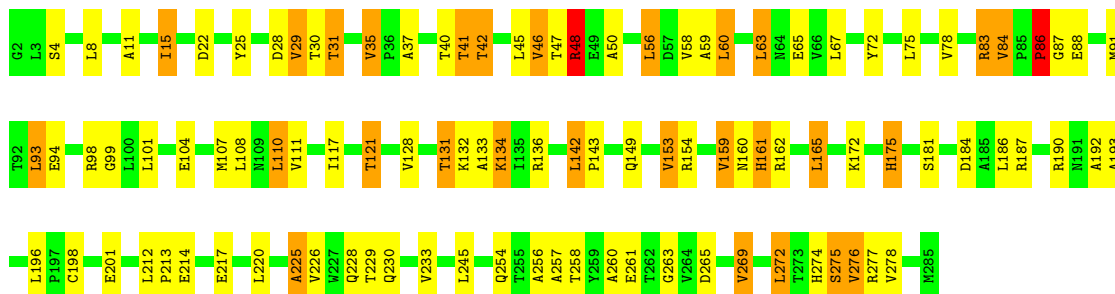
3 Residue-property plots

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. 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. 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.

Note EDS was not executed.

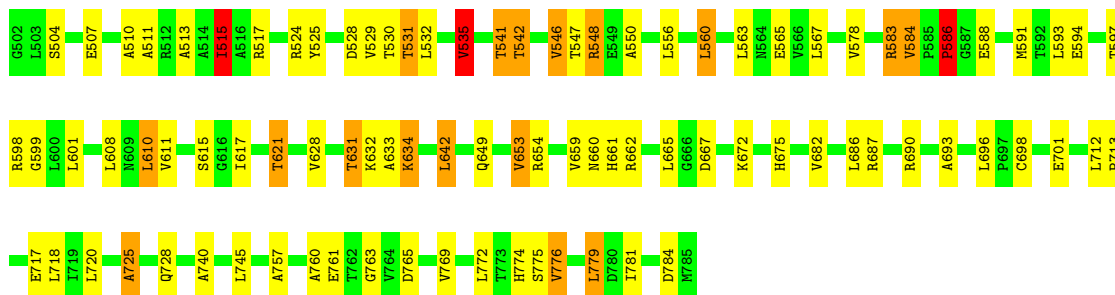
• Molecule 1: QUINOLINATE PHOSPHORIBOSYLTRANSFERASE

Chain A: 



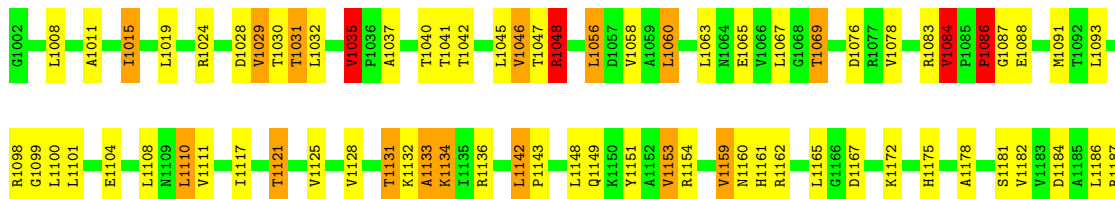
• Molecule 1: QUINOLINATE PHOSPHORIBOSYLTRANSFERASE

Chain B: 



• Molecule 1: QUINOLINATE PHOSPHORIBOSYLTRANSFERASE

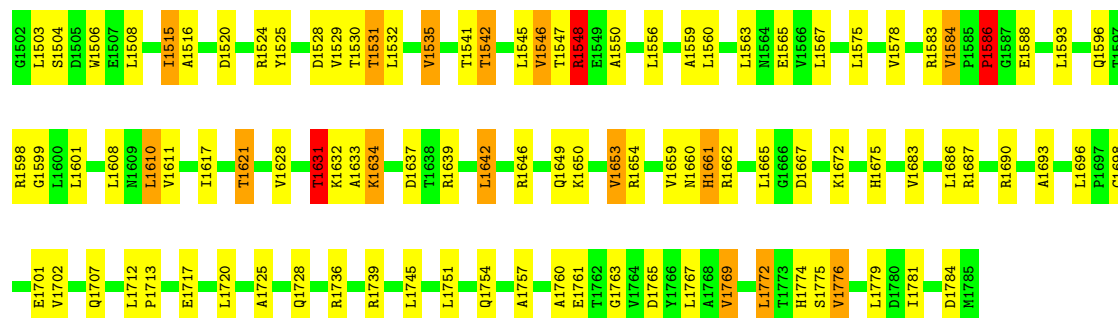
Chain C: 





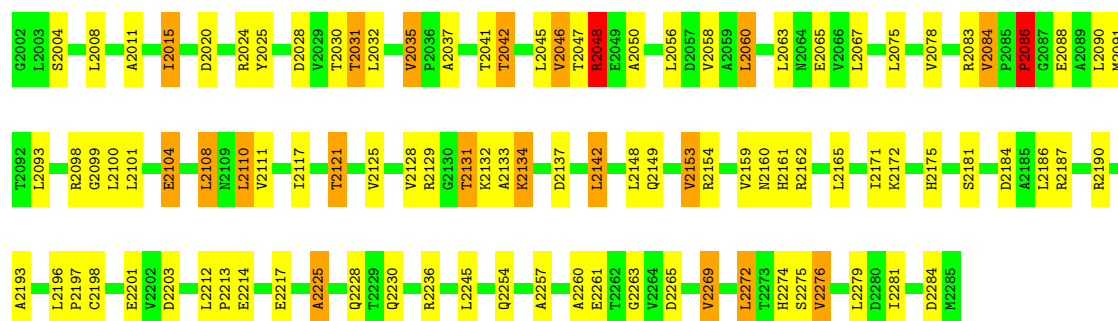
• Molecule 1: QUINOLINATE PHOSPHORIBOSYLTRANSFERASE

Chain D: 65% 29% 5% •



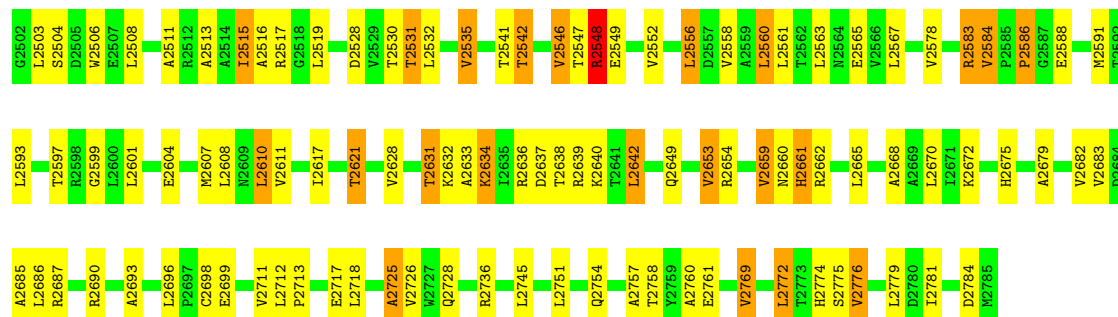
• Molecule 1: QUINOLINATE PHOSPHORIBOSYLTRANSFERASE

Chain E: 65% 28% 7% •



• Molecule 1: QUINOLINATE PHOSPHORIBOSYLTRANSFERASE

Chain F: 63% 29% 8% •



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 31	Depositor
Cell constants a, b, c, α , β , γ	100.34Å 100.34Å 145.66Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	8.00 – 2.45	Depositor
% Data completeness (in resolution range)	97.8 (8.00-2.45)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
Refinement program	X-PLOR 3.1	Depositor
R, R_{free}	0.178 , 0.253	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	12938	wwPDB-VP
Average B, all atoms (Å ²)	27.0	wwPDB-VP

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: NTM, 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	0.89	0/2120	1.20	19/2891 (0.7%)
1	B	0.91	2/2120 (0.1%)	1.20	15/2891 (0.5%)
1	C	0.92	2/2120 (0.1%)	1.19	16/2891 (0.6%)
1	D	0.87	0/2120	1.20	14/2891 (0.5%)
1	E	0.88	0/2120	1.19	13/2891 (0.4%)
1	F	0.87	0/2120	1.19	11/2891 (0.4%)
All	All	0.89	4/12720 (0.0%)	1.20	88/17346 (0.5%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	535	VAL	CA-CB	7.97	1.60	1.54
1	C	1035	VAL	CA-CB	6.35	1.59	1.54
1	B	515	ILE	CA-CB	5.80	1.61	1.54
1	C	1244	MET	SD-CE	-5.21	1.66	1.79

The worst 5 of 88 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	1774	HIS	N-CA-C	-8.78	97.86	110.59
1	A	42	THR	N-CA-C	-8.53	95.33	109.07
1	F	2774	HIS	N-CA-C	-8.09	98.55	110.52
1	B	542	THR	N-CA-C	-7.88	96.06	108.90
1	D	1542	THR	N-CA-C	-7.85	96.43	109.07

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	2095	0	2135	70	0
1	B	2095	0	2135	63	0
1	C	2095	0	2135	78	0
1	D	2095	0	2135	65	0
1	E	2095	0	2135	68	0
1	F	2095	0	2135	70	0
2	A	5	0	0	0	0
2	B	5	0	0	0	0
2	C	5	0	0	0	0
2	D	5	0	0	0	0
2	E	5	0	0	0	0
2	F	5	0	0	0	0
3	A	12	0	3	0	0
3	B	12	0	3	1	0
3	C	12	0	3	0	0
3	D	12	0	3	0	0
3	E	12	0	3	1	0
3	F	12	0	3	2	0
4	A	36	0	0	1	0
4	B	47	0	0	2	0
4	C	60	0	0	8	0
4	D	43	0	0	1	0
4	E	47	0	0	3	0
4	F	33	0	0	0	0
All	All	12938	0	12828	379	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 15.

The worst 5 of 379 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:67:LEU:HD21	1:A:99:GLY:HA3	1.36	1.02
1:C:1175:HIS:HE1	1:D:1531:THR:HG22	1.23	1.02
1:E:2031:THR:HG22	1:F:2675:HIS:HE1	1.30	0.95

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:2175:HIS:HE1	1:F:2531:THR:HG22	1.30	0.94
1:C:1175:HIS:CE1	1:D:1531:THR:HG22	2.06	0.91

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	282/284 (99%)	276 (98%)	5 (2%)	1 (0%)	30	37
1	B	282/284 (99%)	275 (98%)	6 (2%)	1 (0%)	30	37
1	C	282/284 (99%)	276 (98%)	5 (2%)	1 (0%)	30	37
1	D	282/284 (99%)	274 (97%)	7 (2%)	1 (0%)	30	37
1	E	282/284 (99%)	274 (97%)	7 (2%)	1 (0%)	30	37
1	F	282/284 (99%)	276 (98%)	5 (2%)	1 (0%)	30	37
All	All	1692/1704 (99%)	1651 (98%)	35 (2%)	6 (0%)	30	37

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	F	2586	PRO
1	B	586	PRO
1	D	1586	PRO
1	E	2086	PRO
1	A	86	PRO

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	216/216 (100%)	184 (85%)	32 (15%)	3	2
1	B	216/216 (100%)	185 (86%)	31 (14%)	3	2
1	C	216/216 (100%)	180 (83%)	36 (17%)	2	1
1	D	216/216 (100%)	184 (85%)	32 (15%)	3	2
1	E	216/216 (100%)	185 (86%)	31 (14%)	3	2
1	F	216/216 (100%)	184 (85%)	32 (15%)	3	2
All	All	1296/1296 (100%)	1102 (85%)	194 (15%)	3	2

5 of 194 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	1601	LEU
1	E	2078	VAL
1	D	1621	THR
1	D	1776	VAL
1	E	2111	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 32 such sidechains are listed below:

Mol	Chain	Res	Type
1	F	2660	ASN
1	F	2661	HIS
1	C	1161	HIS
1	C	1160	ASN
1	F	2675	HIS

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](#)

12 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	D	2990	-	4,4,4	1.02	0	6,6,6	0.27	0
2	SO4	C	2987	-	4,4,4	1.18	0	6,6,6	0.64	0
2	SO4	B	2986	-	4,4,4	0.98	0	6,6,6	0.43	0
3	NTM	D	2904	-	12,12,12	1.07	1 (8%)	15,16,16	1.41	1 (6%)
3	NTM	E	2905	-	12,12,12	1.38	3 (25%)	15,16,16	1.30	1 (6%)
3	NTM	C	2903	-	12,12,12	1.28	1 (8%)	15,16,16	1.61	3 (20%)
3	NTM	F	2906	-	12,12,12	1.10	1 (8%)	15,16,16	1.39	1 (6%)
2	SO4	A	2985	-	4,4,4	0.92	0	6,6,6	0.41	0
2	SO4	F	2988	-	4,4,4	0.77	0	6,6,6	0.39	0
3	NTM	B	2902	-	12,12,12	0.99	1 (8%)	15,16,16	1.51	4 (26%)
3	NTM	A	2901	-	12,12,12	1.22	1 (8%)	15,16,16	1.38	1 (6%)
2	SO4	E	2989	-	4,4,4	0.84	0	6,6,6	0.40	0

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
3	NTM	D	2904	-	-	2/8/8/8	0/1/1/1
3	NTM	E	2905	-	-	2/8/8/8	0/1/1/1
3	NTM	C	2903	-	-	4/8/8/8	0/1/1/1
3	NTM	F	2906	-	-	2/8/8/8	0/1/1/1
3	NTM	B	2902	-	-	2/8/8/8	0/1/1/1

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NTM	A	2901	-	-	2/8/8/8	0/1/1/1

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	2903	NTM	O3-C8	3.19	1.32	1.22
3	F	2906	NTM	O3-C8	2.47	1.29	1.22
3	E	2905	NTM	O3-C8	2.43	1.29	1.22
3	E	2905	NTM	C2-C7	-2.28	1.47	1.51
3	B	2902	NTM	O3-C8	2.26	1.29	1.22

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	2903	NTM	C6-N1-C2	3.54	123.70	116.80
3	A	2901	NTM	C6-N1-C2	3.52	123.64	116.80
3	F	2906	NTM	C6-N1-C2	3.33	123.29	116.80
3	D	2904	NTM	C6-N1-C2	3.31	123.23	116.80
3	B	2902	NTM	C6-N1-C2	3.27	123.15	116.80

There are no chirality outliers.

5 of 14 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	D	2904	NTM	C2-C3-C8-O4
3	D	2904	NTM	C2-C3-C8-O3
3	C	2903	NTM	C3-C2-C7-O1
3	C	2903	NTM	C3-C2-C7-O2
3	A	2901	NTM	C2-C3-C8-O4

There are no ring outliers.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	E	2905	NTM	1	0
3	F	2906	NTM	2	0
3	B	2902	NTM	1	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

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.