Full wwPDB X-ray Structure Validation Report (i)

Aug 7, 2023 – 10:36 PM EDT

PDB ID	:	1P6X
Title	:	Crystal structure of EHV4-TK complexed with Thy and SO4
Authors	:	Gardberg, A.; Shuvalova, L.; Monnerjahn, C.; Konrad, M.; Lavie, A.
Deposited on	:	2003-04-30
Resolution	:	2.00 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 (i) 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 (1)) were used in the production of this report:

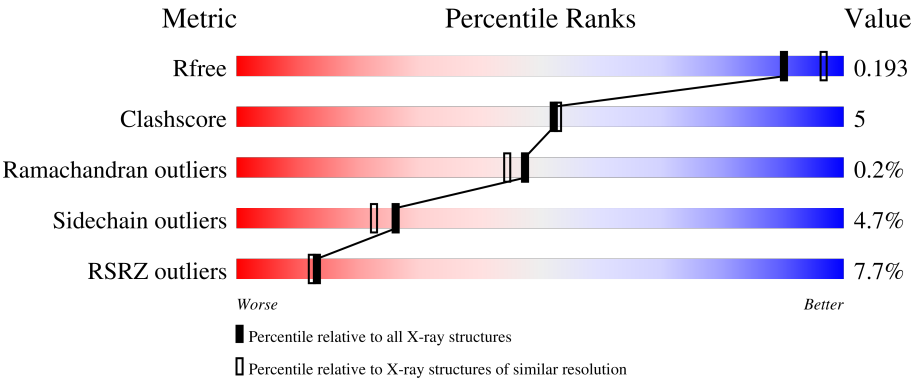
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	8085 (2.00-2.00)
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)
RSRZ outliers	127900	7900 (2.00-2.00)

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 <=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	334	6% 85% 12% .
1	B	334	10% 87% 10% ..

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 5694 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.

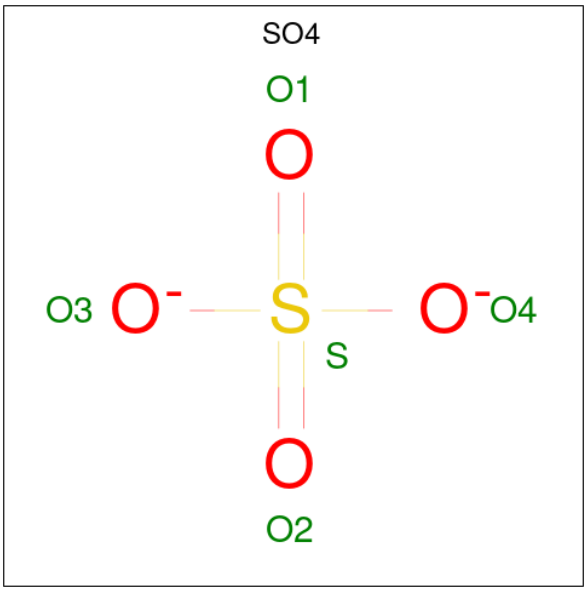
- Molecule 1 is a protein called Thymidine kinase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	333	Total	C	N	O	S	0	4	0
			2597	1638	457	481	21			
1	B	331	Total	C	N	O	S	0	5	0
			2581	1630	452	481	18			

There are 8 discrepancies between the modelled and reference sequences:

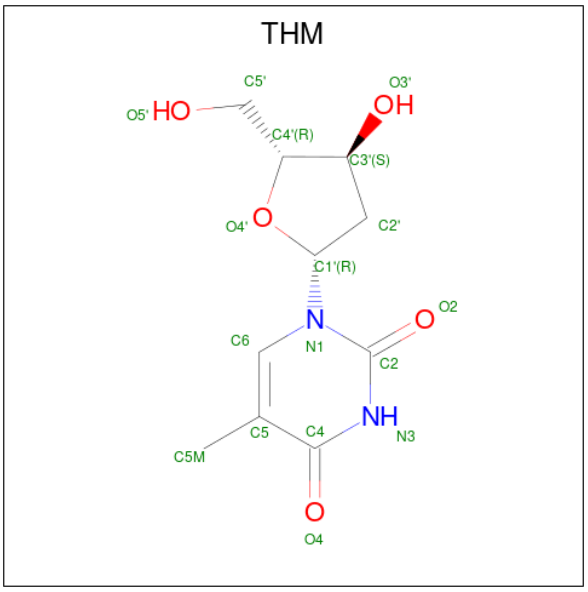
Chain	Residue	Modelled	Actual	Comment	Reference
A	19	GLY	-	cloning artifact	UNP P24425
A	20	SER	-	cloning artifact	UNP P24425
A	21	HIS	-	cloning artifact	UNP P24425
A	22	MET	-	cloning artifact	UNP P24425
B	19	GLY	-	cloning artifact	UNP P24425
B	20	SER	-	cloning artifact	UNP P24425
B	21	HIS	-	cloning artifact	UNP P24425
B	22	MET	-	cloning artifact	UNP P24425

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



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

- Molecule 3 is THYMIDINE (three-letter code: THM) (formula: $C_{10}H_{14}N_2O_5$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C N O 17 10 2 5	0	0
3	B	1	Total C N O 17 10 2 5	0	0

- Molecule 4 is water.

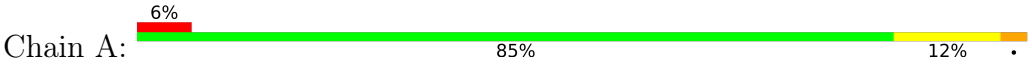
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	249	Total O 249 249	0	0
4	B	203	Total O 203 203	0	0

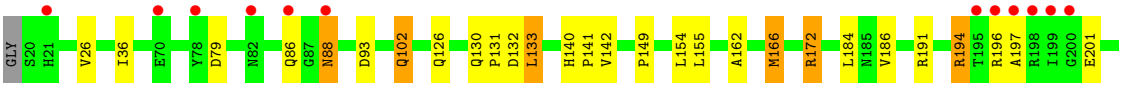
3 Residue-property plots (i)

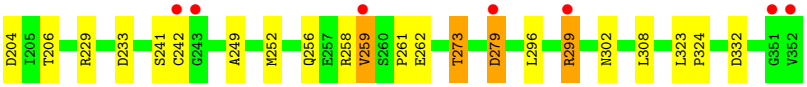
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: Thymidine kinase

Chain A:

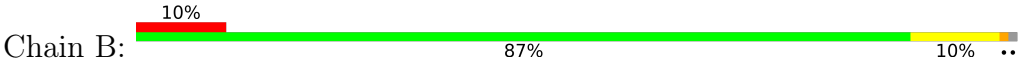


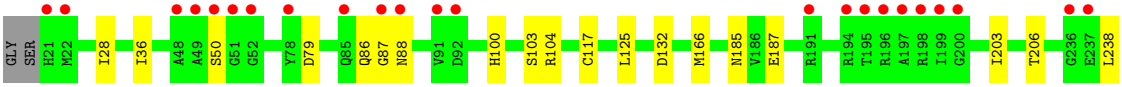


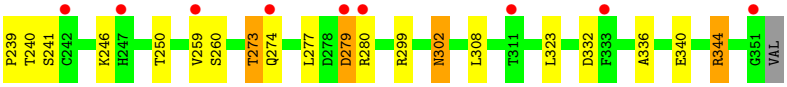


• Molecule 1: Thymidine kinase

Chain B:







4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α, β, γ	111.65Å 121.55Å 118.83Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	24.35 – 2.00 24.35 – 2.00	Depositor EDS
% Data completeness (in resolution range)	99.6 (24.35-2.00) 99.7 (24.35-2.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.60 (at 1.99Å)	Xtriage
Refinement program	REFMAC 5.1.24	Depositor
R, R_{free}	0.187 , 0.237 0.192 , 0.193	Depositor DCC
R_{free} test set	5496 reflections (10.07%)	wwPDB-VP
Wilson B-factor (Å^2)	30.5	Xtriage
Anisotropy	0.106	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 49.4	EDS
L-test for twinning[2]	$< \|L\| > = 0.47$, $< L^2 > = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	5694	wwPDB-VP
Average B, all atoms (Å^2)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.14% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: THM, 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	0.59	0/2667	0.82	9/3621 (0.2%)
1	B	0.56	0/2654	0.76	2/3608 (0.1%)
All	All	0.58	0/5321	0.79	11/7229 (0.2%)

There are no bond length outliers.

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	93	ASP	CB-CG-OD2	6.60	124.24	118.30
1	A	204	ASP	CB-CG-OD2	6.37	124.03	118.30
1	A	279	ASP	CB-CG-OD2	6.31	123.98	118.30
1	A	332	ASP	CB-CG-OD2	6.20	123.88	118.30
1	A	79	ASP	CB-CG-OD2	5.81	123.53	118.30
1	B	332	ASP	CB-CG-OD2	5.80	123.52	118.30
1	A	233	ASP	CB-CG-OD2	5.79	123.51	118.30
1	A	132	ASP	CB-CG-OD2	5.59	123.33	118.30
1	A	172	ARG	NE-CZ-NH2	-5.40	117.60	120.30
1	A	133	LEU	CA-CB-CG	5.10	127.03	115.30
1	B	132	ASP	CB-CG-OD2	5.07	122.86	118.30

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	2597	0	2572	32	0
1	B	2581	0	2541	25	0
2	A	15	0	0	1	0
2	B	15	0	0	0	0
3	A	17	0	14	0	0
3	B	17	0	14	0	0
4	A	249	0	0	6	0
4	B	203	0	0	4	0
All	All	5694	0	5141	57	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 5.

All (57) 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:299:ARG:HG2	1:A:299:ARG:HH11	1.05	1.14
1:A:299:ARG:HG2	1:A:299:ARG:NH1	1.85	0.89
1:A:299:ARG:HH11	1:A:299:ARG:CG	1.85	0.89
1:A:130:GLN:NE2	4:A:1026:HOH:O	2.06	0.87
1:B:100:HIS:CE1	1:B:104:ARG:HE	1.94	0.86
1:A:206:THR:HG23	4:A:985:HOH:O	1.95	0.66
1:A:172:ARG:NH2	2:A:804:SO4:O3	2.30	0.64
1:B:117:CYS:HB3	4:B:918:HOH:O	2.00	0.60
1:B:100:HIS:CE1	1:B:104:ARG:NE	2.69	0.57
1:A:229:ARG:NH2	1:A:261:PRO:O	2.38	0.56
1:B:103:SER:HA	1:B:166:MET:HE1	1.87	0.56
1:B:100:HIS:HE1	1:B:104:ARG:HH21	1.52	0.55
1:B:241:SER:O	1:B:273:THR:CG2	2.54	0.55
1:A:155:LEU:HD21	1:A:206:THR:HG22	1.90	0.54
1:B:100:HIS:HE1	1:B:104:ARG:HE	1.52	0.52
1:B:117:CYS:CB	4:B:918:HOH:O	2.57	0.52
1:A:194:ARG:HD3	4:A:979:HOH:O	2.08	0.52
1:B:240:THR:HG21	1:B:274:GLN:HE21	1.75	0.52
1:A:102:GLN:HG3	1:A:149:PRO:HG3	1.92	0.51
1:A:36:ILE:HG22	1:A:308:LEU:HD12	1.92	0.51
1:B:246:LYS:O	1:B:250:THR:HG23	2.12	0.50
1:B:279:ASP:OD1	1:B:279:ASP:N	2.32	0.50
1:A:259:VAL:HG23	4:A:1003:HOH:O	2.12	0.49
1:A:296:LEU:O	1:A:296:LEU:HG	2.11	0.49
1:B:28:ILE:HD11	1:B:323:LEU:HD21	1.93	0.49
1:A:162:ALA:O	1:A:166:MET:HG2	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:302:ASN:ND2	4:B:950:HOH:O	2.46	0.48
1:A:166:MET:HE2	1:A:166:MET:HB3	1.64	0.48
1:B:100:HIS:HE1	1:B:104:ARG:NH2	2.11	0.48
1:A:88:ASN:HB3	4:A:1031:HOH:O	2.14	0.48
1:B:241:SER:O	1:B:273:THR:HG22	2.15	0.47
1:A:130:GLN:HG2	4:A:963:HOH:O	2.14	0.46
1:B:185:ASN:OD1	1:B:187[A]:GLU:HG2	2.15	0.46
1:B:336:ALA:O	1:B:340:GLU:HG3	2.16	0.45
1:B:259:VAL:HG12	4:B:842:HOH:O	2.17	0.45
1:A:299:ARG:NH1	1:A:299:ARG:CG	2.56	0.45
1:A:155:LEU:CD2	1:A:206:THR:HG22	2.47	0.45
1:B:36:ILE:HG22	1:B:308:LEU:HD12	1.99	0.44
1:A:323:LEU:N	1:A:324:PRO:CD	2.81	0.44
1:A:154:LEU:HD13	1:A:249:ALA:HB1	2.00	0.44
1:A:197:ALA:HB1	1:A:201:GLU:HB3	2.00	0.44
1:B:100:HIS:HE1	1:B:104:ARG:NE	2.12	0.43
1:A:140:HIS:CG	1:A:141:PRO:HD2	2.54	0.43
1:B:86:GLN:HB3	1:B:87:GLY:H	1.70	0.43
1:A:140:HIS:HB3	1:A:142:VAL:HG12	1.99	0.43
1:B:344:ARG:HE	1:B:344:ARG:HB2	1.64	0.43
1:A:196:ARG:HB2	1:A:196:ARG:NH1	2.33	0.42
1:A:166:MET:HG2	1:A:166:MET:H	1.65	0.42
1:A:26:VAL:HG23	1:A:131:PRO:HB3	2.01	0.42
1:A:241:SER:O	1:A:273:THR:HG23	2.19	0.42
1:A:229:ARG:HH12	1:A:262:GLU:HG2	1.85	0.42
1:A:256:GLN:HE21	1:A:258:ARG:NH1	2.18	0.41
1:B:28:ILE:HD11	1:B:323:LEU:CD2	2.51	0.41
1:B:273:THR:O	1:B:277:LEU:HG	2.21	0.41
1:A:36:ILE:HG23	1:A:184:LEU:HB2	2.03	0.41
1:A:186:VAL:HG21	1:A:252[A]:MET:SD	2.61	0.41
1:B:238:LEU:HA	1:B:239:PRO:HD2	1.89	0.41

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	335/334 (100%)	328 (98%)	7 (2%)	0	100 100
1	B	334/334 (100%)	319 (96%)	14 (4%)	1 (0%)	41 37
All	All	669/668 (100%)	647 (97%)	21 (3%)	1 (0%)	47 49

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	88	ASN

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	280/279 (100%)	266 (95%)	14 (5%)	24 20
1	B	277/279 (99%)	264 (95%)	13 (5%)	26 22
All	All	557/558 (100%)	530 (95%)	27 (5%)	26 22

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

Mol	Chain	Res	Type
1	A	86	GLN
1	A	88	ASN
1	A	102	GLN
1	A	126	GLN
1	A	133	LEU
1	A	166	MET
1	A	191	ARG
1	A	194	ARG
1	A	242	CYS
1	A	259	VAL
1	A	273	THR
1	A	279	ASP

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Mol	Chain	Res	Type
1	A	299	ARG
1	A	302	ASN
1	B	50	SER
1	B	79[A]	ASP
1	B	79[B]	ASP
1	B	125	LEU
1	B	203	ILE
1	B	206	THR
1	B	260	SER
1	B	273	THR
1	B	279	ASP
1	B	280	ARG
1	B	299	ARG
1	B	302	ASN
1	B	344	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	256	GLN
1	A	302	ASN
1	B	100	HIS
1	B	126	GLN
1	B	274	GLN
1	B	302	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)

8 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	802	-	4,4,4	0.21	0	6,6,6	0.38	0
2	SO4	A	801	-	4,4,4	0.33	0	6,6,6	0.30	0
3	THM	B	702	-	18,18,18	1.29	3 (16%)	26,26,26	2.41	6 (23%)
2	SO4	B	806	-	4,4,4	0.19	0	6,6,6	0.22	0
2	SO4	B	805	-	4,4,4	0.17	0	6,6,6	0.38	0
2	SO4	A	804	-	4,4,4	0.28	0	6,6,6	0.40	0
2	SO4	A	803	-	4,4,4	0.16	0	6,6,6	0.38	0
3	THM	A	701	-	18,18,18	1.60	6 (33%)	26,26,26	2.14	5 (19%)

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	THM	B	702	-	-	0/6/18/18	0/2/2/2
3	THM	A	701	-	-	0/6/18/18	0/2/2/2

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	701	THM	C6-C5	3.85	1.40	1.34
3	A	701	THM	C4-C5	2.96	1.49	1.44
3	B	702	THM	C6-C5	2.69	1.39	1.34
3	A	701	THM	C2-N1	2.38	1.42	1.38
3	B	702	THM	C4-C5	2.23	1.48	1.44
3	A	701	THM	O2-C2	2.19	1.27	1.23
3	B	702	THM	C4-N3	-2.13	1.34	1.38
3	A	701	THM	C2-N3	-2.07	1.34	1.38
3	A	701	THM	C4-N3	-2.04	1.35	1.38

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	B	702	THM	C4-N3-C2	-5.93	119.67	127.35
3	B	702	THM	C5-C4-N3	5.81	120.27	115.31
3	A	701	THM	C5-C4-N3	5.64	120.13	115.31
3	B	702	THM	O4-C4-C5	-4.93	119.18	124.90
3	B	702	THM	N3-C2-N1	4.91	121.41	114.89
3	A	701	THM	C4-N3-C2	-4.66	121.32	127.35
3	A	701	THM	N3-C2-N1	4.34	120.65	114.89
3	B	702	THM	C5-C6-N1	-3.98	119.25	123.34
3	A	701	THM	C5M-C5-C4	3.91	123.08	118.77
3	A	701	THM	C5-C6-N1	-3.09	120.16	123.34
3	B	702	THM	O2-C2-N1	-2.32	119.70	122.79

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	804	SO4	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

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^{th} 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	333/334 (99%)	0.05	19 (5%)	23	23	20, 30, 55, 67	0
1	B	331/334 (99%)	0.31	32 (9%)	7	7	22, 36, 58, 67	0
All	All	664/668 (99%)	0.18	51 (7%)	13	12	20, 33, 56, 67	0

All (51) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	199	ILE	9.6
1	B	49	ALA	6.4
1	B	50	SER	5.7
1	B	51	GLY	5.6
1	B	52	GLY	5.2
1	A	352	VAL	5.0
1	B	48	ALA	4.9
1	B	85	GLN	4.6
1	A	259	VAL	4.4
1	A	200	GLY	4.2
1	B	21	HIS	4.0
1	B	333	PHE	3.9
1	A	86	GLN	3.8
1	A	351	GLY	3.7
1	A	242	CYS	3.7
1	A	197	ALA	3.6
1	A	196	ARG	3.5
1	B	280	ARG	3.5
1	A	88	ASN	3.4
1	B	351	GLY	3.3
1	B	279	ASP	3.3
1	B	195	THR	3.3
1	B	22	MET	3.0
1	B	87	GLY	3.0

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Mol	Chain	Res	Type	RSRZ
1	B	237	GLU	3.0
1	B	242	CYS	2.9
1	B	88	ASN	2.9
1	B	198	ARG	2.8
1	A	82	ASN	2.8
1	B	199	ILE	2.7
1	B	197	ALA	2.7
1	B	194	ARG	2.7
1	B	91	VAL	2.5
1	A	21	HIS	2.5
1	B	196	ARG	2.5
1	A	195	THR	2.5
1	B	191	ARG	2.5
1	B	274	GLN	2.4
1	B	200	GLY	2.4
1	A	70	GLU	2.4
1	A	299	ARG	2.4
1	B	247[A]	HIS	2.3
1	A	78	TYR	2.3
1	A	243	GLY	2.3
1	B	311	THR	2.2
1	B	92	ASP	2.2
1	B	78	TYR	2.2
1	B	259	VAL	2.1
1	A	198	ARG	2.1
1	B	236	GLY	2.1
1	A	279	ASP	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 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^{th} 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	A	803	5/5	0.96	0.12	48,50,51,51	0
3	THM	A	701	17/17	0.96	0.09	25,28,34,37	0
3	THM	B	702	17/17	0.96	0.08	28,30,35,39	0
2	SO4	B	805	5/5	0.97	0.14	48,49,49,50	0
2	SO4	B	806	5/5	0.98	0.11	42,43,45,45	0
2	SO4	B	802	5/5	0.98	0.08	35,36,37,38	0
2	SO4	A	804	5/5	0.98	0.12	42,44,45,46	0
2	SO4	A	801	5/5	0.99	0.08	31,31,31,33	0

6.5 Other polymers (i)

There are no such residues in this entry.