



Full wwPDB X-ray Structure Validation Report ⓘ

Jun 26, 2017 – 10:24 PM EDT

PDB ID : 1E2J
Title : The nucleoside binding site of Herpes simplex type 1 thymidine kinase analyzed by X-ray crystallography
Authors : Vogt, J.; Scapozza, L.; Schulz, G.E.
Deposited on : 2000-05-23
Resolution : 2.50 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

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20029077
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20029077

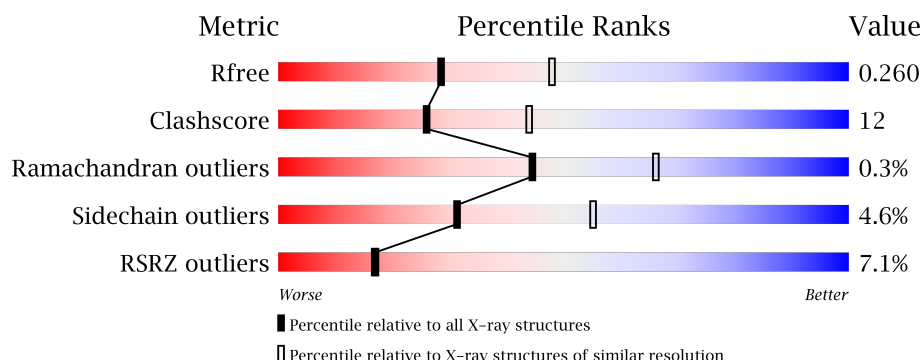
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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}	100719	3846 (2.50-2.50)
Clashscore	112137	4554 (2.50-2.50)
Ramachandran outliers	110173	4463 (2.50-2.50)
Sidechain outliers	110143	4465 (2.50-2.50)
RSRZ outliers	101464	3876 (2.50-2.50)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	331	<div> <div>6%</div> <div>66%</div> <div>23%</div> <div>8%</div> </div>
1	B	331	<div> <div>8%</div> <div>69%</div> <div>24%</div> <div>5%</div> </div>

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 4884 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.

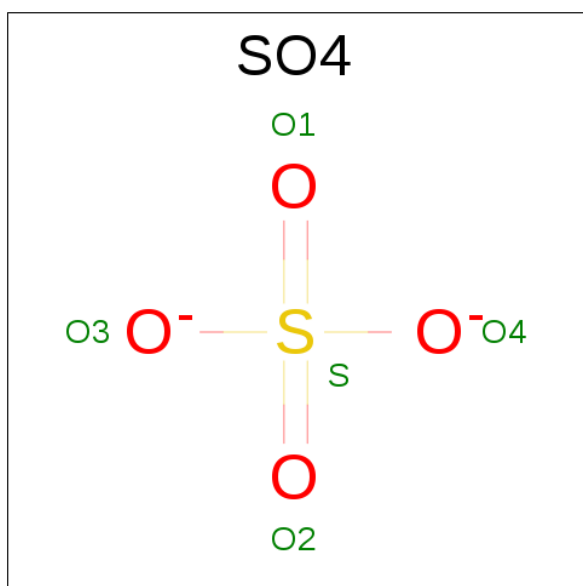
- Molecule 1 is a protein called THYMIDINE KINASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	306	Total	C	N	O	S	0	0	0
			2346	1494	411	425	16			
1	B	314	Total	C	N	O	S	0	0	0
			2383	1518	414	435	16			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	125	ASN	GLN	engineered mutation	UNP P03176
B	125	ASN	GLN	engineered mutation	UNP P03176

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



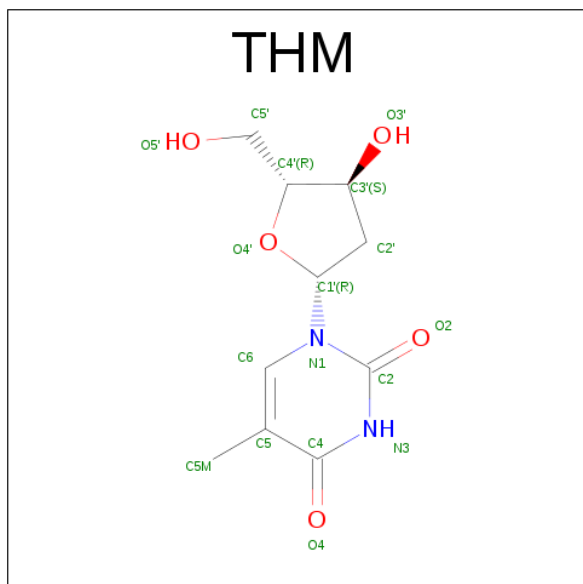
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	O S	0	0
			5	4 1		

Continued on next page...

Continued from previous page...

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

- Molecule 3 is THYMIDINE (three-letter code: THM) (formula: C₁₀H₁₄N₂O₅).



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

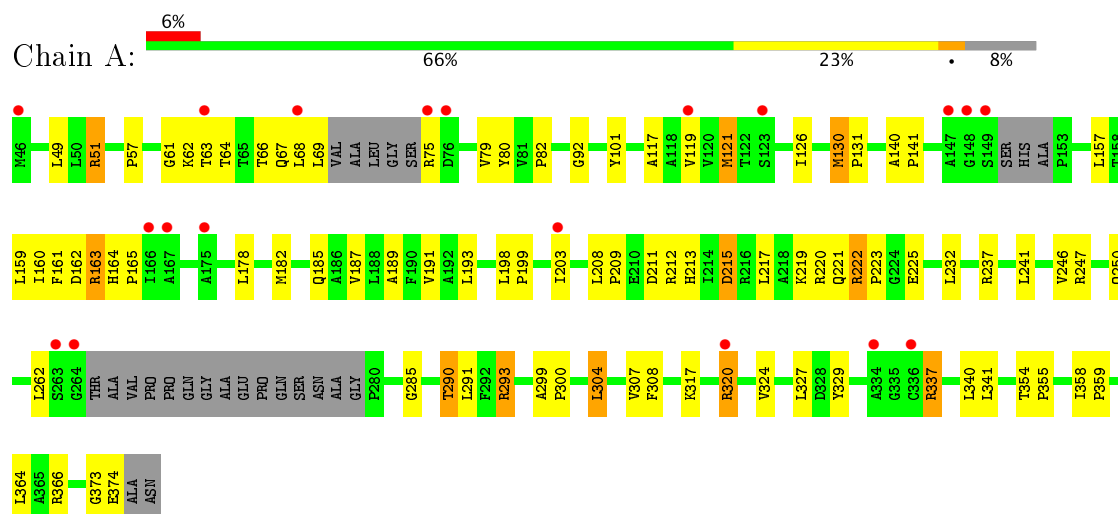
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	57	Total	O	0	0
			57	57		
4	B	54	Total	O	0	0
			54	54		

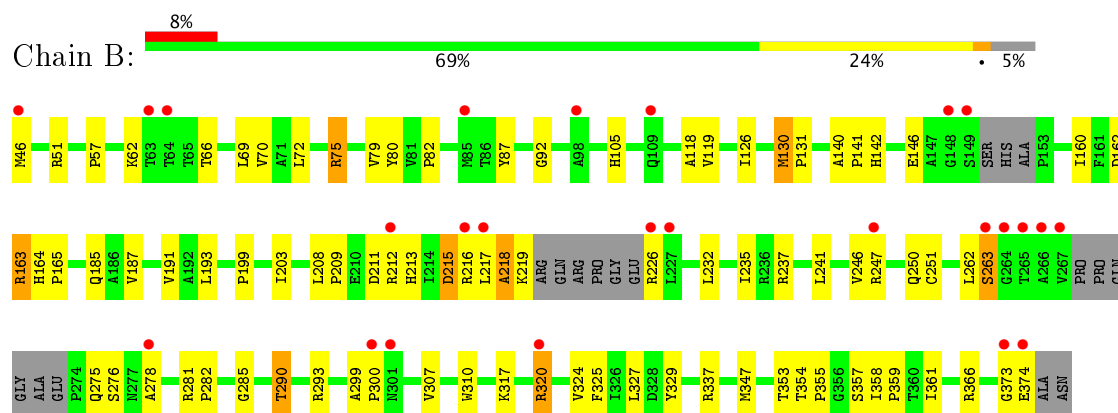
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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



• Molecule 1: THYMIDINE KINASE



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	113.40Å 117.50Å 108.60Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.50 28.35 – 2.44	Depositor EDS
% Data completeness (in resolution range)	91.0 (20.00-2.50) 90.0 (28.35-2.44)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.38 (at 2.45Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.212 , 0.273 0.207 , 0.260	Depositor DCC
R_{free} test set	1168 reflections (5.29%)	DCC
Wilson B-factor (Å ²)	17.4	Xtriage
Anisotropy	0.362	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 47.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	0.030 for -k,-h,-l	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	4884	wwPDB-VP
Average B, all atoms (Å ²)	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.03% 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: 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	0.49	0/2400	1.09	11/3272 (0.3%)
1	B	0.48	0/2437	1.04	8/3326 (0.2%)
All	All	0.48	0/4837	1.06	19/6598 (0.3%)

There are no bond length outliers.

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	51	ARG	CD-NE-CZ	12.57	141.21	123.60
1	A	222	ARG	CD-NE-CZ	12.34	140.88	123.60
1	A	163	ARG	NE-CZ-NH1	11.95	126.27	120.30
1	B	163	ARG	NE-CZ-NH2	11.36	125.98	120.30
1	A	51	ARG	NE-CZ-NH1	11.18	125.89	120.30
1	B	51	ARG	CD-NE-CZ	10.21	137.89	123.60
1	A	163	ARG	NH1-CZ-NH2	-7.92	110.69	119.40
1	B	163	ARG	NH1-CZ-NH2	-7.13	111.56	119.40
1	B	51	ARG	NE-CZ-NH1	7.12	123.86	120.30
1	B	216	ARG	NE-CZ-NH1	7.01	123.81	120.30
1	A	320	ARG	CG-CD-NE	6.88	126.24	111.80
1	B	293	ARG	CD-NE-CZ	6.59	132.83	123.60
1	A	337	ARG	CD-NE-CZ	6.38	132.53	123.60
1	A	222	ARG	NE-CZ-NH1	6.34	123.47	120.30
1	A	51	ARG	NE-CZ-NH2	-6.27	117.17	120.30
1	A	293	ARG	NE-CZ-NH2	-5.56	117.52	120.30
1	A	163	ARG	NE-CZ-NH2	5.47	123.03	120.30
1	B	320	ARG	CG-CD-NE	5.09	122.49	111.80
1	B	51	ARG	NE-CZ-NH2	-5.01	117.79	120.30

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	2346	0	2362	57	0
1	B	2383	0	2400	62	0
2	A	5	0	0	1	0
2	B	5	0	0	0	0
3	A	17	0	14	0	0
3	B	17	0	14	0	0
4	A	57	0	0	2	0
4	B	54	0	0	2	0
All	All	4884	0	4790	113	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 12.

All (113) 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:119:VAL:HG12	1:B:119:VAL:HG12	1.48	0.95
1:B:66:THR:HG23	1:B:160:ILE:HG21	1.58	0.85
1:B:130:MET:HB3	1:B:131:PRO:HD3	1.60	0.83
1:A:358:ILE:HB	1:A:359:PRO:HD3	1.60	0.83
1:B:358:ILE:HB	1:B:359:PRO:HD3	1.63	0.80
1:B:285:GLY:HA2	1:B:290:THR:HG23	1.67	0.76
1:A:69:LEU:HD23	1:A:340:LEU:HD23	1.66	0.76
1:B:246:VAL:HG21	1:B:324:VAL:HG21	1.69	0.75
1:A:285:GLY:HA2	1:A:290:THR:HG23	1.70	0.73
1:B:75:ARG:HE	1:B:75:ARG:H	1.39	0.70
1:B:70:VAL:HG21	1:B:80:TYR:HB2	1.74	0.70
1:B:217:LEU:HD22	1:B:232:LEU:HD13	1.74	0.69
1:B:66:THR:HG21	1:B:80:TYR:CE1	2.27	0.69
1:A:130:MET:HB3	1:A:131:PRO:HD3	1.75	0.69
1:B:140:ALA:HB3	1:B:141:PRO:HD3	1.78	0.66
1:A:217:LEU:HD22	1:A:232:LEU:HD13	1.80	0.63
1:B:354:THR:HB	1:B:355:PRO:HD2	1.82	0.62
1:A:69:LEU:HB2	1:A:337:ARG:HG2	1.83	0.60
1:A:64:THR:O	1:A:68:LEU:HG	2.01	0.60

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:105:HIS:CG	1:B:226:ARG:HH11	2.20	0.59
1:B:187:VAL:O	1:B:191:VAL:HG23	2.02	0.59
1:A:92:GLY:HA2	1:B:185:GLN:HG2	1.84	0.59
1:B:275:GLN:NE2	1:B:278:ALA:HB3	2.19	0.58
1:A:51:ARG:HG3	4:A:2002:HOH:O	2.02	0.58
1:A:62:LYS:HB2	1:A:62:LYS:NZ	2.19	0.58
1:A:61:GLY:HA2	1:A:220:ARG:HH11	1.69	0.57
1:B:62:LYS:NZ	1:B:62:LYS:HB2	2.21	0.56
1:A:354:THR:HB	1:A:355:PRO:HD2	1.87	0.56
1:A:246:VAL:HG21	1:A:324:VAL:HG21	1.88	0.56
1:B:276:SER:HB2	1:B:324:VAL:HB	1.88	0.55
1:B:246:VAL:O	1:B:250:GLN:HG3	2.06	0.55
1:A:185:GLN:HG2	1:B:92:GLY:HA2	1.88	0.55
1:B:262:LEU:O	1:B:263:SER:C	2.45	0.55
1:B:299:ALA:HB1	1:B:300:PRO:HD2	1.88	0.55
1:B:218:ALA:O	1:B:219:LYS:HB2	2.08	0.54
1:B:130:MET:HB3	1:B:131:PRO:CD	2.36	0.54
1:B:72:LEU:CD1	1:B:337:ARG:HD2	2.37	0.54
1:B:208:LEU:HD12	1:B:209:PRO:HD2	1.89	0.54
1:B:162:ASP:O	1:B:163:ARG:HB2	2.08	0.54
1:A:162:ASP:O	1:A:163:ARG:HB2	2.08	0.53
1:A:117:ALA:O	1:A:121:MET:HB2	2.09	0.53
1:B:285:GLY:HA2	1:B:290:THR:CG2	2.37	0.53
1:B:325:PHE:CE1	1:B:347:MET:HG2	2.43	0.53
1:B:75:ARG:NE	1:B:75:ARG:H	2.05	0.53
1:A:304:LEU:HD22	1:A:308:PHE:HB2	1.90	0.52
1:B:105:HIS:CG	1:B:226:ARG:NH1	2.79	0.51
1:A:80:TYR:O	1:A:82:PRO:HD3	2.10	0.51
1:A:159:LEU:HD13	1:A:161:PHE:CZ	2.47	0.50
1:A:164:HIS:CG	1:A:165:PRO:HD2	2.46	0.50
1:B:299:ALA:HB1	1:B:300:PRO:CD	2.41	0.50
1:B:87:TYR:OH	1:B:130:MET:HG3	2.12	0.50
1:B:72:LEU:HD11	1:B:337:ARG:HD2	1.93	0.49
1:A:140:ALA:HB3	1:A:141:PRO:HD3	1.93	0.49
1:B:105:HIS:ND1	1:B:226:ARG:NH1	2.59	0.49
1:B:130:MET:CB	1:B:131:PRO:HD3	2.37	0.49
1:B:164:HIS:CG	1:B:165:PRO:HD2	2.47	0.49
1:A:285:GLY:HA2	1:A:290:THR:CG2	2.42	0.49
1:A:220:ARG:HD2	2:A:400:SO4:O3	2.13	0.49
1:A:63:THR:O	1:A:67:GLN:HG3	2.13	0.49
1:A:69:LEU:HD11	1:A:341:LEU:HD13	1.95	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:178:LEU:HD21	1:A:291:LEU:HD22	1.96	0.48
1:A:203:ILE:HG23	1:A:324:VAL:HG22	1.94	0.48
1:A:187:VAL:O	1:A:191:VAL:HG23	2.13	0.48
1:A:79:VAL:HG12	1:A:80:TYR:N	2.29	0.48
1:A:69:LEU:CD1	1:A:341:LEU:HD13	2.43	0.48
1:B:80:TYR:O	1:B:82:PRO:HD3	2.13	0.47
1:A:221:GLN:HB2	4:A:2041:HOH:O	2.14	0.47
1:A:189:ALA:HB2	4:B:2006:HOH:O	2.13	0.47
1:A:246:VAL:O	1:A:250:GLN:HG3	2.14	0.47
1:B:118:ALA:HB1	4:B:2010:HOH:O	2.15	0.46
1:B:281:ARG:HA	1:B:282:PRO:HD3	1.73	0.46
1:B:373:GLY:O	1:B:374:GLU:HB2	2.15	0.46
1:A:62:LYS:O	1:A:66:THR:HG23	2.15	0.46
1:A:317:LYS:HA	1:A:320:ARG:HD2	1.97	0.45
1:A:317:LYS:HA	1:A:320:ARG:CD	2.47	0.45
1:A:373:GLY:O	1:A:374:GLU:HB2	2.15	0.45
1:B:57:PRO:HB2	1:B:213:HIS:HE1	1.81	0.45
1:A:208:LEU:HD12	1:A:209:PRO:HD2	1.97	0.45
1:A:193:LEU:HD13	1:B:193:LEU:HD13	1.99	0.45
1:B:146:GLU:HG3	1:B:199:PRO:HB3	1.99	0.44
1:B:203:ILE:HG23	1:B:324:VAL:HG22	1.99	0.44
1:A:61:GLY:HA2	1:A:220:ARG:NH1	2.32	0.44
1:A:327:LEU:HD23	1:A:329:TYR:CZ	2.52	0.44
1:B:66:THR:HG23	1:B:160:ILE:CG2	2.39	0.44
1:A:299:ALA:HB1	1:A:300:PRO:HD2	2.00	0.43
1:A:237:ARG:O	1:A:241:LEU:HG	2.18	0.43
1:B:211:ASP:O	1:B:215:ASP:HB2	2.18	0.43
1:A:49:LEU:HD13	1:A:157:LEU:HD23	2.01	0.42
1:B:251:CYS:HB2	1:B:281:ARG:HB2	2.01	0.42
1:B:79:VAL:HG12	1:B:80:TYR:N	2.34	0.42
1:B:358:ILE:CB	1:B:359:PRO:HD3	2.42	0.42
1:B:237:ARG:O	1:B:241:LEU:HG	2.20	0.42
1:B:262:LEU:HD22	1:B:290:THR:CG2	2.50	0.42
1:A:211:ASP:O	1:A:215:ASP:HB2	2.19	0.42
1:B:357:SER:O	1:B:361:ILE:HG13	2.20	0.42
1:A:126:ILE:HD11	1:B:126:ILE:HD11	2.02	0.42
1:A:364:LEU:HD22	1:B:310:TRP:CZ2	2.55	0.42
1:A:262:LEU:HB3	1:A:293:ARG:HD3	2.02	0.41
1:A:198:LEU:HB3	1:A:199:PRO:HD2	2.02	0.41
1:A:130:MET:CB	1:A:131:PRO:HD3	2.47	0.41
1:B:337:ARG:HH11	1:B:337:ARG:HD3	1.68	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:101:TYR:CZ	1:A:225:GLU:HG3	2.56	0.41
1:A:222:ARG:HB3	1:A:223:PRO:HD2	2.01	0.41
1:B:317:LYS:HA	1:B:320:ARG:HD2	2.03	0.41
1:B:327:LEU:HD23	1:B:329:TYR:CZ	2.56	0.41
1:A:62:LYS:HB2	1:A:62:LYS:HZ2	1.84	0.41
1:A:198:LEU:HB3	1:A:199:PRO:CD	2.51	0.41
1:A:63:THR:HG22	1:A:67:GLN:OE1	2.21	0.41
1:B:142:HIS:HA	1:B:353:THR:OG1	2.21	0.41
1:B:235:ILE:HA	1:B:235:ILE:HD12	1.83	0.41
1:B:320:ARG:HH11	1:B:320:ARG:HG3	1.86	0.40
1:A:57:PRO:HB2	1:A:213:HIS:HE1	1.86	0.40
1:B:140:ALA:HB3	1:B:141:PRO:CD	2.50	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	A	298/331 (90%)	282 (95%)	16 (5%)	0	100	100
1	B	306/331 (92%)	287 (94%)	17 (6%)	2 (1%)	25	43
All	All	604/662 (91%)	569 (94%)	33 (6%)	2 (0%)	44	66

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	218	ALA
1	B	263	SER

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	248/264 (94%)	235 (95%)	13 (5%)	27	49
1	B	252/264 (96%)	242 (96%)	10 (4%)	36	62
All	All	500/528 (95%)	477 (95%)	23 (5%)	31	55

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	75	ARG
1	A	121	MET
1	A	130	MET
1	A	160	ILE
1	A	182	MET
1	A	212	ARG
1	A	215	ASP
1	A	219	LYS
1	A	247	ARG
1	A	290	THR
1	A	304	LEU
1	A	307	VAL
1	A	366	ARG
1	B	46	MET
1	B	69	LEU
1	B	75	ARG
1	B	130	MET
1	B	212	ARG
1	B	215	ASP
1	B	247	ARG
1	B	290	THR
1	B	307	VAL
1	B	366	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	67	GLN
1	B	275	GLN

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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

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	400	-	4,4,4	0.70	0	6,6,6	0.13	0
3	THM	A	500	-	13,18,18	1.83	3 (23%)	17,26,26	4.53	8 (47%)
2	SO4	B	400	-	4,4,4	0.74	0	6,6,6	0.17	0
3	THM	B	500	-	13,18,18	1.51	2 (15%)	17,26,26	4.27	9 (52%)

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
2	SO4	A	400	-	-	0/0/0/0	0/0/0/0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	THM	A	500	-	-	0/2/18/18	0/2/2/2
2	SO4	B	400	-	-	0/0/0/0	0/0/0/0
3	THM	B	500	-	-	0/2/18/18	0/2/2/2

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	500	THM	C6-C5	-2.35	1.33	1.40
3	A	500	THM	C6-C5	-2.33	1.33	1.40
3	A	500	THM	O4'-C1'	2.02	1.47	1.42
3	B	500	THM	C4-N3	3.25	1.38	1.33
3	A	500	THM	C4-N3	4.83	1.41	1.33

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	500	THM	C5-C4-N3	-11.87	112.15	125.24
3	A	500	THM	C5-C4-N3	-11.58	112.48	125.24
3	B	500	THM	O4'-C1'-C2'	-5.12	96.42	106.25
3	A	500	THM	O4'-C1'-C2'	-4.77	97.10	106.25
3	A	500	THM	O4'-C4'-C3'	-3.94	96.22	105.68
3	B	500	THM	O4'-C4'-C3'	-2.99	98.50	105.68
3	B	500	THM	C5-C6-N1	-2.76	119.17	122.15
3	B	500	THM	C5M-C5-C4	-2.28	117.53	120.17
3	B	500	THM	O4'-C4'-C5'	2.05	113.55	109.16
3	A	500	THM	O4'-C4'-C5'	2.37	114.24	109.16
3	A	500	THM	C2'-C1'-N1	2.99	121.30	114.23
3	A	500	THM	O4'-C1'-N1	2.99	112.83	107.78
3	B	500	THM	C2'-C1'-N1	3.39	122.24	114.23
3	B	500	THM	C4'-O4'-C1'	3.95	119.07	109.42
3	A	500	THM	C4'-O4'-C1'	3.99	119.18	109.42
3	B	500	THM	C4-N3-C2	9.14	123.15	115.16
3	A	500	THM	C4-N3-C2	11.31	125.05	115.16

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	400	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, 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	306/331 (92%)	0.72	19 (6%)	21 22	7, 24, 48, 88	0
1	B	314/331 (94%)	0.78	25 (7%)	13 13	7, 25, 58, 104	0
All	All	620/662 (93%)	0.75	44 (7%)	17 17	7, 24, 56, 104	0

All (44) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	75	ARG	5.8
1	B	227	LEU	4.7
1	B	148	GLY	4.6
1	A	76	ASP	4.5
1	A	148	GLY	4.5
1	A	264	GLY	4.1
1	B	265	THR	3.9
1	B	226	ARG	3.4
1	B	217	LEU	3.3
1	B	300	PRO	3.1
1	B	263	SER	3.0
1	B	373	GLY	3.0
1	B	247	ARG	2.9
1	B	149	SER	2.8
1	B	264	GLY	2.7
1	A	334	ALA	2.7
1	B	374	GLU	2.7
1	B	267	VAL	2.6
1	A	68	LEU	2.6
1	A	149	SER	2.5
1	B	46	MET	2.5
1	A	166	ILE	2.4
1	B	320	ARG	2.4
1	A	203	ILE	2.3

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	263	SER	2.3
1	B	216	ARG	2.3
1	A	320	ARG	2.2
1	B	212	ARG	2.2
1	A	147	ALA	2.2
1	B	98	ALA	2.2
1	A	167	ALA	2.2
1	B	63	THR	2.2
1	B	266	ALA	2.2
1	A	123	SER	2.1
1	A	46	MET	2.1
1	A	175	ALA	2.1
1	B	64	THR	2.1
1	B	301	ASN	2.1
1	B	85	MET	2.1
1	B	278	ALA	2.1
1	A	336	CYS	2.1
1	A	119	VAL	2.0
1	A	63	THR	2.0
1	B	109	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 carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
3	THM	B	500	17/17	0.84	0.24	1.48	44,46,49,51	0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
3	THM	A	500	17/17	0.86	0.24	1.21	31,33,37,37	0
2	SO4	B	400	5/5	0.96	0.21	-0.29	26,27,29,30	0
2	SO4	A	400	5/5	0.95	0.13	-1.18	30,30,34,35	0

6.5 Other polymers [i](#)

There are no such residues in this entry.