



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 07:06 PM GMT

PDB ID : 1E2P
Title : THYMIDINE KINASE, DHBT
Authors : Schulz, G.E.; Kessler, U.
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 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
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) : trunk26865

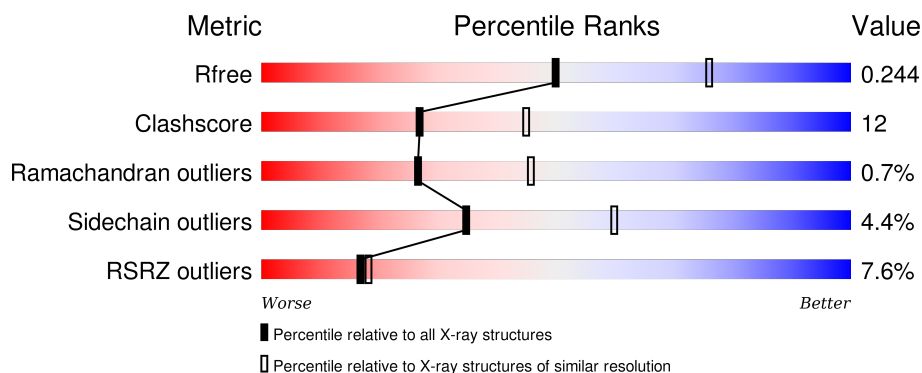
1 Overall quality at a glance

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}	91344	3553 (2.50-2.50)
Clashscore	102246	4242 (2.50-2.50)
Ramachandran outliers	100387	4156 (2.50-2.50)
Sidechain outliers	100360	4158 (2.50-2.50)
RSRZ outliers	91569	3562 (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> <div></div> <div>67%</div> <div>21%</div> <div>•</div> <div>8%</div> </div> </div>
1	B	331	<div> <div>8%</div> <div> <div></div> <div>70%</div> <div>21%</div> <div>•</div> <div>6%</div> </div> </div>

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 4855 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	305	Total	C	N	O	S	0	0	0
			2341	1490	410	425	16			
1	B	310	Total	C	N	O	S	0	0	0
			2359	1502	410	431	16			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	321	SER	PRO	CONFLICT	UNP P03176
B	321	SER	PRO	CONFLICT	UNP P03176

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



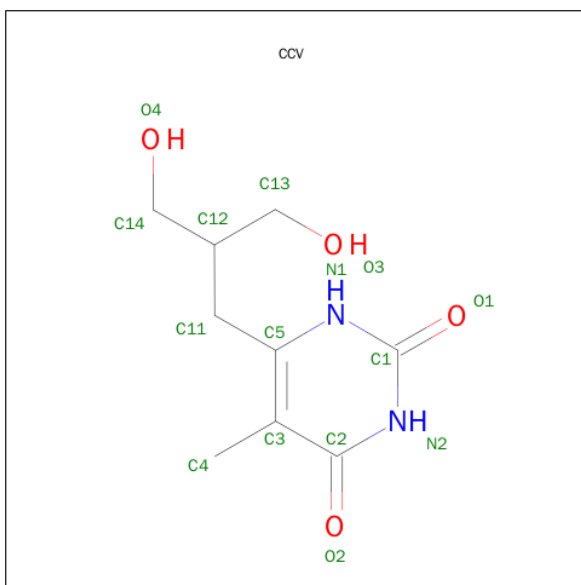
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		

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 6-[3-HYDROXY-2-(HYDROXYMETHYL)PROPYL]-5-METHYL-2,4(1H,3H)-PYRIMIDINEDIONE (three-letter code: CCV) (formula: C₉H₁₄N₂O₄).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			15	9	2	4		
3	B	1	Total	C	N	O	0	0
			15	9	2	4		

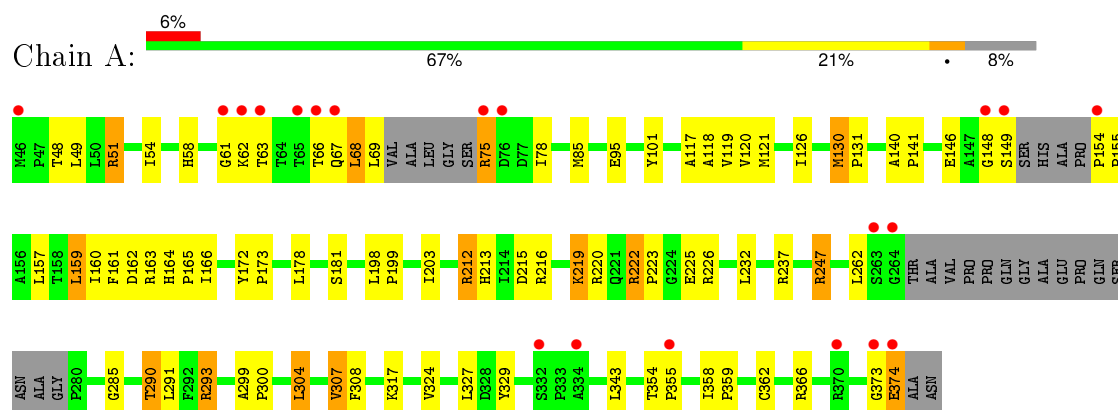
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	52	Total	O	0	0
			52	52		
4	B	63	Total	O	0	0
			63	63		

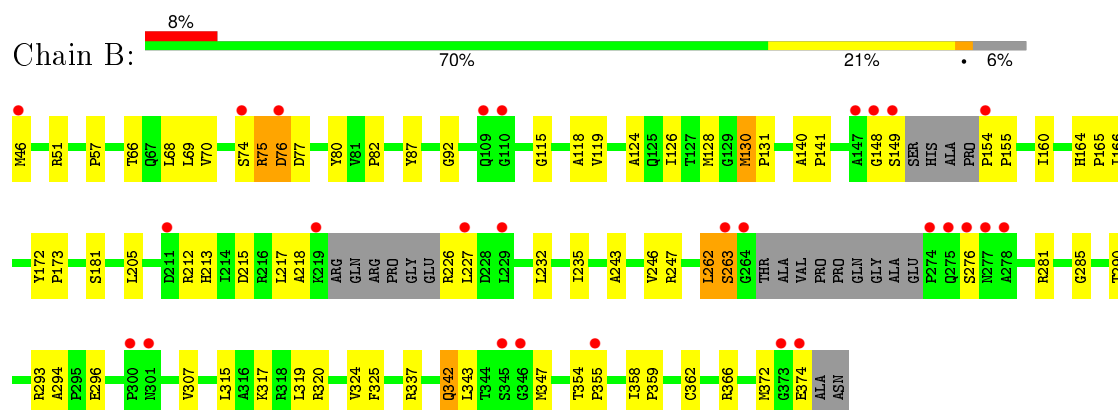
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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	113.70Å 117.60Å 108.30Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.50 19.98 – 2.50	Depositor EDS
% Data completeness (in resolution range)	99.0 (20.00-2.50) 99.8 (19.98-2.50)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.02 (at 2.50Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.209 , 0.261 0.199 , 0.244	Depositor DCC
R_{free} test set	1250 reflections (5.18%)	DCC
Wilson B-factor (Å ²)	41.8	Xtriage
Anisotropy	0.302	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 49.2	EDS
Estimated twinning fraction	0.032 for -k,-h,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 25366 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	4855	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.29% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: CCV, 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	0.45	0/2394	0.93	7/3261 (0.2%)
1	B	0.46	0/2412	1.01	11/3288 (0.3%)
All	All	0.45	0/4806	0.97	18/6549 (0.3%)

There are no bond length outliers.

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	247	ARG	CD-NE-CZ	13.98	143.17	123.60
1	B	247	ARG	NE-CZ-NH1	11.13	125.86	120.30
1	B	281	ARG	CD-NE-CZ	7.75	134.45	123.60
1	B	263	SER	CA-C-N	-7.53	101.14	116.20
1	A	51	ARG	NE-CZ-NH1	6.76	123.68	120.30
1	B	281	ARG	NE-CZ-NH1	6.53	123.56	120.30
1	B	46	MET	CA-CB-CG	6.27	123.96	113.30
1	B	263	SER	CB-CA-C	-6.05	98.60	110.10
1	A	293	ARG	CD-NE-CZ	5.87	131.82	123.60
1	A	237	ARG	CD-NE-CZ	5.81	131.74	123.60
1	A	51	ARG	CD-NE-CZ	5.62	131.47	123.60
1	A	307	VAL	CB-CA-C	-5.55	100.86	111.40
1	B	51	ARG	CD-NE-CZ	5.35	131.09	123.60
1	A	237	ARG	NE-CZ-NH1	5.25	122.92	120.30
1	B	262	LEU	C-N-CA	5.13	134.52	121.70
1	B	263	SER	O-C-N	5.02	131.73	123.20
1	B	247	ARG	NE-CZ-NH2	-5.01	117.79	120.30
1	A	222	ARG	CD-NE-CZ	5.01	130.62	123.60

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	2341	0	2357	62	0
1	B	2359	0	2374	56	0
2	A	5	0	0	0	0
2	B	5	0	0	0	0
3	A	15	0	14	0	0
3	B	15	0	14	1	0
4	A	52	0	0	6	0
4	B	63	0	0	2	0
All	All	4855	0	4759	115	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 (115) 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:126:ILE:HD11	1:B:126:ILE:HD11	1.48	0.95
1:A:119:VAL:HG12	1:B:119:VAL:HG12	1.54	0.88
1:B:154:PRO:HB2	1:B:155:PRO:HD2	1.63	0.80
1:B:358:ILE:HB	1:B:359:PRO:HD3	1.64	0.80
1:B:130:MET:HB3	1:B:131:PRO:HD3	1.65	0.79
1:B:354:THR:HB	1:B:355:PRO:HD2	1.65	0.78
1:A:54:ILE:HD12	1:A:66:THR:HG22	1.65	0.78
1:B:276:SER:HB2	1:B:324:VAL:HB	1.67	0.77
1:A:358:ILE:HB	1:A:359:PRO:HD3	1.66	0.75
1:A:68:LEU:O	1:A:69:LEU:HB2	1.87	0.74
1:B:285:GLY:HA2	1:B:290:THR:HG21	1.70	0.71
1:B:57:PRO:HB3	1:B:235:ILE:HG23	1.73	0.71
1:B:342:GLN:HB2	4:B:2060:HOH:O	1.92	0.70
1:A:61:GLY:HA2	1:A:220:ARG:NH1	2.06	0.69
1:B:140:ALA:HB3	1:B:141:PRO:HD3	1.77	0.67
1:B:262:LEU:HB3	1:B:293:ARG:HD2	1.75	0.67
1:A:285:GLY:HA2	1:A:290:THR:HG23	1.76	0.66
1:B:70:VAL:HG21	1:B:80:TYR:HB2	1.79	0.64
1:B:130:MET:HB3	1:B:131:PRO:CD	2.27	0.64

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:212:ARG:NH1	1:A:216:ARG:HH21	1.95	0.63
1:B:76:ASP:HB3	1:B:366:ARG:HH22	1.63	0.63
1:A:130:MET:HB3	1:A:131:PRO:HD3	1.81	0.62
1:B:217:LEU:HD22	1:B:232:LEU:HD13	1.81	0.62
1:B:317:LYS:HA	1:B:320:ARG:HD3	1.81	0.62
1:A:146:GLU:HG3	1:A:199:PRO:HB3	1.83	0.60
1:A:140:ALA:HB3	1:A:141:PRO:HD3	1.83	0.60
1:B:66:THR:HG23	1:B:160:ILE:HG21	1.84	0.59
1:A:299:ALA:HB1	1:A:300:PRO:HD2	1.83	0.59
1:A:304:LEU:HD22	1:A:308:PHE:HB2	1.86	0.56
1:B:262:LEU:HB3	1:B:293:ARG:CD	2.36	0.56
1:A:85:MET:HE3	1:A:222:ARG:HD3	1.88	0.56
1:B:115:GLY:O	1:B:119:VAL:HG23	2.05	0.55
1:B:262:LEU:HD21	1:B:290:THR:HG22	1.89	0.55
1:B:205:LEU:HD12	1:B:243:ALA:HB2	1.90	0.54
1:A:213:HIS:CE1	1:A:232:LEU:HD11	2.43	0.54
1:A:293:ARG:HH11	1:A:293:ARG:HB3	1.73	0.54
1:B:66:THR:HG21	1:B:80:TYR:CE1	2.43	0.53
1:A:78:ILE:HD11	1:A:160:ILE:HD12	1.90	0.53
1:B:124:ALA:O	1:B:128:MET:HG2	2.09	0.53
1:A:159:LEU:HD13	1:A:161:PHE:CZ	2.44	0.53
1:A:164:HIS:ND1	1:A:166:ILE:HG12	2.24	0.53
1:B:362:CYS:O	1:B:366:ARG:HG2	2.10	0.52
1:A:327:LEU:HD23	1:A:329:TYR:CZ	2.45	0.52
1:A:48:THR:OG1	1:A:155:PRO:HA	2.09	0.51
1:A:154:PRO:CB	1:A:155:PRO:HD2	2.40	0.51
1:B:75:ARG:HE	1:B:75:ARG:H	1.58	0.50
1:A:164:HIS:CG	1:A:165:PRO:HD2	2.46	0.50
1:B:285:GLY:HA2	1:B:290:THR:CG2	2.40	0.50
1:A:62:LYS:HG3	4:A:2003:HOH:O	2.11	0.50
1:B:154:PRO:CB	1:B:155:PRO:HD2	2.38	0.50
1:B:164:HIS:CG	1:B:165:PRO:HD2	2.46	0.50
1:A:317:LYS:HD3	4:B:2020:HOH:O	2.12	0.49
1:A:51:ARG:HG3	4:A:2050:HOH:O	2.12	0.49
1:B:294:ALA:HB1	1:B:296:GLU:OE1	2.12	0.49
1:A:54:ILE:HD12	1:A:66:THR:CG2	2.38	0.49
1:A:362:CYS:O	1:A:366:ARG:HG3	2.12	0.49
1:A:178:LEU:HD21	1:A:291:LEU:HD22	1.95	0.49
1:A:63:THR:HG22	1:A:67:GLN:NE2	2.28	0.48
1:A:198:LEU:HB3	1:A:199:PRO:CD	2.43	0.48
1:A:118:ALA:HA	1:A:181:SER:O	2.15	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:58:HIS:HB3	1:A:163:ARG:NH2	2.29	0.47
1:B:154:PRO:HB2	1:B:155:PRO:CD	2.40	0.47
1:A:154:PRO:HB2	1:A:155:PRO:HD2	1.96	0.47
1:A:62:LYS:HB2	1:A:62:LYS:NZ	2.31	0.46
1:A:157:LEU:HD22	1:A:358:ILE:HG23	1.97	0.46
1:A:285:GLY:HA2	1:A:290:THR:CG2	2.43	0.46
1:A:120:VAL:HA	1:B:119:VAL:CG1	2.46	0.46
1:A:85:MET:CE	1:A:222:ARG:HD3	2.44	0.46
1:B:87:TYR:HB2	1:B:372:MET:HG2	1.98	0.46
4:A:2026:HOH:O	1:B:130:MET:HA	2.16	0.45
1:A:117:ALA:O	1:A:121:MET:HB2	2.17	0.45
1:B:315:LEU:O	1:B:319:LEU:HG	2.16	0.45
3:B:500:CCV:H112	3:B:500:CCV:H43	1.79	0.45
1:B:325:PHE:CE1	1:B:347:MET:HG2	2.51	0.45
1:A:49:LEU:HD12	1:A:157:LEU:O	2.17	0.45
1:A:262:LEU:HD22	1:A:290:THR:CG2	2.47	0.45
1:A:373:GLY:O	1:A:374:GLU:HB2	2.17	0.45
1:B:262:LEU:CD2	1:B:290:THR:HG22	2.47	0.44
1:B:87:TYR:OH	1:B:130:MET:HG3	2.17	0.44
1:A:119:VAL:CG1	1:B:119:VAL:HG12	2.37	0.44
1:B:246:VAL:HG11	1:B:324:VAL:HG23	2.00	0.43
1:B:213:HIS:NE2	1:B:232:LEU:HD11	2.33	0.43
1:A:172:TYR:N	1:A:173:PRO:CD	2.81	0.43
1:B:354:THR:HB	1:B:355:PRO:CD	2.43	0.43
1:A:222:ARG:HB3	1:A:223:PRO:HD2	1.99	0.43
1:B:87:TYR:CE1	1:B:92:GLY:HA3	2.54	0.43
1:B:285:GLY:CA	1:B:290:THR:HG21	2.44	0.43
1:A:148:GLY:O	1:A:149:SER:C	2.57	0.43
1:B:68:LEU:HB3	1:B:337:ARG:HD3	2.00	0.43
1:B:80:TYR:O	1:B:82:PRO:HD3	2.19	0.43
1:B:213:HIS:CE1	1:B:232:LEU:HD11	2.54	0.43
1:A:61:GLY:HA2	1:A:220:ARG:HH12	1.83	0.42
1:A:75:ARG:HE	1:A:75:ARG:N	2.17	0.42
1:A:101:TYR:CZ	1:A:225:GLU:HG3	2.53	0.42
1:B:246:VAL:HG21	1:B:324:VAL:HG21	2.00	0.42
1:A:198:LEU:HB3	1:A:199:PRO:HD2	2.00	0.42
1:A:247:ARG:HD3	4:A:2040:HOH:O	2.19	0.42
1:B:226:ARG:HB2	1:B:227:LEU:H	1.58	0.42
1:A:354:THR:HB	1:A:355:PRO:CD	2.50	0.42
1:A:293:ARG:HB3	1:A:293:ARG:NH1	2.34	0.42
1:B:235:ILE:HA	1:B:235:ILE:HD12	1.90	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:203:ILE:HG23	1:A:324:VAL:HG22	2.01	0.42
1:B:74:SER:HB3	1:B:77:ASP:OD2	2.19	0.42
1:A:62:LYS:HD2	4:A:2020:HOH:O	2.20	0.41
1:B:164:HIS:ND1	1:B:166:ILE:HG12	2.36	0.41
1:A:225:GLU:HG2	1:A:226:ARG:N	2.35	0.41
1:A:54:ILE:CD1	1:A:66:THR:HG22	2.41	0.41
1:B:325:PHE:CZ	1:B:347:MET:HG2	2.56	0.41
1:B:172:TYR:N	1:B:173:PRO:CD	2.84	0.41
1:B:118:ALA:HA	1:B:181:SER:O	2.21	0.41
1:A:304:LEU:HB2	4:A:2047:HOH:O	2.21	0.41
1:A:219:LYS:HB3	1:A:219:LYS:NZ	2.35	0.41
1:A:162:ASP:O	1:A:163:ARG:HB2	2.22	0.40
1:B:148:GLY:O	1:B:149:SER:C	2.59	0.40
1:A:67:GLN:O	1:A:69:LEU:N	2.55	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	297/331 (90%)	280 (94%)	15 (5%)	2 (1%)	26	46
1	B	302/331 (91%)	291 (96%)	9 (3%)	2 (1%)	26	46
All	All	599/662 (90%)	571 (95%)	24 (4%)	4 (1%)	26	46

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	68	LEU
1	B	218	ALA
1	A	95	GLU
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	247/264 (94%)	235 (95%)	12 (5%)	31	55
1	B	249/264 (94%)	239 (96%)	10 (4%)	38	64
All	All	496/528 (94%)	474 (96%)	22 (4%)	35	60

All (22) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	75	ARG
1	A	130	MET
1	A	159	LEU
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	343	LEU
1	A	374	GLU
1	B	69	LEU
1	B	75	ARG
1	B	76	ASP
1	B	130	MET
1	B	212	ARG
1	B	215	ASP
1	B	307	VAL
1	B	342	GLN
1	B	343	LEU
1	B	374	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	349	GLN
1	B	306	ASN
1	B	342	GLN
1	B	349	GLN

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 carbohydrates 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	400	-	4,4,4	0.87	0	6,6,6	0.17	0
3	CCV	A	500	-	11,15,15	1.92	1 (9%)	10,20,20	3.25	3 (30%)
2	SO4	B	400	-	4,4,4	0.95	0	6,6,6	0.33	0
3	CCV	B	500	-	11,15,15	1.89	1 (9%)	10,20,20	2.97	3 (30%)

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
3	CCV	A	500	-	-	0/8/8/8	0/1/1/1
2	SO4	B	400	-	-	0/0/0/0	0/0/0/0
3	CCV	B	500	-	-	0/8/8/8	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	500	CCV	C3-C5	-5.33	1.34	1.39
3	A	500	CCV	C3-C5	-5.32	1.34	1.39

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	500	CCV	C3-C5-N1	-7.41	118.08	124.03
3	B	500	CCV	C3-C5-N1	-5.48	119.62	124.03
3	B	500	CCV	C2-C3-C5	2.01	118.13	115.80
3	A	500	CCV	C2-C3-C5	2.71	118.95	115.80
3	A	500	CCV	C2-N2-C1	6.08	120.50	115.25
3	B	500	CCV	C2-N2-C1	7.17	121.44	115.25

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
3	B	500	CCV	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	305/331 (92%)	0.09	20 (6%) 22 24	20, 35, 79, 114	0
1	B	310/331 (93%)	0.11	27 (8%) 13 13	18, 35, 75, 105	0
All	All	615/662 (92%)	0.10	47 (7%) 17 18	18, 35, 77, 114	0

All (47) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	149	SER	7.8
1	A	264	GLY	7.8
1	B	264	GLY	7.3
1	A	148	GLY	6.7
1	A	75	ARG	6.4
1	B	263	SER	6.1
1	B	148	GLY	5.7
1	A	65	THR	5.6
1	A	76	ASP	4.9
1	B	274	PRO	4.2
1	B	374	GLU	4.2
1	A	62	LYS	4.2
1	A	46	MET	4.2
1	B	227	LEU	4.0
1	B	46	MET	3.8
1	A	61	GLY	3.6
1	B	154	PRO	3.4
1	A	154	PRO	3.3
1	B	149	SER	3.3
1	B	275	GLN	3.2
1	A	370	ARG	3.2
1	A	374	GLU	3.1
1	B	147	ALA	3.1
1	B	277	ASN	3.1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	276	SER	2.9
1	B	219	LYS	2.8
1	B	345	SER	2.7
1	B	300	PRO	2.7
1	B	74	SER	2.7
1	A	67	GLN	2.7
1	B	109	GLN	2.7
1	B	301	ASN	2.7
1	A	263	SER	2.6
1	B	278	ALA	2.5
1	A	373	GLY	2.5
1	A	66	THR	2.5
1	A	355	PRO	2.5
1	B	110	GLY	2.5
1	A	334	ALA	2.4
1	B	211	ASP	2.3
1	A	332	SER	2.3
1	B	346	GLY	2.3
1	B	373	GLY	2.3
1	B	229	LEU	2.2
1	B	355	PRO	2.2
1	B	76	ASP	2.1
1	A	63	THR	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(\AA^2)	Q<0.9
3	CCV	B	500	15/15	0.96	0.18	1.46	27,30,36,41	0
3	CCV	A	500	15/15	0.92	0.27	1.20	26,31,39,40	0
2	SO4	A	400	5/5	0.98	0.16	-0.59	64,64,65,67	0
2	SO4	B	400	5/5	0.99	0.10	-0.94	34,35,36,42	0

6.5 Other polymers [i](#)

There are no such residues in this entry.