



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 07:48 AM GMT

PDB ID : 3C9R
Title : AaThiL complexed with ATP
Authors : McCulloch, K.M.; Kinsland, C.; Begley, T.P.; Ealick, S.E.
Deposited on : 2008-02-18
Resolution : 2.30 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

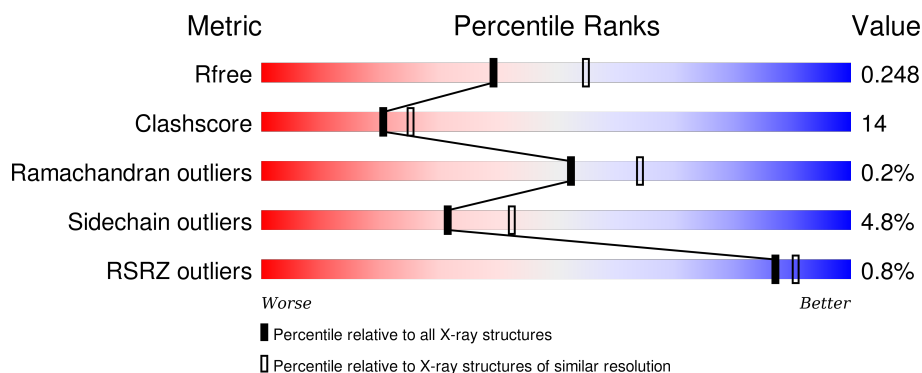
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	3852 (2.30-2.30)
Clashscore	102246	4452 (2.30-2.30)
Ramachandran outliers	100387	4410 (2.30-2.30)
Sidechain outliers	100360	4409 (2.30-2.30)
RSRZ outliers	91569	3857 (2.30-2.30)

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	342	<div> <div style="width: 100%; height: 10px; background-color: red;"></div> <div style="display: flex; justify-content: space-between; align-items: center;"> % <div style="width: 100%; height: 10px; background-color: green;"></div> % </div> <div style="display: flex; justify-content: space-between; align-items: center;"> 68% 19% • 11% </div> </div>
1	B	342	<div> <div style="width: 100%; height: 10px; background-color: red;"></div> <div style="display: flex; justify-content: space-between; align-items: center;"> % <div style="width: 100%; height: 10px; background-color: green;"></div> % </div> <div style="display: flex; justify-content: space-between; align-items: center;"> 56% 29% • 12% </div> </div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4949 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 Thiamine monophosphate kinase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	304	Total	C	N	O	S	0	0	0
			2396	1536	396	455	9			
1	B	302	Total	C	N	O	S	0	0	0
			2382	1526	395	452	9			

There are 72 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-35	MET	-	EXPRESSION TAG	UNP O67883
A	-34	GLY	-	EXPRESSION TAG	UNP O67883
A	-33	SER	-	EXPRESSION TAG	UNP O67883
A	-32	HIS	-	EXPRESSION TAG	UNP O67883
A	-31	HIS	-	EXPRESSION TAG	UNP O67883
A	-30	HIS	-	EXPRESSION TAG	UNP O67883
A	-29	HIS	-	EXPRESSION TAG	UNP O67883
A	-28	HIS	-	EXPRESSION TAG	UNP O67883
A	-27	HIS	-	EXPRESSION TAG	UNP O67883
A	-26	ASP	-	EXPRESSION TAG	UNP O67883
A	-25	ILE	-	EXPRESSION TAG	UNP O67883
A	-24	THR	-	EXPRESSION TAG	UNP O67883
A	-23	SER	-	EXPRESSION TAG	UNP O67883
A	-22	LEU	-	EXPRESSION TAG	UNP O67883
A	-21	TYR	-	EXPRESSION TAG	UNP O67883
A	-20	LYS	-	EXPRESSION TAG	UNP O67883
A	-19	LYS	-	EXPRESSION TAG	UNP O67883
A	-18	ALA	-	EXPRESSION TAG	UNP O67883
A	-17	GLY	-	EXPRESSION TAG	UNP O67883
A	-16	SER	-	EXPRESSION TAG	UNP O67883
A	-15	ALA	-	EXPRESSION TAG	UNP O67883
A	-14	ALA	-	EXPRESSION TAG	UNP O67883
A	-13	ALA	-	EXPRESSION TAG	UNP O67883
A	-12	VAL	-	EXPRESSION TAG	UNP O67883
A	-11	LEU	-	EXPRESSION TAG	UNP O67883

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-10	GLU	-	EXPRESSION TAG	UNP O67883
A	-9	GLU	-	EXPRESSION TAG	UNP O67883
A	-8	ASN	-	EXPRESSION TAG	UNP O67883
A	-7	LEU	-	EXPRESSION TAG	UNP O67883
A	-6	TYR	-	EXPRESSION TAG	UNP O67883
A	-5	PHE	-	EXPRESSION TAG	UNP O67883
A	-4	GLN	-	EXPRESSION TAG	UNP O67883
A	-3	GLY	-	EXPRESSION TAG	UNP O67883
A	-2	SER	-	EXPRESSION TAG	UNP O67883
A	-1	PHE	-	EXPRESSION TAG	UNP O67883
A	0	THR	-	EXPRESSION TAG	UNP O67883
B	-35	MET	-	EXPRESSION TAG	UNP O67883
B	-34	GLY	-	EXPRESSION TAG	UNP O67883
B	-33	SER	-	EXPRESSION TAG	UNP O67883
B	-32	HIS	-	EXPRESSION TAG	UNP O67883
B	-31	HIS	-	EXPRESSION TAG	UNP O67883
B	-30	HIS	-	EXPRESSION TAG	UNP O67883
B	-29	HIS	-	EXPRESSION TAG	UNP O67883
B	-28	HIS	-	EXPRESSION TAG	UNP O67883
B	-27	HIS	-	EXPRESSION TAG	UNP O67883
B	-26	ASP	-	EXPRESSION TAG	UNP O67883
B	-25	ILE	-	EXPRESSION TAG	UNP O67883
B	-24	THR	-	EXPRESSION TAG	UNP O67883
B	-23	SER	-	EXPRESSION TAG	UNP O67883
B	-22	LEU	-	EXPRESSION TAG	UNP O67883
B	-21	TYR	-	EXPRESSION TAG	UNP O67883
B	-20	LYS	-	EXPRESSION TAG	UNP O67883
B	-19	LYS	-	EXPRESSION TAG	UNP O67883
B	-18	ALA	-	EXPRESSION TAG	UNP O67883
B	-17	GLY	-	EXPRESSION TAG	UNP O67883
B	-16	SER	-	EXPRESSION TAG	UNP O67883
B	-15	ALA	-	EXPRESSION TAG	UNP O67883
B	-14	ALA	-	EXPRESSION TAG	UNP O67883
B	-13	ALA	-	EXPRESSION TAG	UNP O67883
B	-12	VAL	-	EXPRESSION TAG	UNP O67883
B	-11	LEU	-	EXPRESSION TAG	UNP O67883
B	-10	GLU	-	EXPRESSION TAG	UNP O67883
B	-9	GLU	-	EXPRESSION TAG	UNP O67883
B	-8	ASN	-	EXPRESSION TAG	UNP O67883
B	-7	LEU	-	EXPRESSION TAG	UNP O67883
B	-6	TYR	-	EXPRESSION TAG	UNP O67883
B	-5	PHE	-	EXPRESSION TAG	UNP O67883

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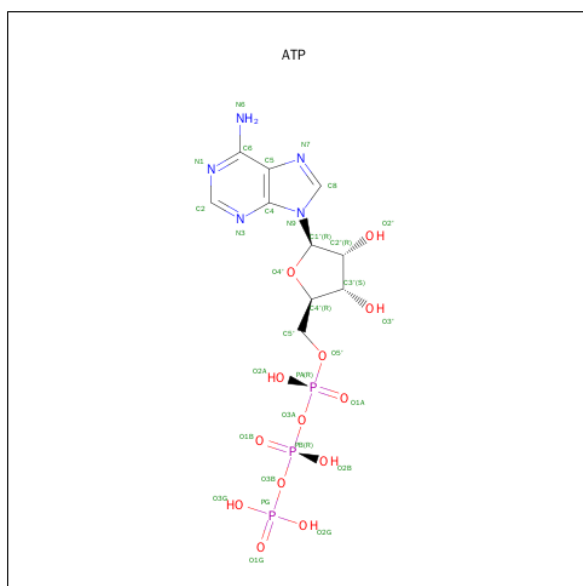
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Chain	Residue	Modelled	Actual	Comment	Reference
B	-4	GLN	-	EXPRESSION TAG	UNP O67883
B	-3	GLY	-	EXPRESSION TAG	UNP O67883
B	-2	SER	-	EXPRESSION TAG	UNP O67883
B	-1	PHE	-	EXPRESSION TAG	UNP O67883
B	0	THR	-	EXPRESSION TAG	UNP O67883

- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	4	Total Mg 4 4	0	0
2	A	4	Total Mg 4 4	0	0

- Molecule 3 is ADENOSINE-5'-TRIPHOSPHATE (three-letter code: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C N O P 31 10 5 13 3	0	0
3	B	1	Total C N O P 31 10 5 13 3	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	57	Total 57	O 57	0	0
4	B	44	Total 44	O 44	0	0

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 ($\text{RSRZ} > 2$). 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.

Chain A:

Sequence logo for Chain A. The y-axis represents information content in bits (0.00 to 0.15). The x-axis lists amino acids. A color scale at the top indicates conservation levels: red (0.00-0.02 bits), yellow (0.02-0.04 bits), green (0.04-0.06 bits), blue (0.06-0.08 bits), and grey (0.08-0.15 bits). A red dot is placed above the 'G' at position 3, and a blue dot is placed above the 'E' at position 245.

Chain B:

56% 29% 12%

Amino Acid	Category
MET	Grey
GLY	Green
SER	Green
HIS	Green
HIS	Green
HIS	Green
HIS	Green
ASP	Green
ASP	Green
ILE	Green
THR	Green
SER	Green
LEU	Green
LEU	Green
TRP	Green
LYS	Green
LYS	Green
ALA	Green
ALA	Green
ALA	Green
VAL	Green
LEU	Green
GLU	Green
GLU	Green
ASN	Green
LEU	Green
TRP	Green
PHE	Green
Q	Yellow
R2	Yellow
L3	Yellow
K4	Yellow
L11	Yellow
L14	Yellow
T18	Yellow
K22	Yellow
T28	Yellow
K36	Yellow
K37	Yellow
L38	Yellow
L39	Yellow
L40	Yellow
T41	Yellow
Y55	Yellow
I56	Yellow
P57	Yellow
E58	Yellow
C61	Yellow

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	61.29 Å 67.14 Å 200.70 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	38.83 – 2.30 38.82 – 2.30	Depositor EDS
% Data completeness (in resolution range)	87.4 (38.83-2.30) 87.5 (38.82-2.30)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.50 (at 2.29 Å)	Xtriage
Refinement program	CNS 1.2	Depositor
R, R_{free}	0.223 , 0.248 0.223 , 0.248	Depositor DCC
R_{free} test set	2053 reflections (6.23%)	DCC
Wilson B-factor (Å ²)	45.0	Xtriage
Anisotropy	0.372	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 33.5	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 34780 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	4949	wwPDB-VP
Average B, all atoms (Å ²)	60.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.39% 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: MG, ATP

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	0.36	0/2442	0.59	0/3294
1	B	0.36	0/2427	0.59	0/3272
All	All	0.36	0/4869	0.59	0/6566

There are no bond length outliers.

There are no bond angle outliers.

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	2396	0	2410	66	0
1	B	2382	0	2396	88	0
2	A	4	0	0	0	0
2	B	4	0	0	0	0
3	A	31	0	12	0	0
3	B	31	0	12	0	0
4	A	57	0	0	1	0
4	B	44	0	0	2	0
All	All	4949	0	4830	140	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 14.

All (140) 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:28:THR:HG21	1:A:39:LEU:HB3	1.28	1.15
1:B:219:LEU:HD12	1:B:227:ILE:HD11	1.52	0.90
1:A:90:GLU:HB2	1:B:4:LYS:HB2	1.51	0.90
1:A:28:THR:HB	1:A:75:ASN:HD22	1.40	0.86
1:B:231:SER:HA	1:B:234:LEU:HD22	1.60	0.82
1:B:218:HIS:O	1:B:222:ARG:HB2	1.83	0.77
1:B:73:ILE:HD12	1:B:195:VAL:HG22	1.67	0.76
1:A:91:ASP:O	1:B:2:ARG:HD2	1.86	0.75
1:A:11:LEU:HD11	1:B:97:VAL:HG11	1.71	0.73
1:B:269:PRO:HD2	1:B:272:ARG:NE	2.05	0.72
1:A:138:ARG:NH2	1:A:202:ALA:O	2.23	0.70
1:B:40:LEU:HD22	1:B:133:VAL:HG22	1.74	0.69
1:B:144:GLY:O	1:B:203:ASN:HB3	1.95	0.67
1:B:148:GLY:HA2	1:B:284:ARG:HH21	1.60	0.66
1:A:28:THR:HB	1:A:75:ASN:ND2	2.10	0.64
1:B:153:VAL:HA	1:B:264:LEU:O	1.97	0.64
1:A:185:HIS:HE1	4:A:354:HOH:O	1.81	0.63
1:B:269:PRO:HD2	1:B:272:ARG:CZ	2.29	0.63
1:A:146:ARG:HH11	1:A:146:ARG:HG3	1.64	0.63
1:B:192:ILE:HD13	1:B:192:ILE:O	2.00	0.61
1:B:58:GLU:OE1	1:B:99:ARG:HB3	2.01	0.61
1:B:228:GLU:HG3	1:B:292:PHE:HB2	1.82	0.61
1:A:201:TYR:CD2	1:A:272:ARG:HD3	2.35	0.60
1:B:226:LYS:HB3	1:B:289:GLU:N	2.15	0.60
1:B:147:LEU:HD12	1:B:147:LEU:H	1.66	0.60
1:B:191:ARG:NH2	1:B:278:ASP:OD1	2.25	0.60
1:A:201:TYR:HD2	1:A:272:ARG:HD3	1.67	0.59
1:A:244:CYS:HB3	1:A:249:LYS:O	2.02	0.59
1:A:28:THR:HG22	1:A:29:ALA:N	2.18	0.59
1:B:166:LEU:HA	1:B:169:MET:HE3	1.84	0.58
1:B:73:ILE:HD12	1:B:195:VAL:CG2	2.33	0.58
1:A:167:LEU:HD11	1:A:186:LEU:HD11	1.85	0.58
1:B:229:ILE:O	1:B:293:VAL:HA	2.04	0.57
1:A:57:PRO:HG2	1:A:58:GLU:OE2	2.04	0.57
1:A:2:ARG:HD2	1:B:91:ASP:O	2.05	0.57
1:B:213:VAL:HG23	1:B:214:ALA:N	2.19	0.56
1:B:138:ARG:HD3	1:B:199:GLN:O	2.06	0.56
1:A:147:LEU:H	1:A:147:LEU:HD22	1.70	0.56
1:A:153:VAL:HA	1:A:264:LEU:O	2.06	0.56
1:A:73:ILE:HD12	1:A:195:VAL:CG2	2.37	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:213:VAL:HG21	1:B:257:PHE:CE2	2.43	0.54
1:A:85:SER:HB3	1:A:129:SER:HB2	1.88	0.54
1:A:299:GLU:HB2	1:A:300:PRO:HD2	1.90	0.54
1:A:28:THR:CG2	1:A:39:LEU:HB3	2.19	0.53
1:A:167:LEU:HD11	1:A:186:LEU:CD1	2.38	0.53
1:B:68:ASN:ND2	1:B:130:VAL:HG13	2.24	0.53
1:B:250:ASN:OD1	1:B:252:ILE:HB	2.08	0.53
1:B:146:ARG:O	1:B:149:ASP:HB2	2.09	0.53
1:B:112:LYS:HD3	1:B:112:LYS:N	2.24	0.53
1:A:200:LYS:HE3	1:A:201:TYR:OH	2.09	0.53
1:A:147:LEU:N	1:A:147:LEU:HD22	2.23	0.53
1:B:234:LEU:HD21	1:B:256:LEU:HD21	1.92	0.52
1:A:250:ASN:HD21	1:A:252:ILE:HB	1.73	0.52
1:B:147:LEU:N	1:B:147:LEU:HD12	2.24	0.52
1:B:184:ARG:HH12	1:B:239:GLU:CG	2.23	0.52
1:B:249:LYS:HG2	1:B:254:TYR:OH	2.10	0.52
1:B:61:GLY:HA2	1:B:100:PHE:CE1	2.45	0.51
1:B:155:GLY:HA3	1:B:263:GLN:NE2	2.25	0.51
1:B:74:ALA:HB1	1:B:206:MET:HA	1.93	0.51
1:A:-2:SER:O	1:A:-1:PHE:HB2	2.11	0.51
1:A:98:GLU:HG3	1:B:14:LEU:HD21	1.93	0.51
1:A:146:ARG:NH1	1:A:146:ARG:HG3	2.24	0.51
1:B:166:LEU:HD23	1:B:169:MET:HE1	1.93	0.51
1:B:161:ARG:O	1:B:165:GLU:HG3	2.11	0.50
1:B:204:ALA:HB1	1:B:219:LEU:HD21	1.93	0.50
1:A:106:ARG:HG2	1:A:106:ARG:HH11	1.77	0.50
1:A:69:VAL:O	1:A:73:ILE:HG12	2.11	0.50
1:B:105:LYS:O	1:B:109:GLU:HG3	2.12	0.50
1:A:299:GLU:HB2	1:A:300:PRO:CD	2.42	0.50
1:A:138:ARG:NH1	1:A:199:GLN:O	2.40	0.49
1:B:78:LEU:CD2	1:B:195:VAL:HG21	2.41	0.49
1:A:78:LEU:HD23	1:A:195:VAL:HG21	1.95	0.49
1:B:56:ILE:HG22	1:B:58:GLU:HG2	1.95	0.49
1:A:226:LYS:HG2	1:A:227:ILE:N	2.28	0.49
1:B:292:PHE:HD2	1:B:295:GLY:O	1.96	0.48
1:B:79:PRO:HB2	1:B:113:CYS:HB3	1.96	0.48
1:A:196:LYS:HG3	1:A:197:HIS:N	2.28	0.48
1:A:42:THR:HG23	1:B:119:ASN:HB2	1.94	0.48
1:A:192:ILE:O	1:A:195:VAL:HG23	2.14	0.48
1:B:58:GLU:OE1	1:B:99:ARG:NE	2.47	0.47
1:A:27:ASP:CG	1:A:142:ARG:HH21	2.16	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:88:LEU:HA	1:B:89:PRO:HD3	1.74	0.47
1:A:131:PHE:CG	1:B:131:PHE:HB2	2.48	0.47
1:B:151:VAL:HG22	1:B:267:THR:HG22	1.95	0.47
1:A:120:ILE:HD13	1:B:11:LEU:HD13	1.95	0.47
1:A:271:GLU:H	1:A:271:GLU:CD	2.18	0.47
1:B:156:THR:HA	1:B:235:PRO:HB2	1.97	0.46
1:A:147:LEU:H	1:A:147:LEU:CD2	2.27	0.46
1:A:47:GLU:HG2	1:A:125:LYS:HE2	1.96	0.46
1:A:105:LYS:HD2	1:B:18:THR:O	2.16	0.46
1:A:34:CYS:C	1:A:36:LYS:H	2.18	0.46
1:B:28:THR:HG22	1:B:41:THR:HB	1.97	0.46
1:B:55:TYR:HB2	4:B:344:HOH:O	2.15	0.46
1:B:268:HIS:HB2	1:B:272:ARG:HD2	1.97	0.46
1:A:28:THR:HG21	1:A:39:LEU:CB	2.21	0.46
1:A:3:LEU:HD12	1:B:94:VAL:HG12	1.98	0.46
1:B:184:ARG:NH1	1:B:239:GLU:HG3	2.31	0.45
1:B:167:LEU:HD21	1:B:186:LEU:CD1	2.45	0.45
1:A:191:ARG:HA	1:A:191:ARG:HD2	1.77	0.45
1:B:78:LEU:HD22	1:B:192:ILE:HD11	1.99	0.45
1:B:235:PRO:HG3	1:B:280:THR:HG21	1.99	0.45
1:A:89:PRO:O	1:B:3:LEU:HD12	2.16	0.45
1:B:81:TRP:O	1:B:132:LEU:HD12	2.16	0.44
1:A:73:ILE:HD12	1:A:195:VAL:HG22	1.98	0.44
1:B:184:ARG:HH12	1:B:239:GLU:HG2	1.82	0.44
1:B:-4:GLN:OE1	1:B:-4:GLN:C	2.56	0.44
1:B:78:LEU:HD23	1:B:195:VAL:HG21	2.00	0.44
1:B:253:GLU:HG3	1:B:257:PHE:HD1	1.83	0.44
1:A:143:ASP:HB2	1:A:222:ARG:O	2.17	0.44
1:B:73:ILE:HD11	1:B:192:ILE:HG12	2.00	0.44
1:A:197:HIS:NE2	1:A:268:HIS:HE1	2.15	0.44
1:B:180:ALA:O	1:B:183:GLN:HB3	2.18	0.44
1:A:98:GLU:HG3	1:B:14:LEU:CD2	2.48	0.43
1:A:137:GLU:HA	1:A:137:GLU:OE1	2.18	0.43
1:B:36:LYS:HG2	1:B:37:LYS:H	1.84	0.43
1:B:192:ILE:O	1:B:195:VAL:HG23	2.18	0.43
1:B:213:VAL:HG22	4:B:352:HOH:O	2.19	0.43
1:A:230:LEU:HB3	1:A:232:GLU:OE2	2.18	0.43
1:A:131:PHE:CD1	1:B:131:PHE:HB2	2.55	0.42
1:A:28:THR:CG2	1:A:29:ALA:N	2.82	0.42
1:A:67:VAL:HG22	1:A:262:TYR:CZ	2.55	0.42
1:B:293:VAL:O	1:B:294:ASP:HB2	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:101:TYR:HA	1:B:104:VAL:HB	2.00	0.42
1:B:219:LEU:HD12	1:B:227:ILE:CD1	2.38	0.42
1:B:93:GLU:N	1:B:93:GLU:OE1	2.48	0.42
1:A:97:VAL:HG11	1:B:11:LEU:HD21	2.02	0.41
1:B:266:PHE:N	1:B:266:PHE:CD2	2.88	0.41
1:A:142:ARG:HB2	1:A:222:ARG:HD3	2.01	0.41
1:B:82:ALA:HB2	1:B:132:LEU:HD13	2.02	0.41
1:B:246:LYS:HE2	1:B:247:TYR:CZ	2.55	0.41
1:B:151:VAL:HG21	1:B:227:ILE:HG23	2.03	0.41
1:A:174:TYR:HB3	1:A:178:GLU:HB2	2.02	0.41
1:B:152:PHE:O	1:B:265:LEU:HD12	2.20	0.41
1:B:58:GLU:CD	1:B:99:ARG:HE	2.23	0.41
1:B:69:VAL:O	1:B:73:ILE:HG12	2.21	0.41
1:A:272:ARG:HA	1:A:272:ARG:NE	2.36	0.40
1:A:106:ARG:HG2	1:A:106:ARG:NH1	2.36	0.40
1:A:4:LYS:O	1:A:4:LYS:HD2	2.22	0.40
1:B:234:LEU:HD12	1:B:234:LEU:HA	1.95	0.40
1:A:81:TRP:O	1:A:132:LEU:HD12	2.21	0.40

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	302/342 (88%)	287 (95%)	14 (5%)	1 (0%)	46	57
1	B	300/342 (88%)	287 (96%)	13 (4%)	0	100	100
All	All	602/684 (88%)	574 (95%)	27 (4%)	1 (0%)	52	64

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	-2	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	260/291 (89%)	253 (97%)	7 (3%)	52	70
1	B	258/291 (89%)	240 (93%)	18 (7%)	19	23
All	All	518/582 (89%)	493 (95%)	25 (5%)	31	42

All (25) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4	LYS
1	A	19	LEU
1	A	106	ARG
1	A	186	LEU
1	A	191	ARG
1	A	232	GLU
1	A	299	GLU
1	B	-4	GLN
1	B	11	LEU
1	B	14	LEU
1	B	22	LYS
1	B	38	LEU
1	B	58	GLU
1	B	112	LYS
1	B	130	VAL
1	B	167	LEU
1	B	168	LEU
1	B	186	LEU
1	B	192	ILE
1	B	222	ARG
1	B	226	LYS
1	B	234	LEU
1	B	236	LEU

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Mol	Chain	Res	Type
1	B	249	LYS
1	B	268	HIS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	75	ASN
1	A	183	GLN
1	A	185	HIS
1	A	203	ASN
1	A	217	ASN
1	A	221	GLN
1	A	238	ASN
1	A	250	ASN
1	A	268	HIS
1	B	46	ASN
1	B	75	ASN
1	B	87	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 10 ligands modelled in this entry, 8 are monoatomic - leaving 2 for Mogul analysis.

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	$\# Z > 2$
3	ATP	A	307	2	24,33,33	1.03	1 (4%)	31,52,52	2.52	12 (38%)
3	ATP	B	307	2	24,33,33	1.02	1 (4%)	31,52,52	2.24	5 (16%)

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	ATP	A	307	2	-	0/18/38/38	0/3/3/3
3	ATP	B	307	2	-	0/18/38/38	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	307	ATP	O4'-C1'	2.24	1.44	1.41
3	A	307	ATP	O4'-C1'	2.38	1.44	1.41

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	307	ATP	N3-C2-N1	-9.48	121.63	128.89
3	A	307	ATP	N3-C2-N1	-9.07	121.95	128.89
3	A	307	ATP	PB-O3B-PG	-4.91	116.21	132.67
3	B	307	ATP	PA-O3A-PB	-4.42	120.31	132.73
3	B	307	ATP	PB-O3B-PG	-4.14	118.79	132.67
3	A	307	ATP	PA-O3A-PB	-3.16	123.85	132.73
3	B	307	ATP	C2'-C1'-N9	-3.06	109.61	114.29
3	A	307	ATP	C2'-C1'-N9	-2.82	109.98	114.29
3	A	307	ATP	O2G-PG-O3B	-2.40	94.20	105.09
3	A	307	ATP	O3G-PG-O3B	-2.35	94.41	105.09
3	A	307	ATP	C4-C5-N7	-2.24	107.42	109.48
3	B	307	ATP	C4-C5-N7	-2.12	107.53	109.48
3	A	307	ATP	O2B-PB-O3A	-2.03	95.87	105.09
3	A	307	ATP	O2B-PB-O1B	2.41	125.61	112.53
3	A	307	ATP	O2B-PB-O3B	2.56	116.69	105.09
3	A	307	ATP	O2G-PG-O1G	3.54	121.96	110.58
3	A	307	ATP	O3G-PG-O1G	3.87	123.02	110.58

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

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	304/342 (88%)	0.05	3 (0%) 84 88	33, 54, 99, 131	1 (0%)
1	B	302/342 (88%)	0.08	2 (0%) 89 92	36, 56, 93, 120	1 (0%)
All	All	606/684 (88%)	0.07	5 (0%) 87 90	33, 55, 96, 131	2 (0%)

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	284	ARG	3.7
1	B	147	LEU	3.2
1	A	298	VAL	2.4
1	A	-3	GLY	2.3
1	A	245	GLU	2.1

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	ATP	B	307	31/31	0.97	0.09	-2.23	30,30,30,30	0
3	ATP	A	307	31/31	0.97	0.07	-2.26	30,30,30,30	0
2	MG	A	309	1/1	0.98	0.23	-	27,27,27,27	0
2	MG	B	312	1/1	0.97	0.15	-	27,27,27,27	0
2	MG	A	311	1/1	0.98	0.06	-	27,27,27,27	0
2	MG	B	311	1/1	0.97	0.07	-	27,27,27,27	0
2	MG	A	310	1/1	0.94	0.28	-	27,27,27,27	0
2	MG	B	310	1/1	0.97	0.32	-	27,27,27,27	0
2	MG	A	312	1/1	0.97	0.18	-	27,27,27,27	0
2	MG	B	309	1/1	0.96	0.23	-	27,27,27,27	0

6.5 Other polymers [i](#)

There are no such residues in this entry.