



Full wwPDB X-ray Structure Validation Report ⓘ

May 21, 2020 – 11:53 pm BST

PDB ID : 3IML
Title : Crystal Structure Of S-Adenosylmethionine Synthetase From Burkholderia Pseudomallei
Authors : Staker, B.L.; Seattle Structural Genomics Center for Infectious Disease (SSG-CID)
Deposited on : 2009-08-10
Resolution : 2.35 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 ⓘ symbol.

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

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.11
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)	:	2.11

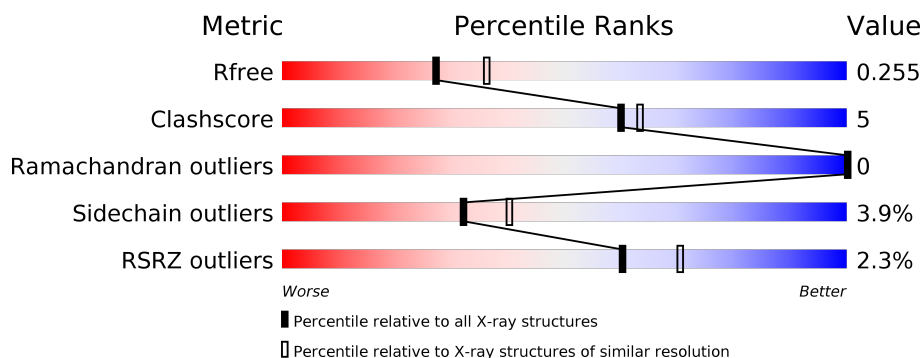
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.35 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	1164 (2.36-2.36)
Clashscore	141614	1232 (2.36-2.36)
Ramachandran outliers	138981	1211 (2.36-2.36)
Sidechain outliers	138945	1212 (2.36-2.36)
RSRZ outliers	127900	1150 (2.36-2.36)

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 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 $\leq 5\%$. 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	399	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 1%, green 84%, grey 14%);"></div> <div style="display: flex; justify-content: space-between; padding: 0 5px;"> % 84% 8% • 8% </div> </div>
1	B	399	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 1%, green 82%, grey 15%);"></div> <div style="display: flex; justify-content: space-between; padding: 0 5px;"> % 82% 7% • 11% </div> </div>
1	C	399	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 4%, orange 1%, yellow 1%, green 75%, grey 19%);"></div> <div style="display: flex; justify-content: space-between; padding: 0 5px;"> 4% 75% 11% • 14% </div> </div>
1	D	399	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 3%, orange 1%, yellow 1%, green 64%, grey 31%);"></div> <div style="display: flex; justify-content: space-between; padding: 0 5px;"> 3% 64% 13% • 22% </div> </div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 10507 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 S-adenosylmethionine synthetase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	368	Total	C	N	O	S	0	0	0
			2751	1737	477	529	8			
1	B	357	Total	C	N	O	S	0	1	0
			2701	1709	471	513	8			
1	C	343	Total	C	N	O	S	0	0	0
			2583	1632	453	490	8			
1	D	311	Total	C	N	O	S	0	0	0
			2339	1488	403	441	7			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-3	GLY	-	EXPRESSION TAG	UNP Q63YH5
A	-2	PRO	-	EXPRESSION TAG	UNP Q63YH5
A	-1	GLY	-	EXPRESSION TAG	UNP Q63YH5
A	0	SER	-	EXPRESSION TAG	UNP Q63YH5
B	-3	GLY	-	EXPRESSION TAG	UNP Q63YH5
B	-2	PRO	-	EXPRESSION TAG	UNP Q63YH5
B	-1	GLY	-	EXPRESSION TAG	UNP Q63YH5
B	0	SER	-	EXPRESSION TAG	UNP Q63YH5
C	-3	GLY	-	EXPRESSION TAG	UNP Q63YH5
C	-2	PRO	-	EXPRESSION TAG	UNP Q63YH5
C	-1	GLY	-	EXPRESSION TAG	UNP Q63YH5
C	0	SER	-	EXPRESSION TAG	UNP Q63YH5
D	-3	GLY	-	EXPRESSION TAG	UNP Q63YH5
D	-2	PRO	-	EXPRESSION TAG	UNP Q63YH5
D	-1	GLY	-	EXPRESSION TAG	UNP Q63YH5
D	0	SER	-	EXPRESSION TAG	UNP Q63YH5

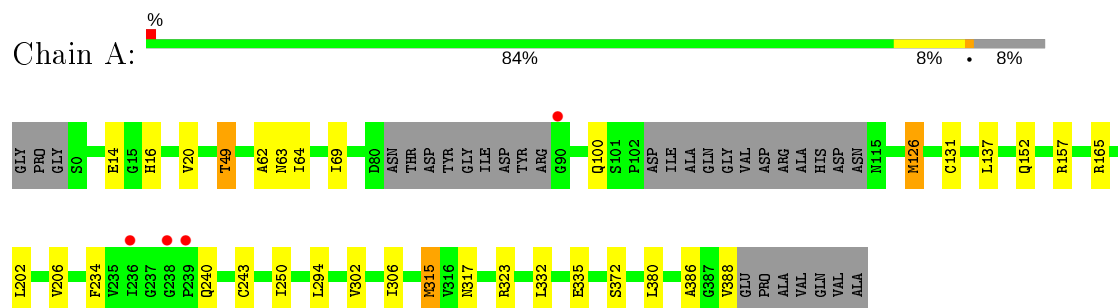
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	44	Total 44	O 44	0	0
2	B	40	Total 40	O 40	0	0
2	C	26	Total 26	O 26	0	0
2	D	23	Total 23	O 23	0	0

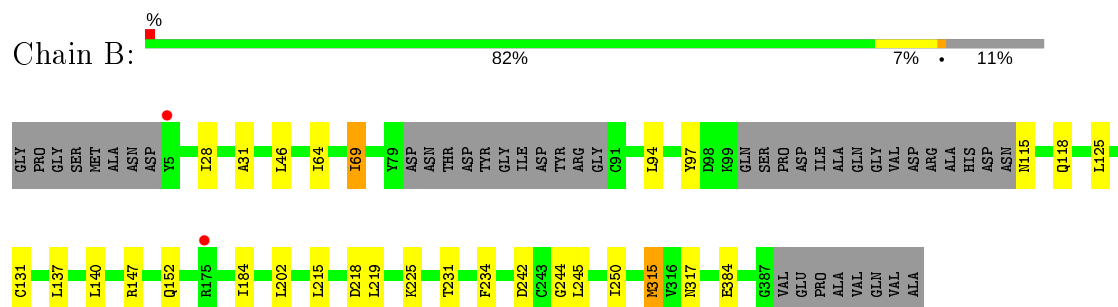
3 Residue-property plots [i](#)

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.

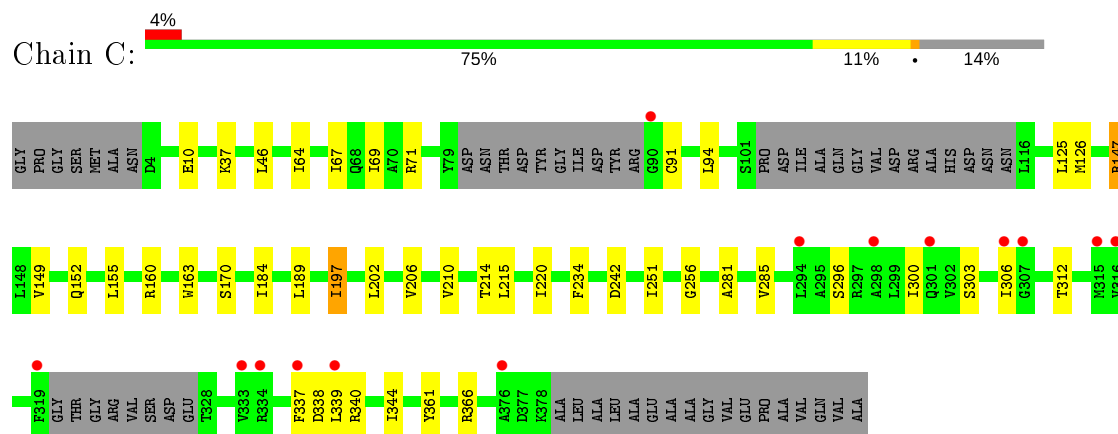
- Molecule 1: S-adenosylmethionine synthetase



- Molecule 1: S-adenosylmethionine synthetase

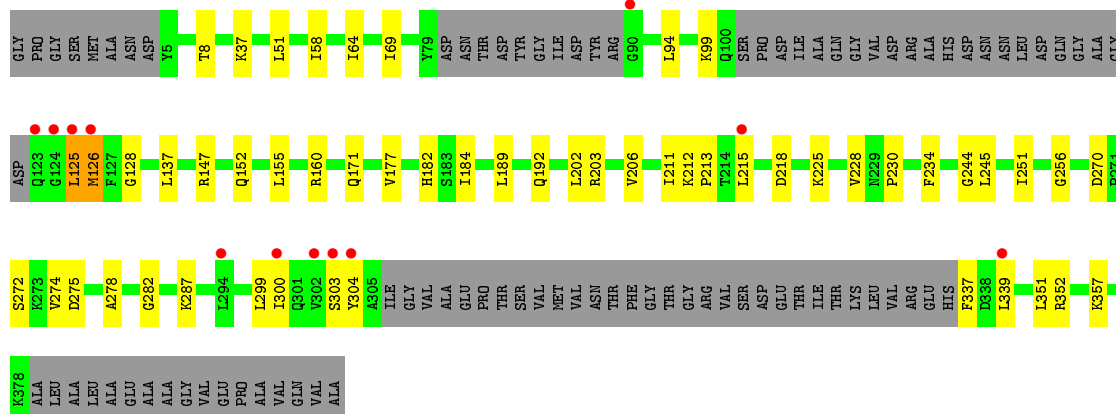


- Molecule 1: S-adenosylmethionine synthetase



- Molecule 1: S-adenosylmethionine synthetase

Chain D:



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	236.30Å 119.44Å 65.35Å 90.00° 105.98° 90.00°	Depositor
Resolution (Å)	28.31 – 2.35 28.31 – 2.35	Depositor EDS
% Data completeness (in resolution range)	(Not available) (28.31-2.35) 97.7 (28.31-2.35)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.49 (at 2.34Å)	Xtriage
Refinement program	REFMAC 5.5.0088	Depositor
R, R_{free}	0.218 , 0.256 0.222 , 0.255	Depositor DCC
R_{free} test set	3602 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	38.7	Xtriage
Anisotropy	0.081	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 13.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.072 for -h-2*k,l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	10507	wwPDB-VP
Average B, all atoms (Å ²)	17.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.68% 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 [i](#)

5.1 Standard geometry [i](#)

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	0.55	1/2802 (0.0%)	0.67	0/3811
1	B	0.53	0/2754	0.64	0/3742
1	C	0.48	0/2631	0.62	0/3574
1	D	0.50	0/2385	0.64	0/3243
All	All	0.52	1/10572 (0.0%)	0.64	0/14370

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	243	CYS	CB-SG	-5.03	1.73	1.81

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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	2751	0	2722	21	0
1	B	2701	0	2701	14	0
1	C	2583	0	2554	33	0
1	D	2339	0	2311	35	0
2	A	44	0	0	1	0
2	B	40	0	0	0	0
2	C	26	0	0	0	0
2	D	23	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	10507	0	10288	94	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 (94) 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:D:177:VAL:HG12	1:D:182:HIS:HB2	1.62	0.80
1:C:285:VAL:CG2	1:C:300:ILE:HD12	2.16	0.74
1:D:37:LYS:O	1:D:351:LEU:HD22	1.92	0.70
1:D:126:MET:HE2	1:D:275:ASP:HA	1.73	0.69
1:C:285:VAL:HG21	1:C:300:ILE:HD12	1.74	0.69
1:A:388:VAL:O	1:A:388:VAL:HG12	1.94	0.67
1:D:189:LEU:HD22	1:D:206:VAL:HG11	1.78	0.66
1:D:64:ILE:CG2	1:D:69:ILE:HD12	2.27	0.64
1:C:184:ILE:HD13	1:C:215:LEU:HD22	1.82	0.62
1:A:380:LEU:HD13	2:A:404:HOH:O	2.00	0.61
1:C:94:LEU:HD21	1:D:51:LEU:HD21	1.81	0.61
1:C:64:ILE:HG23	1:C:69:ILE:CD1	2.31	0.61
1:C:197:ILE:HD13	1:C:202:LEU:HB2	1.81	0.61
1:C:163:TRP:CE2	1:C:197:ILE:HD12	2.37	0.60
1:C:306:ILE:HG23	1:D:230:PRO:HG2	1.84	0.60
1:C:64:ILE:HG23	1:C:69:ILE:HD12	1.84	0.60
1:C:125:LEU:HD13	1:D:8:THR:O	2.02	0.59
1:B:315:MET:HE1	1:B:317:ASN:HB2	1.85	0.58
1:C:285:VAL:HG23	1:C:300:ILE:HD12	1.84	0.58
1:D:64:ILE:CG2	1:D:69:ILE:CD1	2.82	0.57
1:D:202:LEU:HD23	1:D:202:LEU:C	2.26	0.57
1:C:285:VAL:HG12	1:C:337:PHE:CD1	2.40	0.56
1:D:128:GLY:O	1:D:299:LEU:HD12	2.05	0.56
1:C:10:GLU:HG2	1:D:125:LEU:HD21	1.88	0.54
1:D:137:LEU:HD12	1:D:287:LYS:HG3	1.90	0.53
1:B:184:ILE:CD1	1:B:215:LEU:HD22	2.38	0.53
1:A:64:ILE:HG23	1:A:69:ILE:HD12	1.91	0.53
1:C:64:ILE:CG2	1:C:69:ILE:HD12	2.39	0.52
1:A:250:ILE:HD11	1:B:250:ILE:HD11	1.91	0.51
1:D:339:LEU:N	1:D:339:LEU:HD12	2.26	0.51
1:A:202:LEU:O	1:A:206:VAL:HG23	2.12	0.50
1:C:339:LEU:HA	1:C:344:ILE:HD11	1.95	0.49
1:C:312:THR:HG21	1:D:171:GLN:NE2	2.27	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:215:LEU:HD13	1:C:220:ILE:HD11	1.94	0.49
1:D:184:ILE:HD13	1:D:215:LEU:HG	1.95	0.48
1:B:94:LEU:HD13	1:D:94:LEU:HB2	1.95	0.48
1:D:337:PHE:HB2	1:D:339:LEU:HD11	1.94	0.48
1:C:46:LEU:HD23	1:C:46:LEU:C	2.33	0.48
1:C:155:LEU:HD22	1:C:160:ARG:HG2	1.95	0.48
1:B:31:ALA:CB	1:B:69:ILE:HD12	2.45	0.47
1:C:184:ILE:CD1	1:C:215:LEU:HD22	2.43	0.47
1:C:155:LEU:HD12	1:C:210:VAL:HG22	1.97	0.47
1:C:303:SER:OG	1:D:8:THR:HG21	2.15	0.47
1:C:215:LEU:CD1	1:C:220:ILE:HD11	2.45	0.46
1:A:62:ALA:HB1	1:A:64:ILE:CD1	2.45	0.46
1:D:282:GLY:HA2	1:D:300:ILE:HD11	1.98	0.46
1:A:62:ALA:HB1	1:A:64:ILE:HD13	1.96	0.46
1:D:64:ILE:HG23	1:D:69:ILE:HD11	1.96	0.46
1:D:337:PHE:CB	1:D:339:LEU:HD11	2.46	0.46
1:A:315:MET:HE3	1:A:317:ASN:HB2	1.96	0.45
1:D:274:VAL:HG11	1:D:304:TYR:CD2	2.51	0.45
1:A:49:THR:HG23	1:A:240:GLN:HA	1.99	0.45
1:D:203:ARG:HG2	1:D:228:VAL:HB	1.99	0.44
1:A:126:MET:HE2	1:A:126:MET:HB2	1.72	0.44
1:D:189:LEU:HD22	1:D:206:VAL:CG1	2.46	0.44
1:A:294:LEU:CD2	1:A:386:ALA:HB3	2.47	0.44
1:A:294:LEU:CD2	1:A:386:ALA:CB	2.96	0.44
1:B:244:GLY:C	1:B:245:LEU:HD12	2.37	0.44
1:C:338:ASP:O	1:C:344:ILE:HD13	2.18	0.44
1:C:67:ILE:O	1:C:71:ARG:HG3	2.18	0.44
1:B:140:LEU:HD21	1:B:219:LEU:CD1	2.48	0.44
1:C:189:LEU:HD22	1:C:206:VAL:HG11	1.99	0.44
1:C:163:TRP:CD2	1:C:197:ILE:HD12	2.52	0.44
1:B:184:ILE:HD12	1:B:215:LEU:HD22	1.99	0.44
1:D:211:ILE:O	1:D:215:LEU:HD13	2.18	0.44
1:A:14:GLU:CD	1:A:157:ARG:HH12	2.21	0.43
1:C:149:VAL:HG13	1:C:170:SER:HB3	2.00	0.43
1:C:215:LEU:HD13	1:C:220:ILE:CD1	2.48	0.43
1:C:361:TYR:O	1:C:366:ARG:HD2	2.18	0.43
1:C:251:ILE:HG22	1:C:256:GLY:HA2	2.01	0.43
1:D:244:GLY:C	1:D:245:LEU:HD12	2.38	0.43
1:A:126:MET:CE	1:A:302:VAL:HG23	2.49	0.43
1:A:294:LEU:HD21	1:A:386:ALA:HB3	2.01	0.43
1:B:28:ILE:HD13	1:B:97:TYR:OH	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:281:ALA:HB2	1:C:344:ILE:HD12	2.00	0.42
1:B:31:ALA:HB1	1:B:64:ILE:HD12	2.00	0.42
1:A:323:ARG:NH1	1:A:388:VAL:HG13	2.34	0.42
1:D:303:SER:OG	1:D:304:TYR:N	2.51	0.42
1:B:202:LEU:HD23	1:B:202:LEU:C	2.40	0.42
1:A:131:CYS:O	1:A:137:LEU:HA	2.20	0.41
1:A:63:ASN:C	1:A:64:ILE:HD12	2.41	0.41
1:D:251:ILE:HG22	1:D:256:GLY:HA2	2.01	0.41
1:B:46:LEU:HD23	1:B:46:LEU:C	2.41	0.41
1:A:306:ILE:HG21	1:B:231:THR:CG2	2.51	0.41
1:D:192:GLN:HA	1:D:234:PHE:O	2.21	0.41
1:D:245:LEU:N	1:D:245:LEU:HD12	2.36	0.41
1:D:58:ILE:O	1:D:99:LYS:HA	2.20	0.41
1:D:126:MET:HG3	1:D:278:ALA:HB3	2.02	0.41
1:A:49:THR:HA	1:A:240:GLN:HA	2.01	0.41
1:D:270:ASP:OD1	1:D:272:SER:OG	2.31	0.40
1:B:131:CYS:O	1:B:137:LEU:HA	2.21	0.40
1:D:212:LYS:N	1:D:213:PRO:CD	2.84	0.40
1:A:16:HIS:O	1:A:20:VAL:HG23	2.22	0.40
1:C:147:ARG:HB3	1:C:214:THR:HG23	2.04	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	362/399 (91%)	345 (95%)	17 (5%)	0	100	100
1	B	352/399 (88%)	343 (97%)	9 (3%)	0	100	100
1	C	335/399 (84%)	321 (96%)	14 (4%)	0	100	100
1	D	303/399 (76%)	296 (98%)	7 (2%)	0	100	100
All	All	1352/1596 (85%)	1305 (96%)	47 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	283/316 (90%)	273 (96%)	10 (4%)	36	44
1	B	280/316 (89%)	268 (96%)	12 (4%)	29	35
1	C	266/316 (84%)	256 (96%)	10 (4%)	33	41
1	D	239/316 (76%)	229 (96%)	10 (4%)	30	36
All	All	1068/1264 (84%)	1026 (96%)	42 (4%)	32	40

All (42) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	49	THR
1	A	100	GLN
1	A	126	MET
1	A	152	GLN
1	A	165	ARG
1	A	234	PHE
1	A	315	MET
1	A	332	LEU
1	A	335	GLU
1	A	372	SER
1	B	69	ILE
1	B	115	ASN
1	B	118	GLN
1	B	125	LEU
1	B	147	ARG
1	B	152	GLN
1	B	218	ASP
1	B	225	LYS
1	B	234	PHE
1	B	242	ASP
1	B	315	MET
1	B	384	GLU

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Mol	Chain	Res	Type
1	C	37	LYS
1	C	91	CYS
1	C	126	MET
1	C	147	ARG
1	C	152	GLN
1	C	197	ILE
1	C	234	PHE
1	C	242	ASP
1	C	296	SER
1	C	340	ARG
1	D	125	LEU
1	D	126	MET
1	D	147	ARG
1	D	152	GLN
1	D	155	LEU
1	D	160	ARG
1	D	218	ASP
1	D	225	LYS
1	D	352	ARG
1	D	357	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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](#)

There are no ligands in this entry.

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 ⓘ

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	368/399 (92%)	-0.06	4 (1%)	80 87	6, 15, 35, 50	0
1	B	357/399 (89%)	-0.09	2 (0%)	89 93	6, 12, 24, 28	0
1	C	343/399 (85%)	0.18	14 (4%)	37 49	10, 19, 33, 44	0
1	D	311/399 (77%)	0.08	12 (3%)	39 52	9, 18, 32, 43	0
All	All	1379/1596 (86%)	0.02	32 (2%)	60 70	6, 16, 32, 50	0

All (32) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	333	VAL	6.4
1	C	337	PHE	5.4
1	C	90	GLY	5.1
1	D	302	VAL	5.0
1	D	90	GLY	4.4
1	D	125	LEU	4.1
1	C	316	VAL	3.7
1	C	294	LEU	3.4
1	D	123	GLN	3.0
1	D	303	SER	3.0
1	D	304	TYR	3.0
1	D	124	GLY	2.7
1	C	339	LEU	2.7
1	C	307	GLY	2.6
1	D	300	ILE	2.6
1	D	339	LEU	2.5
1	C	319	PHE	2.5
1	B	5	TYR	2.5
1	A	90	GLY	2.5
1	A	239	PRO	2.4
1	C	306	ILE	2.4

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Mol	Chain	Res	Type	RSRZ
1	D	294	LEU	2.4
1	A	238	GLY	2.3
1	D	126	MET	2.3
1	C	376	ALA	2.2
1	C	315	MET	2.2
1	B	175	ARG	2.1
1	C	334	ARG	2.1
1	D	215	LEU	2.1
1	C	298	ALA	2.1
1	A	236	ILE	2.0
1	C	301	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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.