



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 11:08 AM UTC

PDB ID : 4QVG / pdb_00004qvg
Title : Crystal structure of S-adenosylmethionine-dependent methyltransferase SibL in its apo form
Authors : Liu, J.S.; Chen, S.C.; Huang, C.H.; Yang, C.S.; Chen, Y.
Deposited on : 2014-07-15
Resolution : 2.90 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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

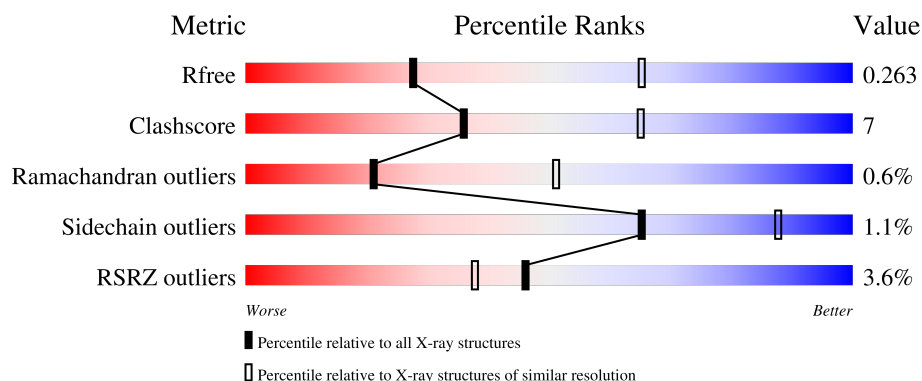
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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}	180053	2481 (2.90-2.90)
Clashscore	190562	2690 (2.90-2.90)
Ramachandran outliers	187476	2623 (2.90-2.90)
Sidechain outliers	187428	2625 (2.90-2.90)
RSRZ outliers	180081	2481 (2.90-2.90)

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 $\leq 5\%$. 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	355	6% 85% 11% .
1	B	355	6% 74% 21% ..
1	C	355	5% 81% 15% ...
1	D	355	3% 75% 19% ..

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 10596 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 SibL.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	341	Total	C	N	O	S	0	0	0
			2639	1673	480	482	4			
1	B	340	Total	C	N	O	S	0	0	0
			2628	1667	476	481	4			
1	C	349	Total	C	N	O	S	0	0	0
			2701	1711	494	492	4			
1	D	340	Total	C	N	O	S	0	0	0
			2628	1667	476	481	4			

There are 44 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	345	ALA	-	expression tag	UNP C0LTM6
A	346	ALA	-	expression tag	UNP C0LTM6
A	347	ALA	-	expression tag	UNP C0LTM6
A	348	LEU	-	expression tag	UNP C0LTM6
A	349	GLU	-	expression tag	UNP C0LTM6
A	350	HIS	-	expression tag	UNP C0LTM6
A	351	HIS	-	expression tag	UNP C0LTM6
A	352	HIS	-	expression tag	UNP C0LTM6
A	353	HIS	-	expression tag	UNP C0LTM6
A	354	HIS	-	expression tag	UNP C0LTM6
A	355	HIS	-	expression tag	UNP C0LTM6
B	345	ALA	-	expression tag	UNP C0LTM6
B	346	ALA	-	expression tag	UNP C0LTM6
B	347	ALA	-	expression tag	UNP C0LTM6
B	348	LEU	-	expression tag	UNP C0LTM6
B	349	GLU	-	expression tag	UNP C0LTM6
B	350	HIS	-	expression tag	UNP C0LTM6
B	351	HIS	-	expression tag	UNP C0LTM6
B	352	HIS	-	expression tag	UNP C0LTM6
B	353	HIS	-	expression tag	UNP C0LTM6
B	354	HIS	-	expression tag	UNP C0LTM6

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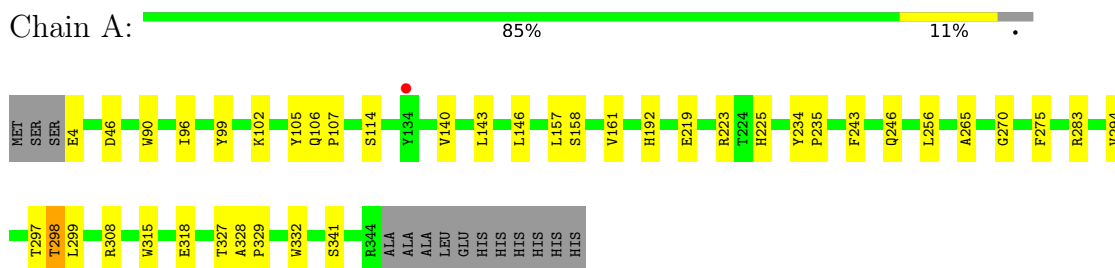
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Chain	Residue	Modelled	Actual	Comment	Reference
B	355	HIS	-	expression tag	UNP C0LTM6
C	345	ALA	-	expression tag	UNP C0LTM6
C	346	ALA	-	expression tag	UNP C0LTM6
C	347	ALA	-	expression tag	UNP C0LTM6
C	348	LEU	-	expression tag	UNP C0LTM6
C	349	GLU	-	expression tag	UNP C0LTM6
C	350	HIS	-	expression tag	UNP C0LTM6
C	351	HIS	-	expression tag	UNP C0LTM6
C	352	HIS	-	expression tag	UNP C0LTM6
C	353	HIS	-	expression tag	UNP C0LTM6
C	354	HIS	-	expression tag	UNP C0LTM6
C	355	HIS	-	expression tag	UNP C0LTM6
D	345	ALA	-	expression tag	UNP C0LTM6
D	346	ALA	-	expression tag	UNP C0LTM6
D	347	ALA	-	expression tag	UNP C0LTM6
D	348	LEU	-	expression tag	UNP C0LTM6
D	349	GLU	-	expression tag	UNP C0LTM6
D	350	HIS	-	expression tag	UNP C0LTM6
D	351	HIS	-	expression tag	UNP C0LTM6
D	352	HIS	-	expression tag	UNP C0LTM6
D	353	HIS	-	expression tag	UNP C0LTM6
D	354	HIS	-	expression tag	UNP C0LTM6
D	355	HIS	-	expression tag	UNP C0LTM6

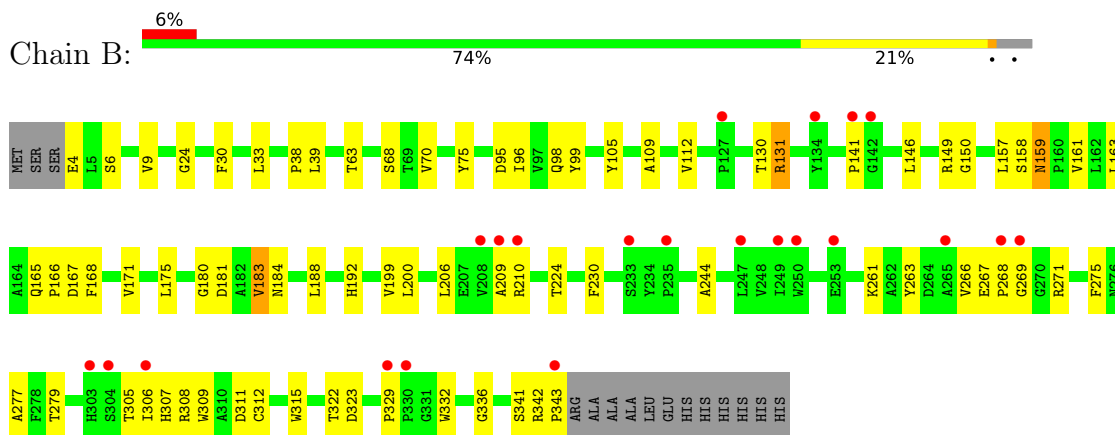
3 Residue-property plots

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.

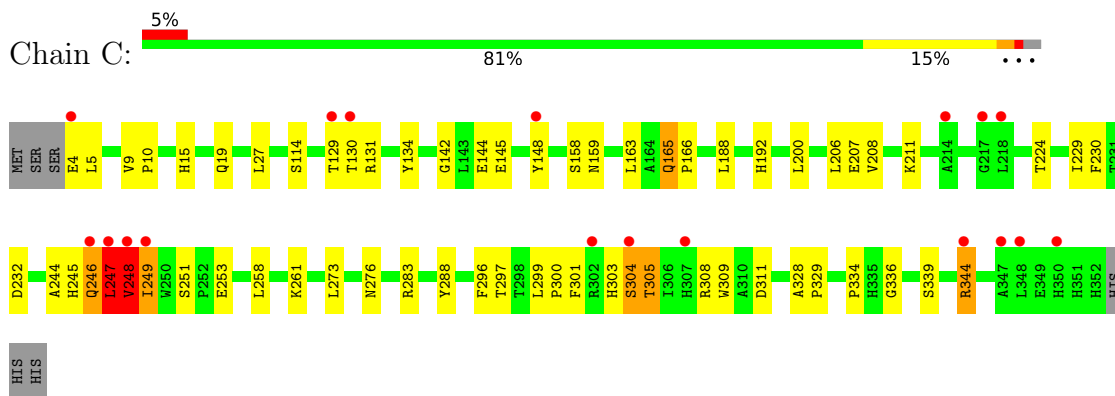
• Molecule 1: SibL



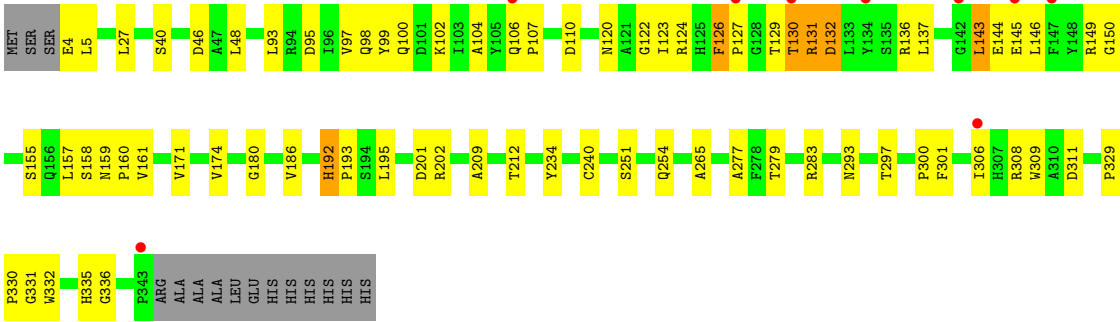
• Molecule 1: SibL



• Molecule 1: SibL



• Molecule 1: SibL



4 Data and refinement statistics

Property	Value	Source
Space group	F 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	102.93Å 295.42Å 322.23Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	28.12 – 2.90 28.12 – 2.90	Depositor EDS
% Data completeness (in resolution range)	99.2 (28.12-2.90) 92.2 (28.12-2.90)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.35 (at 2.90Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.1_1168)	Depositor
R, R_{free}	0.211 , 0.266 0.212 , 0.263	Depositor DCC
R_{free} test set	2003 reflections (3.63%)	wwPDB-VP
Wilson B-factor (Å ²)	60.7	Xtriage
Anisotropy	0.557	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 27.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	10596	wwPDB-VP
Average B, all atoms (Å ²)	69.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.58% 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

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	0.62	0/2707	0.94	5/3696 (0.1%)
1	B	0.63	1/2696 (0.0%)	0.96	5/3682 (0.1%)
1	C	0.64	1/2772 (0.0%)	1.10	23/3785 (0.6%)
1	D	0.60	0/2696	1.04	6/3682 (0.2%)
All	All	0.62	2/10871 (0.0%)	1.01	39/14845 (0.3%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	C	0	1
1	D	0	2
All	All	0	3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	9	VAL	CA-CB	5.23	1.57	1.54
1	C	246	GLN	CA-C	5.23	1.57	1.52

All (39) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	126	PHE	CA-C-N	-10.78	106.37	119.84
1	D	126	PHE	C-N-CA	-10.78	106.37	119.84
1	D	131	ARG	N-CA-C	8.69	123.63	109.72
1	C	249	ILE	N-CA-C	-8.23	96.45	109.20
1	C	305	THR	N-CA-C	7.81	121.25	108.52
1	C	246	GLN	N-CA-C	7.04	122.30	112.93
1	C	329	PRO	CA-C-N	7.03	126.28	118.97
1	C	329	PRO	C-N-CA	7.03	126.28	118.97

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	304	SER	CA-C-N	-6.67	113.71	123.05
1	C	304	SER	C-N-CA	-6.67	113.71	123.05
1	C	244	ALA	N-CA-C	-6.63	99.53	109.94
1	C	344	ARG	N-CA-C	6.52	118.91	108.41
1	C	192	HIS	CA-C-N	6.45	126.38	119.28
1	C	192	HIS	C-N-CA	6.45	126.38	119.28
1	C	131	ARG	N-CA-C	6.28	121.06	107.49
1	A	192	HIS	CA-C-N	6.28	126.18	119.28
1	A	192	HIS	C-N-CA	6.28	126.18	119.28
1	D	132	ASP	N-CA-C	-6.05	99.10	108.42
1	C	159	ASN	CA-C-N	-5.94	112.55	119.32
1	C	159	ASN	C-N-CA	-5.94	112.55	119.32
1	C	248	VAL	CB-CA-C	-5.88	100.23	111.40
1	D	192	HIS	CA-C-N	5.88	125.75	119.28
1	D	192	HIS	C-N-CA	5.88	125.75	119.28
1	B	269	GLY	N-CA-C	-5.69	108.31	115.08
1	A	90	TRP	CA-C-N	-5.63	113.09	119.28
1	A	90	TRP	C-N-CA	-5.63	113.09	119.28
1	C	165	GLN	CA-C-N	5.60	125.27	119.56
1	C	165	GLN	C-N-CA	5.60	125.27	119.56
1	C	276	ASN	N-CA-C	5.50	115.11	107.73
1	C	301	PHE	N-CA-C	-5.42	106.64	113.20
1	C	328	ALA	CA-C-N	-5.32	114.90	120.38
1	C	328	ALA	C-N-CA	-5.32	114.90	120.38
1	B	192	HIS	CA-C-N	5.31	125.12	119.28
1	B	192	HIS	C-N-CA	5.31	125.12	119.28
1	B	159	ASN	CA-C-N	-5.20	113.28	119.05
1	B	159	ASN	C-N-CA	-5.20	113.28	119.05
1	C	245	HIS	CA-C-N	-5.15	114.04	122.79
1	C	245	HIS	C-N-CA	-5.15	114.04	122.79
1	A	105	TYR	N-CA-C	5.00	117.11	111.11

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	247	LEU	Peptide
1	D	130	THR	Peptide
1	D	143	LEU	Peptide

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	2639	0	2587	20	0
1	B	2628	0	2574	50	0
1	C	2701	0	2640	38	0
1	D	2628	0	2574	50	0
All	All	10596	0	10375	152	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 7.

All (152) 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:C:246:GLN:HG3	1:C:248:VAL:HG13	1.55	0.87
1:C:4:GLU:HG3	1:C:5:LEU:H	1.39	0.86
1:B:98:GLN:OE1	1:B:149:ARG:NH2	2.15	0.79
1:A:219:GLU:O	1:A:223:ARG:NH1	2.18	0.77
1:D:283:ARG:NH1	1:D:308:ARG:HD2	2.00	0.77
1:C:247:LEU:HG	1:C:248:VAL:HA	1.68	0.76
1:B:95:ASP:OD1	1:B:149:ARG:NH1	2.23	0.72
1:C:232:ASP:O	1:C:261:LYS:NZ	2.20	0.70
1:A:46:ASP:OD2	1:C:308:ARG:NH2	2.26	0.68
1:D:98:GLN:OE1	1:D:149:ARG:NH1	2.22	0.68
1:B:308:ARG:NH1	1:B:311:ASP:OD1	2.26	0.68
1:C:283:ARG:HH11	1:C:308:ARG:HD2	1.58	0.68
1:D:4:GLU:HG2	1:D:5:LEU:HD12	1.77	0.67
1:B:267:GLU:CD	1:B:268:PRO:HD2	2.19	0.66
1:D:126:PHE:HB3	1:D:127:PRO:HD3	1.76	0.66
1:C:248:VAL:HG23	1:C:303:HIS:HB3	1.77	0.66
1:D:155:SER:OG	1:D:159:ASN:ND2	2.28	0.65
1:B:158:SER:O	1:B:161:VAL:HG12	1.97	0.63
1:B:157:LEU:HD21	1:B:332:TRP:HZ2	1.63	0.63
1:C:308:ARG:NH1	1:C:311:ASP:OD1	2.31	0.63
1:C:283:ARG:NH1	1:C:308:ARG:HD2	2.14	0.62
1:C:4:GLU:HG3	1:C:5:LEU:HD12	1.83	0.61
1:B:175:LEU:HD11	1:B:200:LEU:HB2	1.83	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:127:PRO:HD2	1:D:136:ARG:HD2	1.82	0.61
1:B:263:TYR:O	1:B:342:ARG:NH1	2.34	0.61
1:B:277:ALA:O	1:B:306:ILE:HG23	2.03	0.59
1:C:251:SER:HB2	1:C:253:GLU:OE1	2.03	0.58
1:C:248:VAL:HB	1:C:249:ILE:O	2.03	0.58
1:D:131:ARG:HB2	1:D:301:PHE:CE2	2.39	0.58
1:A:283:ARG:NH1	1:A:308:ARG:HD2	2.20	0.57
1:B:157:LEU:HD21	1:B:332:TRP:CZ2	2.40	0.57
1:B:268:PRO:HB3	1:B:343:PRO:C	2.30	0.56
1:D:171:VAL:HG11	1:D:240:CYS:HB2	1.89	0.55
1:D:234:TYR:HB2	1:D:265:ALA:HB2	1.88	0.55
1:D:137:LEU:HD22	1:D:143:LEU:HD13	1.89	0.55
1:A:158:SER:O	1:A:161:VAL:HG12	2.06	0.55
1:D:95:ASP:OD1	1:D:149:ARG:NH2	2.39	0.54
1:C:299:LEU:HB2	1:C:300:PRO:HD3	1.90	0.54
1:D:158:SER:O	1:D:161:VAL:HG12	2.08	0.53
1:B:180:GLY:O	1:B:209:ALA:HB2	2.09	0.53
1:B:308:ARG:NH2	1:D:46:ASP:OD2	2.41	0.53
1:D:130:THR:HG22	1:D:131:ARG:H	1.73	0.53
1:C:246:GLN:H	1:C:247:LEU:HA	1.74	0.53
1:D:4:GLU:OE1	1:D:4:GLU:N	2.41	0.53
1:B:199:VAL:HB	1:B:224:THR:HG22	1.90	0.53
1:B:130:THR:HG22	1:B:131:ARG:H	1.75	0.52
1:C:273:LEU:HD23	1:C:339:SER:HB3	1.91	0.52
1:C:206:LEU:HD22	1:C:224:THR:HB	1.92	0.52
1:B:167:ASP:OD2	1:B:271:ARG:HD3	2.10	0.51
1:C:207:GLU:O	1:C:211:LYS:HG2	2.09	0.51
1:D:4:GLU:HG2	1:D:5:LEU:H	1.76	0.51
1:B:279:THR:OG1	1:B:306:ILE:HG22	2.10	0.50
1:D:120:ASN:HD22	1:D:300:PRO:C	2.18	0.50
1:C:246:GLN:HG3	1:C:248:VAL:CG1	2.34	0.50
1:D:95:ASP:CG	1:D:149:ARG:HH21	2.19	0.50
1:C:296:PHE:HB3	1:C:304:SER:HA	1.92	0.50
1:A:294:VAL:O	1:A:298:THR:OG1	2.19	0.49
1:C:200:LEU:HD22	1:C:229:ILE:HG22	1.94	0.49
1:D:309:TRP:HH2	1:D:336:GLY:HA3	1.78	0.48
1:B:112:VAL:HG13	1:C:27:LEU:HD21	1.95	0.48
1:B:308:ARG:HH22	1:D:46:ASP:CG	2.21	0.48
1:C:114:SER:HB3	1:C:297:THR:HG22	1.95	0.48
1:D:159:ASN:N	1:D:160:PRO:HD2	2.28	0.48
1:D:180:GLY:O	1:D:209:ALA:HB2	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:161:VAL:HG23	1:B:329:PRO:HG2	1.96	0.47
1:C:142:GLY:HA2	1:C:145:GLU:OE2	2.15	0.47
1:C:246:GLN:N	1:C:247:LEU:HA	2.27	0.47
1:A:161:VAL:HG13	1:A:275:PHE:HE1	1.79	0.47
1:B:70:VAL:HB	1:B:75:TYR:CE2	2.49	0.47
1:A:327:THR:O	1:A:329:PRO:HD3	2.15	0.47
1:B:230:PHE:O	1:B:261:LYS:NZ	2.44	0.47
1:D:120:ASN:ND2	1:D:301:PHE:HA	2.30	0.47
1:D:123:ILE:HD11	1:D:136:ARG:HG3	1.97	0.47
1:B:163:LEU:HD22	1:B:188:LEU:HA	1.96	0.47
1:B:210:ARG:NH2	1:B:224:THR:OG1	2.48	0.47
1:D:129:THR:O	1:D:136:ARG:NH2	2.48	0.47
1:D:293:ASN:O	1:D:297:THR:HG23	2.14	0.47
1:B:168:PHE:HA	1:B:171:VAL:HG22	1.97	0.46
1:B:206:LEU:HB3	1:B:210:ARG:NH1	2.30	0.46
1:D:100:GLN:HA	1:D:104:ALA:HB3	1.97	0.46
1:D:132:ASP:OD1	1:D:132:ASP:N	2.47	0.46
1:B:309:TRP:HH2	1:B:336:GLY:HA3	1.81	0.46
1:B:95:ASP:CG	1:B:149:ARG:NH1	2.74	0.46
1:D:309:TRP:CH2	1:D:336:GLY:HA3	2.50	0.46
1:A:114:SER:HB3	1:A:297:THR:HG22	1.97	0.46
1:B:266:VAL:O	1:B:342:ARG:NH1	2.49	0.45
1:D:4:GLU:HG2	1:D:5:LEU:N	2.31	0.45
1:D:110:ASP:OD2	1:D:122:GLY:HA2	2.16	0.45
1:D:144:GLU:HG2	1:D:145:GLU:H	1.81	0.45
1:B:38:PRO:O	1:B:39:LEU:HD23	2.17	0.45
1:C:134:TYR:HE1	1:C:144:GLU:HG3	1.82	0.45
1:A:4:GLU:N	1:A:4:GLU:OE1	2.49	0.45
1:D:174:VAL:HG23	1:D:195:LEU:HD11	1.99	0.45
1:C:129:THR:OG1	1:C:130:THR:N	2.49	0.45
1:D:99:TYR:CD2	1:D:150:GLY:HA3	2.51	0.45
1:C:288:TYR:CG	1:C:334:PRO:HD3	2.51	0.45
1:A:140:VAL:HB	1:A:143:LEU:HD12	1.98	0.44
1:B:210:ARG:NE	1:B:224:THR:OG1	2.50	0.44
1:D:93:LEU:O	1:D:97:VAL:HG23	2.16	0.44
1:D:123:ILE:HD13	1:D:301:PHE:CZ	2.53	0.44
1:B:33:LEU:HD22	1:B:75:TYR:O	2.17	0.44
1:A:315:TRP:HA	1:A:318:GLU:OE1	2.18	0.44
1:B:96:ILE:O	1:B:99:TYR:HB3	2.17	0.44
1:B:165:GLN:HA	1:B:166:PRO:HD3	1.86	0.44
1:B:268:PRO:HB3	1:B:343:PRO:O	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:279:THR:OG1	1:D:306:ILE:HG22	2.17	0.44
1:D:277:ALA:O	1:D:306:ILE:HG23	2.17	0.44
1:A:157:LEU:HD11	1:A:332:TRP:HZ2	1.83	0.44
1:B:244:ALA:HA	1:B:275:PHE:O	2.18	0.44
1:A:225:HIS:NE2	1:A:235:PRO:HG3	2.33	0.44
1:D:106:GLN:HB3	1:D:107:PRO:HD3	1.99	0.44
1:C:148:TYR:CE1	1:C:208:VAL:HG11	2.52	0.43
1:B:305:THR:HB	1:B:307:HIS:NE2	2.32	0.43
1:B:342:ARG:HA	1:B:343:PRO:HD3	1.85	0.43
1:C:9:VAL:HB	1:C:10:PRO:HD3	2.00	0.43
1:D:251:SER:OG	1:D:254:GLN:OE1	2.34	0.43
1:B:159:ASN:O	1:B:163:LEU:HG	2.17	0.43
1:B:312:CYS:HA	1:B:315:TRP:CE3	2.54	0.43
1:C:247:LEU:N	1:C:248:VAL:HA	2.34	0.43
1:D:308:ARG:NH1	1:D:311:ASP:OD1	2.46	0.43
1:B:99:TYR:HD2	1:B:150:GLY:HA3	1.84	0.43
1:D:192:HIS:HA	1:D:193:PRO:HD2	1.88	0.43
1:D:330:PRO:HA	1:D:331:GLY:HA2	1.70	0.43
1:C:163:LEU:HD22	1:C:188:LEU:HA	2.00	0.43
1:C:309:TRP:HH2	1:C:336:GLY:HA3	1.84	0.42
1:D:126:PHE:HB3	1:D:127:PRO:CD	2.48	0.42
1:B:181:ASP:OD1	1:B:183:VAL:HG13	2.19	0.42
1:D:201:ASP:OD1	1:D:202:ARG:N	2.44	0.42
1:A:96:ILE:O	1:A:99:TYR:HB3	2.20	0.42
1:A:106:GLN:HB3	1:A:107:PRO:HD3	2.02	0.42
1:A:256:LEU:HD21	1:A:318:GLU:HB2	2.02	0.42
1:A:270:GLY:O	1:A:341:SER:HA	2.18	0.42
1:D:157:LEU:HD21	1:D:332:TRP:CZ2	2.55	0.42
1:B:184:ASN:O	1:B:188:LEU:HB2	2.20	0.42
1:B:322:THR:HG22	1:B:323:ASP:N	2.34	0.42
1:C:248:VAL:HG21	1:C:305:THR:OG1	2.20	0.41
1:D:102:LYS:HB2	1:D:146:LEU:HD21	2.02	0.41
1:C:4:GLU:HG3	1:C:5:LEU:N	2.20	0.41
1:B:63:THR:HA	1:B:68:SER:O	2.20	0.41
1:B:109:ALA:HA	1:C:19:GLN:NE2	2.36	0.41
1:A:243:PHE:HB3	1:A:246:GLN:HB2	2.03	0.41
1:C:165:GLN:HA	1:C:166:PRO:HD3	1.87	0.41
1:A:234:TYR:HB2	1:A:265:ALA:HB2	2.02	0.41
1:B:105:TYR:HA	1:C:15:HIS:CD2	2.56	0.40
1:D:27:LEU:O	1:D:48:LEU:HD22	2.21	0.40
1:D:186:VAL:HG21	1:D:212:THR:HG22	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:161:VAL:HG13	1:B:275:PHE:HE1	1.86	0.40
1:B:4:GLU:HG3	1:B:6:SER:H	1.86	0.40
1:B:24:GLY:HA3	1:B:30:PHE:CE2	2.56	0.40
1:A:102:LYS:HB2	1:A:146:LEU:HD21	2.03	0.40
1:C:230:PHE:CZ	1:C:247:LEU:HD11	2.57	0.40
1:D:158:SER:HB2	1:D:335:HIS:CD2	2.57	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	339/355 (96%)	330 (97%)	7 (2%)	2 (1%)	21	51
1	B	262/355 (74%)	252 (96%)	9 (3%)	1 (0%)	30	59
1	C	34/355 (10%)	32 (94%)	2 (6%)	0	100	100
1	D	60/355 (17%)	57 (95%)	2 (3%)	1 (2%)	7	26
All	All	695/1420 (49%)	671 (96%)	20 (3%)	4 (1%)	21	51

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	329	PRO
1	A	299	LEU
1	A	328	ALA
1	B	141	PRO

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	270/281 (96%)	269 (100%)	1 (0%)	84	94
1	B	269/281 (96%)	265 (98%)	4 (2%)	57	84
1	C	275/281 (98%)	270 (98%)	5 (2%)	51	80
1	D	269/281 (96%)	267 (99%)	2 (1%)	76	92
All	All	1083/1124 (96%)	1071 (99%)	12 (1%)	65	88

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	298	THR
1	B	131	ARG
1	B	146	LEU
1	B	183	VAL
1	B	341	SER
1	C	158	SER
1	C	247	LEU
1	C	248	VAL
1	C	258	LEU
1	C	344	ARG
1	D	40	SER
1	D	124	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	172	HIS
1	A	245	HIS
1	A	276	ASN
1	B	22	ASN
1	B	26	GLN
1	B	125	HIS
1	B	172	HIS
1	B	246	GLN
1	C	276	ASN
1	D	26	GLN
1	D	34	HIS

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Mol	Chain	Res	Type
1	D	159	ASN
1	D	246	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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	341/355 (96%)	-0.16	1 (0%) 90 87	34, 55, 84, 104	0
1	B	340/355 (95%)	0.54	22 (6%) 25 20	42, 76, 110, 119	0
1	C	349/355 (98%)	0.22	18 (5%) 33 26	43, 64, 103, 118	0
1	D	340/355 (95%)	0.27	9 (2%) 57 48	46, 69, 105, 131	0
All	All	1370/1420 (96%)	0.22	50 (3%) 46 38	34, 66, 105, 131	0

All (50) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	304	SER	7.1
1	C	246	GLN	5.4
1	B	208	VAL	4.8
1	C	247	LEU	4.5
1	B	253	GLU	4.2
1	C	302	ARG	3.5
1	C	130	THR	3.5
1	A	134	TYR	3.4
1	B	142	GLY	3.4
1	C	350	HIS	3.3
1	B	249	ILE	3.1
1	D	343	PRO	3.0
1	B	269	GLY	3.0
1	D	306	ILE	3.0
1	C	217	GLY	3.0
1	C	218	LEU	2.9
1	C	348	LEU	2.9
1	B	268	PRO	2.8
1	B	330	PRO	2.8
1	B	134	TYR	2.7
1	C	129	THR	2.7

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Mol	Chain	Res	Type	RSRZ
1	C	148	TYR	2.7
1	D	106	GLN	2.7
1	B	233	SER	2.6
1	C	214	ALA	2.5
1	B	306	ILE	2.5
1	B	209	ALA	2.5
1	C	248	VAL	2.5
1	D	142	GLY	2.4
1	D	147	PHE	2.4
1	B	343	PRO	2.4
1	D	145	GLU	2.4
1	D	130	THR	2.4
1	B	303	HIS	2.3
1	B	304	SER	2.3
1	D	134	TYR	2.3
1	B	235	PRO	2.3
1	B	127	PRO	2.2
1	C	307	HIS	2.2
1	B	329	PRO	2.1
1	B	265	ALA	2.1
1	C	347	ALA	2.1
1	C	4	GLU	2.1
1	B	141	PRO	2.1
1	D	127	PRO	2.1
1	B	247	LEU	2.0
1	B	210	ARG	2.0
1	C	344	ARG	2.0
1	C	249	ILE	2.0
1	B	250	TRP	2.0

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.