



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 06:35 AM UTC

PDB ID : 1SR9 / pdb_00001sr9
Title : Crystal Structure of LeuA from Mycobacterium tuberculosis
Authors : Koon, N.; Squire, C.J.; Baker, E.N.
Deposited on : 2004-03-22
Resolution : 2.00 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
Mogul	:	2022.3.0, CSD as543be (2022)
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

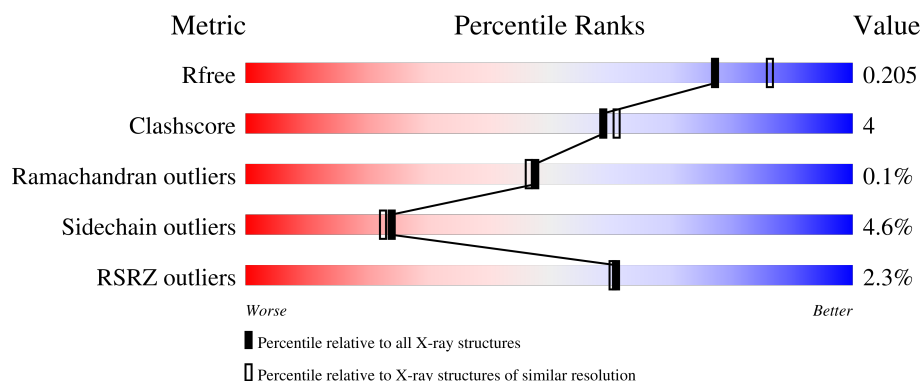
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

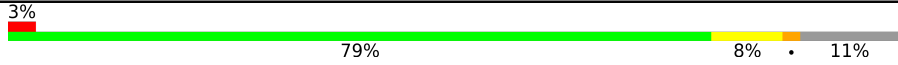
The reported resolution of this entry is 2.00 Å.

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	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

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	644	 3% 79% 8% • 11%
1	B	644	 0% 79% 10% • 10%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 9153 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 2-isopropylmalate synthase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	573	Total	C	N	O	S	Se	0	0	0
			4319	2717	752	830	9	11			
1	B	577	Total	C	N	O	S	Se	0	0	0
			4349	2733	761	835	9	11			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MSE	MET	modified residue	UNP P96420
A	41	MSE	MET	modified residue	UNP P96420
A	90	MSE	MET	modified residue	UNP P96420
A	98	MSE	MET	modified residue	UNP P96420
A	105	MSE	MET	modified residue	UNP P96420
A	257	MSE	MET	modified residue	UNP P96420
A	270	MSE	MET	modified residue	UNP P96420
A	390	MSE	MET	modified residue	UNP P96420
A	404	MSE	MET	modified residue	UNP P96420
A	441	MSE	MET	modified residue	UNP P96420
A	480	MSE	MET	modified residue	UNP P96420
A	559	MSE	MET	modified residue	UNP P96420
B	1	MSE	MET	modified residue	UNP P96420
B	41	MSE	MET	modified residue	UNP P96420
B	90	MSE	MET	modified residue	UNP P96420
B	98	MSE	MET	modified residue	UNP P96420
B	105	MSE	MET	modified residue	UNP P96420
B	257	MSE	MET	modified residue	UNP P96420
B	270	MSE	MET	modified residue	UNP P96420
B	390	MSE	MET	modified residue	UNP P96420
B	404	MSE	MET	modified residue	UNP P96420
B	441	MSE	MET	modified residue	UNP P96420
B	480	MSE	MET	modified residue	UNP P96420
B	559	MSE	MET	modified residue	UNP P96420

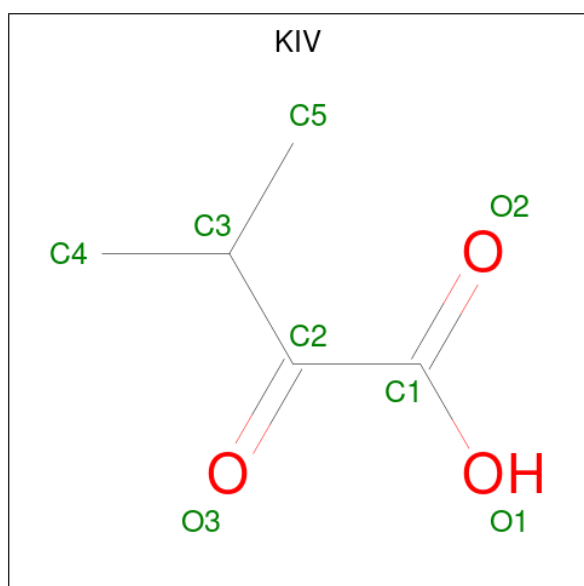
- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Zn	0	0
			1	1		
2	B	1	Total	Zn	0	0
			1	1		

- Molecule 3 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Cl	0	0
			1	1		

- Molecule 4 is 3-METHYL-2-OXOBUTANOIC ACID (CCD ID: KIV) (formula: C₅H₈O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			8	5	3		
4	B	1	Total	C	O	0	0
			8	5	3		

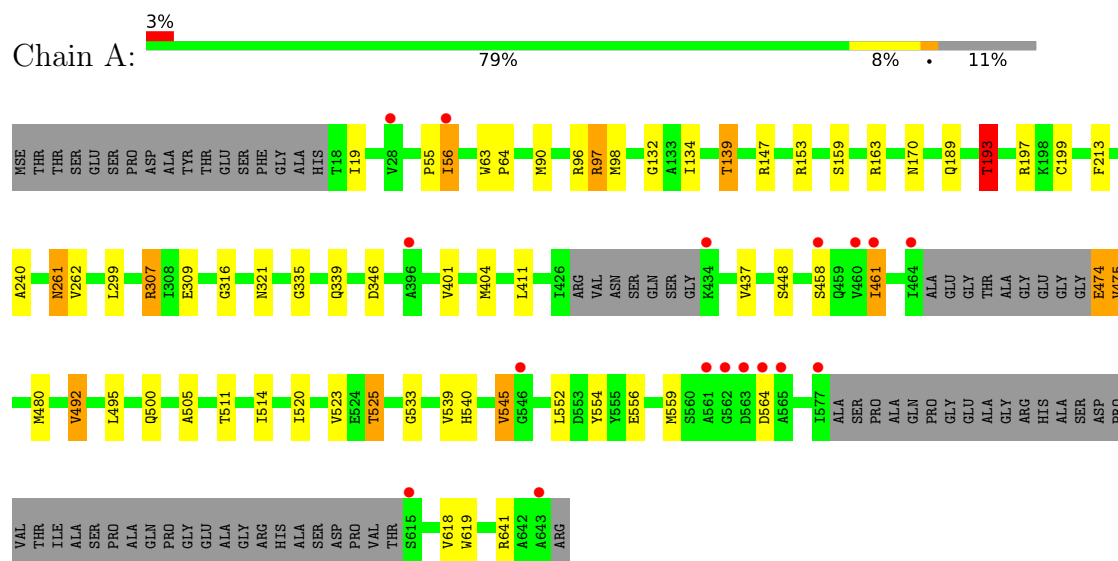
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	236	Total	O	0	0
			236	236		
5	B	230	Total	O	0	0
			230	230		

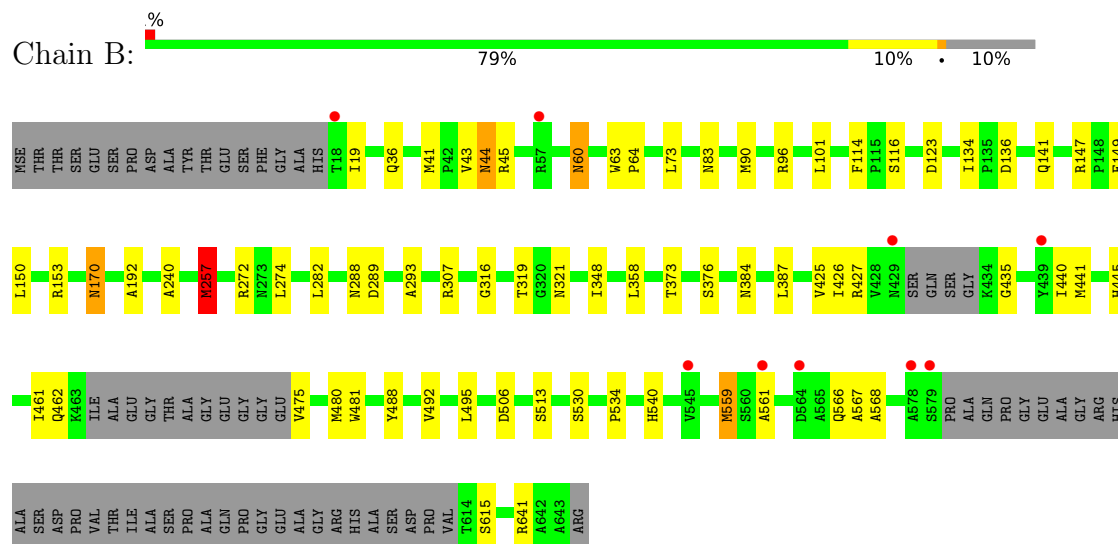
3 Residue-property plots [i](#)

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: 2-isopropylmalate synthase



• Molecule 1: 2-isopropylmalate synthase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	54.25Å 154.73Å 68.82Å 90.00° 98.05° 90.00°	Depositor
Resolution (Å)	30.00 – 2.00 30.00 – 2.00	Depositor EDS
% Data completeness (in resolution range)	(Not available) (30.00-2.00) 98.4 (30.00-2.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.83 (at 1.91Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.169 , 0.197 0.181 , 0.205	Depositor DCC
R_{free} test set	4367 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å ²)	32.2	Xtriage
Anisotropy	0.108	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 39.3	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	0.96	EDS
Total number of atoms	9153	wwPDB-VP
Average B, all atoms (Å ²)	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.07% 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](#)

Bond lengths and bond angles in the following residue types are not validated in this section: CL, ZN, KIV

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	0.94	6/4403 (0.1%)	0.99	11/5999 (0.2%)
1	B	0.92	4/4433 (0.1%)	0.95	4/6036 (0.1%)
All	All	0.93	10/8836 (0.1%)	0.97	15/12035 (0.1%)

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	559	MSE	SE-CE	-8.38	1.70	1.95
1	B	441	MSE	SE-CE	-6.63	1.75	1.95
1	B	257	MSE	SE-CE	-6.41	1.76	1.95
1	B	240	ALA	CA-CB	6.30	1.57	1.52
1	A	475	VAL	CA-CB	6.09	1.61	1.54
1	A	559	MSE	CG-SE	-6.09	1.77	1.95
1	A	98	MSE	SE-CE	-5.26	1.79	1.95
1	A	96	ARG	CA-CB	5.21	1.61	1.53
1	A	240	ALA	CA-CB	5.21	1.61	1.53
1	A	90	MSE	SE-CE	5.13	2.10	1.95

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	307	ARG	NE-CZ-NH1	-8.22	113.28	121.50
1	A	307	ARG	NE-CZ-NH2	7.80	126.22	119.20
1	A	492	VAL	CB-CA-C	7.25	117.88	110.70
1	B	257	MSE	CG-SE-CE	-6.70	84.18	98.92
1	B	41	MSE	CG-SE-CE	-6.16	85.38	98.92
1	A	55	PRO	CA-C-N	5.89	129.29	120.69
1	A	55	PRO	C-N-CA	5.89	129.29	120.69
1	A	134	ILE	N-CA-C	5.77	113.26	107.55
1	A	56	ILE	CB-CA-C	-5.75	102.63	111.71

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	492	VAL	N-CA-CB	-5.55	104.18	112.67
1	A	492	VAL	N-CA-C	-5.53	107.89	113.20
1	A	193	THR	N-CA-CB	-5.36	102.05	110.30
1	A	307	ARG	CD-NE-CZ	5.16	131.62	124.40
1	B	134	ILE	N-CA-C	5.09	112.59	107.55
1	B	561	ALA	N-CA-C	5.08	121.68	114.16

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	4319	0	4106	41	0
1	B	4349	0	4134	41	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	1	0	0	1	0
4	A	8	0	7	0	0
4	B	8	0	7	0	0
5	A	236	0	0	12	0
5	B	230	0	0	4	0
All	All	9153	0	8254	75	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 4.

All (75) 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:56:ILE:HG13	5:A:1180:HOH:O	1.71	0.88
1:A:56:ILE:HD11	1:A:262:VAL:HG13	1.58	0.85
1:A:404:MSE:O	1:B:45:ARG:HD2	1.78	0.83
1:B:141:GLN:HE22	1:B:307:ARG:HH22	1.21	0.83
1:B:83:ASN:HD21	1:B:90:MSE:H	1.27	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:474:GLU:OE1	5:A:1081:HOH:O	2.00	0.79
1:A:641:ARG:NH1	5:A:924:HOH:O	2.16	0.77
1:A:139:THR:HG21	5:A:1265:HOH:O	1.85	0.76
1:A:139:THR:HB	1:A:163:ARG:HG3	1.72	0.71
1:A:523:VAL:O	1:A:525:THR:HG22	1.90	0.70
5:A:1115:HOH:O	1:B:257:MSE:HE1	1.92	0.69
1:B:123:ASP:OD2	5:B:1261:HOH:O	2.11	0.67
1:B:141:GLN:HE22	1:B:307:ARG:NH2	1.93	0.67
1:A:193:THR:HG21	5:A:1121:HOH:O	1.95	0.66
1:B:440:ILE:HG22	1:B:480:MSE:HE1	1.77	0.66
1:A:505:ALA:HB2	1:A:511:THR:O	1.97	0.63
1:A:56:ILE:CD1	1:A:262:VAL:HG13	2.29	0.63
1:B:559:MSE:HE2	1:B:567:ALA:C	2.24	0.63
1:A:193:THR:HG23	1:A:197:ARG:HH12	1.64	0.62
1:A:193:THR:HG23	1:A:197:ARG:NH1	2.15	0.62
1:A:339:GLN:NE2	1:B:36:GLN:HE21	1.99	0.60
1:A:316:GLY:HA3	1:A:321:ASN:HD22	1.68	0.58
1:A:19:ILE:HD11	1:B:348:ILE:HG13	1.84	0.58
1:B:530:SER:O	1:B:540:HIS:HD2	1.86	0.58
1:A:261:ASN:HD22	1:A:261:ASN:H	1.50	0.57
1:B:44:ASN:ND2	5:B:1133:HOH:O	2.31	0.56
1:B:83:ASN:ND2	1:B:90:MSE:H	2.00	0.56
1:A:437:VAL:HG21	1:A:458:SER:HB3	1.89	0.55
1:A:520:ILE:HD11	1:A:545:VAL:CG2	2.36	0.55
1:A:307:ARG:NH1	1:A:309:GLU:OE1	2.40	0.55
1:A:500:GLN:HG3	1:A:514:ILE:HD11	1.90	0.54
1:A:339:GLN:HE21	1:B:36:GLN:HE21	1.54	0.54
1:B:150:LEU:HD13	5:B:1273:HOH:O	2.08	0.54
1:A:404:MSE:O	1:B:45:ARG:CD	2.55	0.53
5:A:1195:HOH:O	1:B:19:ILE:HG12	2.09	0.53
1:B:559:MSE:HE3	1:B:566:GLN:CB	2.39	0.53
1:B:60:ASN:ND2	1:B:272:ARG:HH22	2.07	0.52
1:A:97:ARG:HD3	5:A:1251:HOH:O	2.10	0.52
1:A:193:THR:CG2	1:A:197:ARG:HH12	2.22	0.52
1:B:488:TYR:CE2	1:B:641:ARG:HD3	2.45	0.52
1:A:56:ILE:CD1	5:A:1180:HOH:O	2.57	0.51
1:B:288:ASN:HD22	1:B:293:ALA:H	1.59	0.51
1:B:384:ASN:HD21	1:B:462:GLN:NE2	2.08	0.50
1:A:619:TRP:N	5:A:924:HOH:O	2.44	0.50
1:B:114:PHE:HE2	5:B:1273:HOH:O	1.93	0.49
1:A:554:TYR:OH	1:A:556:GLU:OE1	2.17	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:533:GLY:HA3	3:A:705:CL:CL	2.49	0.49
1:B:63:TRP:N	1:B:64:PRO:CD	2.77	0.48
1:A:461:ILE:CD1	1:A:480:MSE:HG3	2.44	0.47
1:B:316:GLY:HA3	1:B:321:ASN:HD22	1.79	0.47
1:B:373:THR:HG23	1:B:425:VAL:HG23	1.95	0.47
1:A:520:ILE:HD11	1:A:545:VAL:HG22	1.98	0.46
1:B:288:ASN:ND2	1:B:293:ALA:H	2.14	0.46
1:B:513:SER:OG	1:B:530:SER:OG	2.25	0.46
1:A:461:ILE:HD11	1:A:480:MSE:HG3	1.98	0.45
1:B:435:GLY:HA2	1:B:440:ILE:HD11	1.99	0.45
1:B:116:SER:HA	1:B:153:ARG:HG2	1.99	0.43
1:B:289:ASP:HA	1:B:319:THR:HG21	2.00	0.43
1:A:316:GLY:HA3	1:A:321:ASN:ND2	2.32	0.43
1:B:445:HIS:CE1	1:B:481:TRP:CD2	3.07	0.43
1:B:559:MSE:HE3	1:B:566:GLN:HB3	2.01	0.43
1:B:426:ILE:HG21	1:B:461:ILE:HG21	2.00	0.43
1:B:73:LEU:O	1:B:307:ARG:HA	2.19	0.43
1:A:139:THR:HG22	1:A:163:ARG:HD2	2.01	0.42
1:B:170:ASN:HD21	1:B:192:ALA:HB2	1.85	0.42
1:A:63:TRP:CG	1:A:64:PRO:HD3	2.56	0.41
1:B:60:ASN:HD21	1:B:272:ARG:HH22	1.66	0.41
1:A:132:GLY:HA2	5:A:1165:HOH:O	2.21	0.41
1:A:500:GLN:O	1:B:506:ASP:HA	2.20	0.41
1:A:539:VAL:HG23	1:A:540:HIS:CD2	2.56	0.41
1:A:199:CYS:HB3	1:A:213:PHE:CE2	2.56	0.40
1:A:335:GLY:C	1:B:43:VAL:CG1	2.94	0.40
5:A:1258:HOH:O	1:B:534:PRO:HG3	2.21	0.40
1:B:559:MSE:HE2	1:B:568:ALA:N	2.37	0.40
1:A:189:GLN:O	1:A:193:THR:HB	2.22	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	565/644 (88%)	553 (98%)	11 (2%)	1 (0%)	43	42
1	B	569/644 (88%)	553 (97%)	16 (3%)	0	100	100
All	All	1134/1288 (88%)	1106 (98%)	27 (2%)	1 (0%)	48	46

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	564	ASP

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	441/508 (87%)	419 (95%)	22 (5%)	22	20
1	B	443/508 (87%)	424 (96%)	19 (4%)	26	25
All	All	884/1016 (87%)	843 (95%)	41 (5%)	24	22

All (41) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	97	ARG
1	A	139	THR
1	A	147	ARG
1	A	153	ARG
1	A	159	SER
1	A	170	ASN
1	A	193	THR
1	A	261	ASN
1	A	299	LEU
1	A	346	ASP
1	A	401	VAL
1	A	411	LEU
1	A	448	SER
1	A	461	ILE
1	A	474	GLU

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Mol	Chain	Res	Type
1	A	475	VAL
1	A	492	VAL
1	A	495	LEU
1	A	525	THR
1	A	545	VAL
1	A	552	LEU
1	A	618	VAL
1	B	44	ASN
1	B	60	ASN
1	B	96	ARG
1	B	101	LEU
1	B	136	ASP
1	B	147	ARG
1	B	149	GLU
1	B	170	ASN
1	B	257	MSE
1	B	274	LEU
1	B	282	LEU
1	B	358	LEU
1	B	376	SER
1	B	387	LEU
1	B	427	ARG
1	B	475	VAL
1	B	492	VAL
1	B	495	LEU
1	B	615	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (25) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	170	ASN
1	A	189	GLN
1	A	210	GLN
1	A	250	ASN
1	A	261	ASN
1	A	321	ASN
1	A	339	GLN
1	A	454	GLN
1	A	566	GLN
1	B	44	ASN
1	B	60	ASN
1	B	83	ASN

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Mol	Chain	Res	Type
1	B	119	GLN
1	B	131	GLN
1	B	141	GLN
1	B	170	ASN
1	B	276	ASN
1	B	288	ASN
1	B	321	ASN
1	B	357	GLN
1	B	380	GLN
1	B	384	ASN
1	B	459	GLN
1	B	462	GLN
1	B	540	HIS

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](#)

Of 5 ligands modelled in this entry, 3 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	$\# Z > 2$
4	KIV	A	701	2	7,7,7	2.38	1 (14%)	8,9,9	1.10	1 (12%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	KIV	B	702	2	7,7,7	2.47	1 (14%)	8,9,9	0.92	0

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
4	KIV	A	701	2	-	0/7/8/8	-
4	KIV	B	702	2	-	0/7/8/8	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	702	KIV	C2-C1	-6.40	1.47	1.54
4	A	701	KIV	C2-C1	-6.20	1.47	1.54

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	701	KIV	O1-C1-O2	-2.08	118.95	123.90

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 [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	562/644 (87%)	0.06	17 (3%) 52 51	25, 38, 55, 72	0
1	B	566/644 (87%)	-0.05	9 (1%) 70 70	25, 37, 55, 64	0
All	All	1128/1288 (87%)	0.01	26 (2%) 61 60	25, 37, 55, 72	0

All (26) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	563	ASP	5.5
1	A	565	ALA	4.4
1	A	564	ASP	3.8
1	B	579	SER	3.4
1	A	434	LYS	3.3
1	A	562	GLY	3.3
1	B	57	ARG	3.1
1	A	396	ALA	2.9
1	B	18	THR	2.8
1	A	615	SER	2.7
1	B	561	ALA	2.7
1	B	545	VAL	2.6
1	A	458	SER	2.6
1	A	461	ILE	2.5
1	A	464	ILE	2.5
1	A	561	ALA	2.4
1	B	429	ASN	2.4
1	A	56	ILE	2.4
1	B	564	ASP	2.4
1	A	643	ALA	2.3
1	A	577	ILE	2.3
1	A	460	VAL	2.3
1	A	546	GLY	2.2
1	B	578	ALA	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	439	TYR	2.1
1	A	28	VAL	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 oligosaccharides 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. 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	B-factors($\text{\AA}^2$)	Q<0.9
4	KIV	A	701	8/8	0.93	0.08	33,37,38,38	0
3	CL	A	705	1/1	0.94	0.26	39,39,39,39	1
4	KIV	B	702	8/8	0.95	0.08	29,35,39,40	0
2	ZN	B	703	1/1	0.99	0.04	35,35,35,35	0
2	ZN	A	704	1/1	0.99	0.02	39,39,39,39	0

6.5 Other polymers [i](#)

There are no such residues in this entry.