



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 4, 2026 – 09:57 PM UTC

PDB ID : 1CNZ / pdb_00001cnz
Title : 3-ISOPROPYLMALATE DEHYDROGENASE (IPMDH) FROM
SALMONELLA TYPHIMURIUM
Authors : Wallon, G.; Kryger, G.; Lovett, S.T.; Oshima, T.; Ringe, D.; Petsko, G.A.
Deposited on : 1999-05-24
Resolution : 1.76 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)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

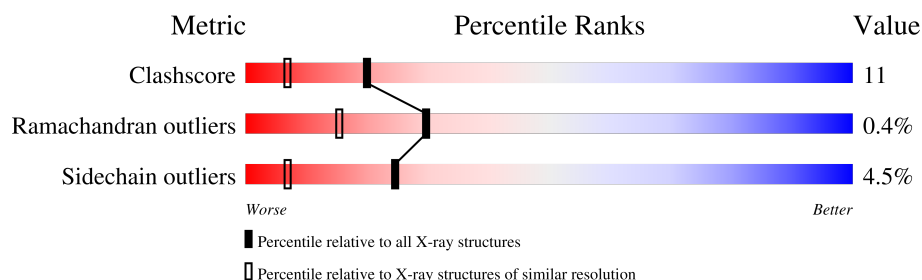
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.76 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))
Clashscore	190562	3299 (1.76-1.76)
Ramachandran outliers	187476	3274 (1.76-1.76)
Sidechain outliers	187428	3274 (1.76-1.76)

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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	363	 80% 16% . .
1	B	363	 83% 16% .

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 6229 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 PROTEIN (3-ISOPROPYLMALATE DEHYDROGENASE).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	363	Total	C	N	O	S	0	0	0
			2776	1747	486	528	15			
1	B	363	Total	C	N	O	S	0	0	0
			2776	1747	486	528	15			

- Molecule 2 is MANGANESE (II) ION (CCD ID: MN) (formula: Mn).

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

- Molecule 3 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



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

- Molecule 4 is water.

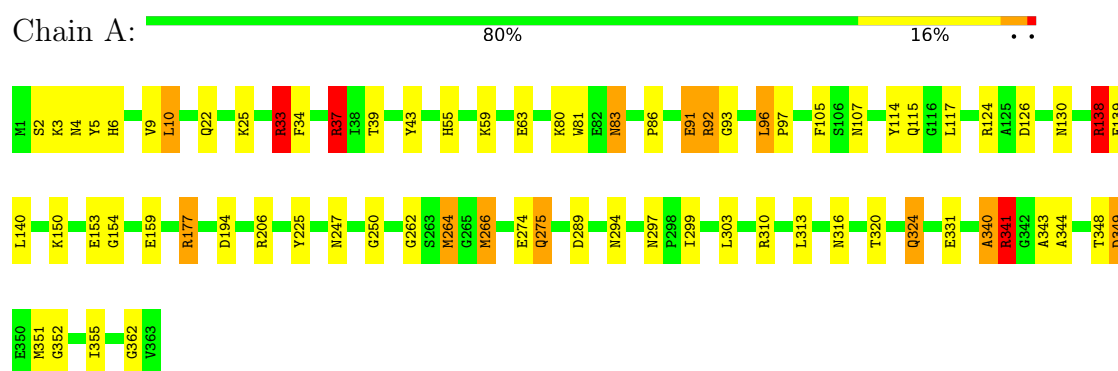
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	287	Total O 287 287	0	0
4	B	348	Total O 348 348	0	0

3 Residue-property plots

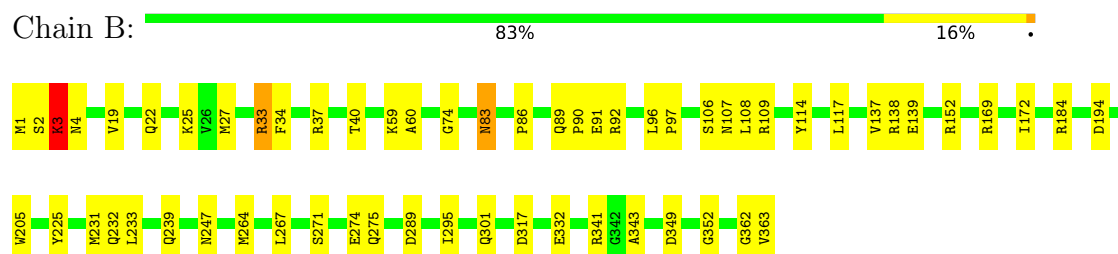
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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. 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.

Note EDS was not executed.

• Molecule 1: PROTEIN (3-ISOPROPYLMALATE DEHYDROGENASE)



• Molecule 1: PROTEIN (3-ISOPROPYLMALATE DEHYDROGENASE)



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	75.90Å 100.80Å 109.30Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	6.00 – 1.76	Depositor
% Data completeness (in resolution range)	79.0 (6.00-1.76)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
Refinement program	X-PLOR 3.1	Depositor
R, R_{free}	0.198 , 0.257	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	6229	wwPDB-VP
Average B, all atoms (Å ²)	18.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MN, 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	0.77	1/2828 (0.0%)	1.02	7/3825 (0.2%)
1	B	0.79	2/2828 (0.1%)	0.95	3/3825 (0.1%)
All	All	0.78	3/5656 (0.1%)	0.98	10/7650 (0.1%)

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	A	0	2
1	B	0	1
All	All	0	3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	231	MET	SD-CE	-6.31	1.63	1.79
1	B	90	PRO	C-O	5.78	1.32	1.24
1	A	81	TRP	NE1-CE2	-5.39	1.31	1.37

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	33	ARG	CD-NE-CZ	7.75	135.26	124.40
1	A	340	ALA	N-CA-C	-7.51	103.96	113.72
1	B	89	GLN	CA-C-N	7.19	126.71	119.24
1	B	89	GLN	C-N-CA	7.19	126.71	119.24
1	A	340	ALA	O-C-N	6.54	130.40	122.35
1	A	37	ARG	CD-NE-CZ	5.90	132.66	124.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	341	ARG	CD-NE-CZ	5.38	131.93	124.40
1	A	349	ASP	N-CA-C	5.34	116.78	111.07
1	A	341	ARG	NE-CZ-NH2	5.29	123.96	119.20
1	A	33	ARG	NE-CZ-NH1	5.20	126.70	121.50

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	138	ARG	Sidechain
1	A	206	ARG	Sidechain
1	B	184	ARG	Sidechain

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	2776	0	2762	68	3
1	B	2776	0	2762	60	3
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	20	0	0	1	0
3	B	20	0	0	0	0
4	A	287	0	0	10	1
4	B	348	0	0	6	1
All	All	6229	0	5524	127	4

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 11.

All (127) 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:4:ASN:HB2	1:A:37:ARG:NH2	1.46	1.26
1:A:92:ARG:CD	1:A:92:ARG:C	2.21	1.12

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:92:ARG:O	1:A:92:ARG:HD3	1.55	1.04
1:A:274:GLU:HB3	4:A:1107:HOH:O	1.61	1.00
1:B:4:ASN:HB2	1:B:37:ARG:NH2	1.81	0.96
1:A:92:ARG:C	1:A:92:ARG:HD3	1.87	0.94
1:A:4:ASN:CB	1:A:37:ARG:NH2	2.31	0.93
1:A:275:GLN:HA	1:A:275:GLN:OE1	1.68	0.92
1:A:4:ASN:HB2	1:A:37:ARG:HH21	1.12	0.91
1:A:92:ARG:C	1:A:92:ARG:HD2	1.95	0.89
1:A:4:ASN:CB	1:A:37:ARG:HH21	1.85	0.89
1:B:275:GLN:N	1:B:275:GLN:OE1	2.07	0.88
1:A:275:GLN:OE1	1:A:275:GLN:CA	2.21	0.87
1:A:92:ARG:CD	1:A:92:ARG:O	2.20	0.87
1:B:4:ASN:HB2	1:B:37:ARG:HH21	1.38	0.86
1:A:4:ASN:HB2	1:A:37:ARG:CZ	2.07	0.83
1:B:2:SER:O	1:B:3:LYS:HB2	1.79	0.82
1:B:83:ASN:HD22	1:B:83:ASN:H	1.29	0.81
1:B:74:GLY:HA2	1:B:301:GLN:HE22	1.47	0.78
1:B:3:LYS:NZ	1:B:37:ARG:HD3	1.98	0.77
1:A:33:ARG:NH1	4:A:1175:HOH:O	2.18	0.76
1:B:91:GLU:HG2	4:B:981:HOH:O	1.85	0.76
1:A:341:ARG:NH2	4:A:1192:HOH:O	2.09	0.75
1:A:107:ASN:HB2	1:A:140:LEU:HD22	1.69	0.74
1:B:138:ARG:HH11	1:B:247:ASN:HD21	1.32	0.74
1:A:310:ARG:HE	1:A:316:ASN:HD22	1.40	0.70
1:A:33:ARG:NH2	1:A:34:PHE:CZ	2.59	0.70
1:B:349:ASP:HB2	4:B:1127:HOH:O	1.91	0.70
1:B:22:GLN:HE21	1:B:352:GLY:HA3	1.58	0.69
1:A:96:LEU:HB2	1:A:97:PRO:HD3	1.74	0.69
1:B:22:GLN:HE22	1:B:25:LYS:NZ	1.90	0.69
1:A:150:LYS:HE2	4:A:1097:HOH:O	1.92	0.69
1:A:138:ARG:HG3	1:A:250:GLY:HA3	1.73	0.69
1:A:22:GLN:HE21	1:A:352:GLY:HA3	1.59	0.68
1:B:3:LYS:HZ1	1:B:37:ARG:CD	2.06	0.68
1:A:92:ARG:HD2	1:A:93:GLY:N	2.09	0.68
1:A:59:LYS:O	1:A:63:GLU:HG3	1.93	0.67
1:B:3:LYS:HG2	1:B:37:ARG:HD3	1.75	0.66
1:B:3:LYS:NZ	1:B:37:ARG:CD	2.58	0.66
1:B:232:GLN:HE21	1:B:239:GLN:HE22	1.44	0.66
1:B:1:MET:SD	4:B:1059:HOH:O	2.53	0.65
1:A:320:THR:O	1:A:324:GLN:HG2	1.99	0.61
1:A:275:GLN:OE1	1:A:275:GLN:N	2.33	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:310:ARG:HE	1:A:316:ASN:ND2	1.99	0.59
1:B:3:LYS:CE	1:B:37:ARG:HD3	2.32	0.59
1:B:138:ARG:HH11	1:B:247:ASN:ND2	1.99	0.59
1:A:9:VAL:C	1:A:10:LEU:HD23	2.27	0.58
1:A:274:GLU:C	1:A:275:GLN:OE1	2.47	0.58
1:A:159:GLU:OE1	1:B:169:ARG:NH2	2.37	0.56
1:A:33:ARG:HH11	1:A:362:GLY:HA2	1.70	0.56
1:A:114:TYR:HB2	1:A:117:LEU:HD12	1.88	0.55
1:A:139:GLU:O	1:A:247:ASN:HA	2.07	0.55
1:B:33:ARG:CD	1:B:363:VAL:HB	2.38	0.54
1:B:92:ARG:HA	1:B:96:LEU:HD13	1.89	0.54
1:A:351:MET:O	1:A:355:ILE:HG12	2.08	0.53
1:B:3:LYS:HZ1	1:B:37:ARG:HD2	1.74	0.53
1:A:22:GLN:HE22	1:A:25:LYS:NZ	2.07	0.53
1:B:96:LEU:HB2	1:B:97:PRO:HD3	1.91	0.52
1:A:5:TYR:CD2	1:A:313:LEU:HD22	2.44	0.52
1:B:83:ASN:HD22	1:B:83:ASN:N	2.03	0.52
1:A:297:ASN:ND2	1:A:299:ILE:H	2.08	0.52
1:A:105:PHE:HE2	1:A:274:GLU:HG3	1.75	0.51
1:B:3:LYS:CG	1:B:37:ARG:HD3	2.41	0.51
1:A:274:GLU:CB	4:A:1107:HOH:O	2.38	0.51
1:A:3:LYS:O	1:A:3:LYS:HG2	2.10	0.50
1:A:105:PHE:CE2	1:A:274:GLU:HG3	2.46	0.50
1:A:124:ARG:HD2	1:A:126:ASP:OD1	2.11	0.50
1:B:2:SER:O	1:B:3:LYS:CB	2.52	0.50
1:B:138:ARG:HE	1:B:247:ASN:HD22	1.59	0.50
1:B:138:ARG:HE	1:B:247:ASN:ND2	2.10	0.49
1:A:86:PRO:O	1:A:92:ARG:HG3	2.12	0.49
1:B:4:ASN:CB	1:B:37:ARG:HH21	2.18	0.49
1:A:80:LYS:HG2	1:A:80:LYS:O	2.12	0.48
1:A:92:ARG:HD2	1:A:93:GLY:CA	2.44	0.48
1:B:33:ARG:HD3	1:B:363:VAL:O	2.14	0.48
1:B:96:LEU:HD12	1:B:96:LEU:H	1.79	0.48
1:B:27:MET:HE1	1:B:40:THR:CG2	2.45	0.47
1:B:138:ARG:NH1	1:B:247:ASN:HD21	2.07	0.47
1:A:6:HIS:HA	1:A:39:THR:O	2.15	0.46
1:A:177:ARG:NH2	3:A:908:SO4:O4	2.48	0.46
1:A:274:GLU:HG2	4:A:955:HOH:O	2.15	0.46
1:B:172:ILE:HD13	1:B:205:TRP:HA	1.96	0.46
1:B:83:ASN:H	1:B:83:ASN:ND2	2.07	0.46
1:A:343:ALA:O	1:A:344:ALA:HB3	2.14	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:59:LYS:HG3	1:B:60:ALA:N	2.30	0.45
1:A:91:GLU:HB3	4:A:1158:HOH:O	2.16	0.45
1:A:92:ARG:HD2	1:A:93:GLY:HA2	1.98	0.45
1:B:3:LYS:HB3	1:B:37:ARG:CZ	2.46	0.45
1:A:264:MET:HG3	4:A:1189:HOH:O	2.16	0.45
1:A:55:HIS:HB3	4:A:1153:HOH:O	2.16	0.45
1:B:106:SER:O	1:B:271:SER:HA	2.17	0.45
1:B:19:VAL:HG23	1:B:301:GLN:HE21	1.81	0.45
1:A:262:GLY:HA2	4:A:1190:HOH:O	2.15	0.45
1:B:114:TYR:HB2	1:B:117:LEU:HD12	1.99	0.45
1:B:317:ASP:HB2	4:B:1061:HOH:O	2.17	0.45
1:B:33:ARG:HG2	1:B:34:PHE:CE1	2.51	0.44
1:B:362:GLY:O	1:B:363:VAL:HG23	2.16	0.44
1:B:22:GLN:NE2	1:B:352:GLY:HA3	2.30	0.44
1:B:194:ASP:O	1:B:225:TYR:HA	2.17	0.44
1:B:169:ARG:NH2	4:B:1172:HOH:O	2.50	0.44
1:B:139:GLU:O	1:B:247:ASN:HA	2.18	0.44
1:B:264:MET:HE2	1:B:264:MET:HB2	1.77	0.44
1:A:10:LEU:HD22	1:A:43:TYR:HB2	2.00	0.44
1:A:297:ASN:C	1:A:297:ASN:HD22	2.26	0.44
1:A:340:ALA:C	1:A:341:ARG:HG2	2.43	0.44
1:B:107:ASN:HD21	1:B:109:ARG:HG3	1.82	0.44
1:B:108:LEU:HD22	1:B:137:VAL:HG22	2.00	0.44
1:A:2:SER:CB	1:A:37:ARG:H	2.31	0.43
1:A:194:ASP:O	1:A:225:TYR:HA	2.18	0.43
1:B:264:MET:HA	1:B:267:LEU:HD12	2.01	0.43
1:B:33:ARG:HD3	1:B:363:VAL:HB	2.00	0.43
1:B:96:LEU:HD12	1:B:96:LEU:N	2.33	0.43
1:B:3:LYS:HG2	1:B:37:ARG:CD	2.48	0.42
1:A:340:ALA:O	1:A:341:ARG:HG3	2.20	0.42
1:B:232:GLN:NE2	1:B:239:GLN:HE22	2.14	0.42
1:A:340:ALA:O	1:A:341:ARG:CG	2.68	0.42
1:A:340:ALA:C	1:A:341:ARG:CG	2.93	0.41
1:A:6:HIS:CE1	1:A:39:THR:HG22	2.55	0.41
1:A:117:LEU:CD1	1:A:266:MET:HE2	2.51	0.41
1:A:153:GLU:HG2	1:A:154:GLY:N	2.35	0.41
1:B:4:ASN:H	1:B:37:ARG:HB2	1.86	0.41
1:A:3:LYS:O	1:A:3:LYS:CG	2.68	0.41
1:B:274:GLU:HG3	4:B:1177:HOH:O	2.20	0.41
1:A:303:LEU:HD23	1:A:303:LEU:HA	1.91	0.40
1:B:22:GLN:HE22	1:B:25:LYS:HZ2	1.64	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:22:GLN:HE22	1:B:25:LYS:HZ1	1.69	0.40
1:A:294:ASN:OD1	1:A:348:THR:HB	2.22	0.40

All (4) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:349:ASP:OD2	1:B:343:ALA:CB[3_645]	1.67	0.53
1:A:349:ASP:CG	1:B:343:ALA:CB[3_645]	1.96	0.24
1:A:349:ASP:OD1	1:B:343:ALA:CB[3_645]	1.96	0.24
4:A:1180:HOH:O	4:B:1136:HOH:O[3_645]	2.19	0.01

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	361/363 (99%)	345 (96%)	14 (4%)	2 (1%)	21	8
1	B	361/363 (99%)	347 (96%)	13 (4%)	1 (0%)	36	21
All	All	722/726 (99%)	692 (96%)	27 (4%)	3 (0%)	30	15

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	3	LYS
1	A	83	ASN
1	A	33	ARG

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	289/289 (100%)	272 (94%)	17 (6%)	18 4
1	B	289/289 (100%)	280 (97%)	9 (3%)	35 15
All	All	578/578 (100%)	552 (96%)	26 (4%)	24 7

All (26) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	10	LEU
1	A	37	ARG
1	A	83	ASN
1	A	91	GLU
1	A	92	ARG
1	A	96	LEU
1	A	115	GLN
1	A	130	ASN
1	A	138	ARG
1	A	177	ARG
1	A	264	MET
1	A	266	MET
1	A	275	GLN
1	A	289	ASP
1	A	324	GLN
1	A	331	GLU
1	A	341	ARG
1	B	3	LYS
1	B	33	ARG
1	B	83	ASN
1	B	86	PRO
1	B	152	ARG
1	B	233	LEU
1	B	289	ASP
1	B	295	ILE
1	B	332	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	22	GLN
1	A	55	HIS
1	A	107	ASN
1	A	228	ASN
1	A	232	GLN
1	A	239	GLN
1	A	297	ASN
1	A	316	ASN
1	A	324	GLN
1	B	22	GLN
1	B	83	ASN
1	B	107	ASN
1	B	157	GLN
1	B	228	ASN
1	B	232	GLN
1	B	247	ASN
1	B	301	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](#)

Of 10 ligands modelled in this entry, 2 are monoatomic - leaving 8 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	SO4	A	907	-	4,4,4	0.44	0	6,6,6	0.40	0
3	SO4	A	903	-	4,4,4	0.51	0	6,6,6	0.28	0
3	SO4	B	904	-	4,4,4	0.40	0	6,6,6	0.87	0
3	SO4	A	902	-	4,4,4	0.51	0	6,6,6	0.47	0
3	SO4	A	908	-	4,4,4	0.49	0	6,6,6	0.11	0
3	SO4	B	905	-	4,4,4	0.55	0	6,6,6	0.35	0
3	SO4	B	906	-	4,4,4	0.54	0	6,6,6	0.49	0
3	SO4	B	901	-	4,4,4	0.44	0	6,6,6	0.20	0

There are no bond length outliers.

There are no bond angle outliers.

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	A	908	SO4	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

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.