



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 07:37 AM GMT

PDB ID : 3BIC
Title : Crystal structure of human methylmalonyl-CoA mutase
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Deposited on : 2007-11-30
Resolution : 2.60 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

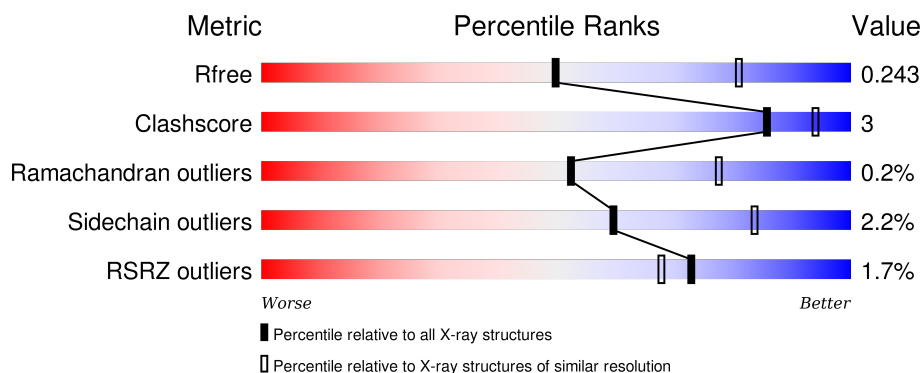
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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	2328 (2.60-2.60)
Clashscore	102246	2679 (2.60-2.60)
Ramachandran outliers	100387	2635 (2.60-2.60)
Sidechain outliers	100360	2635 (2.60-2.60)
RSRZ outliers	91569	2334 (2.60-2.60)

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	762	<div> <div>2%</div> <div>85%</div> <div>8%</div> <div>6%</div> </div>
1	B	762	<div> <div>%</div> <div>87%</div> <div>6%</div> <div>6%</div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 10752 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 Methylmalonyl-CoA mutase, mitochondrial precursor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	715	Total	C	N	O	S	0	2	0
			5340	3396	908	1007	29			
1	B	715	Total	C	N	O	S	0	1	0
			5324	3376	909	1008	31			

There are 48 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	11	MET	-	EXPRESSION TAG	UNP P22033
A	499	THR	ALA	VARIANT	UNP P22033
A	751	ALA	-	EXPRESSION TAG	UNP P22033
A	752	GLU	-	EXPRESSION TAG	UNP P22033
A	753	ASN	-	EXPRESSION TAG	UNP P22033
A	754	LEU	-	EXPRESSION TAG	UNP P22033
A	755	TYR	-	EXPRESSION TAG	UNP P22033
A	756	PHE	-	EXPRESSION TAG	UNP P22033
A	757	GLN	-	EXPRESSION TAG	UNP P22033
A	758	SER	-	EXPRESSION TAG	UNP P22033
A	759	HIS	-	EXPRESSION TAG	UNP P22033
A	760	HIS	-	EXPRESSION TAG	UNP P22033
A	761	HIS	-	EXPRESSION TAG	UNP P22033
A	762	HIS	-	EXPRESSION TAG	UNP P22033
A	763	HIS	-	EXPRESSION TAG	UNP P22033
A	764	HIS	-	EXPRESSION TAG	UNP P22033
A	765	ASP	-	EXPRESSION TAG	UNP P22033
A	766	TYR	-	EXPRESSION TAG	UNP P22033
A	767	LYS	-	EXPRESSION TAG	UNP P22033
A	768	ASP	-	EXPRESSION TAG	UNP P22033
A	769	ASP	-	EXPRESSION TAG	UNP P22033
A	770	ASP	-	EXPRESSION TAG	UNP P22033
A	771	ASP	-	EXPRESSION TAG	UNP P22033
A	772	LYS	-	EXPRESSION TAG	UNP P22033
B	11	MET	-	EXPRESSION TAG	UNP P22033

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Chain	Residue	Modelled	Actual	Comment	Reference
B	499	THR	ALA	VARIANT	UNP P22033
B	751	ALA	-	EXPRESSION TAG	UNP P22033
B	752	GLU	-	EXPRESSION TAG	UNP P22033
B	753	ASN	-	EXPRESSION TAG	UNP P22033
B	754	LEU	-	EXPRESSION TAG	UNP P22033
B	755	TYR	-	EXPRESSION TAG	UNP P22033
B	756	PHE	-	EXPRESSION TAG	UNP P22033
B	757	GLN	-	EXPRESSION TAG	UNP P22033
B	758	SER	-	EXPRESSION TAG	UNP P22033
B	759	HIS	-	EXPRESSION TAG	UNP P22033
B	760	HIS	-	EXPRESSION TAG	UNP P22033
B	761	HIS	-	EXPRESSION TAG	UNP P22033
B	762	HIS	-	EXPRESSION TAG	UNP P22033
B	763	HIS	-	EXPRESSION TAG	UNP P22033
B	764	HIS	-	EXPRESSION TAG	UNP P22033
B	765	ASP	-	EXPRESSION TAG	UNP P22033
B	766	TYR	-	EXPRESSION TAG	UNP P22033
B	767	LYS	-	EXPRESSION TAG	UNP P22033
B	768	ASP	-	EXPRESSION TAG	UNP P22033
B	769	ASP	-	EXPRESSION TAG	UNP P22033
B	770	ASP	-	EXPRESSION TAG	UNP P22033
B	771	ASP	-	EXPRESSION TAG	UNP P22033
B	772	LYS	-	EXPRESSION TAG	UNP P22033

- Molecule 2 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	2	Total Cl 2 2	0	0
2	A	2	Total Cl 2 2	0	0

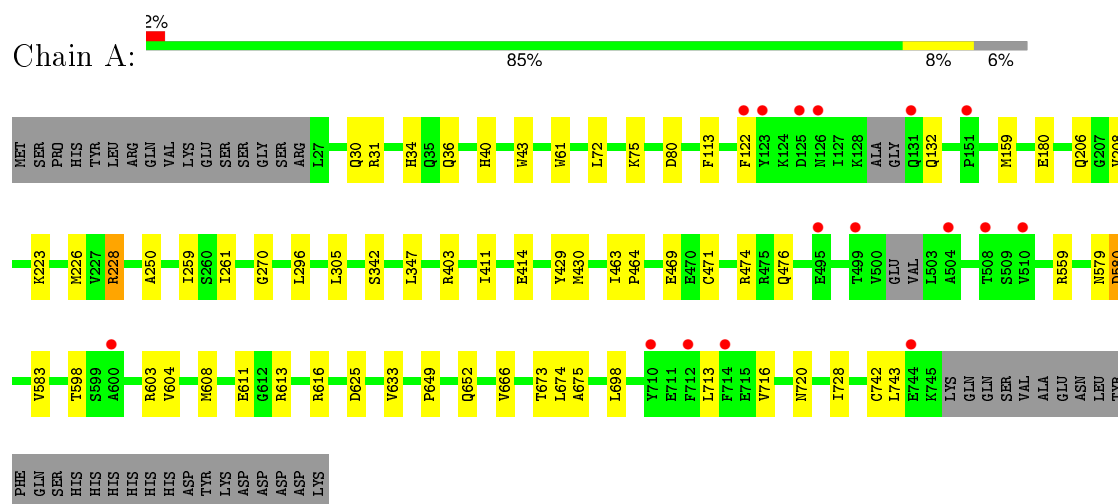
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	33	Total O 33 33	0	0
3	B	51	Total O 51 51	0	0

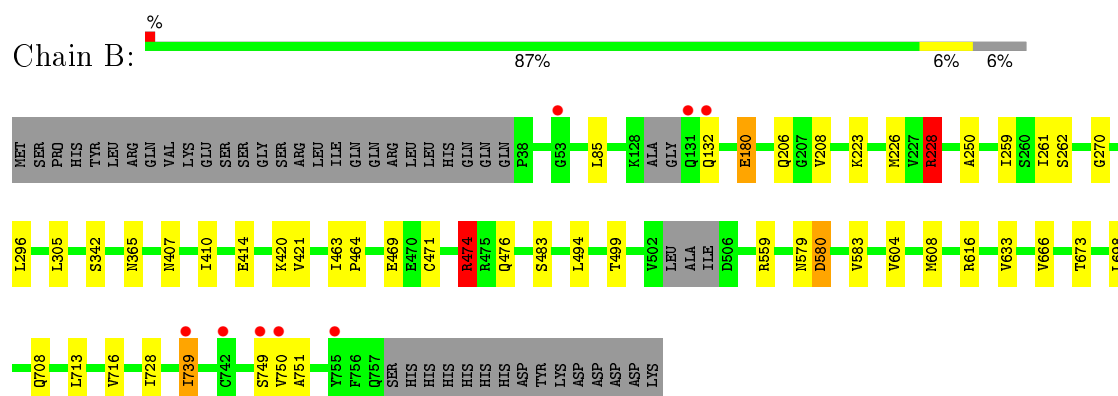
3 Residue-property plots

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 ($RSRZ > 2$). 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: Methylmalonyl-CoA mutase, mitochondrial precursor



- Molecule 1: Methylmalonyl-CoA mutase, mitochondrial precursor



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	103.75Å 95.15Å 119.16Å 90.00° 108.31° 90.00°	Depositor
Resolution (Å)	37.42 – 2.60 37.43 – 2.60	Depositor EDS
% Data completeness (in resolution range)	99.5 (37.42-2.60) 99.6 (37.43-2.60)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	0.12	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.68 (at 2.61Å)	Xtriage
Refinement program	REFMAC 5.3.0040	Depositor
R, R_{free}	0.217 , 0.243 0.221 , 0.243	Depositor DCC
R_{free} test set	1152 reflections (1.73%)	DCC
Wilson B-factor (Å ²)	44.5	Xtriage
Anisotropy	0.051	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 51.7	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 67598 reflections	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	10752	wwPDB-VP
Average B, all atoms (Å ²)	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.57% 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:
CL

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	0.41	0/5451	0.68	7/7407 (0.1%)
1	B	0.42	0/5431	0.70	7/7382 (0.1%)
All	All	0.42	0/10882	0.69	14/14789 (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	1
1	B	0	2
All	All	0	3

There are no bond length outliers.

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	474	ARG	NE-CZ-NH2	-19.12	110.74	120.30
1	B	228	ARG	NE-CZ-NH1	-19.00	110.80	120.30
1	A	228	ARG	NE-CZ-NH2	-18.03	111.28	120.30
1	B	228	ARG	NE-CZ-NH2	15.60	128.10	120.30
1	A	228	ARG	NE-CZ-NH1	15.60	128.10	120.30
1	A	474	ARG	NE-CZ-NH1	-15.35	112.63	120.30
1	A	474	ARG	NE-CZ-NH2	15.00	127.80	120.30
1	B	474	ARG	CD-NE-CZ	13.23	142.12	123.60
1	B	228	ARG	CD-NE-CZ	9.86	137.40	123.60
1	A	474	ARG	CD-NE-CZ	9.26	136.57	123.60
1	A	228	ARG	CD-NE-CZ	9.03	136.25	123.60
1	B	474	ARG	NE-CZ-NH1	6.69	123.65	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	474	ARG	CG-CD-NE	6.41	125.26	111.80
1	B	474	ARG	CG-CD-NE	-5.13	101.02	111.80

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	228	ARG	Sidechain
1	B	228	ARG	Sidechain
1	B	474	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	5340	0	5103	32	0
1	B	5324	0	5077	31	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
3	A	33	0	0	0	0
3	B	51	0	0	0	0
All	All	10752	0	10180	58	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 3.

All (58) 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:579:ASN:HA	1:A:580:ASP:CB	2.01	0.91
1:B:579:ASN:HA	1:B:580:ASP:HB2	1.63	0.80
1:A:604:VAL:HG12	1:A:608:MET:CE	2.14	0.78
1:B:579:ASN:HA	1:B:580:ASP:CB	2.14	0.78
1:B:604:VAL:HG12	1:B:608:MET:CE	2.26	0.64
1:A:43:TRP:CG	1:A:72:LEU:HD22	2.31	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:611:GLU:OE1	1:A:743:LEU:HD13	1.97	0.64
1:A:604:VAL:HG12	1:A:608:MET:HE2	1.80	0.63
1:B:223:LYS:HA	1:B:226:MET:HE3	1.82	0.60
1:A:223:LYS:HA	1:A:226:MET:HE3	1.84	0.59
1:B:579:ASN:CA	1:B:580:ASP:HB2	2.32	0.56
1:A:34:HIS:HA	1:A:80:ASP:OD2	2.07	0.55
1:B:604:VAL:HG12	1:B:608:MET:HE3	1.87	0.55
1:A:206:GLN:HB3	1:A:208:VAL:HG23	1.88	0.54
1:A:579:ASN:CA	1:A:580:ASP:CB	2.78	0.54
1:A:713:LEU:O	1:A:716:VAL:HG12	2.09	0.53
1:B:616:ARG:HG2	1:B:666:VAL:HG12	1.89	0.53
1:A:616:ARG:HG2	1:A:666:VAL:HG12	1.90	0.53
1:A:476:GLN:HG2	1:A:633:VAL:HG11	1.92	0.52
1:A:159:MET:HE2	1:A:675:ALA:HB1	1.92	0.52
1:A:61:TRP:CD2	1:B:420:LYS:HD3	2.45	0.51
1:A:633:VAL:HG12	1:A:728:ILE:HD11	1.93	0.51
1:B:270:GLY:O	1:B:471:CYS:HB3	2.11	0.50
1:A:259:ILE:HG23	1:A:305:LEU:HD23	1.93	0.50
1:B:633:VAL:HG12	1:B:728:ILE:HD11	1.93	0.50
1:B:713:LEU:O	1:B:716:VAL:HG12	2.12	0.49
1:B:499:THR:HG23	1:B:708:GLN:NE2	2.27	0.49
1:B:206:GLN:HB3	1:B:208:VAL:HG23	1.94	0.49
1:B:259:ILE:HG23	1:B:305:LEU:HD23	1.94	0.48
1:B:261:ILE:HD11	1:B:305:LEU:HD22	1.95	0.48
1:A:270:GLY:O	1:A:471:CYS:HB3	2.14	0.47
1:B:476:GLN:HG2	1:B:633:VAL:HG11	1.95	0.47
1:A:698:LEU:HD21	1:A:742:CYS:SG	2.55	0.47
1:A:40:HIS:CE1	1:B:85:LEU:HD11	2.50	0.46
1:A:261:ILE:HD11	1:A:305:LEU:HD22	1.98	0.46
1:B:471:CYS:HA	1:B:474:ARG:HH21	1.81	0.45
1:B:499:THR:HG23	1:B:708:GLN:HE21	1.81	0.45
1:A:113:PHE:HE2	1:A:122:PHE:CD1	2.36	0.44
1:A:43:TRP:CD2	1:A:72:LEU:HD22	2.52	0.44
1:B:407:ASN:HD22	1:B:410:ILE:HD12	1.83	0.44
1:B:698:LEU:HD12	1:B:739:ILE:HG22	1.99	0.43
1:B:469:GLU:HB3	1:B:583:VAL:HG21	2.00	0.43
1:B:463:ILE:HB	1:B:464:PRO:HD3	2.00	0.42
1:B:749:SER:C	1:B:751:ALA:H	2.23	0.42
1:A:430:MET:HG3	1:B:421:VAL:HG11	2.02	0.41
1:A:75:LYS:HA	1:A:429:TYR:CE2	2.54	0.41
1:A:625:ASP:CG	1:A:674:LEU:HD22	2.41	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:250:ALA:CB	1:A:296:LEU:HD21	2.51	0.41
1:A:469:GLU:HB3	1:A:583:VAL:HG21	2.02	0.41
1:A:403:ARG:CZ	1:B:494:LEU:HD21	2.51	0.41
1:A:347:LEU:HD23	1:A:347:LEU:C	2.41	0.41
1:A:463:ILE:HB	1:A:464:PRO:HD3	2.01	0.41
1:B:250:ALA:CB	1:B:296:LEU:HD21	2.50	0.41
1:B:579:ASN:CA	1:B:580:ASP:CB	2.89	0.41
1:B:180:GLU:HG3	1:B:208:VAL:HG22	2.03	0.40
1:A:649:PRO:O	1:A:652:GLN:HG3	2.21	0.40
1:B:259:ILE:CG2	1:B:305:LEU:HD23	2.52	0.40
1:A:411:ILE:HD11	1:B:365:ASN:HB3	2.03	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	711/762 (93%)	691 (97%)	19 (3%)	1 (0%)	56 81
1	B	710/762 (93%)	687 (97%)	21 (3%)	2 (0%)	46 72
All	All	1421/1524 (93%)	1378 (97%)	40 (3%)	3 (0%)	52 77

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	580	ASP
1	B	580	ASP
1	B	750	VAL

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	520/636 (82%)	507 (98%)	13 (2%)	55	81
1	B	522/636 (82%)	512 (98%)	10 (2%)	65	86
All	All	1042/1272 (82%)	1019 (98%)	23 (2%)	60	83

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	30	GLN
1	A	31	ARG
1	A	36	GLN
1	A	132	GLN
1	A	180	GLU
1	A	342	SER
1	A	414	GLU
1	A	559	ARG
1	A	598	THR
1	A	603	ARG
1	A	613	ARG
1	A	673	THR
1	A	720	ASN
1	B	132	GLN
1	B	180	GLU
1	B	228	ARG
1	B	262	SER
1	B	342	SER
1	B	414	GLU
1	B	483	SER
1	B	559	ARG
1	B	673	THR
1	B	739	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	30	GLN
1	A	36	GLN
1	A	132	GLN
1	A	206	GLN
1	A	407	ASN
1	A	605	HIS
1	B	132	GLN
1	B	206	GLN
1	B	407	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 4 ligands modelled in this entry, 4 are monoatomic - leaving 0 for Mogul analysis.

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.

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 ⓘ

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	715/762 (93%)	-0.03	16 (2%) 65 59	30, 40, 56, 68	0
1	B	715/762 (93%)	-0.10	8 (1%) 82 79	29, 40, 55, 65	0
All	All	1430/1524 (93%)	-0.06	24 (1%) 73 68	29, 40, 55, 68	0

All (24) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	504	ALA	6.1
1	A	126	ASN	4.3
1	A	131	GLN	3.7
1	B	131	GLN	3.3
1	A	714	PHE	3.2
1	A	744	GLU	2.7
1	B	132	GLN	2.7
1	A	600	ALA	2.6
1	A	510	VAL	2.6
1	B	749	SER	2.5
1	B	53	GLY	2.5
1	B	750	VAL	2.4
1	A	508	THR	2.4
1	A	710	TYR	2.4
1	A	499	THR	2.4
1	B	742	CYS	2.3
1	A	495	GLU	2.3
1	A	122	PHE	2.3
1	B	739	ILE	2.3
1	A	151	PRO	2.3
1	A	712	PHE	2.3
1	B	755	TYR	2.3
1	A	125	ASP	2.2
1	A	123	TYR	2.2

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
2	CL	B	802	1/1	0.99	0.26	-	41,41,41,41	0
2	CL	A	803	1/1	0.80	0.13	-	78,78,78,78	0
2	CL	A	801	1/1	0.98	0.21	-	45,45,45,45	0
2	CL	B	804	1/1	0.87	0.10	-	61,61,61,61	0

6.5 Other polymers [i](#)

There are no such residues in this entry.