



Full wwPDB X-ray Structure Validation Report ⓘ

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PDB ID : 3BIC / pdb_00003bic
Title : Crystal structure of human methylmalonyl-CoA mutase
Authors : Ugochukwu, E.; Kochan, G.; Pantic, N.; Parizotto, E.; Pilka, E.S.; Pike, A.C.W.; Gileadi, O.; von Delft, F.; Arrowsmith, C.H.; Weigelt, J.; Edwards, A.M.; Oppermann, U.; Structural Genomics Consortium (SGC)
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

<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

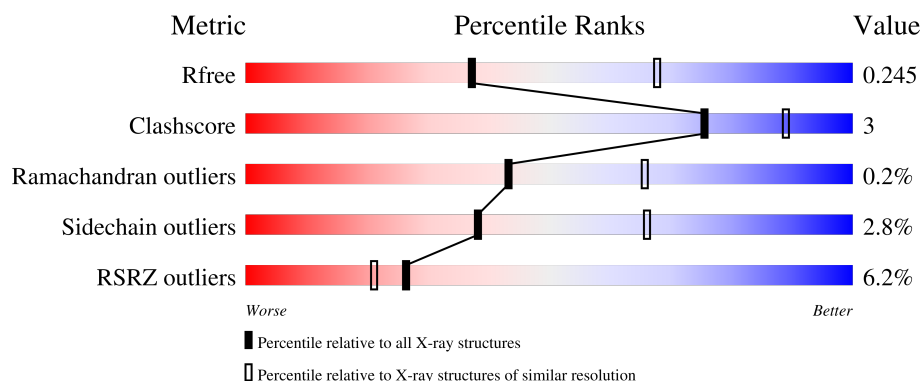
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

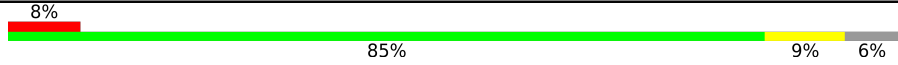
The reported resolution of this entry is 2.60 Å.

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}	180053	4008 (2.60-2.60)
Clashscore	190562	4347 (2.60-2.60)
Ramachandran outliers	187476	4277 (2.60-2.60)
Sidechain outliers	187428	4277 (2.60-2.60)
RSRZ outliers	180081	4008 (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 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	762	
1	B	762	

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 (CCD ID: CL) (formula: Cl).

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

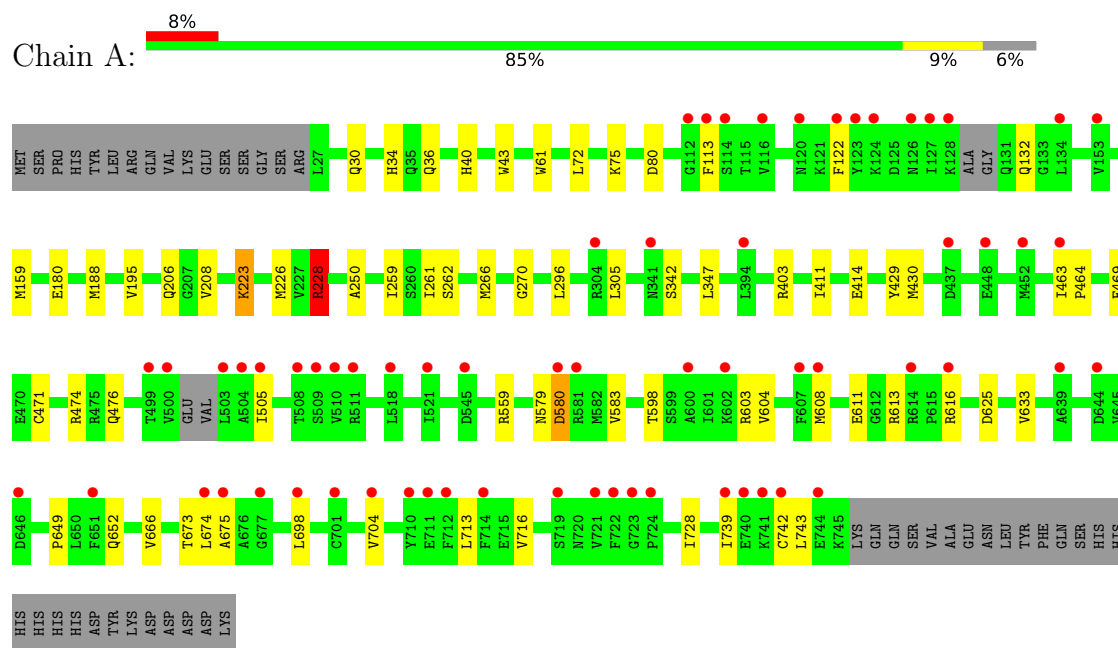
- Molecule 3 is water.

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

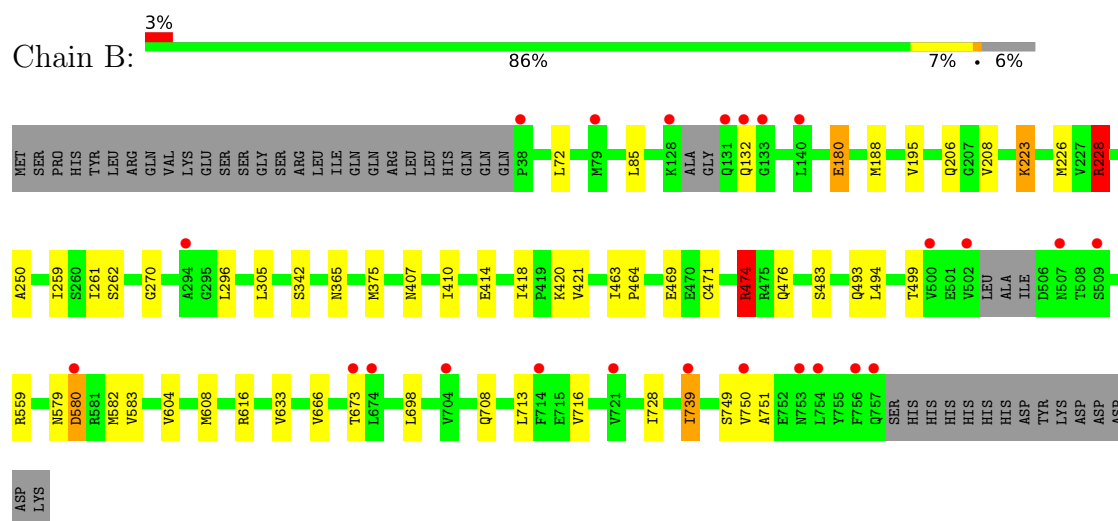
3 Residue-property plots [i](#)

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: 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 37.42 – 2.60	Depositor EDS
% Data completeness (in resolution range)	99.5 (37.42-2.60) 99.5 (37.42-2.60)	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 (Not available) , 0.245	Depositor DCC
R_{free} test set	1152 reflections (1.70%)	wwPDB-VP
Wilson B-factor (Å ²)	44.5	Xtriage
Anisotropy	0.051	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 50.6	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	0.92	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, 0.333 respectively for untwinned datasets, and 0.375, 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	0.55	0/5451	0.80	7/7407 (0.1%)
1	B	0.57	0/5431	0.81	5/7382 (0.1%)
All	All	0.56	0/10882	0.80	12/14789 (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 (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	474	ARG	CD-NE-CZ	12.66	142.12	124.40
1	B	228	ARG	NE-CZ-NH1	-10.70	110.80	121.50
1	B	228	ARG	NE-CZ-NH2	9.89	128.10	119.20
1	A	474	ARG	NE-CZ-NH2	9.55	127.80	119.20
1	B	474	ARG	NE-CZ-NH2	-9.40	110.74	119.20
1	B	228	ARG	CD-NE-CZ	9.29	137.40	124.40
1	A	474	ARG	NE-CZ-NH1	-8.87	112.63	121.50
1	A	228	ARG	NE-CZ-NH2	-8.79	111.28	119.20
1	A	474	ARG	CD-NE-CZ	8.69	136.57	124.40
1	A	228	ARG	CD-NE-CZ	8.46	136.25	124.40
1	A	228	ARG	NE-CZ-NH1	6.60	128.10	121.50
1	A	474	ARG	CG-CD-NE	6.03	125.26	112.00

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	35	0
1	B	5324	0	5077	32	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	62	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 (62) 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:A:188:MET:HE3	1:A:195:VAL:HG21	1.69	0.75
1:B:188:MET:HE3	1:B:195:VAL:HG21	1.70	0.74
1:A:159:MET:HE2	1:A:675:ALA:HB1	1.70	0.74
1:A:159:MET:HE1	1:A:505:ILE:HG21	1.78	0.64
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
1:A:611:GLU:OE1	1:A:743:LEU:HD13	1.97	0.64
1:B:223:LYS:HA	1:B:226:MET:HE3	1.83	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:604:VAL:HG12	1:A:608:MET:HE2	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:B:604:VAL:HG12	1:B:608:MET:HE3	1.87	0.56
1:A:34:HIS:HA	1:A:80:ASP:OD2	2.07	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:616:ARG:HG2	1:A:666:VAL:HG12	1.90	0.53
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:476:GLN:HG2	1:A:633:VAL:HG11	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:375:MET:HE3	1:B:418:ILE:CD1	2.44	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:B:749:SER:C	1:B:751:ALA:H	2.23	0.47
1:A:40:HIS:CE1	1:B:85:LEU:HD11	2.50	0.46
1:A:625:ASP:CG	1:A:674:LEU:HD22	2.41	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:347:LEU:C	1:A:347:LEU:HD23	2.41	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:A:262:SER:O	1:A:266:MET:HE3	2.19	0.43
1:B:463:ILE:HB	1:B:464:PRO:HD3	2.00	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

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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: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:A:649:PRO:O	1:A:652:GLN:HG3	2.21	0.40
1:B:180:GLU:HG3	1:B:208:VAL:HG22	2.03	0.40
1:A:411:ILE:HD11	1:B:365:ASN:HB3	2.03	0.40
1:B:259:ILE:CG2	1:B:305:LEU:HD23	2.52	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%)	48	70
1	B	710/762 (93%)	687 (97%)	21 (3%)	2 (0%)	36	58
All	All	1421/1524 (93%)	1378 (97%)	40 (3%)	3 (0%)	43	66

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 [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	520/636 (82%)	505 (97%)	15 (3%)	37	65
1	B	522/636 (82%)	508 (97%)	14 (3%)	39	67
All	All	1042/1272 (82%)	1013 (97%)	29 (3%)	38	66

All (29) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	30	GLN
1	A	36	GLN
1	A	132	GLN
1	A	180	GLU
1	A	223	LYS
1	A	228	ARG
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	704	VAL
1	A	739	ILE
1	B	72	LEU
1	B	132	GLN
1	B	180	GLU
1	B	223	LYS
1	B	228	ARG
1	B	262	SER
1	B	342	SER
1	B	414	GLU
1	B	483	SER
1	B	493	GLN
1	B	559	ARG
1	B	582	MET
1	B	673	THR
1	B	739	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	30	GLN
1	A	34	HIS
1	A	36	GLN
1	A	40	HIS
1	A	132	GLN
1	A	206	GLN
1	A	407	ASN
1	A	476	GLN
1	B	40	HIS
1	B	132	GLN
1	B	206	GLN
1	B	407	ASN
1	B	476	GLN
1	B	690	ASN
1	B	720	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

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 [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	715/762 (93%)	0.64	64 (8%)	15 11	18, 40, 56, 68	2 (0%)
1	B	715/762 (93%)	0.33	24 (3%)	48 42	20, 40, 55, 65	1 (0%)
All	All	1430/1524 (93%)	0.48	88 (6%)	26 21	18, 40, 55, 68	3 (0%)

All (88) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	126	ASN	4.8
1	B	131	GLN	4.7
1	A	123	TYR	4.6
1	B	674	LEU	4.4
1	B	750	VAL	4.4
1	A	504	ALA	4.0
1	A	644	ASP	3.7
1	B	757	GLN	3.7
1	A	500	VAL	3.7
1	A	674	LEU	3.6
1	B	704	VAL	3.4
1	A	127	ILE	3.4
1	B	79	MET	3.4
1	B	502	VAL	3.3
1	B	133	GLY	3.2
1	B	132	GLN	3.1
1	A	722	PHE	3.1
1	A	510	VAL	3.1
1	B	673	THR	3.0
1	A	710	TYR	3.0
1	A	113	PHE	3.0
1	A	122	PHE	3.0
1	A	714	PHE	2.9
1	A	602	LYS	2.9

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Mol	Chain	Res	Type	RSRZ
1	A	505	ILE	2.9
1	A	509	SER	2.9
1	A	124	LYS	2.9
1	A	128	LYS	2.9
1	A	607	PHE	2.9
1	B	38	PRO	2.8
1	A	719	SER	2.8
1	A	704	VAL	2.8
1	A	116	VAL	2.8
1	A	724	PRO	2.8
1	B	753	ASN	2.8
1	B	500	VAL	2.8
1	B	128	LYS	2.7
1	B	509	SER	2.7
1	B	739	ILE	2.6
1	A	394	LEU	2.6
1	A	112	GLY	2.6
1	A	698	LEU	2.6
1	A	600	ALA	2.6
1	A	712	PHE	2.6
1	A	521	ILE	2.5
1	A	114	SER	2.5
1	A	739	ILE	2.5
1	A	711	GLU	2.5
1	A	580	ASP	2.4
1	A	616	ARG	2.4
1	A	744	GLU	2.4
1	A	614	ARG	2.4
1	A	742	CYS	2.4
1	A	721	VAL	2.4
1	B	140	LEU	2.3
1	B	507	ASN	2.3
1	B	756	PHE	2.3
1	B	754	LEU	2.3
1	A	120	ASN	2.3
1	A	448	GLU	2.3
1	A	153	VAL	2.3
1	A	740	GLU	2.3
1	A	508	THR	2.2
1	B	721	VAL	2.2
1	A	639	ALA	2.2
1	A	723	GLY	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	580	ASP	2.2
1	B	294	ALA	2.2
1	A	701	CYS	2.2
1	A	304	ARG	2.2
1	A	651	PHE	2.2
1	A	452	MET	2.1
1	A	463	ILE	2.1
1	A	511	ARG	2.1
1	A	503	LEU	2.1
1	A	741	LYS	2.1
1	A	437	ASP	2.1
1	A	545	ASP	2.1
1	A	581	ARG	2.1
1	A	134	LEU	2.1
1	A	341	ASN	2.1
1	A	677	GLY	2.1
1	B	714	PHE	2.1
1	A	499	THR	2.0
1	A	646	ASP	2.0
1	A	675	ALA	2.0
1	A	608	MET	2.0
1	A	518	LEU	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(Å ²)	Q<0.9
2	CL	B	804	1/1	0.88	0.12	61,61,61,61	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	CL	A	803	1/1	0.89	0.10	78,78,78,78	0
2	CL	A	801	1/1	0.95	0.08	45,45,45,45	0
2	CL	B	802	1/1	0.97	0.06	41,41,41,41	0

6.5 Other polymers [i](#)

There are no such residues in this entry.