



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 03:50 AM UTC

PDB ID : 3E4P / pdb_00003e4p
Title : Crystal structure of malonate occupied DctB
Authors : Zhou, Y.F.; Nan, J.; Nan, B.Y.; Liang, Y.H.; Panjikar, S.; Su, X.D.
Deposited on : 2008-08-12
Resolution : 2.30 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

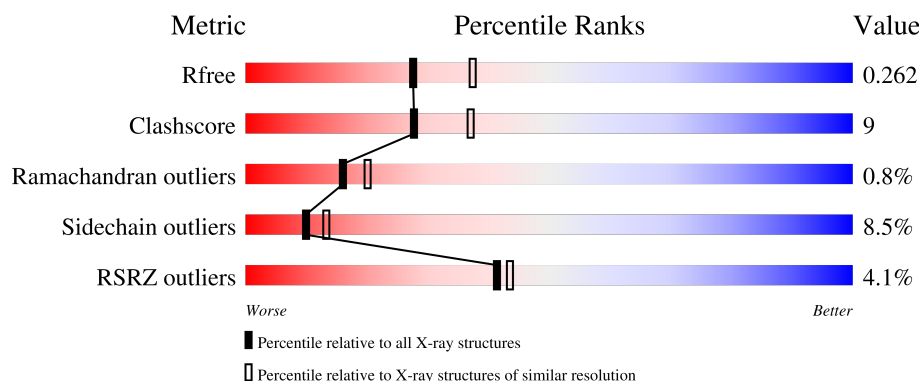
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	6319 (2.30-2.30)
Clashscore	190562	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (2.30-2.30)
RSRZ outliers	180081	6325 (2.30-2.30)

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	305	
1	B	305	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 3984 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 C4-dicarboxylate transport sensor protein dctB.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	254	Total	C	N	O	S	3	0	0
			1945	1232	349	360	4			
1	B	253	Total	C	N	O	S	0	0	0
			1909	1207	344	354	4			

There are 72 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	8	MET	-	expression tag	UNP P13633
A	9	GLY	-	expression tag	UNP P13633
A	10	SER	-	expression tag	UNP P13633
A	11	SER	-	expression tag	UNP P13633
A	12	HIS	-	expression tag	UNP P13633
A	13	HIS	-	expression tag	UNP P13633
A	14	HIS	-	expression tag	UNP P13633
A	15	HIS	-	expression tag	UNP P13633
A	16	HIS	-	expression tag	UNP P13633
A	17	HIS	-	expression tag	UNP P13633
A	18	SER	-	expression tag	UNP P13633
A	19	SER	-	expression tag	UNP P13633
A	20	GLY	-	expression tag	UNP P13633
A	21	LEU	-	expression tag	UNP P13633
A	22	VAL	-	expression tag	UNP P13633
A	23	PRO	-	expression tag	UNP P13633
A	24	ARG	-	expression tag	UNP P13633
A	25	GLY	-	expression tag	UNP P13633
A	26	SER	-	expression tag	UNP P13633
A	27	HIS	-	expression tag	UNP P13633
A	28	MET	-	expression tag	UNP P13633
A	29	ALA	-	expression tag	UNP P13633
A	30	SER	-	expression tag	UNP P13633
A	31	MET	-	expression tag	UNP P13633
A	32	THR	-	expression tag	UNP P13633

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Chain	Residue	Modelled	Actual	Comment	Reference
A	33	GLY	-	expression tag	UNP P13633
A	34	GLY	-	expression tag	UNP P13633
A	35	GLU	-	expression tag	UNP P13633
A	36	GLU	-	expression tag	UNP P13633
A	37	MET	-	expression tag	UNP P13633
A	38	GLY	-	expression tag	UNP P13633
A	39	ARG	-	expression tag	UNP P13633
A	40	GLY	-	expression tag	UNP P13633
A	41	SER	-	expression tag	UNP P13633
A	174	LYS	ASN	SEE REMARK 999	UNP P13633
A	309	ASN	LYS	SEE REMARK 999	UNP P13633
B	8	MET	-	expression tag	UNP P13633
B	9	GLY	-	expression tag	UNP P13633
B	10	SER	-	expression tag	UNP P13633
B	11	SER	-	expression tag	UNP P13633
B	12	HIS	-	expression tag	UNP P13633
B	13	HIS	-	expression tag	UNP P13633
B	14	HIS	-	expression tag	UNP P13633
B	15	HIS	-	expression tag	UNP P13633
B	16	HIS	-	expression tag	UNP P13633
B	17	HIS	-	expression tag	UNP P13633
B	18	SER	-	expression tag	UNP P13633
B	19	SER	-	expression tag	UNP P13633
B	20	GLY	-	expression tag	UNP P13633
B	21	LEU	-	expression tag	UNP P13633
B	22	VAL	-	expression tag	UNP P13633
B	23	PRO	-	expression tag	UNP P13633
B	24	ARG	-	expression tag	UNP P13633
B	25	GLY	-	expression tag	UNP P13633
B	26	SER	-	expression tag	UNP P13633
B	27	HIS	-	expression tag	UNP P13633
B	28	MET	-	expression tag	UNP P13633
B	29	ALA	-	expression tag	UNP P13633
B	30	SER	-	expression tag	UNP P13633
B	31	MET	-	expression tag	UNP P13633
B	32	THR	-	expression tag	UNP P13633
B	33	GLY	-	expression tag	UNP P13633
B	34	GLY	-	expression tag	UNP P13633
B	35	GLU	-	expression tag	UNP P13633
B	36	GLU	-	expression tag	UNP P13633
B	37	MET	-	expression tag	UNP P13633
B	38	GLY	-	expression tag	UNP P13633

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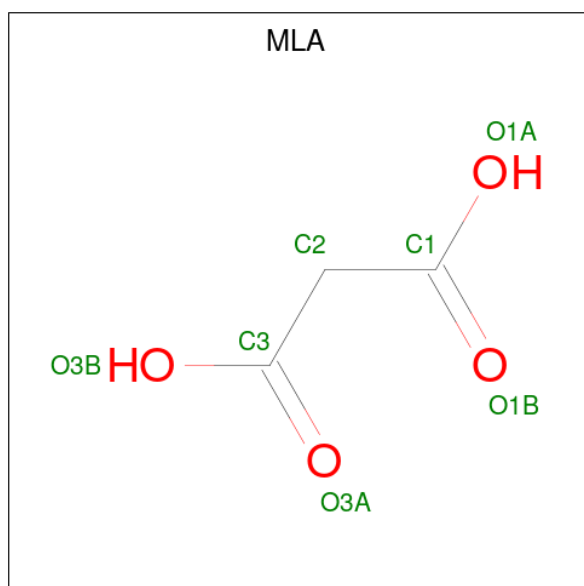
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Chain	Residue	Modelled	Actual	Comment	Reference
B	39	ARG	-	expression tag	UNP P13633
B	40	GLY	-	expression tag	UNP P13633
B	41	SER	-	expression tag	UNP P13633
B	174	LYS	ASN	SEE REMARK 999	UNP P13633
B	309	ASN	LYS	SEE REMARK 999	UNP P13633

- Molecule 2 is STRONTIUM ION (CCD ID: SR) (formula: Sr).

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

- Molecule 3 is MALONIC ACID (CCD ID: MLA) (formula: C₃H₄O₄).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 7 3 4	0	0
3	B	1	Total C O 7 3 4	0	0

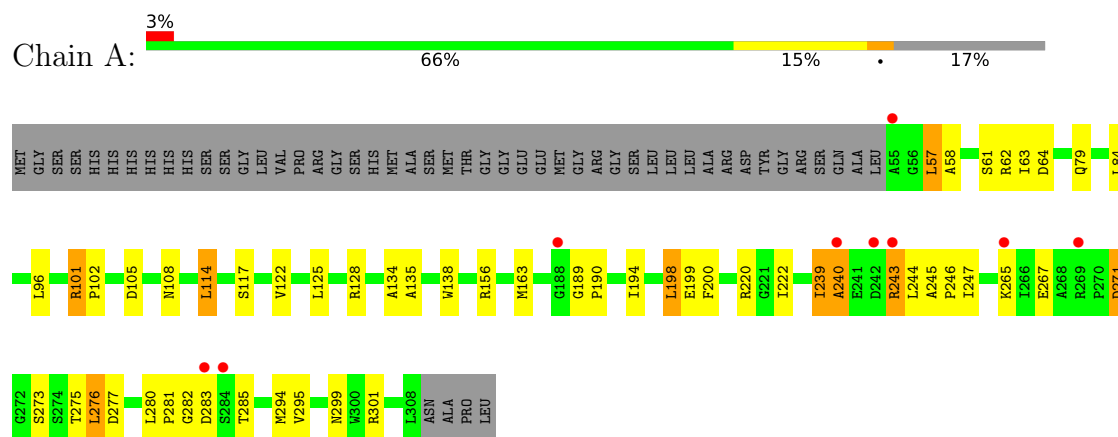
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	55	Total 55	O 55	0	0
4	B	58	Total 58	O 58	0	0

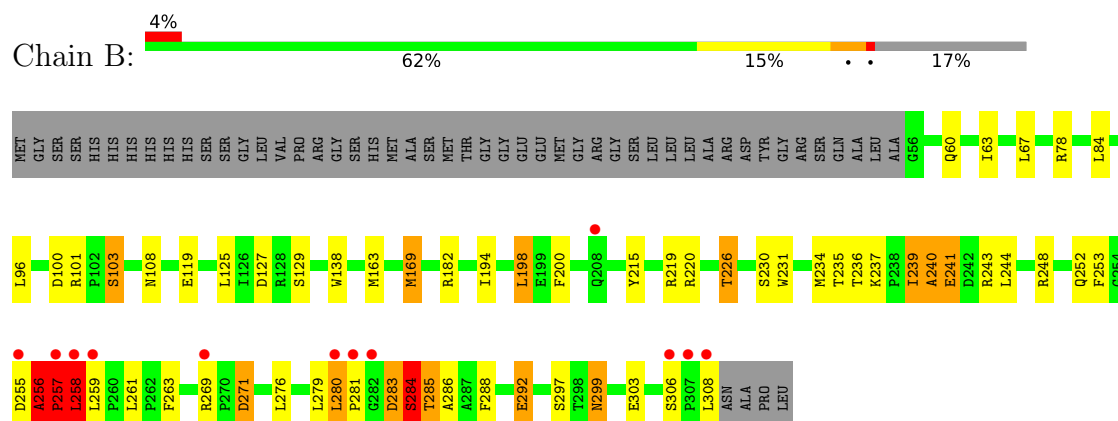
3 Residue-property plots [i](#)

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: C4-dicarboxylate transport sensor protein dctB



- Molecule 1: C4-dicarboxylate transport sensor protein dctB



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	57.98Å 39.10Å 111.54Å 90.00° 94.78° 90.00°	Depositor
Resolution (Å)	30.00 – 2.30 30.00 – 2.30	Depositor EDS
% Data completeness (in resolution range)	97.6 (30.00-2.30) 97.6 (30.00-2.30)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.47 (at 2.31Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.196 , 0.262 0.204 , 0.262	Depositor DCC
R_{free} test set	1142 reflections (5.18%)	wwPDB-VP
Wilson B-factor (Å ²)	32.5	Xtriage
Anisotropy	0.665	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 42.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	3984	wwPDB-VP
Average B, all atoms (Å ²)	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.81% 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: SR, MLA

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	0.86	1/1985 (0.1%)	1.09	9/2699 (0.3%)
1	B	0.88	0/1949	1.32	9/2649 (0.3%)
All	All	0.87	1/3934 (0.0%)	1.21	18/5348 (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	A	1	7
1	B	1	7
All	All	2	14

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	194	ILE	CA-CB	5.39	1.60	1.54

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	280	LEU	CA-C-N	-26.74	89.86	119.28
1	B	280	LEU	C-N-CA	-26.74	89.86	119.28
1	B	280	LEU	N-CA-C	9.53	130.88	109.81
1	B	280	LEU	C-N-CD	8.04	157.96	125.00
1	B	256	ALA	CA-C-N	-7.55	110.40	119.84
1	B	256	ALA	C-N-CA	-7.55	110.40	119.84
1	A	295	VAL	CA-C-N	-6.67	113.12	119.85
1	A	295	VAL	C-N-CA	-6.67	113.12	119.85

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	276	LEU	CA-CB-CG	6.17	137.90	116.30
1	B	256	ALA	N-CA-C	6.11	123.30	109.81
1	A	189	GLY	CA-C-N	5.69	125.62	119.76
1	A	189	GLY	C-N-CA	5.69	125.62	119.76
1	A	57	LEU	N-CA-C	-5.68	104.70	111.69
1	B	101	ARG	CA-C-N	-5.32	113.55	119.19
1	B	101	ARG	C-N-CA	-5.32	113.55	119.19
1	A	138	TRP	N-CA-C	5.30	117.80	111.71
1	A	294	MET	CA-C-N	-5.02	118.97	122.59
1	A	294	MET	C-N-CA	-5.02	118.97	122.59

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	240	ALA	CA
1	B	256	ALA	CA

All (14) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	239	ILE	Peptide
1	A	240	ALA	Peptide
1	A	271	ASP	Peptide
1	A	275	THR	Peptide
1	A	281	PRO	Peptide
1	A	282	GLY	Peptide
1	A	283	ASP	Peptide
1	B	256	ALA	Peptide
1	B	257	PRO	Peptide
1	B	258	LEU	Peptide
1	B	271	ASP	Peptide
1	B	279	LEU	Peptide
1	B	283	ASP	Peptide
1	B	284	SER	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	1945	0	1975	29	0
1	B	1909	0	1913	42	0
2	A	1	0	0	0	0
2	B	2	0	0	0	0
3	A	7	0	2	0	0
3	B	7	0	2	0	0
4	A	55	0	0	2	0
4	B	58	0	0	1	0
All	All	3984	0	3892	70	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 9.

All (70) 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:239:ILE:HG22	1:A:240:ALA:CB	1.69	1.23
1:A:239:ILE:CG2	1:A:240:ALA:HB3	1.68	1.22
1:B:256:ALA:CB	1:B:257:PRO:HD2	1.82	1.09
1:B:261:LEU:O	4:B:645:HOH:O	1.72	1.06
1:A:101:ARG:NH1	1:A:105:ASP:OD1	2.01	0.94
1:B:256:ALA:HB1	1:B:257:PRO:HD2	1.47	0.93
1:B:256:ALA:CB	1:B:257:PRO:CD	2.46	0.92
1:B:256:ALA:HB2	1:B:257:PRO:HD2	1.54	0.87
1:A:265:LYS:HD2	1:A:277:ASP:OD2	1.78	0.83
1:B:256:ALA:HB2	1:B:257:PRO:CD	2.09	0.78
1:B:215:TYR:HB3	1:B:226:THR:HG23	1.64	0.78
1:A:128:ARG:HD2	1:A:190:PRO:O	1.86	0.75
1:A:101:ARG:HD3	1:A:101:ARG:O	1.87	0.75
1:A:79:GLN:HG3	1:A:198:LEU:HG	1.70	0.73
1:A:245:ALA:HB3	1:A:246:PRO:HD3	1.69	0.73
1:A:243:ARG:O	1:A:247:ILE:HD12	1.90	0.71
1:B:239:ILE:HG13	1:B:240:ALA:N	2.05	0.71
1:B:299:ASN:HD22	1:B:299:ASN:C	1.98	0.71
1:A:267:GLU:OE1	4:A:720:HOH:O	2.11	0.68
1:B:169:MET:O	1:B:252:GLN:NE2	2.27	0.67
1:A:79:GLN:CG	1:A:198:LEU:HG	2.25	0.66
1:B:163:MET:HE3	1:B:182:ARG:NH1	2.12	0.65
1:B:286:ALA:HB3	1:B:288:PHE:CE2	2.33	0.64
1:A:58:ALA:O	1:A:62:ARG:HG3	1.99	0.61
1:B:258:LEU:HD23	1:B:258:LEU:H	1.67	0.60
1:B:256:ALA:O	1:B:257:PRO:C	2.46	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:239:ILE:O	1:B:240:ALA:HB2	2.02	0.59
1:B:244:LEU:O	1:B:248:ARG:HG3	2.03	0.58
1:B:256:ALA:O	1:B:257:PRO:O	2.21	0.58
1:B:239:ILE:HG23	1:B:240:ALA:H	1.69	0.57
1:B:292:GLU:HG3	1:B:303:GLU:HG2	1.86	0.56
1:A:108:ASN:ND2	1:A:135:ALA:H	2.07	0.53
1:B:256:ALA:HB1	1:B:257:PRO:CD	2.22	0.53
1:B:253:PHE:C	1:B:253:PHE:CD1	2.87	0.52
1:B:280:LEU:O	1:B:281:PRO:C	2.43	0.52
1:B:258:LEU:HD23	1:B:258:LEU:N	2.25	0.52
1:A:240:ALA:HB1	1:A:244:LEU:HG	1.93	0.51
1:B:100:ASP:OD1	1:B:103:SER:HB3	2.12	0.50
1:A:271:ASP:HB3	1:A:273:SER:H	1.77	0.50
1:B:241:GLU:C	1:B:243:ARG:H	2.20	0.49
1:A:198:LEU:HD13	1:A:200:PHE:CZ	2.48	0.49
1:A:96:LEU:HD11	1:A:125:LEU:HD11	1.95	0.49
1:A:61:SER:HB3	4:A:732:HOH:O	2.13	0.48
1:A:239:ILE:HG22	1:A:240:ALA:HB3	0.75	0.48
1:B:253:PHE:C	1:B:253:PHE:HD1	2.22	0.48
1:B:108:ASN:HB3	1:B:138:TRP:CD1	2.50	0.47
1:B:96:LEU:HD11	1:B:125:LEU:HD11	1.97	0.46
1:B:241:GLU:HA	1:B:244:LEU:HD12	1.98	0.45
1:A:198:LEU:HD13	1:A:200:PHE:CE1	2.50	0.45
1:A:101:ARG:HD3	1:A:101:ARG:C	2.37	0.45
1:A:63:ILE:HG13	1:A:64:ASP:N	2.32	0.45
1:B:127:ASP:OD1	1:B:129:SER:OG	2.33	0.44
1:A:198:LEU:HD22	1:A:199:GLU:O	2.17	0.44
1:A:114:LEU:HD12	1:B:84:LEU:HG	2.00	0.43
1:B:219:ARG:O	1:B:237:LYS:NZ	2.50	0.43
1:B:78:ARG:NH2	1:B:119:GLU:OE2	2.42	0.43
1:A:220:ARG:HB2	1:A:222:ILE:HD12	2.01	0.43
1:A:271:ASP:CB	1:A:273:SER:H	2.31	0.43
1:B:231:TRP:CE3	1:B:261:LEU:HD22	2.54	0.43
1:B:263:PHE:CD2	1:B:276:LEU:HD11	2.53	0.43
1:B:60:GLN:HA	1:B:63:ILE:HD12	2.01	0.42
1:B:299:ASN:C	1:B:299:ASN:ND2	2.71	0.42
1:A:108:ASN:HD21	1:A:134:ALA:HA	1.85	0.41
1:B:284:SER:HB3	1:B:285:THR:H	1.57	0.41
1:B:198:LEU:HD13	1:B:200:PHE:CZ	2.56	0.41
1:B:234:MET:SD	1:B:259:LEU:HB2	2.61	0.41
1:B:236:THR:HG22	1:B:261:LEU:HD12	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:79:GLN:HG2	1:A:198:LEU:HG	2.02	0.40
1:A:101:ARG:N	1:A:102:PRO:CD	2.84	0.40
1:B:269:ARG:C	1:B:271:ASP:N	2.78	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	252/305 (83%)	241 (96%)	11 (4%)	0	100	100
1	B	251/305 (82%)	235 (94%)	12 (5%)	4 (2%)	7	7
All	All	503/610 (82%)	476 (95%)	23 (5%)	4 (1%)	16	20

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	257	PRO
1	B	283	ASP
1	B	240	ALA
1	B	239	ILE

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	203/242 (84%)	188 (93%)	15 (7%)	13	17
1	B	196/242 (81%)	177 (90%)	19 (10%)	8	10
All	All	399/484 (82%)	365 (92%)	34 (8%)	10	13

All (34) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	57	LEU
1	A	84	LEU
1	A	101	ARG
1	A	114	LEU
1	A	117	SER
1	A	122	VAL
1	A	156	ARG
1	A	163	MET
1	A	198	LEU
1	A	243	ARG
1	A	276	LEU
1	A	280	LEU
1	A	285	THR
1	A	299	ASN
1	A	301	ARG
1	B	67	LEU
1	B	103	SER
1	B	169	MET
1	B	194	ILE
1	B	198	LEU
1	B	220	ARG
1	B	226	THR
1	B	230	SER
1	B	235	THR
1	B	241	GLU
1	B	255	ASP
1	B	258	LEU
1	B	284	SER
1	B	285	THR
1	B	292	GLU
1	B	297	SER
1	B	299	ASN
1	B	306	SER
1	B	308	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	79	GLN
1	A	108	ASN
1	A	299	ASN
1	B	299	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 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	$\# Z > 2$
3	MLA	B	601	-	6,6,6	2.44	2 (33%)	7,7,7	0.94	0
3	MLA	A	701	-	6,6,6	1.62	1 (16%)	7,7,7	1.05	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
3	MLA	B	601	-	-	0/4/4/4	-
3	MLA	A	701	-	-	0/4/4/4	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	601	MLA	C2-C1	4.26	1.57	1.51
3	B	601	MLA	C2-C3	2.71	1.55	1.51
3	A	701	MLA	O1A-C1	-2.29	1.23	1.30

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	254/305 (83%)	0.05	9 (3%) 47 49	11, 31, 45, 53	2 (0%)
1	B	253/305 (82%)	0.18	12 (4%) 36 38	22, 31, 50, 57	0
All	All	507/610 (83%)	0.11	21 (4%) 41 43	11, 31, 48, 57	2 (0%)

All (21) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	283	ASP	5.7
1	B	258	LEU	5.0
1	A	240	ALA	4.4
1	A	269	ARG	3.8
1	A	55	ALA	3.4
1	B	280	LEU	3.3
1	B	281	PRO	3.1
1	B	269	ARG	3.0
1	B	307	PRO	3.0
1	B	259	LEU	2.6
1	B	257	PRO	2.5
1	B	282	GLY	2.5
1	A	188	GLY	2.4
1	B	208	GLN	2.4
1	B	255	ASP	2.4
1	A	265	LYS	2.3
1	A	242	ASP	2.2
1	A	284	SER	2.1
1	B	308	LEU	2.0
1	B	306	SER	2.0
1	A	243	ARG	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
2	SR	A	502	1/1	0.95	0.07	43,43,43,43	1
3	MLA	A	701	7/7	0.95	0.07	25,26,30,30	0
3	MLA	B	601	7/7	0.96	0.08	21,23,24,25	0
2	SR	B	503	1/1	0.97	0.06	38,38,38,38	1
2	SR	B	501	1/1	0.98	0.04	54,54,54,54	1

6.5 Other polymers [i](#)

There are no such residues in this entry.