



Full wwPDB X-ray Structure Validation Report ⓘ

Jun 13, 2021 – 02:09 PM JST

PDB ID : 7EBC
Title : Crystal structure of Isocitrate lyase-1 from *Saccharomyces cerevisiae*
Authors : Hiragi, K.; Nishio, K.; Moriyama, S.; Hamaguchi, T.; Mizoguchi, A.; Yonekura, K.; Tani, K.; Mizushima, T.
Deposited on : 2021-03-09
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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.20
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.20

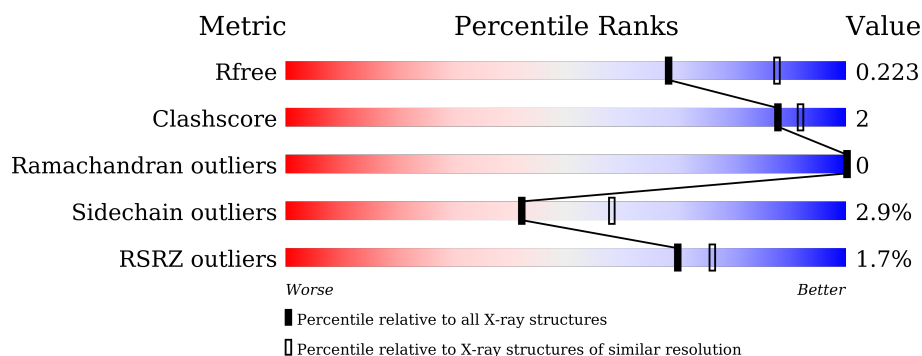
1 Overall quality at a glance

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}	130704	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (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	563	<div> <div>2%</div> <div>87% 5% • 7%</div> </div>
1	B	563	<div> <div>%</div> <div>88% 6% 6%</div> </div>
1	C	563	<div> <div>2%</div> <div>85% 7% • 7%</div> </div>
1	D	563	<div> <div>%</div> <div>87% 7% 6%</div> </div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 17254 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 Isocitrate lyase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	524	Total	C	N	O	S	0	0	0
			4158	2628	724	785	21			
1	B	527	Total	C	N	O	S	0	0	0
			4175	2638	727	789	21			
1	C	523	Total	C	N	O	S	0	0	0
			4154	2626	723	784	21			
1	D	527	Total	C	N	O	S	0	0	0
			4175	2638	727	789	21			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-5	HIS	-	expression tag	UNP P28240
A	-4	HIS	-	expression tag	UNP P28240
A	-3	HIS	-	expression tag	UNP P28240
A	-2	HIS	-	expression tag	UNP P28240
A	-1	HIS	-	expression tag	UNP P28240
A	0	HIS	-	expression tag	UNP P28240
B	-5	HIS	-	expression tag	UNP P28240
B	-4	HIS	-	expression tag	UNP P28240
B	-3	HIS	-	expression tag	UNP P28240
B	-2	HIS	-	expression tag	UNP P28240
B	-1	HIS	-	expression tag	UNP P28240
B	0	HIS	-	expression tag	UNP P28240
C	-5	HIS	-	expression tag	UNP P28240
C	-4	HIS	-	expression tag	UNP P28240
C	-3	HIS	-	expression tag	UNP P28240
C	-2	HIS	-	expression tag	UNP P28240
C	-1	HIS	-	expression tag	UNP P28240
C	0	HIS	-	expression tag	UNP P28240
D	-5	HIS	-	expression tag	UNP P28240
D	-4	HIS	-	expression tag	UNP P28240
D	-3	HIS	-	expression tag	UNP P28240

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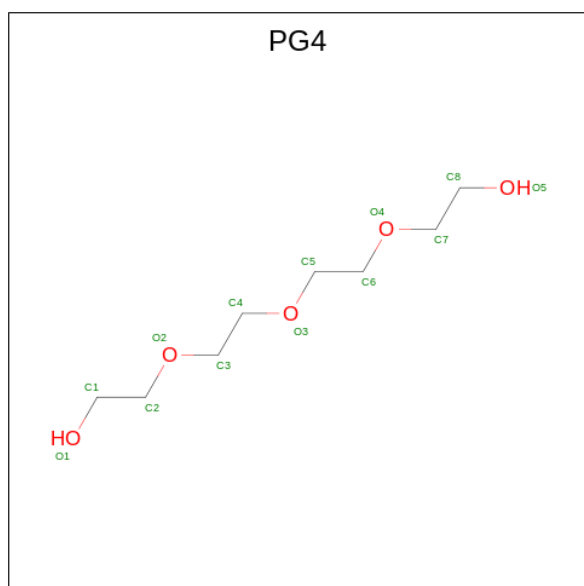
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Chain	Residue	Modelled	Actual	Comment	Reference
D	-2	HIS	-	expression tag	UNP P28240
D	-1	HIS	-	expression tag	UNP P28240
D	0	HIS	-	expression tag	UNP P28240

- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Mg 1 1	0	0
2	B	1	Total Mg 1 1	0	0
2	C	1	Total Mg 1 1	0	0
2	D	1	Total Mg 1 1	0	0

- Molecule 3 is TETRAETHYLENE GLYCOL (three-letter code: PG4) (formula: C₈H₁₈O₅).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	1	Total C O 13 8 5	0	0

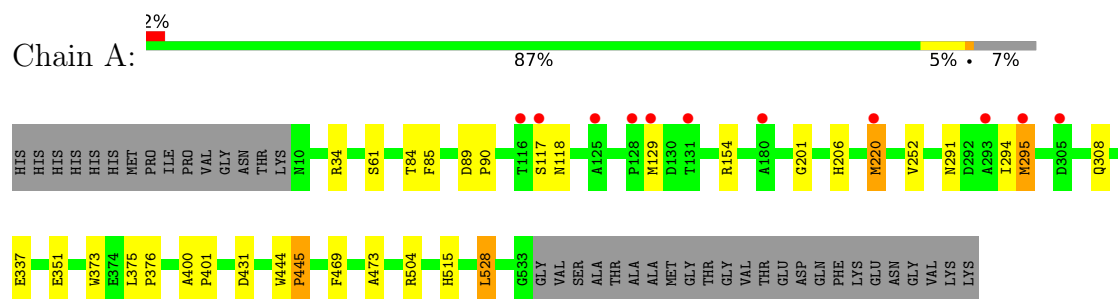
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	165	Total 165	O 165	0	0
4	B	127	Total 127	O 127	0	0
4	C	130	Total 130	O 130	0	0
4	D	153	Total 153	O 153	0	0

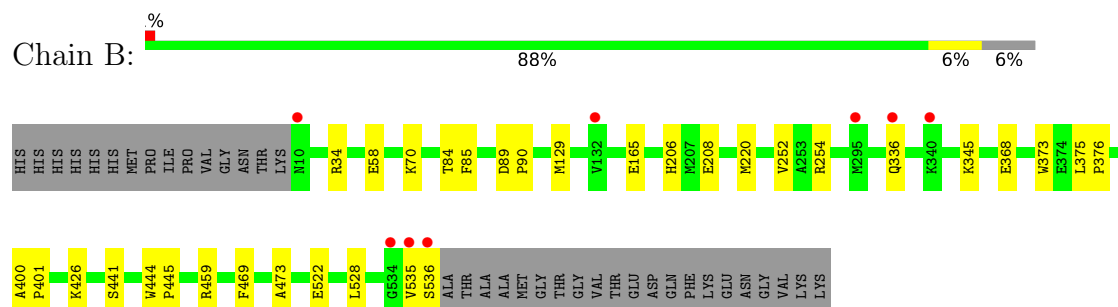
3 Residue-property plots [i](#)

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.

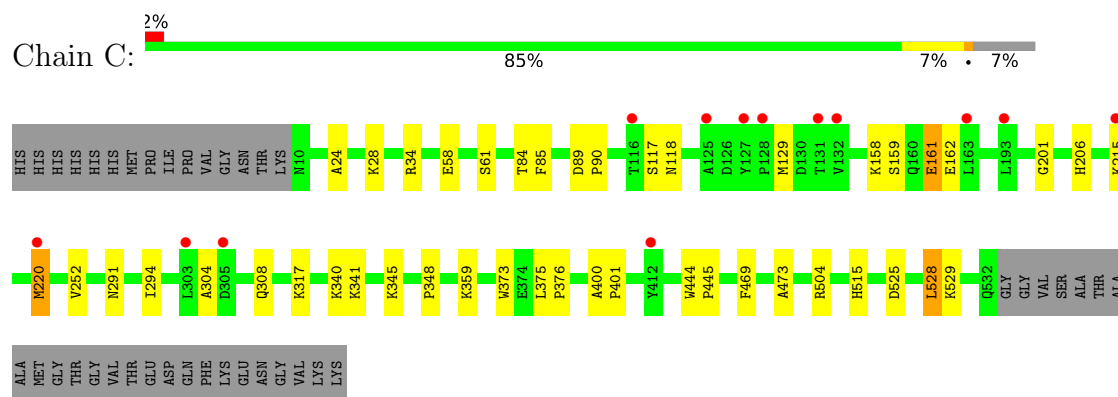
• Molecule 1: Isocitrate lyase



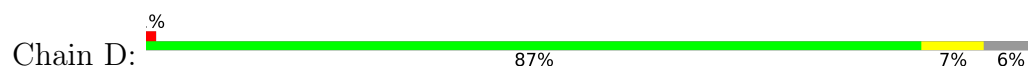
• Molecule 1: Isocitrate lyase

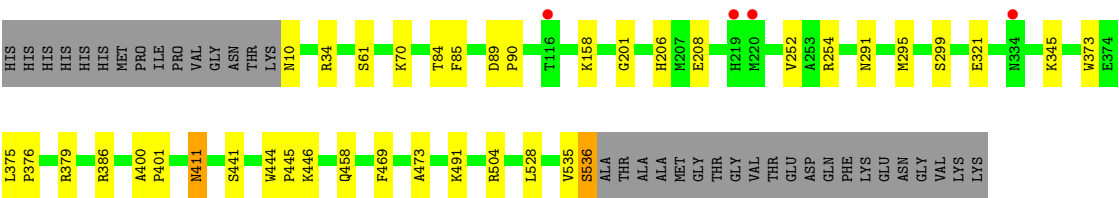


• Molecule 1: Isocitrate lyase



• Molecule 1: Isocitrate lyase





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	95.52Å 129.38Å 210.79Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.80 – 2.30 48.80 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.7 (48.80-2.30) 99.7 (48.80-2.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.04 (at 2.29Å)	Xtriage
Refinement program	REFMAC 5.8.0135	Depositor
R, R_{free}	0.189 , 0.220 0.194 , 0.223	Depositor DCC
R_{free} test set	5823 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	33.8	Xtriage
Anisotropy	0.089	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 23.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	17254	wwPDB-VP
Average B, all atoms (Å ²)	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.30% 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: MG, PG4

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	0.28	0/4254	0.40	0/5752
1	B	0.27	0/4271	0.38	0/5775
1	C	0.27	0/4250	0.38	0/5747
1	D	0.27	0/4271	0.38	0/5775
All	All	0.27	0/17046	0.39	0/23049

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	1
1	C	0	1
All	All	0	3

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	220	MET	Peptide
1	B	220	MET	Peptide
1	C	220	MET	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	4158	0	4062	20	0
1	B	4175	0	4079	18	0
1	C	4154	0	4059	19	0
1	D	4175	0	4079	18	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	B	13	0	18	0	0
4	A	165	0	0	1	0
4	B	127	0	0	2	0
4	C	130	0	0	0	0
4	D	153	0	0	0	0
All	All	17254	0	16297	65	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 2.

All (65) 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:295:MET:HA	1:B:535:VAL:HG21	1.60	0.82
1:A:291:ASN:HD21	1:B:536:SER:HB2	1.56	0.70
1:A:295:MET:HA	1:B:535:VAL:CG2	2.23	0.68
1:D:321:GLU:OE2	1:D:386:ARG:NH2	2.34	0.57
1:B:444:TRP:N	1:B:445:PRO:HD2	2.20	0.57
1:C:525:ASP:O	1:C:529:LYS:HG2	2.06	0.55
1:A:444:TRP:N	1:A:445:PRO:HD2	2.22	0.55
1:D:411:ASN:OD1	1:D:411:ASN:N	2.36	0.54
1:B:459:ARG:HD2	4:B:703:HOH:O	2.08	0.51
1:D:444:TRP:N	1:D:445:PRO:CD	2.74	0.51
1:A:515:HIS:CE1	1:B:441:SER:HB3	2.45	0.50
1:C:294:ILE:HG22	1:D:535:VAL:HG22	1.94	0.50
1:A:375:LEU:N	1:A:376:PRO:CD	2.75	0.49
1:C:444:TRP:N	1:C:445:PRO:CD	2.75	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:400:ALA:N	1:D:401:PRO:CD	2.76	0.49
1:B:375:LEU:N	1:B:376:PRO:CD	2.75	0.49
1:B:444:TRP:N	1:B:445:PRO:CD	2.76	0.49
1:C:375:LEU:N	1:C:376:PRO:CD	2.76	0.49
1:A:400:ALA:N	1:A:401:PRO:CD	2.76	0.48
1:D:375:LEU:N	1:D:376:PRO:CD	2.76	0.48
1:B:400:ALA:N	1:B:401:PRO:CD	2.76	0.48
1:A:444:TRP:N	1:A:445:PRO:CD	2.76	0.48
1:C:84:THR:O	1:C:469:PHE:HA	2.13	0.48
1:A:294:ILE:HG22	1:B:535:VAL:HG22	1.96	0.47
1:C:159:SER:OG	1:C:162:GLU:HG3	2.13	0.47
1:B:84:THR:O	1:B:469:PHE:HA	2.13	0.47
1:C:206:HIS:HB3	1:C:252:VAL:HB	1.96	0.47
1:A:89:ASP:HB2	1:A:90:PRO:HD2	1.98	0.46
1:A:206:HIS:HB3	1:A:252:VAL:HB	1.97	0.46
1:C:400:ALA:N	1:C:401:PRO:CD	2.78	0.46
1:A:84:THR:O	1:A:469:PHE:HA	2.15	0.46
1:C:291:ASN:OD1	1:D:536:SER:HB2	2.14	0.46
1:B:206:HIS:HB3	1:B:252:VAL:HB	1.97	0.46
1:D:84:THR:O	1:D:469:PHE:HA	2.16	0.45
1:B:85:PHE:HB2	1:B:473:ALA:HB3	1.98	0.45
1:B:89:ASP:HB2	1:B:90:PRO:HD2	1.99	0.45
1:D:85:PHE:HB2	1:D:473:ALA:HB3	1.98	0.45
1:C:85:PHE:HB2	1:C:473:ALA:HB3	1.99	0.45
1:A:375:LEU:N	1:A:376:PRO:HD3	2.32	0.44
1:D:206:HIS:HB3	1:D:252:VAL:HB	1.98	0.44
1:A:291:ASN:ND2	1:B:536:SER:HB2	2.28	0.44
1:C:89:ASP:HB2	1:C:90:PRO:HD2	1.98	0.44
1:C:159:SER:OG	1:C:161:GLU:HG2	2.17	0.44
1:D:89:ASP:HB2	1:D:90:PRO:HD2	2.00	0.44
1:C:117:SER:O	1:C:118:ASN:HB2	2.17	0.44
1:B:375:LEU:N	1:B:376:PRO:HD3	2.34	0.43
1:D:375:LEU:N	1:D:376:PRO:HD3	2.34	0.43
1:C:375:LEU:N	1:C:376:PRO:HD3	2.34	0.42
1:A:154:ARG:NH1	1:D:10:ASN:OD1	2.39	0.42
1:A:85:PHE:HB2	1:A:473:ALA:HB3	2.01	0.42
1:A:351:GLU:OE2	4:A:701:HOH:O	2.22	0.42
1:C:528:LEU:HD12	1:C:528:LEU:HA	1.89	0.42
1:D:295:MET:O	1:D:295:MET:HG2	2.19	0.42
1:A:61:SER:HB3	1:A:201:GLY:HA2	2.02	0.42
1:C:304:ALA:O	1:C:308:GLN:HG2	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:208:GLU:HA	1:B:254:ARG:O	2.20	0.42
1:D:291:ASN:CB	1:D:379:ARG:HH12	2.33	0.41
1:C:61:SER:HB3	1:C:201:GLY:HA2	2.02	0.41
1:C:24:ALA:O	1:C:28:LYS:HG3	2.21	0.41
1:A:117:SER:O	1:A:118:ASN:HB2	2.21	0.41
1:A:528:LEU:HD12	1:A:528:LEU:HA	1.89	0.41
1:D:61:SER:HB3	1:D:201:GLY:HA2	2.02	0.41
1:D:208:GLU:HA	1:D:254:ARG:O	2.21	0.41
1:C:515:HIS:CE1	1:D:441:SER:HB3	2.56	0.40
1:B:522:GLU:OE1	4:B:701:HOH:O	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	522/563 (93%)	513 (98%)	9 (2%)	0	100	100
1	B	525/563 (93%)	514 (98%)	11 (2%)	0	100	100
1	C	521/563 (92%)	514 (99%)	7 (1%)	0	100	100
1	D	525/563 (93%)	518 (99%)	7 (1%)	0	100	100
All	All	2093/2252 (93%)	2059 (98%)	34 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	439/470 (93%)	428 (98%)	11 (2%)	47	65
1	B	441/470 (94%)	430 (98%)	11 (2%)	47	65
1	C	439/470 (93%)	423 (96%)	16 (4%)	35	49
1	D	441/470 (94%)	428 (97%)	13 (3%)	42	58
All	All	1760/1880 (94%)	1709 (97%)	51 (3%)	42	58

All (51) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	34	ARG
1	A	129	MET
1	A	220	MET
1	A	295	MET
1	A	308	GLN
1	A	337	GLU
1	A	373	TRP
1	A	431	ASP
1	A	445	PRO
1	A	504	ARG
1	A	528	LEU
1	B	34	ARG
1	B	58	GLU
1	B	70	LYS
1	B	129	MET
1	B	165	GLU
1	B	336	GLN
1	B	345	LYS
1	B	368	GLU
1	B	373	TRP
1	B	426	LYS
1	B	528	LEU
1	C	34	ARG
1	C	58	GLU
1	C	129	MET
1	C	158	LYS
1	C	161	GLU
1	C	215	LYS
1	C	220	MET
1	C	317	LYS

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Mol	Chain	Res	Type
1	C	340	LYS
1	C	341	LYS
1	C	345	LYS
1	C	348	PRO
1	C	359	LYS
1	C	373	TRP
1	C	504	ARG
1	C	528	LEU
1	D	34	ARG
1	D	70	LYS
1	D	158	LYS
1	D	299	SER
1	D	345	LYS
1	D	373	TRP
1	D	411	ASN
1	D	446	LYS
1	D	458	GLN
1	D	491	LYS
1	D	504	ARG
1	D	528	LEU
1	D	536	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	308	GLN
1	A	515	HIS
1	B	308	GLN
1	C	515	HIS
1	D	515	HIS

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 [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 5 ligands modelled in this entry, 4 are monoatomic - leaving 1 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	PG4	B	602	-	12,12,12	0.55	0	11,11,11	0.11	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	PG4	B	602	-	-	8/10/10/10	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	602	PG4	O1-C1-C2-O2
3	B	602	PG4	O3-C5-C6-O4
3	B	602	PG4	O4-C7-C8-O5
3	B	602	PG4	O2-C3-C4-O3
3	B	602	PG4	C5-C6-O4-C7
3	B	602	PG4	C4-C3-O2-C2
3	B	602	PG4	C6-C5-O3-C4
3	B	602	PG4	C8-C7-O4-C6

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

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	524/563 (93%)	-0.24	11 (2%) 63 70	21, 30, 57, 88	0
1	B	527/563 (93%)	-0.19	8 (1%) 73 79	23, 33, 76, 101	0
1	C	523/563 (92%)	-0.07	13 (2%) 57 64	22, 34, 66, 91	0
1	D	527/563 (93%)	-0.30	4 (0%) 86 89	23, 33, 63, 98	0
All	All	2101/2252 (93%)	-0.20	36 (1%) 70 76	21, 33, 66, 101	0

All (36) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	535	VAL	8.4
1	C	220	MET	4.1
1	B	534	GLY	3.6
1	B	536	SER	3.1
1	A	128	PRO	3.0
1	A	295	MET	2.8
1	B	295	MET	2.8
1	C	131	THR	2.7
1	A	117	SER	2.7
1	C	127	TYR	2.7
1	A	220	MET	2.6
1	C	125	ALA	2.6
1	A	116	THR	2.5
1	C	132	VAL	2.5
1	A	293	ALA	2.5
1	C	412	TYR	2.5
1	C	163	LEU	2.4
1	C	303	LEU	2.4
1	C	128	PRO	2.4
1	D	116	THR	2.4
1	D	334	ASN	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	340	LYS	2.3
1	B	336	GLN	2.3
1	C	305	ASP	2.2
1	A	180	ALA	2.2
1	A	125	ALA	2.2
1	C	215	LYS	2.2
1	D	220	MET	2.1
1	C	116	THR	2.1
1	A	129	MET	2.1
1	C	193	LEU	2.1
1	A	131	THR	2.0
1	A	305	ASP	2.0
1	B	132	VAL	2.0
1	D	219	HIS	2.0
1	B	10	ASN	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 monosaccharides 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(\AA^2)	Q<0.9
3	PG4	B	602	13/13	0.79	0.19	48,70,76,83	0
2	MG	C	601	1/1	0.90	0.44	46,46,46,46	0
2	MG	D	601	1/1	0.92	0.23	45,45,45,45	0
2	MG	B	601	1/1	0.96	0.22	38,38,38,38	0
2	MG	A	601	1/1	0.97	0.34	39,39,39,39	0

6.5 Other polymers [i](#)

There are no such residues in this entry.