



wwPDB X-ray Structure Validation Summary Report ⓘ

May 22, 2020 – 03:16 am BST

PDB ID : 1G5H
Title : CRYSTAL STRUCTURE OF THE ACCESSORY SUBUNIT OF MURINE MITOCHONDRIAL POLYMERASE GAMMA
Authors : Carrodegua, J.A.; Theis, K.; Bogenhagen, D.F.; Kisker, C.
Deposited on : 2000-11-01
Resolution : 1.95 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

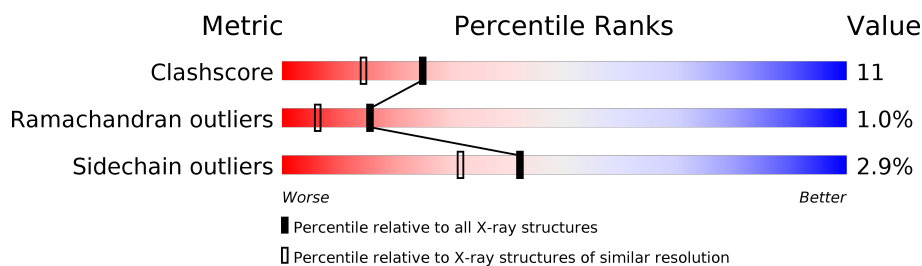
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.95 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	141614	2705 (1.96-1.96)
Ramachandran outliers	138981	2678 (1.96-1.96)
Sidechain outliers	138945	2678 (1.96-1.96)

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 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	454	
1	B	454	
1	C	454	
1	D	454	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 13779 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 MITOCHONDRIAL DNA POLYMERASE ACCESSORY SUBUNIT.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	405	Total	C	N	O	S	Se	0	0	0
			3220	2050	570	586	8	6			
1	B	397	Total	C	N	O	S	Se	0	0	0
			3153	2010	554	575	8	6			
1	C	405	Total	C	N	O	S	Se	0	0	0
			3213	2045	568	586	8	6			
1	D	415	Total	C	N	O	S	Se	0	0	0
			3305	2103	587	601	8	6			

There are 68 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	92	MSE	MET	MODIFIED RESIDUE	UNP Q9QZM2
A	242	MSE	MET	MODIFIED RESIDUE	UNP Q9QZM2
A	409	MSE	MET	MODIFIED RESIDUE	UNP Q9QZM2
A	436	MSE	MET	MODIFIED RESIDUE	UNP Q9QZM2
A	439	MSE	MET	MODIFIED RESIDUE	UNP Q9QZM2
A	440	MSE	MET	MODIFIED RESIDUE	UNP Q9QZM2
A	460	ALA	-	EXPRESSION TAG	UNP Q9QZM2
A	461	ALA	-	EXPRESSION TAG	UNP Q9QZM2
A	462	ALA	-	EXPRESSION TAG	UNP Q9QZM2
A	463	LEU	-	EXPRESSION TAG	UNP Q9QZM2
A	464	ASP	-	EXPRESSION TAG	UNP Q9QZM2
A	465	HIS	-	EXPRESSION TAG	UNP Q9QZM2
A	466	HIS	-	EXPRESSION TAG	UNP Q9QZM2
A	467	HIS	-	EXPRESSION TAG	UNP Q9QZM2
A	468	HIS	-	EXPRESSION TAG	UNP Q9QZM2
A	469	HIS	-	EXPRESSION TAG	UNP Q9QZM2
A	470	HIS	-	EXPRESSION TAG	UNP Q9QZM2
B	92	MSE	MET	MODIFIED RESIDUE	UNP Q9QZM2
B	242	MSE	MET	MODIFIED RESIDUE	UNP Q9QZM2
B	409	MSE	MET	MODIFIED RESIDUE	UNP Q9QZM2

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Chain	Residue	Modelled	Actual	Comment	Reference
B	436	MSE	MET	MODIFIED RESIDUE	UNP Q9QZM2
B	439	MSE	MET	MODIFIED RESIDUE	UNP Q9QZM2
B	440	MSE	MET	MODIFIED RESIDUE	UNP Q9QZM2
B	460	ALA	-	EXPRESSION TAG	UNP Q9QZM2
B	461	ALA	-	EXPRESSION TAG	UNP Q9QZM2
B	462	ALA	-	EXPRESSION TAG	UNP Q9QZM2
B	463	LEU	-	EXPRESSION TAG	UNP Q9QZM2
B	464	ASP	-	EXPRESSION TAG	UNP Q9QZM2
B	465	HIS	-	EXPRESSION TAG	UNP Q9QZM2
B	466	HIS	-	EXPRESSION TAG	UNP Q9QZM2
B	467	HIS	-	EXPRESSION TAG	UNP Q9QZM2
B	468	HIS	-	EXPRESSION TAG	UNP Q9QZM2
B	469	HIS	-	EXPRESSION TAG	UNP Q9QZM2
B	470	HIS	-	EXPRESSION TAG	UNP Q9QZM2
C	92	MSE	MET	MODIFIED RESIDUE	UNP Q9QZM2
C	242	MSE	MET	MODIFIED RESIDUE	UNP Q9QZM2
C	409	MSE	MET	MODIFIED RESIDUE	UNP Q9QZM2
C	436	MSE	MET	MODIFIED RESIDUE	UNP Q9QZM2
C	439	MSE	MET	MODIFIED RESIDUE	UNP Q9QZM2
C	440	MSE	MET	MODIFIED RESIDUE	UNP Q9QZM2
C	460	ALA	-	EXPRESSION TAG	UNP Q9QZM2
C	461	ALA	-	EXPRESSION TAG	UNP Q9QZM2
C	462	ALA	-	EXPRESSION TAG	UNP Q9QZM2
C	463	LEU	-	EXPRESSION TAG	UNP Q9QZM2
C	464	ASP	-	EXPRESSION TAG	UNP Q9QZM2
C	465	HIS	-	EXPRESSION TAG	UNP Q9QZM2
C	466	HIS	-	EXPRESSION TAG	UNP Q9QZM2
C	467	HIS	-	EXPRESSION TAG	UNP Q9QZM2
C	468	HIS	-	EXPRESSION TAG	UNP Q9QZM2
C	469	HIS	-	EXPRESSION TAG	UNP Q9QZM2
C	470	HIS	-	EXPRESSION TAG	UNP Q9QZM2
D	92	MSE	MET	MODIFIED RESIDUE	UNP Q9QZM2
D	242	MSE	MET	MODIFIED RESIDUE	UNP Q9QZM2
D	409	MSE	MET	MODIFIED RESIDUE	UNP Q9QZM2
D	436	MSE	MET	MODIFIED RESIDUE	UNP Q9QZM2
D	439	MSE	MET	MODIFIED RESIDUE	UNP Q9QZM2
D	440	MSE	MET	MODIFIED RESIDUE	UNP Q9QZM2
D	460	ALA	-	EXPRESSION TAG	UNP Q9QZM2
D	461	ALA	-	EXPRESSION TAG	UNP Q9QZM2
D	462	ALA	-	EXPRESSION TAG	UNP Q9QZM2
D	463	LEU	-	EXPRESSION TAG	UNP Q9QZM2
D	464	ASP	-	EXPRESSION TAG	UNP Q9QZM2

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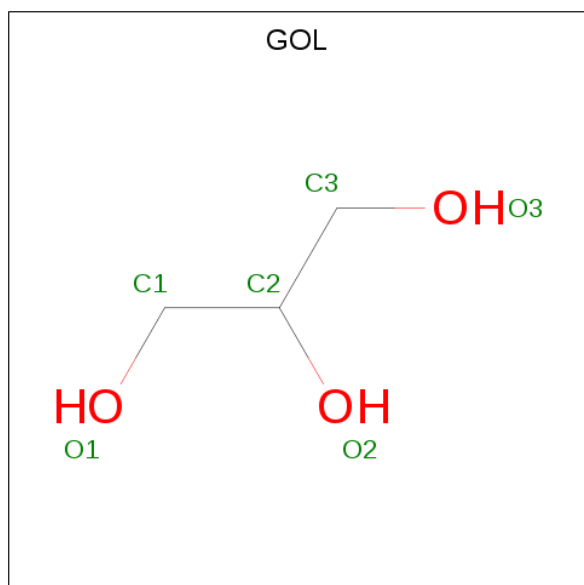
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Chain	Residue	Modelled	Actual	Comment	Reference
D	465	HIS	-	EXPRESSION TAG	UNP Q9QZM2
D	466	HIS	-	EXPRESSION TAG	UNP Q9QZM2
D	467	HIS	-	EXPRESSION TAG	UNP Q9QZM2
D	468	HIS	-	EXPRESSION TAG	UNP Q9QZM2
D	469	HIS	-	EXPRESSION TAG	UNP Q9QZM2
D	470	HIS	-	EXPRESSION TAG	UNP Q9QZM2

- Molecule 2 is SODIUM ION (three-letter code: NA) (formula: Na).

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

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	1	Total C O 6 3 3	0	0
3	D	1	Total C O 6 3 3	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	220	Total 220	O 220	0	0
4	B	234	Total 234	O 234	0	0
4	C	214	Total 214	O 214	0	0
4	D	204	Total 204	O 204	0	0

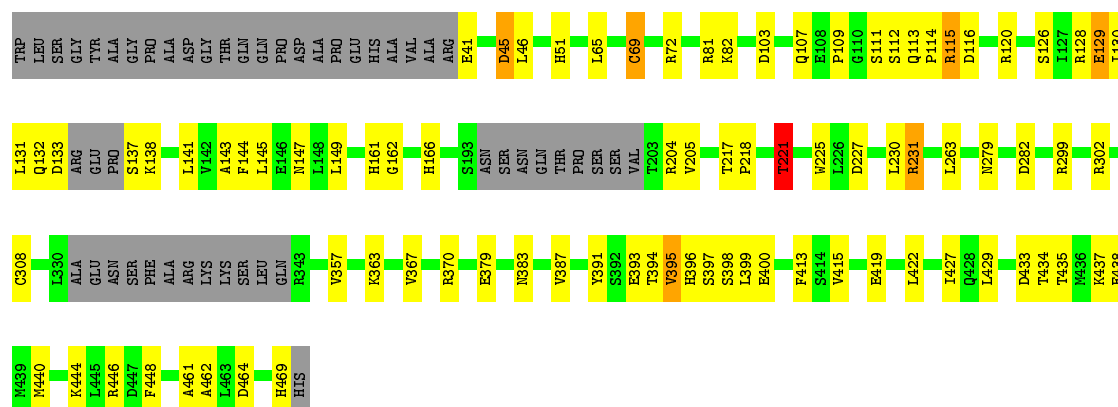
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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.

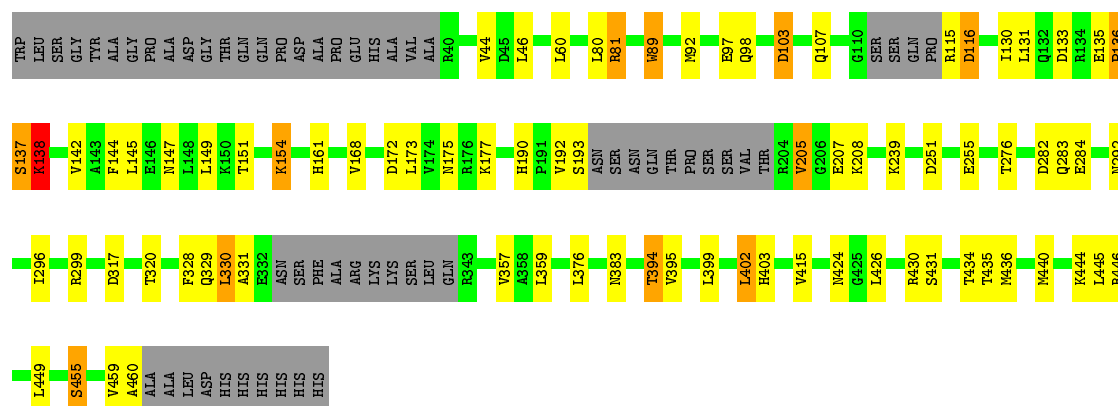
• Molecule 1: MITOCHONDRIAL DNA POLYMERASE ACCESSORY SUBUNIT

Chain A: 



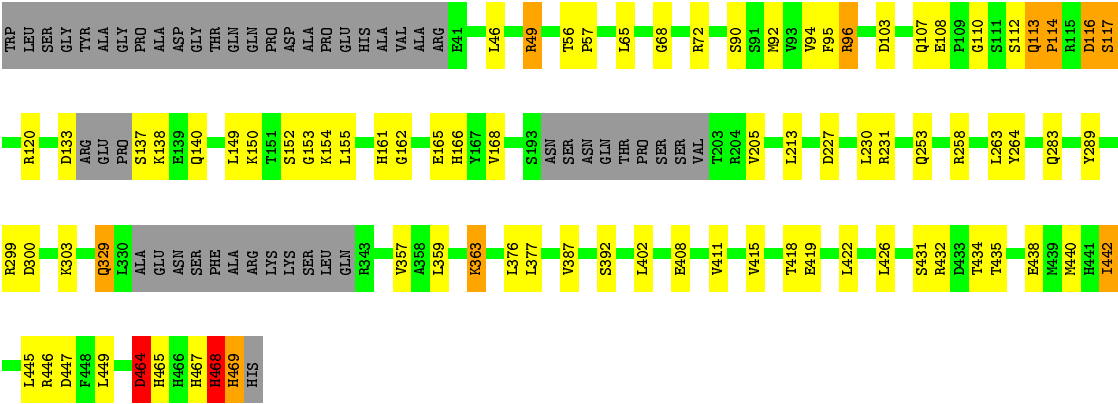
• Molecule 1: MITOCHONDRIAL DNA POLYMERASE ACCESSORY SUBUNIT

Chain B: 

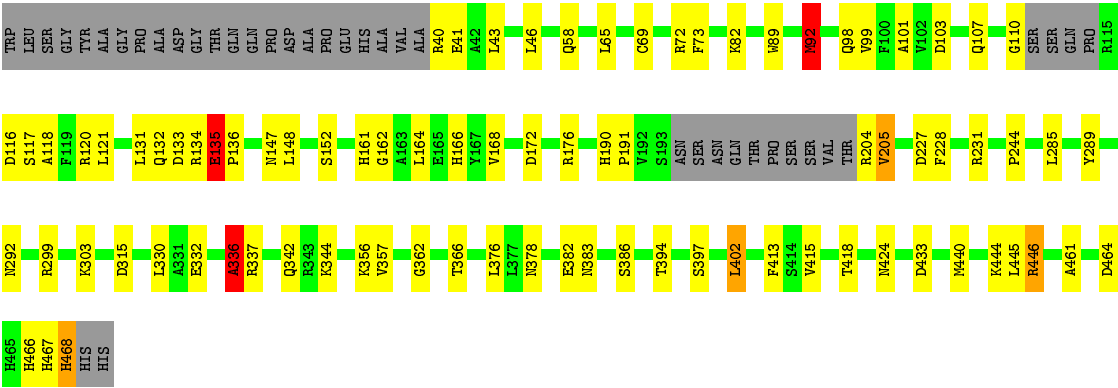


• Molecule 1: MITOCHONDRIAL DNA POLYMERASE ACCESSORY SUBUNIT

Chain C: 



● Molecule 1: MITOCHONDRIAL DNA POLYMERASE ACCESSORY SUBUNIT



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	96.62Å 133.42Å 135.04Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 1.95	Depositor
% Data completeness (in resolution range)	100.0 (20.00-1.95)	Depositor
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	REFMAC	Depositor
R, R_{free}	0.183 , 0.224	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	13779	wwPDB-VP
Average B, all atoms (Å ²)	45.0	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: GOL, NA

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	0.81	0/3289	0.90	7/4447 (0.2%)
1	B	0.81	1/3217 (0.0%)	0.98	10/4348 (0.2%)
1	C	0.80	1/3281 (0.0%)	0.92	7/4436 (0.2%)
1	D	0.80	2/3375 (0.1%)	0.96	11/4561 (0.2%)
All	All	0.80	4/13162 (0.0%)	0.94	35/17792 (0.2%)

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	C	0	2
1	D	0	2
All	All	0	4

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	264	TYR	CD2-CE2	-5.64	1.30	1.39
1	D	73	PHE	CD2-CE2	5.24	1.49	1.39
1	B	89	TRP	CB-CG	-5.10	1.41	1.50
1	D	92	MSE	SE-CE	-5.08	1.65	1.95

The worst 5 of 35 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	464	ASP	CB-CG-OD2	11.39	128.55	118.30
1	B	81	ARG	NE-CZ-NH2	-11.05	114.77	120.30
1	B	81	ARG	NE-CZ-NH1	10.15	125.38	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	161	HIS	CA-CB-CG	-7.53	100.81	113.60
1	D	103	ASP	CB-CG-OD2	6.98	124.58	118.30

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	468	HIS	Sidechain
1	C	469	HIS	Sidechain
1	D	466	HIS	Sidechain
1	D	468	HIS	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	3220	0	3206	81	0
1	B	3153	0	3154	86	0
1	C	3213	0	3194	67	0
1	D	3305	0	3300	70	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	6	0	8	1	0
3	D	6	0	8	0	0
4	A	220	0	0	5	0
4	B	234	0	0	9	0
4	C	214	0	0	4	0
4	D	204	0	0	5	0
All	All	13779	0	12870	277	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 11.

The worst 5 of 277 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:D:135:GLU:H	1:D:136:PRO:CD	1.36	1.26
1:D:134:ARG:HA	1:D:136:PRO:HD3	1.24	1.18
1:A:394:THR:O	1:A:395:VAL:HG22	1.01	1.17
1:A:394:THR:O	1:A:395:VAL:CG2	1.93	1.17
1:C:205:VAL:HG13	1:D:107:GLN:NE2	1.60	1.14

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	397/454 (87%)	383 (96%)	10 (2%)	4 (1%)	15	6
1	B	389/454 (86%)	378 (97%)	6 (2%)	5 (1%)	12	3
1	C	397/454 (87%)	385 (97%)	9 (2%)	3 (1%)	19	9
1	D	409/454 (90%)	387 (95%)	18 (4%)	4 (1%)	15	6
All	All	1592/1816 (88%)	1533 (96%)	43 (3%)	16 (1%)	15	6

5 of 16 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	116	ASP
1	A	395	VAL
1	B	116	ASP
1	B	137	SER
1	B	138	LYS

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	357/391 (91%)	349 (98%)	8 (2%)	52	44
1	B	349/391 (89%)	338 (97%)	11 (3%)	39	27
1	C	355/391 (91%)	343 (97%)	12 (3%)	37	25
1	D	365/391 (93%)	354 (97%)	11 (3%)	41	30
All	All	1426/1564 (91%)	1384 (97%)	42 (3%)	42	31

5 of 42 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	455	SER
1	C	329	GLN
1	D	292	ASN
1	C	49	ARG
1	C	117	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 22 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	383	ASN
1	C	140	GLN
1	D	349	HIS
1	B	403	HIS
1	B	428	GLN

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 carbohydrates in this entry.

5.6 Ligand geometry

Of 6 ligands modelled in this entry, 4 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	GOL	D	5	-	5,5,5	0.50	0	5,5,5	0.30	0
3	GOL	B	6	-	5,5,5	0.37	0	5,5,5	0.79	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	GOL	D	5	-	-	2/4/4/4	-
3	GOL	B	6	-	-	4/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	6	GOL	O1-C1-C2-O2
3	D	5	GOL	C1-C2-C3-O3
3	B	6	GOL	O1-C1-C2-C3
3	B	6	GOL	C1-C2-C3-O3
3	B	6	GOL	O2-C2-C3-O3

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	6	GOL	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.