



# Full wwPDB X-ray Structure Validation Report ⓘ

May 16, 2020 – 05:48 am BST

PDB ID : 3QIA  
Title : Crystal structure of P-loop G237A mutant of subunit A of the A1AO ATP synthase  
Authors : Ragunathan, P.; Manimekalai, M.S.S.; Jeyakanthan, J.; Gruber, G.  
Deposited on : 2011-01-26  
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](mailto: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.

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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	:	2.11
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)	:	2.11

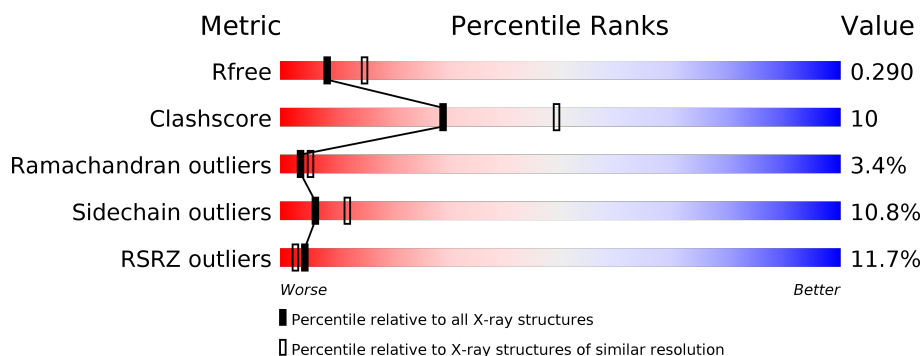
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 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))
$R_{free}$	130704	3163 (2.60-2.60)
Clashscore	141614	3518 (2.60-2.60)
Ramachandran outliers	138981	3455 (2.60-2.60)
Sidechain outliers	138945	3455 (2.60-2.60)
RSRZ outliers	127900	3104 (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  $\geq 3$ , 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	588	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	MPD	A	594	-	-	-	X

## 2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 4700 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.

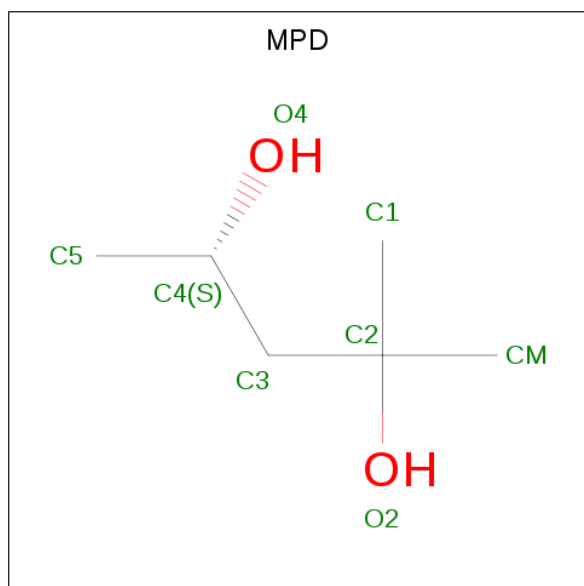
- Molecule 1 is a protein called V-type ATP synthase alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	564	4457	2849	759	830	19	0	3	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	237	ALA	GLY	ENGINEERED MUTATION	UNP O57728

- Molecule 2 is (4S)-2-METHYL-2,4-PENTANEDIOL (three-letter code: MPD) (formula: C<sub>6</sub>H<sub>14</sub>O<sub>2</sub>).



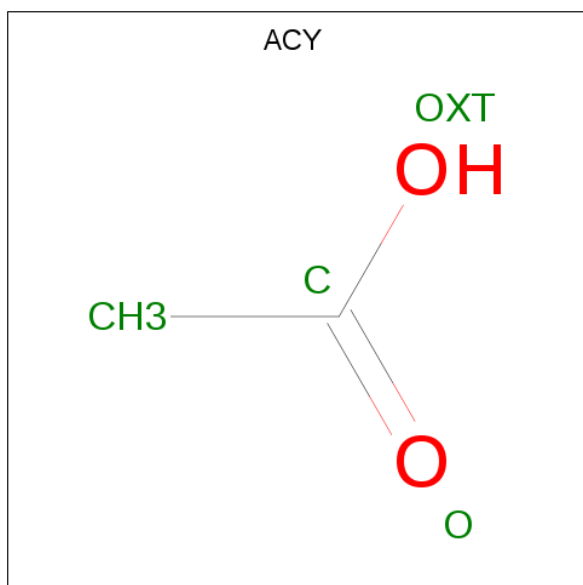
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			8	6	2		
2	A	1	Total	C	O	0	0
			8	6	2		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			8	6	2		
2	A	1	Total	C	O	0	0
			8	6	2		

- Molecule 3 is ACETIC ACID (three-letter code: ACY) (formula: C<sub>2</sub>H<sub>4</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		

- Molecule 4 is 2-AMINO-2-HYDROXYMETHYL-PROPANE-1,3-DIOL (three-letter code: TRS) (formula: C<sub>4</sub>H<sub>12</sub>NO<sub>3</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			8	4	1	3		

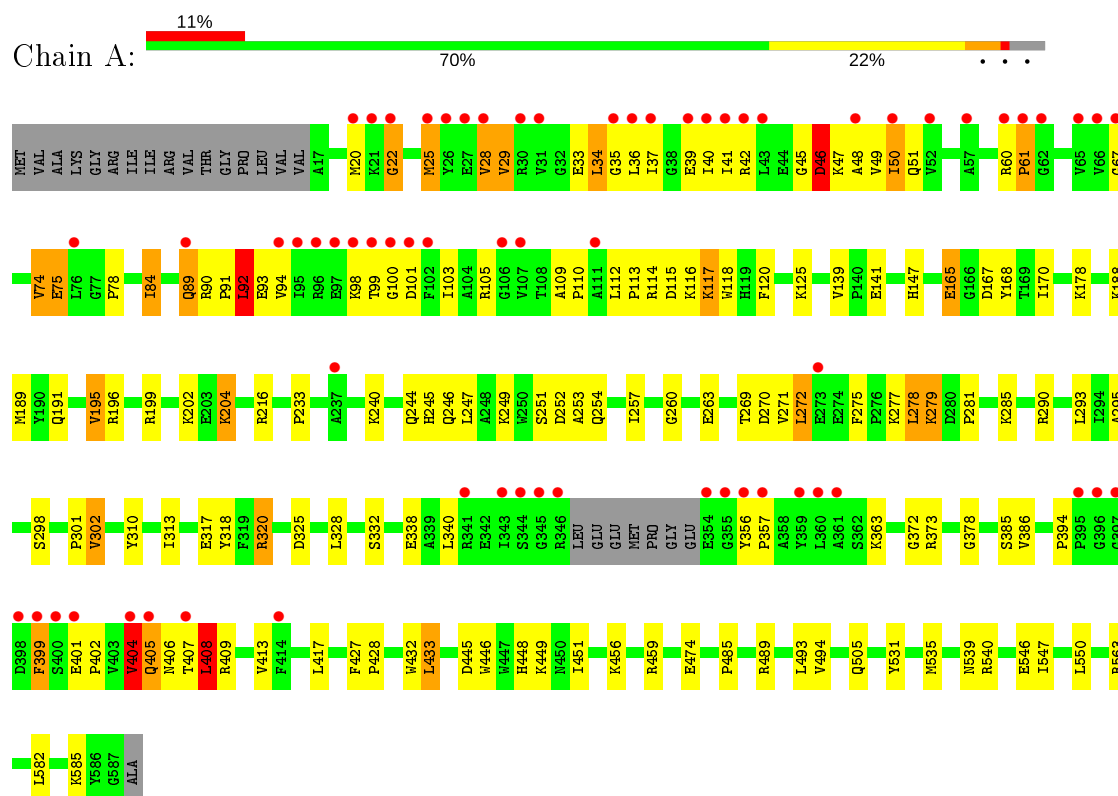
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	175	Total	O	0	0
			175	175		

### 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 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: V-type ATP synthase alpha chain



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	128.69Å 128.69Å 106.29Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	27.32 – 2.60 27.32 – 2.60	Depositor EDS
% Data completeness (in resolution range)	99.7 (27.32-2.60) 99.7 (27.32-2.60)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.22 (at 2.61Å)	Xtriage
Refinement program	REFMAC 5.5.0072	Depositor
R, $R_{free}$	0.240 , 0.297 0.237 , 0.290	Depositor DCC
$R_{free}$ test set	1406 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	49.3	Xtriage
Anisotropy	0.042	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.28 , 55.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	4700	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	66.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.27% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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 [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: ACY, MPD, TRS

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	0.42	0/4559	0.59	0/6171

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts [i](#)

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	4457	0	4524	87	0
2	A	32	0	56	4	0
3	A	28	0	21	0	0
4	A	8	0	12	0	0
5	A	175	0	0	3	0
All	All	4700	0	4613	88	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 10.

All (88) 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:216:ARG:H	1:A:505:GLN:HE22	1.21	0.86
1:A:60:ARG:HB2	1:A:61:PRO:HD2	1.64	0.79
1:A:22:GLY:HA3	1:A:37:ILE:HG23	1.65	0.79
1:A:247:LEU:O	1:A:251:SER:HB3	1.83	0.78
1:A:373:ARG:HG3	1:A:385:SER:HB3	1.67	0.77
1:A:320:ARG:HG2	1:A:386:VAL:HG23	1.67	0.76
1:A:260:GLY:HA2	1:A:332:SER:HB3	1.69	0.74
1:A:78:PRO:O	1:A:112:LEU:HD21	1.93	0.67
1:A:401:GLU:HA	1:A:405:GLN:HB2	1.77	0.65
1:A:253:ALA:O	1:A:290:ARG:NH2	2.32	0.63
1:A:114:ARG:HA	1:A:170:ILE:CG2	2.29	0.62
1:A:254:GLN:NE2	1:A:325:ASP:H	1.97	0.62
1:A:275:PHE:HA	1:A:278:LEU:HD22	1.82	0.62
1:A:249:LYS:HE2	2:A:589:MPD:H52	1.82	0.60
1:A:254:GLN:HE22	1:A:325:ASP:H	1.48	0.59
1:A:195:VAL:HG13	1:A:310:TYR:CB	2.32	0.59
1:A:34:LEU:HD13	1:A:49:VAL:H	1.67	0.59
1:A:112:LEU:HD22	1:A:170:ILE:HD12	1.85	0.58
1:A:257:ILE:HB	1:A:328:LEU:HD12	1.85	0.58
1:A:191:GLN:NE2	1:A:199:ARG:HH12	2.02	0.58
1:A:202:LYS:NZ	1:A:378:GLY:O	2.35	0.58
1:A:147:HIS:HE1	1:A:318:TYR:OH	1.87	0.58
1:A:448:HIS:HE1	1:A:456:LYS:H	1.53	0.57
1:A:216:ARG:H	1:A:505:GLN:NE2	1.99	0.56
1:A:114:ARG:HA	1:A:170:ILE:HG22	1.88	0.56
1:A:60:ARG:CB	1:A:61:PRO:HD2	2.35	0.56
1:A:94:VAL:HG12	1:A:272:LEU:HD11	1.88	0.56
1:A:120:PHE:HB2	1:A:189:MET:CE	2.36	0.55
1:A:75:GLU:HG2	5:A:753:HOH:O	2.07	0.54
1:A:92:LEU:HG	1:A:93:GLU:H	1.73	0.54
1:A:407:THR:C	1:A:409:ARG:H	2.11	0.54
1:A:50:ILE:HD13	1:A:50:ILE:H	1.73	0.53
1:A:401:GLU:N	1:A:402:PRO:HD2	2.23	0.53
1:A:310:TYR:OH	1:A:363:LYS:HB2	2.10	0.52
1:A:84:ILE:HD11	1:A:295:ALA:HB2	1.92	0.51
1:A:195:VAL:HG13	1:A:310:TYR:HB2	1.92	0.51
1:A:195:VAL:HG13	1:A:310:TYR:HB3	1.91	0.51
1:A:245[A]:HIS:CD2	2:A:589:MPD:HM2	2.46	0.50
1:A:141:GLU:OE2	1:A:147:HIS:HD2	1.94	0.50
1:A:546:GLU:HG3	1:A:582:LEU:HD11	1.94	0.49
1:A:407:THR:O	1:A:409:ARG:N	2.46	0.49
1:A:540:ARG:HD2	5:A:728:HOH:O	2.11	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:204:LYS:HD2	1:A:372:GLY:HA3	1.93	0.49
1:A:92:LEU:HD23	1:A:92:LEU:H	1.77	0.48
1:A:84:ILE:O	1:A:293:LEU:O	2.30	0.48
1:A:427:PHE:HA	1:A:428:PRO:C	2.33	0.48
1:A:74:VAL:HG13	1:A:89:GLN:NE2	2.28	0.48
1:A:34:LEU:HD22	1:A:48:ALA:HB3	1.95	0.48
1:A:394:PRO:HG3	1:A:399:PHE:HD2	1.79	0.48
1:A:260:GLY:HA2	1:A:332:SER:CB	2.42	0.47
1:A:279:LYS:H	1:A:279:LYS:HE2	1.80	0.46
1:A:245[A]:HIS:HE1	1:A:278:LEU:HG	1.80	0.46
1:A:39:GLU:HG3	1:A:40:ILE:H	1.80	0.46
1:A:36:LEU:HD22	1:A:37:ILE:H	1.81	0.45
1:A:117:LYS:O	1:A:117:LYS:HD2	2.16	0.45
1:A:310:TYR:HA	1:A:313:ILE:HG22	1.97	0.45
1:A:249:LYS:HD2	1:A:281:PRO:HG3	1.97	0.45
1:A:317:GLU:O	1:A:320:ARG:HG3	2.17	0.45
2:A:594:MPD:H13	5:A:685:HOH:O	2.16	0.44
1:A:263:GLU:CD	1:A:332:SER:HA	2.38	0.44
1:A:494:VAL:HG11	1:A:531:TYR:HB2	1.99	0.44
1:A:120:PHE:HB2	1:A:189:MET:HE3	1.99	0.44
1:A:404:VAL:HG22	1:A:408:LEU:HG	2.00	0.44
1:A:448:HIS:CE1	1:A:456:LYS:H	2.34	0.44
1:A:446:TRP:CZ3	1:A:451:ILE:CD1	3.01	0.43
1:A:432:TRP:CD1	1:A:433:LEU:HD13	2.54	0.43
1:A:535:MET:O	1:A:539:ASN:HB2	2.18	0.43
1:A:25:MET:HB2	1:A:35:GLY:HA3	2.01	0.42
1:A:45:GLY:O	1:A:46:ASP:C	2.57	0.42
1:A:271:VAL:O	1:A:275:PHE:HB2	2.19	0.42
1:A:141:GLU:OE2	1:A:147:HIS:CD2	2.72	0.42
1:A:356:TYR:HB3	1:A:357:PRO:HD3	2.01	0.42
1:A:109:ALA:HB1	1:A:110:PRO:HD2	2.02	0.42
1:A:90:ARG:HA	1:A:91:PRO:HD3	1.82	0.42
1:A:33:GLU:H	1:A:34:LEU:HG	1.84	0.41
1:A:120:PHE:HA	1:A:139:VAL:HG12	2.01	0.41
1:A:245[A]:HIS:CE1	1:A:278:LEU:HG	2.56	0.41
1:A:100:GLY:HA3	1:A:269:THR:HG21	2.02	0.41
1:A:113:PRO:HB2	1:A:116:LYS:HB2	2.02	0.41
1:A:45:GLY:HA2	1:A:67:GLY:HA2	2.02	0.41
1:A:485:PRO:O	1:A:489:ARG:HG3	2.21	0.41
1:A:313:ILE:HD12	1:A:328:LEU:HD22	2.03	0.41
1:A:216:ARG:N	1:A:505:GLN:HE22	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:246:GLN:OE1	2:A:589:MPD:HM1	2.21	0.41
1:A:408:LEU:HD13	1:A:408:LEU:O	2.21	0.41
1:A:118:TRP:N	1:A:168:TYR:O	2.50	0.40
1:A:28:VAL:HG13	1:A:29:VAL:H	1.86	0.40
1:A:547:ILE:O	1:A:550:LEU:HB2	2.21	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	563/588 (96%)	487 (86%)	57 (10%)	19 (3%)	<b>3</b> <b>5</b>

All (19) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	28	VAL
1	A	301	PRO
1	A	302	VAL
1	A	22	GLY
1	A	46	ASP
1	A	89	GLN
1	A	92	LEU
1	A	165	GLU
1	A	408	LEU
1	A	99	THR
1	A	101	ASP
1	A	252	ASP
1	A	42	ARG
1	A	61	PRO
1	A	98	LYS
1	A	406	ASN

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Mol	Chain	Res	Type
1	A	195	VAL
1	A	41	ILE
1	A	404	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	476/492 (97%)	425 (89%)	51 (11%)	6 12

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

Mol	Chain	Res	Type
1	A	20	MET
1	A	25	MET
1	A	29	VAL
1	A	34	LEU
1	A	46	ASP
1	A	47	LYS
1	A	50	ILE
1	A	51	GLN
1	A	74	VAL
1	A	75	GLU
1	A	84	ILE
1	A	92	LEU
1	A	103	ILE
1	A	105	ARG
1	A	115	ASP
1	A	117	LYS
1	A	125	LYS
1	A	165	GLU
1	A	167	ASP
1	A	178	LYS
1	A	188	LYS
1	A	196	ARG
1	A	204	LYS

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Mol	Chain	Res	Type
1	A	233	PRO
1	A	240	LYS
1	A	244	GLN
1	A	270	ASP
1	A	272	LEU
1	A	277	LYS
1	A	278	LEU
1	A	279	LYS
1	A	285	LYS
1	A	298	SER
1	A	302	VAL
1	A	320	ARG
1	A	338	GLU
1	A	340	LEU
1	A	399	PHE
1	A	404	VAL
1	A	405	GLN
1	A	408	LEU
1	A	413	VAL
1	A	417	LEU
1	A	433	LEU
1	A	445	ASP
1	A	449	LYS
1	A	459	ARG
1	A	474	GLU
1	A	493	LEU
1	A	563	ARG
1	A	585	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	89	GLN
1	A	147	HIS
1	A	191	GLN
1	A	254	GLN
1	A	266	ASN
1	A	406	ASN
1	A	426	HIS
1	A	448	HIS
1	A	504	GLN
1	A	505	GLN

### 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](#)

12 ligands are modelled in this entry.

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	$\# Z  > 2$
2	MPD	A	599	-	7,7,7	0.28	0	9,10,10	0.21	0
3	ACY	A	591	-	1,3,3	1.35	0	0,3,3	0.00	-
3	ACY	A	592	-	1,3,3	1.26	0	0,3,3	0.00	-
3	ACY	A	596	-	1,3,3	1.51	0	0,3,3	0.00	-
3	ACY	A	598	-	1,3,3	1.53	0	0,3,3	0.00	-
4	TRS	A	595	-	7,7,7	0.30	0	9,9,9	0.34	0
2	MPD	A	589	-	7,7,7	0.24	0	9,10,10	0.47	0
3	ACY	A	590	-	1,3,3	1.59	0	0,3,3	0.00	-
3	ACY	A	597	-	1,3,3	1.63	0	0,3,3	0.00	-
2	MPD	A	600	-	7,7,7	0.27	0	9,10,10	0.33	0
2	MPD	A	594	-	7,7,7	0.27	0	9,10,10	0.33	0
3	ACY	A	593	-	1,3,3	1.45	0	0,3,3	0.00	-

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
2	MPD	A	599	-	-	1/5/5/5	-
2	MPD	A	589	-	-	1/5/5/5	-
2	MPD	A	594	-	-	3/5/5/5	-
4	TRS	A	595	-	-	4/9/9/9	-
2	MPD	A	600	-	-	0/5/5/5	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	595	TRS	C2-C-C1-O1
4	A	595	TRS	C3-C-C1-O1
2	A	599	MPD	O2-C2-C3-C4
2	A	594	MPD	O2-C2-C3-C4
4	A	595	TRS	N-C-C1-O1
2	A	594	MPD	C2-C3-C4-C5
2	A	594	MPD	C2-C3-C4-O4
4	A	595	TRS	C1-C-C3-O3
2	A	589	MPD	C2-C3-C4-C5

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	589	MPD	3	0
2	A	594	MPD	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 ⓘ

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	564/588 (95%)	0.32	66 (11%) 4 3	25, 55, 151, 178	0

All (66) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	96	ARG	7.6
1	A	57	ALA	7.0
1	A	28	VAL	6.3
1	A	395	PRO	6.2
1	A	396	GLY	5.8
1	A	61	PRO	5.7
1	A	40	ILE	5.2
1	A	404	VAL	5.2
1	A	37	ILE	5.0
1	A	98	LYS	4.6
1	A	36	LEU	4.6
1	A	102	PHE	4.6
1	A	30	ARG	4.3
1	A	27	GLU	4.3
1	A	22	GLY	4.2
1	A	355	GLY	4.1
1	A	357	PRO	4.1
1	A	26	TYR	4.1
1	A	39	GLU	4.0
1	A	31	VAL	4.0
1	A	407	THR	3.9
1	A	401	GLU	3.9
1	A	67	GLY	3.8
1	A	237	ALA	3.8
1	A	62	GLY	3.7
1	A	356	TYR	3.6
1	A	414	PHE	3.6

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Mol	Chain	Res	Type	RSRZ
1	A	343	ILE	3.5
1	A	360	LEU	3.3
1	A	95	ILE	3.3
1	A	25	MET	3.2
1	A	100	GLY	3.1
1	A	89	GLN	3.1
1	A	99	THR	3.0
1	A	359	TYR	3.0
1	A	397	GLY	3.0
1	A	97	GLU	2.9
1	A	66	VAL	2.9
1	A	361	ALA	2.9
1	A	345	GLY	2.9
1	A	35	GLY	2.9
1	A	354	GLU	2.9
1	A	399	PHE	2.8
1	A	42	ARG	2.8
1	A	94	VAL	2.7
1	A	48	ALA	2.7
1	A	111	ALA	2.7
1	A	41	ILE	2.6
1	A	107	VAL	2.6
1	A	341	ARG	2.5
1	A	65	VAL	2.4
1	A	346	ARG	2.4
1	A	398	ASP	2.3
1	A	76	LEU	2.3
1	A	101	ASP	2.3
1	A	21	LYS	2.2
1	A	52	VAL	2.2
1	A	344	SER	2.2
1	A	43	LEU	2.2
1	A	273	GLU	2.2
1	A	405	GLN	2.1
1	A	400	SER	2.1
1	A	106	GLY	2.1
1	A	50	ILE	2.0
1	A	20	MET	2.0
1	A	60	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 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. The B-factors column lists the minimum, median, 95<sup>th</sup> 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	MPD	A	594	8/8	0.48	0.61	103,103,104,105	0
3	ACY	A	593	4/4	0.60	0.31	115,116,116,118	0
2	MPD	A	600	8/8	0.70	0.37	81,82,83,83	0
3	ACY	A	596	4/4	0.81	0.31	99,100,100,101	0
2	MPD	A	589	8/8	0.81	0.37	77,79,80,81	0
4	TRS	A	595	8/8	0.84	0.30	73,74,75,75	0
2	MPD	A	599	8/8	0.84	0.30	94,96,98,98	0
3	ACY	A	597	4/4	0.85	0.24	65,66,66,66	0
3	ACY	A	590	4/4	0.86	0.15	73,73,73,73	0
3	ACY	A	592	4/4	0.91	0.61	95,96,96,97	0
3	ACY	A	591	4/4	0.92	0.50	78,79,79,79	0
3	ACY	A	598	4/4	0.96	0.12	89,89,89,90	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.