



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 03:52 PM UTC

PDB ID : 3QIA / pdb_00003qia
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

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

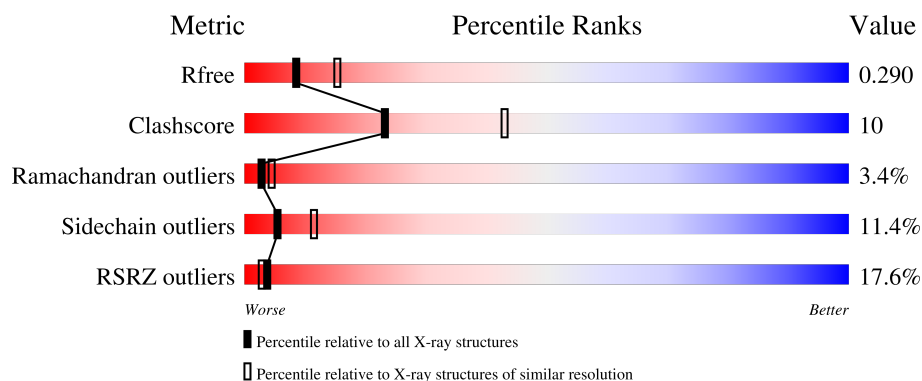
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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	588	17% 69% 21% 5% • •

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.

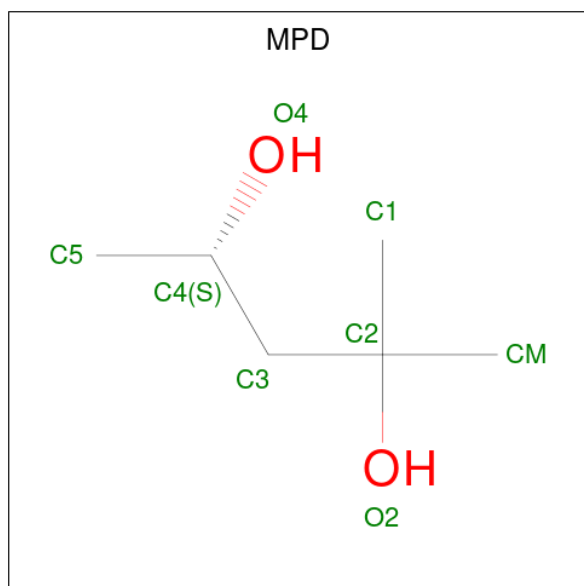
- Molecule 1 is a protein called V-type ATP synthase alpha chain.

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 (CCD ID: MPD) (formula: C₆H₁₄O₂).



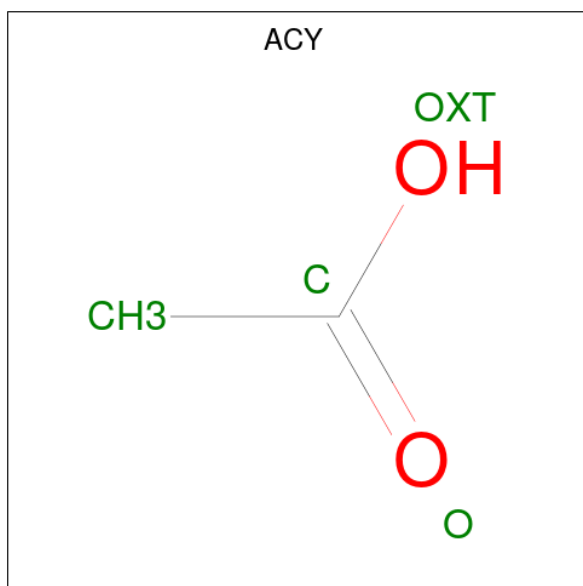
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
2	A	1	8	6	2	0	0
2	A	1	8	6	2	0	0
2	A	1	8	6	2	0	0

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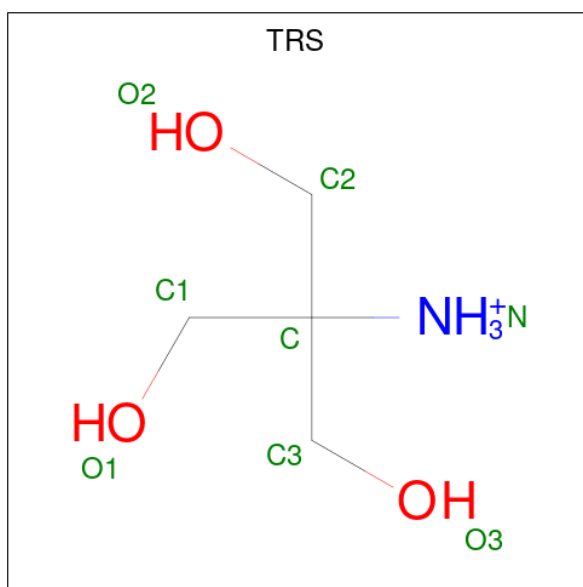
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			8	6	2		

- Molecule 3 is ACETIC ACID (CCD ID: ACY) (formula: $C_2H_4O_2$).



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 (CCD ID: TRS) (formula: $C_4H_{12}NO_3$).



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

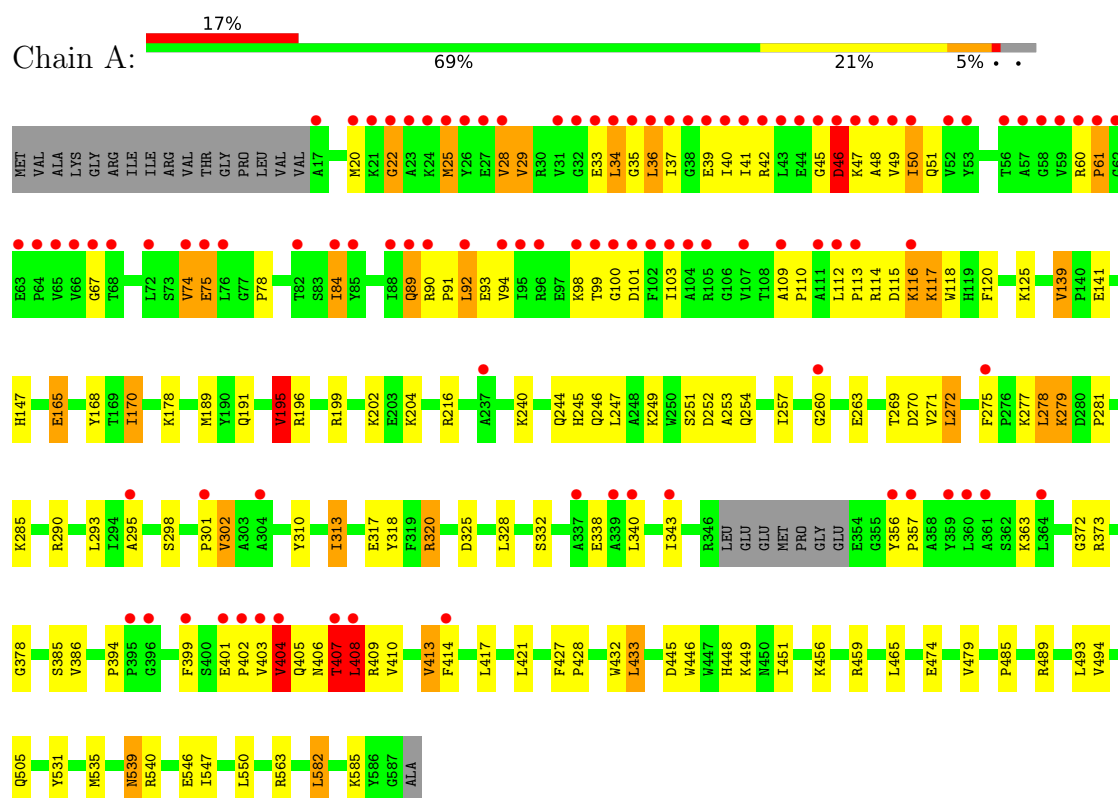
- Molecule 5 is water.

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, 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: 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, α , β , γ	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) 99.6 (27.32-2.60)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	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 (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	49.3	Xtriage
Anisotropy	0.042	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 53.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	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 ²)	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.*

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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: MPD, ACY, 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	0.56	0/4559	0.87	4/6171 (0.1%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	479	VAL	N-CA-C	5.53	118.51	113.20
1	A	170	ILE	N-CA-C	5.31	116.67	110.62
1	A	407	THR	N-CA-C	-5.30	105.61	111.71
1	A	459	ARG	N-CA-CB	5.20	117.77	110.12

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	93	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	94	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 (94) 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:407:THR:C	1:A:409:ARG:H	2.11	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:147:HIS:HE1	1:A:318:TYR:OH	1.87	0.58
1:A:202:LYS:NZ	1:A:378:GLY:O	2.35	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:60:ARG:CB	1:A:61:PRO:HD2	2.35	0.56
1:A:114:ARG:HA	1:A:170:ILE:HG22	1.88	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: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:427:PHE:HA	1:A:428:PRO:C	2.33	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
1:A:204:LYS:HD2	1:A:372:GLY:HA3	1.93	0.49
1:A:263:GLU:CD	1:A:332:SER:HA	2.38	0.49
1:A:92:LEU:H	1:A:92:LEU:HD23	1.77	0.48
1:A:84:ILE:O	1:A:293:LEU:O	2.30	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:45:GLY:O	1:A:46:ASP:C	2.57	0.47
1:A:120:PHE:HB2	1:A:189:MET:HE3	1.96	0.47
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:HD2	1:A:117:LYS:O	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:139:VAL:HG11	1:A:189:MET:HE2	2.00	0.44
1:A:494:VAL:HG11	1:A:531:TYR:HB2	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: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:90:ARG:HA	1:A:91:PRO:HD3	1.82	0.42
1:A:109:ALA:HB1	1:A:110:PRO:HD2	2.02	0.42
1:A:413:VAL:C	1:A:414:PHE:HD1	2.28	0.42
1:A:407:THR:C	1:A:409:ARG:N	2.77	0.42
1:A:33:GLU:H	1:A:34:LEU:HG	1.84	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:401:GLU:CD	1:A:405:GLN:HG3	2.45	0.41
1:A:36:LEU:HD13	1:A:37:ILE:C	2.46	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:45:GLY:HA2	1:A:67:GLY:HA2	2.02	0.41
1:A:113:PRO:HB2	1:A:116:LYS:HB2	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
1:A:246:GLN:OE1	2:A:589:MPD:HM1	2.21	0.41
1:A:408:LEU:O	1:A:408:LEU:HD13	2.21	0.41
1:A:28:VAL:HG13	1:A:29:VAL:H	1.86	0.40
1:A:118:TRP:N	1:A:168:TYR:O	2.50	0.40
1:A:408:LEU:C	1:A:410:VAL:H	2.29	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%)	3 4

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

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Mol	Chain	Res	Type
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
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%)	422 (89%)	54 (11%)	5 12

All (54) 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	36	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

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Mol	Chain	Res	Type
1	A	103	ILE
1	A	115	ASP
1	A	116	LYS
1	A	117	LYS
1	A	125	LYS
1	A	139	VAL
1	A	165	GLU
1	A	178	LYS
1	A	195	VAL
1	A	196	ARG
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	313	ILE
1	A	320	ARG
1	A	338	GLU
1	A	340	LEU
1	A	343	ILE
1	A	403	VAL
1	A	404	VAL
1	A	407	THR
1	A	408	LEU
1	A	413	VAL
1	A	417	LEU
1	A	421	LEU
1	A	433	LEU
1	A	445	ASP
1	A	449	LYS
1	A	465	LEU
1	A	474	GLU
1	A	493	LEU
1	A	539	ASN
1	A	563	ARG
1	A	582	LEU
1	A	585	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	89	GLN
1	A	147	HIS
1	A	191	GLN
1	A	224	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
1	A	529	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](#)

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	$\# Z > 2$
3	ACY	A	591	-	3,3,3	0.83	0	3,3,3	0.74	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	ACY	A	592	-	3,3,3	0.80	0	3,3,3	0.91	0
3	ACY	A	596	-	3,3,3	0.81	0	3,3,3	0.82	0
4	TRS	A	595	-	7,7,7	0.31	0	9,9,9	0.35	0
3	ACY	A	598	-	3,3,3	0.82	0	3,3,3	0.76	0
3	ACY	A	590	-	3,3,3	0.81	0	3,3,3	0.74	0
3	ACY	A	593	-	3,3,3	0.81	0	3,3,3	0.83	0
3	ACY	A	597	-	3,3,3	0.81	0	3,3,3	0.84	0
2	MPD	A	594	-	7,7,7	0.29	0	9,10,10	0.35	0
2	MPD	A	599	-	7,7,7	0.29	0	9,10,10	0.22	0
2	MPD	A	600	-	7,7,7	0.29	0	9,10,10	0.36	0
2	MPD	A	589	-	7,7,7	0.25	0	9,10,10	0.44	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
4	TRS	A	595	-	-	6/9/9/9	-
2	MPD	A	594	-	-	3/5/5/5	-
2	MPD	A	599	-	-	2/5/5/5	-
2	MPD	A	600	-	-	0/5/5/5	-
2	MPD	A	589	-	-	2/5/5/5	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (13) 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
4	A	595	TRS	N-C-C1-O1
2	A	594	MPD	C2-C3-C4-O4
4	A	595	TRS	C1-C-C3-O3
2	A	594	MPD	C2-C3-C4-C5
4	A	595	TRS	C2-C-C3-O3
2	A	589	MPD	O2-C2-C3-C4
2	A	594	MPD	O2-C2-C3-C4
2	A	599	MPD	O2-C2-C3-C4

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Mol	Chain	Res	Type	Atoms
2	A	589	MPD	CM-C2-C3-C4
2	A	599	MPD	C1-C2-C3-C4
4	A	595	TRS	N-C-C3-O3

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	594	MPD	1	0
2	A	589	MPD	3	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, 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	564/588 (95%)	0.76	99 (17%) 4 3	18, 54, 151, 178	3 (0%)

All (99) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	25	MET	7.2
1	A	37	ILE	7.0
1	A	36	LEU	6.7
1	A	59	VAL	6.3
1	A	26	TYR	6.2
1	A	404	VAL	6.2
1	A	35	GLY	5.8
1	A	22	GLY	5.8
1	A	57	ALA	5.7
1	A	58	GLY	5.6
1	A	48	ALA	5.5
1	A	17	ALA	5.4
1	A	340	LEU	5.3
1	A	24	LYS	5.1
1	A	31	VAL	5.0
1	A	28	VAL	4.8
1	A	395	PRO	4.7
1	A	41	ILE	4.6
1	A	46	ASP	4.5
1	A	72	LEU	4.5
1	A	403	VAL	4.4
1	A	34	LEU	4.4
1	A	100	GLY	4.3
1	A	23	ALA	4.3
1	A	43	LEU	4.2
1	A	102	PHE	4.1
1	A	20	MET	4.1

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Mol	Chain	Res	Type	RSRZ
1	A	396	GLY	4.0
1	A	414	PHE	3.9
1	A	65	VAL	3.9
1	A	92	LEU	3.8
1	A	111	ALA	3.8
1	A	47	LYS	3.8
1	A	104	ALA	3.8
1	A	89	GLN	3.7
1	A	66	VAL	3.6
1	A	45	GLY	3.6
1	A	96	ARG	3.6
1	A	32	GLY	3.6
1	A	402	PRO	3.5
1	A	399	PHE	3.5
1	A	103	ILE	3.5
1	A	74	VAL	3.5
1	A	40	ILE	3.4
1	A	237	ALA	3.4
1	A	21	LYS	3.3
1	A	42	ARG	3.3
1	A	99	THR	3.3
1	A	53	TYR	3.3
1	A	56	THR	3.3
1	A	49	VAL	3.3
1	A	50	ILE	3.2
1	A	275	PHE	3.2
1	A	64	PRO	3.2
1	A	39	GLU	3.2
1	A	75	GLU	3.2
1	A	67	GLY	3.2
1	A	60	ARG	3.1
1	A	44	GLU	3.1
1	A	61	PRO	3.0
1	A	88	ILE	3.0
1	A	98	LYS	2.9
1	A	95	ILE	2.9
1	A	112	LEU	2.9
1	A	360	LEU	2.9
1	A	356	TYR	2.8
1	A	359	TYR	2.8
1	A	107	VAL	2.8
1	A	401	GLU	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	84	ILE	2.8
1	A	364	LEU	2.8
1	A	38	GLY	2.7
1	A	343	ILE	2.7
1	A	82	THR	2.7
1	A	85	TYR	2.6
1	A	52	VAL	2.6
1	A	94	VAL	2.6
1	A	408	LEU	2.6
1	A	33	GLU	2.6
1	A	339	ALA	2.6
1	A	63	GLU	2.6
1	A	62	GLY	2.6
1	A	113	PRO	2.6
1	A	68	THR	2.5
1	A	90	ARG	2.5
1	A	295	ALA	2.4
1	A	361	ALA	2.4
1	A	27	GLU	2.4
1	A	116	LYS	2.4
1	A	101	ASP	2.3
1	A	301	PRO	2.3
1	A	407	THR	2.2
1	A	105	ARG	2.2
1	A	357	PRO	2.2
1	A	76	LEU	2.2
1	A	109	ALA	2.1
1	A	260	GLY	2.1
1	A	337	ALA	2.1
1	A	304	ALA	2.1

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
3	ACY	A	593	4/4	0.59	0.20	115,116,116,118	0
3	ACY	A	597	4/4	0.60	0.21	65,66,66,66	0
3	ACY	A	596	4/4	0.69	0.16	99,100,100,101	0
2	MPD	A	594	8/8	0.69	0.30	103,103,104,105	0
3	ACY	A	598	4/4	0.71	0.20	89,89,89,90	0
2	MPD	A	600	8/8	0.72	0.26	81,82,83,83	0
3	ACY	A	590	4/4	0.77	0.16	73,73,73,73	0
3	ACY	A	591	4/4	0.80	0.29	78,79,79,79	0
2	MPD	A	599	8/8	0.81	0.26	94,96,98,98	0
2	MPD	A	589	8/8	0.82	0.28	77,79,80,81	0
3	ACY	A	592	4/4	0.82	0.30	95,96,96,97	0
4	TRS	A	595	8/8	0.82	0.14	73,74,75,75	0

6.5 Other polymers [i](#)

There are no such residues in this entry.