



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 08:24 AM GMT

PDB ID : 3EIU
Title : A second transient position of ATP on its trail to the nucleotide-binding site of subunit B of the motor protein A1Ao ATP synthase
Authors : Manimekalai, S.M.S.; Kumar, A.; Balakrishna, A.M.; Gruber, G.
Deposited on : 2008-09-17
Resolution : 3.43 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
<http://wwpdb.org/validation/2016/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 : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

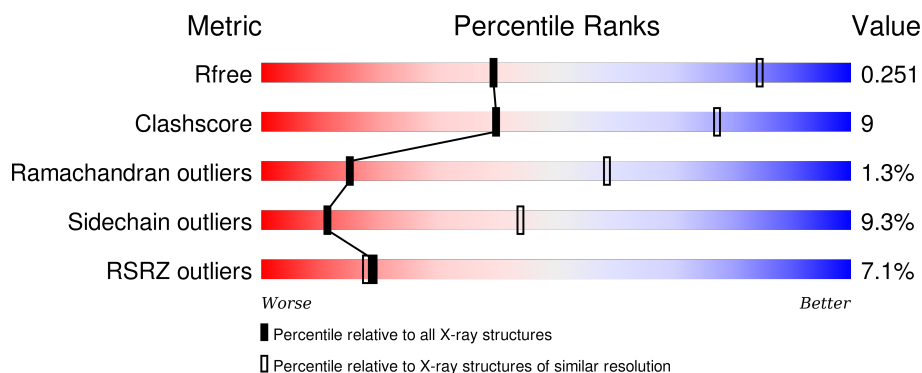
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.43 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}	91344	1007 (3.54-3.34)
Clashscore	102246	1044 (3.52-3.36)
Ramachandran outliers	100387	1013 (3.52-3.36)
Sidechain outliers	100360	1014 (3.52-3.36)
RSRZ outliers	91569	1012 (3.54-3.34)

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. 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	469	<div> <div>8%</div> <div>65%</div> <div>22%</div> <div>•</div> <div>11%</div> </div>
1	B	469	<div> <div>5%</div> <div>66%</div> <div>22%</div> <div>•</div> <div>9%</div> </div>

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	ATP	A	461	-	-	-	X
3	AES	B	461	-	-	-	X

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 6550 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.

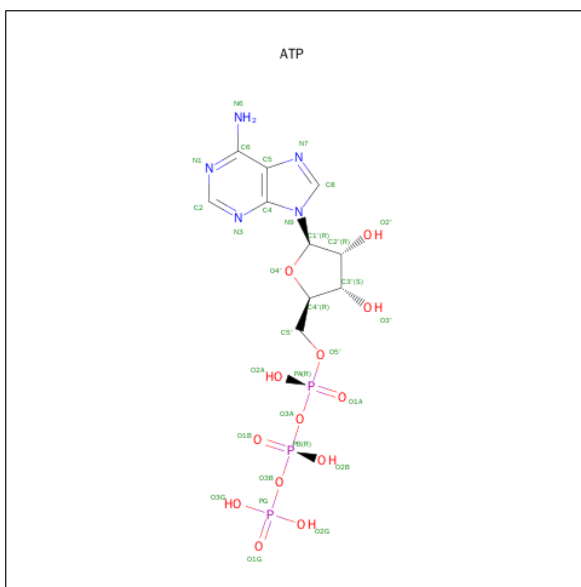
- Molecule 1 is a protein called V-type ATP synthase beta chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	418	Total	C	N	O	S	0	0	0
			3221	2044	552	614	11			
1	B	426	Total	C	N	O	S	0	0	0
			3285	2085	566	623	11			

There are 22 discrepancies between the modelled and reference sequences:

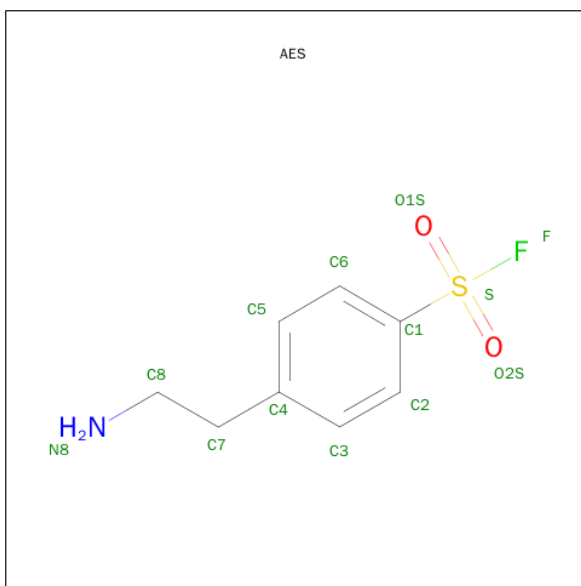
Chain	Residue	Modelled	Actual	Comment	Reference
A	-8	MET	-	EXPRESSION TAG	UNP Q60187
A	-7	LYS	-	EXPRESSION TAG	UNP Q60187
A	-6	HIS	-	EXPRESSION TAG	UNP Q60187
A	-5	HIS	-	EXPRESSION TAG	UNP Q60187
A	-4	HIS	-	EXPRESSION TAG	UNP Q60187
A	-3	HIS	-	EXPRESSION TAG	UNP Q60187
A	-2	HIS	-	EXPRESSION TAG	UNP Q60187
A	-1	HIS	-	EXPRESSION TAG	UNP Q60187
A	0	PRO	-	EXPRESSION TAG	UNP Q60187
A	2	VAL	ALA	SEE REMARK 999	UNP Q60187
A	416	TRP	ARG	ENGINEERED	UNP Q60187
B	-8	MET	-	EXPRESSION TAG	UNP Q60187
B	-7	LYS	-	EXPRESSION TAG	UNP Q60187
B	-6	HIS	-	EXPRESSION TAG	UNP Q60187
B	-5	HIS	-	EXPRESSION TAG	UNP Q60187
B	-4	HIS	-	EXPRESSION TAG	UNP Q60187
B	-3	HIS	-	EXPRESSION TAG	UNP Q60187
B	-2	HIS	-	EXPRESSION TAG	UNP Q60187
B	-1	HIS	-	EXPRESSION TAG	UNP Q60187
B	0	PRO	-	EXPRESSION TAG	UNP Q60187
B	2	VAL	ALA	SEE REMARK 999	UNP Q60187
B	416	TRP	ARG	ENGINEERED	UNP Q60187

- Molecule 2 is ADENOSINE-5'-TRIPHOSPHATE (three-letter code: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			31	10	5	13	3		

- Molecule 3 is 4-(2-AMINOETHYL)BENZENESULFONYL FLUORIDE (three-letter code: AES) (formula: $C_8H_{10}FNO_2S$).

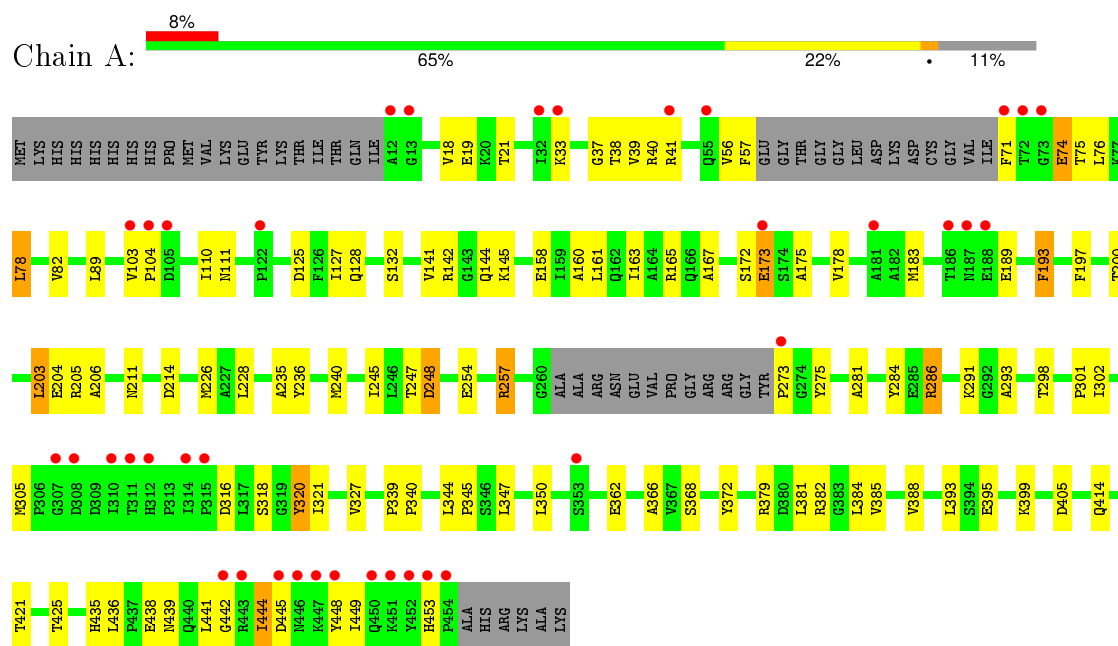


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	B	1	Total	C	F	N	O	S	
			13	8	1	1	2	1	0

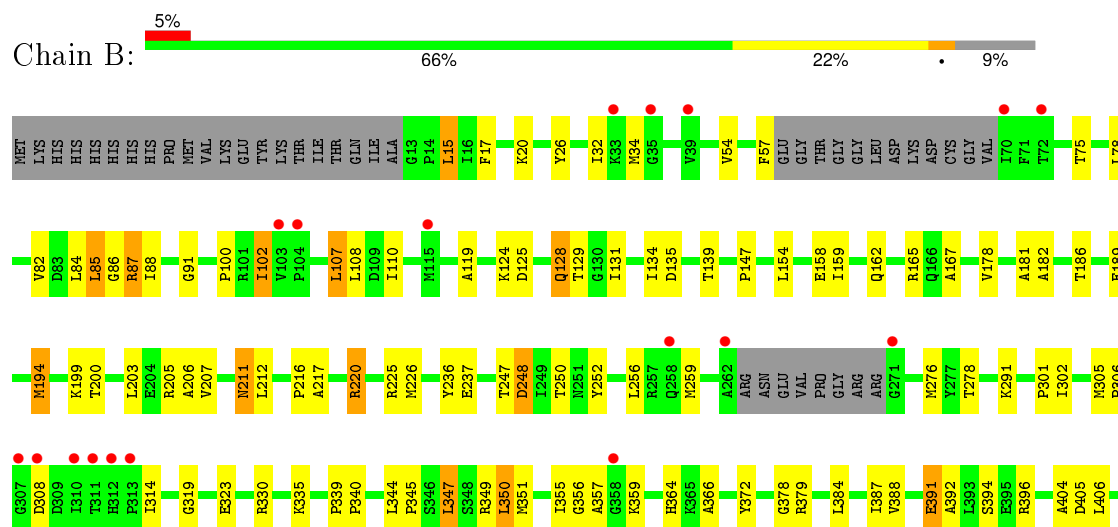
3 Residue-property plots

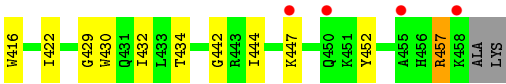
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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 beta chain



• Molecule 1: V-type ATP synthase beta chain





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	75.69 Å 96.87 Å 129.63 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	24.62 – 3.43 24.62 – 3.43	Depositor EDS
% Data completeness (in resolution range)	90.5 (24.62-3.43) 90.5 (24.62-3.43)	Depositor EDS
R_{merge}	0.17	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.98 (at 3.46 Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.246 , 0.315 0.241 , 0.251	Depositor DCC
R_{free} test set	599 reflections (5.24%)	DCC
Wilson B-factor (Å ²)	76.7	Xtriage
Anisotropy	0.143	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 50.7	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	0 of 12032 reflections	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	6550	wwPDB-VP
Average B, all atoms (Å ²)	72.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.97% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: AES, ATP

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	0.33	0/3283	0.53	0/4453
1	B	0.32	0/3349	0.51	0/4542
All	All	0.33	0/6632	0.52	0/8995

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

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	3221	0	3222	58	0
1	B	3285	0	3287	61	0
2	A	31	0	12	0	0
3	B	13	0	10	1	0
All	All	6550	0	6531	115	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 (115) 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:B:388:VAL:O	1:B:392:ALA:HB3	1.49	1.12
1:A:327:VAL:HG21	1:A:345:PRO:HB2	1.67	0.76
1:B:248:ASP:H	1:B:302:ILE:HB	1.51	0.74
1:A:248:ASP:H	1:A:302:ILE:HB	1.54	0.73
1:A:385:VAL:HG22	1:A:393:LEU:HD11	1.73	0.71
1:A:197:PHE:HB3	1:A:203:LEU:HD22	1.72	0.71
1:B:452:TYR:HA	1:B:457:ARG:HD3	1.76	0.68
1:A:347:LEU:HB3	1:B:349:ARG:HH22	1.59	0.67
1:A:132:SER:HB2	1:A:425:THR:HG23	1.76	0.67
1:A:128:GLN:HE22	1:A:421:THR:HA	1.58	0.66
1:A:127:ILE:HG13	1:A:142:ARG:HG2	1.79	0.65
1:B:139:THR:HB	1:B:351:MET:HG3	1.81	0.62
1:B:129:THR:HG23	1:B:131:ILE:H	1.64	0.62
1:A:366:ALA:HB1	1:A:444:ILE:HG22	1.80	0.61
1:A:128:GLN:NE2	1:A:421:THR:HA	2.16	0.61
1:A:438:GLU:HA	1:A:441:LEU:HD13	1.82	0.60
1:A:197:PHE:HB3	1:A:203:LEU:CD2	2.32	0.58
1:A:19:GLU:HG3	1:A:76:LEU:HA	1.86	0.58
1:B:323:GLU:HG2	1:B:350:LEU:HD21	1.86	0.57
1:B:158:GLU:HB3	1:B:416:TRP:CZ2	2.39	0.57
1:A:281:ALA:HA	1:A:284:TYR:CZ	2.40	0.57
1:B:88:ILE:HD13	1:B:194:MET:HG3	1.86	0.57
1:A:347:LEU:HD21	1:B:347:LEU:HD22	1.87	0.57
1:B:211:ASN:HD21	1:B:220:ARG:CD	2.18	0.56
1:A:344:LEU:HB2	1:A:345:PRO:HD3	1.87	0.56
1:B:344:LEU:HD11	1:B:379:ARG:HG3	1.87	0.56
1:A:381:LEU:O	1:A:385:VAL:HG23	2.06	0.55
1:A:144:GLN:HG3	1:A:350:LEU:HD12	1.90	0.53
1:B:306:PRO:HD2	1:B:314:ILE:HG22	1.90	0.53
1:A:125:ASP:HB3	1:A:142:ARG:NH1	2.25	0.52
1:A:144:GLN:H	1:A:298:THR:HG23	1.74	0.52
1:B:87:ARG:HH11	1:B:100:PRO:HG2	1.74	0.51
1:A:247:THR:HA	1:A:302:ILE:HD13	1.91	0.51
1:B:129:THR:HG21	1:B:134:ILE:HB	1.92	0.51
1:A:273:PRO:HB3	1:A:275:TYR:CE2	2.46	0.51
1:B:388:VAL:O	1:B:392:ALA:CB	2.41	0.51
1:A:183:MET:HA	1:A:211:ASN:HB3	1.92	0.51
1:B:86:GLY:HA2	1:B:203:LEU:HG	1.92	0.50
1:A:40:ARG:HD2	1:A:56:VAL:HG21	1.92	0.50
1:B:344:LEU:HB2	1:B:345:PRO:HD3	1.92	0.50
1:A:254:GLU:HA	1:A:257:ARG:HB3	1.93	0.50
1:B:178:VAL:O	1:B:206:ALA:HA	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:429:GLY:O	1:B:432:ILE:HG22	2.12	0.50
1:B:85:LEU:H	1:B:207:VAL:HG22	1.77	0.49
1:B:236:TYR:HD2	1:B:237:GLU:HG3	1.76	0.49
1:A:193:PHE:N	1:A:193:PHE:CD2	2.81	0.49
1:A:165:ARG:HD2	1:A:200:THR:HG21	1.95	0.48
1:A:235:ALA:HA	1:A:240:MET:O	2.13	0.48
1:B:344:LEU:HA	1:B:372:TYR:CE1	2.49	0.48
1:A:284:TYR:HB3	1:A:320:TYR:CE2	2.47	0.48
1:A:379:ARG:HH21	1:B:319:GLY:HA2	1.78	0.48
1:A:193:PHE:HD2	1:A:193:PHE:N	2.11	0.48
1:B:211:ASN:HD21	1:B:220:ARG:HD2	1.78	0.47
1:B:225:ARG:NH1	1:B:252:TYR:OH	2.46	0.47
1:A:178:VAL:O	1:A:206:ALA:HA	2.15	0.47
1:B:442:GLY:C	1:B:444:ILE:H	2.19	0.46
1:A:103:VAL:HA	1:A:104:PRO:HD3	1.85	0.46
1:B:366:ALA:HB1	1:B:444:ILE:HG13	1.97	0.46
1:A:160:ALA:HB1	1:A:245:ILE:HG21	1.96	0.45
1:B:186:THR:HG23	1:B:189:GLU:H	1.81	0.45
1:B:384:LEU:HA	1:B:387:ILE:HD12	1.98	0.45
1:A:173:GLU:H	1:A:173:GLU:HG2	1.55	0.45
1:A:145:LYS:HD3	1:A:284:TYR:O	2.15	0.45
1:B:87:ARG:NH1	1:B:100:PRO:HG2	2.32	0.45
1:A:379:ARG:O	1:A:382:ARG:HB2	2.17	0.45
1:B:182:ALA:HA	1:B:247:THR:CG2	2.46	0.44
1:B:339:PRO:HA	1:B:340:PRO:HD3	1.80	0.44
1:A:316:ASP:OD2	1:B:330:ARG:HB2	2.16	0.44
1:B:256:LEU:HD13	1:B:276:MET:HG2	1.99	0.44
1:B:162:GLN:CA	1:B:165:ARG:HH21	2.31	0.44
1:B:165:ARG:HD3	1:B:200:THR:HG21	1.98	0.44
1:B:129:THR:HG22	1:B:135:ASP:CG	2.38	0.44
1:A:78:LEU:HB2	1:A:226:MET:SD	2.58	0.43
1:A:228:LEU:HD13	1:A:286:ARG:HG3	1.99	0.43
1:B:355:ILE:HG13	1:B:364:HIS:CG	2.53	0.43
1:A:236:TYR:HE1	1:A:291:LYS:HB2	1.84	0.43
1:B:378:GLY:HA3	1:B:404:ALA:HB2	1.99	0.43
1:B:181:ALA:O	1:B:247:THR:HG22	2.19	0.43
1:B:154:LEU:HD21	1:B:330:ARG:HG2	2.01	0.43
1:B:26:TYR:OH	3:B:461:AES:H72	2.17	0.43
1:A:141:VAL:HG21	1:A:350:LEU:O	2.19	0.43
1:B:124:LYS:HG3	1:B:125:ASP:H	1.83	0.43
1:B:430:TRP:O	1:B:434:THR:HG23	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:391:GLU:OE1	1:B:391:GLU:HA	2.17	0.43
1:A:175:ALA:O	1:A:240:MET:HB2	2.19	0.43
1:A:445:ASP:HB3	1:A:448:TYR:CD1	2.54	0.43
1:B:131:ILE:HB	1:B:134:ILE:HD12	2.01	0.43
1:B:356:GLY:O	1:B:359:LYS:HB2	2.18	0.43
1:B:162:GLN:HA	1:B:165:ARG:HE	1.84	0.42
1:A:33:LYS:HB2	1:A:74:GLU:HB3	2.00	0.42
1:B:182:ALA:HA	1:B:247:THR:HG22	2.00	0.42
1:A:449:ILE:O	1:A:453:HIS:HB2	2.20	0.42
1:A:127:ILE:CG1	1:A:142:ARG:HG2	2.48	0.42
1:B:78:LEU:O	1:B:107:LEU:HA	2.19	0.42
1:A:132:SER:H	1:A:414:GLN:HE22	1.67	0.42
1:A:301:PRO:HG3	1:A:320:TYR:CE2	2.54	0.42
1:B:128:GLN:O	1:B:167:ALA:HA	2.20	0.42
1:B:335:LYS:HG3	1:B:335:LYS:O	2.20	0.42
1:A:286:ARG:H	1:A:286:ARG:HG2	1.72	0.41
1:B:91:GLY:O	1:B:226:MET:HG3	2.21	0.41
1:B:147:PRO:HB3	1:B:301:PRO:HG2	2.02	0.41
1:A:18:VAL:HA	1:A:75:THR:HA	2.02	0.41
1:A:167:ALA:O	1:A:205:ARG:NH1	2.53	0.41
1:A:318:SER:HA	1:A:321:ILE:HD12	2.03	0.41
1:B:102:ILE:H	1:B:102:ILE:HG13	1.66	0.41
1:B:159:ILE:HD12	1:B:339:PRO:HB3	2.03	0.41
1:B:17:PHE:HB2	1:B:110:ILE:HD11	2.02	0.40
1:A:110:ILE:HD12	1:A:111:ASN:H	1.86	0.40
1:A:125:ASP:C	1:A:142:ARG:HG3	2.42	0.40
1:A:339:PRO:HA	1:A:340:PRO:HD3	2.00	0.40
1:A:384:LEU:O	1:A:388:VAL:HG22	2.22	0.40
1:B:15:LEU:HA	1:B:54:VAL:O	2.21	0.40
1:B:119:ALA:HB2	1:B:291:LYS:HA	2.03	0.40
1:A:344:LEU:HA	1:A:372:TYR:CE2	2.56	0.40
1:B:217:ALA:HA	1:B:220:ARG:HG3	2.04	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	412/469 (88%)	367 (89%)	40 (10%)	5 (1%)	16	60
1	B	420/469 (90%)	371 (88%)	43 (10%)	6 (1%)	14	56
All	All	832/938 (89%)	738 (89%)	83 (10%)	11 (1%)	15	58

All (11) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	38	THR
1	A	442	GLY
1	B	84	LEU
1	B	457	ARG
1	B	85	LEU
1	B	248	ASP
1	B	357	ALA
1	A	293	ALA
1	A	204	GLU
1	A	37	GLY
1	B	216	PRO

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	343/384 (89%)	311 (91%)	32 (9%)	11	44
1	B	348/384 (91%)	316 (91%)	32 (9%)	11	44
All	All	691/768 (90%)	627 (91%)	64 (9%)	11	44

All (64) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	21	THR

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Mol	Chain	Res	Type
1	A	39	VAL
1	A	41	ARG
1	A	57	PHE
1	A	71	PHE
1	A	74	GLU
1	A	78	LEU
1	A	82	VAL
1	A	89	LEU
1	A	158	GLU
1	A	161	LEU
1	A	163	ILE
1	A	172	SER
1	A	173	GLU
1	A	189	GLU
1	A	193	PHE
1	A	203	LEU
1	A	214	ASP
1	A	248	ASP
1	A	257	ARG
1	A	286	ARG
1	A	305	MET
1	A	320	TYR
1	A	362	GLU
1	A	368	SER
1	A	395	GLU
1	A	399	LYS
1	A	405	ASP
1	A	435	HIS
1	A	436	LEU
1	A	439	ASN
1	A	444	ILE
1	B	15	LEU
1	B	20	LYS
1	B	32	ILE
1	B	34	MET
1	B	57	PHE
1	B	75	THR
1	B	82	VAL
1	B	87	ARG
1	B	102	ILE
1	B	107	LEU
1	B	108	LEU

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Mol	Chain	Res	Type
1	B	128	GLN
1	B	194	MET
1	B	199	LYS
1	B	205	ARG
1	B	211	ASN
1	B	212	LEU
1	B	220	ARG
1	B	250	THR
1	B	259	MET
1	B	278	THR
1	B	305	MET
1	B	308	ASP
1	B	347	LEU
1	B	350	LEU
1	B	391	GLU
1	B	394	SER
1	B	396	ARG
1	B	405	ASP
1	B	406	LEU
1	B	422	ILE
1	B	447	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	55	GLN
1	A	128	GLN
1	A	138	ASN
1	A	238	HIS
1	A	299	GLN
1	A	312	HIS
1	A	414	GLN
1	A	417	ASN
1	A	439	ASN
1	B	111	ASN
1	B	116	ASN
1	B	128	GLN
1	B	211	ASN
1	B	299	GLN
1	B	414	GLN
1	B	417	ASN
1	B	450	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 ⓘ

2 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	ATP	A	461	-	24,33,33	1.02	1 (4%)	31,52,52	1.88	5 (16%)
3	AES	B	461	-	11,13,13	0.74	0	17,18,18	1.32	2 (11%)

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	ATP	A	461	-	-	0/18/38/38	0/3/3/3
3	AES	B	461	-	-	0/9/9/9	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	461	ATP	C5-C4	3.19	1.47	1.40

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	461	ATP	N3-C2-N1	-7.24	123.35	128.89
2	A	461	ATP	C4-C5-N7	-3.03	106.69	109.48
2	A	461	ATP	PB-O3B-PG	-2.96	122.75	132.67
2	A	461	ATP	PA-O3A-PB	-2.94	124.46	132.73
3	B	461	AES	O2S-S-O1S	-2.83	109.98	118.95
2	A	461	ATP	C2'-C1'-N9	-2.43	110.58	114.29
3	B	461	AES	F-S-C1	3.67	110.84	102.39

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	461	AES	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, 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	418/469 (89%)	0.36	38 (9%) 11 11	55, 70, 89, 104	0
1	B	426/469 (90%)	0.19	22 (5%) 31 27	26, 70, 89, 93	0
All	All	844/938 (89%)	0.27	60 (7%) 19 18	26, 70, 89, 104	0

All (60) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	311	THR	5.3
1	A	308	ASP	4.5
1	A	311	THR	3.9
1	A	273	PRO	3.8
1	A	454	PRO	3.6
1	A	12	ALA	3.4
1	B	312	HIS	3.3
1	A	188	GLU	3.3
1	A	73	GLY	3.3
1	A	442	GLY	3.2
1	A	446	ASN	3.1
1	A	452	TYR	3.1
1	B	271	GLY	3.0
1	A	103	VAL	3.0
1	B	458	LYS	3.0
1	A	453	HIS	3.0
1	B	35	GLY	3.0
1	A	307	GLY	3.0
1	A	445	ASP	2.9
1	B	307	GLY	2.9
1	A	315	PRO	2.9
1	B	455	ALA	2.9
1	A	447	LYS	2.9
1	A	450	GLN	2.9

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Mol	Chain	Res	Type	RSRZ
1	B	310	ILE	2.9
1	B	103	VAL	2.8
1	A	312	HIS	2.7
1	A	55	GLN	2.7
1	B	72	THR	2.7
1	A	187	ASN	2.7
1	A	104	PRO	2.6
1	A	314	ILE	2.6
1	B	115	MET	2.6
1	A	443	ARG	2.6
1	A	41	ARG	2.6
1	A	33	LYS	2.5
1	B	262	ALA	2.5
1	B	450	GLN	2.5
1	A	181	ALA	2.4
1	A	32	ILE	2.3
1	A	451	LYS	2.3
1	A	353	SER	2.3
1	A	122	PRO	2.3
1	A	186	THR	2.3
1	B	104	PRO	2.2
1	A	173	GLU	2.2
1	A	13	GLY	2.2
1	A	71	PHE	2.2
1	A	105	ASP	2.2
1	B	70	ILE	2.2
1	A	72	THR	2.2
1	B	447	LYS	2.2
1	A	310	ILE	2.2
1	B	358	GLY	2.2
1	B	33	LYS	2.1
1	B	308	ASP	2.1
1	B	39	VAL	2.1
1	A	448	TYR	2.1
1	B	313	PRO	2.0
1	B	258	GLN	2.0

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(\AA^2)	Q<0.9
3	AES	B	461	13/13	0.86	0.42	3.17	72,73,74,74	0
2	ATP	A	461	31/31	0.58	0.53	2.96	78,78,80,80	31

6.5 Other polymers [i](#)

There are no such residues in this entry.