



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 06:47 PM GMT

PDB ID : 1CG0
Title : STRUCTURE OF ADENYLOSUCCINATE SYNTHETASE FROM E. COLI
COMPLEXED WITH HADACIDIN, GDP, 6-PHOSPHORYL-IMP, AND
MG2+
Authors : Choe, J.Y.; Poland, B.W.; Fromm, H.; Honzatko, R.
Deposited on : 1999-03-26
Resolution : 2.50 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

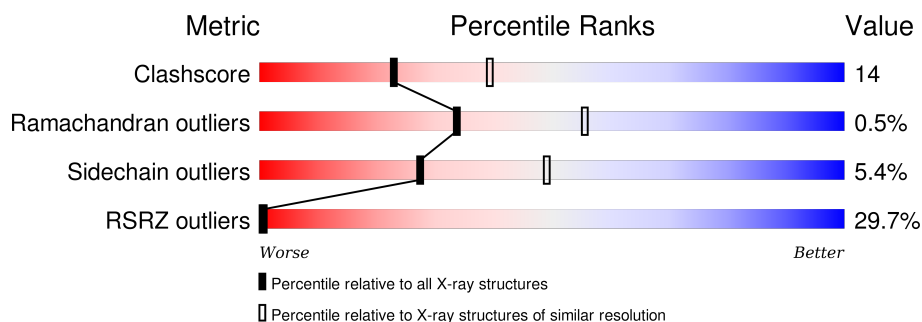
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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	102246	4242 (2.50-2.50)
Ramachandran outliers	100387	4156 (2.50-2.50)
Sidechain outliers	100360	4158 (2.50-2.50)
RSRZ outliers	91569	3562 (2.50-2.50)

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	431	<div> <div>30%</div> <div>71%</div> <div>27%</div> <div>.</div> </div>

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 3585 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.

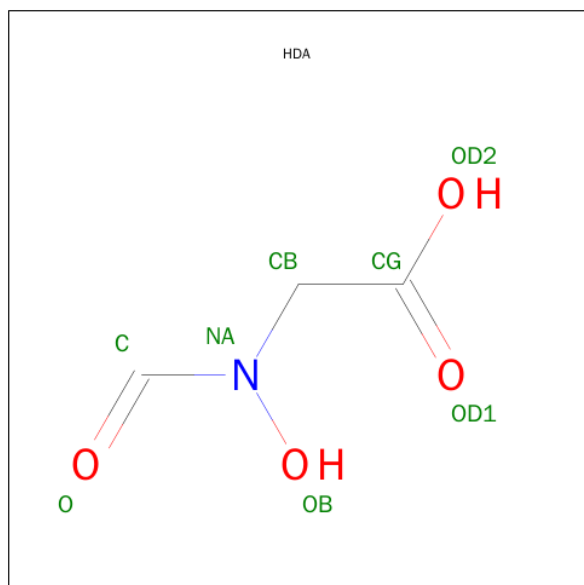
- Molecule 1 is a protein called PROTEIN (ADENYLOSUCCINATE SYNTHETASE).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	431	Total	C	N	O	S	0	0	0
			3321	2092	576	640	13			

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

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

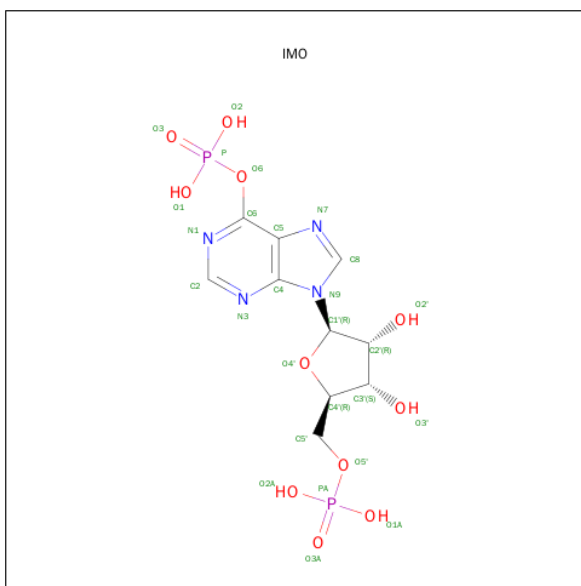
- Molecule 3 is HADACIDIN (three-letter code: HDA) (formula: C₃H₅NO₄).



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

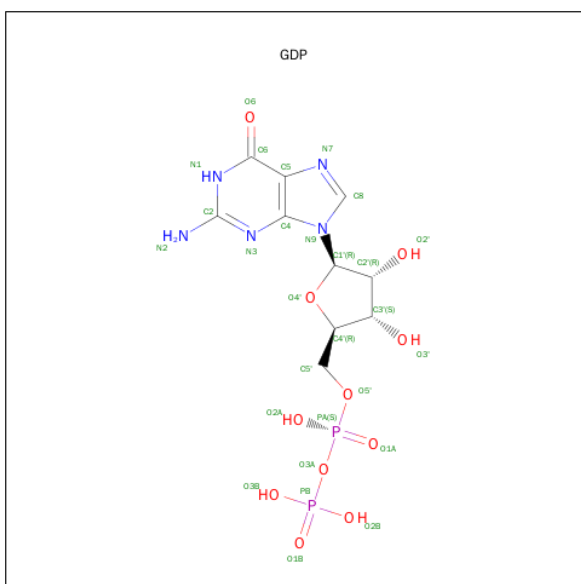
- Molecule 4 is 6-O-PHOSPHORYL INOSINE MONOPHOSPHATE (three-letter code: IMO)

(formula: C₁₀H₁₄N₄O₁₁P₂).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	0	0
			27	10	4	11	2		

- Molecule 5 is GUANOSINE-5'-DIPHOSPHATE (three-letter code: GDP) (formula: $\text{C}_{10}\text{H}_{15}\text{N}_5\text{O}_{11}\text{P}_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
5	A	1	Total	C	N	O	P	0	0
			28	10	5	11	2		

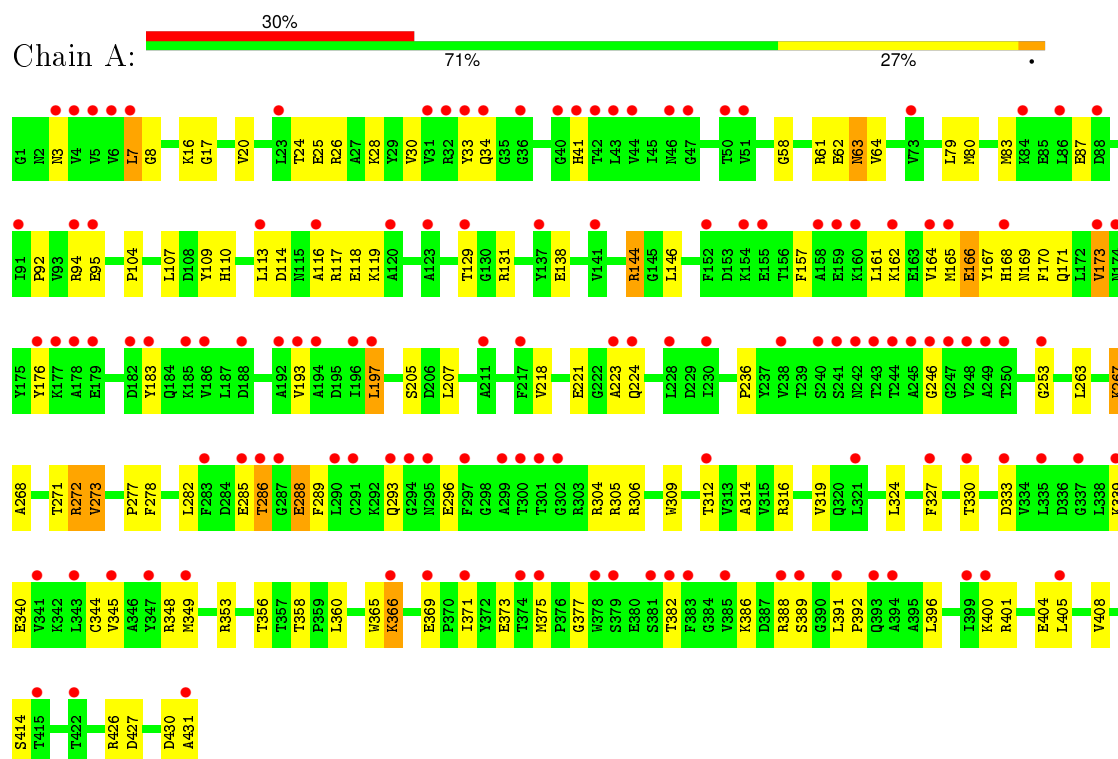
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	200	Total 200	O 200	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 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: PROTEIN (ADENYLOSUCCINATE SYNTHETASE)



4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α , β , γ	79.86 Å 79.86 Å 158.43 Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	5.00 – 2.50 41.97 – 2.46	Depositor EDS
% Data completeness (in resolution range)	79.2 (5.00-2.50) 85.0 (41.97-2.46)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.53 (at 2.45 Å)	Xtriage
Refinement program	X-PLOR 3.851	Depositor
R, R_{free}	0.160 , 0.259 0.327 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	DCC
Wilson B-factor (Å ²)	24.0	Xtriage
Anisotropy	0.563	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 73.9	EDS
Estimated twinning fraction	0.045 for -h,-k,l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	8 of 18562 reflections (0.043%)	Xtriage
F_o, F_c correlation	0.76	EDS
Total number of atoms	3585	wwPDB-VP
Average B, all atoms (Å ²)	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.46% of the height of the origin peak. No significant pseudotranslation is detected.*

¹ Intensities estimated from amplitudes.

² Theoretical 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: GDP, MG, IMO, HDA

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	0.70	0/3379	0.92	5/4577 (0.1%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	61	ARG	NE-CZ-NH2	-6.70	116.95	120.30
1	A	61	ARG	NE-CZ-NH1	6.26	123.43	120.30
1	A	7	LEU	CA-CB-CG	6.24	129.65	115.30
1	A	273	VAL	N-CA-C	-5.29	96.71	111.00
1	A	267	LYS	N-CA-C	5.07	124.69	111.00

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	3321	0	3326	91	0
2	A	1	0	0	0	0
3	A	8	0	4	0	0
4	A	27	0	10	0	0
5	A	28	0	12	0	0
6	A	200	0	0	8	2

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	3585	0	3352	91	2

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 14.

All (91) 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:34:GLN:HE22	1:A:223:ALA:H	1.23	0.86
1:A:83:MET:O	1:A:87:GLU:HG3	1.78	0.82
1:A:312:THR:HG22	1:A:316:ARG:HH11	1.46	0.77
1:A:30:VAL:HG23	1:A:64:VAL:HG11	1.67	0.76
1:A:169:ASN:O	1:A:173:VAL:HG13	1.86	0.74
1:A:20:VAL:HG21	1:A:221:GLU:HG3	1.72	0.71
1:A:79:LEU:O	1:A:83:MET:HG3	1.94	0.68
1:A:246:GLY:HA2	6:A:700:HOH:O	1.94	0.68
1:A:267:LYS:HA	1:A:330:THR:OG1	1.96	0.65
1:A:3:ASN:HD22	1:A:218:VAL:HB	1.61	0.65
1:A:289:PHE:CE1	1:A:293:GLN:HG3	2.32	0.64
1:A:157:PHE:CE2	1:A:161:LEU:HD22	2.32	0.64
1:A:80:MET:HG3	1:A:193:VAL:HG11	1.81	0.63
1:A:34:GLN:HE22	1:A:223:ALA:N	1.96	0.62
1:A:267:LYS:HG2	1:A:267:LYS:O	1.98	0.62
1:A:33:TYR:CD1	1:A:34:GLN:HG3	2.36	0.60
1:A:30:VAL:HG21	1:A:58:GLY:HA3	1.84	0.60
1:A:146:LEU:HD23	1:A:157:PHE:CE1	2.37	0.60
1:A:316:ARG:HH21	1:A:356:THR:HB	1.68	0.58
1:A:30:VAL:HG23	1:A:64:VAL:CG1	2.31	0.57
1:A:271:THR:HA	1:A:306:ARG:O	2.04	0.57
1:A:24:THR:HG21	1:A:30:VAL:HG22	1.85	0.57
1:A:345:VAL:HG11	1:A:373:GLU:HG3	1.84	0.57
1:A:348:ARG:HB2	1:A:371:ILE:HD11	1.87	0.57
1:A:267:LYS:O	1:A:268:ALA:HB3	2.05	0.56
1:A:366:LYS:HA	6:A:693:HOH:O	2.06	0.55
1:A:144:ARG:NH2	6:A:699:HOH:O	2.39	0.55
1:A:314:ALA:HA	1:A:358:THR:HG21	1.88	0.55
1:A:104:PRO:HB3	6:A:571:HOH:O	2.08	0.54
1:A:282:LEU:HD21	1:A:309:TRP:NE1	2.24	0.52
1:A:296:GLU:HB3	1:A:305:ARG:HB2	1.90	0.52
1:A:312:THR:HG21	1:A:405:LEU:HB3	1.92	0.52
1:A:272:ARG:NH1	1:A:277:PRO:O	2.40	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:129:THR:O	1:A:131:ARG:NH1	2.43	0.51
1:A:157:PHE:HE2	1:A:161:LEU:HD22	1.75	0.51
1:A:63:ASN:HD22	1:A:63:ASN:H	1.58	0.51
1:A:267:LYS:O	1:A:330:THR:O	2.28	0.51
1:A:117:ARG:NH2	1:A:138:GLU:OE1	2.44	0.50
1:A:3:ASN:ND2	1:A:218:VAL:HB	2.26	0.50
1:A:205:SER:HB3	1:A:253:GLY:HA3	1.92	0.50
1:A:107:LEU:O	1:A:110:HIS:HB2	2.12	0.50
1:A:25:GLU:CD	6:A:675:HOH:O	2.49	0.49
1:A:116:ALA:HB1	1:A:176:TYR:CD1	2.48	0.48
1:A:207:LEU:HD23	1:A:207:LEU:C	2.33	0.48
1:A:388:ARG:HA	1:A:391:LEU:HG	1.95	0.47
1:A:304:ARG:HG2	1:A:304:ARG:HH11	1.77	0.47
1:A:349:MET:HG3	1:A:353:ARG:NH2	2.29	0.47
1:A:17:GLY:HA3	1:A:41:HIS:HB3	1.97	0.47
1:A:267:LYS:CG	1:A:267:LYS:O	2.63	0.47
1:A:109:TYR:O	1:A:113:LEU:HG	2.15	0.47
1:A:168:HIS:HD2	1:A:171:GLN:NE2	2.13	0.46
1:A:164:VAL:O	1:A:167:TYR:HB3	2.15	0.46
1:A:285:GLU:H	1:A:285:GLU:CD	2.18	0.46
1:A:312:THR:HB	1:A:344:CYS:O	2.15	0.46
1:A:87:GLU:OE2	1:A:94:ARG:NE	2.46	0.46
1:A:165:MET:SD	1:A:183:TYR:HA	2.56	0.46
1:A:28:LYS:HD3	6:A:665:HOH:O	2.16	0.46
1:A:345:VAL:HG11	1:A:373:GLU:CG	2.46	0.45
1:A:382:THR:HG22	1:A:392:PRO:HD2	1.98	0.45
1:A:24:THR:HG21	1:A:30:VAL:CG2	2.46	0.45
1:A:161:LEU:O	1:A:164:VAL:HG12	2.16	0.45
1:A:348:ARG:HB3	1:A:369:GLU:HB2	1.98	0.45
1:A:113:LEU:O	1:A:117:ARG:HG3	2.17	0.45
1:A:426:ARG:NH1	1:A:431:ALA:OXT	2.51	0.44
1:A:400:LYS:HE3	1:A:404:GLU:HG3	1.99	0.44
1:A:8:GLY:N	1:A:16:LYS:HD3	2.33	0.44
1:A:165:MET:O	1:A:169:ASN:HB2	2.17	0.44
1:A:170:PHE:C	1:A:170:PHE:CD2	2.91	0.44
1:A:333:ASP:HA	1:A:382:THR:OG1	2.18	0.44
1:A:118:GLU:OE2	1:A:118:GLU:HA	2.18	0.43
1:A:34:GLN:NE2	1:A:223:ALA:H	2.02	0.43
1:A:375:MET:HE2	1:A:401:ARG:HG2	1.99	0.43
1:A:312:THR:CG2	1:A:316:ARG:HH11	2.24	0.43
1:A:30:VAL:CG2	1:A:64:VAL:HG11	2.43	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:430:ASP:O	1:A:431:ALA:HB2	2.19	0.43
1:A:285:GLU:HA	1:A:288:GLU:OE1	2.19	0.43
1:A:330:THR:HA	1:A:414:SER:HB3	2.01	0.42
1:A:118:GLU:HG2	6:A:669:HOH:O	2.19	0.42
1:A:92:PRO:HB2	1:A:95:GLU:HG3	2.01	0.42
1:A:286:THR:HG21	6:A:532:HOH:O	2.20	0.42
1:A:388:ARG:HH21	1:A:396:LEU:HD22	1.85	0.42
1:A:162:LYS:O	1:A:166:GLU:HB2	2.20	0.41
1:A:197:LEU:HD12	1:A:197:LEU:O	2.20	0.41
1:A:319:VAL:HA	1:A:324:LEU:HD12	2.02	0.41
1:A:316:ARG:NH2	1:A:356:THR:HB	2.36	0.41
1:A:114:ASP:OD1	1:A:131:ARG:O	2.39	0.41
1:A:373:GLU:CD	1:A:401:ARG:HH21	2.24	0.41
1:A:340:GLU:HA	1:A:377:GLY:N	2.36	0.41
1:A:327:PHE:CE1	1:A:408:VAL:HB	2.56	0.40
1:A:365:TRP:O	1:A:366:LYS:C	2.59	0.40
1:A:26:ARG:NH1	1:A:427:ASP:OD1	2.55	0.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:A:699:HOH:O	6:A:699:HOH:O[6_555]	2.02	0.18
6:A:700:HOH:O	6:A:700:HOH:O[6_555]	2.09	0.11

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	429/431 (100%)	397 (92%)	30 (7%)	2 (0%)	34 55

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	366	LYS
1	A	224	GLN

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	353/353 (100%)	334 (95%)	19 (5%)	27 49

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	7	LEU
1	A	62	GLU
1	A	63	ASN
1	A	119	LYS
1	A	144	ARG
1	A	166	GLU
1	A	173	VAL
1	A	197	LEU
1	A	236	PRO
1	A	263	LEU
1	A	272	ARG
1	A	273	VAL
1	A	278	PHE
1	A	286	THR
1	A	288	GLU
1	A	339	LYS
1	A	360	LEU
1	A	386	LYS
1	A	389	SER

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	2	ASN

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Mol	Chain	Res	Type
1	A	3	ASN
1	A	34	GLN
1	A	63	ASN
1	A	115	ASN
1	A	168	HIS
1	A	295	ASN
1	A	320	GLN
1	A	393	GLN
1	A	397	ASN

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 4 ligands modelled in this entry, 1 is monoatomic - leaving 3 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	$\# Z > 2$
5	GDP	A	432	2	23,30,30	1.58	4 (17%)	30,47,47	2.15	6 (20%)
3	HDA	A	437	2	1,7,7	0.32	0	1,8,8	1.69	0
4	IMO	A	440	2	23,29,29	2.61	6 (26%)	29,45,45	2.85	6 (20%)

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
5	GDP	A	432	2	-	0/12/32/32	0/3/3/3
3	HDA	A	437	2	-	0/1/6/6	0/0/0/0
4	IMO	A	440	2	-	0/9/31/31	0/3/3/3

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	440	IMO	PA-O2A	-2.37	1.46	1.54
4	A	440	IMO	C8-N7	-2.27	1.30	1.34
5	A	432	GDP	PB-O2B	-2.24	1.46	1.54
4	A	440	IMO	O3'-C3'	2.15	1.48	1.43
5	A	432	GDP	C2-N1	2.55	1.39	1.35
4	A	440	IMO	C6-N1	2.66	1.36	1.32
5	A	432	GDP	O4'-C1'	3.20	1.45	1.41
5	A	432	GDP	C6-N1	4.12	1.40	1.33
4	A	440	IMO	O4'-C1'	5.83	1.48	1.41
4	A	440	IMO	O6-C6	8.83	1.51	1.40

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	432	GDP	C5-C6-N1	-7.16	113.80	123.59
4	A	440	IMO	N3-C2-N1	-6.85	123.65	128.89
4	A	440	IMO	C5-C6-N1	-6.76	108.83	123.63
5	A	432	GDP	C1'-N9-C4	-3.29	121.97	126.94
4	A	440	IMO	C2'-C1'-N9	-2.91	109.84	114.29
5	A	432	GDP	N3-C2-N1	-2.88	123.06	127.44
5	A	432	GDP	O5'-C5'-C4'	-2.42	100.20	109.12
5	A	432	GDP	C4'-O4'-C1'	2.48	112.44	109.72
4	A	440	IMO	O6-C6-N1	3.89	124.00	116.56
4	A	440	IMO	O4'-C1'-N9	4.87	118.30	108.10
5	A	432	GDP	C6-N1-C2	5.41	123.45	115.94
4	A	440	IMO	C2-N1-C6	8.48	128.12	116.05

There are no chirality outliers.

There are no torsion outliers.

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	431/431 (100%)	1.60	128 (29%) 1 0	16, 30, 47, 63	0

All (128) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	192	ALA	5.9
1	A	299	ALA	4.8
1	A	337	GLY	4.4
1	A	178	ALA	4.2
1	A	196	ILE	4.1
1	A	158	ALA	4.1
1	A	297	PHE	4.0
1	A	50	THR	3.9
1	A	155	GLU	3.9
1	A	141	VAL	3.9
1	A	283	PHE	3.8
1	A	194	ALA	3.8
1	A	389	SER	3.7
1	A	137	TYR	3.7
1	A	179	GLU	3.7
1	A	165	MET	3.6
1	A	293	GLN	3.6
1	A	188	ASP	3.6
1	A	249	ALA	3.5
1	A	43	LEU	3.5
1	A	371	ILE	3.5
1	A	400	LYS	3.4
1	A	394	ALA	3.4
1	A	343	LEU	3.4
1	A	159	GLU	3.4
1	A	431	ALA	3.3
1	A	375	MET	3.3

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Mol	Chain	Res	Type	RSRZ
1	A	391	LEU	3.3
1	A	197	LEU	3.2
1	A	182	ASP	3.1
1	A	164	VAL	3.1
1	A	385	VAL	3.1
1	A	86	LEU	3.1
1	A	330	THR	3.1
1	A	378	TRP	3.1
1	A	177	LYS	3.0
1	A	415	THR	3.0
1	A	44	VAL	3.0
1	A	379	SER	2.9
1	A	321	LEU	2.9
1	A	217	PHE	2.9
1	A	176	TYR	2.9
1	A	173	VAL	2.9
1	A	349	MET	2.9
1	A	243	THR	2.9
1	A	339	LYS	2.9
1	A	5	VAL	2.9
1	A	91	ILE	2.8
1	A	183	TYR	2.8
1	A	369	GLU	2.8
1	A	94	ARG	2.8
1	A	383	PHE	2.8
1	A	291	CYS	2.8
1	A	33	TYR	2.8
1	A	154	LYS	2.8
1	A	300	THR	2.8
1	A	246	GLY	2.7
1	A	253	GLY	2.7
1	A	84	LYS	2.7
1	A	290	LEU	2.7
1	A	335	LEU	2.7
1	A	241	SER	2.7
1	A	51	VAL	2.7
1	A	193	VAL	2.7
1	A	295	ASN	2.7
1	A	40	GLY	2.6
1	A	287	GLY	2.6
1	A	162	LYS	2.6
1	A	393	GLN	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	302	GLY	2.6
1	A	327	PHE	2.6
1	A	174	ASN	2.6
1	A	422	THR	2.6
1	A	223	ALA	2.6
1	A	7	LEU	2.5
1	A	240	SER	2.5
1	A	47	GLY	2.5
1	A	247	GLY	2.5
1	A	116	ALA	2.5
1	A	382	THR	2.5
1	A	345	VAL	2.4
1	A	31	VAL	2.4
1	A	34	GLN	2.4
1	A	73	VAL	2.4
1	A	374	THR	2.4
1	A	95	GLU	2.4
1	A	242	ASN	2.4
1	A	46	ASN	2.4
1	A	285	GLU	2.4
1	A	168	HIS	2.3
1	A	228	LEU	2.3
1	A	250	THR	2.3
1	A	42	THR	2.3
1	A	238	VAL	2.3
1	A	245	ALA	2.3
1	A	286	THR	2.3
1	A	244	THR	2.2
1	A	248	VAL	2.2
1	A	388	ARG	2.2
1	A	185	LYS	2.2
1	A	3	ASN	2.2
1	A	366	LYS	2.2
1	A	88	ASP	2.2
1	A	123	ALA	2.1
1	A	152	PHE	2.1
1	A	129	THR	2.1
1	A	301	THR	2.1
1	A	294	GLY	2.1
1	A	4	VAL	2.1
1	A	32	ARG	2.1
1	A	347	TYR	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	230	ILE	2.1
1	A	36	GLY	2.1
1	A	381	SER	2.1
1	A	6	VAL	2.1
1	A	41	HIS	2.1
1	A	113	LEU	2.1
1	A	405	LEU	2.1
1	A	312	THR	2.1
1	A	341	VAL	2.0
1	A	224	GLN	2.0
1	A	120	ALA	2.0
1	A	211	ALA	2.0
1	A	160	LYS	2.0
1	A	186	VAL	2.0
1	A	333	ASP	2.0
1	A	399	ILE	2.0
1	A	23	LEU	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. 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(Å ²)	Q<0.9
4	IMO	A	440	27/27	0.81	0.26	0.03	20,26,34,39	0
3	HDA	A	437	8/8	0.76	0.28	-0.17	28,35,36,37	0
5	GDP	A	432	28/28	0.89	0.23	-0.72	21,29,32,33	0
2	MG	A	435	1/1	0.85	0.17	-1.55	26,26,26,26	0

6.5 Other polymers [i](#)

There are no such residues in this entry.