



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 03:10 PM UTC

PDB ID : 3SUC / pdb_00003suc
Title : Crystal structure of the pre-mature bacteriophage phi29 gene product 12
Authors : Xiang, Y.; Rossmann, M.G.
Deposited on : 2011-07-11
Resolution : 2.15 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
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
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

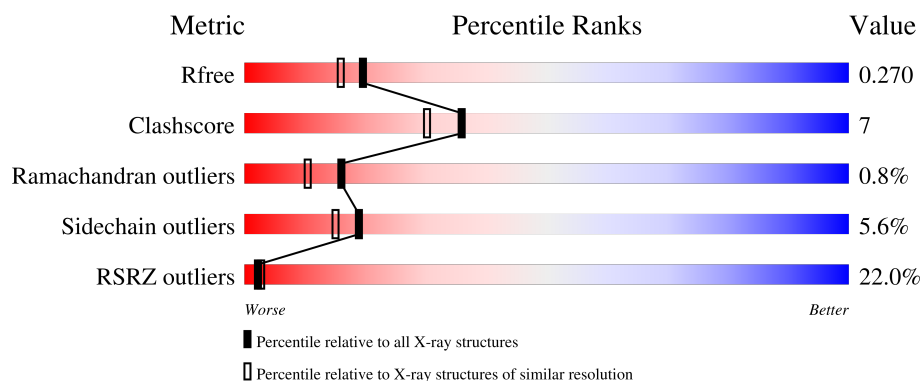
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.15 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	2057 (2.16-2.16)
Clashscore	190562	2159 (2.16-2.16)
Ramachandran outliers	187476	2134 (2.16-2.16)
Sidechain outliers	187428	2133 (2.16-2.16)
RSRZ outliers	180081	2059 (2.16-2.16)

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	772	22% 81% 16% ..

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 5875 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 Preneck appendage protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	767	Total	C	N	O	S	0	5	0
			5767	3587	1006	1159	15			

There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	83	HIS	-	expression tag	UNP B3VMP8
A	84	HIS	-	expression tag	UNP B3VMP8
A	85	HIS	-	expression tag	UNP B3VMP8
A	86	HIS	-	expression tag	UNP B3VMP8
A	87	HIS	-	expression tag	UNP B3VMP8
A	88	HIS	-	expression tag	UNP B3VMP8
A	166	ARG	LYS	variant	UNP B3VMP8
A	627	GLN	LYS	variant	UNP B3VMP8
A	695	GLN	GLU	engineered mutation	UNP B3VMP8
A	701	GLY	ASP	variant	UNP B3VMP8
A	817	SER	GLY	variant	UNP B3VMP8

- Molecule 2 is CALCIUM ION (CCD ID: CA) (formula: Ca).

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

- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

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

- Molecule 4 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: C₁₀H₁₆N₅O₁₃P₃).

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: Preneck appendage protein



4 Data and refinement statistics

Property	Value	Source
Space group	H 3 2	Depositor
Cell constants a, b, c, α , β , γ	95.89Å 95.89Å 795.39Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	49.27 – 2.15 49.27 – 2.15	Depositor EDS
% Data completeness (in resolution range)	65.5 (49.27-2.15) 65.5 (49.27-2.15)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	15.88 (at 2.16Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.261 , 0.291 (Not available) , 0.270	Depositor DCC
R_{free} test set	2533 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	42.6	Xtriage
Anisotropy	0.466	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 35.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.53$, $\langle L^2 \rangle = 0.37$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	5875	wwPDB-VP
Average B, all atoms (Å ²)	48.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.62% 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: ATP, MG, CA

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	0.51	0/5882	0.79	2/7972 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	575	SER	N-CA-C	5.55	117.95	111.02
1	A	437	GLN	N-CA-C	5.18	115.07	108.24

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	5767	0	5628	84	0
2	A	1	0	0	0	0
3	A	2	0	0	0	0
4	A	31	0	12	0	0
5	A	74	0	0	3	0
All	All	5875	0	5640	84	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 7.

All (84) 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:644:ASN:HD21	1:A:654:THR:CG2	1.55	1.18
1:A:644:ASN:ND2	1:A:654:THR:HG22	1.66	1.11
1:A:644:ASN:HD21	1:A:654:THR:HG22	0.85	1.00
1:A:517:THR:HG22	1:A:519:ASN:O	1.78	0.82
1:A:558:THR:HG21	1:A:570:ILE:HG22	1.59	0.82
1:A:792:ARG:HG2	1:A:792:ARG:HH11	1.43	0.81
1:A:336:ALA:HB2	1:A:342:ALA:HA	1.65	0.79
1:A:496[B]:VAL:HG23	1:A:522:PRO:HB3	1.67	0.77
1:A:514:LEU:HG	1:A:529:SER:HB3	1.73	0.71
1:A:578:GLU:HB3	1:A:593:LYS:HG2	1.74	0.70
1:A:572:GLY:O	1:A:588:THR:HA	1.93	0.68
1:A:644:ASN:ND2	1:A:654:THR:CG2	2.39	0.65
1:A:517:THR:HG21	1:A:522:PRO:HG2	1.77	0.65
1:A:519:ASN:HD21	1:A:521:ASN:CG	2.05	0.64
1:A:182:ASN:H	1:A:187:ASN:HD21	1.45	0.63
1:A:696:TYR:CE1	1:A:741:GLU:HG2	2.36	0.60
1:A:451:THR:HB	1:A:480:ASN:HB3	1.84	0.60
1:A:641:GLY:H	1:A:644:ASN:HD22	1.49	0.59
1:A:792:ARG:HG2	1:A:792:ARG:NH1	2.15	0.58
1:A:521:ASN:HA	1:A:551:ASN:ND2	2.19	0.58
1:A:494:GLU:HG3	5:A:72:HOH:O	2.03	0.58
1:A:473[B]:ASN:ND2	5:A:12:HOH:O	2.38	0.56
1:A:656:GLY:HA3	1:A:659:LYS:HG3	1.86	0.56
1:A:517:THR:CG2	1:A:522:PRO:HG2	2.36	0.55
1:A:288:GLN:HE21	1:A:316:ARG:HE	1.52	0.55
1:A:696:TYR:HE1	1:A:741:GLU:HG2	1.70	0.55
1:A:512:VAL:HG12	1:A:537:ARG:HH12	1.71	0.54
1:A:502:SER:HA	1:A:528:SER:O	2.07	0.54
1:A:277:PHE:CE2	1:A:300:PRO:HB3	2.43	0.54
1:A:312:ASP:CG	1:A:313:ASP:H	2.15	0.54
1:A:646:ILE:HD11	1:A:654:THR:HB	1.89	0.53
1:A:496[B]:VAL:CG2	1:A:522:PRO:HB3	2.36	0.53
1:A:564:ILE:HG12	1:A:570:ILE:CD1	2.39	0.53
1:A:521:ASN:N	1:A:522:PRO:CD	2.73	0.52
1:A:636:GLN:O	1:A:651:GLY:HA2	2.10	0.52
1:A:577:CYS:HB2	5:A:3:HOH:O	2.10	0.51
1:A:514:LEU:HD13	1:A:515:VAL:HG23	1.92	0.51
1:A:159:GLY:HA2	1:A:194:SER:HB3	1.92	0.51
1:A:517:THR:CG2	1:A:519:ASN:O	2.56	0.51
1:A:446:ASN:HD21	1:A:476:ASN:HD22	1.58	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:710:LEU:HD23	1:A:730:VAL:HG22	1.94	0.49
1:A:803:GLN:HG2	1:A:834:GLN:HE22	1.77	0.49
1:A:521:ASN:HA	1:A:551:ASN:HD21	1.77	0.49
1:A:472:VAL:HG13	1:A:496[B]:VAL:HG12	1.95	0.48
1:A:475:SER:HA	1:A:499:THR:O	2.13	0.48
1:A:480:ASN:C	1:A:480:ASN:HD22	2.22	0.47
1:A:403:PRO:HG2	1:A:428:LEU:O	2.14	0.47
1:A:564:ILE:HG12	1:A:570:ILE:HD13	1.95	0.47
1:A:558:THR:HB	1:A:573:SER:O	2.15	0.46
1:A:315:SER:O	1:A:343:ALA:HA	2.15	0.46
1:A:704:VAL:HG22	1:A:793:ARG:HG2	1.97	0.46
1:A:336:ALA:CB	1:A:342:ALA:HA	2.41	0.46
1:A:239:LEU:HB3	1:A:240:HIS:H	1.55	0.46
1:A:288:GLN:NE2	1:A:316:ARG:HE	2.14	0.45
1:A:324:ARG:HG3	1:A:352:MET:HB3	1.98	0.45
1:A:404:ARG:HD3	1:A:432:THR:O	2.16	0.45
1:A:326:LYS:HA	1:A:354:VAL:O	2.16	0.45
1:A:808:ILE:HG22	1:A:825:ALA:HB3	1.99	0.45
1:A:662:GLY:HA3	1:A:669:TRP:CE2	2.52	0.45
1:A:763:VAL:HB	1:A:771:PHE:CE2	2.52	0.44
1:A:556:ALA:HB3	1:A:571:MET:HE3	1.98	0.44
1:A:281:GLY:HA3	1:A:297[A]:SER:OG	2.16	0.44
1:A:326:LYS:HG3	1:A:354:VAL:HB	1.99	0.44
1:A:309:PHE:CZ	1:A:323:ASN:HB3	2.53	0.44
1:A:443[B]:CYS:HB3	1:A:472:VAL:HB	1.99	0.44
1:A:672:ASP:OD1	1:A:675:ASN:HB2	2.18	0.44
1:A:311:ILE:HD11	1:A:320:LEU:HD21	2.01	0.42
1:A:240:HIS:CE1	1:A:279:ASP:HB3	2.54	0.42
1:A:437:GLN:HB3	1:A:463:ILE:HD12	2.01	0.42
1:A:211:ILE:H	1:A:211:ILE:HG13	1.70	0.42
1:A:710:LEU:HD22	1:A:727:ILE:HG21	2.02	0.42
1:A:775:LEU:HA	1:A:776:PRO:HD3	1.92	0.42
1:A:642:ASN:HB3	1:A:657:SER:HB3	2.02	0.41
1:A:446:ASN:ND2	1:A:475:SER:OG	2.50	0.41
1:A:700:LEU:O	1:A:703:GLN:HG3	2.20	0.41
1:A:772:LYS:HB3	1:A:772:LYS:HE2	1.88	0.41
1:A:165:ILE:HB	1:A:197:LEU:HD23	2.02	0.41
1:A:409:SER:HB3	1:A:438:PHE:HB2	2.02	0.41
1:A:649:SER:OG	1:A:662:GLY:HA2	2.21	0.41
1:A:430:THR:O	1:A:456:SER:HA	2.21	0.41
1:A:173:ARG:HH12	1:A:208:ILE:HG21	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:787:ILE:HA	1:A:788:PRO:HD3	1.90	0.40
1:A:746:TRP:HA	1:A:786:TYR:CE2	2.57	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	770/772 (100%)	717 (93%)	47 (6%)	6 (1%)	16 10

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	606	THR
1	A	689	THR
1	A	304	ALA
1	A	380	ASN
1	A	216	GLU
1	A	521	ASN

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	629/630 (100%)	593 (94%)	36 (6%)	18 14

All (36) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	143	VAL
1	A	156	THR
1	A	167	PHE
1	A	177	LEU
1	A	180	ASN
1	A	211	ILE
1	A	239	LEU
1	A	259	THR
1	A	379	LYS
1	A	451	THR
1	A	466	SER
1	A	467	ARG
1	A	472	VAL
1	A	478	THR
1	A	514	LEU
1	A	518	ILE
1	A	519	ASN
1	A	547	LEU
1	A	549	LEU
1	A	558	THR
1	A	567[A]	GLU
1	A	567[B]	GLU
1	A	570	ILE
1	A	606	THR
1	A	610	LYS
1	A	636	GLN
1	A	654	THR
1	A	655	THR
1	A	674	LEU
1	A	703	GLN
1	A	707	THR
1	A	738	VAL
1	A	747	GLN
1	A	792	ARG
1	A	793	ARG
1	A	843	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (26) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	180	ASN

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Mol	Chain	Res	Type
1	A	187	ASN
1	A	200	ASN
1	A	285	HIS
1	A	288	GLN
1	A	294	ASN
1	A	361	ASN
1	A	398	GLN
1	A	417	ASN
1	A	437	GLN
1	A	446	ASN
1	A	480	ASN
1	A	495	ASN
1	A	519	ASN
1	A	551	ASN
1	A	614	ASN
1	A	636	GLN
1	A	644	ASN
1	A	661	ASN
1	A	668	ASN
1	A	688	ASN
1	A	703	GLN
1	A	747	GLN
1	A	777	ASN
1	A	791	GLN
1	A	834	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 oligosaccharides in this entry.

5.6 Ligand geometry

Of 4 ligands modelled in this entry, 3 are monoatomic - leaving 1 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
4	ATP	A	856	3	32,33,33	1.55	7 (21%)	48,52,52	1.78	9 (18%)

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	ATP	A	856	3	-	3/22/38/38	0/3/3/3

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	856	ATP	C5-C4	5.06	1.48	1.39
4	A	856	ATP	C5-C6	2.93	1.49	1.41
4	A	856	ATP	PB-O3B	2.54	1.62	1.59
4	A	856	ATP	PB-O3A	2.49	1.62	1.59
4	A	856	ATP	C8-N7	2.38	1.36	1.31
4	A	856	ATP	PA-O3A	2.35	1.62	1.59
4	A	856	ATP	C5-N7	-2.28	1.34	1.39

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	856	ATP	C5-C4-N3	-6.01	118.44	126.72
4	A	856	ATP	N3-C4-N9	4.72	135.20	127.17
4	A	856	ATP	C2-N3-C4	3.77	121.03	111.83
4	A	856	ATP	C4-C5-N7	-3.53	106.55	110.58
4	A	856	ATP	N3-C2-N1	-3.23	123.69	128.58
4	A	856	ATP	C5-N7-C8	2.55	107.46	103.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	856	ATP	C3'-C2'-C1'	2.53	106.25	101.46
4	A	856	ATP	C4-N9-C8	2.30	108.15	105.74
4	A	856	ATP	C6-C5-N7	2.05	136.05	132.09

There are no chirality outliers.

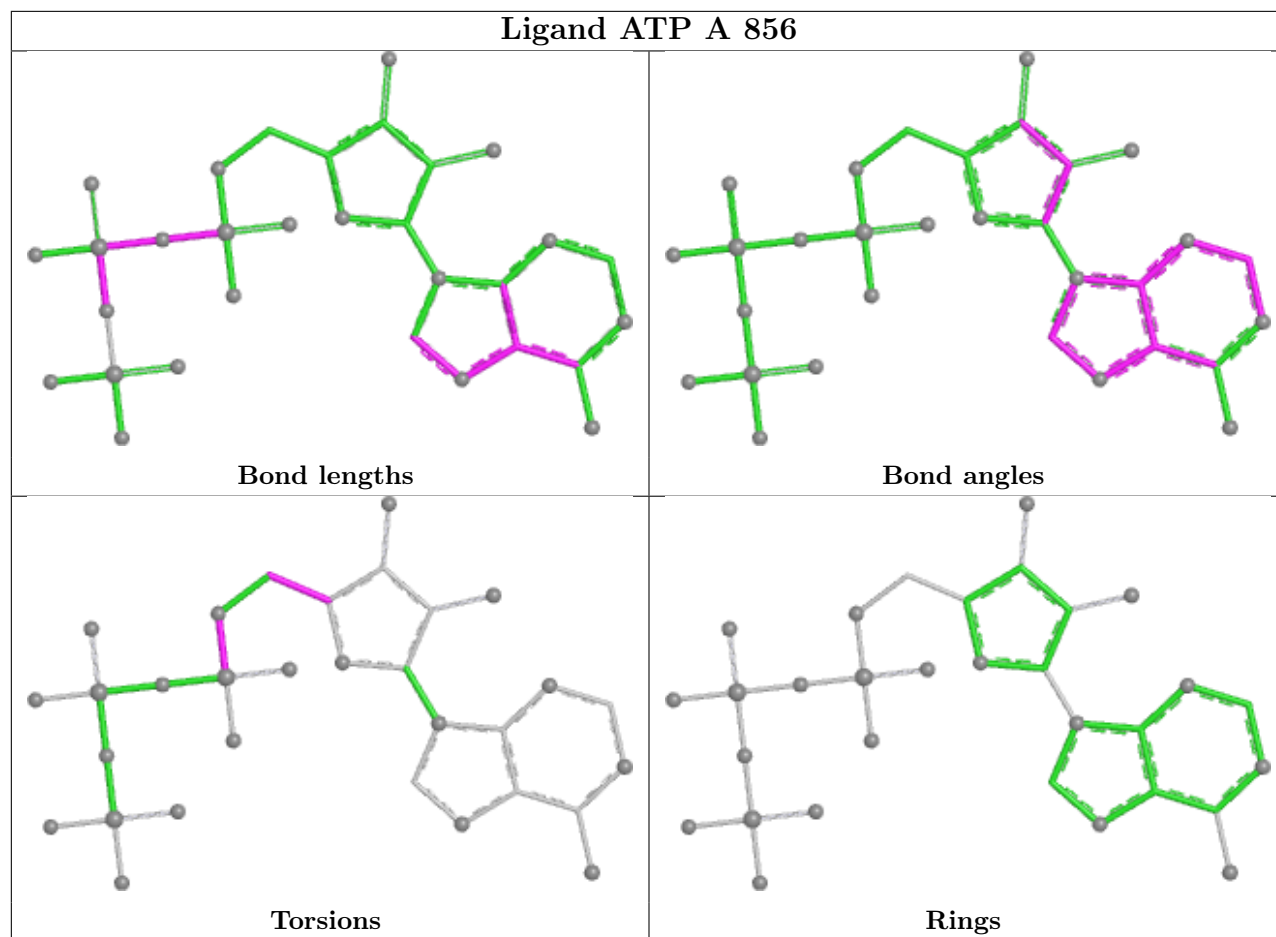
All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	856	ATP	C5'-O5'-PA-O1A
4	A	856	ATP	O4'-C4'-C5'-O5'
4	A	856	ATP	C3'-C4'-C5'-O5'

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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	767/772 (99%)	1.27	169 (22%) 2 3	12, 42, 96, 155	8 (1%)

All (169) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	810	GLU	9.1
1	A	88	HIS	8.7
1	A	690	TRP	8.4
1	A	184	THR	7.1
1	A	117	VAL	6.7
1	A	385	ASN	6.7
1	A	89	PHE	6.5
1	A	103	PHE	5.8
1	A	100	LEU	5.8
1	A	174	GLY	5.4
1	A	116	GLY	5.3
1	A	208	ILE	5.1
1	A	744	PHE	5.0
1	A	691	SER	4.9
1	A	199	GLY	4.9
1	A	132	PHE	4.7
1	A	746	TRP	4.5
1	A	762	GLU	4.5
1	A	689	THR	4.5
1	A	205	GLY	4.5
1	A	688	ASN	4.5
1	A	92	LEU	4.5
1	A	131	GLY	4.4
1	A	782	PRO	4.3
1	A	124	PHE	4.2
1	A	745	GLU	4.1
1	A	769	VAL	4.0

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Mol	Chain	Res	Type	RSRZ
1	A	786	TYR	4.0
1	A	107	VAL	3.9
1	A	135	TYR	3.9
1	A	466	SER	3.8
1	A	96	VAL	3.8
1	A	177	LEU	3.7
1	A	110	TYR	3.7
1	A	303	THR	3.7
1	A	170	SER	3.7
1	A	102	GLN	3.6
1	A	767	ASP	3.5
1	A	164	VAL	3.5
1	A	167	PHE	3.5
1	A	90	ALA	3.5
1	A	741	GLU	3.5
1	A	766	GLU	3.4
1	A	153	THR	3.4
1	A	687	GLY	3.4
1	A	302	LEU	3.4
1	A	101	LYS	3.4
1	A	94	ILE	3.4
1	A	743	SER	3.4
1	A	141	PHE	3.4
1	A	842	LYS	3.4
1	A	105	VAL	3.4
1	A	165	ILE	3.4
1	A	832	ILE	3.4
1	A	114	GLY	3.3
1	A	211	ILE	3.3
1	A	259	THR	3.3
1	A	134	VAL	3.3
1	A	780	PHE	3.3
1	A	115	ASP	3.3
1	A	788	PRO	3.3
1	A	765	THR	3.2
1	A	191	PHE	3.2
1	A	130	SER	3.2
1	A	742	SER	3.2
1	A	210	GLY	3.2
1	A	128	ILE	3.1
1	A	133	PRO	3.1
1	A	147	ILE	3.1

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Mol	Chain	Res	Type	RSRZ
1	A	146	GLY	3.1
1	A	747	GLN	3.1
1	A	113	LYS	3.1
1	A	108	LYS	3.0
1	A	793	ARG	3.0
1	A	787	ILE	3.0
1	A	171	VAL	3.0
1	A	192	LEU	3.0
1	A	544	ASN	3.0
1	A	190	ILE	3.0
1	A	241	GLY	2.9
1	A	503	GLY	2.9
1	A	172	GLY	2.9
1	A	93	VAL	2.9
1	A	97	ILE	2.9
1	A	122	ARG	2.8
1	A	156	THR	2.8
1	A	129	GLU	2.8
1	A	202	LYS	2.8
1	A	112	ALA	2.8
1	A	204	LEU	2.8
1	A	118	THR	2.8
1	A	127	ALA	2.7
1	A	158	ALA	2.7
1	A	230	ARG	2.7
1	A	748	GLY	2.7
1	A	269	ILE	2.7
1	A	530	ILE	2.7
1	A	181	GLU	2.6
1	A	183	VAL	2.6
1	A	232	ILE	2.6
1	A	145	ARG	2.6
1	A	111	GLY	2.6
1	A	207	GLY	2.6
1	A	155	LEU	2.6
1	A	95	GLN	2.6
1	A	213	GLY	2.6
1	A	160	LYS	2.6
1	A	138	TYR	2.6
1	A	249	LEU	2.5
1	A	173	ARG	2.5
1	A	219	LEU	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	168	MET	2.5
1	A	339	ASP	2.5
1	A	399	ASP	2.5
1	A	178	MET	2.5
1	A	201	ASN	2.5
1	A	238	THR	2.4
1	A	532	TYR	2.4
1	A	162	ASN	2.4
1	A	206	GLN	2.4
1	A	334	ILE	2.4
1	A	244	ILE	2.4
1	A	365	ILE	2.4
1	A	289	TYR	2.3
1	A	149	LEU	2.3
1	A	282	ILE	2.3
1	A	494	GLU	2.3
1	A	505	GLY	2.3
1	A	215	ARG	2.3
1	A	143	VAL	2.3
1	A	791	GLN	2.3
1	A	157	GLY	2.3
1	A	144	SER	2.3
1	A	506	ASP	2.3
1	A	221	ILE	2.2
1	A	136	VAL	2.2
1	A	126	LYS	2.2
1	A	401	ALA	2.2
1	A	150	PRO	2.2
1	A	772	LYS	2.2
1	A	231	ASP	2.2
1	A	137	PRO	2.2
1	A	185	THR	2.2
1	A	518	ILE	2.2
1	A	227	VAL	2.2
1	A	216	GLU	2.2
1	A	123	ALA	2.2
1	A	161	ARG	2.2
1	A	711	VAL	2.1
1	A	214	SER	2.1
1	A	200	ASN	2.1
1	A	228	TYR	2.1
1	A	393	ASN	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	98	ASP	2.1
1	A	247	GLY	2.1
1	A	106	SER	2.1
1	A	284	THR	2.1
1	A	104	GLY	2.1
1	A	537	ARG	2.1
1	A	195	PHE	2.1
1	A	304	ALA	2.1
1	A	197	LEU	2.1
1	A	445	LEU	2.1
1	A	120	ASP	2.0
1	A	813	LYS	2.0
1	A	121	ILE	2.0
1	A	508	ILE	2.0
1	A	187	ASN	2.0
1	A	109	THR	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 oligosaccharides in this entry.

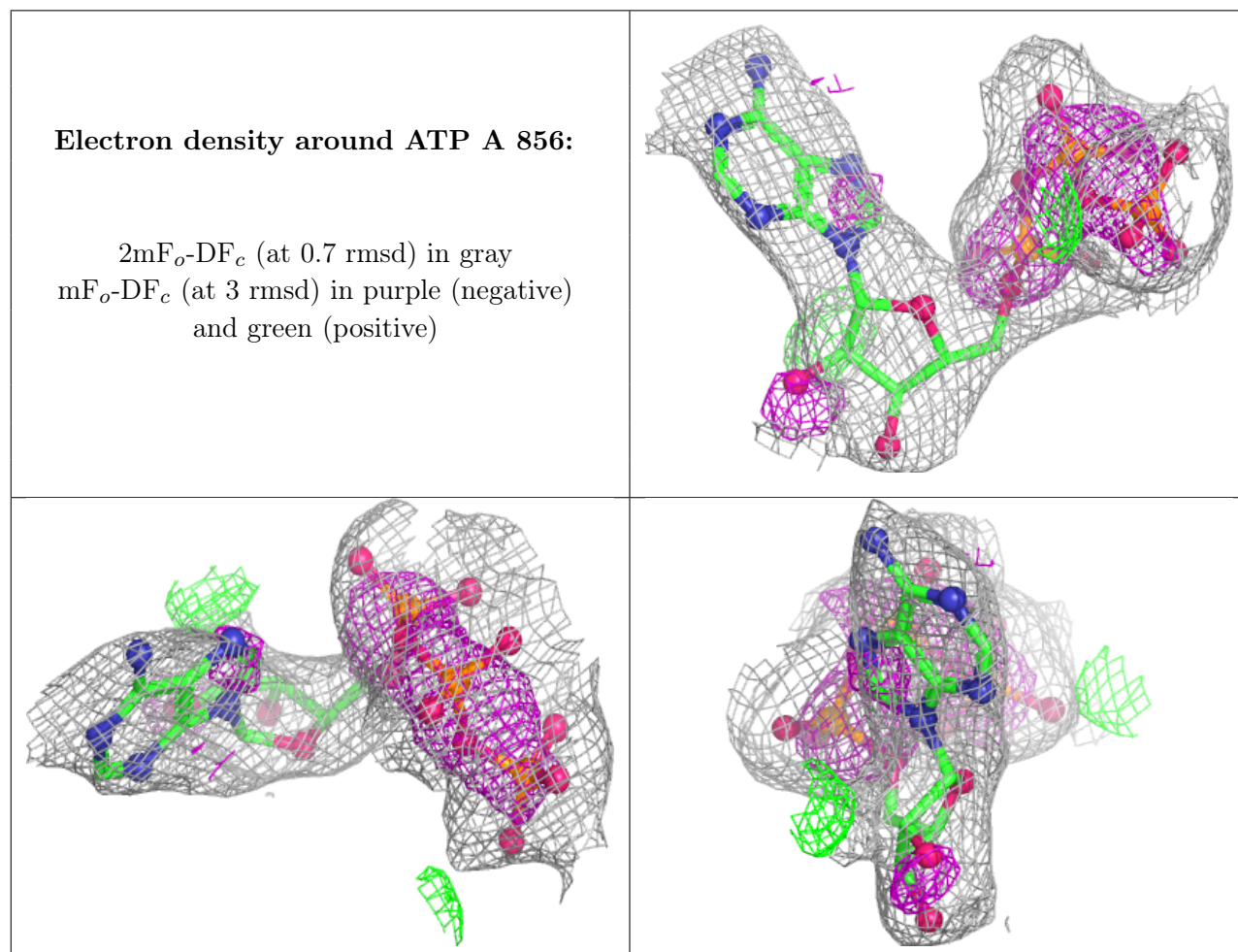
6.4 Ligands [i](#)

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($\text{\AA}^2$)	Q<0.9
4	ATP	A	856	31/31	0.79	0.14	49,59,60,62	0
3	MG	A	855	1/1	0.82	0.10	47,47,47,47	0
3	MG	A	857	1/1	0.87	0.07	47,47,47,47	0
2	CA	A	1	1/1	0.95	0.05	49,49,49,49	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers

as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.



6.5 Other polymers ⓘ

There are no such residues in this entry.