



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 05:04 AM UTC

PDB ID : 4RQF / pdb_00004rqf
Title : human Seryl-tRNA synthetase dimer complexed with one molecule of tRNA^{sec}
Authors : Xie, W.; Wang, C.; Guo, Y.; Tian, Q.; Jia, Q.
Deposited on : 2014-11-03
Resolution : 3.50 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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

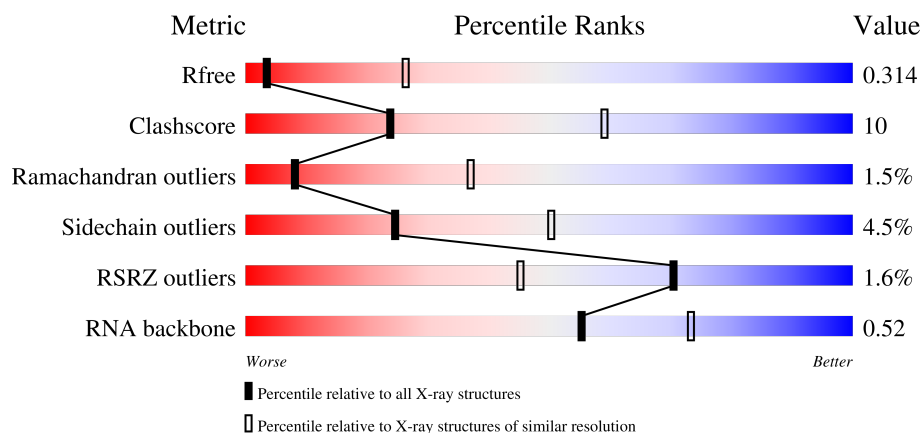
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.50 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))
R_{free}	180053	1085 (3.54-3.46)
Clashscore	190562	1140 (3.54-3.46)
Ramachandran outliers	187476	1113 (3.54-3.46)
Sidechain outliers	187428	1114 (3.54-3.46)
RSRZ outliers	180081	1084 (3.54-3.46)
RNA backbone	3983	1010 (3.98-3.02)

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	C	90	46% 19% • 30%
2	A	522	64% 20% • 14%
2	B	522	68% 20% • 9%

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
3	ANP	A	602	-	-	X	-
3	ANP	B	602	-	-	X	-

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 8619 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 RNA chain called selenocysteine tRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	C	63	Total	C	N	O	P	0	0	0
			1341	598	233	447	63			

- Molecule 2 is a protein called Serine-tRNA ligase, cytoplasmic.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	A	451	Total	C	N	O	S	0	0	0
			3535	2245	612	662	16			
2	B	474	Total	C	N	O	S	0	0	0
			3667	2326	637	686	18			

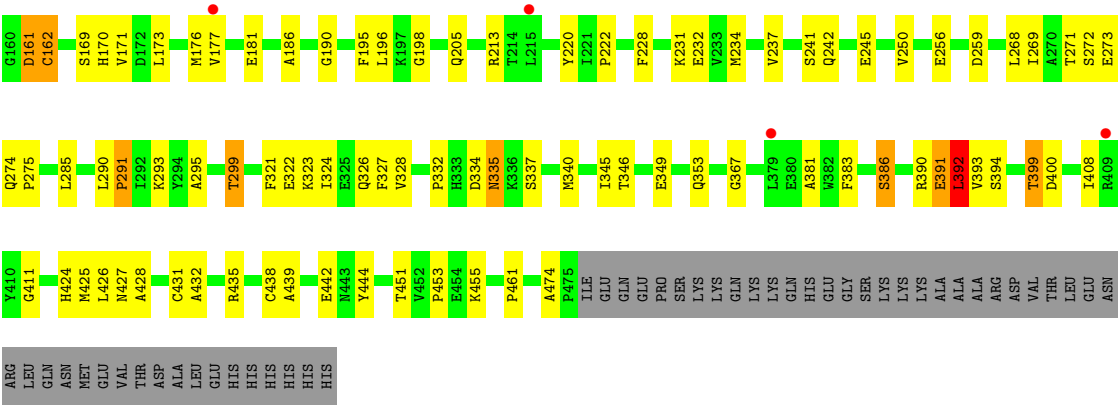
There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	447	LYS	GLU	engineered mutation	UNP P49591
A	515	LEU	-	expression tag	UNP P49591
A	516	GLU	-	expression tag	UNP P49591
A	517	HIS	-	expression tag	UNP P49591
A	518	HIS	-	expression tag	UNP P49591
A	519	HIS	-	expression tag	UNP P49591
A	520	HIS	-	expression tag	UNP P49591
A	521	HIS	-	expression tag	UNP P49591
A	522	HIS	-	expression tag	UNP P49591
B	447	LYS	GLU	engineered mutation	UNP P49591
B	515	LEU	-	expression tag	UNP P49591
B	516	GLU	-	expression tag	UNP P49591
B	517	HIS	-	expression tag	UNP P49591
B	518	HIS	-	expression tag	UNP P49591
B	519	HIS	-	expression tag	UNP P49591
B	520	HIS	-	expression tag	UNP P49591
B	521	HIS	-	expression tag	UNP P49591
B	522	HIS	-	expression tag	UNP P49591

- # ANP

Chemical structure of Serine (SER) is shown. The side chain consists of a hydroxyl group (OH) attached to a methylene group (CH₂), which is attached to the alpha-carbon (Cα). The alpha-carbon is also bonded to an amino group (NH₂) and a carboxyl group (COOH). The carboxyl group is shown as a carbonyl (C=O) and a hydroxyl (OH) group. The amino group is shown as a nitrogen (N) atom bonded to two hydrogen atoms (H). The hydroxyl group is shown as an oxygen (O) atom bonded to a hydrogen atom (H). The side chain is labeled CB (backbone carbon) and CA(S) (alpha-carbon). The carboxyl group is labeled C (carbonyl carbon) and OXT (oxygen atom).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			7	3	1	3		
4	B	1	Total	C	N	O	0	0
			7	3	1	3		



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	160.38Å 108.89Å 89.49Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	37.62 – 3.50 37.62 – 3.50	Depositor EDS
% Data completeness (in resolution range)	96.9 (37.62-3.50) 96.9 (37.62-3.50)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.18 (at 3.48Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.2_1309)	Depositor
R, R_{free}	0.253 , 0.314 0.253 , 0.314	Depositor DCC
R_{free} test set	1008 reflections (2.55%)	wwPDB-VP
Wilson B-factor (Å ²)	115.9	Xtriage
Anisotropy	0.394	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 70.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	8619	wwPDB-VP
Average B, all atoms (Å ²)	135.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.18% 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: ANP

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	C	0.44	0/1496	0.75	1/2327 (0.0%)
2	A	0.65	0/3605	0.89	0/4875
2	B	0.61	0/3739	0.89	3/5061 (0.1%)
All	All	0.60	0/8840	0.87	4/12263 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	392	LEU	N-CA-C	5.62	122.78	110.80
1	C	66	C	C2'-C3'-O3'	5.38	121.77	113.70
2	B	391	GLU	N-CA-C	5.34	119.28	112.87
2	B	399	THR	CB-CA-C	-5.20	110.56	116.54

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	C	1341	0	677	13	0
2	A	3535	0	3426	78	0
2	B	3667	0	3557	77	0
3	A	31	0	13	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	31	0	13	11	0
4	A	7	0	4	2	0
4	B	7	0	4	2	0
All	All	8619	0	7694	163	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.

The worst 5 of 163 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:C:19:G:H1	1:C:56:C:H42	1.32	0.76
2:B:435:ARG:NH1	3:B:602:ANP:H2'	2.02	0.75
1:C:19:G:H1	1:C:56:C:N4	1.85	0.75
2:B:332:PRO:HB3	2:B:424:HIS:CD2	2.25	0.72
2:A:432:ALA:HB1	3:A:602:ANP:O2'	1.90	0.72

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	
2	A	445/522 (85%)	399 (90%)	40 (9%)	6 (1%)	9	39
2	B	472/522 (90%)	421 (89%)	43 (9%)	8 (2%)	7	35
All	All	917/1044 (88%)	820 (89%)	83 (9%)	14 (2%)	8	37

5 of 14 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	A	100	VAL

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Mol	Chain	Res	Type
2	B	162	CYS
2	B	392	LEU
2	A	191	SER
2	A	334	ASP

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	
2	A	369/461 (80%)	352 (95%)	17 (5%)	24	50
2	B	380/461 (82%)	363 (96%)	17 (4%)	24	50
All	All	749/922 (81%)	715 (96%)	34 (4%)	24	50

5 of 34 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	259	ASP
2	B	299	THR
2	B	394	SER
2	A	330	SER
2	A	290	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such sidechains are listed below:

Mol	Chain	Res	Type
2	A	427	ASN
2	B	242	GLN
2	B	274	GLN
2	A	209	GLN
2	A	205	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	C	61/90 (67%)	10 (16%)	3 (4%)

5 of 10 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	C	7	G
1	C	9	U
1	C	18	G
1	C	20	U
1	C	20(A)	C

All (3) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	C	6	U
1	C	19	G
1	C	66	C

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](#)

4 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
4	SER	B	601	-	4,6,6	1.19	1 (25%)	2,7,7	1.76	1 (50%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	SER	A	601	-	4,6,6	1.37	1 (25%)	2,7,7	1.48	1 (50%)
3	ANP	B	602	-	33,33,33	1.84	8 (24%)	45,52,52	2.49	16 (35%)
3	ANP	A	602	-	33,33,33	1.91	8 (24%)	45,52,52	2.47	19 (42%)

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	SER	B	601	-	-	2/6/6/6	-
4	SER	A	601	-	-	2/6/6/6	-
3	ANP	B	602	-	-	5/18/38/38	0/3/3/3
3	ANP	A	602	-	-	6/18/38/38	0/3/3/3

The worst 5 of 18 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	602	ANP	PB-O1B	4.72	1.53	1.46
3	A	602	ANP	PG-N3B	4.44	1.75	1.63
3	B	602	ANP	C5-C4	4.32	1.46	1.39
3	A	602	ANP	C5-C4	4.23	1.46	1.39
3	A	602	ANP	PB-N3B	4.20	1.74	1.63

The worst 5 of 37 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	602	ANP	O1G-PG-N3B	-6.21	102.63	111.77
3	B	602	ANP	C5-C4-N3	-6.11	118.30	126.72
3	B	602	ANP	O1G-PG-N3B	-6.06	102.84	111.77
3	B	602	ANP	O2B-PB-O1B	5.29	121.22	109.87
3	A	602	ANP	C5-C4-N3	-5.12	119.66	126.72

There are no chirality outliers.

5 of 15 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	602	ANP	PB-N3B-PG-O1G
3	A	602	ANP	C5'-O5'-PA-O2A
3	A	602	ANP	C5'-O5'-PA-O3A

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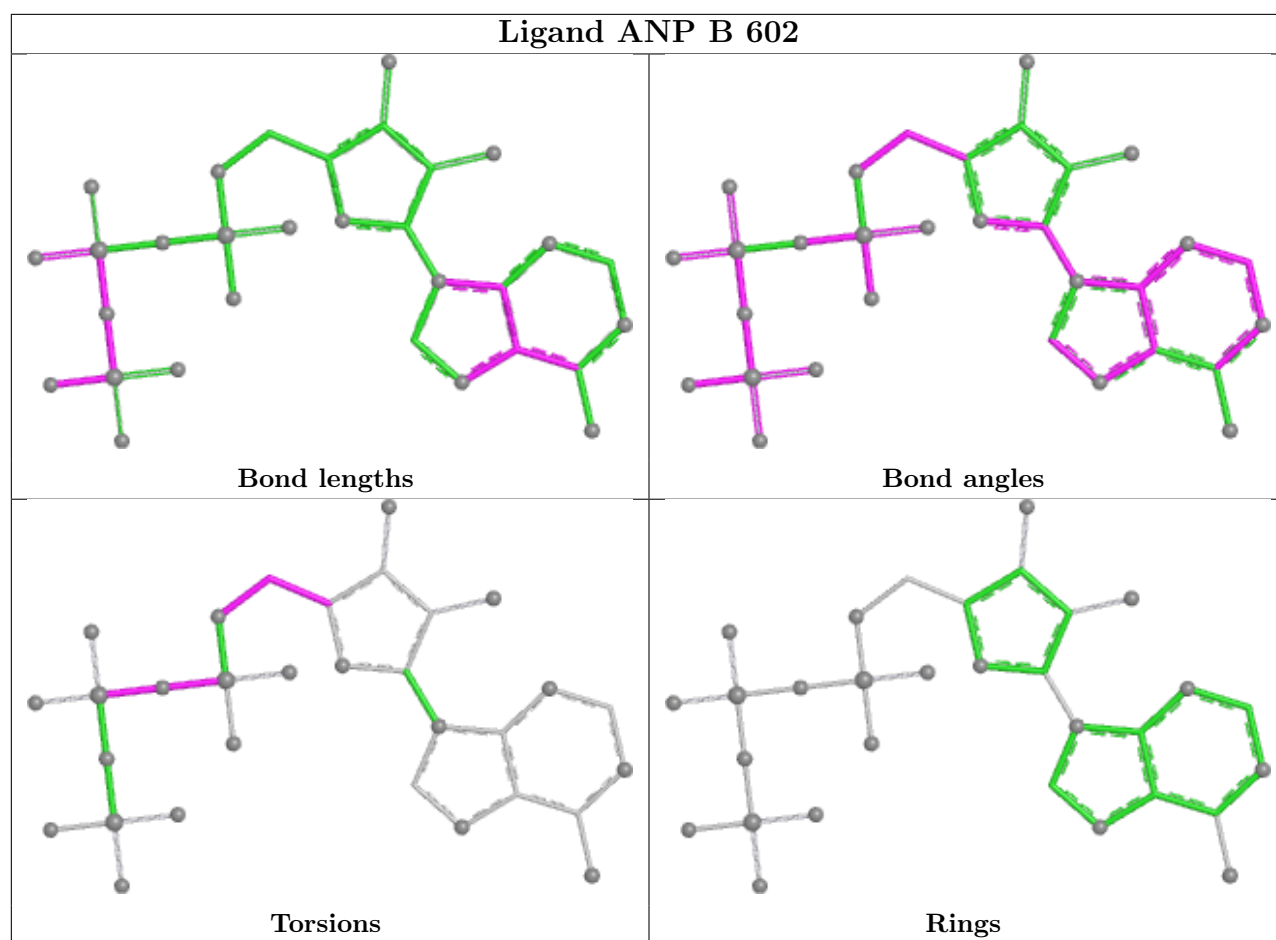
Mol	Chain	Res	Type	Atoms
3	A	602	ANP	O4'-C4'-C5'-O5'
3	B	602	ANP	PA-O3A-PB-O2B

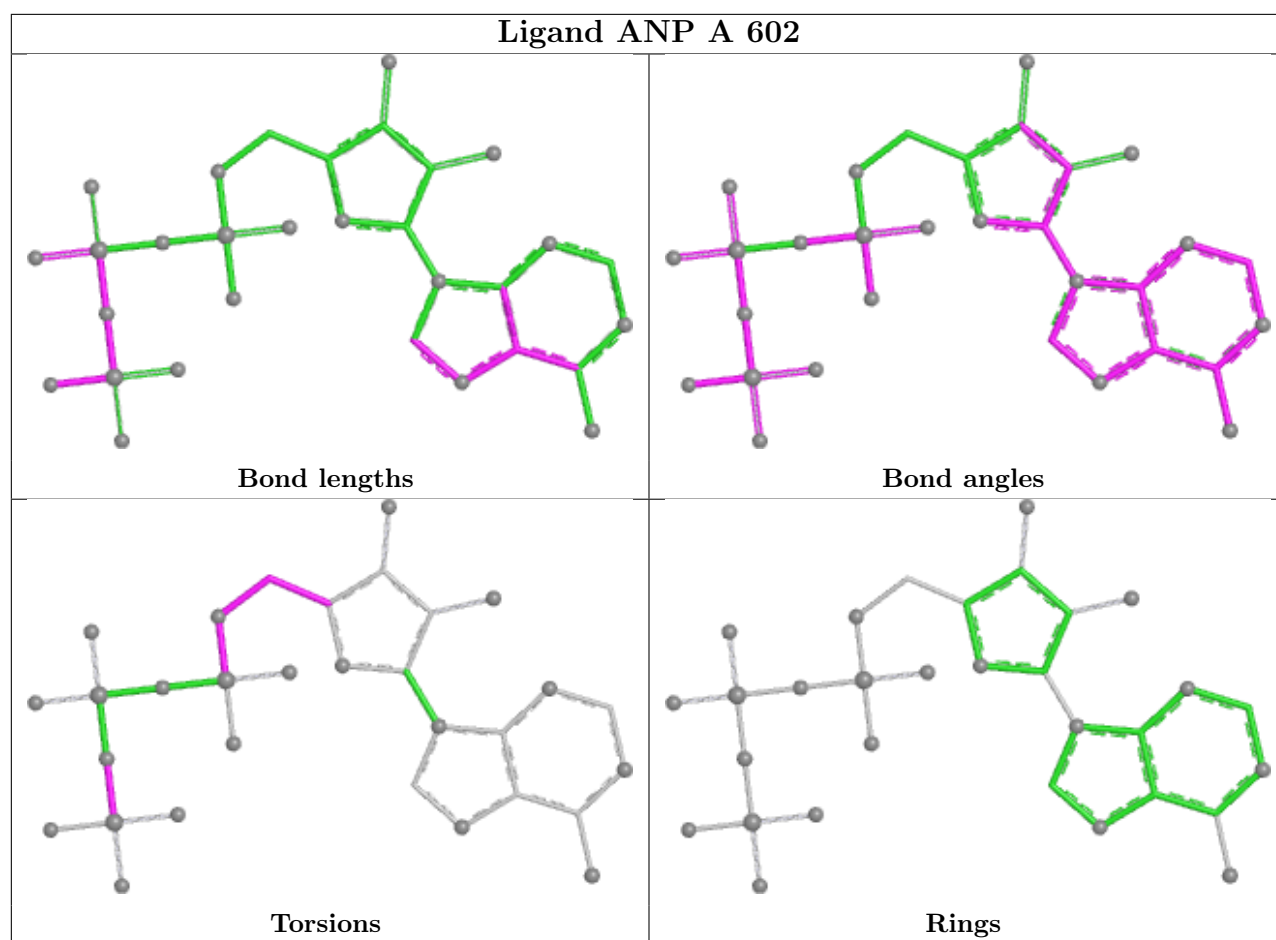
There are no ring outliers.

4 monomers are involved in 24 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	601	SER	2	0
4	A	601	SER	2	0
3	B	602	ANP	11	0
3	A	602	ANP	9	0

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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	C	63/90 (70%)	0.33	1 (1%) 70 45	106, 185, 254, 294	0
2	A	451/522 (86%)	-0.02	9 (1%) 65 39	85, 120, 161, 197	0
2	B	474/522 (90%)	-0.04	6 (1%) 75 50	81, 131, 176, 199	0
All	All	988/1134 (87%)	-0.01	16 (1%) 70 45	81, 127, 185, 294	0

The worst 5 of 16 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	A	300	CYS	4.4
2	A	285	LEU	4.1
2	A	60	CYS	4.0
2	A	438	CYS	3.6
2	B	51	ASP	3.5

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](#)

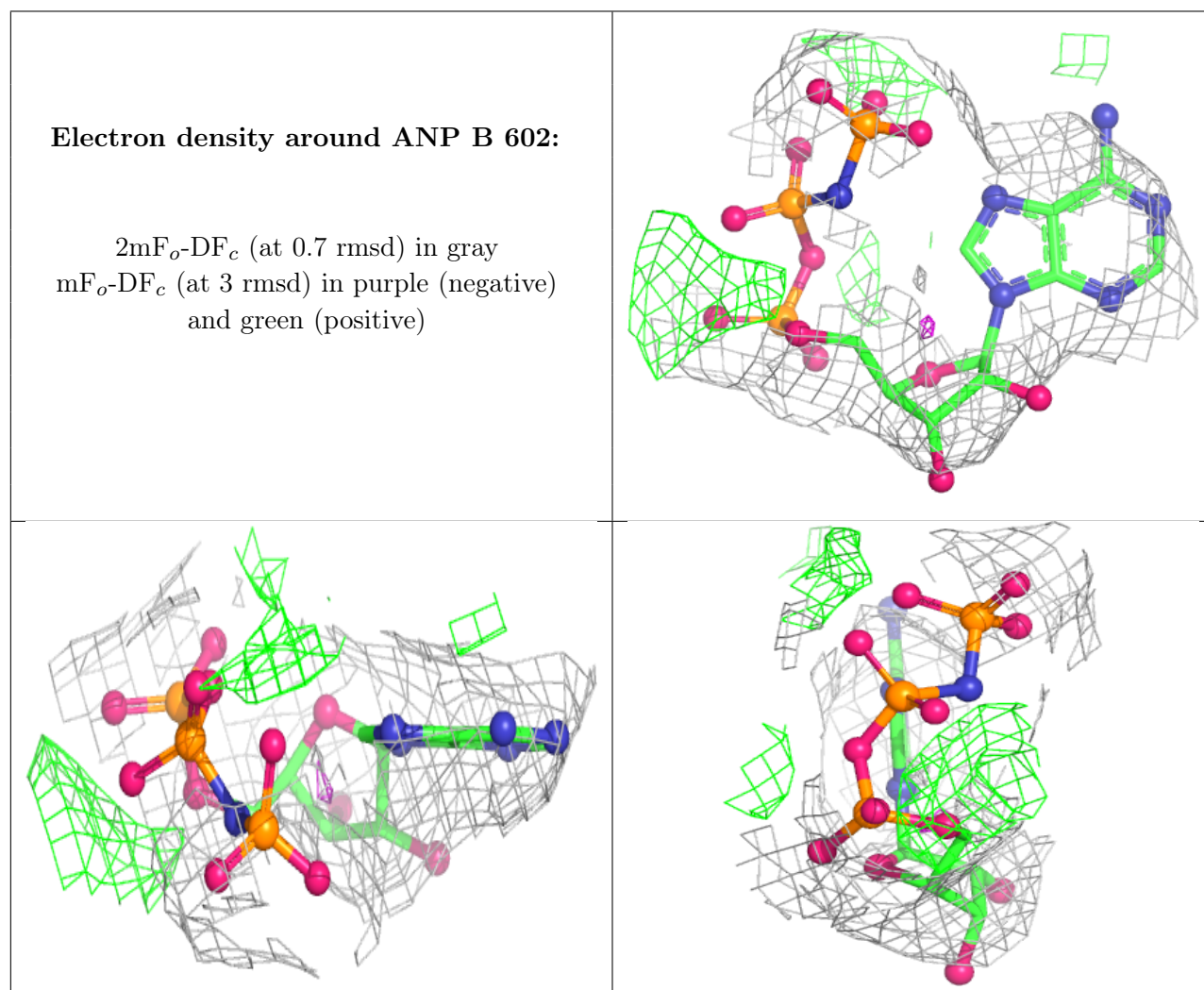
There are no oligosaccharides in this entry.

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.

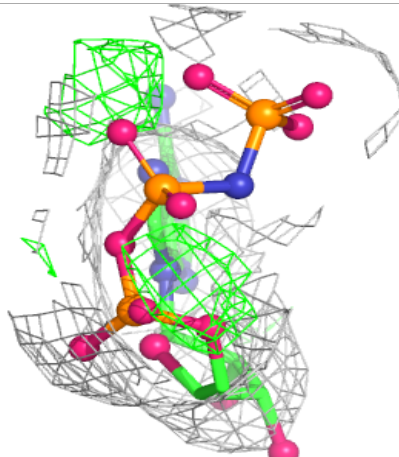
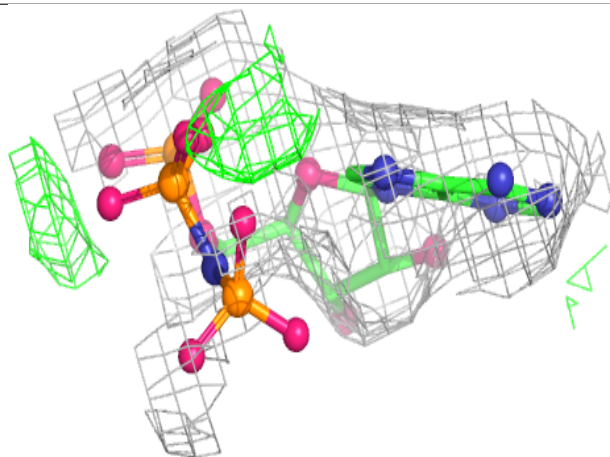
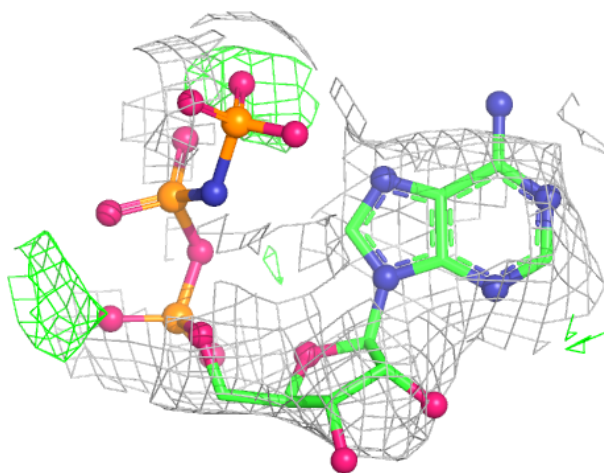
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	ANP	B	602	31/31	0.85	0.10	104,115,131,136	0
3	ANP	A	602	31/31	0.88	0.10	114,122,137,140	0
4	SER	B	601	7/7	0.90	0.11	134,137,139,140	0
4	SER	A	601	7/7	0.91	0.19	105,110,116,117	0

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.



Electron density around ANP A 602:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers [i](#)

There are no such residues in this entry.