



wwPDB EM Validation Summary Report ⓘ

Mar 20, 2026 – 12:30 AM UTC

PDB ID : 7RL7 / pdb_00007rl7
EMDB ID : EMD-24519
Title : Cryo-EM structure of human p97-R155H mutant bound to ATPgS.
Authors : Caffrey, B.; Zhu, X.; Berezuk, A.; Tuttle, K.; Chittori, S.; Subramaniam, S.
Deposited on : 2021-07-23
Resolution : 3.00 Å (reported)

This is a wwPDB EM 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/EMValidationReportHelp>

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:

EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : **NOT EXECUTED**
MapQ : **FAILED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

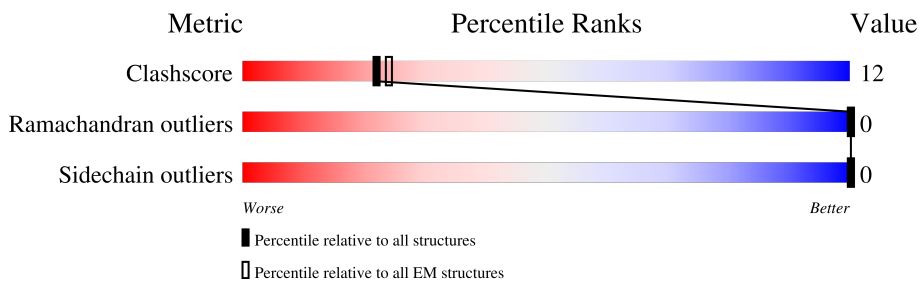
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.00 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)	EM structures (#Entries)
Clashscore	229148	23984
Ramachandran outliers	224038	23583
Sidechain outliers	223484	23102

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the 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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	A	821	
1	B	821	
1	C	821	
1	D	821	
1	E	821	
1	F	821	

2 Entry composition i

There are 3 unique types of molecules in this entry. The entry contains 34950 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, 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 Transitional endoplasmic reticulum ATPase.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	737	5761	3627	1013	1091	30	0	0
1	B	737	5761	3627	1013	1091	30	0	0
1	C	737	5761	3627	1013	1091	30	0	0
1	D	737	5761	3627	1013	1091	30	0	0
1	E	737	5761	3627	1013	1091	30	0	0
1	F	737	5761	3627	1013	1091	30	0	0

There are 102 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-14	HIS	-	expression tag	UNP P55072
A	-13	HIS	-	expression tag	UNP P55072
A	-12	HIS	-	expression tag	UNP P55072
A	-11	HIS	-	expression tag	UNP P55072
A	-10	HIS	-	expression tag	UNP P55072
A	-9	HIS	-	expression tag	UNP P55072
A	-8	GLY	-	expression tag	UNP P55072
A	-7	THR	-	expression tag	UNP P55072
A	-6	SER	-	expression tag	UNP P55072
A	-5	GLU	-	expression tag	UNP P55072
A	-4	ASN	-	expression tag	UNP P55072
A	-3	LEU	-	expression tag	UNP P55072
A	-2	TYR	-	expression tag	UNP P55072
A	-1	PHE	-	expression tag	UNP P55072
A	0	GLN	-	expression tag	UNP P55072
A	1	GLY	-	expression tag	UNP P55072
A	155	HIS	ARG	engineered mutation	UNP P55072
B	-14	HIS	-	expression tag	UNP P55072

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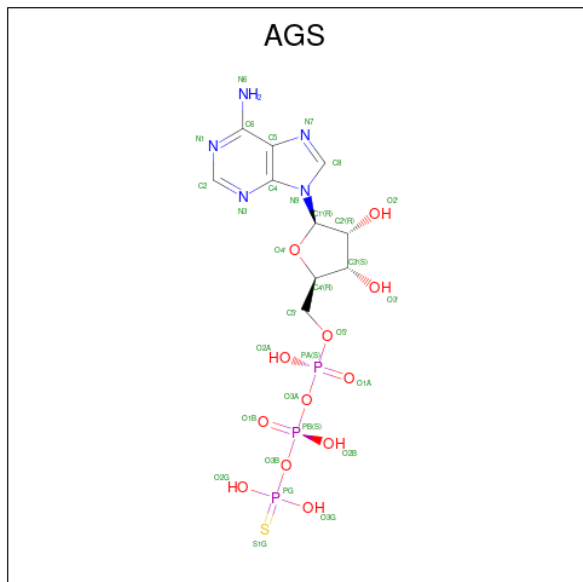
Chain	Residue	Modelled	Actual	Comment	Reference
B	-13	HIS	-	expression tag	UNP P55072
B	-12	HIS	-	expression tag	UNP P55072
B	-11	HIS	-	expression tag	UNP P55072
B	-10	HIS	-	expression tag	UNP P55072
B	-9	HIS	-	expression tag	UNP P55072
B	-8	GLY	-	expression tag	UNP P55072
B	-7	THR	-	expression tag	UNP P55072
B	-6	SER	-	expression tag	UNP P55072
B	-5	GLU	-	expression tag	UNP P55072
B	-4	ASN	-	expression tag	UNP P55072
B	-3	LEU	-	expression tag	UNP P55072
B	-2	TYR	-	expression tag	UNP P55072
B	-1	PHE	-	expression tag	UNP P55072
B	0	GLN	-	expression tag	UNP P55072
B	1	GLY	-	expression tag	UNP P55072
B	155	HIS	ARG	engineered mutation	UNP P55072
C	-14	HIS	-	expression tag	UNP P55072
C	-13	HIS	-	expression tag	UNP P55072
C	-12	HIS	-	expression tag	UNP P55072
C	-11	HIS	-	expression tag	UNP P55072
C	-10	HIS	-	expression tag	UNP P55072
C	-9	HIS	-	expression tag	UNP P55072
C	-8	GLY	-	expression tag	UNP P55072
C	-7	THR	-	expression tag	UNP P55072
C	-6	SER	-	expression tag	UNP P55072
C	-5	GLU	-	expression tag	UNP P55072
C	-4	ASN	-	expression tag	UNP P55072
C	-3	LEU	-	expression tag	UNP P55072
C	-2	TYR	-	expression tag	UNP P55072
C	-1	PHE	-	expression tag	UNP P55072
C	0	GLN	-	expression tag	UNP P55072
C	1	GLY	-	expression tag	UNP P55072
C	155	HIS	ARG	engineered mutation	UNP P55072
D	-14	HIS	-	expression tag	UNP P55072
D	-13	HIS	-	expression tag	UNP P55072
D	-12	HIS	-	expression tag	UNP P55072
D	-11	HIS	-	expression tag	UNP P55072
D	-10	HIS	-	expression tag	UNP P55072
D	-9	HIS	-	expression tag	UNP P55072
D	-8	GLY	-	expression tag	UNP P55072
D	-7	THR	-	expression tag	UNP P55072
D	-6	SER	-	expression tag	UNP P55072

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-5	GLU	-	expression tag	UNP P55072
D	-4	ASN	-	expression tag	UNP P55072
D	-3	LEU	-	expression tag	UNP P55072
D	-2	TYR	-	expression tag	UNP P55072
D	-1	PHE	-	expression tag	UNP P55072
D	0	GLN	-	expression tag	UNP P55072
D	1	GLY	-	expression tag	UNP P55072
D	155	HIS	ARG	engineered mutation	UNP P55072
E	-14	HIS	-	expression tag	UNP P55072
E	-13	HIS	-	expression tag	UNP P55072
E	-12	HIS	-	expression tag	UNP P55072
E	-11	HIS	-	expression tag	UNP P55072
E	-10	HIS	-	expression tag	UNP P55072
E	-9	HIS	-	expression tag	UNP P55072
E	-8	GLY	-	expression tag	UNP P55072
E	-7	THR	-	expression tag	UNP P55072
E	-6	SER	-	expression tag	UNP P55072
E	-5	GLU	-	expression tag	UNP P55072
E	-4	ASN	-	expression tag	UNP P55072
E	-3	LEU	-	expression tag	UNP P55072
E	-2	TYR	-	expression tag	UNP P55072
E	-1	PHE	-	expression tag	UNP P55072
E	0	GLN	-	expression tag	UNP P55072
E	1	GLY	-	expression tag	UNP P55072
E	155	HIS	ARG	engineered mutation	UNP P55072
F	-14	HIS	-	expression tag	UNP P55072
F	-13	HIS	-	expression tag	UNP P55072
F	-12	HIS	-	expression tag	UNP P55072
F	-11	HIS	-	expression tag	UNP P55072
F	-10	HIS	-	expression tag	UNP P55072
F	-9	HIS	-	expression tag	UNP P55072
F	-8	GLY	-	expression tag	UNP P55072
F	-7	THR	-	expression tag	UNP P55072
F	-6	SER	-	expression tag	UNP P55072
F	-5	GLU	-	expression tag	UNP P55072
F	-4	ASN	-	expression tag	UNP P55072
F	-3	LEU	-	expression tag	UNP P55072
F	-2	TYR	-	expression tag	UNP P55072
F	-1	PHE	-	expression tag	UNP P55072
F	0	GLN	-	expression tag	UNP P55072
F	1	GLY	-	expression tag	UNP P55072
F	155	HIS	ARG	engineered mutation	UNP P55072

- Molecule 2 is PHOSPHOTHIOPHOSPHORIC ACID-ADENYLATE ESTER (CCD ID: AGS) (formula: C₁₀H₁₆N₅O₁₂P₃S).



Mol	Chain	Residues	Atoms					AltConf	
			Total	C	N	O	P		S
2	A	1	Total	C	N	O	P	S	0
			31	10	5	12	3	1	
2	A	1	Total	C	N	O	P	S	0
			31	10	5	12	3	1	
2	B	1	Total	C	N	O	P	S	0
			31	10	5	12	3	1	
2	B	1	Total	C	N	O	P	S	0
			31	10	5	12	3	1	
2	C	1	Total	C	N	O	P	S	0
			31	10	5	12	3	1	
2	C	1	Total	C	N	O	P	S	0
			31	10	5	12	3	1	
2	D	1	Total	C	N	O	P	S	0
			31	10	5	12	3	1	
2	D	1	Total	C	N	O	P	S	0
			31	10	5	12	3	1	
2	E	1	Total	C	N	O	P	S	0
			31	10	5	12	3	1	
2	E	1	Total	C	N	O	P	S	0
			31	10	5	12	3	1	
2	F	1	Total	C	N	O	P	S	0
			31	10	5	12	3	1	
2	F	1	Total	C	N	O	P	S	0
			31	10	5	12	3	1	

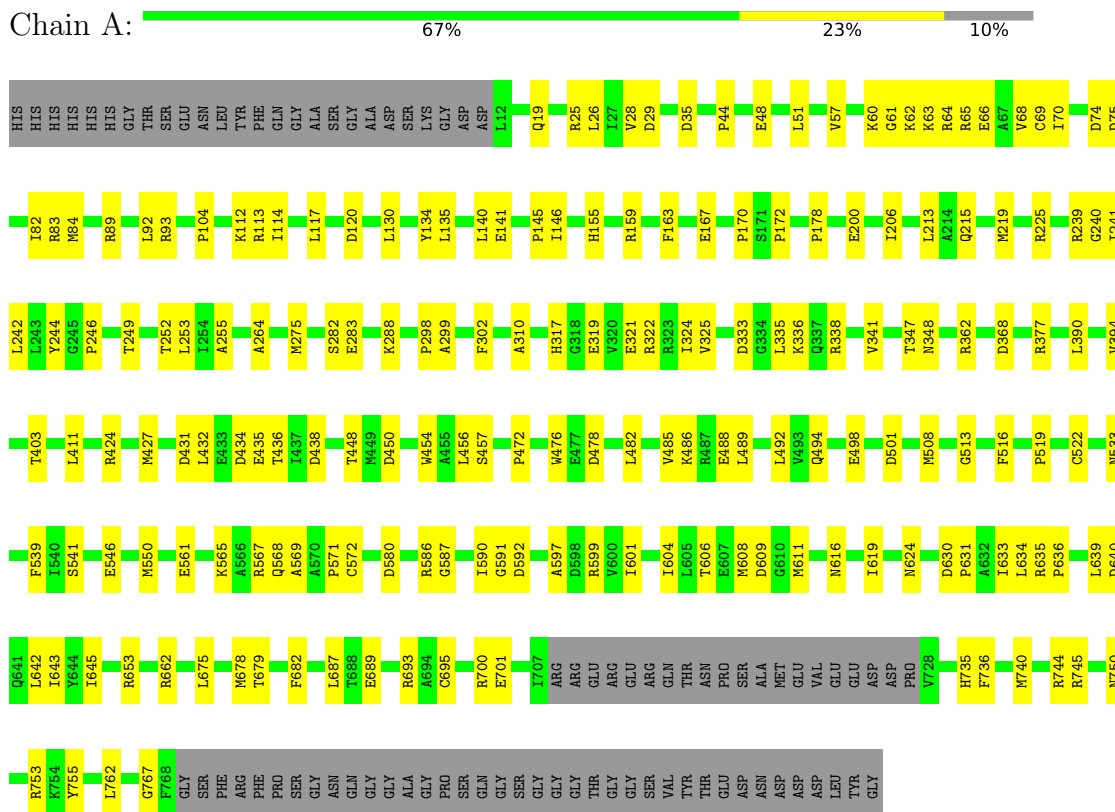
- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
3	A	2	Total 2	Mg 2	0
3	B	2	Total 2	Mg 2	0
3	C	2	Total 2	Mg 2	0
3	D	2	Total 2	Mg 2	0
3	E	2	Total 2	Mg 2	0
3	F	2	Total 2	Mg 2	0

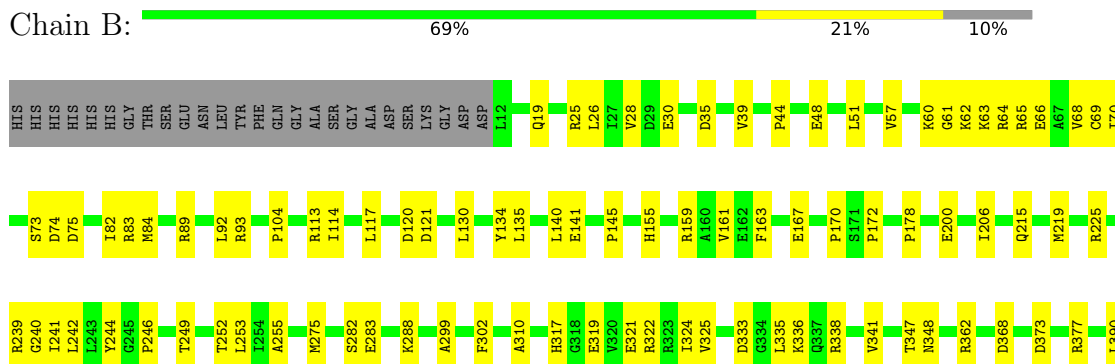
3 Residue-property plots

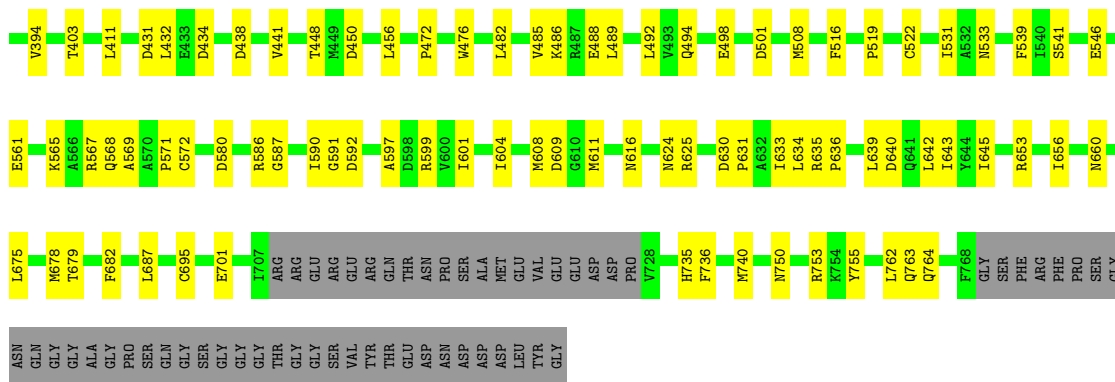
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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. 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: Transitional endoplasmic reticulum ATPase

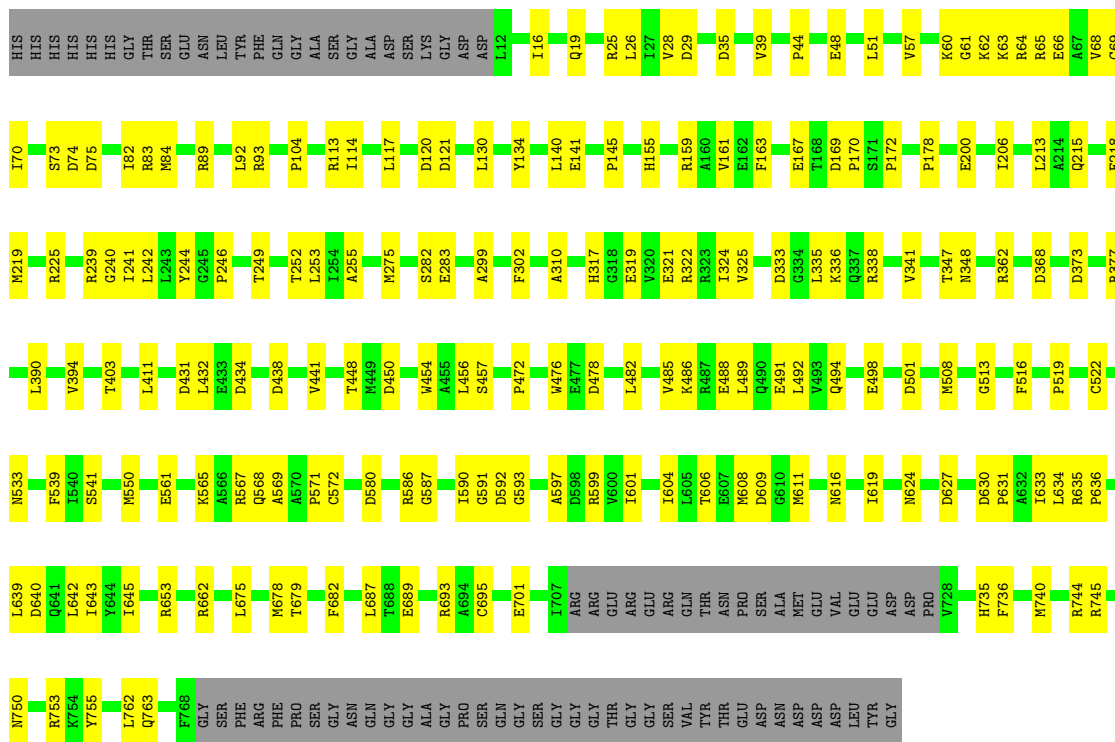


- Molecule 1: Transitional endoplasmic reticulum ATPase

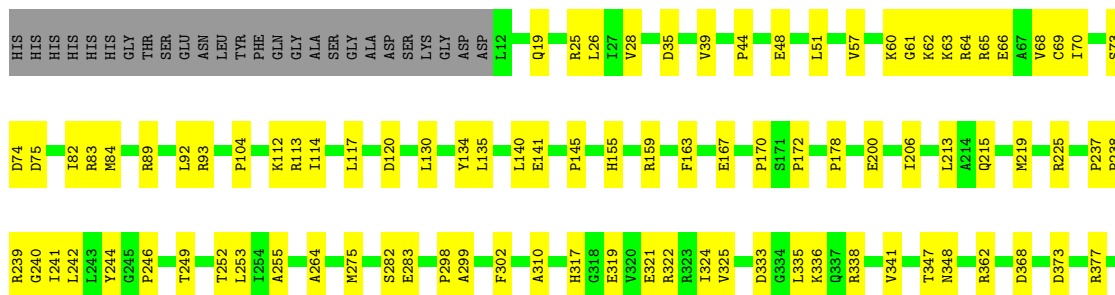


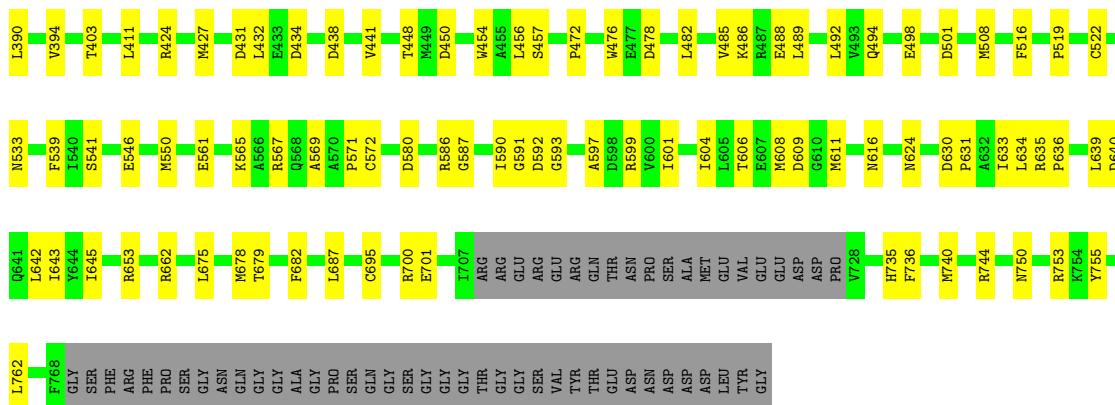


● Molecule 1: Transitional endoplasmic reticulum ATPase

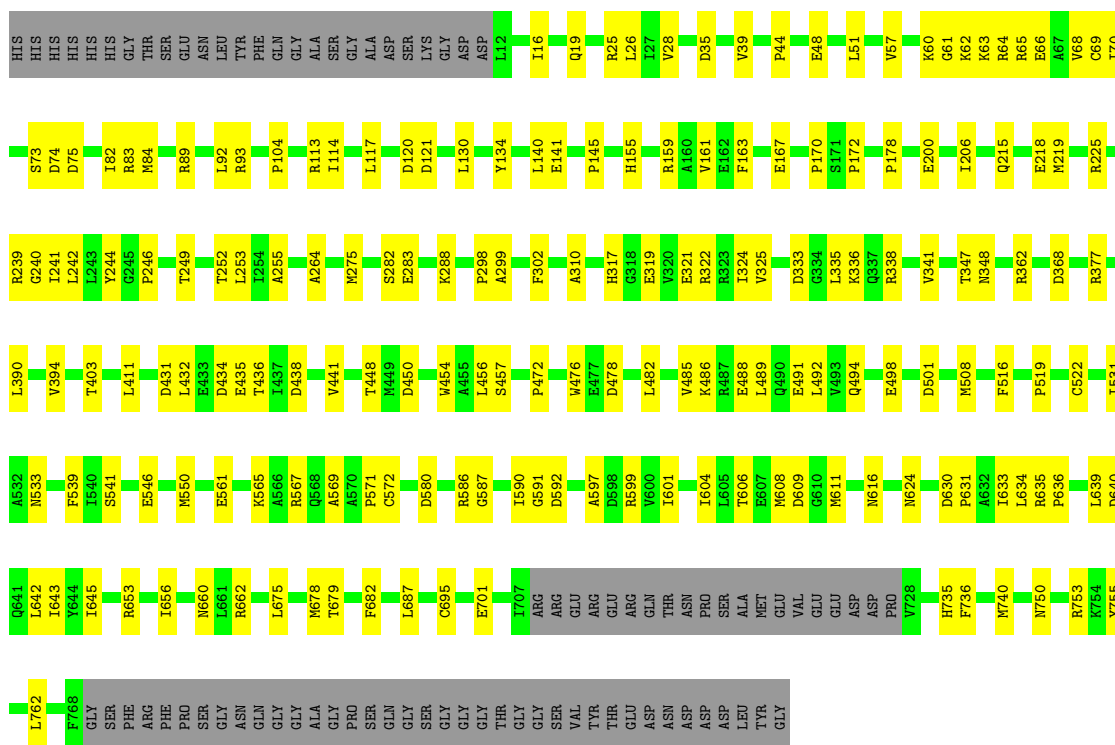


● Molecule 1: Transitional endoplasmic reticulum ATPase

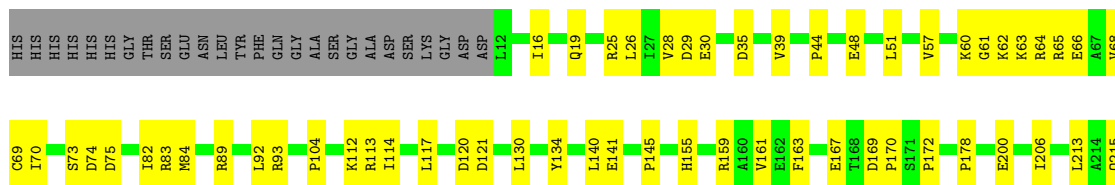




• Molecule 1: Transitional endoplasmic reticulum ATPase



• Molecule 1: Transitional endoplasmic reticulum ATPase



LEU	E218	D373	M508	I619	GLU
TTR	M219	R377	G513	N624	VAL
GLY	R225	L390	F516	D627	GLU
	P237	V394	P519	D630	ASP
	P238	T403	G521	P631	PRO
	G240	L411	C522	A632	Y728
	I241	R424	I531	L633	H735
	L242	M427	A532	L634	F736
	L243	D431	M533	R635	M740
	Y244	L432	F539	P636	N750
	G246	E433	I540	L639	R753
	P246	D434	S541	D640	K754
	T249	E435	I546	D641	Y755
	T252	E436	M550	L642	L762
	L253	T436	E561	I643	Q763
	I254	I437	R565	Y644	Q764
	A255	D438	R662	I645	F768
	M275	T448	L675	D649	GLY
	S282	D450	M678	R653	SER
	E283	A454	T679	R662	SER
	A299	L455	F682	L687	PHE
	F302	S457	F682	T688	ARG
	A310	L464	L689	E689	ARG
	H317	P472	R693	R693	PHE
	G318	W476	A694	C695	PHE
	E319	D478	C695	R700	PRO
	V320	L482	R700	E701	SER
	E321	V485	A597	I707	GLY
	R322	K486	D598	ARG	GLY
	I324	R487	R599	GLY	GLY
	V325	E488	I601	THR	THR
	D333	L489	I604	GLY	GLY
	L335	Q490	L606	ARG	SER
	K336	E491	T606	GLU	VAL
	Q337	L492	M608	ARG	TYR
	R338	V493	M609	GLN	THR
	V341	Q494	M611	THR	THR
	T347	E498	M616	GLU	GLU
	N348	D501		ASN	ASP
	R362			ASN	ASN
	D368			ASP	ASP
				ALA	ALA
				MET	MET

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	284092	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor

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: AGS, MG

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	0.15	0/5855	0.39	0/7906
1	B	0.15	0/5855	0.39	0/7906
1	C	0.15	0/5855	0.39	0/7906
1	D	0.14	0/5855	0.39	0/7906
1	E	0.15	0/5855	0.39	0/7906
1	F	0.14	0/5855	0.39	0/7906
All	All	0.15	0/35130	0.39	0/47436

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 [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	5761	0	5833	144	0
1	B	5761	0	5833	135	0
1	C	5761	0	5833	145	0
1	D	5761	0	5833	140	0
1	E	5761	0	5833	137	0
1	F	5761	0	5833	151	0
2	A	62	0	24	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	62	0	24	2	0
2	C	62	0	24	3	0
2	D	62	0	24	4	0
2	E	62	0	24	3	0
2	F	62	0	24	2	0
3	A	2	0	0	0	0
3	B	2	0	0	0	0
3	C	2	0	0	0	0
3	D	2	0	0	0	0
3	E	2	0	0	0	0
3	F	2	0	0	0	0
All	All	34950	0	35142	807	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 12.

The worst 5 of 807 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:65:ARG:HB3	1:C:92:LEU:CD2	1.58	1.33
1:D:65:ARG:HB3	1:D:92:LEU:CD2	1.57	1.33
1:A:65:ARG:HB3	1:A:92:LEU:CD2	1.58	1.32
1:B:65:ARG:HB3	1:B:92:LEU:CD2	1.58	1.32
1:F:65:ARG:HB3	1:F:92:LEU:CD2	1.58	1.31

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 PDB entries followed by that with respect to all EM entries.

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	733/821 (89%)	686 (94%)	47 (6%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	733/821 (89%)	689 (94%)	44 (6%)	0	100	100
1	C	733/821 (89%)	688 (94%)	45 (6%)	0	100	100
1	D	733/821 (89%)	688 (94%)	45 (6%)	0	100	100
1	E	733/821 (89%)	688 (94%)	45 (6%)	0	100	100
1	F	733/821 (89%)	688 (94%)	45 (6%)	0	100	100
All	All	4398/4926 (89%)	4127 (94%)	271 (6%)	0	100	100

There are no Ramachandran outliers to report.

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 PDB entries followed by that with respect to all EM entries.

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	626/691 (91%)	626 (100%)	0	100	100
1	B	626/691 (91%)	626 (100%)	0	100	100
1	C	626/691 (91%)	626 (100%)	0	100	100
1	D	626/691 (91%)	626 (100%)	0	100	100
1	E	626/691 (91%)	626 (100%)	0	100	100
1	F	626/691 (91%)	626 (100%)	0	100	100
All	All	3756/4146 (91%)	3756 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 30 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	499	HIS
1	F	398	GLN
1	D	285	ASN
1	F	499	HIS
1	E	602	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](#)

Of 24 ligands modelled in this entry, 12 are monoatomic - leaving 12 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
2	AGS	A	901	3	32,33,33	0.50	1 (3%)	45,52,52	0.69	1 (2%)
2	AGS	F	902	3	32,33,33	0.49	1 (3%)	45,52,52	0.68	1 (2%)
2	AGS	C	901	3	32,33,33	0.50	1 (3%)	45,52,52	0.69	1 (2%)
2	AGS	F	901	3	32,33,33	0.50	1 (3%)	45,52,52	0.69	1 (2%)
2	AGS	B	901	3	32,33,33	0.50	1 (3%)	45,52,52	0.69	1 (2%)
2	AGS	C	902	3	32,33,33	0.50	1 (3%)	45,52,52	0.68	1 (2%)
2	AGS	D	902	3	32,33,33	0.49	1 (3%)	45,52,52	0.68	1 (2%)
2	AGS	B	902	3	32,33,33	0.50	1 (3%)	45,52,52	0.68	1 (2%)
2	AGS	E	902	3	32,33,33	0.50	1 (3%)	45,52,52	0.68	1 (2%)
2	AGS	D	901	3	32,33,33	0.50	1 (3%)	45,52,52	0.69	1 (2%)
2	AGS	E	901	3	32,33,33	0.51	1 (3%)	45,52,52	0.69	1 (2%)
2	AGS	A	902	3	32,33,33	0.50	1 (3%)	45,52,52	0.68	1 (2%)

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	AGS	A	901	3	-	7/21/38/38	0/3/3/3
2	AGS	F	902	3	-	3/21/38/38	0/3/3/3
2	AGS	C	901	3	-	7/21/38/38	0/3/3/3
2	AGS	F	901	3	-	7/21/38/38	0/3/3/3
2	AGS	B	901	3	-	7/21/38/38	0/3/3/3
2	AGS	C	902	3	-	3/21/38/38	0/3/3/3
2	AGS	D	902	3	-	3/21/38/38	0/3/3/3
2	AGS	B	902	3	-	3/21/38/38	0/3/3/3
2	AGS	E	902	3	-	3/21/38/38	0/3/3/3
2	AGS	D	901	3	-	7/21/38/38	0/3/3/3
2	AGS	E	901	3	-	7/21/38/38	0/3/3/3
2	AGS	A	902	3	-	3/21/38/38	0/3/3/3

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	901	AGS	PG-S1G	2.09	1.95	1.90
2	B	902	AGS	PG-S1G	2.09	1.95	1.90
2	A	902	AGS	PG-S1G	2.07	1.95	1.90
2	D	901	AGS	PG-S1G	2.07	1.95	1.90
2	A	901	AGS	PG-S1G	2.06	1.95	1.90

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	901	AGS	PB-O3B-PG	-3.82	119.17	133.17
2	C	901	AGS	PB-O3B-PG	-3.82	119.18	133.17
2	A	901	AGS	PB-O3B-PG	-3.82	119.19	133.17
2	E	901	AGS	PB-O3B-PG	-3.81	119.22	133.17
2	F	901	AGS	PB-O3B-PG	-3.81	119.22	133.17

There are no chirality outliers.

5 of 60 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	901	AGS	C5'-O5'-PA-O1A
2	A	901	AGS	C5'-O5'-PA-O2A

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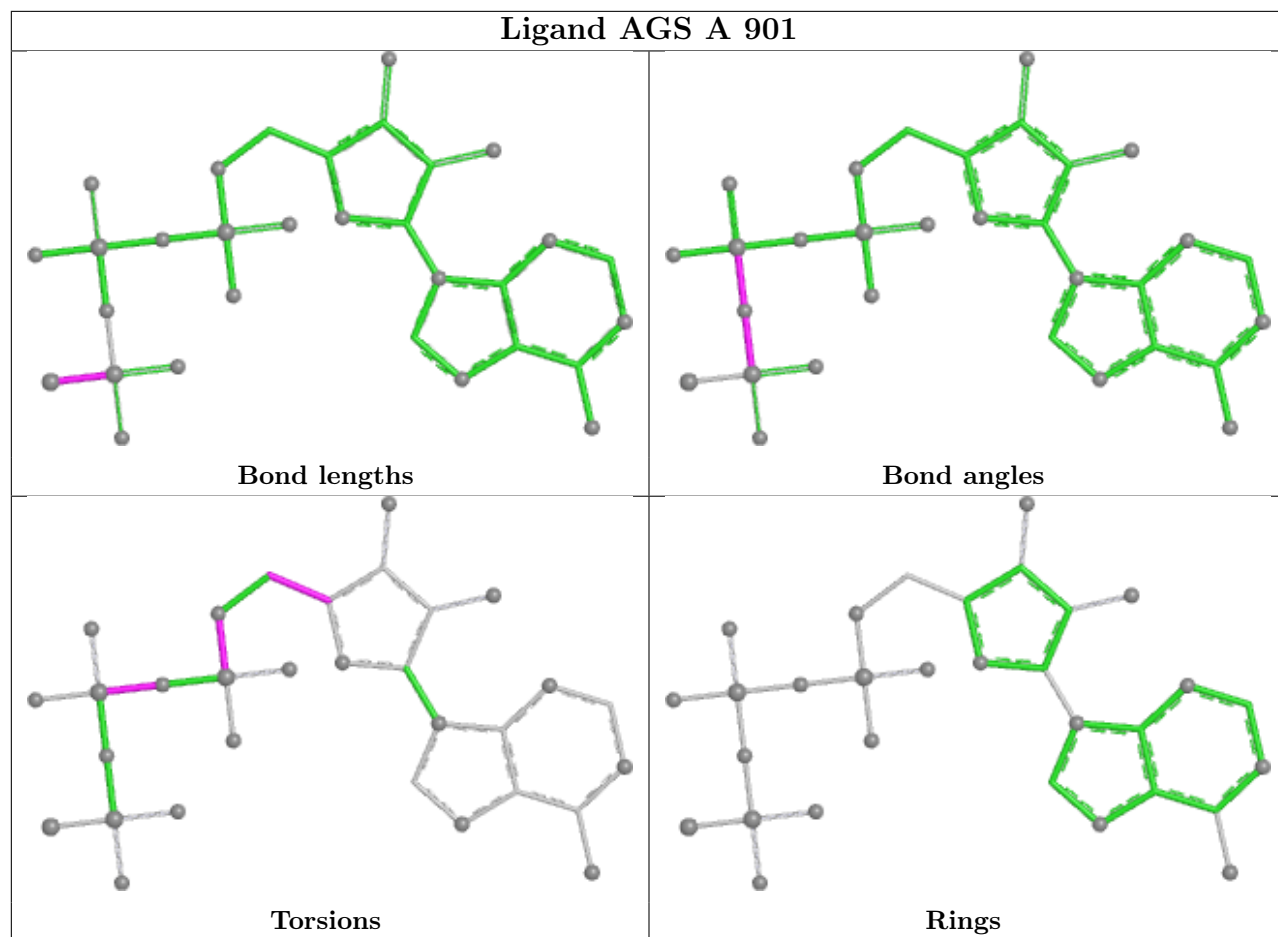
Mol	Chain	Res	Type	Atoms
2	A	901	AGS	C5'-O5'-PA-O3A
2	B	901	AGS	C5'-O5'-PA-O1A
2	B	901	AGS	C5'-O5'-PA-O2A

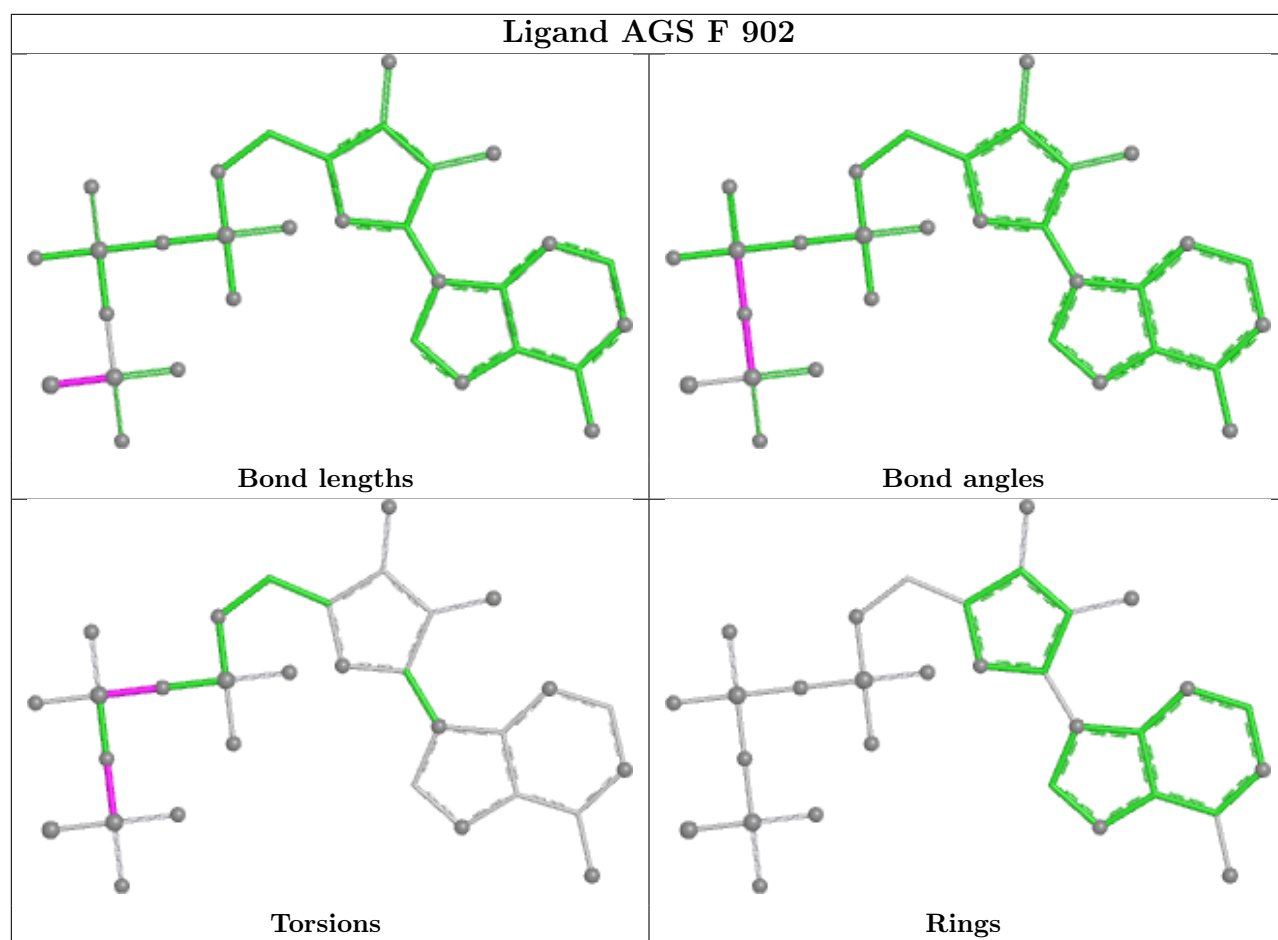
There are no ring outliers.

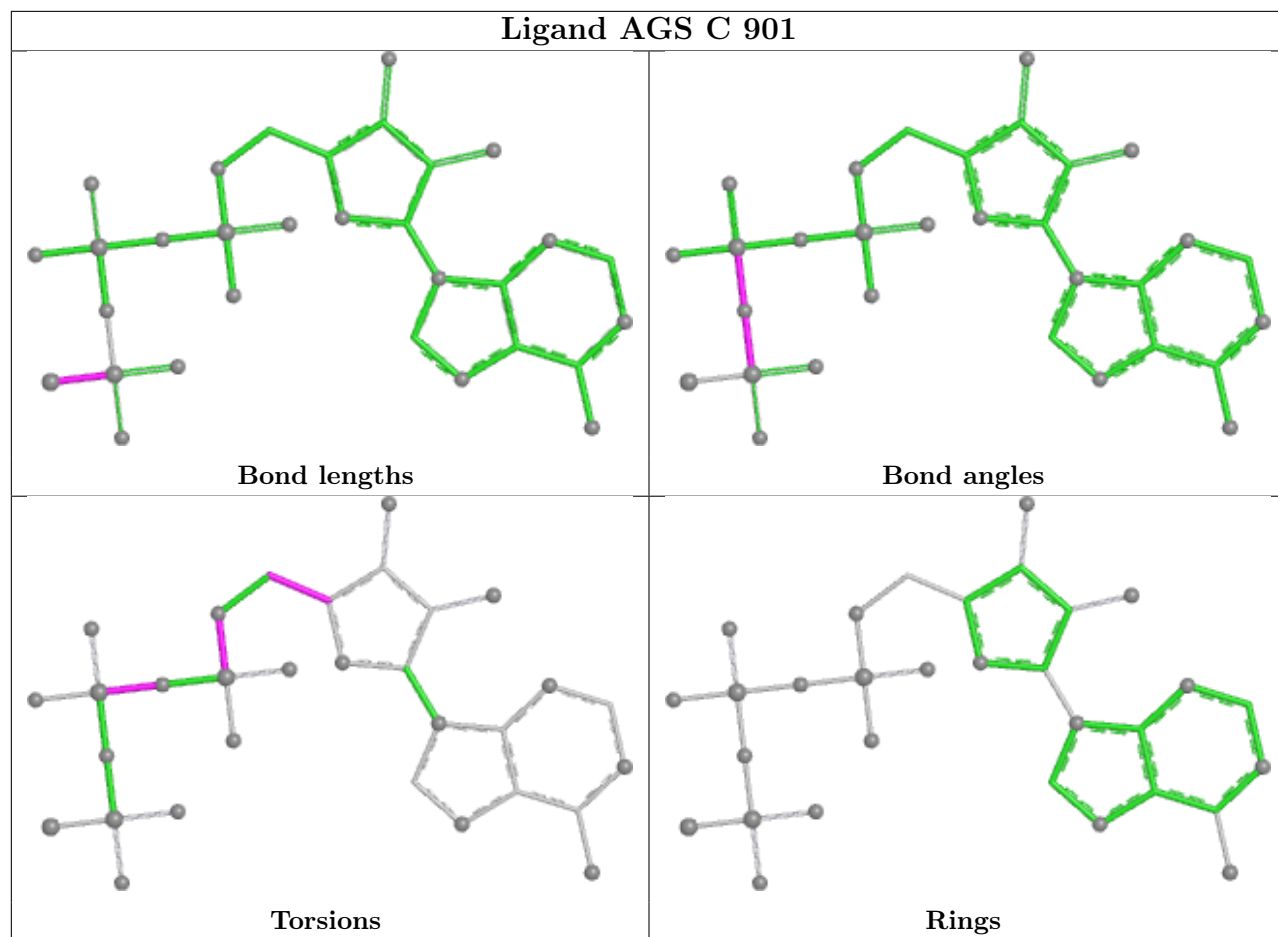
7 monomers are involved in 16 short contacts:

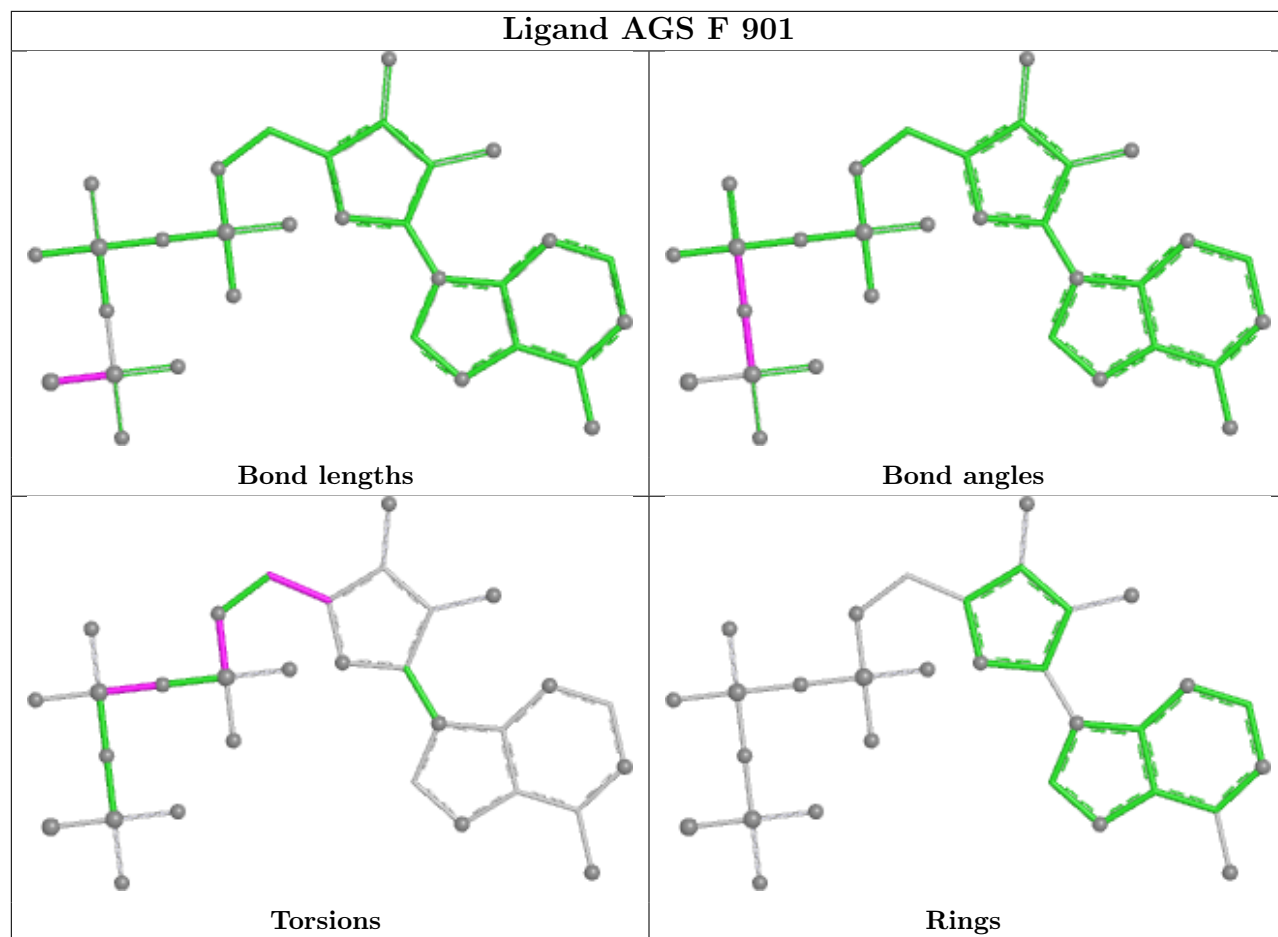
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	901	AGS	2	0
2	C	901	AGS	3	0
2	F	901	AGS	2	0
2	B	901	AGS	2	0
2	D	902	AGS	1	0
2	D	901	AGS	3	0
2	E	901	AGS	3	0

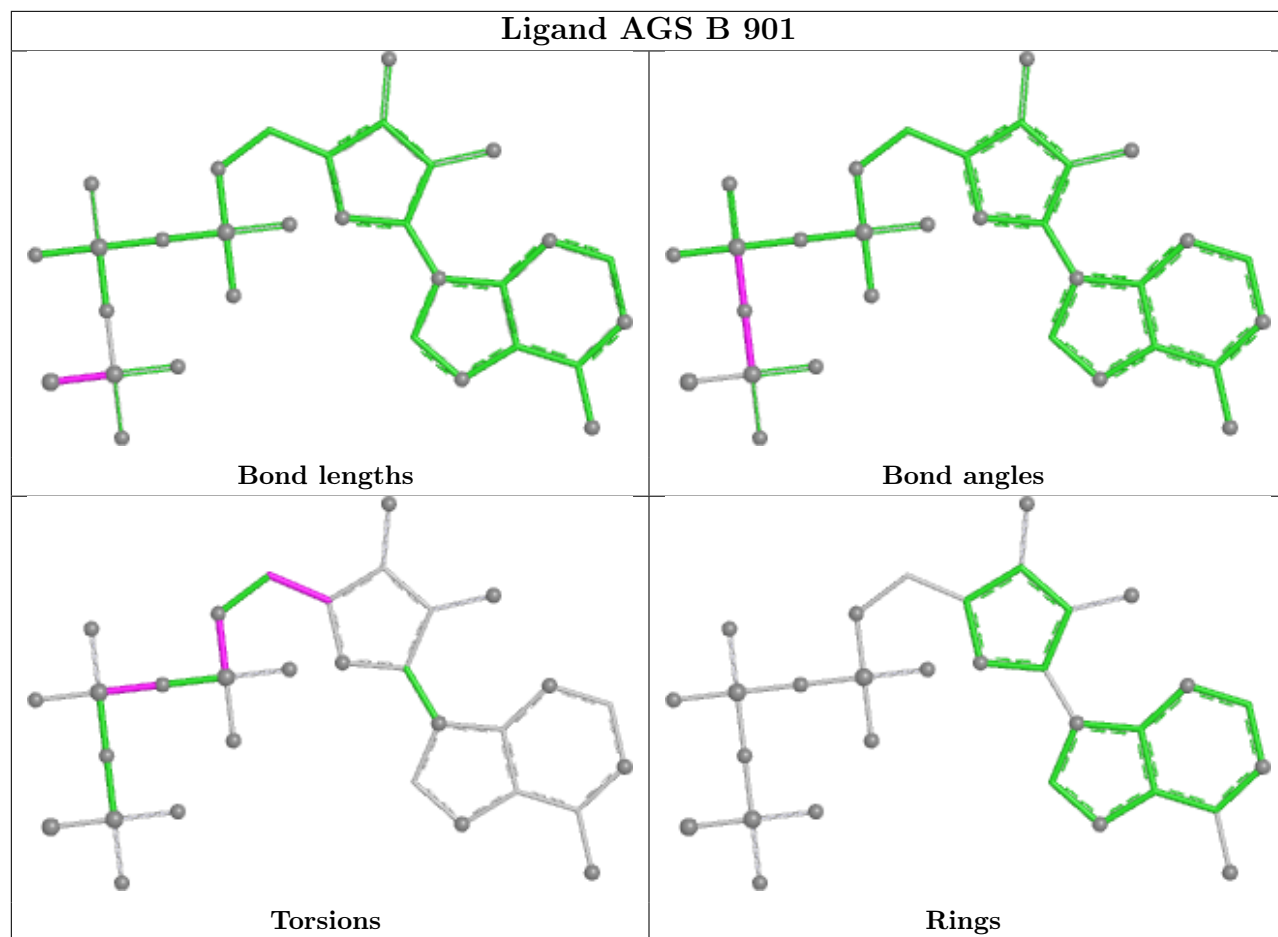
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.

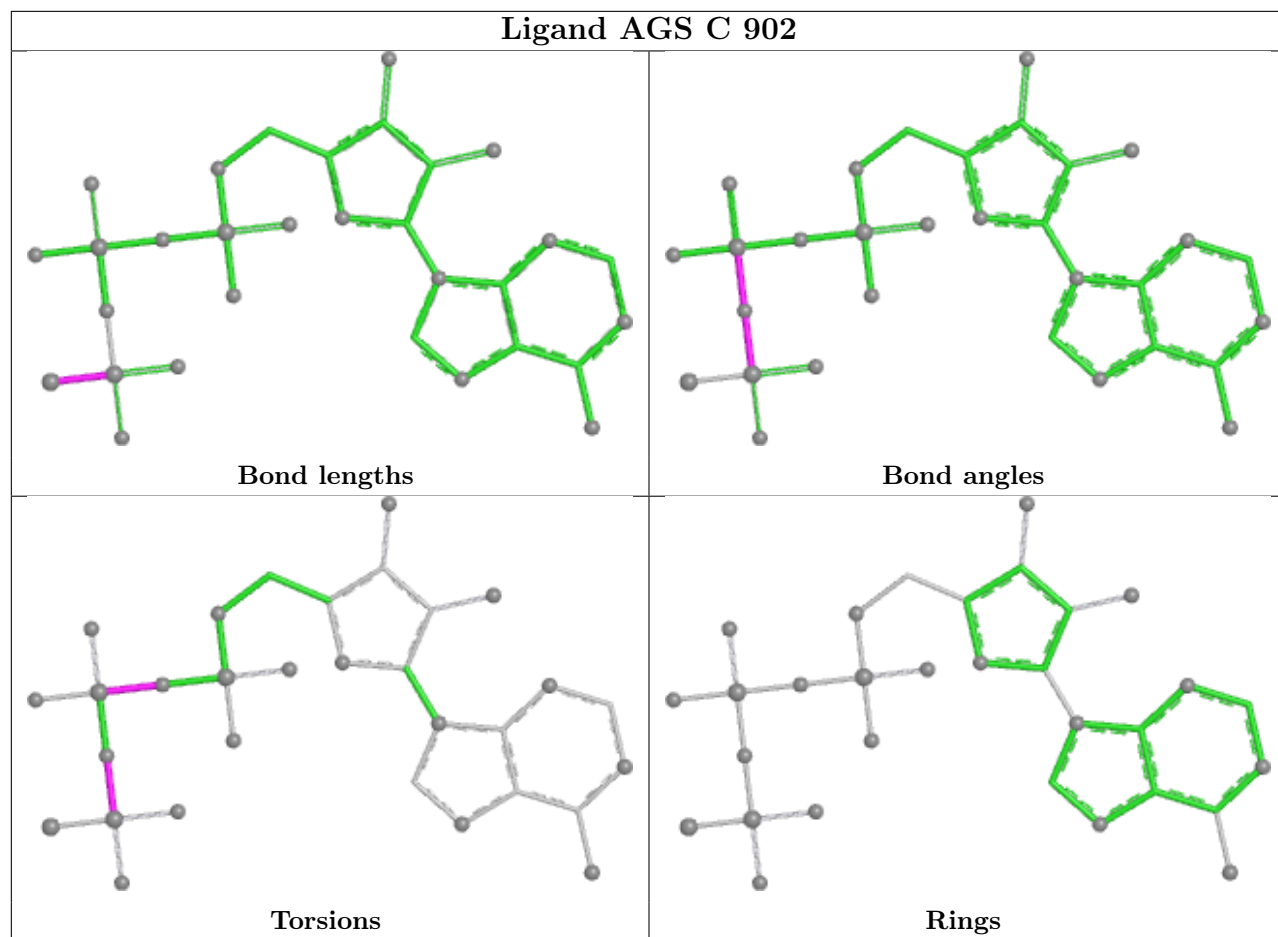


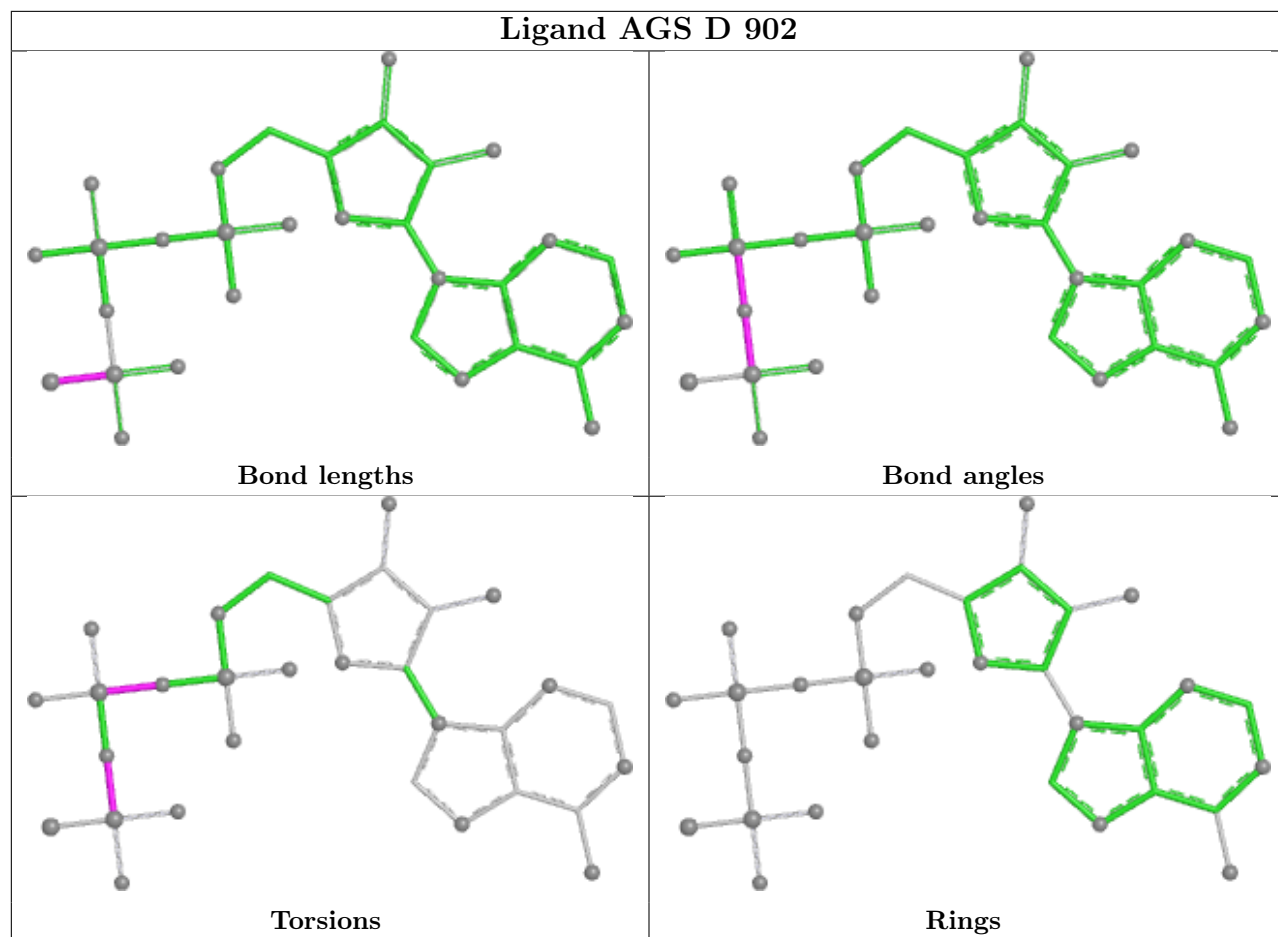


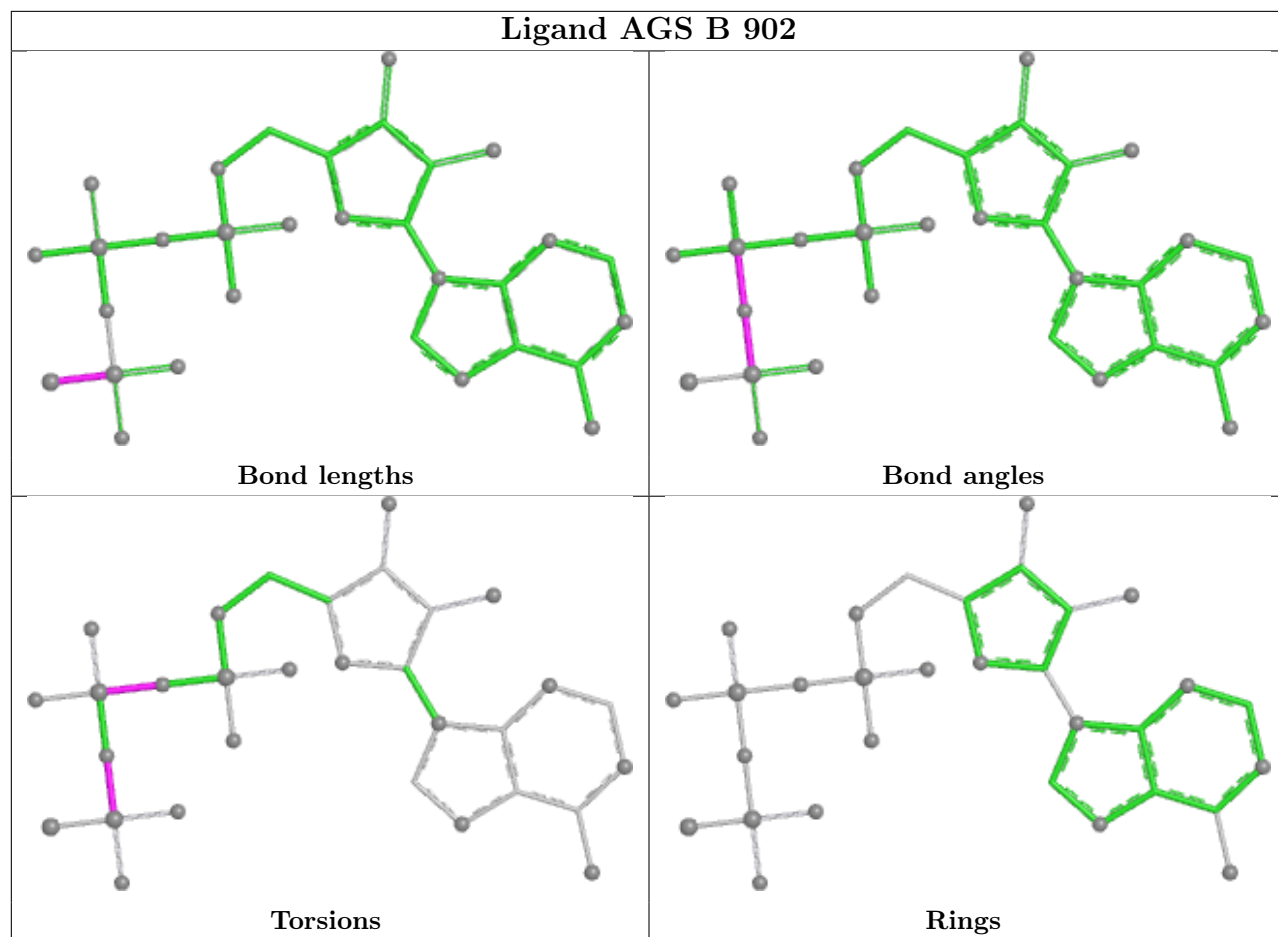


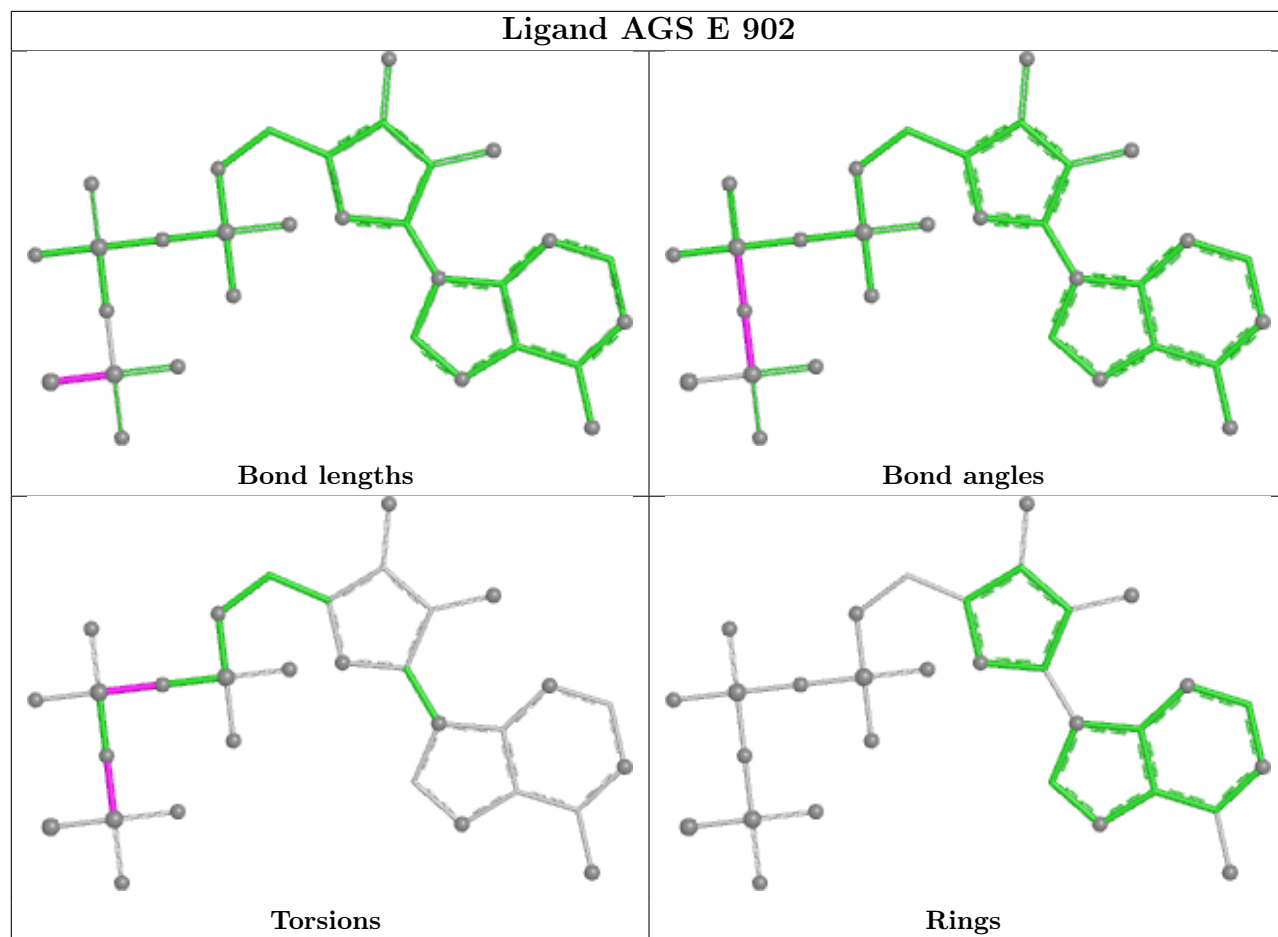


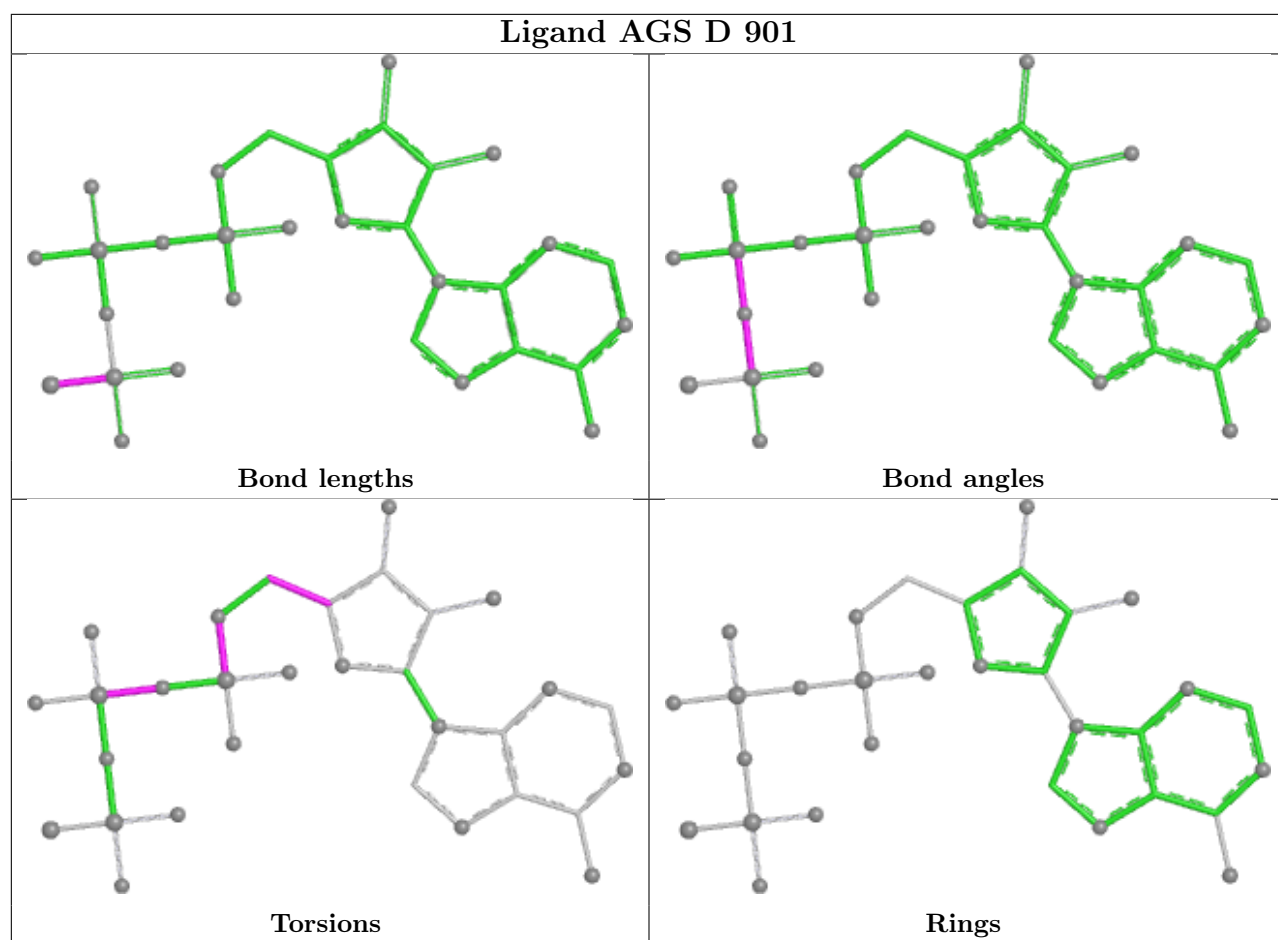


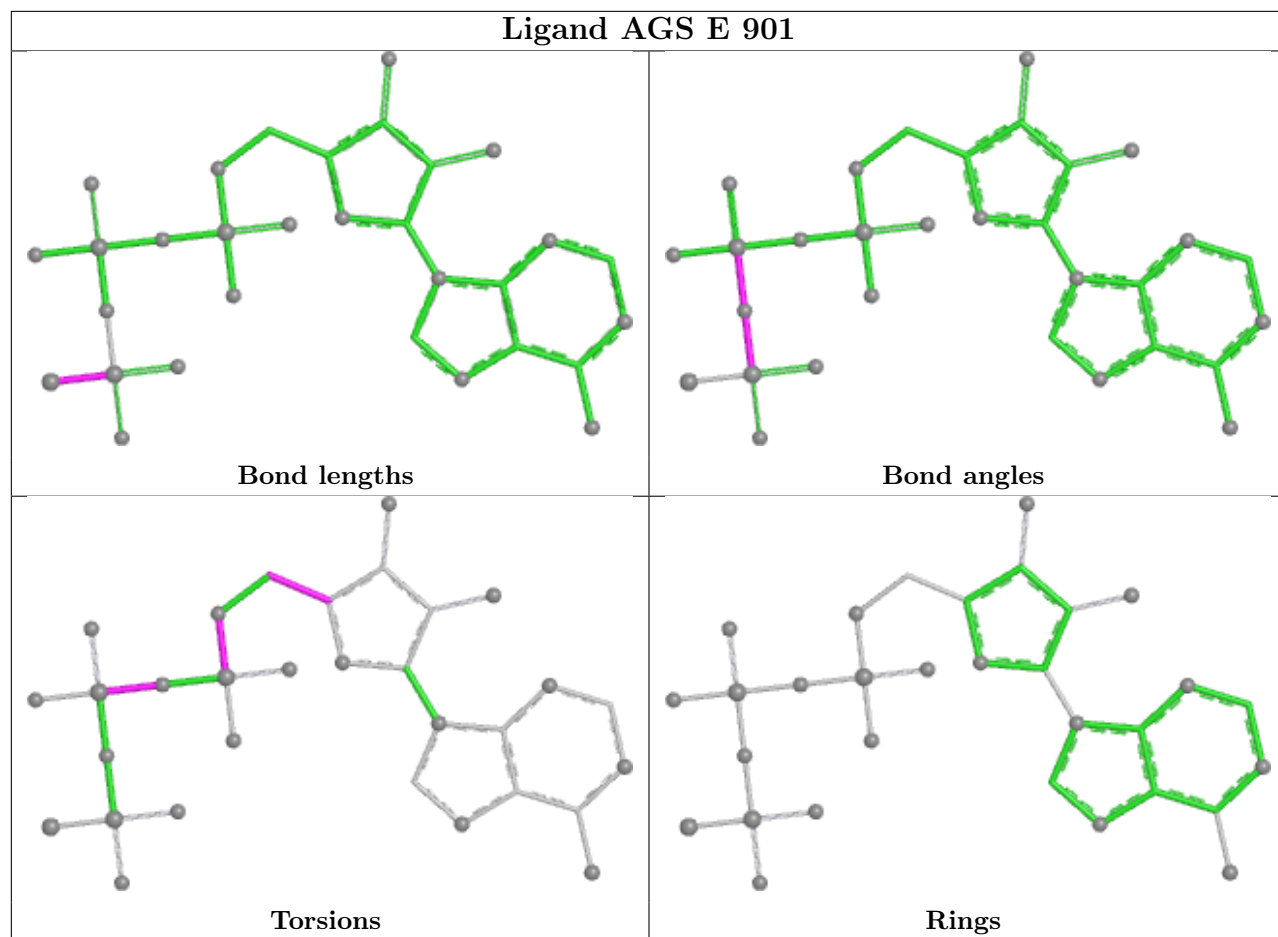


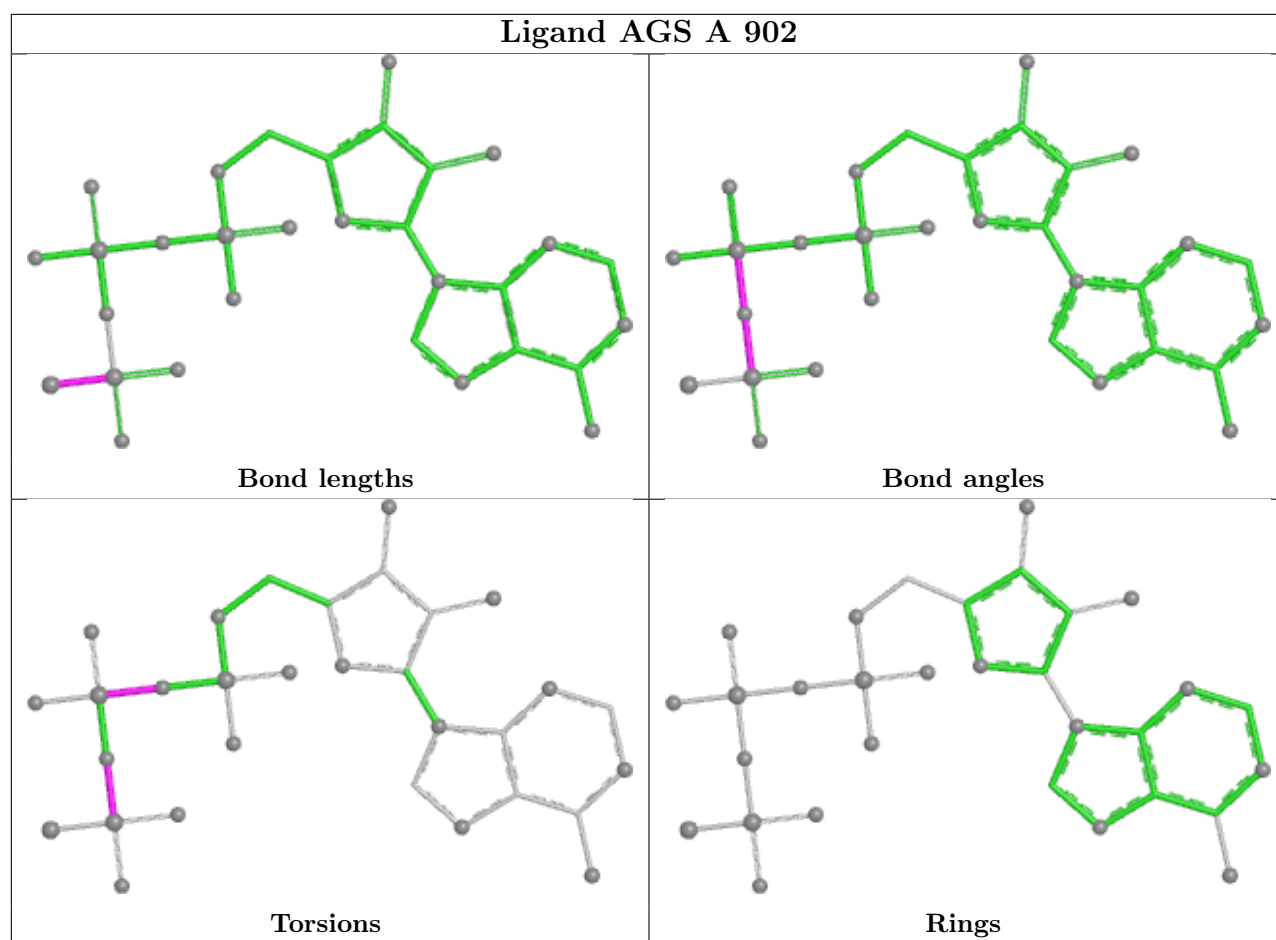












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Map visualisation

This section contains visualisations of the EMDB entry EMD-24519. These allow visual inspection of the internal detail of the map and identification of artifacts.

No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

This section was not generated.

6.2 Central slices

This section was not generated.

6.3 Largest variance slices

This section was not generated.

6.4 Orthogonal standard-deviation projections (False-color)

This section was not generated.

6.5 Orthogonal surface views

This section was not generated.

6.6 Mask visualisation

This section was not generated. No masks/segmentation were deposited.

7 Map analysis

This section contains the results of statistical analysis of the map.

7.1 Map-value distribution

This section was not generated.

7.2 Volume estimate versus contour level

This section was not generated.

7.3 Rotationally averaged power spectrum

This section was not generated. The rotationally averaged power spectrum had issues being displayed.

8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit

This section was not generated.