



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 3, 2024 – 10:05 pm GMT

PDB ID : 5C1B
Title : p97-delta709-728 in complex with a UFD1-SHP peptide
Authors : Haenzelmann, P.; Schindelin, H.
Deposited on : 2015-06-13
Resolution : 3.08 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 : 4.02b-467
Mogul : 1.8.4, CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.36
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36

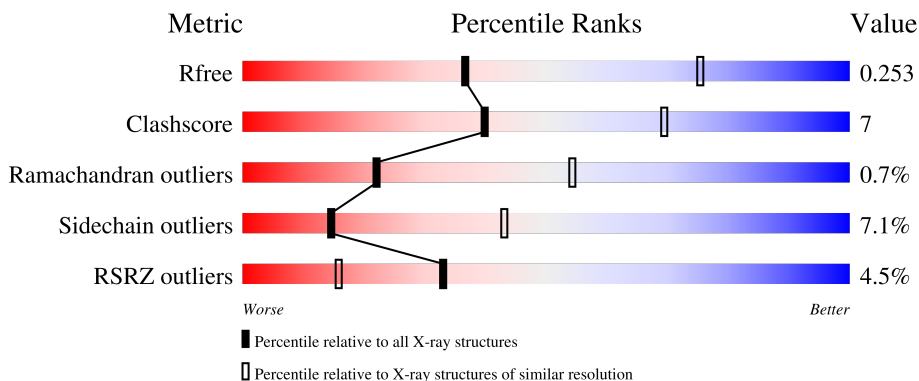
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.08 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.



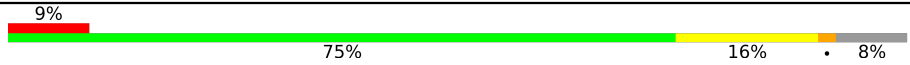


Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1447 (3.10-3.06)
Clashscore	141614	1546 (3.10-3.06)
Ramachandran outliers	138981	1487 (3.10-3.06)
Sidechain outliers	138945	1486 (3.10-3.06)
RSRZ outliers	127900	1416 (3.10-3.06)

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	785	 4% 70% 19% • 8%
1	B	785	 3% 74% 16% • 8%
1	C	785	 2% 75% 14% • 8%
1	D	785	 4% 74% 16% • 8%
1	E	785	 2% 74% 16% • 8%

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Mol	Chain	Length	Quality of chain
1	F	785	
2	U	21	
2	V	21	

2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 69385 atoms, of which 34726 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 Transitional endoplasmic reticulum ATPase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
1	A	724	11417	3572	5739	1003	1073	30	0	0	0
1	B	724	11426	3572	5748	1003	1073	30	0	0	0
1	C	724	11427	3572	5749	1003	1073	30	0	0	0
1	D	724	11427	3572	5749	1003	1073	30	0	0	0
1	E	724	11426	3572	5748	1003	1073	30	0	0	0
1	F	724	11427	3572	5749	1003	1073	30	0	0	0

There are 120 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	ARG	deletion	UNP P55072
A	?	-	GLU	deletion	UNP P55072
A	?	-	ARG	deletion	UNP P55072
A	?	-	GLU	deletion	UNP P55072
A	?	-	ARG	deletion	UNP P55072
A	?	-	GLN	deletion	UNP P55072
A	?	-	THR	deletion	UNP P55072
A	?	-	ASN	deletion	UNP P55072
A	?	-	PRO	deletion	UNP P55072
A	?	-	SER	deletion	UNP P55072
A	?	-	ALA	deletion	UNP P55072
A	?	-	MET	deletion	UNP P55072
A	?	-	GLU	deletion	UNP P55072
A	?	-	VAL	deletion	UNP P55072
A	?	-	GLU	deletion	UNP P55072
A	?	-	GLU	deletion	UNP P55072
A	?	-	ASP	deletion	UNP P55072

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Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	ASP	deletion	UNP P55072
A	?	-	PRO	deletion	UNP P55072
A	?	-	VAL	deletion	UNP P55072
B	?	-	ARG	deletion	UNP P55072
B	?	-	GLU	deletion	UNP P55072
B	?	-	ARG	deletion	UNP P55072
B	?	-	GLU	deletion	UNP P55072
B	?	-	ARG	deletion	UNP P55072
B	?	-	GLN	deletion	UNP P55072
B	?	-	THR	deletion	UNP P55072
B	?	-	ASN	deletion	UNP P55072
B	?	-	PRO	deletion	UNP P55072
B	?	-	SER	deletion	UNP P55072
B	?	-	ALA	deletion	UNP P55072
B	?	-	MET	deletion	UNP P55072
B	?	-	GLU	deletion	UNP P55072
B	?	-	VAL	deletion	UNP P55072
B	?	-	GLU	deletion	UNP P55072
B	?	-	GLU	deletion	UNP P55072
B	?	-	ASP	deletion	UNP P55072
B	?	-	ASP	deletion	UNP P55072
B	?	-	PRO	deletion	UNP P55072
B	?	-	VAL	deletion	UNP P55072
C	?	-	ARG	deletion	UNP P55072
C	?	-	GLU	deletion	UNP P55072
C	?	-	ARG	deletion	UNP P55072
C	?	-	GLU	deletion	UNP P55072
C	?	-	ARG	deletion	UNP P55072
C	?	-	GLN	deletion	UNP P55072
C	?	-	THR	deletion	UNP P55072
C	?	-	ASN	deletion	UNP P55072
C	?	-	PRO	deletion	UNP P55072
C	?	-	SER	deletion	UNP P55072
C	?	-	ALA	deletion	UNP P55072
C	?	-	MET	deletion	UNP P55072
C	?	-	GLU	deletion	UNP P55072
C	?	-	VAL	deletion	UNP P55072
C	?	-	GLU	deletion	UNP P55072
C	?	-	GLU	deletion	UNP P55072
C	?	-	ASP	deletion	UNP P55072
C	?	-	ASP	deletion	UNP P55072
C	?	-	PRO	deletion	UNP P55072

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Chain	Residue	Modelled	Actual	Comment	Reference
C	?	-	VAL	deletion	UNP P55072
D	?	-	ARG	deletion	UNP P55072
D	?	-	GLU	deletion	UNP P55072
D	?	-	ARG	deletion	UNP P55072
D	?	-	GLU	deletion	UNP P55072
D	?	-	ARG	deletion	UNP P55072
D	?	-	GLN	deletion	UNP P55072
D	?	-	THR	deletion	UNP P55072
D	?	-	ASN	deletion	UNP P55072
D	?	-	PRO	deletion	UNP P55072
D	?	-	SER	deletion	UNP P55072
D	?	-	ALA	deletion	UNP P55072
D	?	-	MET	deletion	UNP P55072
D	?	-	GLU	deletion	UNP P55072
D	?	-	VAL	deletion	UNP P55072
D	?	-	GLU	deletion	UNP P55072
D	?	-	GLU	deletion	UNP P55072
D	?	-	ASP	deletion	UNP P55072
D	?	-	ASP	deletion	UNP P55072
D	?	-	PRO	deletion	UNP P55072
D	?	-	VAL	deletion	UNP P55072
E	?	-	ARG	deletion	UNP P55072
E	?	-	GLU	deletion	UNP P55072
E	?	-	ARG	deletion	UNP P55072
E	?	-	GLU	deletion	UNP P55072
E	?	-	ARG	deletion	UNP P55072
E	?	-	GLN	deletion	UNP P55072
E	?	-	THR	deletion	UNP P55072
E	?	-	ASN	deletion	UNP P55072
E	?	-	PRO	deletion	UNP P55072
E	?	-	SER	deletion	UNP P55072
E	?	-	ALA	deletion	UNP P55072
E	?	-	MET	deletion	UNP P55072
E	?	-	GLU	deletion	UNP P55072
E	?	-	VAL	deletion	UNP P55072
E	?	-	GLU	deletion	UNP P55072
E	?	-	GLU	deletion	UNP P55072
E	?	-	ASP	deletion	UNP P55072
E	?	-	ASP	deletion	UNP P55072
E	?	-	PRO	deletion	UNP P55072
E	?	-	VAL	deletion	UNP P55072
F	?	-	ARG	deletion	UNP P55072

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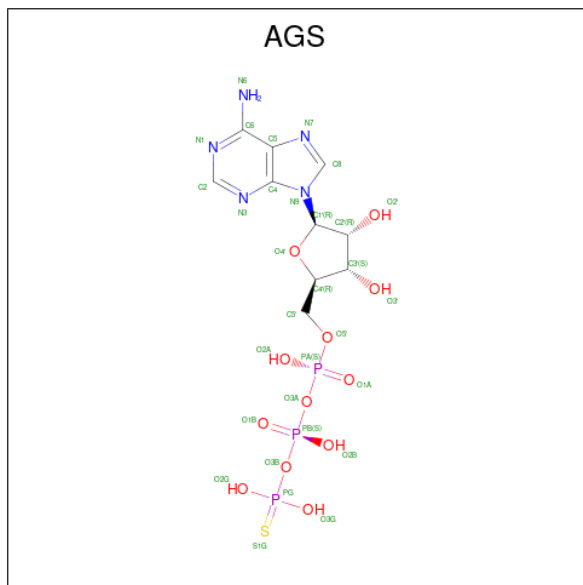
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Chain	Residue	Modelled	Actual	Comment	Reference
F	?	-	GLU	deletion	UNP P55072
F	?	-	ARG	deletion	UNP P55072
F	?	-	GLU	deletion	UNP P55072
F	?	-	ARG	deletion	UNP P55072
F	?	-	GLN	deletion	UNP P55072
F	?	-	THR	deletion	UNP P55072
F	?	-	ASN	deletion	UNP P55072
F	?	-	PRO	deletion	UNP P55072
F	?	-	SER	deletion	UNP P55072
F	?	-	ALA	deletion	UNP P55072
F	?	-	MET	deletion	UNP P55072
F	?	-	GLU	deletion	UNP P55072
F	?	-	VAL	deletion	UNP P55072
F	?	-	GLU	deletion	UNP P55072
F	?	-	GLU	deletion	UNP P55072
F	?	-	ASP	deletion	UNP P55072
F	?	-	ASP	deletion	UNP P55072
F	?	-	PRO	deletion	UNP P55072
F	?	-	VAL	deletion	UNP P55072

- Molecule 2 is a protein called Ubiquitin fusion degradation protein 1 homolog.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	V	11	Total	C	H	N	O	0	0	0
			125	53	40	18	14			
2	U	10	Total	C	H	N	O	0	0	0
			106	44	32	17	13			

- Molecule 3 is PHOSPHOTHIOPHOSPHORIC ACID-ADENYLATE ESTER (three-letter code: AGS) (formula: C₁₀H₁₆N₅O₁₂P₃S).



Mol	Chain	Residues	Atoms							ZeroOcc	AltConf
			Total	C	H	N	O	P	S		
3	A	1	Total	C	H	N	O	P	S	0	0
			44	10	13	5	12	3	1		
3	A	1	Total	C	H	N	O	P	S	0	0
			44	10	13	5	12	3	1		
3	B	1	Total	C	H	N	O	P	S	0	0
			44	10	13	5	12	3	1		
3	B	1	Total	C	H	N	O	P	S	0	0
			44	10	13	5	12	3	1		
3	C	1	Total	C	H	N	O	P	S	0	0
			44	10	13	5	12	3	1		
3	C	1	Total	C	H	N	O	P	S	0	0
			44	10	13	5	12	3	1		
3	D	1	Total	C	H	N	O	P	S	0	0
			44	10	13	5	12	3	1		
3	D	1	Total	C	H	N	O	P	S	0	0
			44	10	13	5	12	3	1		
3	E	1	Total	C	H	N	O	P	S	0	0
			44	10	13	5	12	3	1		
3	E	1	Total	C	H	N	O	P	S	0	0
			44	10	13	5	12	3	1		
3	F	1	Total	C	H	N	O	P	S	0	0
			44	10	13	5	12	3	1		
3	F	1	Total	C	H	N	O	P	S	0	0
			44	10	13	5	12	3	1		

- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

- Molecule 5 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total Cl 1 1	0	0
5	B	1	Total Cl 1 1	0	0
5	C	1	Total Cl 1 1	0	0
5	D	1	Total Cl 1 1	0	0
5	E	1	Total Cl 1 1	0	0
5	F	1	Total Cl 1 1	0	0

- Molecule 6 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	
6	F	1	Total	C	H	O	0	0
			14	3	8	3		
6	F	1	Total	C	H	O	0	0
			14	3	8	3		

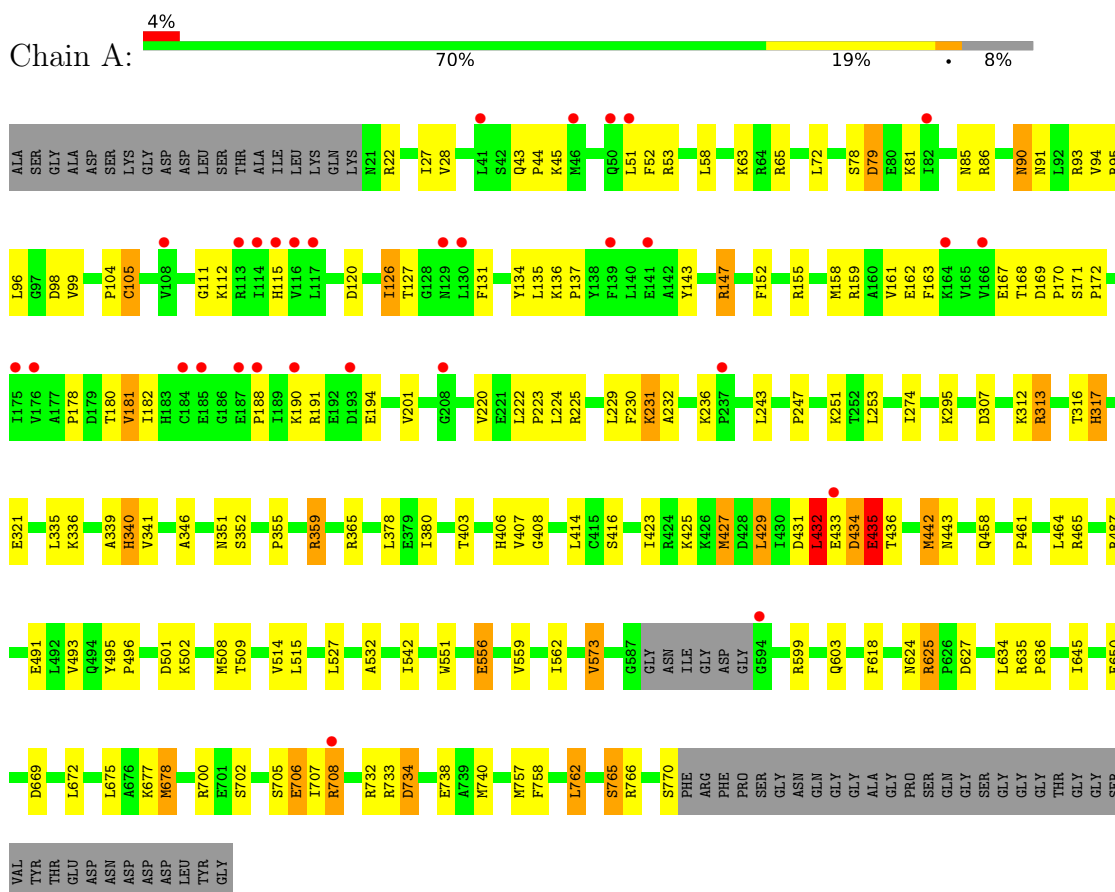
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	5	Total	O	0	0
			5	5		
7	B	5	Total	O	0	0
			5	5		
7	C	5	Total	O	0	0
			5	5		
7	D	5	Total	O	0	0
			5	5		
7	E	5	Total	O	0	0
			5	5		
7	F	5	Total	O	0	0
			5	5		

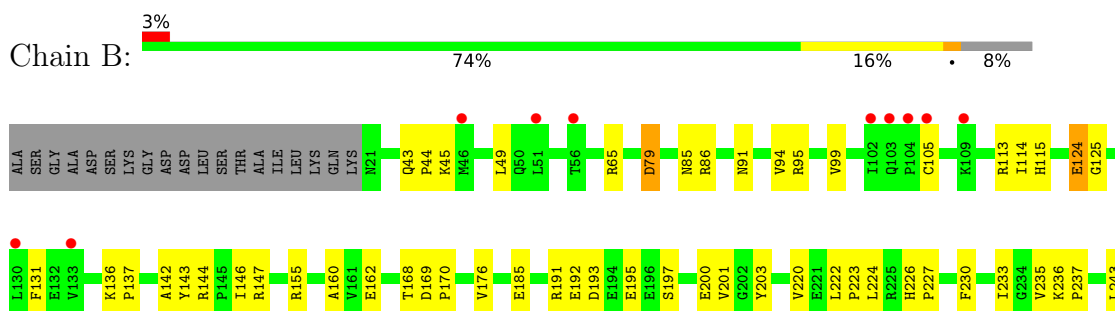
3 Residue-property plots

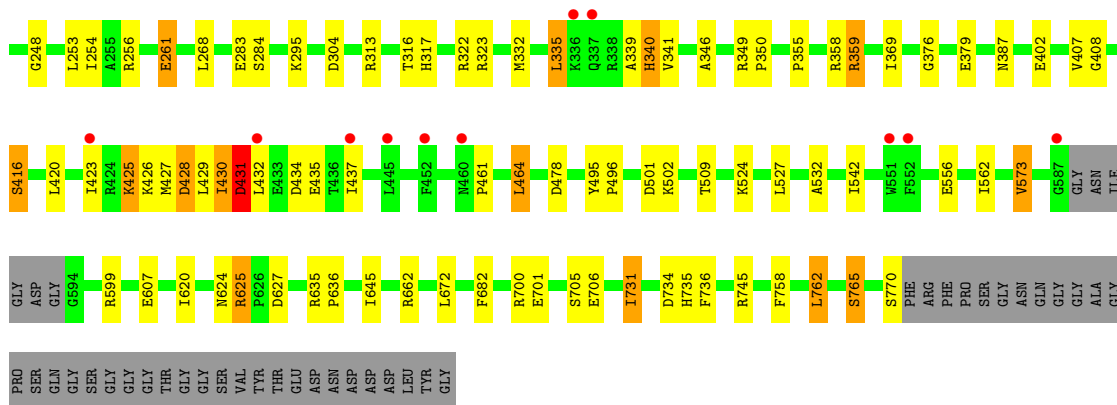
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density.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

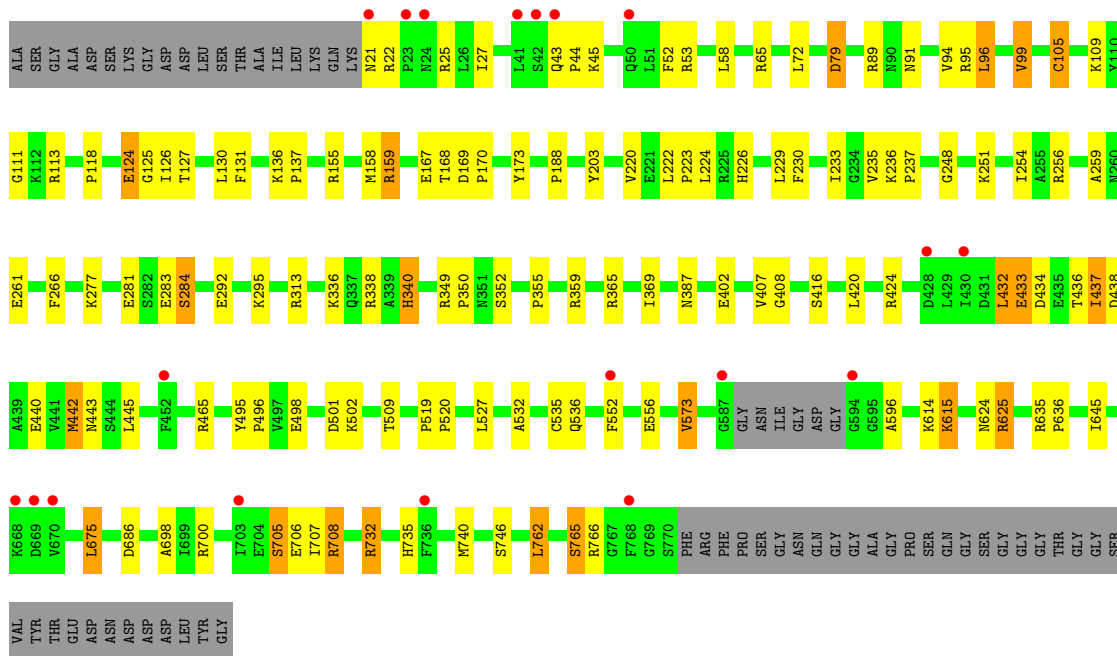
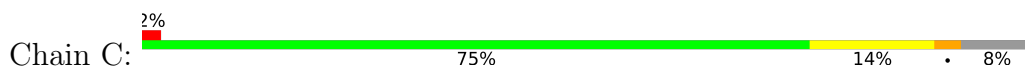


• Molecule 1: Transitional endoplasmic reticulum ATPase

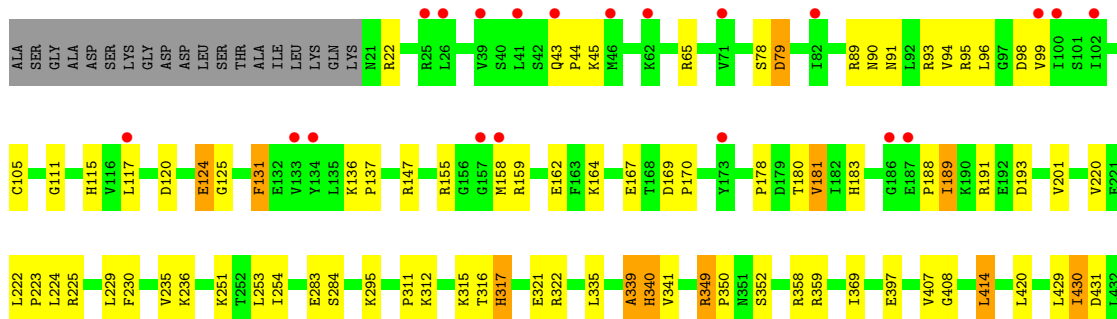
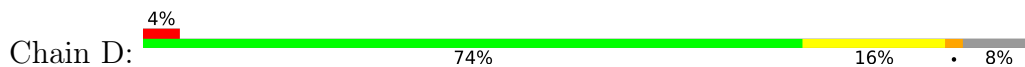


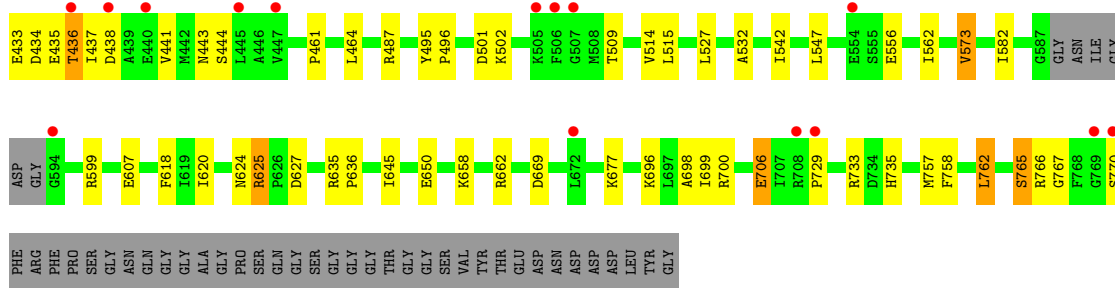


• Molecule 1: Transitional endoplasmic reticulum ATPase

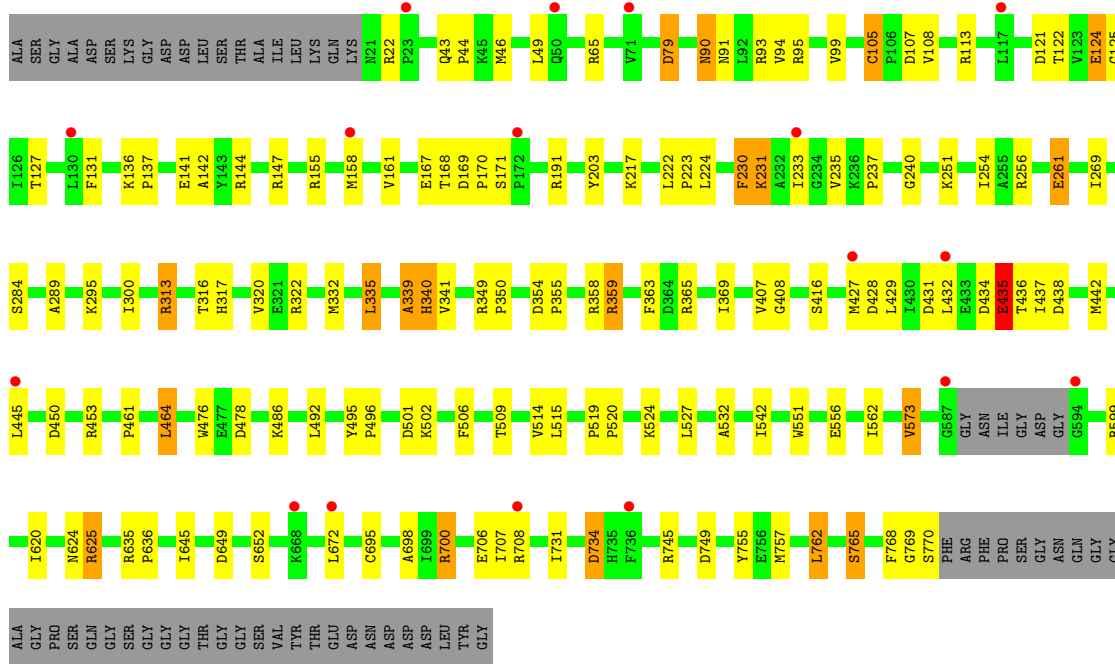
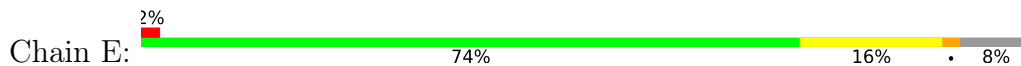


• Molecule 1: Transitional endoplasmic reticulum ATPase

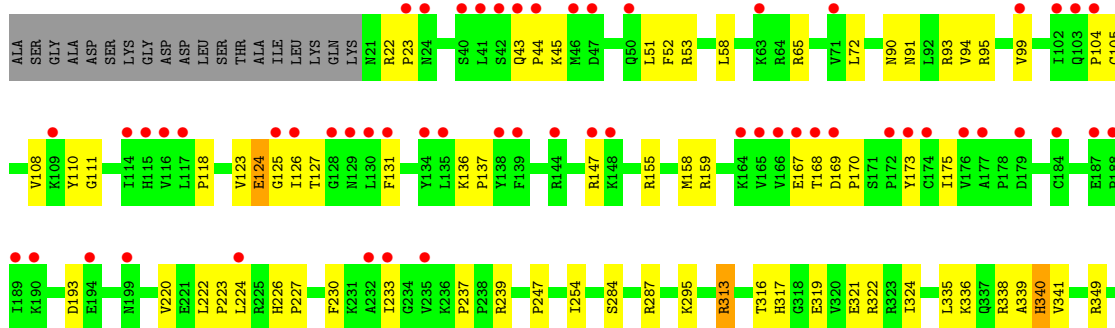
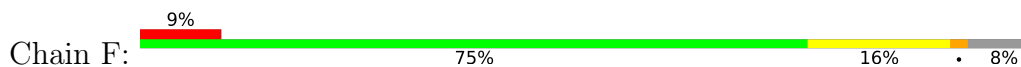


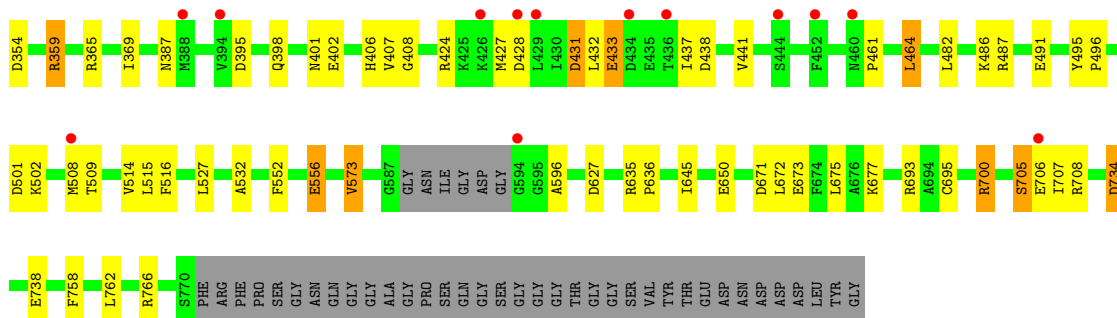


• Molecule 1: Transitional endoplasmic reticulum ATPase

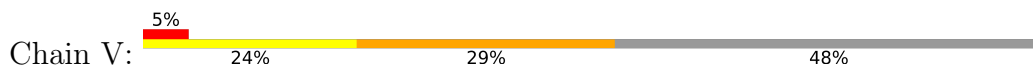


• Molecule 1: Transitional endoplasmic reticulum ATPase

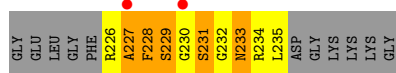
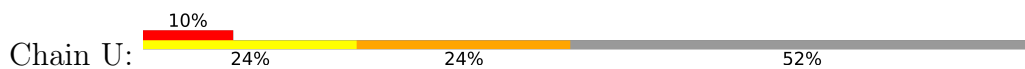




● Molecule 2: Ubiquitin fusion degradation protein 1 homolog



● Molecule 2: Ubiquitin fusion degradation protein 1 homolog



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	140.72Å 180.66Å 254.96Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.14 – 3.08 49.14 – 3.08	Depositor EDS
% Data completeness (in resolution range)	100.0 (49.14-3.08) 100.0 (49.14-3.08)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.76 (at 3.07Å)	Xtrriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.198 , 0.240 0.210 , 0.253	Depositor DCC
R_{free} test set	6055 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	108.5	Xtrriage
Anisotropy	0.333	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 85.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	69385	wwPDB-VP
Average B, all atoms (Å ²)	145.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.35% 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: AGS, GOL, CL, 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	0.22	0/5771	0.44	0/7791
1	B	0.22	0/5771	0.43	0/7791
1	C	0.22	0/5771	0.44	0/7791
1	D	0.23	0/5771	0.44	0/7791
1	E	0.22	0/5771	0.42	0/7791
1	F	0.22	0/5771	0.44	0/7791
2	U	0.25	0/74	0.51	0/96
2	V	0.26	0/86	0.56	0/112
All	All	0.22	0/34786	0.44	0/46954

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	5678	5739	5749	107	1
1	B	5678	5748	5749	84	0
1	C	5678	5749	5749	74	1
1	D	5678	5749	5749	88	1
1	E	5678	5748	5749	90	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	F	5678	5749	5749	74	1
2	U	74	32	72	17	0
2	V	85	40	81	22	0
3	A	62	26	24	4	0
3	B	62	26	24	1	0
3	C	62	26	24	3	0
3	D	62	26	24	1	0
3	E	62	26	24	4	0
3	F	62	26	24	4	0
4	A	2	0	0	0	0
4	B	2	0	0	0	0
4	C	2	0	0	0	0
4	D	2	0	0	0	0
4	E	2	0	0	0	0
4	F	2	0	0	0	0
5	A	1	0	0	0	0
5	B	1	0	0	0	0
5	C	1	0	0	0	0
5	D	1	0	0	0	0
5	E	1	0	0	0	0
5	F	1	0	0	0	0
6	F	12	16	16	0	0
7	A	5	0	0	1	0
7	B	5	0	0	2	0
7	C	5	0	0	1	0
7	D	5	0	0	0	0
7	E	5	0	0	1	0
7	F	5	0	0	1	0
All	All	34659	34726	34807	510	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 7.

All (510) 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:162:GLU:OE1	1:A:191:ARG:NH2	1.83	1.10
2:V:227:ALA:HB1	2:V:228:PHE:CD1	2.02	0.94
1:D:162:GLU:OE1	1:D:191:ARG:NH2	2.04	0.91
1:B:429:LEU:O	1:B:431:ASP:N	2.04	0.90
1:D:181:VAL:HA	2:V:233:ASN:HB3	1.55	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:U:227:ALA:HB1	2:U:228:PHE:CD1	2.08	0.87
1:E:339:ALA:O	1:E:341:VAL:N	2.10	0.84
1:A:321:GLU:OE2	1:B:322:ARG:NH2	2.10	0.83
1:A:766:ARG:NH1	3:F:902:AGS:S1G	2.52	0.82
1:D:65:ARG:NH1	1:D:91:ASN:O	2.12	0.81
1:A:181:VAL:HA	2:U:233:ASN:HB3	1.60	0.81
3:F:901:AGS:O1A	7:F:1001:HOH:O	1.98	0.80
1:B:304:ASP:OD2	7:B:1001:HOH:O	1.99	0.79
1:C:65:ARG:NH1	1:C:91:ASN:O	2.15	0.79
3:A:901:AGS:O3G	7:A:1001:HOH:O	2.00	0.79
1:D:339:ALA:O	1:D:341:VAL:N	2.15	0.79
1:E:65:ARG:NH1	1:E:91:ASN:O	2.16	0.79
1:C:251:LYS:NZ	3:C:902:AGS:O1B	2.18	0.77
1:A:434:ASP:OD2	1:B:226:HIS:ND1	2.19	0.76
1:A:339:ALA:O	1:A:341:VAL:N	2.22	0.73
1:D:251:LYS:NZ	3:D:902:AGS:O1B	2.22	0.73
1:B:304:ASP:OD1	7:B:1002:HOH:O	2.06	0.72
1:E:434:ASP:O	1:E:435:GLU:HG2	1.88	0.72
1:A:178:PRO:HA	2:U:235:LEU:HD13	1.71	0.72
1:E:124:GLU:OE1	1:E:125:GLY:N	2.23	0.72
3:E:901:AGS:O1A	7:E:1001:HOH:O	2.08	0.71
1:A:79:ASP:OD1	1:A:79:ASP:N	2.24	0.71
1:D:79:ASP:N	1:D:79:ASP:OD1	2.24	0.70
1:D:321:GLU:OE2	1:E:322:ARG:NH2	2.24	0.70
1:B:65:ARG:NH1	1:B:91:ASN:O	2.25	0.69
1:D:650:GLU:OE1	1:D:677:LYS:HG3	1.93	0.69
2:U:232:GLY:O	2:U:234:ARG:N	2.24	0.69
2:V:233:ASN:OD1	2:V:234:ARG:N	2.25	0.68
1:E:79:ASP:OD1	1:E:79:ASP:N	2.27	0.68
1:E:434:ASP:O	1:E:435:GLU:CG	2.42	0.67
1:C:79:ASP:OD1	1:C:79:ASP:N	2.27	0.67
2:V:232:GLY:O	2:V:234:ARG:N	2.26	0.67
1:D:178:PRO:HA	2:V:235:LEU:HD13	1.77	0.66
1:F:65:ARG:NH1	1:F:91:ASN:O	2.29	0.66
1:A:65:ARG:NH1	1:A:91:ASN:O	2.28	0.66
2:U:233:ASN:OD1	2:U:234:ARG:N	2.27	0.66
1:E:700:ARG:NH1	1:F:491:GLU:OE2	2.29	0.65
1:F:734:ASP:OD1	1:F:734:ASP:N	2.28	0.65
1:D:131:PHE:CE2	2:V:234:ARG:NH1	2.65	0.65
1:F:339:ALA:O	1:F:341:VAL:N	2.30	0.65
2:V:227:ALA:HB1	2:V:228:PHE:CE1	2.31	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:432:LEU:HD11	1:F:226:HIS:CG	2.32	0.64
1:A:339:ALA:O	1:A:341:VAL:HG23	1.97	0.64
2:V:228:PHE:O	2:V:229:SER:HB3	1.98	0.64
1:C:113:ARG:NH1	1:C:169:ASP:OD1	2.31	0.63
1:A:115:HIS:NE2	2:U:227:ALA:O	2.32	0.62
1:E:158:MET:HE1	1:E:445:LEU:HD13	1.81	0.62
2:U:228:PHE:O	2:U:229:SER:HB3	1.99	0.62
1:A:251:LYS:NZ	3:A:901:AGS:O1B	2.33	0.61
2:V:226:ARG:HG3	2:V:227:ALA:N	2.15	0.61
1:A:158:MET:CE	1:B:235:VAL:HG21	2.30	0.61
1:E:339:ALA:O	1:E:341:VAL:HG23	2.00	0.61
1:E:434:ASP:OD2	1:E:437:ILE:HD13	2.00	0.61
1:D:222:LEU:HB2	1:D:223:PRO:HD3	1.83	0.60
1:E:169:ASP:HB3	1:E:170:PRO:HD3	1.82	0.60
1:E:43:GLN:N	1:E:44:PRO:HD2	2.16	0.60
1:B:43:GLN:N	1:B:44:PRO:HD2	2.16	0.59
1:F:43:GLN:N	1:F:44:PRO:HD2	2.17	0.59
2:V:228:PHE:O	2:V:229:SER:CB	2.50	0.59
1:A:169:ASP:HB3	1:A:170:PRO:HD3	1.85	0.59
1:A:231:LYS:HD3	1:A:232:ALA:N	2.16	0.59
1:D:339:ALA:O	1:D:341:VAL:HG23	2.02	0.59
1:C:43:GLN:N	1:C:44:PRO:HD2	2.17	0.59
1:E:90:ASN:O	1:E:93:ARG:NH1	2.35	0.59
1:A:222:LEU:HB2	1:A:223:PRO:HD3	1.84	0.58
1:B:142:ALA:HB1	1:B:144:ARG:HG3	1.84	0.58
1:C:169:ASP:HB3	1:C:170:PRO:HD3	1.86	0.58
2:U:228:PHE:O	2:U:229:SER:CB	2.52	0.58
1:B:162:GLU:OE1	1:B:191:ARG:NH2	2.36	0.58
1:A:247:PRO:HB3	3:A:901:AGS:S1G	2.44	0.57
1:B:79:ASP:N	1:B:79:ASP:OD1	2.37	0.57
1:D:43:GLN:N	1:D:44:PRO:HD2	2.20	0.57
1:A:43:GLN:N	1:A:44:PRO:HD2	2.19	0.57
1:B:350:PRO:O	1:B:358:ARG:NH2	2.38	0.57
1:B:461:PRO:HG2	1:B:464:LEU:HD21	1.87	0.57
1:F:169:ASP:HB3	1:F:170:PRO:HD3	1.87	0.57
1:B:427:MET:O	1:B:428:ASP:C	2.43	0.57
1:A:96:LEU:O	1:A:225:ARG:NH2	2.38	0.57
1:C:338:ARG:CG	1:C:338:ARG:O	2.52	0.57
1:B:339:ALA:O	1:B:341:VAL:N	2.35	0.56
1:D:169:ASP:HB3	1:D:170:PRO:HD3	1.87	0.56
1:B:169:ASP:HB3	1:B:170:PRO:HD3	1.86	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:220:VAL:CG1	1:C:224:LEU:HD12	2.35	0.56
1:B:230:PHE:HA	1:B:233:ILE:HG22	1.88	0.56
1:A:678:MET:HA	1:A:678:MET:CE	2.36	0.56
2:U:227:ALA:HB1	2:U:228:PHE:CE1	2.39	0.56
1:D:90:ASN:O	1:D:93:ARG:NH1	2.38	0.56
1:B:115:HIS:NE2	1:B:185:GLU:OE2	2.38	0.56
3:B:902:AGS:S1G	1:C:766:ARG:NH1	2.79	0.55
1:D:433:GLU:HG2	1:D:438:ASP:OD2	2.06	0.55
1:A:115:HIS:CD2	2:U:227:ALA:O	2.60	0.55
1:E:695:CYS:SG	1:F:508:MET:SD	3.04	0.55
2:U:226:ARG:HG3	2:U:227:ALA:N	2.22	0.55
1:F:127:THR:HG22	1:F:437:ILE:HB	1.89	0.54
1:F:247:PRO:HB3	3:F:901:AGS:S1G	2.47	0.54
1:B:635:ARG:NH1	1:B:636:PRO:O	2.39	0.54
1:F:707:ILE:HG22	1:F:708:ARG:N	2.22	0.54
1:D:434:ASP:O	1:D:435:GLU:C	2.46	0.54
1:E:203:TYR:CE2	1:E:261:GLU:HG2	2.43	0.54
1:E:542:ILE:HD13	1:E:562:ILE:HD13	1.90	0.54
3:E:902:AGS:S1G	1:F:766:ARG:NH1	2.81	0.54
1:C:420:LEU:CD1	1:D:235:VAL:HG11	2.38	0.54
2:U:230:GLY:O	2:U:231:SER:HB3	2.08	0.54
1:C:158:MET:N	1:C:387:ASN:O	2.40	0.54
1:C:707:ILE:HG22	1:C:708:ARG:N	2.23	0.54
3:C:902:AGS:O2A	7:C:1001:HOH:O	2.18	0.54
1:D:696:LYS:HE2	1:E:492:LEU:HD23	1.90	0.54
2:V:230:GLY:O	2:V:231:SER:HB3	2.08	0.54
1:B:124:GLU:OE1	1:B:125:GLY:N	2.41	0.53
1:D:254:ILE:HD12	1:D:369:ILE:HD13	1.90	0.53
1:C:237:PRO:HG2	1:C:340:HIS:HE1	1.72	0.53
1:A:650:GLU:OE1	1:A:677:LYS:HG3	2.08	0.53
1:C:615:LYS:HE2	1:C:615:LYS:HA	1.91	0.53
1:F:136:LYS:HB3	1:F:137:PRO:HD3	1.90	0.53
1:D:124:GLU:OE1	1:D:125:GLY:N	2.41	0.53
3:C:903:AGS:S1G	1:D:766:ARG:NH1	2.82	0.53
1:D:158:MET:CE	1:E:235:VAL:HG21	2.39	0.53
1:A:312:LYS:HE3	1:A:351:ASN:O	2.07	0.53
1:A:434:ASP:OD2	1:B:226:HIS:CE1	2.62	0.53
1:C:136:LYS:HB3	1:C:137:PRO:HD3	1.89	0.53
1:B:160:ALA:HB2	1:B:387:ASN:OD1	2.09	0.53
1:E:435:GLU:HG3	1:E:436:THR:N	2.24	0.53
1:A:635:ARG:NH1	1:A:636:PRO:O	2.42	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:136:LYS:HB3	1:B:137:PRO:HD3	1.90	0.53
1:C:465:ARG:NH2	1:D:607:GLU:OE1	2.42	0.53
1:A:442:MET:SD	1:B:233:ILE:HD13	2.49	0.52
1:A:542:ILE:HD13	1:A:562:ILE:HD13	1.92	0.52
1:D:136:LYS:HB3	1:D:137:PRO:HD3	1.92	0.52
1:E:121:ASP:OD2	1:E:191:ARG:HD2	2.09	0.52
1:F:461:PRO:HG2	1:F:464:LEU:HD21	1.90	0.52
1:B:355:PRO:O	1:B:359:ARG:NH1	2.42	0.52
1:D:220:VAL:CG1	1:D:224:LEU:HD12	2.39	0.52
1:C:203:TYR:CE2	1:C:261:GLU:HG2	2.44	0.52
1:E:136:LYS:HB3	1:E:137:PRO:HD3	1.90	0.52
1:C:53:ARG:HB2	1:C:72:LEU:HD23	1.92	0.52
1:D:317:HIS:CE1	1:E:322:ARG:NH1	2.78	0.52
1:F:124:GLU:C	1:F:124:GLU:OE1	2.48	0.52
1:C:349:ARG:HG3	1:C:352:SER:CB	2.40	0.52
1:D:698:ALA:HA	1:D:735:HIS:CE1	2.44	0.52
1:B:203:TYR:CE2	1:B:261:GLU:HG2	2.45	0.51
1:B:430:ILE:O	1:B:431:ASP:CB	2.58	0.51
1:E:222:LEU:HB2	1:E:223:PRO:HD3	1.92	0.51
1:A:111:GLY:O	1:A:180:THR:HG22	2.09	0.51
1:A:120:ASP:N	1:A:188:PRO:HB2	2.26	0.51
1:A:136:LYS:HB3	1:A:137:PRO:HD3	1.92	0.51
1:A:313:ARG:O	1:A:316:THR:OG1	2.29	0.51
1:A:434:ASP:O	1:A:436:THR:N	2.44	0.51
1:B:430:ILE:O	1:B:431:ASP:HB2	2.10	0.51
1:C:438:ASP:OD1	1:C:440:GLU:N	2.43	0.51
1:E:105:CYS:HB3	1:E:108:VAL:HG13	1.92	0.51
1:A:431:ASP:O	1:A:433:GLU:N	2.44	0.51
1:A:508:MET:SD	1:F:695:CYS:SG	3.07	0.51
1:E:339:ALA:O	1:E:340:HIS:C	2.49	0.51
1:A:495:TYR:N	1:A:496:PRO:HD2	2.26	0.51
1:C:338:ARG:O	1:C:338:ARG:HG2	2.11	0.51
1:D:433:GLU:O	1:D:433:GLU:HG3	2.11	0.51
1:D:115:HIS:NE2	2:V:227:ALA:O	2.44	0.50
1:F:222:LEU:HB3	1:F:223:PRO:HD3	1.93	0.50
1:B:222:LEU:HB3	1:B:223:PRO:HD3	1.93	0.50
1:C:124:GLU:OE1	1:C:125:GLY:N	2.45	0.50
1:C:237:PRO:HG2	1:C:340:HIS:CE1	2.46	0.50
1:C:437:ILE:HD11	1:D:229:LEU:CD1	2.41	0.50
1:B:283:GLU:OE2	1:B:323:ARG:HD2	2.12	0.50
1:D:201:VAL:HG11	1:D:253:LEU:HD12	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:167:GLU:HG3	1:C:168:THR:N	2.26	0.50
1:C:338:ARG:C	1:C:340:HIS:N	2.63	0.50
1:D:436:THR:OG1	1:D:437:ILE:N	2.45	0.50
1:D:527:LEU:HD12	1:D:645:ILE:HD13	1.92	0.50
1:F:94:VAL:HG12	1:F:95:ARG:N	2.26	0.50
1:E:461:PRO:HG2	1:E:464:LEU:HD21	1.93	0.50
2:V:226:ARG:CG	2:V:227:ALA:N	2.74	0.50
1:C:707:ILE:CG2	1:C:708:ARG:N	2.75	0.50
1:F:527:LEU:HD12	1:F:645:ILE:HD13	1.93	0.50
1:B:700:ARG:HG3	1:B:701:GLU:N	2.25	0.50
1:C:222:LEU:HB3	1:C:223:PRO:HD3	1.94	0.50
1:A:131:PHE:HD1	1:A:135:LEU:HD12	1.77	0.50
1:C:94:VAL:HG12	1:C:95:ARG:N	2.27	0.50
1:F:431:ASP:O	1:F:433:GLU:N	2.45	0.50
1:A:702:SER:O	1:A:706:GLU:HA	2.12	0.49
1:B:420:LEU:CD1	1:C:235:VAL:HG11	2.42	0.49
1:B:313:ARG:O	1:B:316:THR:OG1	2.29	0.49
1:C:705:SER:HB2	1:C:707:ILE:CD1	2.42	0.49
1:D:124:GLU:OE1	1:D:124:GLU:C	2.50	0.49
1:F:516:PHE:CD1	1:F:645:ILE:HD11	2.46	0.49
1:C:237:PRO:CG	1:C:340:HIS:CE1	2.95	0.49
1:C:527:LEU:HD12	1:C:645:ILE:HD13	1.95	0.49
1:C:762:LEU:O	1:C:765:SER:OG	2.29	0.49
1:D:495:TYR:N	1:D:496:PRO:HD2	2.27	0.49
1:A:152:PHE:CZ	1:A:163:PHE:HB2	2.47	0.49
1:B:542:ILE:HD13	1:B:562:ILE:HD13	1.92	0.49
1:F:158:MET:N	1:F:387:ASN:O	2.45	0.49
1:C:136:LYS:HB3	1:C:137:PRO:CD	2.42	0.49
1:F:705:SER:HB2	1:F:707:ILE:CD1	2.43	0.49
1:A:94:VAL:HG12	1:A:95:ARG:N	2.28	0.49
1:C:254:ILE:HD12	1:C:369:ILE:HD13	1.94	0.49
1:D:94:VAL:HG12	1:D:95:ARG:N	2.27	0.49
1:F:58:LEU:HB2	1:F:105:CYS:SG	2.53	0.49
1:E:94:VAL:HG12	1:E:95:ARG:N	2.28	0.49
1:E:450:ASP:OD1	1:E:453:ARG:NH1	2.45	0.49
1:E:707:ILE:CG2	1:E:708:ARG:N	2.74	0.49
1:A:359:ARG:HG2	3:F:901:AGS:S1G	2.53	0.49
1:D:317:HIS:ND1	1:D:317:HIS:N	2.61	0.49
1:D:339:ALA:O	1:D:340:HIS:C	2.51	0.49
1:F:438:ASP:OD2	1:F:441:VAL:HB	2.13	0.49
1:E:254:ILE:HD12	1:E:369:ILE:HD13	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:635:ARG:NH1	1:E:636:PRO:O	2.46	0.48
2:V:228:PHE:CD1	2:V:228:PHE:N	2.81	0.48
1:C:349:ARG:HG3	1:C:352:SER:HB3	1.94	0.48
1:B:427:MET:SD	1:B:432:LEU:HD21	2.53	0.48
1:F:635:ARG:NH1	1:F:636:PRO:O	2.46	0.48
1:D:96:LEU:O	1:D:225:ARG:NH2	2.47	0.48
1:A:220:VAL:CG1	1:A:224:LEU:HD12	2.43	0.48
1:D:699:ILE:HG12	1:E:506:PHE:CE2	2.49	0.48
1:F:239:ARG:HB2	1:F:335:LEU:HD12	1.94	0.48
1:B:136:LYS:HB3	1:B:137:PRO:CD	2.43	0.48
1:E:532:ALA:HB2	1:E:573:VAL:HG11	1.94	0.48
1:A:339:ALA:O	1:A:340:HIS:C	2.52	0.48
1:B:420:LEU:HD13	1:C:235:VAL:HG11	1.95	0.48
3:E:901:AGS:S1G	1:F:359:ARG:HG2	2.53	0.48
1:F:707:ILE:CG2	1:F:708:ARG:N	2.77	0.48
1:B:227:PRO:HB2	1:B:340:HIS:CE1	2.48	0.48
1:B:495:TYR:N	1:B:496:PRO:HD2	2.28	0.48
1:D:624:ASN:C	1:D:625:ARG:HG2	2.34	0.48
1:E:142:ALA:HB1	1:E:144:ARG:HG3	1.95	0.48
1:F:673:GLU:OE1	1:F:673:GLU:N	2.45	0.48
2:U:227:ALA:HB1	2:U:228:PHE:HD1	1.73	0.48
1:B:124:GLU:OE1	1:B:124:GLU:C	2.52	0.48
1:D:669:ASP:HB2	1:D:733:ARG:HD2	1.95	0.48
1:F:124:GLU:OE1	1:F:125:GLY:N	2.47	0.48
1:A:678:MET:HA	1:A:678:MET:HE2	1.95	0.47
1:B:430:ILE:HG23	1:B:431:ASP:N	2.29	0.47
1:A:316:THR:O	1:A:317:HIS:C	2.52	0.47
1:A:465:ARG:NH2	1:B:607:GLU:OE1	2.47	0.47
1:A:514:VAL:HG23	1:A:618:PHE:CE2	2.50	0.47
1:B:94:VAL:HG12	1:B:95:ARG:N	2.29	0.47
1:D:94:VAL:HG13	1:D:98:ASP:HB2	1.97	0.47
1:D:350:PRO:O	1:D:358:ARG:NH2	2.47	0.47
1:D:111:GLY:O	1:D:180:THR:HG22	2.15	0.47
1:C:442:MET:HA	1:C:442:MET:CE	2.44	0.47
1:C:495:TYR:N	1:C:496:PRO:HD2	2.30	0.47
1:E:230:PHE:CZ	1:E:237:PRO:HB3	2.50	0.47
1:E:495:TYR:N	1:E:496:PRO:HD2	2.29	0.47
1:F:136:LYS:HB3	1:F:137:PRO:CD	2.44	0.47
1:A:201:VAL:HG11	1:A:253:LEU:HD12	1.96	0.47
1:A:434:ASP:O	1:A:435:GLU:C	2.53	0.47
1:B:762:LEU:O	1:B:765:SER:OG	2.31	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:136:LYS:HB3	1:D:137:PRO:CD	2.45	0.47
1:F:650:GLU:OE1	1:F:677:LYS:HG3	2.15	0.47
1:C:407:VAL:CG1	1:C:408:GLY:N	2.78	0.47
1:E:355:PRO:O	1:E:359:ARG:NH1	2.48	0.47
1:D:117:LEU:HD11	2:V:225:PHE:CZ	2.50	0.47
1:E:167:GLU:HG3	1:E:168:THR:N	2.30	0.47
1:F:495:TYR:N	1:F:496:PRO:HD2	2.30	0.47
1:A:431:ASP:C	1:A:433:GLU:N	2.69	0.46
1:E:649:ASP:OD1	1:E:652:SER:OG	2.25	0.46
1:E:745:ARG:NH2	1:E:749:ASP:OD1	2.47	0.46
1:B:254:ILE:HD12	1:B:369:ILE:HD13	1.98	0.46
1:B:416:SER:OG	1:C:235:VAL:HG13	2.16	0.46
1:E:136:LYS:HB3	1:E:137:PRO:CD	2.45	0.46
1:F:90:ASN:O	1:F:93:ARG:NH1	2.48	0.46
1:F:431:ASP:C	1:F:433:GLU:N	2.66	0.46
2:U:228:PHE:CD1	2:U:228:PHE:N	2.83	0.46
1:A:527:LEU:HD12	1:A:645:ILE:HD13	1.98	0.46
1:D:573:VAL:HG23	1:D:620:ILE:CD1	2.45	0.46
1:E:316:THR:HG22	1:E:316:THR:O	2.15	0.46
1:F:53:ARG:HB2	1:F:72:LEU:HD23	1.98	0.46
1:C:248:GLY:O	1:C:407:VAL:CG1	2.64	0.46
1:F:51:LEU:HD21	1:F:104:PRO:HB3	1.98	0.46
1:A:63:LYS:HE2	1:A:194:GLU:OE1	2.15	0.46
1:A:432:LEU:O	1:A:433:GLU:HG3	2.16	0.46
1:C:532:ALA:HB2	1:C:573:VAL:HG11	1.98	0.46
1:C:635:ARG:NH1	1:C:636:PRO:O	2.49	0.46
1:E:762:LEU:O	1:E:765:SER:OG	2.33	0.46
1:F:110:TYR:N	1:F:110:TYR:CD1	2.84	0.46
1:A:53:ARG:HB2	1:A:72:LEU:HD23	1.97	0.46
1:A:232:ALA:CB	1:F:437:ILE:HD11	2.46	0.46
1:A:624:ASN:C	1:A:625:ARG:HG2	2.35	0.46
1:A:136:LYS:HB3	1:A:137:PRO:CD	2.46	0.46
1:B:524:LYS:HG2	1:B:645:ILE:HD12	1.97	0.46
1:B:734:ASP:OD1	1:B:735:HIS:N	2.49	0.46
1:D:414:LEU:HD12	1:D:414:LEU:C	2.36	0.46
2:V:234:ARG:O	2:V:235:LEU:HB2	2.16	0.46
1:A:126:ILE:HD12	1:A:127:THR:H	1.81	0.45
1:C:111:GLY:HA2	1:C:170:PRO:HG2	1.98	0.45
1:C:432:LEU:C	1:C:434:ASP:H	2.19	0.45
1:D:115:HIS:CE1	2:V:227:ALA:O	2.69	0.45
1:F:227:PRO:HB2	1:F:340:HIS:CE1	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:395:ASP:OD2	1:F:398:GLN:NE2	2.49	0.45
1:A:493:VAL:HG22	1:A:618:PHE:CD2	2.52	0.45
1:B:672:LEU:N	1:B:672:LEU:HD12	2.31	0.45
1:D:441:VAL:O	1:D:444:SER:OG	2.28	0.45
1:E:407:VAL:CG1	1:E:408:GLY:N	2.79	0.45
1:A:317:HIS:HB3	1:F:317:HIS:NE2	2.31	0.45
1:C:118:PRO:HG2	1:C:188:PRO:HB3	1.98	0.45
1:C:124:GLU:OE1	1:C:124:GLU:C	2.54	0.45
1:C:552:PHE:CD1	1:C:596:ALA:HB2	2.52	0.45
1:E:527:LEU:HD12	1:E:645:ILE:HD13	1.98	0.45
1:F:110:TYR:N	1:F:110:TYR:HD1	2.14	0.45
1:D:542:ILE:CD1	1:D:562:ILE:HD13	2.46	0.45
1:E:230:PHE:HA	1:E:233:ILE:HG22	1.98	0.45
2:U:226:ARG:CG	2:U:227:ALA:N	2.79	0.45
1:A:542:ILE:HD12	1:A:562:ILE:HG21	1.97	0.45
1:A:672:LEU:N	1:A:672:LEU:HD12	2.31	0.45
1:A:762:LEU:O	1:A:765:SER:OG	2.32	0.45
1:B:192:GLU:HB2	1:B:195:GLU:CD	2.37	0.45
1:F:254:ILE:HD12	1:F:369:ILE:HD13	1.99	0.45
1:F:407:VAL:CG1	1:F:408:GLY:N	2.80	0.45
1:A:90:ASN:O	1:A:93:ARG:NH1	2.46	0.45
1:C:96:LEU:N	1:C:96:LEU:CD2	2.79	0.45
1:C:432:LEU:O	1:C:434:ASP:N	2.49	0.45
1:E:551:TRP:CZ2	1:F:556:GLU:HG2	2.51	0.45
1:B:114:ILE:CD1	1:B:176:VAL:HG22	2.47	0.45
1:E:240:GLY:HA3	1:E:363:PHE:HA	1.99	0.45
1:E:313:ARG:HD2	1:E:354:ASP:OD2	2.17	0.45
1:E:332:MET:O	1:E:335:LEU:HB2	2.16	0.45
1:F:118:PRO:HB2	1:F:123:VAL:HG11	1.98	0.45
1:C:226:HIS:HB3	1:C:229:LEU:HD23	1.98	0.45
1:F:424:ARG:O	1:F:427:MET:HG2	2.17	0.45
1:C:437:ILE:HD11	1:D:229:LEU:HD11	1.98	0.45
1:F:108:VAL:CG1	1:F:175:ILE:HG13	2.47	0.45
1:A:669:ASP:OD1	1:A:733:ARG:HB2	2.16	0.45
1:E:731:ILE:HG13	1:E:731:ILE:O	2.17	0.45
1:F:220:VAL:CG1	1:F:224:LEU:HD12	2.47	0.45
2:V:227:ALA:HB1	2:V:228:PHE:HD1	1.69	0.44
1:B:407:VAL:CG1	1:B:408:GLY:N	2.80	0.44
1:D:311:PRO:HG2	1:D:316:THR:HG22	2.00	0.44
1:A:134:TYR:CD2	1:A:161:VAL:HG11	2.52	0.44
1:E:434:ASP:N	1:E:434:ASP:OD1	2.50	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:51:LEU:HD21	1:A:104:PRO:HB3	1.98	0.44
2:U:234:ARG:O	2:U:235:LEU:HB2	2.17	0.44
1:A:85:ASN:OD1	1:A:86:ARG:N	2.51	0.44
1:A:94:VAL:HG13	1:A:98:ASP:CB	2.47	0.44
1:A:532:ALA:HB2	1:A:573:VAL:HG11	1.99	0.44
1:C:127:THR:O	1:C:438:ASP:HA	2.18	0.44
1:B:423:ILE:O	1:B:427:MET:N	2.51	0.44
1:C:89:ARG:NH1	1:C:96:LEU:HD21	2.33	0.44
1:D:547:LEU:HD12	1:D:582:ILE:HD11	2.00	0.44
1:E:672:LEU:HD12	1:E:672:LEU:N	2.33	0.44
1:A:461:PRO:HG2	1:A:464:LEU:HD11	1.99	0.44
1:D:420:LEU:HD21	1:E:230:PHE:CZ	2.52	0.44
1:C:259:ALA:HB2	1:C:266:PHE:CD1	2.52	0.44
1:C:686:ASP:OD1	1:C:746:SER:OG	2.29	0.44
1:C:698:ALA:HA	1:C:735:HIS:CE1	2.53	0.44
1:D:312:LYS:N	1:D:352:SER:O	2.49	0.44
1:B:201:VAL:HG11	1:B:253:LEU:HD12	2.00	0.44
1:A:94:VAL:CG1	1:A:98:ASP:HB2	2.48	0.43
1:A:423:ILE:O	1:A:427:MET:HB2	2.18	0.43
1:A:707:ILE:HG23	1:A:708:ARG:N	2.32	0.43
1:C:624:ASN:C	1:C:625:ARG:HG2	2.38	0.43
1:D:131:PHE:CZ	2:V:234:ARG:NH1	2.85	0.43
1:E:141:GLU:O	1:E:141:GLU:CD	2.57	0.43
1:E:624:ASN:C	1:E:625:ARG:HG2	2.37	0.43
1:A:134:TYR:CE2	1:A:161:VAL:HG11	2.54	0.43
1:C:501:ASP:OD1	1:C:502:LYS:N	2.51	0.43
1:E:734:ASP:OD1	1:E:734:ASP:N	2.49	0.43
1:E:320:VAL:HB	1:F:319:GLU:OE1	2.18	0.43
2:V:225:PHE:CG	2:V:226:ARG:N	2.86	0.43
1:A:403:THR:HB	1:A:406:HIS:CG	2.54	0.43
1:D:89:ARG:NH1	1:D:96:LEU:HD21	2.33	0.43
1:D:627:ASP:HB3	1:D:758:PHE:CZ	2.53	0.43
1:A:243:LEU:O	1:A:346:ALA:HA	2.19	0.43
1:A:407:VAL:CG1	1:A:408:GLY:N	2.81	0.43
1:B:501:ASP:OD1	1:B:502:LYS:N	2.51	0.43
1:B:682:PHE:CD1	1:B:745:ARG:HG3	2.53	0.43
1:E:519:PRO:HA	1:E:755:TYR:CE2	2.54	0.43
1:F:167:GLU:HG3	1:F:168:THR:N	2.32	0.43
1:A:158:MET:HE3	1:B:235:VAL:HG21	2.00	0.43
1:B:332:MET:O	1:B:335:LEU:HB2	2.18	0.43
1:C:625:ARG:HD2	1:D:767:GLY:O	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:120:ASP:CA	1:A:188:PRO:HB2	2.48	0.43
1:A:147:ARG:NH1	1:A:172:PRO:HB2	2.33	0.43
1:B:197:SER:HB3	1:B:200:GLU:HG2	2.01	0.43
1:B:220:VAL:CG1	1:B:224:LEU:HD22	2.49	0.43
1:B:627:ASP:HB3	1:B:758:PHE:CZ	2.54	0.43
1:D:729:PRO:HB2	1:E:506:PHE:CZ	2.54	0.43
1:E:122:THR:HB	1:E:161:VAL:HA	2.01	0.43
1:E:251:LYS:NZ	3:E:901:AGS:O1B	2.51	0.43
1:E:542:ILE:HD12	1:E:562:ILE:HG21	1.99	0.43
1:F:501:ASP:OD1	1:F:502:LYS:N	2.51	0.43
1:A:312:LYS:N	1:A:352:SER:O	2.52	0.43
1:A:491:GLU:OE2	1:F:700:ARG:NE	2.51	0.43
1:B:532:ALA:HB2	1:B:573:VAL:HG11	1.99	0.43
1:E:524:LYS:HG2	1:E:645:ILE:HD12	2.01	0.43
1:F:552:PHE:CD1	1:F:596:ALA:HB2	2.53	0.43
1:B:624:ASN:C	1:B:625:ARG:HG2	2.38	0.43
1:D:461:PRO:O	1:D:464:LEU:HD11	2.18	0.43
1:A:317:HIS:CE1	1:B:322:ARG:NH1	2.87	0.42
1:A:556:GLU:HA	1:A:603:GLN:OE1	2.19	0.42
1:C:58:LEU:HB2	1:C:105:CYS:SG	2.58	0.42
1:C:89:ARG:HD3	1:C:96:LEU:HD22	2.01	0.42
1:E:191:ARG:NH1	1:E:191:ARG:HB3	2.34	0.42
1:F:313:ARG:O	1:F:316:THR:OG1	2.32	0.42
1:A:58:LEU:HB2	1:A:105:CYS:SG	2.58	0.42
1:A:380:ILE:CD1	3:A:901:AGS:N1	2.82	0.42
1:A:515:LEU:HD22	1:A:634:LEU:HD21	2.00	0.42
1:A:627:ASP:HB3	1:A:758:PHE:CZ	2.54	0.42
1:C:118:PRO:HG3	1:C:130:LEU:HD13	2.01	0.42
1:F:313:ARG:NE	1:F:354:ASP:OD2	2.53	0.42
1:A:675:LEU:HD11	1:A:740:MET:HE3	2.02	0.42
1:D:433:GLU:O	1:D:434:ASP:C	2.57	0.42
1:E:698:ALA:CB	1:E:731:ILE:HG22	2.50	0.42
1:F:230:PHE:CE1	1:F:237:PRO:HB3	2.54	0.42
1:B:243:LEU:O	1:B:346:ALA:HA	2.19	0.42
1:B:425:LYS:HG3	1:B:426:LYS:N	2.33	0.42
1:E:350:PRO:O	1:E:358:ARG:NH2	2.53	0.42
1:F:406:HIS:CE1	1:F:461:PRO:HB3	2.54	0.42
1:B:376:GLY:O	1:B:379:GLU:HB2	2.19	0.42
1:B:527:LEU:HD12	1:B:645:ILE:HD13	2.02	0.42
1:D:438:ASP:HB3	1:D:441:VAL:HB	2.01	0.42
1:F:125:GLY:O	1:F:437:ILE:HG13	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:120:ASP:N	1:D:188:PRO:HB2	2.35	0.42
1:D:407:VAL:CG1	1:D:408:GLY:N	2.81	0.42
1:D:532:ALA:HB2	1:D:573:VAL:HG11	2.00	0.42
2:V:225:PHE:CD1	2:V:225:PHE:C	2.93	0.42
1:A:94:VAL:HG13	1:A:98:ASP:HB2	2.02	0.42
1:A:131:PHE:HE1	1:A:182:ILE:HD13	1.83	0.42
1:A:442:MET:SD	1:B:233:ILE:CD1	3.07	0.42
1:A:501:ASP:OD1	1:A:502:LYS:N	2.52	0.42
1:C:349:ARG:HA	1:C:350:PRO:HD2	1.90	0.42
1:D:115:HIS:CD2	2:V:227:ALA:O	2.73	0.42
1:E:230:PHE:CE1	1:E:237:PRO:HB3	2.55	0.42
1:F:159:ARG:N	1:F:387:ASN:HB3	2.35	0.42
1:A:167:GLU:HG3	1:A:168:THR:N	2.33	0.42
1:D:349:ARG:HA	1:D:350:PRO:HD2	1.92	0.42
1:D:542:ILE:HD13	1:D:562:ILE:HD13	1.99	0.42
1:A:442:MET:CE	1:A:442:MET:HA	2.49	0.42
1:E:22:ARG:NH1	1:E:22:ARG:HB2	2.35	0.42
1:E:127:THR:O	1:E:438:ASP:HA	2.19	0.42
1:E:269:ILE:HD11	1:E:289:ALA:CB	2.50	0.42
1:F:321:GLU:HA	1:F:324:ILE:HD12	2.01	0.42
1:B:573:VAL:CG2	1:B:620:ILE:HD12	2.50	0.42
1:E:141:GLU:O	1:E:141:GLU:CG	2.67	0.42
1:E:317:HIS:O	1:F:322:ARG:NH2	2.53	0.42
1:A:28:VAL:HG21	1:A:94:VAL:HG11	2.02	0.41
1:B:248:GLY:O	1:B:407:VAL:CG1	2.68	0.41
1:D:514:VAL:HG12	1:D:515:LEU:N	2.34	0.41
1:E:43:GLN:N	1:E:44:PRO:CD	2.83	0.41
1:E:203:TYR:CE2	1:E:217:LYS:HD3	2.54	0.41
1:E:231:LYS:HD3	1:E:231:LYS:C	2.40	0.41
1:E:501:ASP:OD1	1:E:502:LYS:N	2.52	0.41
1:F:532:ALA:HB2	1:F:573:VAL:HG11	2.01	0.41
1:A:559:VAL:HA	1:A:562:ILE:HD12	2.02	0.41
1:C:277:LYS:HB3	1:C:281:GLU:HB3	2.02	0.41
1:D:635:ARG:NH1	1:D:636:PRO:O	2.53	0.41
1:F:126:ILE:HD11	1:F:159:ARG:HD3	2.02	0.41
1:A:143:TYR:CE2	1:A:178:PRO:HD3	2.54	0.41
1:B:115:HIS:NE2	1:B:185:GLU:HG3	2.35	0.41
1:B:427:MET:O	1:B:429:LEU:N	2.53	0.41
1:C:732:ARG:NH1	1:C:735:HIS:CE1	2.88	0.41
1:F:22:ARG:HG2	1:F:23:PRO:HD2	2.02	0.41
1:A:732:ARG:NE	1:A:734:ASP:OD2	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:27:ILE:HD13	1:C:99:VAL:HG13	2.01	0.41
1:D:501:ASP:OD1	1:D:502:LYS:N	2.53	0.41
1:F:111:GLY:HA2	1:F:170:PRO:HG2	2.02	0.41
1:A:115:HIS:CE1	2:U:227:ALA:O	2.74	0.41
1:D:94:VAL:CG1	1:D:98:ASP:HB2	2.51	0.41
1:E:313:ARG:CD	1:E:354:ASP:OD2	2.68	0.41
1:F:482:LEU:O	1:F:486:LYS:HG3	2.21	0.41
1:B:731:ILE:HD11	1:B:736:PHE:CE2	2.55	0.41
1:D:321:GLU:OE2	1:E:322:ARG:HD2	2.20	0.41
1:E:476:TRP:CE3	1:E:486:LYS:HD3	2.55	0.41
1:E:573:VAL:HG23	1:E:620:ILE:HD12	2.03	0.41
1:F:672:LEU:N	1:F:672:LEU:HD12	2.36	0.41
1:A:734:ASP:OD1	1:A:734:ASP:N	2.36	0.41
1:D:430:ILE:HG22	1:D:431:ASP:N	2.35	0.41
1:E:769:GLY:O	1:E:770:SER:C	2.59	0.41
1:A:435:GLU:HG3	1:A:436:THR:N	2.35	0.41
1:B:142:ALA:O	1:B:143:TYR:CG	2.74	0.41
1:B:230:PHE:CE1	1:B:237:PRO:HB3	2.56	0.41
1:D:94:VAL:HG13	1:D:98:ASP:CB	2.50	0.41
1:E:435:GLU:CG	1:E:436:THR:N	2.84	0.41
1:F:627:ASP:HB3	1:F:758:PHE:CZ	2.55	0.41
1:B:113:ARG:HG2	1:B:169:ASP:HB2	2.03	0.41
1:B:423:ILE:O	1:B:427:MET:HB2	2.21	0.41
1:B:434:ASP:O	1:B:435:GLU:C	2.57	0.41
1:B:478:ASP:OD1	1:B:662:ARG:NH2	2.53	0.41
1:D:98:ASP:OD1	1:D:225:ARG:NH1	2.51	0.41
1:D:120:ASP:CA	1:D:188:PRO:HB2	2.51	0.41
1:D:461:PRO:HG2	1:D:464:LEU:HD11	2.02	0.41
1:A:429:LEU:HD12	1:A:429:LEU:H	1.86	0.40
1:B:705:SER:OG	1:B:706:GLU:N	2.50	0.40
1:D:222:LEU:HB2	1:D:223:PRO:CD	2.51	0.40
1:E:224:LEU:HD21	1:E:300:ILE:HG13	2.03	0.40
1:E:514:VAL:HG12	1:E:515:LEU:N	2.36	0.40
1:A:307:ASP:OD1	1:A:307:ASP:N	2.55	0.40
1:D:658:LYS:O	1:D:662:ARG:HG3	2.21	0.40
1:D:762:LEU:O	1:D:765:SER:OG	2.38	0.40
1:E:442:MET:CE	1:F:233:ILE:HD13	2.50	0.40
1:F:428:ASP:O	1:F:431:ASP:HB3	2.21	0.40
1:B:85:ASN:OD1	1:B:86:ARG:N	2.54	0.40
1:C:675:LEU:HD21	1:C:740:MET:CE	2.52	0.40
1:D:706:GLU:CA	1:D:706:GLU:OE2	2.69	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:514:VAL:HG12	1:F:515:LEU:N	2.36	0.40
1:A:134:TYR:CE2	1:A:161:VAL:CG1	3.04	0.40
1:C:159:ARG:N	1:C:387:ASN:HB3	2.36	0.40
1:E:427:MET:SD	1:E:445:LEU:HD12	2.62	0.40
1:A:27:ILE:HB	1:A:81:LYS:HG2	2.04	0.40
1:A:231:LYS:HD3	1:A:231:LYS:C	2.42	0.40
1:B:146:ILE:HD11	1:B:168:THR:HG21	2.04	0.40
1:B:437:ILE:HG12	1:C:229:LEU:HD12	2.04	0.40
1:C:519:PRO:HA	1:C:520:PRO:HD3	1.94	0.40
1:C:535:CYS:O	1:C:536:GLN:CG	2.70	0.40
1:D:115:HIS:ND1	1:D:183:HIS:O	2.55	0.40
1:D:164:LYS:HE2	1:D:189:ILE:HD13	2.04	0.40
1:E:519:PRO:HA	1:E:520:PRO:HD3	1.95	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)
1:C:284:SER:OG	1:F:671:ASP:OD2[3_555]	2.02	0.18
1:A:112:LYS:NZ	1:D:397:GLU:OE1[1_455]	2.17	0.03

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	720/785 (92%)	690 (96%)	25 (4%)	5 (1%)	22 54
1	B	720/785 (92%)	696 (97%)	20 (3%)	4 (1%)	25 57
1	C	720/785 (92%)	698 (97%)	20 (3%)	2 (0%)	41 71
1	D	720/785 (92%)	697 (97%)	21 (3%)	2 (0%)	41 71
1	E	720/785 (92%)	695 (96%)	20 (3%)	5 (1%)	22 54

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	F	720/785 (92%)	693 (96%)	23 (3%)	4 (1%)	25	57
2	U	8/21 (38%)	1 (12%)	3 (38%)	4 (50%)	0	0
2	V	9/21 (43%)	2 (22%)	3 (33%)	4 (44%)	0	0
All	All	4337/4752 (91%)	4172 (96%)	135 (3%)	30 (1%)	22	54

All (30) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	340	HIS
1	B	428	ASP
1	B	430	ILE
1	B	431	ASP
1	C	706	GLU
1	D	340	HIS
1	E	340	HIS
1	F	340	HIS
2	V	229	SER
2	V	233	ASN
2	U	229	SER
2	U	233	ASN
1	A	432	LEU
1	A	435	GLU
1	B	340	HIS
1	E	435	GLU
1	E	706	GLU
1	F	432	LEU
1	E	431	ASP
1	A	706	GLU
1	C	433	GLU
1	D	339	ALA
2	V	227	ALA
2	V	231	SER
2	U	227	ALA
2	U	231	SER
1	A	434	ASP
1	E	339	ALA
1	F	433	GLU
1	F	706	GLU

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	617/658 (94%)	561 (91%)	56 (9%)	9	31
1	B	617/658 (94%)	583 (94%)	34 (6%)	21	52
1	C	617/658 (94%)	563 (91%)	54 (9%)	10	34
1	D	617/658 (94%)	573 (93%)	44 (7%)	14	43
1	E	617/658 (94%)	576 (93%)	41 (7%)	16	45
1	F	617/658 (94%)	584 (95%)	33 (5%)	22	53
2	U	7/14 (50%)	6 (86%)	1 (14%)	3	13
2	V	8/14 (57%)	6 (75%)	2 (25%)	0	1
All	All	3717/3976 (94%)	3452 (93%)	265 (7%)	14	43

All (265) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	22	ARG
1	A	45	LYS
1	A	52	PHE
1	A	78	SER
1	A	79	ASP
1	A	90	ASN
1	A	99	VAL
1	A	105	CYS
1	A	126	ILE
1	A	147	ARG
1	A	155	ARG
1	A	159	ARG
1	A	171	SER
1	A	181	VAL
1	A	190	LYS
1	A	229	LEU
1	A	230	PHE
1	A	231	LYS
1	A	236	LYS

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Mol	Chain	Res	Type
1	A	274	ILE
1	A	295	LYS
1	A	313	ARG
1	A	317	HIS
1	A	335	LEU
1	A	336	LYS
1	A	355	PRO
1	A	359	ARG
1	A	365	ARG
1	A	378	LEU
1	A	414	LEU
1	A	416	SER
1	A	425	LYS
1	A	427	MET
1	A	429	LEU
1	A	432	LEU
1	A	435	GLU
1	A	442	MET
1	A	443	ASN
1	A	458	GLN
1	A	487	ARG
1	A	509	THR
1	A	551	TRP
1	A	556	GLU
1	A	573	VAL
1	A	599	ARG
1	A	625	ARG
1	A	678	MET
1	A	700	ARG
1	A	705	SER
1	A	708	ARG
1	A	734	ASP
1	A	738	GLU
1	A	757	MET
1	A	762	LEU
1	A	765	SER
1	A	770	SER
1	B	45	LYS
1	B	49	LEU
1	B	79	ASP
1	B	99	VAL
1	B	105	CYS

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Mol	Chain	Res	Type
1	B	124	GLU
1	B	131	PHE
1	B	147	ARG
1	B	155	ARG
1	B	193	ASP
1	B	236	LYS
1	B	256	ARG
1	B	261	GLU
1	B	268	LEU
1	B	284	SER
1	B	295	LYS
1	B	317	HIS
1	B	335	LEU
1	B	349	ARG
1	B	359	ARG
1	B	402	GLU
1	B	416	SER
1	B	425	LYS
1	B	431	ASP
1	B	464	LEU
1	B	509	THR
1	B	556	GLU
1	B	573	VAL
1	B	599	ARG
1	B	625	ARG
1	B	731	ILE
1	B	762	LEU
1	B	765	SER
1	B	770	SER
1	C	21	ASN
1	C	22	ARG
1	C	25	ARG
1	C	45	LYS
1	C	52	PHE
1	C	79	ASP
1	C	96	LEU
1	C	99	VAL
1	C	105	CYS
1	C	109	LYS
1	C	124	GLU
1	C	126	ILE
1	C	131	PHE

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Mol	Chain	Res	Type
1	C	155	ARG
1	C	159	ARG
1	C	173	TYR
1	C	230	PHE
1	C	233	ILE
1	C	236	LYS
1	C	256	ARG
1	C	283	GLU
1	C	284	SER
1	C	292	GLU
1	C	295	LYS
1	C	313	ARG
1	C	336	LYS
1	C	340	HIS
1	C	355	PRO
1	C	359	ARG
1	C	365	ARG
1	C	402	GLU
1	C	416	SER
1	C	424	ARG
1	C	432	LEU
1	C	433	GLU
1	C	436	THR
1	C	437	ILE
1	C	442	MET
1	C	443	ASN
1	C	445	LEU
1	C	498	GLU
1	C	509	THR
1	C	556	GLU
1	C	573	VAL
1	C	614	LYS
1	C	615	LYS
1	C	625	ARG
1	C	675	LEU
1	C	700	ARG
1	C	705	SER
1	C	708	ARG
1	C	732	ARG
1	C	762	LEU
1	C	765	SER
1	D	22	ARG

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Mol	Chain	Res	Type
1	D	45	LYS
1	D	78	SER
1	D	79	ASP
1	D	99	VAL
1	D	105	CYS
1	D	124	GLU
1	D	131	PHE
1	D	147	ARG
1	D	155	ARG
1	D	159	ARG
1	D	167	GLU
1	D	181	VAL
1	D	189	ILE
1	D	193	ASP
1	D	230	PHE
1	D	236	LYS
1	D	283	GLU
1	D	284	SER
1	D	295	LYS
1	D	315	LYS
1	D	317	HIS
1	D	322	ARG
1	D	335	LEU
1	D	349	ARG
1	D	359	ARG
1	D	414	LEU
1	D	429	LEU
1	D	430	ILE
1	D	436	THR
1	D	443	ASN
1	D	487	ARG
1	D	509	THR
1	D	556	GLU
1	D	573	VAL
1	D	599	ARG
1	D	618	PHE
1	D	625	ARG
1	D	700	ARG
1	D	706	GLU
1	D	757	MET
1	D	762	LEU
1	D	765	SER

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Mol	Chain	Res	Type
1	D	770	SER
1	E	46	MET
1	E	49	LEU
1	E	79	ASP
1	E	90	ASN
1	E	99	VAL
1	E	105	CYS
1	E	107	ASP
1	E	113	ARG
1	E	124	GLU
1	E	131	PHE
1	E	147	ARG
1	E	155	ARG
1	E	171	SER
1	E	230	PHE
1	E	231	LYS
1	E	256	ARG
1	E	261	GLU
1	E	284	SER
1	E	295	LYS
1	E	313	ARG
1	E	335	LEU
1	E	349	ARG
1	E	359	ARG
1	E	365	ARG
1	E	416	SER
1	E	428	ASP
1	E	429	LEU
1	E	435	GLU
1	E	464	LEU
1	E	478	ASP
1	E	509	THR
1	E	556	GLU
1	E	573	VAL
1	E	599	ARG
1	E	625	ARG
1	E	700	ARG
1	E	734	ASP
1	E	757	MET
1	E	762	LEU
1	E	765	SER
1	E	768	PHE

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Mol	Chain	Res	Type
1	F	45	LYS
1	F	52	PHE
1	F	99	VAL
1	F	124	GLU
1	F	131	PHE
1	F	147	ARG
1	F	155	ARG
1	F	173	TYR
1	F	193	ASP
1	F	284	SER
1	F	287	ARG
1	F	295	LYS
1	F	313	ARG
1	F	336	LYS
1	F	338	ARG
1	F	349	ARG
1	F	359	ARG
1	F	365	ARG
1	F	401	ASN
1	F	402	GLU
1	F	431	ASP
1	F	464	LEU
1	F	487	ARG
1	F	509	THR
1	F	556	GLU
1	F	573	VAL
1	F	675	LEU
1	F	693	ARG
1	F	700	ARG
1	F	705	SER
1	F	734	ASP
1	F	738	GLU
1	F	762	LEU
2	V	225	PHE
2	V	228	PHE
2	U	228	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	340	HIS
1	D	90	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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 32 ligands modelled in this entry, 18 are monoatomic - leaving 14 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
3	AGS	B	901	4	26,33,33	1.44	5 (19%)	26,52,52	1.70	4 (15%)
3	AGS	E	901	4	26,33,33	1.51	7 (26%)	26,52,52	1.65	3 (11%)
3	AGS	F	901	4	26,33,33	1.43	5 (19%)	26,52,52	1.72	5 (19%)
6	GOL	F	906	-	5,5,5	0.41	0	5,5,5	0.21	0
3	AGS	D	902	4	26,33,33	1.47	5 (19%)	26,52,52	1.73	5 (19%)
3	AGS	C	903	4	26,33,33	1.47	5 (19%)	26,52,52	1.68	4 (15%)
3	AGS	E	902	4	26,33,33	1.46	5 (19%)	26,52,52	1.66	6 (23%)
3	AGS	A	901	4	26,33,33	1.48	6 (23%)	26,52,52	1.57	3 (11%)
3	AGS	D	903	4	26,33,33	1.46	5 (19%)	26,52,52	1.69	6 (23%)
6	GOL	F	907	-	5,5,5	0.37	0	5,5,5	0.24	0
3	AGS	F	902	4	26,33,33	1.47	6 (23%)	26,52,52	1.64	4 (15%)
3	AGS	A	902	4	26,33,33	1.45	5 (19%)	26,52,52	1.66	5 (19%)
3	AGS	B	902	4	26,33,33	1.45	6 (23%)	26,52,52	1.72	5 (19%)
3	AGS	C	902	4	26,33,33	1.49	6 (23%)	26,52,52	1.58	3 (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
3	AGS	B	901	4	-	7/17/38/38	0/3/3/3
3	AGS	E	901	4	-	5/17/38/38	0/3/3/3
3	AGS	F	901	4	-	4/17/38/38	0/3/3/3
6	GOL	F	906	-	-	2/4/4/4	-
3	AGS	D	902	4	-	5/17/38/38	0/3/3/3
3	AGS	C	903	4	-	7/17/38/38	0/3/3/3
3	AGS	E	902	4	-	6/17/38/38	0/3/3/3
3	AGS	A	901	4	-	3/17/38/38	0/3/3/3
3	AGS	D	903	4	-	9/17/38/38	0/3/3/3
6	GOL	F	907	-	-	2/4/4/4	-
3	AGS	F	902	4	-	4/17/38/38	0/3/3/3
3	AGS	A	902	4	-	3/17/38/38	0/3/3/3
3	AGS	B	902	4	-	7/17/38/38	0/3/3/3
3	AGS	C	902	4	-	4/17/38/38	0/3/3/3

All (66) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	E	901	AGS	C2-N3	3.28	1.37	1.32
3	D	903	AGS	C2-N3	3.19	1.37	1.32
3	C	903	AGS	C2-N3	3.17	1.37	1.32
3	E	902	AGS	C2-N3	3.17	1.37	1.32
3	C	902	AGS	C2-N3	3.14	1.37	1.32
3	D	902	AGS	C2-N3	3.10	1.37	1.32
3	B	902	AGS	C2-N3	3.10	1.37	1.32
3	F	902	AGS	C2-N3	3.10	1.37	1.32
3	A	902	AGS	C2-N3	3.10	1.37	1.32
3	A	901	AGS	C2-N3	3.04	1.37	1.32
3	F	901	AGS	C2-N3	3.02	1.37	1.32
3	B	901	AGS	C6-N6	2.91	1.44	1.34
3	E	902	AGS	C6-N6	2.86	1.44	1.34
3	D	902	AGS	C6-N6	2.85	1.44	1.34
3	F	902	AGS	C6-N6	2.84	1.44	1.34
3	B	902	AGS	C6-N6	2.84	1.44	1.34
3	A	901	AGS	C6-N6	2.84	1.44	1.34
3	C	902	AGS	C6-N6	2.84	1.44	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	903	AGS	C6-N6	2.83	1.44	1.34
3	C	903	AGS	C6-N6	2.83	1.44	1.34
3	A	902	AGS	C6-N6	2.82	1.44	1.34
3	F	901	AGS	C6-N6	2.81	1.44	1.34
3	E	901	AGS	C6-N6	2.73	1.44	1.34
3	B	901	AGS	C2-N3	2.67	1.36	1.32
3	E	901	AGS	C2'-C1'	-2.67	1.49	1.53
3	A	901	AGS	O2'-C2'	-2.55	1.37	1.43
3	B	901	AGS	O2'-C2'	-2.53	1.37	1.43
3	C	902	AGS	O2'-C2'	-2.52	1.37	1.43
3	C	903	AGS	O2'-C2'	-2.51	1.37	1.43
3	E	902	AGS	O2'-C2'	-2.48	1.37	1.43
3	B	902	AGS	O2'-C2'	-2.47	1.37	1.43
3	D	903	AGS	O2'-C2'	-2.47	1.37	1.43
3	A	902	AGS	O2'-C2'	-2.46	1.37	1.43
3	D	902	AGS	O2'-C2'	-2.46	1.37	1.43
3	E	901	AGS	O2'-C2'	-2.45	1.37	1.43
3	F	901	AGS	O2'-C2'	-2.45	1.37	1.43
3	F	902	AGS	O2'-C2'	-2.44	1.37	1.43
3	A	901	AGS	C2'-C3'	-2.32	1.47	1.53
3	A	901	AGS	O3'-C3'	-2.29	1.37	1.43
3	D	902	AGS	O3'-C3'	-2.28	1.37	1.43
3	C	902	AGS	C2'-C3'	-2.27	1.47	1.53
3	F	902	AGS	C2'-C3'	-2.26	1.47	1.53
3	C	902	AGS	O3'-C3'	-2.26	1.37	1.43
3	A	902	AGS	C2'-C3'	-2.24	1.47	1.53
3	C	903	AGS	C2'-C3'	-2.24	1.47	1.53
3	B	902	AGS	C2'-C3'	-2.21	1.47	1.53
3	F	902	AGS	O3'-C3'	-2.21	1.37	1.43
3	A	902	AGS	O3'-C3'	-2.20	1.37	1.43
3	D	903	AGS	O3'-C3'	-2.20	1.37	1.43
3	E	902	AGS	O3'-C3'	-2.20	1.37	1.43
3	C	903	AGS	O3'-C3'	-2.20	1.37	1.43
3	B	901	AGS	C2'-C3'	-2.19	1.47	1.53
3	B	902	AGS	O3'-C3'	-2.19	1.37	1.43
3	F	901	AGS	O3'-C3'	-2.18	1.37	1.43
3	D	902	AGS	C2'-C3'	-2.18	1.47	1.53
3	F	901	AGS	C2'-C3'	-2.15	1.47	1.53
3	D	903	AGS	C2'-C3'	-2.15	1.47	1.53
3	E	901	AGS	O3'-C3'	-2.13	1.38	1.43
3	A	901	AGS	C2'-C1'	-2.13	1.50	1.53
3	E	902	AGS	C2'-C3'	-2.08	1.47	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	901	AGS	O3'-C3'	-2.07	1.38	1.43
3	F	902	AGS	C2'-C1'	-2.06	1.50	1.53
3	C	902	AGS	C2'-C1'	-2.03	1.50	1.53
3	E	901	AGS	C2'-C3'	-2.01	1.47	1.53
3	E	901	AGS	PG-S1G	2.01	1.95	1.90
3	B	902	AGS	C2'-C1'	-2.01	1.50	1.53

All (53) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	901	AGS	N3-C2-N1	-5.76	119.67	128.68
3	A	902	AGS	N3-C2-N1	-5.68	119.80	128.68
3	B	902	AGS	N3-C2-N1	-5.58	119.95	128.68
3	C	903	AGS	N3-C2-N1	-5.56	119.98	128.68
3	F	902	AGS	N3-C2-N1	-5.56	119.99	128.68
3	F	901	AGS	N3-C2-N1	-5.56	119.99	128.68
3	D	903	AGS	N3-C2-N1	-5.53	120.04	128.68
3	A	901	AGS	N3-C2-N1	-5.52	120.05	128.68
3	D	902	AGS	N3-C2-N1	-5.52	120.05	128.68
3	E	901	AGS	N3-C2-N1	-5.51	120.06	128.68
3	E	902	AGS	N3-C2-N1	-5.49	120.10	128.68
3	C	902	AGS	N3-C2-N1	-5.48	120.11	128.68
3	F	901	AGS	PA-O3A-PB	-4.22	118.34	132.83
3	F	902	AGS	PA-O3A-PB	-4.14	118.61	132.83
3	D	902	AGS	PA-O3A-PB	-3.94	119.31	132.83
3	C	903	AGS	PA-O3A-PB	-3.93	119.34	132.83
3	B	902	AGS	PA-O3A-PB	-3.90	119.46	132.83
3	A	901	AGS	PA-O3A-PB	-3.61	120.42	132.83
3	A	902	AGS	PA-O3A-PB	-3.60	120.46	132.83
3	E	902	AGS	PA-O3A-PB	-3.59	120.49	132.83
3	C	902	AGS	PA-O3A-PB	-3.59	120.50	132.83
3	E	901	AGS	PA-O3A-PB	-3.53	120.72	132.83
3	D	903	AGS	PA-O3A-PB	-3.42	121.10	132.83
3	B	901	AGS	PA-O3A-PB	-3.11	122.16	132.83
3	D	903	AGS	C3'-C2'-C1'	2.82	105.23	100.98
3	D	902	AGS	C3'-C2'-C1'	2.79	105.18	100.98
3	B	901	AGS	O2G-PG-O3B	2.74	113.77	104.64
3	B	902	AGS	C3'-C2'-C1'	2.69	105.03	100.98
3	B	901	AGS	C4-C5-N7	-2.67	106.61	109.40
3	E	902	AGS	C3'-C2'-C1'	2.43	104.64	100.98
3	D	902	AGS	O4'-C4'-C3'	2.41	109.88	105.11
3	D	903	AGS	O2G-PG-O3B	2.40	112.67	104.64

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	E	901	AGS	C5'-C4'-C3'	-2.36	106.33	115.18
3	C	903	AGS	C3'-C2'-C1'	2.35	104.52	100.98
3	F	901	AGS	C3'-C2'-C1'	2.33	104.49	100.98
3	E	902	AGS	O2G-PG-O3B	2.32	112.40	104.64
3	A	902	AGS	O2G-PG-O3B	2.25	112.14	104.64
3	F	901	AGS	O4'-C4'-C3'	2.20	109.46	105.11
3	A	902	AGS	C3'-C2'-C1'	2.17	104.25	100.98
3	F	901	AGS	C4-C5-N7	-2.16	107.15	109.40
3	B	902	AGS	C4-C5-N7	-2.15	107.16	109.40
3	D	903	AGS	C4-C5-N7	-2.13	107.18	109.40
3	C	902	AGS	C4-C5-N7	-2.12	107.19	109.40
3	B	902	AGS	O4'-C4'-C3'	2.12	109.31	105.11
3	A	902	AGS	C4-C5-N7	-2.11	107.20	109.40
3	D	902	AGS	C4-C5-N7	-2.10	107.21	109.40
3	F	902	AGS	C4-C5-N7	-2.08	107.23	109.40
3	C	903	AGS	C4-C5-N7	-2.08	107.23	109.40
3	F	902	AGS	O3G-PG-O3B	2.05	111.47	104.64
3	E	902	AGS	O4'-C4'-C3'	2.04	109.15	105.11
3	E	902	AGS	C4-C5-N7	-2.02	107.29	109.40
3	A	901	AGS	C4-C5-N7	-2.01	107.31	109.40
3	D	903	AGS	O4'-C4'-C3'	2.00	109.08	105.11

There are no chirality outliers.

All (68) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	901	AGS	C5'-O5'-PA-O1A
3	A	901	AGS	C5'-O5'-PA-O2A
3	A	901	AGS	C5'-O5'-PA-O3A
3	A	902	AGS	PB-O3B-PG-O2G
3	A	902	AGS	PB-O3B-PG-O3G
3	B	901	AGS	PB-O3B-PG-O2G
3	B	901	AGS	PB-O3B-PG-O3G
3	B	901	AGS	C5'-O5'-PA-O2A
3	B	901	AGS	C5'-O5'-PA-O3A
3	B	901	AGS	O4'-C4'-C5'-O5'
3	B	901	AGS	C3'-C4'-C5'-O5'
3	B	902	AGS	PB-O3B-PG-O2G
3	B	902	AGS	PB-O3B-PG-O3G
3	C	902	AGS	C5'-O5'-PA-O2A
3	C	902	AGS	C5'-O5'-PA-O3A
3	C	903	AGS	C5'-O5'-PA-O3A

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Mol	Chain	Res	Type	Atoms
3	D	903	AGS	PB-O3B-PG-O2G
3	D	903	AGS	PB-O3B-PG-O3G
3	D	903	AGS	C5'-O5'-PA-O2A
3	E	902	AGS	PB-O3B-PG-O2G
3	E	902	AGS	C5'-O5'-PA-O1A
3	F	901	AGS	C5'-O5'-PA-O1A
3	F	901	AGS	C5'-O5'-PA-O2A
3	F	901	AGS	C5'-O5'-PA-O3A
3	F	902	AGS	C5'-O5'-PA-O1A
3	F	902	AGS	C5'-O5'-PA-O2A
6	F	906	GOL	O1-C1-C2-C3
6	F	907	GOL	C1-C2-C3-O3
3	D	903	AGS	PG-O3B-PB-O1B
6	F	906	GOL	O1-C1-C2-O2
6	F	907	GOL	O2-C2-C3-O3
3	C	903	AGS	C3'-C4'-C5'-O5'
3	B	902	AGS	O4'-C4'-C5'-O5'
3	C	903	AGS	O4'-C4'-C5'-O5'
3	D	902	AGS	O4'-C4'-C5'-O5'
3	B	902	AGS	C3'-C4'-C5'-O5'
3	C	903	AGS	PB-O3A-PA-O1A
3	B	902	AGS	PG-O3B-PB-O1B
3	D	902	AGS	C3'-C4'-C5'-O5'
3	D	902	AGS	C5'-O5'-PA-O3A
3	D	903	AGS	C5'-O5'-PA-O3A
3	E	901	AGS	C5'-O5'-PA-O3A
3	E	902	AGS	C5'-O5'-PA-O3A
3	D	903	AGS	PB-O3A-PA-O2A
3	E	901	AGS	PB-O3A-PA-O1A
3	B	901	AGS	C5'-O5'-PA-O1A
3	C	902	AGS	C5'-O5'-PA-O1A
3	C	903	AGS	C5'-O5'-PA-O1A
3	D	902	AGS	C5'-O5'-PA-O1A
3	D	903	AGS	C5'-O5'-PA-O1A
3	E	901	AGS	C5'-O5'-PA-O2A
3	E	902	AGS	C5'-O5'-PA-O2A
3	C	903	AGS	PG-O3B-PB-O2B
3	B	902	AGS	PA-O3A-PB-O2B
3	F	901	AGS	O4'-C4'-C5'-O5'
3	E	902	AGS	PB-O3B-PG-O3G
3	D	903	AGS	O4'-C4'-C5'-O5'
3	D	903	AGS	C3'-C4'-C5'-O5'

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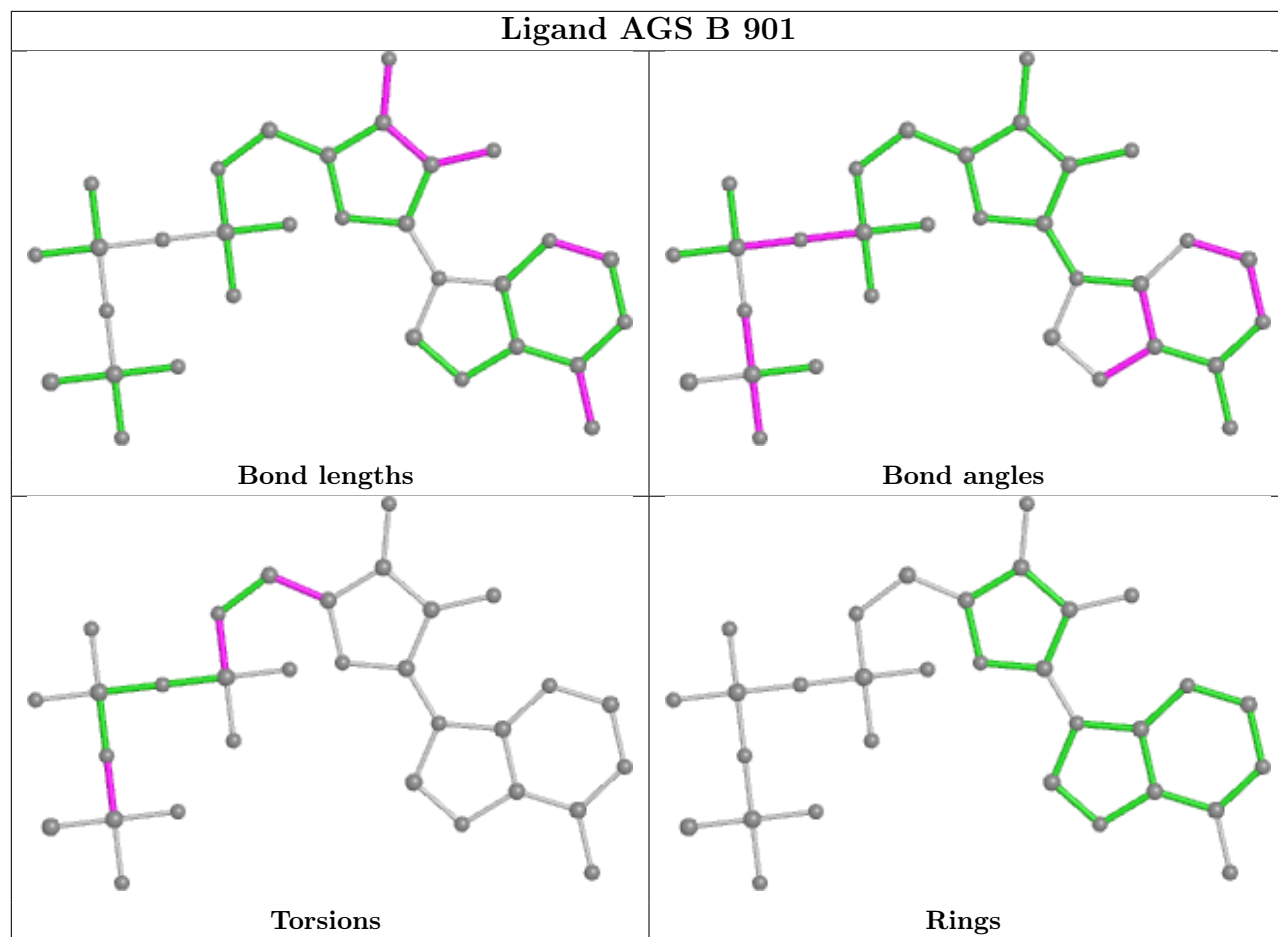
Mol	Chain	Res	Type	Atoms
3	F	902	AGS	PG-O3B-PB-O2B
3	F	902	AGS	C5'-O5'-PA-O3A
3	A	902	AGS	PA-O3A-PB-O2B
3	B	902	AGS	PA-O3A-PB-O1B
3	C	902	AGS	PB-O3A-PA-O2A
3	C	903	AGS	PB-O3A-PA-O2A
3	E	901	AGS	PB-O3A-PA-O2A
3	E	902	AGS	PB-O3A-PA-O1A
3	D	902	AGS	C5'-O5'-PA-O2A
3	E	901	AGS	O4'-C4'-C5'-O5'

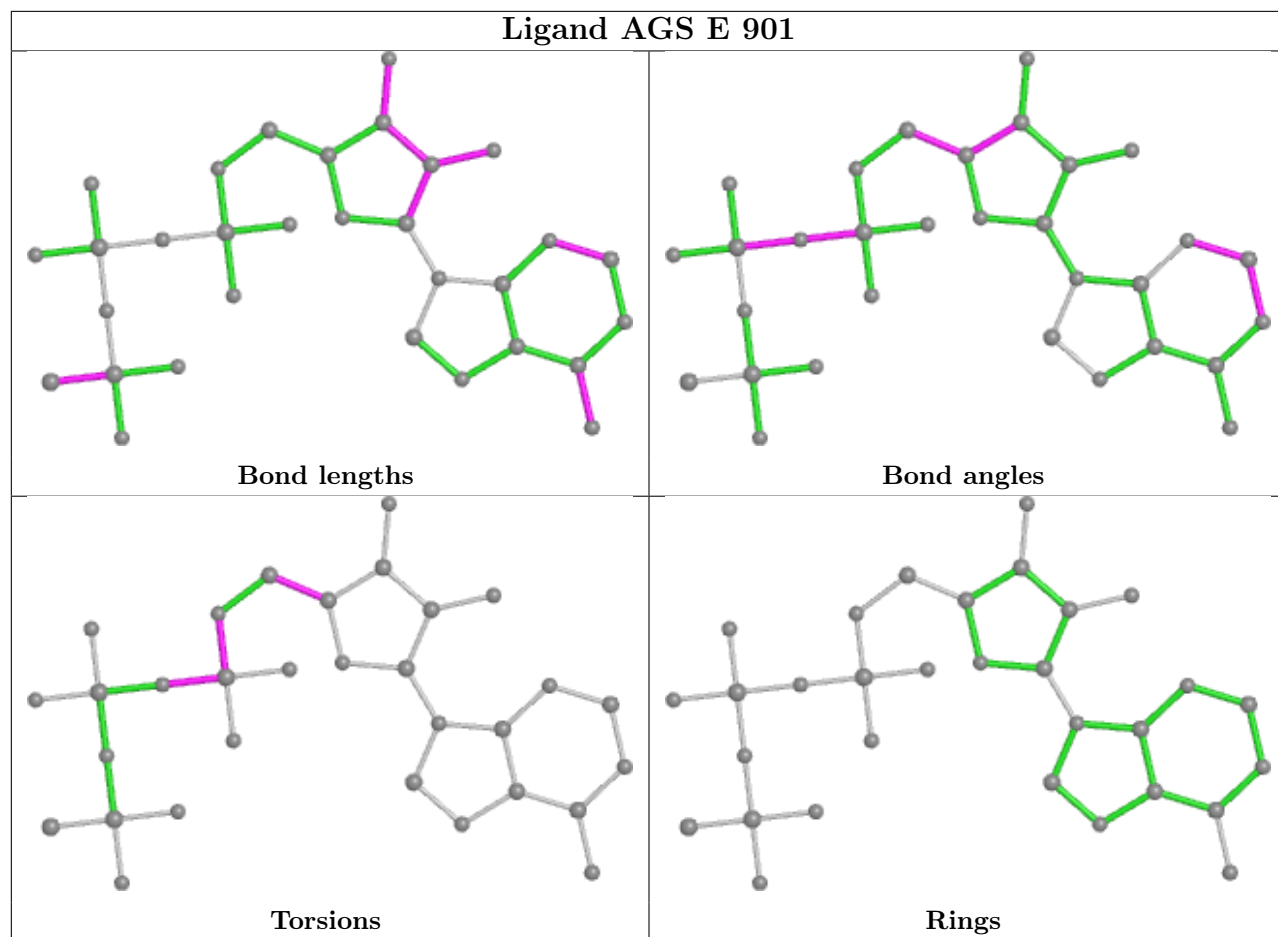
There are no ring outliers.

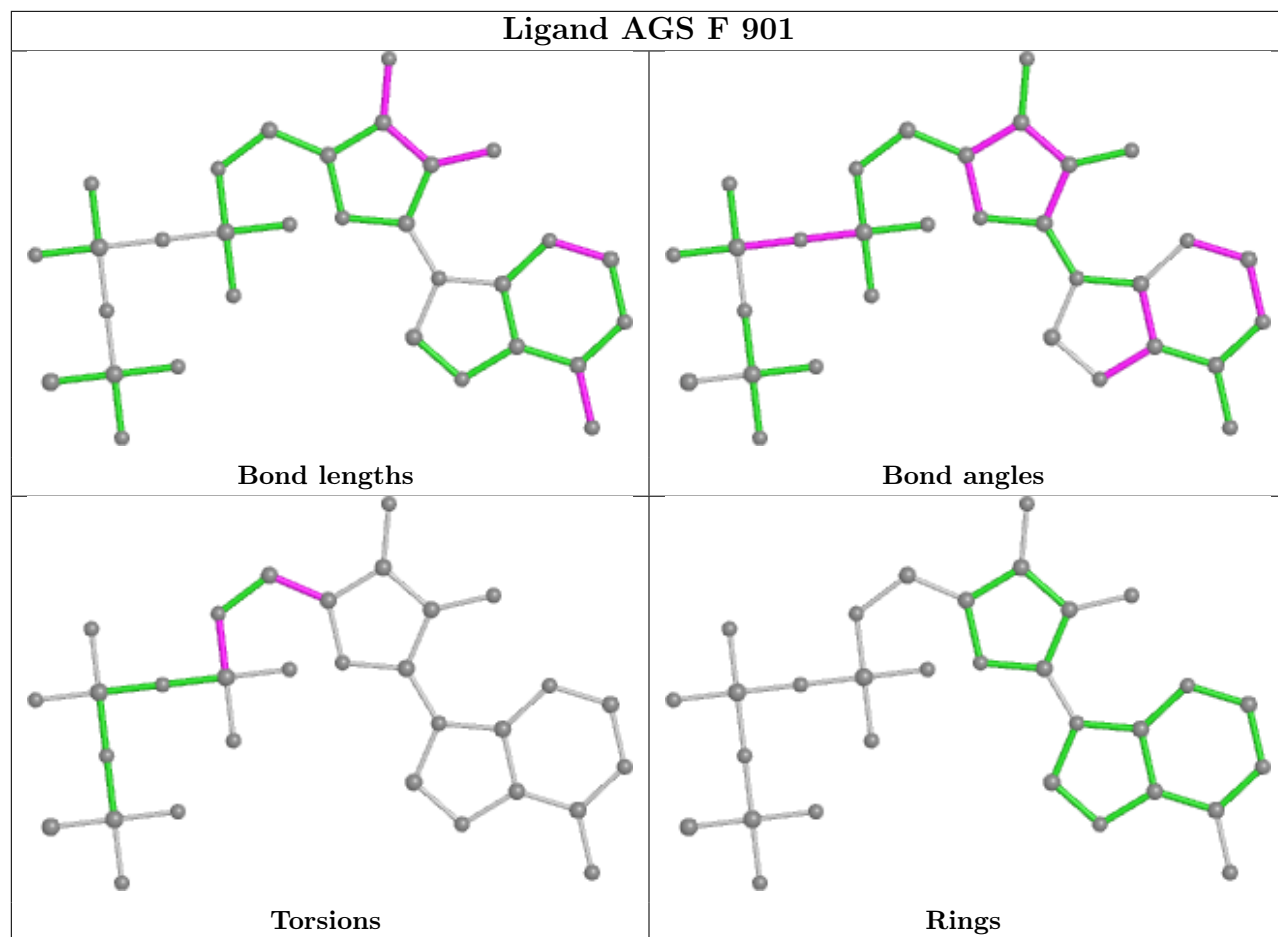
9 monomers are involved in 17 short contacts:

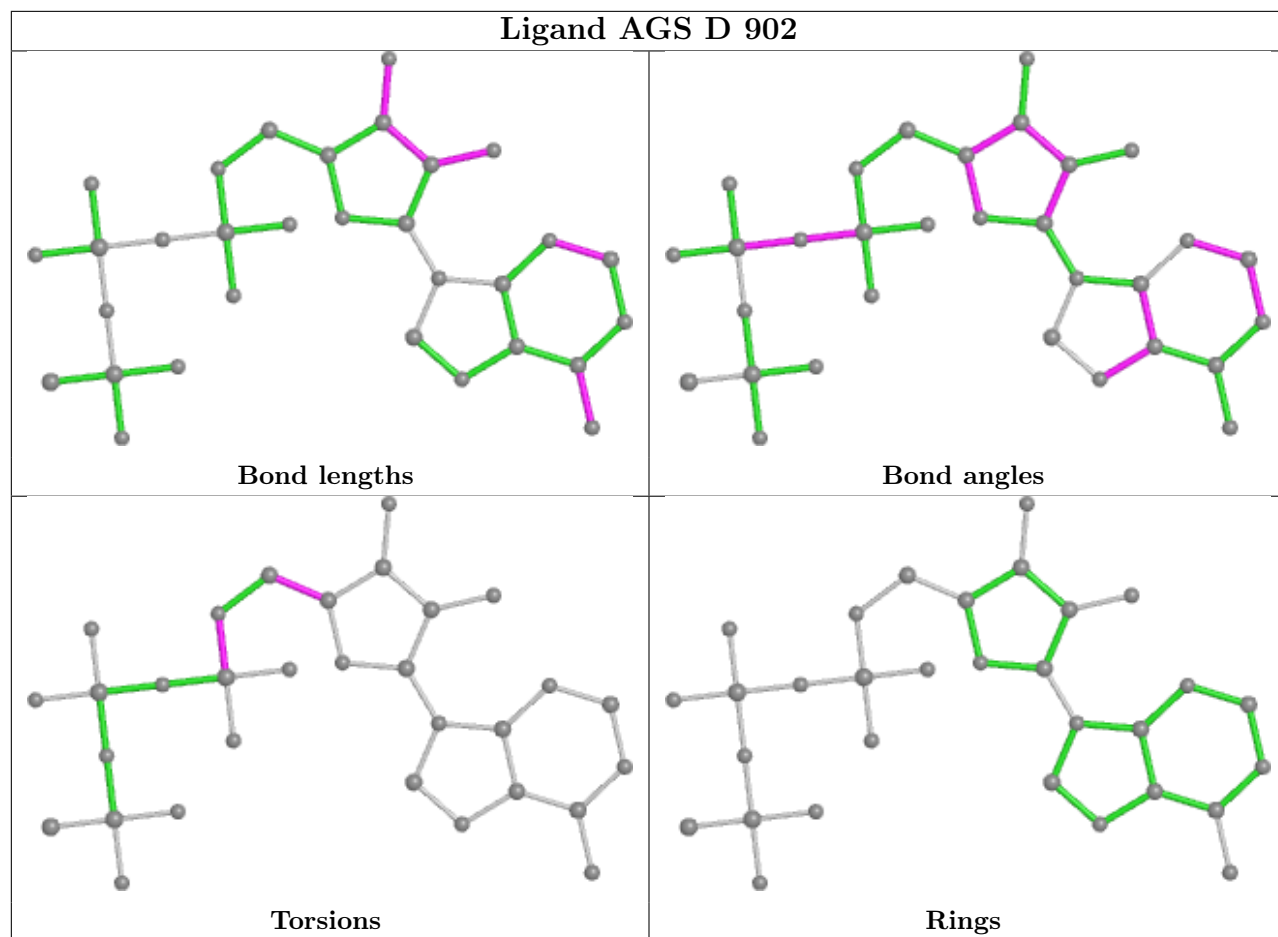
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	E	901	AGS	3	0
3	F	901	AGS	3	0
3	D	902	AGS	1	0
3	C	903	AGS	1	0
3	E	902	AGS	1	0
3	A	901	AGS	4	0
3	F	902	AGS	1	0
3	B	902	AGS	1	0
3	C	902	AGS	2	0

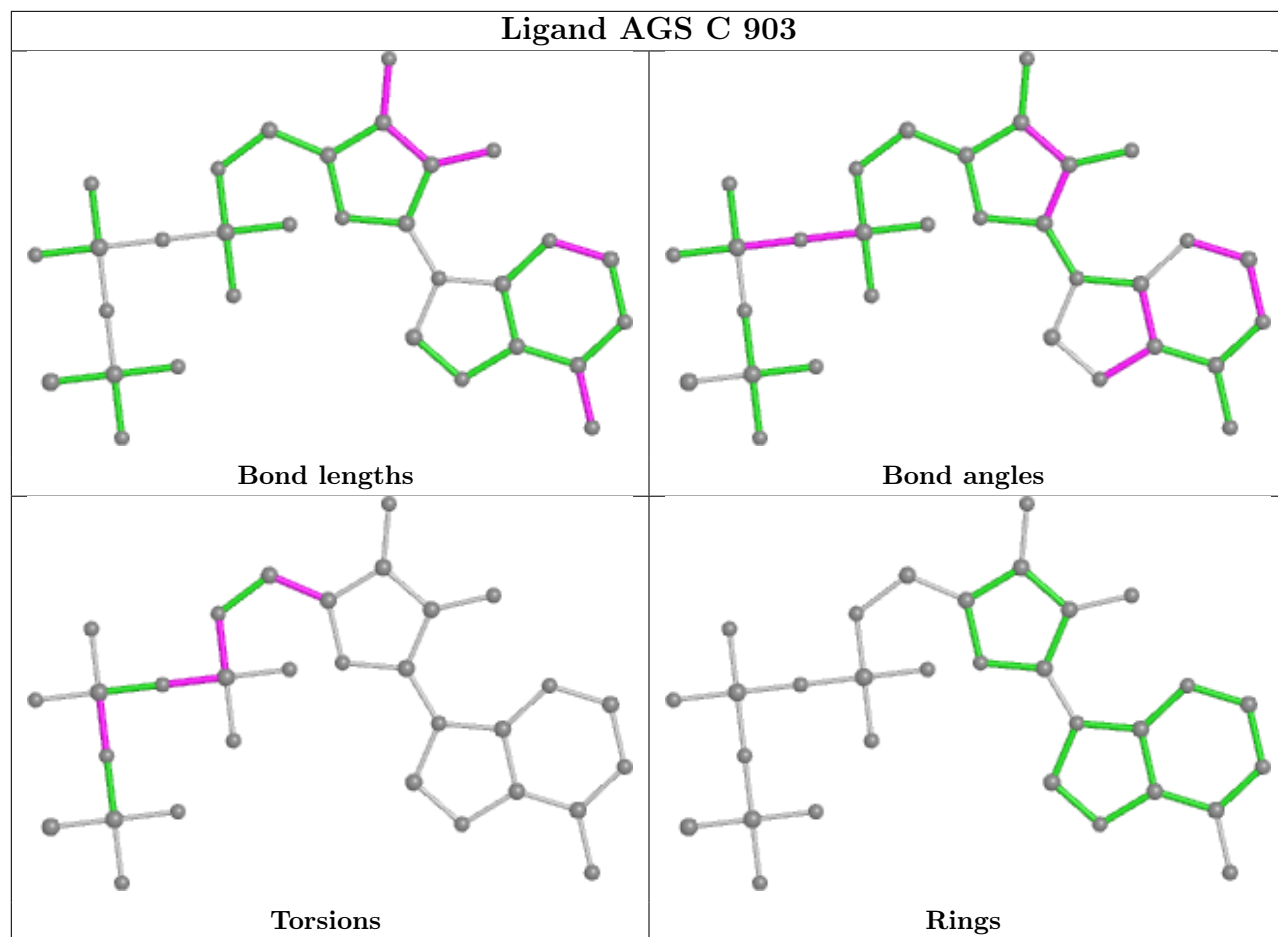
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

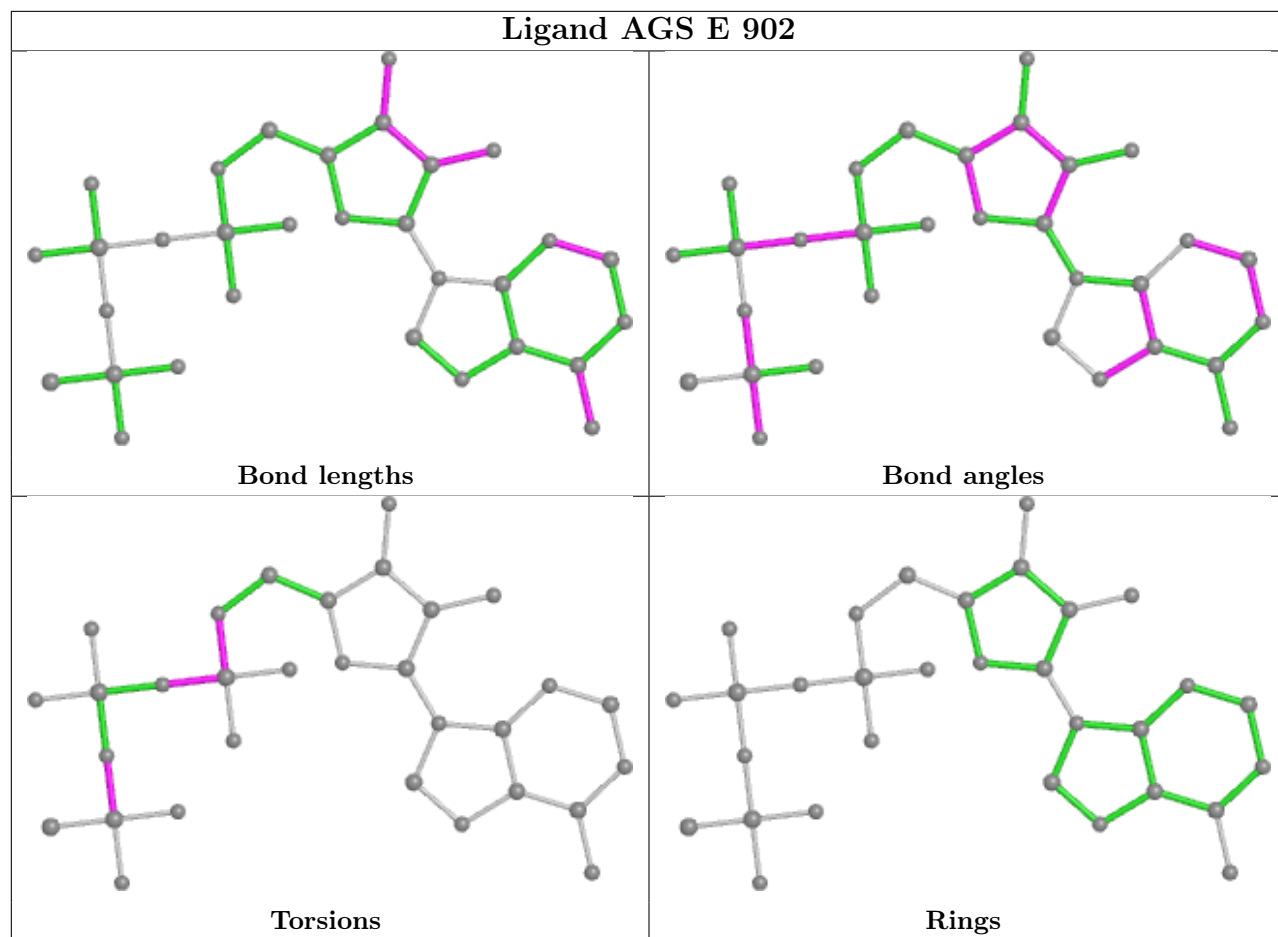


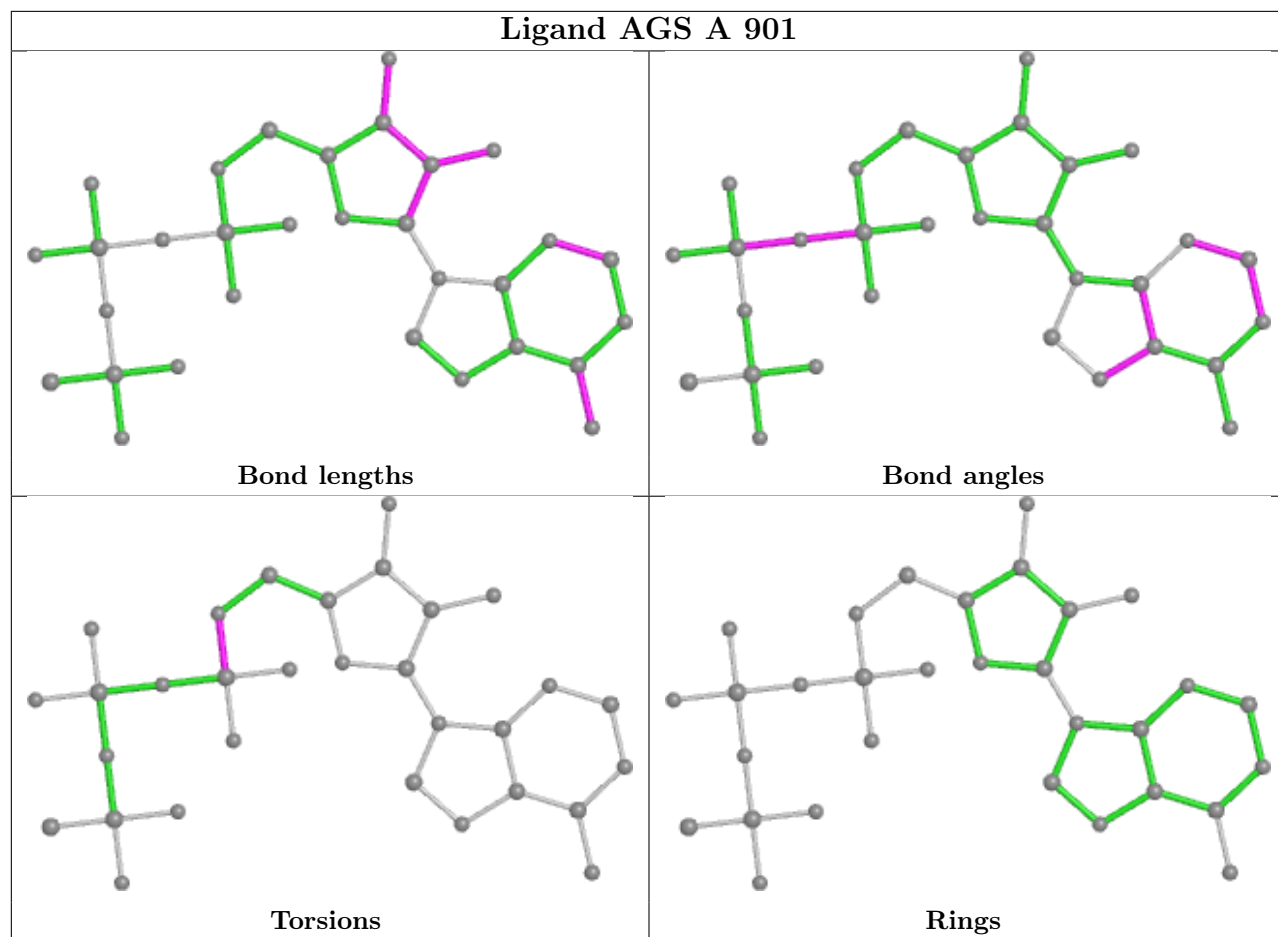


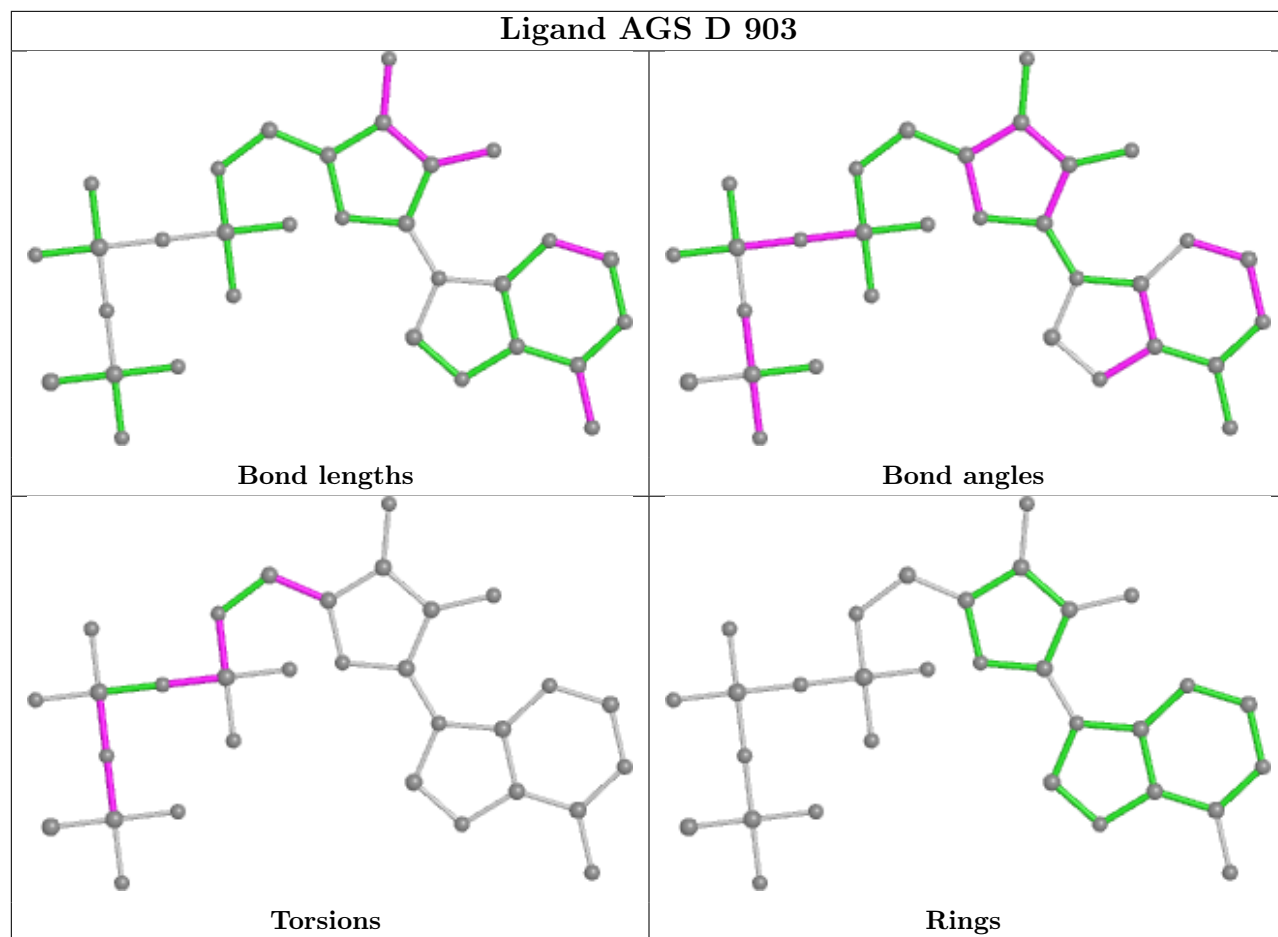


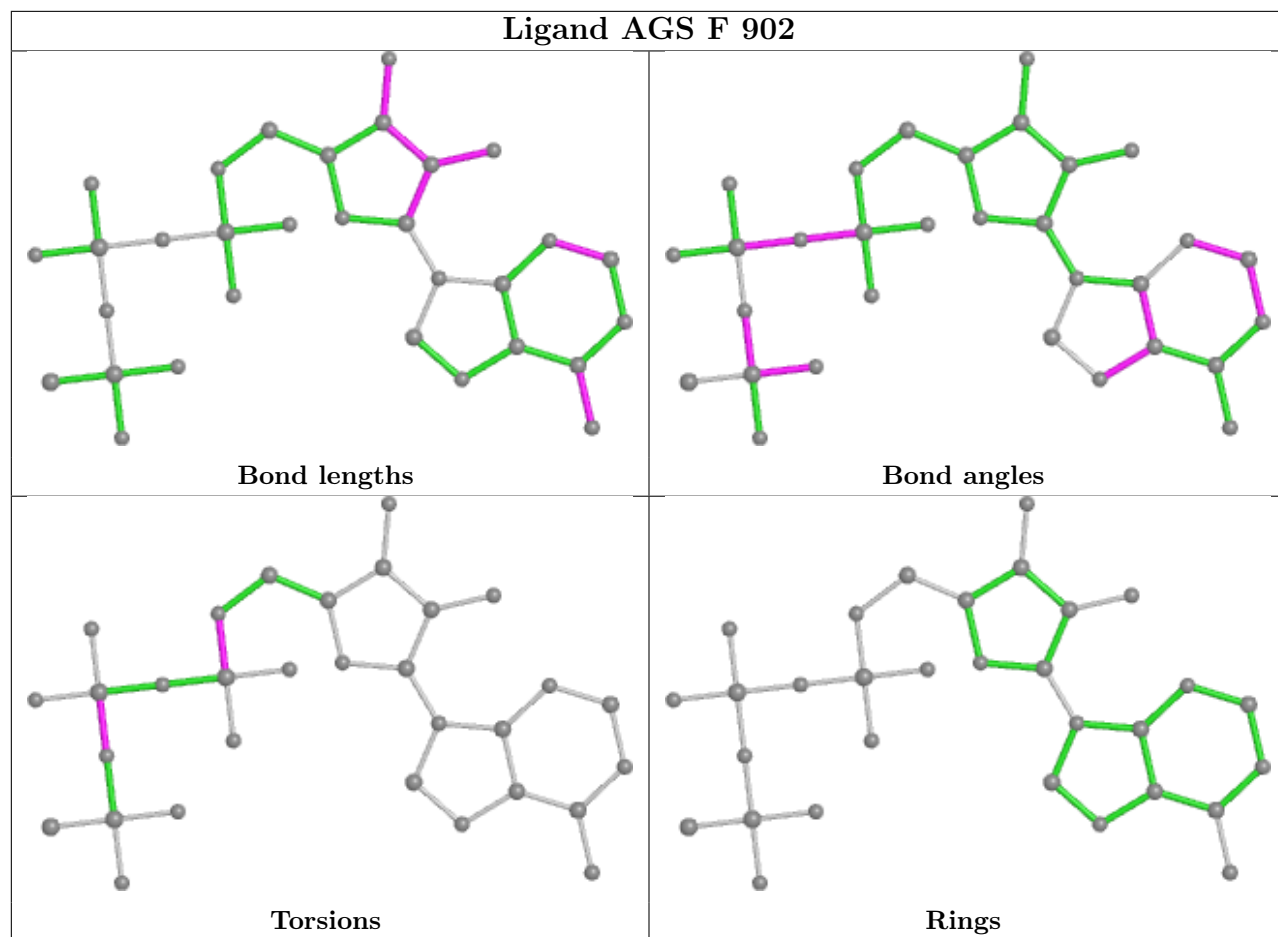


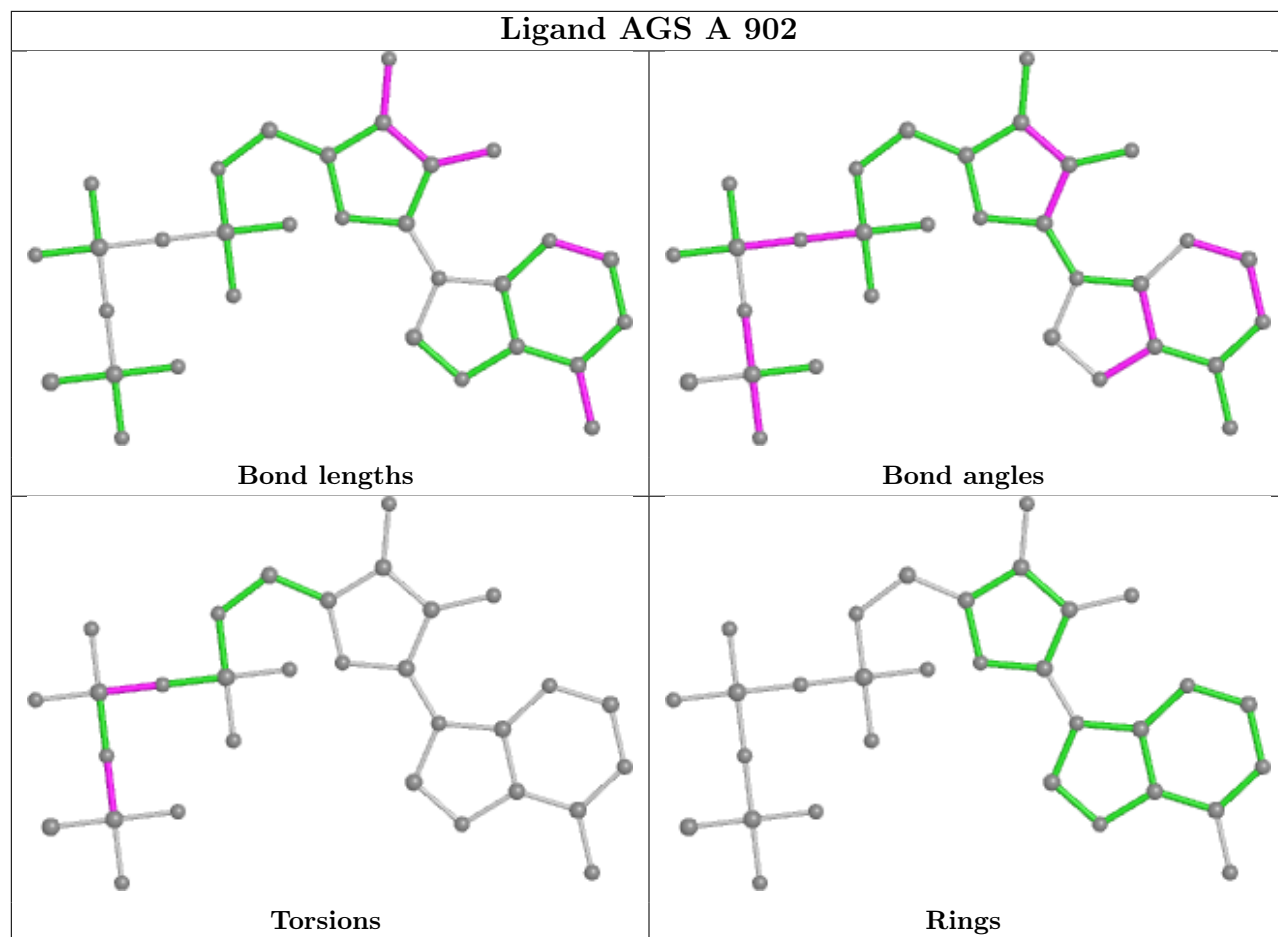


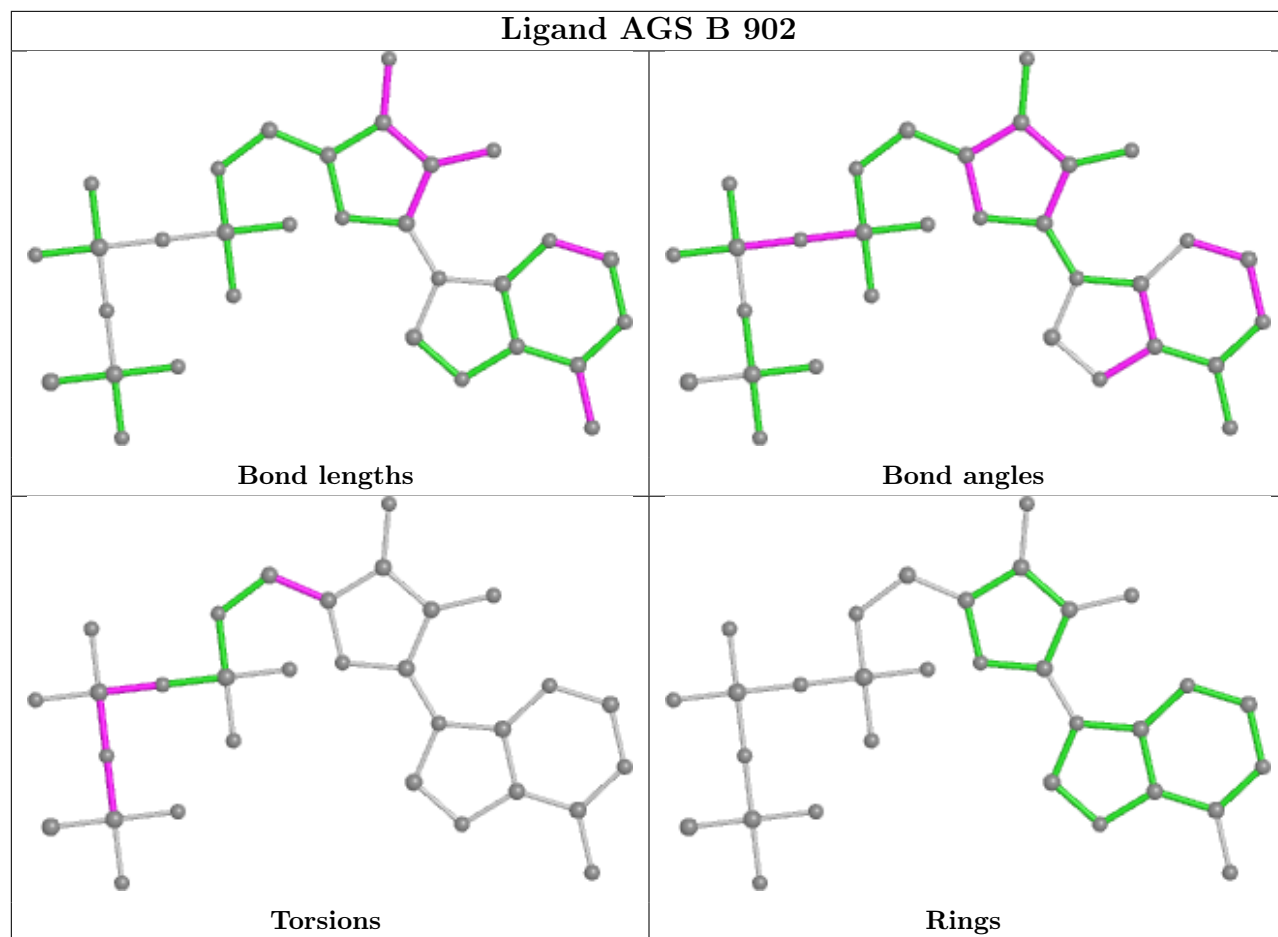


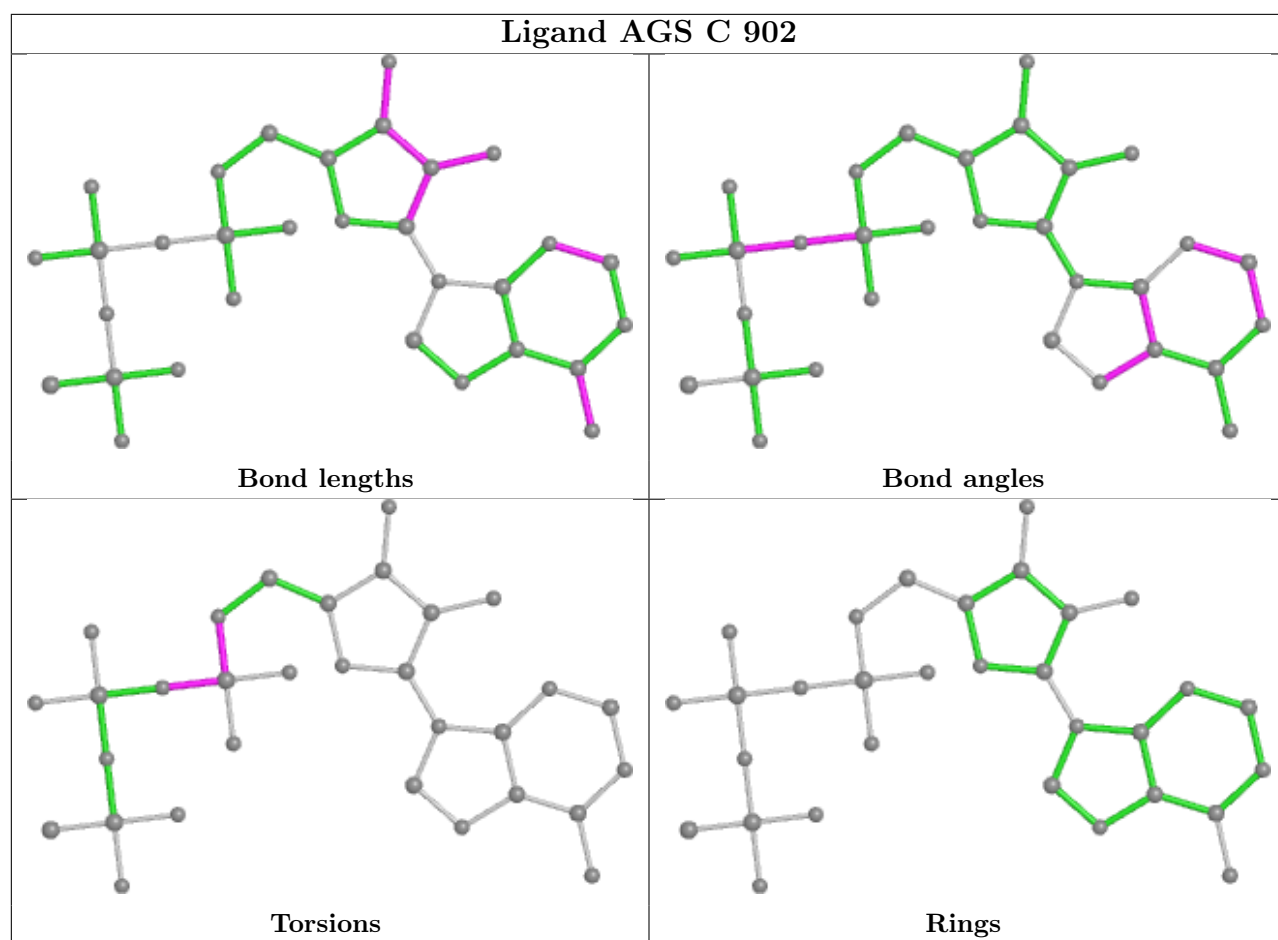












5.7 Other polymers [i](#)

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

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	724/785 (92%)	0.36	30 (4%) 37 18	69, 126, 205, 276	0
1	B	724/785 (92%)	0.15	21 (2%) 51 27	66, 118, 184, 264	0
1	C	724/785 (92%)	0.19	19 (2%) 56 31	55, 121, 199, 301	0
1	D	724/785 (92%)	0.25	35 (4%) 30 14	68, 130, 211, 317	0
1	E	724/785 (92%)	0.17	17 (2%) 60 37	75, 121, 192, 287	0
1	F	724/785 (92%)	0.52	70 (9%) 7 2	68, 131, 258, 320	0
2	U	10/21 (47%)	0.80	2 (20%) 1 0	170, 229, 262, 283	0
2	V	11/21 (52%)	1.04	1 (9%) 9 3	167, 186, 232, 328	0
All	All	4365/4752 (91%)	0.28	195 (4%) 33 16	55, 124, 217, 328	0

All (195) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	164	LYS	7.3
1	F	166	VAL	7.1
1	F	116	VAL	6.6
1	F	117	LEU	6.6
1	A	139	PHE	5.7
1	F	41	LEU	5.5
1	B	552	PHE	5.4
1	F	43	GLN	5.4
1	F	594	GLY	5.4
1	F	176	VAL	5.4
1	F	173	TYR	5.3
1	F	187	GLU	5.2
1	A	115	HIS	5.1
1	A	176	VAL	5.0
1	A	114	ILE	4.8
1	F	130	LEU	4.6

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Mol	Chain	Res	Type	RSRZ
1	C	587	GLY	4.5
1	B	587	GLY	4.4
1	F	172	PRO	4.4
1	F	179	ASP	4.3
1	F	452	PHE	4.3
1	F	134	TYR	4.3
2	V	234	ARG	4.1
1	B	102	ILE	4.1
1	F	104	PRO	4.1
1	A	108	VAL	4.1
1	B	551	TRP	4.0
1	D	436	THR	4.0
1	A	184	CYS	3.9
1	A	50	GLN	3.8
1	D	186	GLY	3.8
1	E	427	MET	3.8
1	F	125	GLY	3.8
1	F	508	MET	3.8
1	F	174	CYS	3.7
1	F	102	ILE	3.7
1	F	139	PHE	3.7
1	C	23	PRO	3.6
1	D	708	ARG	3.6
1	F	190	LYS	3.6
1	E	668	LYS	3.6
1	F	167	GLU	3.5
1	F	50	GLN	3.5
1	F	23	PRO	3.5
1	F	235	VAL	3.5
1	F	426	LYS	3.5
1	B	46	MET	3.5
1	D	117	LEU	3.4
1	A	708	ARG	3.4
1	D	594	GLY	3.4
1	A	594	GLY	3.3
1	F	168	THR	3.3
1	D	26	LEU	3.3
1	F	46	MET	3.3
1	C	552	PHE	3.3
1	E	587	GLY	3.2
1	F	63	LYS	3.2
1	F	165	VAL	3.2

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Mol	Chain	Res	Type	RSRZ
1	F	115	HIS	3.2
1	D	41	LEU	3.1
1	E	158	MET	3.1
1	F	233	ILE	3.1
1	C	669	ASP	3.1
1	F	169	ASP	3.1
1	F	184	CYS	3.1
1	F	232	ALA	3.0
1	D	187	GLU	3.0
1	A	185	GLU	3.0
1	F	129	ASN	3.0
1	F	436	THR	3.0
1	D	157	GLY	2.9
1	F	131	PHE	2.9
1	C	43	GLN	2.9
1	F	177	ALA	2.9
1	B	103	GLN	2.9
1	C	594	GLY	2.9
1	D	770	SER	2.9
1	B	105	CYS	2.8
1	C	24	ASN	2.8
1	C	703	ILE	2.8
1	D	100	ILE	2.8
1	B	445	LEU	2.8
1	C	670	VAL	2.8
1	B	130	LEU	2.8
1	B	337	GLN	2.7
1	A	164	LYS	2.7
1	A	116	VAL	2.7
1	E	594	GLY	2.7
1	A	130	LEU	2.7
1	A	208	GLY	2.7
1	B	423	ILE	2.7
1	D	82	ILE	2.7
1	A	190	LYS	2.7
1	C	41	LEU	2.7
1	A	187	GLU	2.6
1	F	189	ILE	2.6
1	F	103	GLN	2.6
1	E	432	LEU	2.6
1	F	144	ARG	2.6
1	C	428	ASP	2.6

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Mol	Chain	Res	Type	RSRZ
1	F	188	PRO	2.6
1	A	193	ASP	2.6
1	D	672	LEU	2.6
1	D	39	VAL	2.6
1	A	113	ARG	2.6
1	F	444	SER	2.5
1	F	40	SER	2.5
1	D	134	TYR	2.5
1	E	50	GLN	2.5
1	F	126	ILE	2.5
1	F	194	GLU	2.5
1	C	668	LYS	2.5
1	F	71	VAL	2.5
1	E	130	LEU	2.5
1	D	173	TYR	2.5
1	D	445	LEU	2.5
1	A	141	GLU	2.5
1	F	109	LYS	2.5
1	C	21	ASN	2.5
1	D	133	VAL	2.5
1	F	388	MET	2.4
1	C	50	GLN	2.4
1	F	148	LYS	2.4
1	D	62	LYS	2.4
1	D	25	ARG	2.4
1	A	41	LEU	2.4
1	E	233	ILE	2.4
1	E	445	LEU	2.4
1	A	129	ASN	2.4
1	D	46	MET	2.4
1	D	507	GLY	2.4
1	F	128	GLY	2.4
1	B	437	ILE	2.3
1	A	166	VAL	2.3
1	F	706	GLU	2.3
1	A	117	LEU	2.3
1	C	768	PHE	2.3
1	A	188	PRO	2.3
1	F	460	ASN	2.3
1	C	430	ILE	2.3
1	C	736	PHE	2.3
1	D	554	GLU	2.3

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Mol	Chain	Res	Type	RSRZ
1	F	428	ASP	2.3
1	D	440	GLU	2.3
1	D	438	ASP	2.3
2	U	230	GLY	2.2
1	B	56	THR	2.2
1	D	43	GLN	2.2
1	B	460	ASN	2.2
1	F	44	PRO	2.2
1	B	104	PRO	2.2
1	F	434	ASP	2.2
1	F	47	ASP	2.2
1	D	506	PHE	2.2
1	F	394	VAL	2.2
1	A	51	LEU	2.2
1	C	452	PHE	2.2
1	D	102	ILE	2.2
2	U	227	ALA	2.1
1	E	172	PRO	2.1
1	F	99	VAL	2.1
1	F	114	ILE	2.1
1	A	237	PRO	2.1
1	E	117	LEU	2.1
1	E	672	LEU	2.1
1	B	336	LYS	2.1
1	D	71	VAL	2.1
1	E	71	VAL	2.1
1	D	447	VAL	2.1
1	A	433	GLU	2.1
1	B	452	PHE	2.1
1	F	138	TYR	2.1
1	D	769	GLY	2.1
1	E	736	PHE	2.1
1	D	729	PRO	2.1
1	A	82	ILE	2.1
1	B	133	VAL	2.1
1	F	429	LEU	2.1
1	F	24	ASN	2.1
1	D	505	LYS	2.1
1	C	42	SER	2.1
1	F	42	SER	2.1
1	B	109	LYS	2.0
1	F	199	ASN	2.0

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Mol	Chain	Res	Type	RSRZ
1	A	175	ILE	2.0
1	B	51	LEU	2.0
1	F	135	LEU	2.0
1	D	99	VAL	2.0
1	F	147	ARG	2.0
1	E	23	PRO	2.0
1	A	46	MET	2.0
1	D	158	MET	2.0
1	B	432	LEU	2.0
1	E	708	ARG	2.0
1	F	224	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 monosaccharides 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(Å ²)	Q<0.9
5	CL	C	901	1/1	0.70	0.31	130,130,130,130	0
5	CL	D	901	1/1	0.73	0.31	117,117,117,117	0
4	MG	A	903	1/1	0.78	0.19	243,243,243,243	0
5	CL	E	905	1/1	0.80	0.36	118,118,118,118	0
6	GOL	F	906	6/6	0.81	0.38	108,130,150,155	0
5	CL	A	905	1/1	0.84	0.32	98,98,98,98	0
4	MG	D	905	1/1	0.88	0.28	100,100,100,100	0
4	MG	B	903	1/1	0.89	0.17	139,139,139,139	0
5	CL	B	905	1/1	0.89	0.28	105,105,105,105	0
5	CL	F	905	1/1	0.91	0.36	109,109,109,109	0
3	AGS	F	902	31/31	0.92	0.28	55,88,149,575	0
4	MG	C	904	1/1	0.92	0.29	111,111,111,111	0

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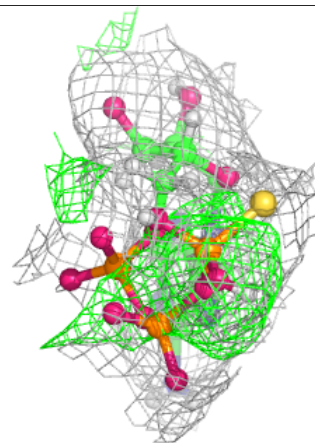
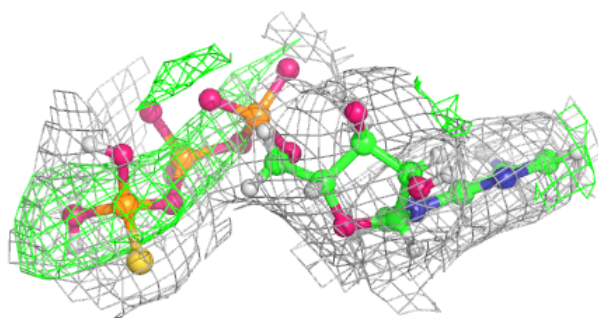
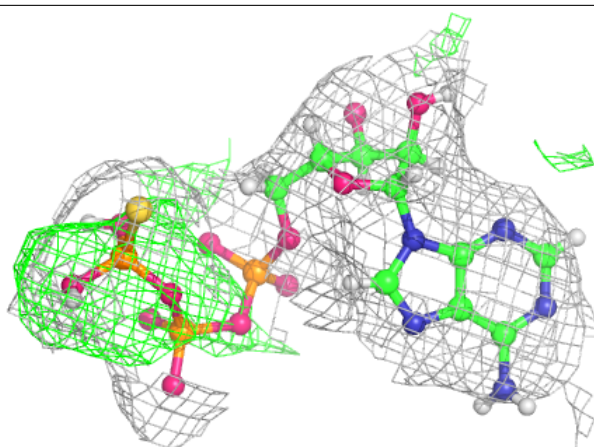
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	AGS	E	902	31/31	0.94	0.23	57,97,116,136	0
3	AGS	F	901	31/31	0.94	0.30	83,125,164,219	0
6	GOL	F	907	6/6	0.94	0.24	92,114,131,144	0
3	AGS	B	902	31/31	0.95	0.23	70,99,130,144	0
4	MG	E	904	1/1	0.95	0.33	100,100,100,100	0
3	AGS	D	903	31/31	0.96	0.23	66,97,120,134	0
4	MG	E	903	1/1	0.96	0.11	115,115,115,115	0
3	AGS	E	901	31/31	0.96	0.18	81,106,140,164	0
4	MG	F	904	1/1	0.96	0.29	70,70,70,70	0
3	AGS	A	902	31/31	0.96	0.24	55,100,134,142	0
3	AGS	B	901	31/31	0.96	0.24	63,101,152,169	0
3	AGS	A	901	31/31	0.96	0.29	71,108,176,255	0
3	AGS	C	902	31/31	0.96	0.30	72,100,145,218	0
3	AGS	C	903	31/31	0.96	0.21	79,114,143,164	0
4	MG	B	904	1/1	0.96	0.28	99,99,99,99	0
3	AGS	D	902	31/31	0.96	0.18	79,106,154,239	0
4	MG	D	904	1/1	0.96	0.10	139,139,139,139	0
4	MG	F	903	1/1	0.97	0.19	199,199,199,199	0
4	MG	C	905	1/1	0.97	0.25	102,102,102,102	0
4	MG	A	904	1/1	0.98	0.29	86,86,86,86	0

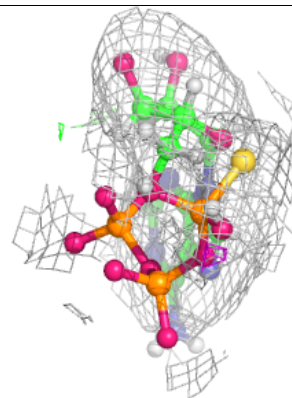
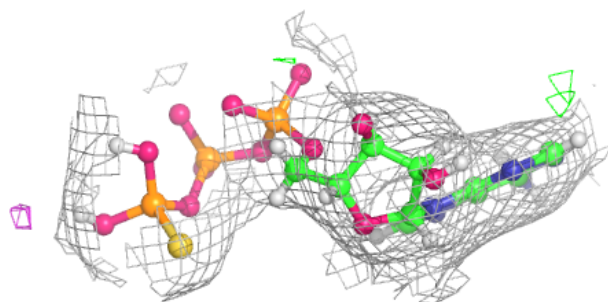
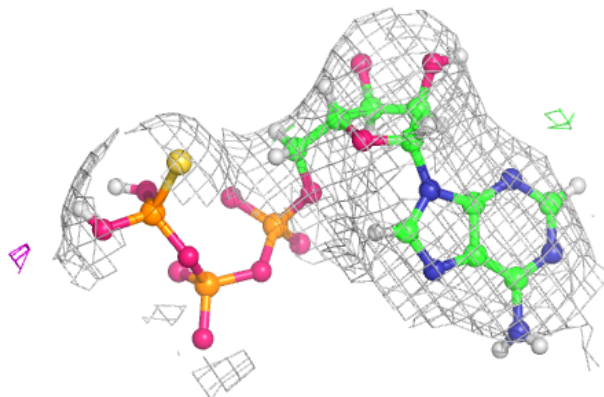
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around AGS F 902:

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

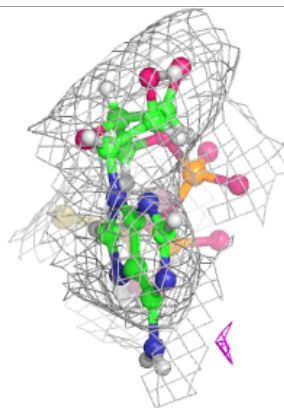
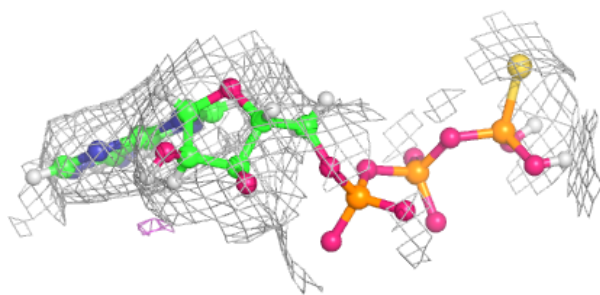
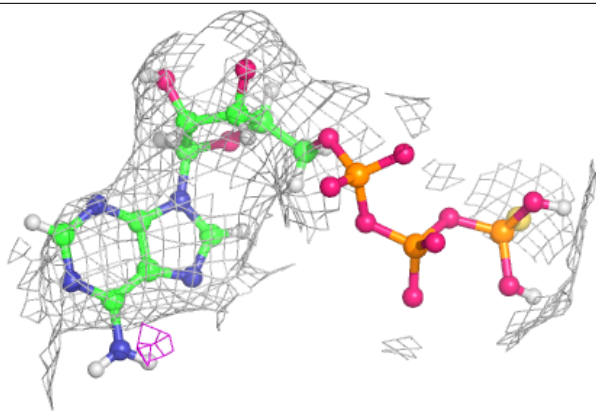
**Electron density around AGS E 902:**

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

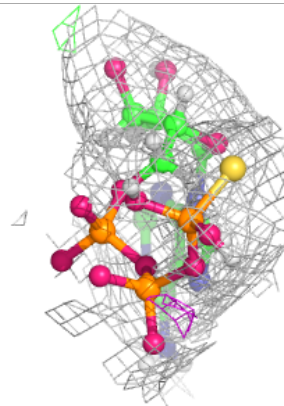
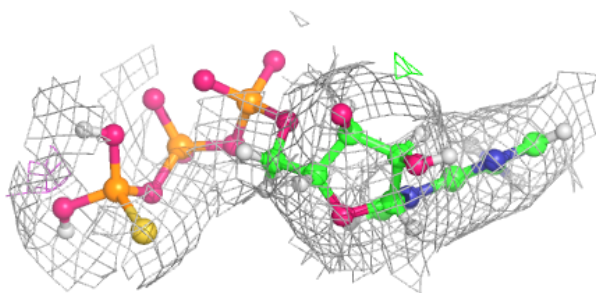
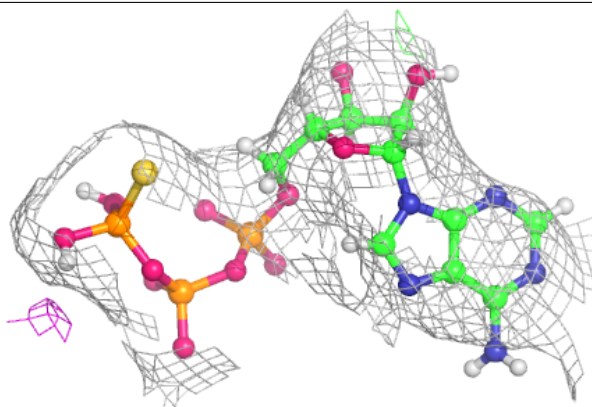


Electron density around AGS F 901:

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

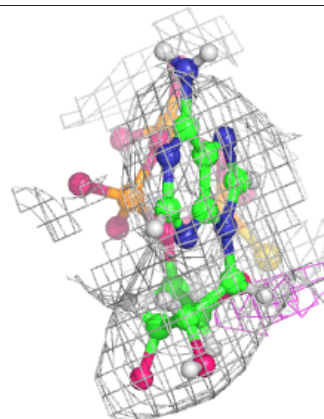
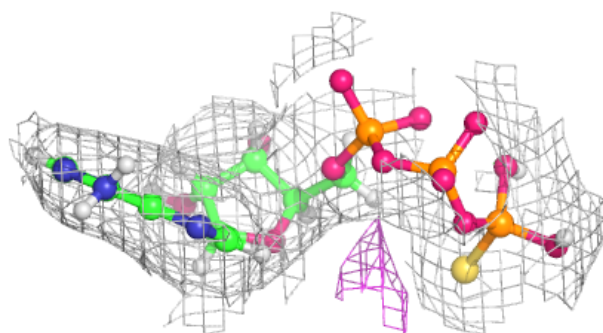
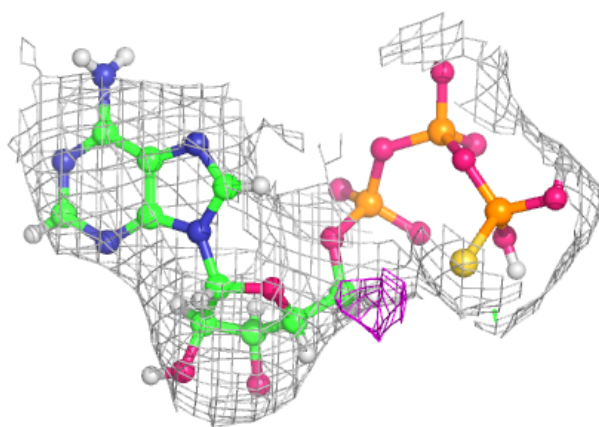
**Electron density around AGS B 902:**

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

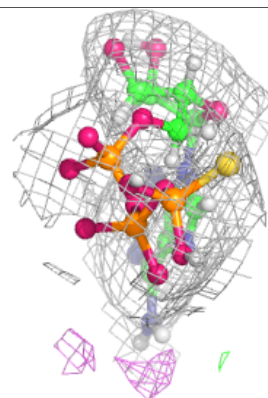
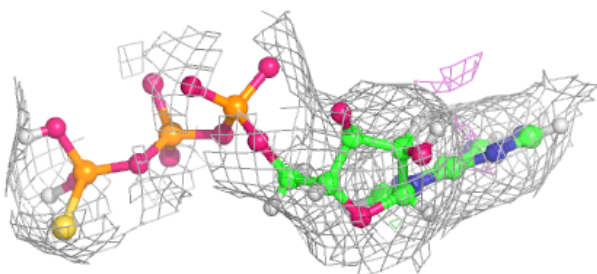
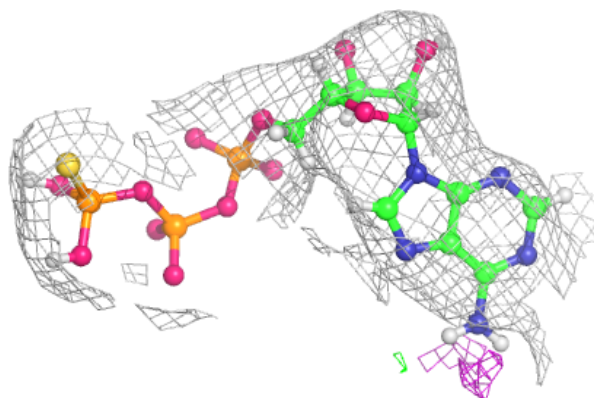


Electron density around AGS D 903:

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

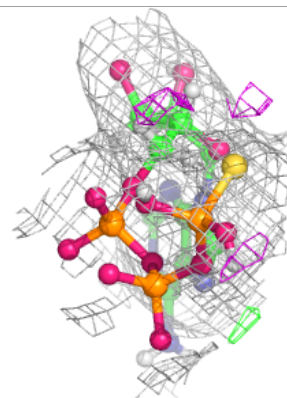
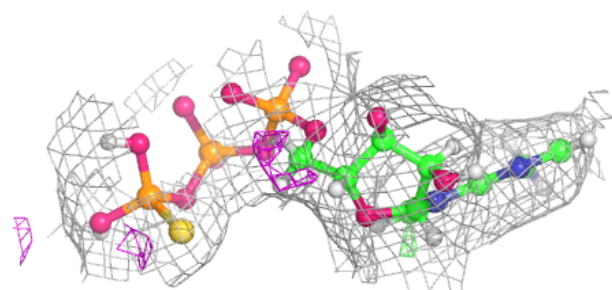
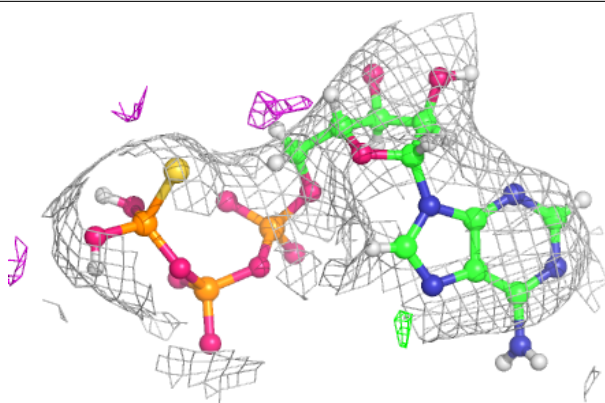
**Electron density around AGS E 901:**

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

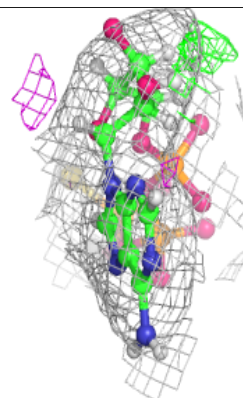
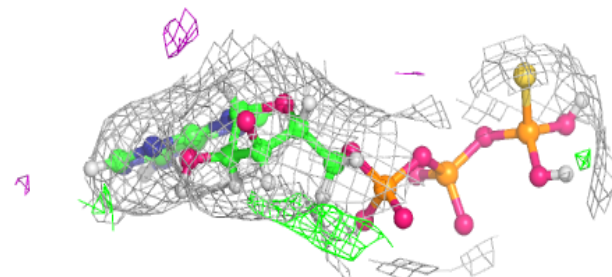
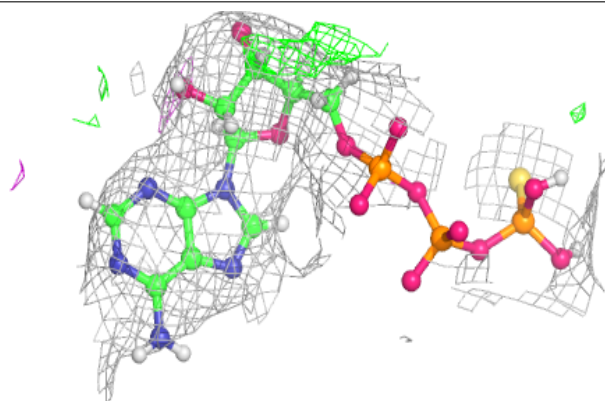


Electron density around AGS A 902:

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

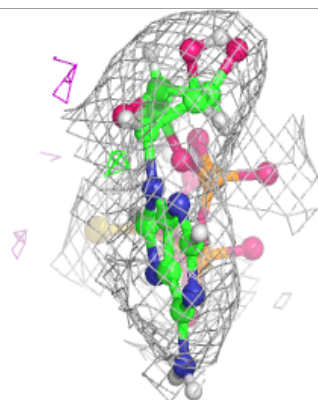
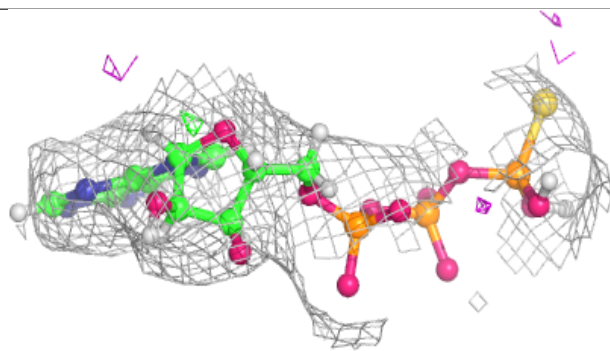
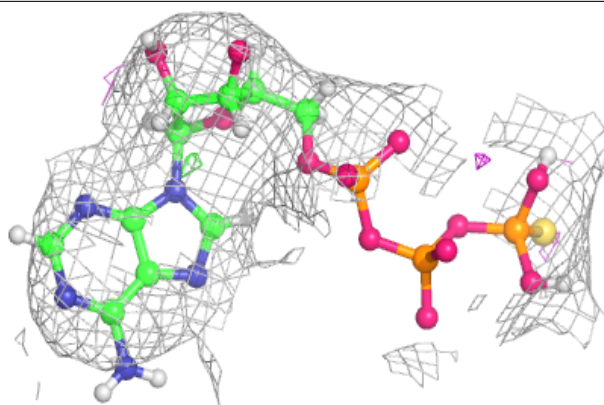
**Electron density around AGS B 901:**

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

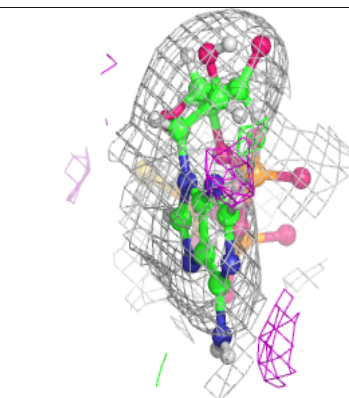
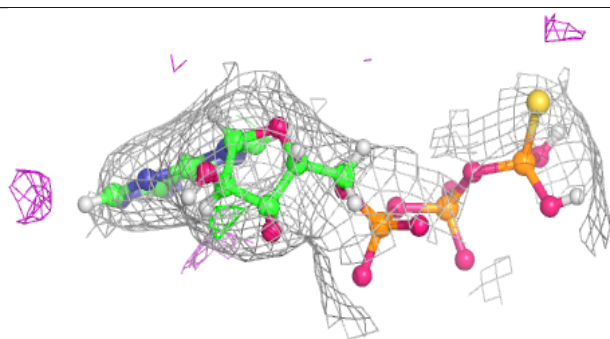
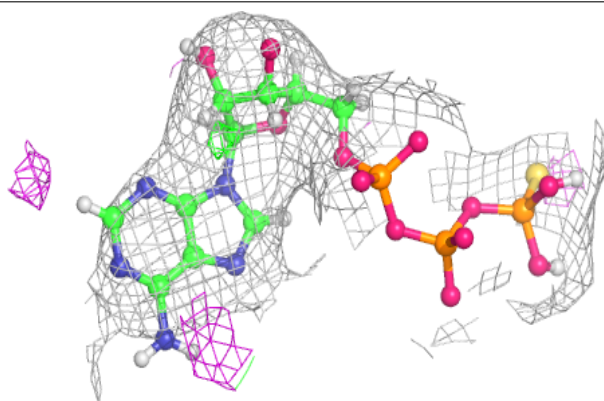


Electron density around AGS A 901:

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

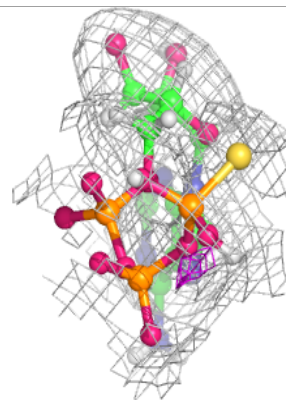
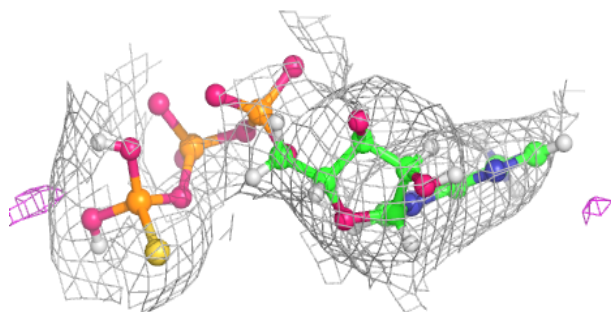
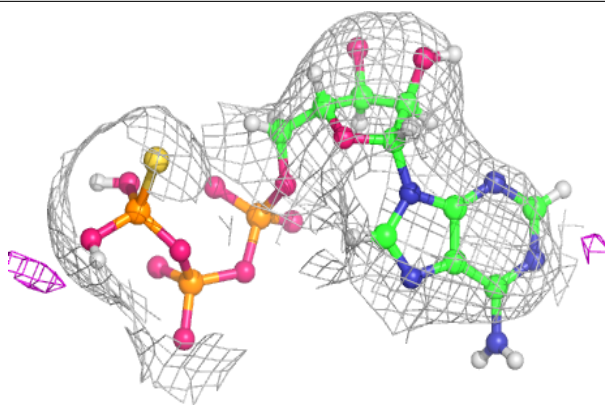
**Electron density around AGS C 902:**

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

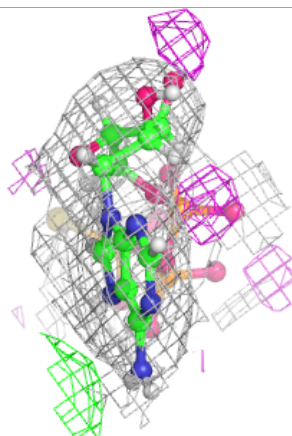
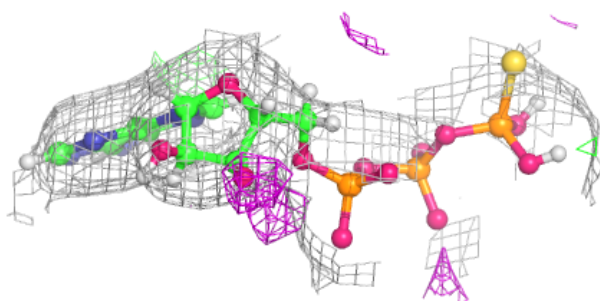
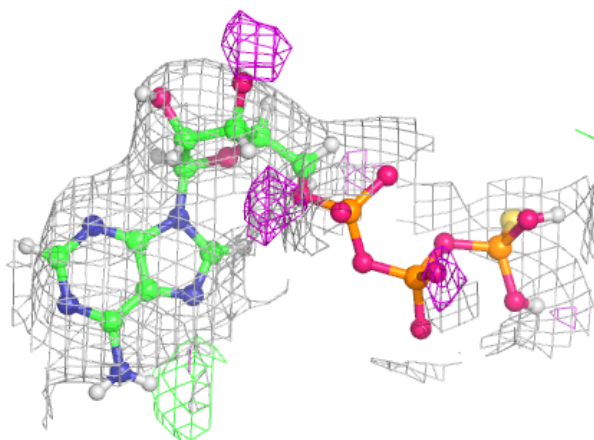


Electron density around AGS C 903:

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

**Electron density around AGS D 902:**

$2mF_o-DF_c$ (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.