



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 25, 2026 – 12:42 PM JST

PDB ID : 9WED / pdb_00009wed
Title : Plasmodium vivax aspartyl-tRNA synthetase in complex with AMP, Asp-AMP, Partially occupied ASP, Mg ion and Butanetriol
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Deposited on : 2025-08-19
Resolution : 2.16 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.015 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.50

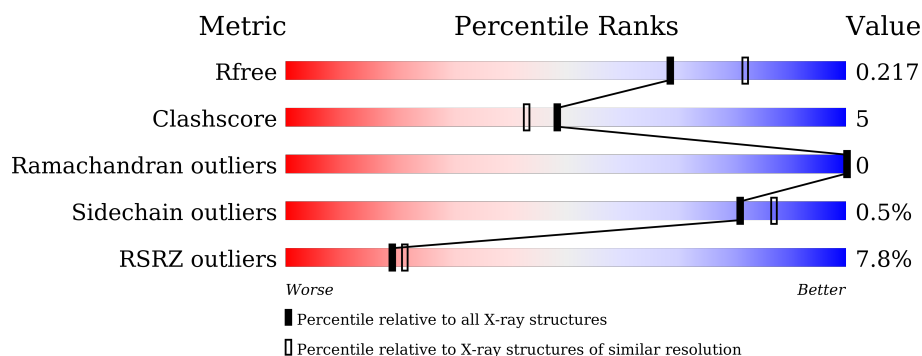
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.16 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	2057 (2.16-2.16)
Clashscore	190562	2159 (2.16-2.16)
Ramachandran outliers	187476	2134 (2.16-2.16)
Sidechain outliers	187428	2133 (2.16-2.16)
RSRZ outliers	180081	2059 (2.16-2.16)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	536	5% 85% 9% 6%
1	B	536	10% 79% 13% 7%

2 Entry composition [i](#)

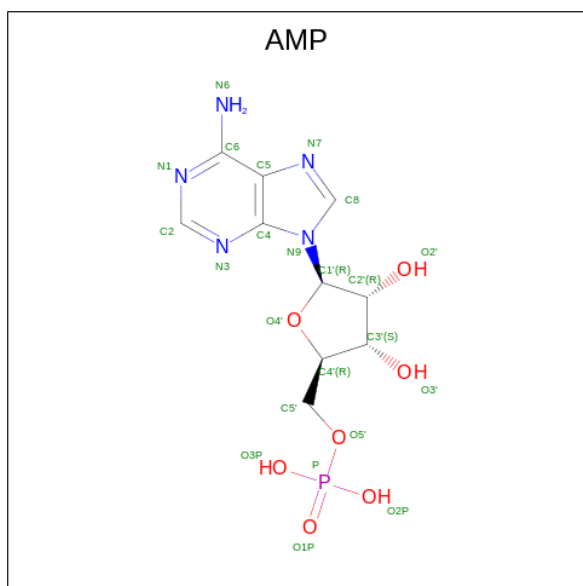
There are 8 unique types of molecules in this entry. The entry contains 8472 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called aspartate-tRNA ligase.

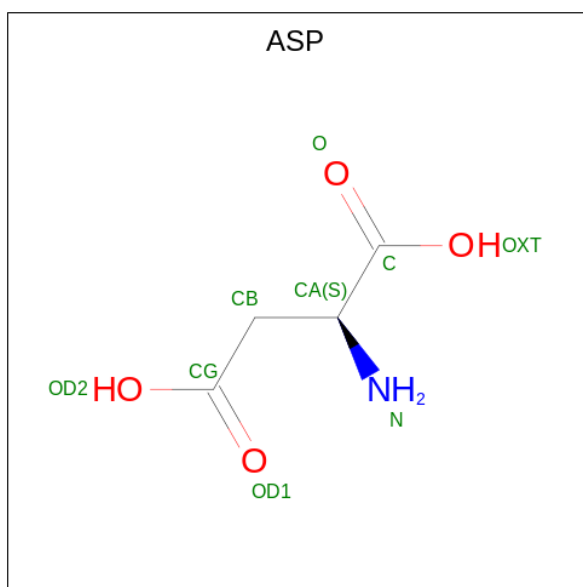
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	503	Total	C	N	O	S	0	1	0
			4055	2602	676	750	27			
1	B	498	Total	C	N	O	S	0	2	0
			3955	2541	655	731	28			

- Molecule 2 is ADENOSINE MONOPHOSPHATE (CCD ID: AMP) (formula: $C_{10}H_{14}N_5O_7P$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			23	10	5	7	1		

- Molecule 3 is ASPARTIC ACID (CCD ID: ASP) (formula: $C_4H_7NO_4$) (labeled as "Ligand of Interest" by depositor).

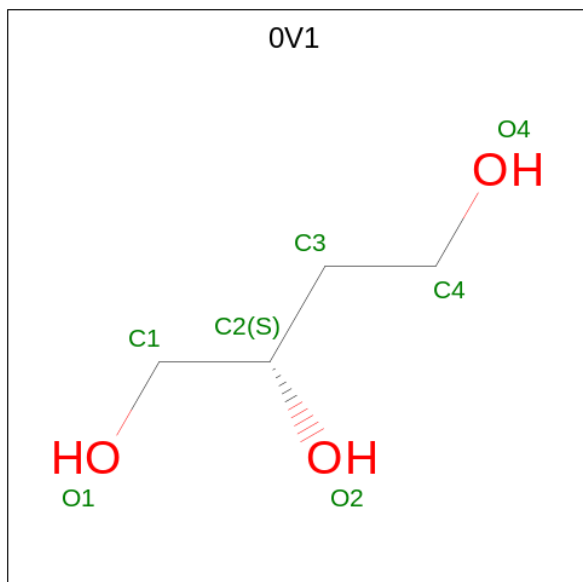


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			6	3	1	2		

- Molecule 4 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

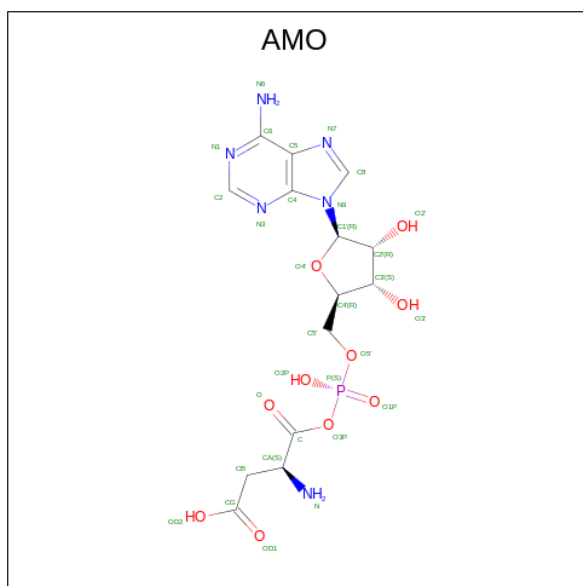
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	3	Total	Cl	0	0
			3	3		
4	B	3	Total	Cl	0	0
			3	3		

- Molecule 5 is (2 {S})-butane-1,2,4-triol (CCD ID: 0V1) (formula: C₄H₁₀O₃).



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

- Molecule 6 is ASPARTYL-ADENOSINE-5'-MONOPHOSPHATE (CCD ID: AMO) (formula: $C_{14}H_{19}N_6O_{10}P$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	B	1	Total C N O P 31 14 6 10 1	0	0

- Molecule 7 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	B	1	Total Mg 1 1	0	0

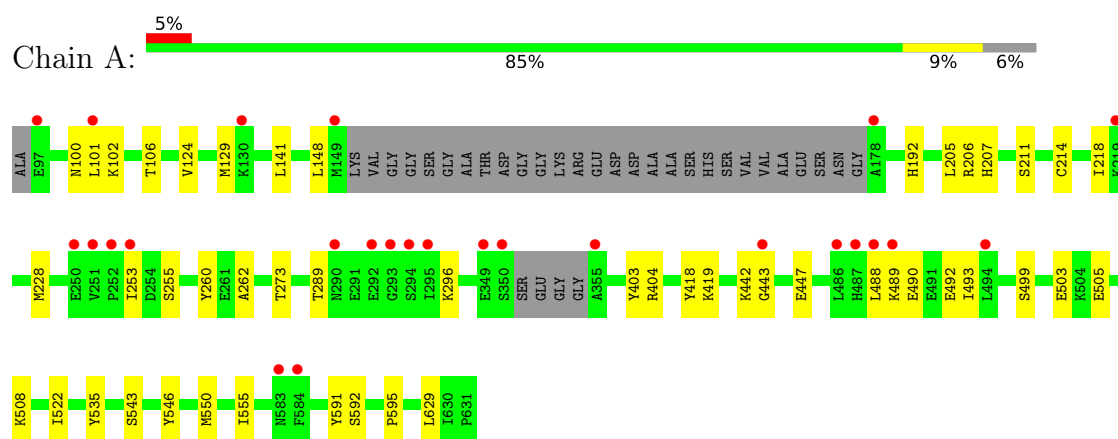
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	190	Total 194	O 194	0	6
8	B	162	Total 166	O 166	0	6

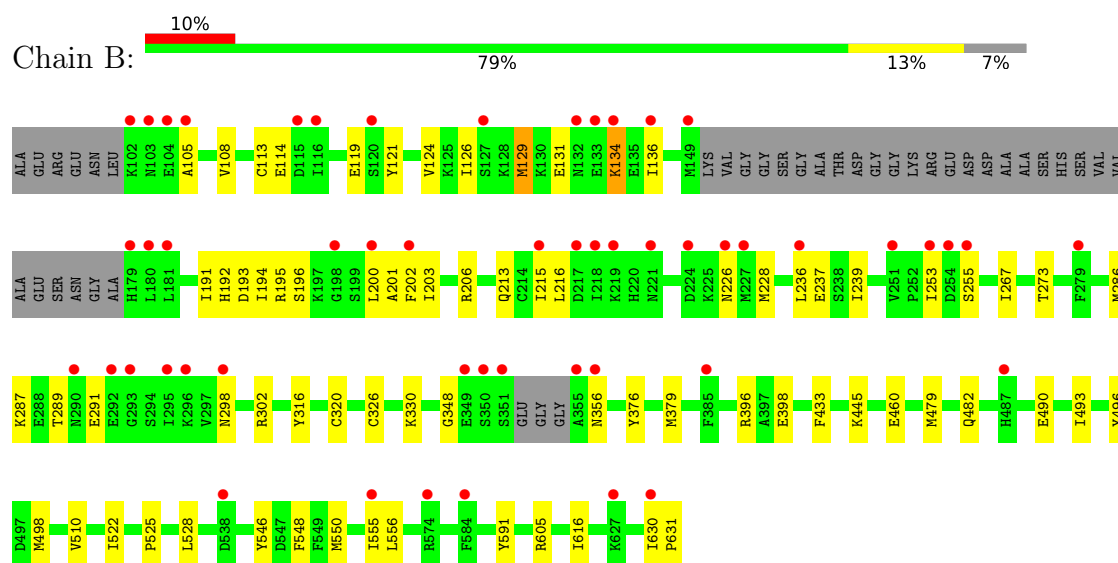
3 Residue-property plots

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: aspartate-tRNA ligase



• Molecule 1: aspartate-tRNA ligase



4 Data and refinement statistics

Property	Value	Source
Space group	P 61 2 2	Depositor
Cell constants a, b, c, α , β , γ	137.91Å 137.91Å 271.74Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	59.72 – 2.16 59.72 – 2.16	Depositor EDS
% Data completeness (in resolution range)	98.7 (59.72-2.16) 98.8 (59.72-2.16)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.34 (at 2.16Å)	Xtriage
Refinement program	PHENIX (1.15rc1_3423: ???)	Depositor
R, R_{free}	0.189 , 0.216 0.193 , 0.217	Depositor DCC
R_{free} test set	3988 reflections (4.84%)	wwPDB-VP
Wilson B-factor (Å ²)	58.4	Xtriage
Anisotropy	0.268	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 63.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	8472	wwPDB-VP
Average B, all atoms (Å ²)	74.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.20% 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: CL, AMP, AMO, 0V1, 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	0.31	0/4146	0.50	0/5598
1	B	0.52	0/4049	0.70	6/5477 (0.1%)
All	All	0.43	0/8195	0.61	6/11075 (0.1%)

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	226	ASN	N-CA-C	-13.42	97.04	113.41
1	B	134	LYS	N-CA-C	10.26	122.92	110.91
1	B	136	ILE	N-CA-C	8.94	121.89	109.55
1	B	289	THR	N-CA-C	8.44	120.56	111.36
1	B	286	MET	N-CA-C	6.07	119.46	110.48
1	B	134	LYS	CB-CA-C	-5.23	103.12	112.27

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	4055	0	3928	34	0
1	B	3955	0	3764	57	0
2	A	23	0	12	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	6	0	2	1	0
4	A	3	0	0	0	0
4	B	3	0	0	0	0
5	A	21	0	0	0	0
5	B	14	0	0	0	0
6	B	31	0	17	0	0
7	B	1	0	0	0	0
8	A	194	0	0	1	0
8	B	166	0	0	2	0
All	All	8472	0	7723	87	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 5.

All (87) 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:B:194:ILE:HD13	1:B:203:ILE:HG12	1.72	0.71
1:B:124:VAL:HG11	1:B:129:MET:SD	2.33	0.69
1:B:196:SER:HB2	1:B:228:MET:CE	2.27	0.65
1:A:102:LYS:O	1:A:106:THR:HG23	1.98	0.64
1:A:591:TYR:HA	1:B:273:THR:HG23	1.80	0.64
1:A:499:SER:O	1:A:503:GLU:HG3	1.98	0.63
1:A:289:THR:H	1:A:296:LYS:HZ1	1.45	0.63
1:B:630:ILE:HG23	1:B:631:PRO:HA	1.79	0.62
1:B:550:MET:SD	1:B:555:ILE:HD13	2.39	0.62
1:A:489:LYS:HB2	1:A:492:GLU:H	1.65	0.61
1:B:194:ILE:CD1	1:B:203:ILE:HG12	2.30	0.61
1:B:201:ALA:HB2	1:B:228:MET:HE3	1.83	0.60
1:B:326:CYS:O	1:B:330:LYS:HG3	2.01	0.60
1:B:196:SER:HB2	1:B:228:MET:HE2	1.82	0.60
1:B:253:ILE:H	1:B:253:ILE:HD12	1.67	0.60
1:B:131:GLU:N	1:B:134:LYS:H	2.04	0.56
1:B:605:ARG:HG2	1:B:616:ILE:HD12	1.88	0.56
1:A:218:ILE:HG23	1:A:228:MET:HE2	1.87	0.55
1:A:443:GLY:O	1:A:447:GLU:HG2	2.08	0.54
1:B:253:ILE:HG22	1:B:255:SER:H	1.72	0.54
1:A:419:LYS:O	1:B:126:ILE:HD11	2.08	0.54
1:B:445:LYS:NZ	8:B:805:HOH:O	2.40	0.53
1:A:591:TYR:O	1:A:592:SER:OG	2.25	0.52
1:B:113:CYS:SG	1:B:114:GLU:N	2.83	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:548:PHE:HB2	1:B:556:LEU:HB3	1.92	0.51
1:B:121:TYR:HA	1:B:267:ILE:O	2.12	0.50
1:B:525:PRO:HG2	1:B:528:LEU:HD12	1.92	0.50
1:B:196:SER:CB	1:B:228:MET:HE2	2.42	0.50
1:B:376:TYR:HA	1:B:379:MET:HE3	1.94	0.50
1:B:291:GLU:HA	1:B:291:GLU:OE1	2.12	0.50
1:B:193:ASP:OD2	1:B:195:ARG:NH1	2.45	0.49
1:B:496:TYR:CE2	1:B:498:MET:HA	2.47	0.49
1:B:298:ASN:O	1:B:302:ARG:HG3	2.12	0.49
1:A:100:ASN:C	1:A:100:ASN:HD22	2.20	0.48
1:B:460:GLU:HG3	8:B:807:HOH:O	2.13	0.48
1:B:356:ASN:ND2	1:B:398:GLU:HG3	2.28	0.48
1:B:433:PHE:CE1	1:B:555:ILE:HD12	2.47	0.48
1:A:522:ILE:HG22	1:A:546:TYR:HB3	1.95	0.47
1:B:124:VAL:CG1	1:B:129:MET:SD	3.02	0.47
1:B:129:MET:HB3	1:B:129:MET:HE3	1.50	0.47
1:B:195:ARG:HB2	1:B:202:PHE:HB2	1.95	0.47
1:B:192:HIS:HB2	1:B:206:ARG:HB2	1.97	0.46
1:A:192:HIS:HB2	1:A:206:ARG:HB2	1.95	0.46
1:A:100:ASN:C	1:A:100:ASN:ND2	2.73	0.46
1:B:201:ALA:HB2	1:B:228:MET:CE	2.45	0.46
1:A:442:LYS:HG2	1:A:443:GLY:N	2.30	0.46
1:A:124:VAL:HG21	1:A:129:MET:SD	2.55	0.45
1:B:105:ALA:O	1:B:108:VAL:HG12	2.17	0.45
1:B:630:ILE:CG2	1:B:631:PRO:HA	2.47	0.45
1:A:289:THR:H	1:A:296:LYS:NZ	2.12	0.44
1:A:205:LEU:O	1:A:211:SER:HA	2.18	0.44
1:B:396:ARG:HB3	1:B:398:GLU:OE1	2.18	0.44
1:A:101:LEU:HA	1:A:101:LEU:HD23	1.78	0.44
1:A:403:TYR:CZ	1:A:404:ARG:HD2	2.52	0.44
1:B:126:ILE:HA	1:B:129:MET:HG3	2.00	0.44
1:B:196:SER:HB2	1:B:228:MET:HE1	1.98	0.44
1:A:488:LEU:HD12	1:A:488:LEU:HA	1.79	0.43
1:B:316:TYR:CZ	1:B:320[A]:CYS:SG	3.11	0.43
1:B:555:ILE:HG13	1:B:556:LEU:N	2.33	0.43
1:A:550:MET:SD	1:A:555:ILE:HD13	2.59	0.43
1:B:253:ILE:HD12	1:B:253:ILE:N	2.33	0.43
1:B:131:GLU:H	1:B:134:LYS:HA	1.84	0.43
1:A:550:MET:SD	1:A:555:ILE:HG21	2.59	0.43
3:A:702:ASP:N	8:A:813:HOH:O	2.52	0.43
1:A:100:ASN:ND2	1:A:100:ASN:O	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:479:MET:HE1	1:B:510:VAL:HG22	2.01	0.42
1:A:214:CYS:HA	1:A:262:ALA:O	2.20	0.42
1:A:141:LEU:HB2	1:A:207:HIS:HB3	2.02	0.42
1:B:522:ILE:HG22	1:B:546:TYR:HB3	2.01	0.42
1:B:200:LEU:HA	1:B:216:LEU:O	2.20	0.42
1:A:273:THR:HG23	1:B:591:TYR:HA	2.02	0.41
1:B:131:GLU:O	1:B:134:LYS:N	2.53	0.41
1:A:418:TYR:CE1	1:A:595:PRO:HB2	2.56	0.41
1:A:535:TYR:HA	1:A:543:SER:HA	2.03	0.41
1:B:213:GLN:OE1	1:B:215:ILE:HD11	2.20	0.41
1:A:629:LEU:HD21	1:B:348:GLY:HA2	2.01	0.41
1:B:126:ILE:HA	1:B:129:MET:CG	2.50	0.41
1:A:490:GLU:HA	1:A:493:ILE:HG13	2.03	0.41
1:A:253:ILE:HG22	1:A:255:SER:H	1.86	0.41
1:B:194:ILE:HD12	1:B:202:PHE:O	2.21	0.41
1:B:479:MET:HA	1:B:482:GLN:HG2	2.03	0.41
1:B:236:LEU:O	1:B:237:GLU:HB2	2.21	0.40
1:A:148:LEU:HD13	1:A:260:TYR:CD2	2.56	0.40
1:B:490:GLU:HG2	1:B:493:ILE:HD12	2.02	0.40
1:A:505:GLU:HA	1:A:508:LYS:HD3	2.03	0.40
1:A:592:SER:HB2	1:B:239:ILE:HG13	2.02	0.40
1:B:191:ILE:HG23	1:B:203:ILE:HG23	2.04	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	498/536 (93%)	484 (97%)	14 (3%)	0	100	100
1	B	494/536 (92%)	474 (96%)	20 (4%)	0	100	100
All	All	992/1072 (92%)	958 (97%)	34 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	438/485 (90%)	438 (100%)	0	100	100
1	B	418/485 (86%)	415 (99%)	3 (1%)	76	82
All	All	856/970 (88%)	853 (100%)	3 (0%)	81	89

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	119	GLU
1	B	129	MET
1	B	287	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	100	ASN
1	A	299	GLN
1	A	305	ASN
1	A	405	HIS
1	B	301	ASN
1	B	371	GLN
1	B	374	GLN
1	B	482	GLN

5.3.3 RNA ⓘ

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 15 ligands modelled in this entry, 7 are monoatomic - leaving 8 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	AMP	A	701	-	25,25,25	1.37	3 (12%)	38,38,38	1.93	7 (18%)
3	ASP	A	702	-	5,5,8	1.03	1 (20%)	5,5,10	0.84	0
5	0V1	A	707	-	6,6,6	0.06	0	4,6,6	0.14	0
5	0V1	A	706	-	6,6,6	0.06	0	4,6,6	0.14	0
5	0V1	B	706	-	6,6,6	0.06	0	4,6,6	0.14	0
5	0V1	B	707	-	6,6,6	0.05	0	4,6,6	0.14	0
5	0V1	A	708	-	6,6,6	0.05	0	4,6,6	0.14	0
6	AMO	B	701	-	31,33,33	0.29	0	44,49,49	0.66	2 (4%)

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	AMP	A	701	-	-	0/10/26/26	0/3/3/3
3	ASP	A	702	-	-	2/3/3/8	-
5	0V1	A	707	-	-	0/5/5/5	-
5	0V1	A	706	-	-	2/5/5/5	-
5	0V1	B	706	-	-	2/5/5/5	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	0V1	B	707	-	-	2/5/5/5	-
5	0V1	A	708	-	-	2/5/5/5	-
6	AMO	B	701	-	-	5/21/39/39	0/3/3/3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	701	AMP	C5-C4	4.77	1.47	1.39
2	A	701	AMP	C5-C6	2.63	1.48	1.41
2	A	701	AMP	C8-N7	2.44	1.36	1.31
3	A	702	ASP	OD2-CG	-2.14	1.23	1.30

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	701	AMP	C5-C4-N3	-6.55	118.20	126.75
2	A	701	AMP	N3-C4-N9	5.22	135.69	127.08
2	A	701	AMP	C2-N3-C4	4.21	121.69	111.75
2	A	701	AMP	N3-C2-N1	-3.29	123.46	128.60
6	B	701	AMO	O-C-CA	2.72	129.92	120.95
2	A	701	AMP	C4-C5-N7	-2.69	107.35	110.62
2	A	701	AMP	C5-N7-C8	2.19	106.62	103.51
6	B	701	AMO	O3P-P-O1P	2.10	115.94	109.45
2	A	701	AMP	C4-N9-C8	2.04	107.94	105.73

There are no chirality outliers.

All (15) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	706	0V1	C1-C2-C3-C4
5	A	706	0V1	O2-C2-C3-C4
5	A	708	0V1	C1-C2-C3-C4
5	A	708	0V1	O2-C2-C3-C4
5	B	706	0V1	C1-C2-C3-C4
5	B	707	0V1	C1-C2-C3-C4
5	B	707	0V1	O2-C2-C3-C4
6	B	701	AMO	CA-CB-CG-OD1
6	B	701	AMO	CA-CB-CG-OD2
6	B	701	AMO	O4'-C4'-C5'-O5'
5	B	706	0V1	O2-C2-C3-C4

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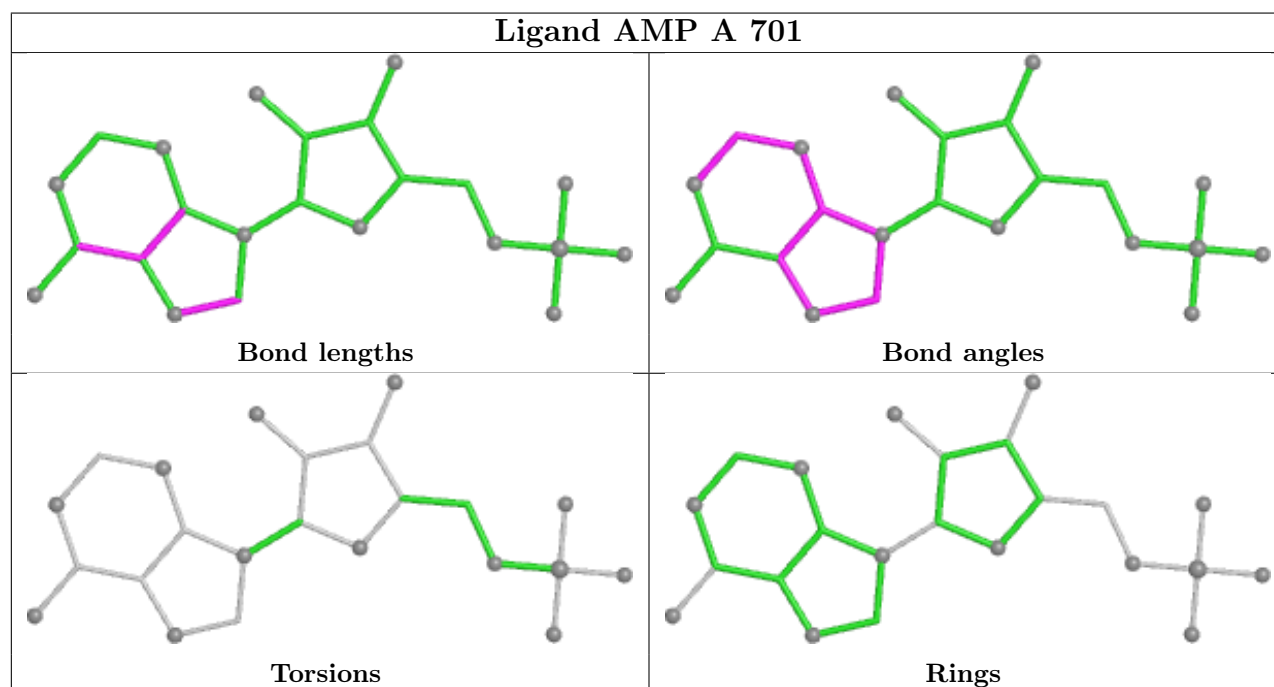
Mol	Chain	Res	Type	Atoms
3	A	702	ASP	CA-CB-CG-OD1
3	A	702	ASP	CA-CB-CG-OD2
6	B	701	AMO	C-O3P-P-O5'
6	B	701	AMO	C3'-C4'-C5'-O5'

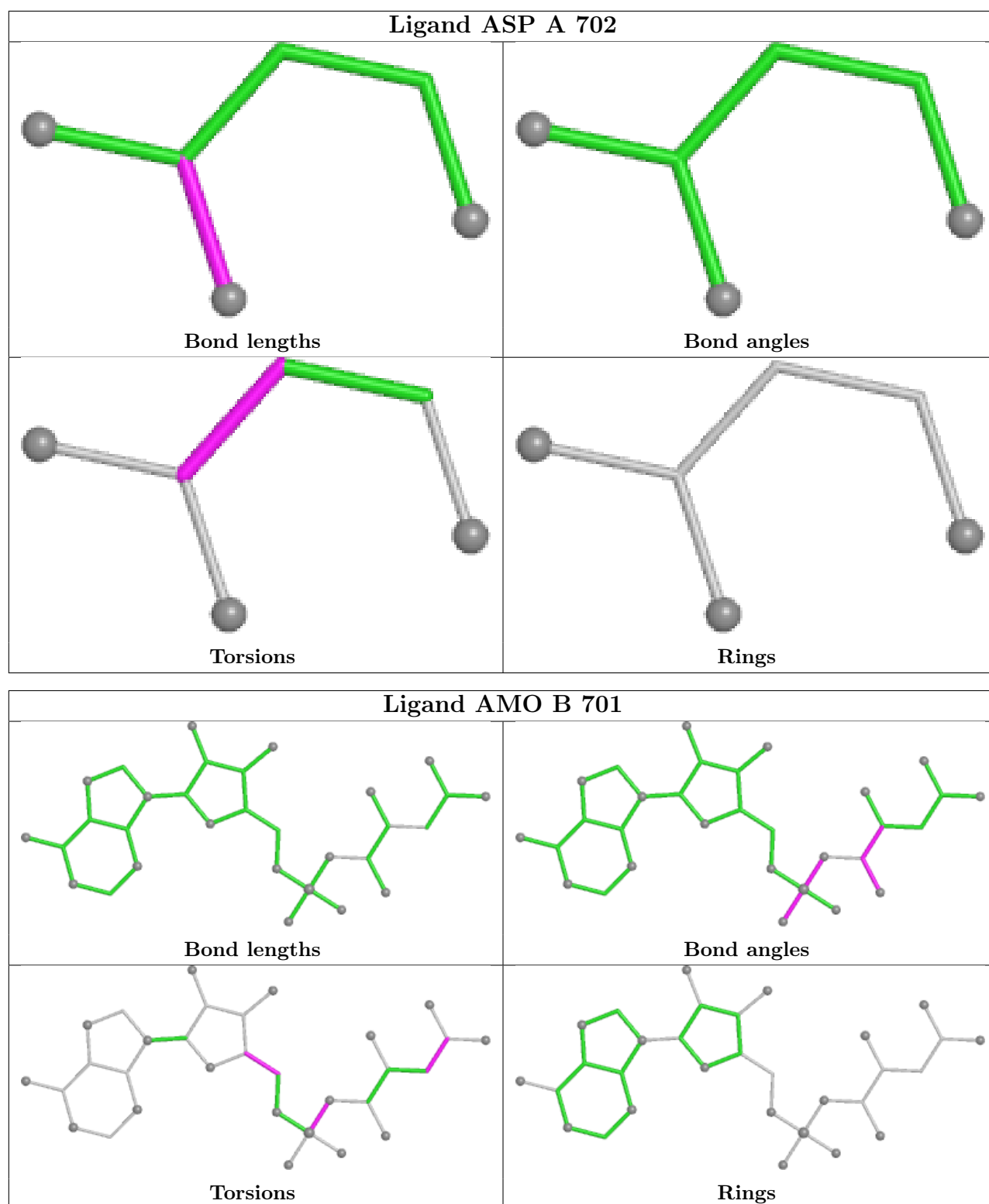
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	702	ASP	1	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 ⓘ

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	503/536 (93%)	0.34	26 (5%)	33 36	38, 66, 112, 172	2 (0%)
1	B	498/536 (92%)	0.60	52 (10%)	11 13	38, 72, 137, 184	4 (0%)
All	All	1001/1072 (93%)	0.47	78 (7%)	19 21	38, 68, 129, 184	6 (0%)

All (78) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	350	SER	9.1
1	B	351	SER	7.6
1	B	349	GLU	6.9
1	B	136	ILE	6.3
1	A	97	GLU	6.0
1	A	487	HIS	5.6
1	A	295	ILE	5.4
1	B	350	SER	5.3
1	B	116	ILE	5.2
1	B	224	ASP	4.9
1	A	584	PHE	4.7
1	B	217	ASP	4.7
1	B	295	ILE	4.6
1	A	355	ALA	4.6
1	B	103	ASN	4.5
1	A	583	ASN	4.4
1	B	253	ILE	4.3
1	B	355	ALA	4.1
1	A	488	LEU	4.1
1	B	179	HIS	4.1
1	B	290	ASN	4.1
1	B	115	ASP	4.1
1	A	494	LEU	3.8
1	A	489	LYS	3.7

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Mol	Chain	Res	Type	RSRZ
1	B	226	ASN	3.6
1	A	349	GLU	3.6
1	A	292	GLU	3.5
1	A	293	GLY	3.4
1	A	290	ASN	3.4
1	B	133	GLU	3.4
1	B	254	ASP	3.4
1	B	102	LYS	3.3
1	B	385	PHE	3.1
1	A	294	SER	3.1
1	B	132	ASN	3.1
1	B	584	PHE	3.0
1	B	215	ILE	3.0
1	A	149	MET	3.0
1	A	178	ALA	2.9
1	A	252	PRO	2.9
1	B	255	SER	2.9
1	B	104	GLU	2.9
1	B	149	MET	2.9
1	A	101	LEU	2.8
1	B	180	LEU	2.8
1	B	221	ASN	2.8
1	A	253	ILE	2.8
1	B	227	MET	2.7
1	B	356	ASN	2.7
1	B	555	ILE	2.7
1	B	202	PHE	2.7
1	A	251	VAL	2.6
1	A	219	LYS	2.6
1	B	134	LYS	2.6
1	B	219	LYS	2.5
1	B	251	VAL	2.5
1	B	293	GLY	2.4
1	B	218	ILE	2.4
1	B	298	ASN	2.4
1	B	630	ILE	2.4
1	B	574	ARG	2.4
1	A	486	LEU	2.3
1	B	181	LEU	2.3
1	B	200	LEU	2.3
1	B	538	ASP	2.3
1	A	130	LYS	2.3

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Mol	Chain	Res	Type	RSRZ
1	B	198	GLY	2.2
1	A	250	GLU	2.2
1	B	487	HIS	2.2
1	B	296	LYS	2.2
1	B	105	ALA	2.1
1	B	120	SER	2.1
1	B	236	LEU	2.1
1	B	279	PHE	2.1
1	B	627	LYS	2.0
1	B	292	GLU	2.0
1	B	127	SER	2.0
1	A	443	GLY	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	ASP	A	702	6/9	0.69	0.24	62,77,86,87	0
5	0V1	A	708	7/7	0.71	0.18	104,105,106,107	7
5	0V1	B	706	7/7	0.82	0.18	94,96,103,104	0
5	0V1	A	706	7/7	0.83	0.13	91,92,94,96	0
5	0V1	A	707	7/7	0.84	0.15	75,81,85,90	0
7	MG	B	702	1/1	0.87	0.09	101,101,101,101	0
5	0V1	B	707	7/7	0.90	0.19	77,81,87,87	7
4	CL	A	704	1/1	0.91	0.15	109,109,109,109	0
4	CL	B	705	1/1	0.91	0.11	90,90,90,90	0
2	AMP	A	701	23/23	0.94	0.08	51,61,78,82	23
4	CL	A	703	1/1	0.94	0.11	89,89,89,89	0

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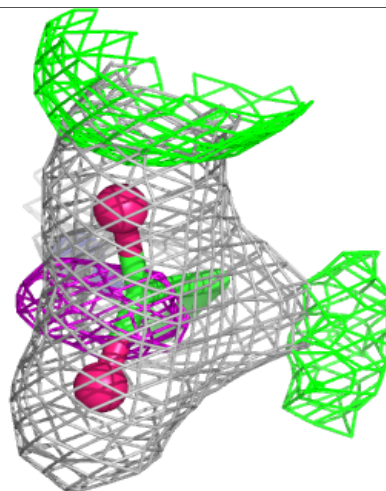
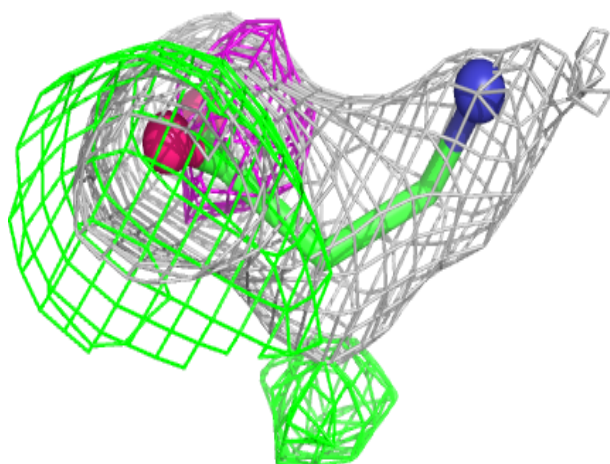
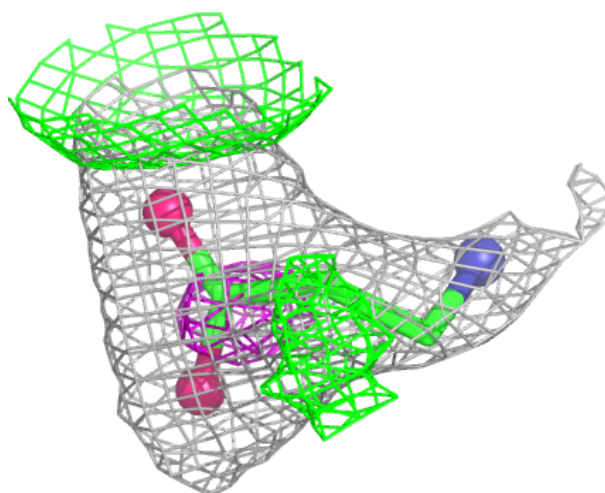
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	CL	B	704	1/1	0.95	0.17	116,116,116,116	0
6	AMO	B	701	31/31	0.95	0.10	52,67,98,102	31
4	CL	B	703	1/1	0.95	0.21	100,100,100,100	0
4	CL	A	705	1/1	0.96	0.19	103,103,103,103	0

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.

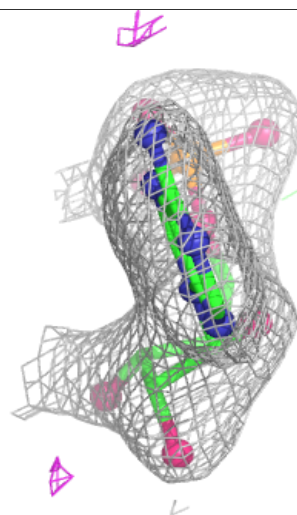
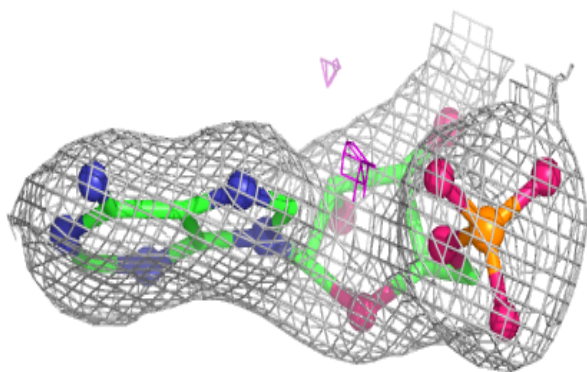
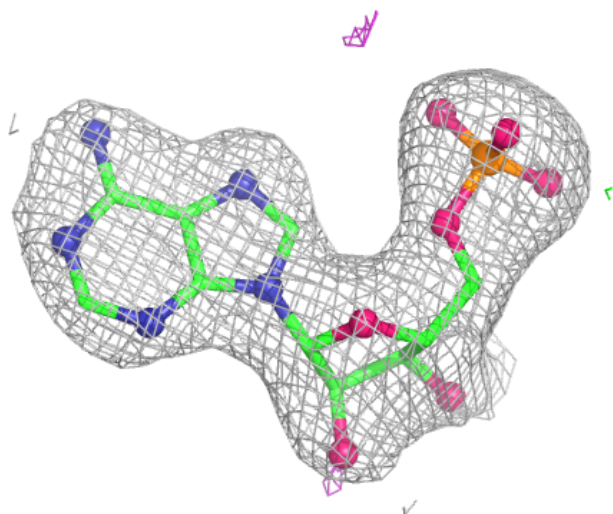
Electron density around ASP A 702:

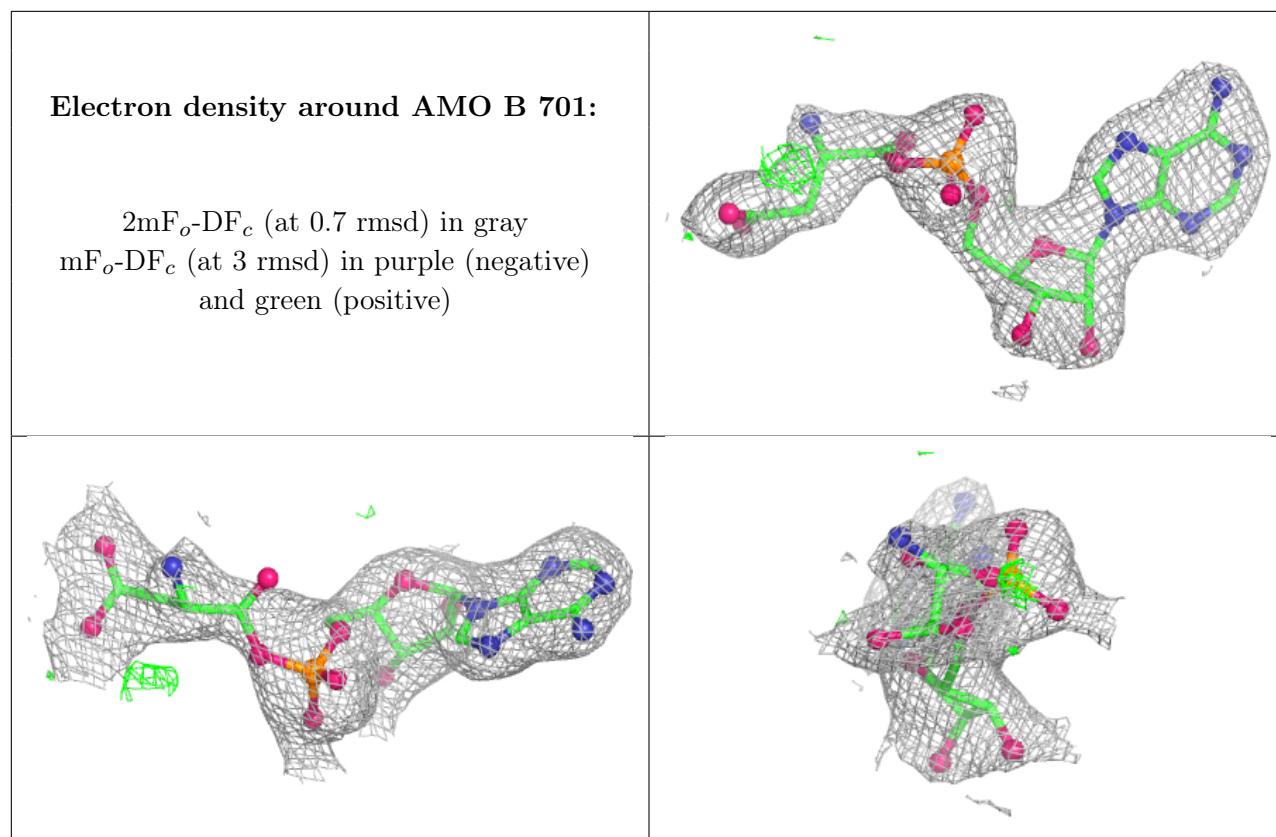
2mF_o-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around AMP A 701:

$2mF_o-DF_c$ (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.