



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 3, 2023 – 10:15 PM EDT

PDB ID : 6PAM
Title : Structure of a bacterial Atm1-family ABC transporter with MgADP bound
Authors : Fan, C.; Kaiser, J.T.; Rees, D.C.
Deposited on : 2019-06-11
Resolution : 3.70 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 : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.35.1
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) : 2.35.1

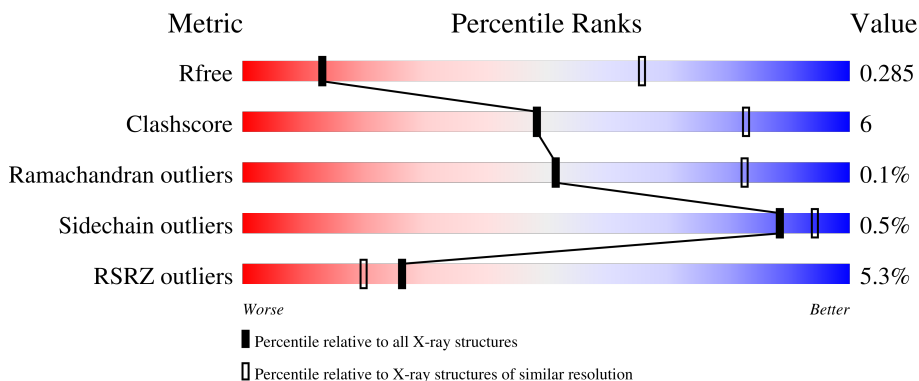
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.70 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.



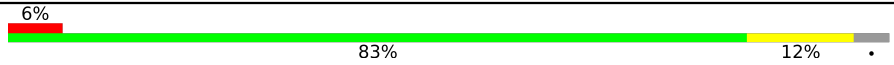
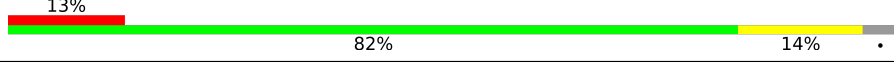

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1049 (3.88-3.52)
Clashscore	141614	1027 (3.86-3.54)
Ramachandran outliers	138981	1069 (3.88-3.52)
Sidechain outliers	138945	1065 (3.88-3.52)
RSRZ outliers	127900	1578 (3.90-3.50)

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	614	79% 16% 5%
1	B	614	76% 19% 5%
1	C	614	79% 17% . 2%
1	D	614	79% 16% 5% 3%
1	E	614	82% 14% . 5%

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Mol	Chain	Length	Quality of chain
1	F	614	 6% 83% 12% •
1	G	614	 13% 82% 14% •
1	H	614	 10% 84% 12% •

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 36839 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 ATM1-type heavy metal exporter.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	586	4561	2913	812	823	13	0	0	0
1	B	586	4561	2913	812	823	13	0	0	0
1	C	590	4590	2929	816	832	13	0	0	0
1	D	586	4561	2913	812	823	13	0	0	0
1	E	589	4581	2924	815	829	13	0	0	0
1	F	589	4581	2924	815	829	13	0	0	0
1	G	590	4590	2929	816	832	13	0	0	0
1	H	590	4590	2929	816	832	13	0	0	0

There are 56 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	527	CYS	ALA	engineered mutation	UNP Q2G506
A	609	HIS	-	expression tag	UNP Q2G506
A	610	HIS	-	expression tag	UNP Q2G506
A	611	HIS	-	expression tag	UNP Q2G506
A	612	HIS	-	expression tag	UNP Q2G506
A	613	HIS	-	expression tag	UNP Q2G506
A	614	HIS	-	expression tag	UNP Q2G506
B	527	CYS	ALA	engineered mutation	UNP Q2G506
B	609	HIS	-	expression tag	UNP Q2G506
B	610	HIS	-	expression tag	UNP Q2G506
B	611	HIS	-	expression tag	UNP Q2G506
B	612	HIS	-	expression tag	UNP Q2G506
B	613	HIS	-	expression tag	UNP Q2G506

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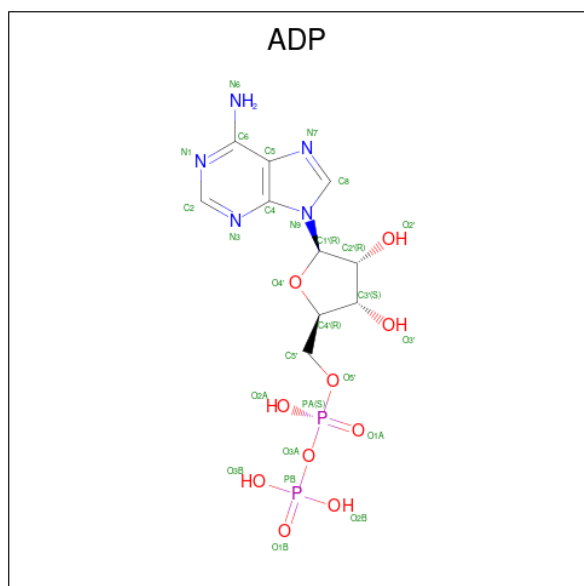
Chain	Residue	Modelled	Actual	Comment	Reference
B	614	HIS	-	expression tag	UNP Q2G506
C	527	CYS	ALA	engineered mutation	UNP Q2G506
C	609	HIS	-	expression tag	UNP Q2G506
C	610	HIS	-	expression tag	UNP Q2G506
C	611	HIS	-	expression tag	UNP Q2G506
C	612	HIS	-	expression tag	UNP Q2G506
C	613	HIS	-	expression tag	UNP Q2G506
C	614	HIS	-	expression tag	UNP Q2G506
D	527	CYS	ALA	engineered mutation	UNP Q2G506
D	609	HIS	-	expression tag	UNP Q2G506
D	610	HIS	-	expression tag	UNP Q2G506
D	611	HIS	-	expression tag	UNP Q2G506
D	612	HIS	-	expression tag	UNP Q2G506
D	613	HIS	-	expression tag	UNP Q2G506
D	614	HIS	-	expression tag	UNP Q2G506
E	527	CYS	ALA	engineered mutation	UNP Q2G506
E	609	HIS	-	expression tag	UNP Q2G506
E	610	HIS	-	expression tag	UNP Q2G506
E	611	HIS	-	expression tag	UNP Q2G506
E	612	HIS	-	expression tag	UNP Q2G506
E	613	HIS	-	expression tag	UNP Q2G506
E	614	HIS	-	expression tag	UNP Q2G506
F	527	CYS	ALA	engineered mutation	UNP Q2G506
F	609	HIS	-	expression tag	UNP Q2G506
F	610	HIS	-	expression tag	UNP Q2G506
F	611	HIS	-	expression tag	UNP Q2G506
F	612	HIS	-	expression tag	UNP Q2G506
F	613	HIS	-	expression tag	UNP Q2G506
F	614	HIS	-	expression tag	UNP Q2G506
G	527	CYS	ALA	engineered mutation	UNP Q2G506
G	609	HIS	-	expression tag	UNP Q2G506
G	610	HIS	-	expression tag	UNP Q2G506
G	611	HIS	-	expression tag	UNP Q2G506
G	612	HIS	-	expression tag	UNP Q2G506
G	613	HIS	-	expression tag	UNP Q2G506
G	614	HIS	-	expression tag	UNP Q2G506
H	527	CYS	ALA	engineered mutation	UNP Q2G506
H	609	HIS	-	expression tag	UNP Q2G506
H	610	HIS	-	expression tag	UNP Q2G506
H	611	HIS	-	expression tag	UNP Q2G506
H	612	HIS	-	expression tag	UNP Q2G506
H	613	HIS	-	expression tag	UNP Q2G506

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Chain	Residue	Modelled	Actual	Comment	Reference
H	614	HIS	-	expression tag	UNP Q2G506

- Molecule 2 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
2	A	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
2	B	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
2	C	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
2	D	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
2	E	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
2	F	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
2	G	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
2	H	1	Total	C	N	O	P	0	0
			27	10	5	10	2		

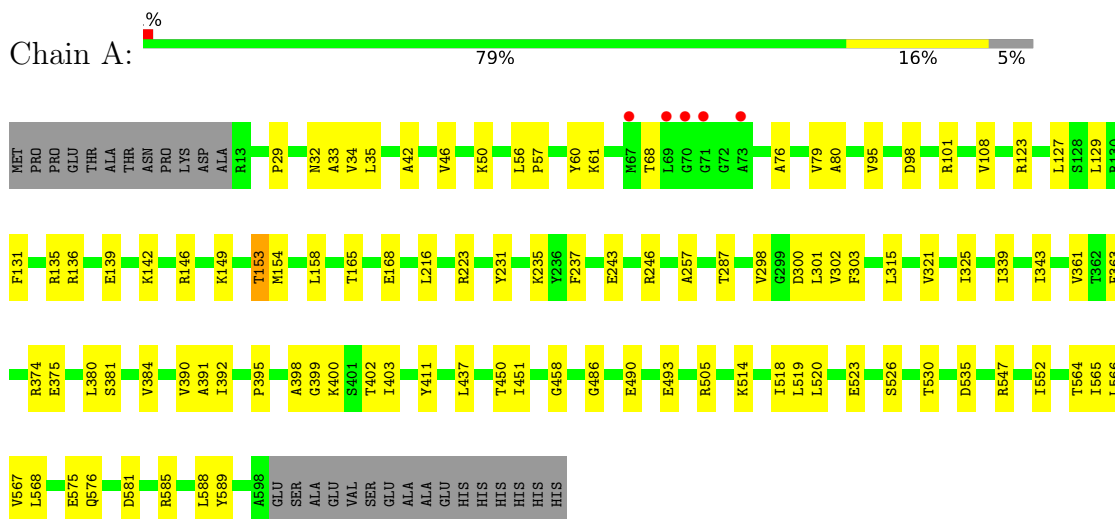
- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total Mg 1 1	0	0
3	B	1	Total Mg 1 1	0	0
3	C	1	Total Mg 1 1	0	0
3	D	1	Total Mg 1 1	0	0
3	E	1	Total Mg 1 1	0	0
3	F	1	Total Mg 1 1	0	0
3	G	1	Total Mg 1 1	0	0
3	H	1	Total Mg 1 1	0	0

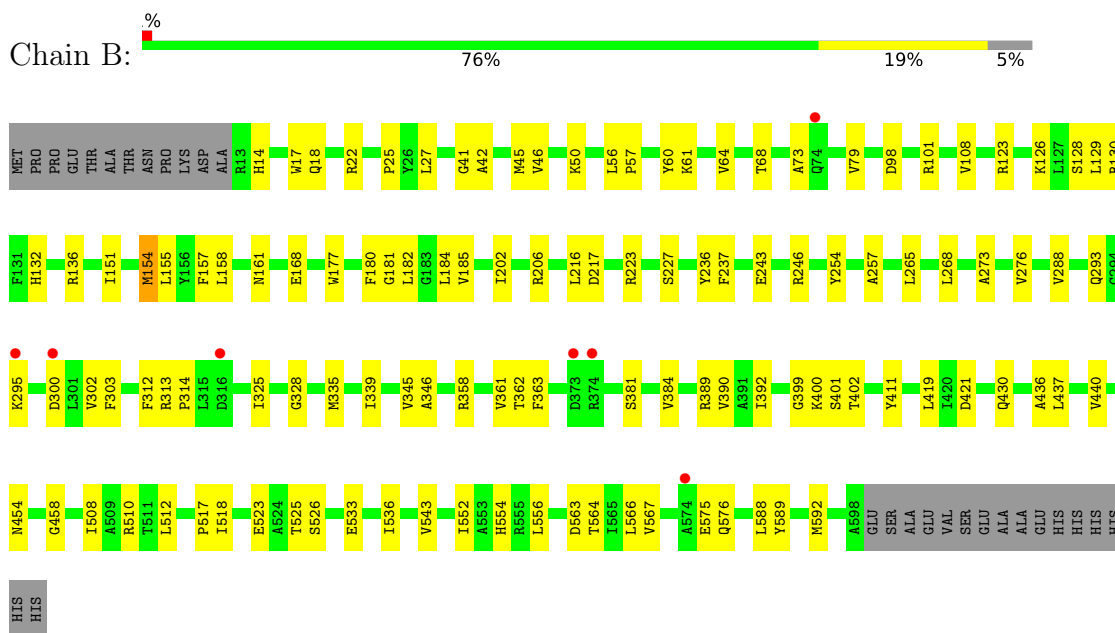
3 Residue-property plots

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

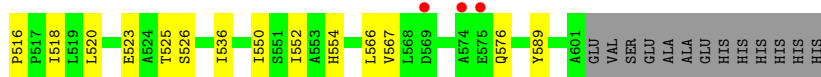
- Molecule 1: ATM1-type heavy metal exporter



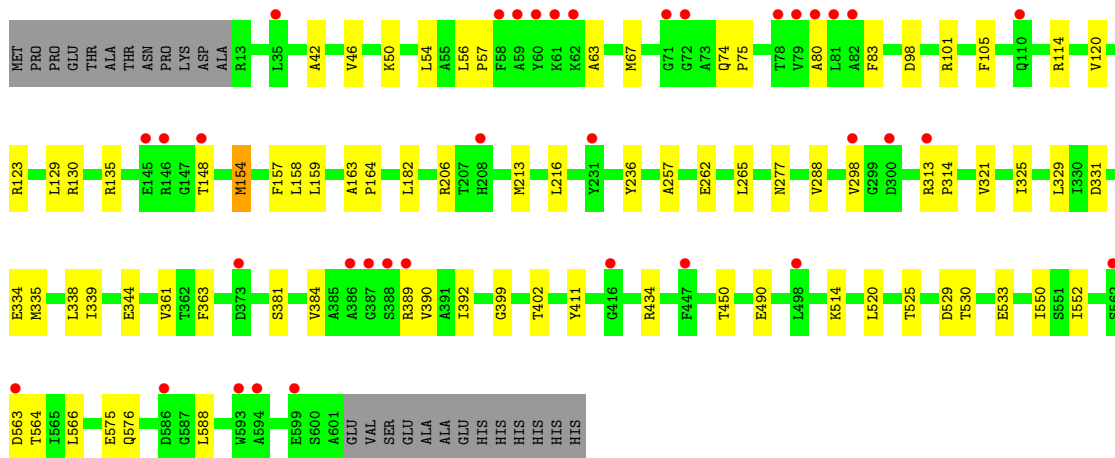
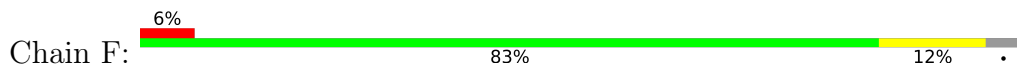
- Molecule 1: ATM1-type heavy metal exporter



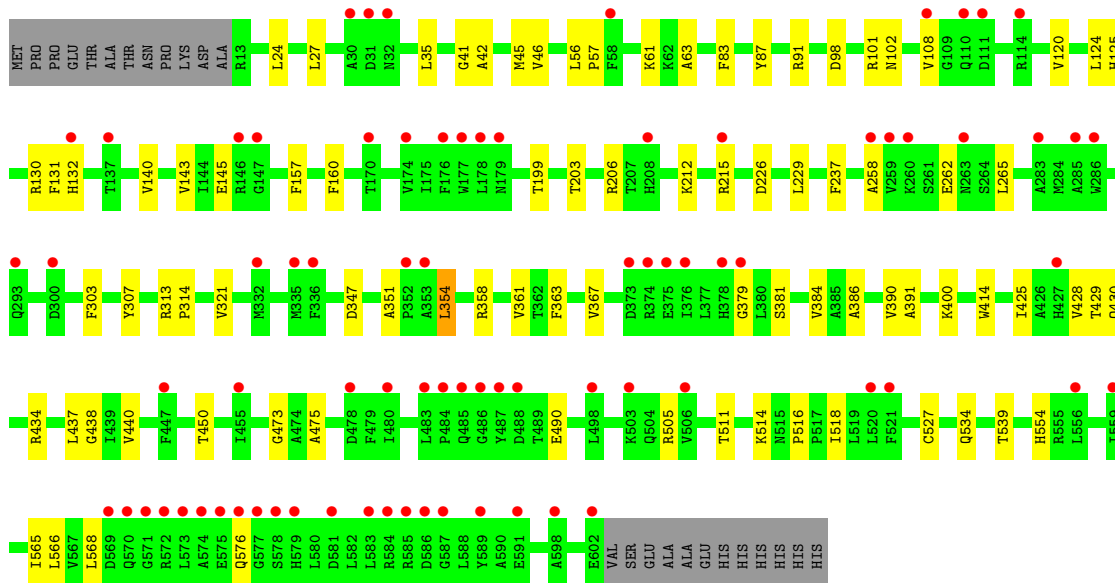
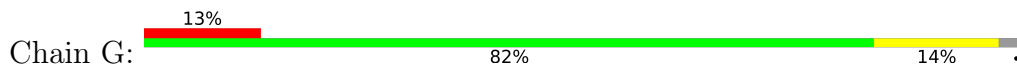
- Molecule 1: ATM1-type heavy metal exporter



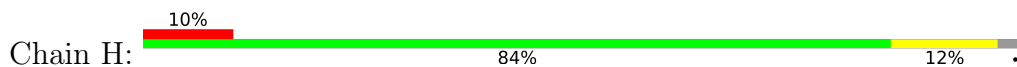
- Molecule 1: ATM1-type heavy metal exporter

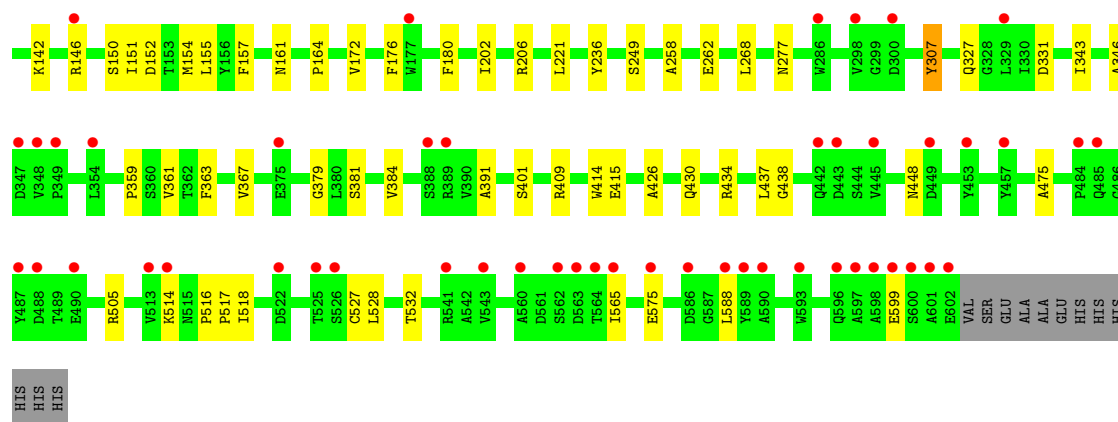


- Molecule 1: ATM1-type heavy metal exporter



- Molecule 1: ATM1-type heavy metal exporter





4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	129.18Å 133.61Å 134.26Å 110.62° 98.28° 101.20°	Depositor
Resolution (Å)	39.61 – 3.70 39.61 – 3.70	Depositor EDS
% Data completeness (in resolution range)	97.6 (39.61-3.70) 97.8 (39.61-3.70)	Depositor EDS
R_{merge}	0.17	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.51 (at 3.66Å)	Xtrriage
Refinement program	PHENIX 1.15.2_3472, REFMAC	Depositor
R, R_{free}	0.238 , 0.286 0.240 , 0.285	Depositor DCC
R_{free} test set	4195 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	146.7	Xtrriage
Anisotropy	0.110	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.23 , 86.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.38$, $\langle L^2 \rangle = 0.22$	Xtrriage
Estimated twinning fraction	0.055 for -h,-l,-k	Xtrriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	36839	wwPDB-VP
Average B, all atoms (Å ²)	178.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.66% 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: MG, ADP

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	0.25	0/4646	0.42	0/6310
1	B	0.25	0/4646	0.43	0/6310
1	C	0.25	0/4675	0.41	0/6349
1	D	0.24	0/4646	0.41	0/6310
1	E	0.25	0/4666	0.42	1/6337 (0.0%)
1	F	0.24	0/4666	0.41	0/6337
1	G	0.24	0/4675	0.43	2/6349 (0.0%)
1	H	0.24	0/4675	0.40	0/6349
All	All	0.24	0/37295	0.42	3/50651 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	354	LEU	CB-CG-CD2	-7.04	99.03	111.00
1	G	354	LEU	CA-CB-CG	-6.41	100.55	115.30
1	E	400	LYS	CD-CE-NZ	5.59	124.55	111.70

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	4561	0	4645	65	0
1	B	4561	0	4645	78	0
1	C	4590	0	4667	68	0
1	D	4561	0	4645	72	0
1	E	4581	0	4661	53	0
1	F	4581	0	4660	54	0
1	G	4590	0	4667	53	0
1	H	4590	0	4667	53	0
2	A	27	0	12	2	0
2	B	27	0	12	2	0
2	C	27	0	12	2	0
2	D	27	0	12	0	0
2	E	27	0	12	3	0
2	F	27	0	12	1	0
2	G	27	0	12	1	0
2	H	27	0	12	1	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
3	E	1	0	0	0	0
3	F	1	0	0	0	0
3	G	1	0	0	0	0
3	H	1	0	0	0	0
All	All	36839	0	37353	447	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 6.

All (447) 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:G:354:LEU:HD11	1:G:428:VAL:HB	1.41	1.02
1:B:128:SER:HB3	1:B:345:VAL:HG21	1.59	0.84
1:D:146:ARG:NH1	1:D:335:MET:SD	2.55	0.79
1:F:154:MET:HG3	1:F:325:ILE:HA	1.65	0.79
1:A:136:ARG:HB2	1:A:139:GLU:HB2	1.64	0.78
1:C:73:ALA:HB1	1:C:79:VAL:HG21	1.65	0.78
1:B:525:THR:HG22	1:B:536:ILE:HD11	1.69	0.74
1:D:113:THR:HB	1:D:151:ILE:HD13	1.70	0.73
1:G:363:PHE:O	1:G:381:SER:HA	1.88	0.73
1:H:136:ARG:NH2	1:H:139:GLU:OE1	2.22	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:154:MET:HE3	1:F:329:LEU:HG	1.72	0.70
1:A:363:PHE:O	1:A:381:SER:HA	1.93	0.69
1:A:390:VAL:HG13	1:A:564:THR:HG23	1.74	0.68
1:A:29:PRO:HB2	1:A:32:ASN:HB3	1.75	0.68
1:A:35:LEU:HD12	1:A:35:LEU:H	1.57	0.68
1:C:374:ARG:HH22	2:C:701:ADP:H1'	1.59	0.67
1:D:567:VAL:HG21	1:D:589:TYR:HB2	1.75	0.67
1:E:363:PHE:O	1:E:381:SER:HA	1.95	0.67
1:E:315:LEU:HD22	1:E:318:LEU:HD22	1.75	0.67
1:E:123:ARG:NH2	1:E:341:THR:O	2.28	0.67
1:E:123:ARG:HG2	1:E:339:ILE:HA	1.77	0.66
1:B:177:TRP:HA	1:B:181:GLY:HA3	1.76	0.66
1:D:153:THR:HB	1:D:324:THR:HB	1.76	0.66
1:E:236:TYR:O	1:F:514:LYS:NZ	2.28	0.65
1:G:527:CYS:HB3	1:H:527:CYS:HA	1.79	0.65
1:B:18:GLN:NE2	1:D:364:ASP:OD1	2.28	0.65
1:C:229:LEU:HD11	1:D:136:ARG:HH22	1.62	0.65
1:F:123:ARG:HG3	1:F:339:ILE:HG23	1.78	0.65
1:A:149:LYS:O	1:A:153:THR:HG23	1.97	0.64
1:G:226:ASP:OD2	1:H:448:ASN:N	2.25	0.64
1:E:567:VAL:HG21	1:E:589:TYR:HB2	1.80	0.64
1:D:177:TRP:HZ3	1:D:182:LEU:HD13	1.63	0.64
1:A:68:THR:HG21	1:A:298:VAL:HG11	1.81	0.63
1:A:165:THR:HG21	1:A:315:LEU:HD21	1.80	0.63
1:D:384:VAL:HG11	1:D:550:ILE:HD11	1.79	0.63
1:F:216:LEU:HD12	1:F:257:ALA:HB2	1.80	0.63
1:G:46:VAL:HG22	1:G:101:ARG:HD2	1.79	0.63
1:E:401:SER:OG	2:E:701:ADP:O1A	2.16	0.63
1:B:400:LYS:NZ	2:B:701:ADP:O1B	2.30	0.63
1:G:91:ARG:NH1	1:H:277:ASN:OD1	2.33	0.62
1:E:392:ILE:HB	1:E:552:ILE:HG12	1.80	0.62
1:E:64:VAL:O	1:E:68:THR:HG23	1.99	0.62
1:B:128:SER:O	1:B:129:LEU:HG	1.98	0.62
1:C:236:TYR:O	1:D:514:LYS:NZ	2.29	0.62
1:B:123:ARG:HG2	1:B:339:ILE:HA	1.82	0.62
1:E:429:THR:HG1	1:E:432:SER:HG	1.48	0.61
1:E:298:VAL:HG23	1:F:67:MET:HE1	1.82	0.61
1:C:523:GLU:HB3	1:C:526:SER:OG	1.98	0.61
1:C:363:PHE:O	1:C:381:SER:HA	2.01	0.61
1:C:75:PRO:HG2	1:C:78:THR:HB	1.83	0.61
1:E:525:THR:HG22	1:E:536:ILE:HD11	1.83	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:567:VAL:HG21	1:C:589:TYR:HB2	1.83	0.60
1:A:374:ARG:NH2	2:A:701:ADP:N3	2.49	0.60
1:C:575:GLU:OE2	1:C:588:LEU:N	2.33	0.60
1:H:146:ARG:O	1:H:150:SER:N	2.34	0.60
1:A:154:MET:HG3	1:A:325:ILE:HA	1.83	0.60
1:D:150:SER:HB2	1:D:331:ASP:HB2	1.83	0.60
1:G:514:LYS:NZ	1:H:236:TYR:O	2.34	0.60
1:A:123:ARG:HG2	1:A:339:ILE:HA	1.83	0.60
1:F:361:VAL:HB	1:F:384:VAL:HB	1.83	0.60
1:A:129:LEU:HD13	1:A:411:TYR:HE2	1.66	0.60
1:F:206:ARG:HD2	1:F:265:LEU:HA	1.83	0.60
1:G:63:ALA:HB2	1:G:83:PHE:HB3	1.83	0.60
1:G:56:LEU:HG	1:G:57:PRO:HD3	1.84	0.59
1:C:448:ASN:ND2	1:C:493:GLU:OE2	2.35	0.59
1:E:91:ARG:NH1	1:F:277:ASN:OD1	2.35	0.59
1:B:64:VAL:O	1:B:68:THR:HG23	2.02	0.59
1:D:399:GLY:O	1:D:402:THR:OG1	2.15	0.59
1:B:361:VAL:HB	1:B:384:VAL:HB	1.84	0.58
1:D:504:GLN:HG3	1:D:528:LEU:HD11	1.84	0.58
1:E:554:HIS:CE1	1:F:530:THR:H	2.22	0.57
1:B:567:VAL:HG21	1:B:589:TYR:HB2	1.85	0.57
1:H:98:ASP:OD1	1:H:101:ARG:NH1	2.38	0.57
1:C:56:LEU:HG	1:C:57:PRO:HD3	1.87	0.57
1:B:73:ALA:HB2	1:B:79:VAL:HG23	1.85	0.57
1:D:177:TRP:CZ3	1:D:182:LEU:HD13	2.40	0.57
1:C:127:LEU:O	1:D:231:TYR:OH	2.19	0.57
1:E:374:ARG:NH1	2:E:701:ADP:O3'	2.38	0.57
1:C:101:ARG:HE	1:C:160:PHE:HD2	1.51	0.56
1:D:56:LEU:HG	1:D:57:PRO:HD3	1.87	0.56
1:H:391:ALA:HB3	1:H:565:ILE:HG12	1.87	0.56
1:D:123:ARG:HG3	1:D:339:ILE:HG23	1.88	0.56
1:F:363:PHE:O	1:F:381:SER:HA	2.06	0.56
1:F:399:GLY:O	1:F:402:THR:OG1	2.22	0.56
1:G:157:PHE:HD1	1:G:321:VAL:HA	1.70	0.56
1:A:80:ALA:HB1	1:B:288:VAL:HG21	1.88	0.56
1:A:399:GLY:O	1:A:402:THR:OG1	2.20	0.56
1:C:361:VAL:HB	1:C:384:VAL:HB	1.87	0.56
1:E:50:LYS:HE3	1:E:164:PRO:HB3	1.86	0.56
1:F:450:THR:HA	1:F:490:GLU:HA	1.87	0.56
1:D:101:ARG:HE	1:D:160:PHE:HD1	1.52	0.56
1:B:401:SER:OG	2:B:701:ADP:O1A	2.21	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:180:PHE:HE2	1:B:182:LEU:HB2	1.71	0.56
1:F:50:LYS:HE3	1:F:164:PRO:HB3	1.88	0.56
1:H:475:ALA:O	1:H:505:ARG:NH1	2.38	0.56
1:F:46:VAL:HG22	1:F:101:ARG:HD2	1.88	0.55
1:H:56:LEU:HG	1:H:57:PRO:HD3	1.88	0.55
1:B:50:LYS:NZ	1:B:168:GLU:OE1	2.37	0.55
1:G:361:VAL:HB	1:G:384:VAL:HB	1.87	0.55
1:C:64:VAL:O	1:C:68:THR:HG23	2.06	0.55
1:G:554:HIS:NE2	2:G:701:ADP:O2B	2.33	0.55
1:E:361:VAL:HB	1:E:384:VAL:HB	1.89	0.55
1:C:392:ILE:HB	1:C:552:ILE:HG12	1.88	0.55
1:E:56:LEU:HG	1:E:57:PRO:HD3	1.89	0.54
1:B:56:LEU:HG	1:B:57:PRO:HD3	1.89	0.54
1:B:525:THR:HB	1:B:533:GLU:HG3	1.89	0.54
1:F:63:ALA:HB2	1:F:83:PHE:HB3	1.88	0.54
1:H:363:PHE:O	1:H:381:SER:HA	2.07	0.54
1:C:27:LEU:HD21	1:C:155:LEU:HD21	1.88	0.54
1:G:475:ALA:O	1:G:505:ARG:NH1	2.41	0.54
1:H:41:GLY:O	1:H:45:MET:HG2	2.08	0.54
1:H:50:LYS:HE3	1:H:164:PRO:HB3	1.90	0.54
1:B:358:ARG:N	1:B:421:ASP:OD1	2.37	0.54
1:F:157:PHE:HD2	1:F:321:VAL:HG22	1.71	0.54
1:A:361:VAL:HB	1:A:384:VAL:HB	1.90	0.54
1:B:18:GLN:HE22	1:D:365:ASN:HB2	1.73	0.54
1:B:399:GLY:O	1:B:402:THR:OG1	2.21	0.54
1:G:425:ILE:O	1:G:428:VAL:HG22	2.08	0.54
1:A:56:LEU:HG	1:A:57:PRO:HD3	1.90	0.54
1:E:315:LEU:HA	1:E:318:LEU:HB2	1.88	0.53
1:A:575:GLU:OE2	1:A:588:LEU:N	2.37	0.53
1:B:384:VAL:HG13	1:B:390:VAL:HG21	1.91	0.53
1:F:56:LEU:HG	1:F:57:PRO:HD3	1.90	0.53
1:G:450:THR:HA	1:G:490:GLU:HA	1.90	0.53
1:C:221:LEU:HD21	1:D:144:ILE:HA	1.90	0.53
1:F:129:LEU:HD12	1:F:411:TYR:HE2	1.73	0.53
1:H:172:VAL:HG22	1:H:307:TYR:HD2	1.74	0.53
1:C:140:VAL:HG22	1:D:229:LEU:HD21	1.91	0.53
1:D:575:GLU:OE2	1:D:588:LEU:N	2.40	0.53
1:H:146:ARG:NH1	1:H:331:ASP:OD2	2.42	0.53
1:A:61:LYS:HB2	1:A:303:PHE:HB2	1.90	0.53
1:H:202:ILE:HG21	1:H:268:LEU:HB2	1.91	0.53
1:H:151:ILE:HA	1:H:154:MET:HG2	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:33:ALA:O	1:A:35:LEU:N	2.42	0.52
1:A:142:LYS:O	1:A:146:ARG:HB3	2.09	0.52
1:G:354:LEU:CD1	1:G:428:VAL:HB	2.25	0.52
1:H:35:LEU:HD22	1:H:108:VAL:HG22	1.91	0.52
1:B:158:LEU:HD23	1:B:325:ILE:HD13	1.91	0.52
1:A:451:ILE:HD11	1:A:486:GLY:O	2.09	0.52
1:B:512:LEU:HD21	1:B:543:VAL:HG13	1.91	0.52
1:H:367:VAL:HG22	1:H:379:GLY:H	1.74	0.52
1:F:392:ILE:HB	1:F:552:ILE:HG12	1.92	0.52
1:C:395:PRO:HD2	1:C:398:ALA:HB2	1.92	0.52
1:B:392:ILE:HB	1:B:552:ILE:HG12	1.92	0.52
1:H:505:ARG:NH2	1:H:532:THR:OG1	2.43	0.52
1:D:361:VAL:HB	1:D:384:VAL:HB	1.91	0.52
1:B:129:LEU:HA	1:B:132:HIS:ND1	2.24	0.52
1:G:199:THR:O	1:G:203:THR:OG1	2.20	0.52
1:A:223:ARG:HD3	1:A:246:ARG:HG2	1.92	0.52
1:B:14:HIS:NE2	1:B:17:TRP:HB2	2.25	0.51
1:H:142:LYS:HE3	1:H:146:ARG:HH21	1.75	0.51
1:H:438:GLY:HA3	1:H:516:PRO:HG3	1.91	0.51
1:B:363:PHE:O	1:B:381:SER:HA	2.10	0.51
1:F:74:GLN:HB2	1:F:75:PRO:HD3	1.93	0.51
1:C:402:THR:HA	1:C:405:ARG:HG2	1.91	0.51
1:A:567:VAL:HG21	1:A:589:TYR:HB2	1.92	0.51
1:H:361:VAL:HB	1:H:384:VAL:HB	1.93	0.51
1:H:157:PHE:O	1:H:161:ASN:HB3	2.11	0.51
1:B:126:LYS:NZ	1:D:349:PRO:O	2.44	0.51
1:B:129:LEU:HD22	1:B:411:TYR:CE2	2.45	0.51
1:G:140:VAL:HA	1:G:143:VAL:HG22	1.92	0.51
1:C:74:GLN:HB2	1:C:75:PRO:HD3	1.92	0.51
1:D:363:PHE:O	1:D:381:SER:HA	2.11	0.51
1:B:575:GLU:OE2	1:B:588:LEU:N	2.42	0.51
1:E:474:ALA:HB2	1:E:512:LEU:HD12	1.93	0.51
1:A:375:GLU:OE1	1:E:378:HIS:NE2	2.44	0.50
1:A:520:LEU:HD11	1:A:552:ILE:HD12	1.91	0.50
1:C:35:LEU:HD22	1:C:108:VAL:HG12	1.93	0.50
1:C:276:VAL:HG13	1:C:312:PHE:HD2	1.75	0.50
1:E:523:GLU:HB3	1:E:526:SER:OG	2.11	0.50
1:C:384:VAL:HG13	1:C:390:VAL:HG21	1.91	0.50
1:E:384:VAL:HG13	1:E:390:VAL:HG21	1.93	0.50
1:A:380:LEU:HD23	1:A:403:ILE:HD11	1.93	0.50
1:H:367:VAL:O	1:H:414:TRP:N	2.44	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:523:GLU:HB3	1:A:526:SER:OG	2.12	0.50
1:G:438:GLY:HA3	1:G:516:PRO:HG3	1.93	0.50
1:A:530:THR:H	1:B:554:HIS:CE1	2.30	0.50
1:D:434:ARG:O	1:D:514:LYS:NZ	2.43	0.50
1:A:60:TYR:CE1	1:A:302:VAL:HG11	2.47	0.49
1:E:288:VAL:HG21	1:F:80:ALA:HB1	1.93	0.49
1:B:180:PHE:CE2	1:B:182:LEU:HB2	2.48	0.49
1:C:165:THR:HG21	1:C:315:LEU:HD21	1.94	0.49
1:B:206:ARG:HD2	1:B:265:LEU:HA	1.93	0.49
1:C:136:ARG:O	1:C:140:VAL:HG23	2.12	0.49
1:D:46:VAL:HG22	1:D:101:ARG:HD2	1.95	0.49
1:G:347:ASP:HB3	1:G:430:GLN:HG3	1.94	0.49
1:B:440:VAL:HG21	1:B:508:ILE:HD13	1.94	0.49
1:F:331:ASP:O	1:F:335:MET:HG2	2.13	0.49
1:B:362:THR:HB	1:B:419:LEU:HB2	1.94	0.49
1:D:165:THR:HG21	1:D:315:LEU:HD21	1.95	0.49
1:A:50:LYS:NZ	1:A:168:GLU:OE1	2.44	0.49
1:B:151:ILE:HD11	1:B:335:MET:SD	2.53	0.49
1:B:566:LEU:HD23	1:B:576:GLN:HG3	1.95	0.49
1:D:358:ARG:HD2	1:D:359:PRO:HD2	1.94	0.49
1:A:400:LYS:HB3	1:A:568:LEU:HD12	1.95	0.48
1:D:63:ALA:HB2	1:D:83:PHE:HB3	1.94	0.48
1:F:434:ARG:O	1:F:514:LYS:NZ	2.42	0.48
1:E:130:ARG:HH21	1:E:341:THR:HG21	1.78	0.48
1:A:395:PRO:HD2	1:A:398:ALA:HB2	1.95	0.48
1:C:144:ILE:HG13	1:C:145:GLU:H	1.79	0.48
1:F:130:ARG:NH1	1:F:338:LEU:HD22	2.29	0.48
1:B:129:LEU:HA	1:B:132:HIS:H	1.79	0.48
1:C:144:ILE:HB	1:D:221:LEU:HG	1.94	0.48
1:G:367:VAL:HG22	1:G:379:GLY:H	1.78	0.48
1:C:150:SER:OG	1:C:328:GLY:HA2	2.13	0.48
1:G:440:VAL:HG22	1:G:511:THR:HG21	1.95	0.48
1:H:172:VAL:HG22	1:H:307:TYR:CD2	2.48	0.48
1:G:367:VAL:O	1:G:414:TRP:N	2.45	0.48
1:D:65:ASP:HA	1:D:68:THR:HG22	1.94	0.48
1:E:459:ARG:NH2	1:E:466:GLU:OE2	2.35	0.48
1:A:391:ALA:HB3	1:A:565:ILE:HD13	1.94	0.48
1:A:392:ILE:HB	1:A:552:ILE:HG12	1.96	0.47
1:C:80:ALA:HB1	1:D:288:VAL:HG21	1.96	0.47
1:D:68:THR:HG23	1:D:69:LEU:HD13	1.95	0.47
1:A:321:VAL:O	1:A:325:ILE:HG12	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:113:THR:HG21	1:D:151:ILE:HG21	1.95	0.47
1:E:63:ALA:HB2	1:E:83:PHE:HB3	1.96	0.47
1:C:60:TYR:CE1	1:C:302:VAL:HG11	2.48	0.47
1:H:346:ALA:O	1:H:409:ARG:NH2	2.47	0.47
1:C:465:ALA:H	1:H:249:SER:HB2	1.80	0.47
1:D:390:VAL:HG13	1:D:564:THR:HG23	1.97	0.47
1:E:80:ALA:HB1	1:F:288:VAL:HG21	1.95	0.47
1:G:42:ALA:O	1:G:46:VAL:HG23	2.14	0.47
1:F:157:PHE:CD2	1:F:321:VAL:HG22	2.49	0.47
1:B:129:LEU:HB2	1:B:132:HIS:HB2	1.96	0.47
1:F:154:MET:O	1:F:158:LEU:HB2	2.15	0.47
1:G:384:VAL:HG13	1:G:390:VAL:HG11	1.95	0.47
1:A:231:TYR:OH	1:A:235:LYS:HE2	2.14	0.47
1:B:276:VAL:HG13	1:B:312:PHE:HD2	1.80	0.47
1:C:367:VAL:HB	1:C:415:GLU:HB2	1.96	0.47
1:F:399:GLY:HA2	2:F:701:ADP:H5'2	1.95	0.47
1:G:430:GLN:HE21	1:G:434:ARG:HH22	1.62	0.47
1:A:95:VAL:HG11	1:B:273:ALA:HB2	1.97	0.47
1:A:505:ARG:HH22	1:A:535:ASP:HB3	1.79	0.47
1:A:519:LEU:HD13	1:A:547:ARG:HD3	1.96	0.47
1:F:575:GLU:OE2	1:F:588:LEU:N	2.44	0.47
1:G:87:TYR:CZ	1:G:91:ARG:HD2	2.50	0.47
1:D:113:THR:HG21	1:D:151:ILE:CG2	2.45	0.47
1:D:216:LEU:HD12	1:D:257:ALA:HB2	1.97	0.47
1:A:437:LEU:HD23	1:A:518:ILE:HB	1.96	0.46
1:G:132:HIS:O	1:G:132:HIS:ND1	2.48	0.46
1:H:45:MET:HB2	1:H:101:ARG:HB3	1.97	0.46
1:E:566:LEU:HD23	1:E:576:GLN:HG3	1.97	0.46
1:H:437:LEU:HD23	1:H:518:ILE:HB	1.96	0.46
1:A:384:VAL:HG13	1:A:390:VAL:HG21	1.97	0.46
1:B:216:LEU:HD12	1:B:257:ALA:HB2	1.97	0.46
1:C:41:GLY:O	1:C:45:MET:HG2	2.15	0.46
1:D:384:VAL:HG13	1:D:390:VAL:HG21	1.97	0.46
1:A:32:ASN:ND2	1:A:35:LEU:HD13	2.30	0.46
1:A:98:ASP:O	1:A:101:ARG:HG2	2.15	0.46
1:B:227:SER:OG	1:B:243:GLU:HG2	2.16	0.46
1:C:50:LYS:NZ	1:C:168:GLU:OE1	2.43	0.46
1:H:126:LYS:HD3	1:H:343:ILE:HD11	1.97	0.46
1:B:293:GLN:OE1	1:B:295:LYS:NZ	2.48	0.46
1:C:370:TYR:OH	1:C:405:ARG:NH1	2.48	0.46
1:F:42:ALA:O	1:F:46:VAL:HG23	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:46:VAL:HG22	1:A:101:ARG:HD2	1.97	0.46
1:A:392:ILE:HG12	1:A:566:LEU:HD12	1.98	0.46
1:H:146:ARG:NH1	1:H:327:GLN:OE1	2.49	0.46
1:H:359:PRO:HB2	1:H:518:ILE:HD11	1.97	0.46
1:B:27:LEU:HD21	1:B:155:LEU:HD21	1.98	0.46
1:B:154:MET:HB2	1:B:328:GLY:HA3	1.97	0.46
1:C:237:PHE:CD1	1:D:458:GLY:HA2	2.51	0.46
1:E:348:VAL:HG23	1:E:351:ALA:HB2	1.98	0.46
1:G:35:LEU:HD22	1:G:108:VAL:HG22	1.97	0.46
1:E:280:MET:HE1	1:E:308:LEU:HB2	1.97	0.46
1:D:276:VAL:HG13	1:D:312:PHE:HD2	1.81	0.46
1:E:399:GLY:O	1:E:402:THR:OG1	2.29	0.46
1:G:212:LYS:HG3	1:G:215:ARG:NH2	2.30	0.46
1:B:98:ASP:O	1:B:101:ARG:HG2	2.16	0.45
1:C:27:LEU:HD11	1:C:155:LEU:HD11	1.97	0.45
1:B:436:ALA:HA	1:B:517:PRO:HD2	1.97	0.45
1:B:556:LEU:HD11	1:B:592:MET:HB3	1.98	0.45
1:D:380:LEU:HD23	1:D:403:ILE:HD11	1.97	0.45
1:H:154:MET:HG3	1:H:155:LEU:N	2.31	0.45
1:H:528:LEU:HD13	1:H:532:THR:HG22	1.98	0.45
1:C:61:LYS:HB2	1:C:303:PHE:HB2	1.98	0.45
1:C:390:VAL:HG13	1:C:564:THR:HG23	1.98	0.45
1:C:399:GLY:O	1:C:402:THR:OG1	2.22	0.45
1:D:556:LEU:HD11	1:D:592:MET:HB3	1.97	0.45
1:E:158:LEU:HD23	1:E:162:ILE:HG13	1.97	0.45
1:F:344:GLU:O	1:F:344:GLU:HG2	2.16	0.45
1:G:400:LYS:HB3	1:G:568:LEU:HD12	1.98	0.45
1:A:61:LYS:NZ	1:A:300:ASP:OD1	2.38	0.45
1:C:525:THR:HB	1:C:533:GLU:HG3	1.97	0.45
1:C:46:VAL:HG22	1:C:101:ARG:HD2	1.99	0.45
1:C:154:MET:HB2	1:C:328:GLY:HA3	1.99	0.45
1:B:437:LEU:HD23	1:B:518:ILE:HB	1.97	0.45
1:B:523:GLU:HB3	1:B:526:SER:HB2	1.99	0.45
1:G:358:ARG:HG3	1:G:386:ALA:HB1	1.98	0.45
1:G:61:LYS:HB2	1:G:303:PHE:HB2	1.99	0.45
1:C:130:ARG:HA	1:C:130:ARG:HD2	1.83	0.45
1:C:273:ALA:HB2	1:D:95:VAL:HG11	1.98	0.45
1:E:67:MET:HE2	1:F:298:VAL:HG23	1.99	0.45
1:F:390:VAL:HG13	1:F:564:THR:HG23	1.98	0.45
1:H:359:PRO:HG3	1:H:517:PRO:HB2	1.99	0.45
1:D:129:LEU:HD13	1:D:344:GLU:OE2	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:120:VAL:HG11	1:F:335:MET:CE	2.47	0.44
1:A:514:LYS:NZ	1:B:236:TYR:O	2.45	0.44
1:B:22:ARG:HH22	1:D:419:LEU:HD11	1.82	0.44
1:C:434:ARG:O	1:C:514:LYS:NZ	2.49	0.44
1:D:50:LYS:HE3	1:D:164:PRO:HB3	1.98	0.44
1:E:438:GLY:HA3	1:E:516:PRO:HG3	2.00	0.44
1:H:142:LYS:HG2	1:H:146:ARG:HH21	1.82	0.44
1:A:127:LEU:HD23	1:A:343:ILE:HG12	1.99	0.44
1:D:157:PHE:O	1:D:161:ASN:HB3	2.18	0.44
1:G:41:GLY:O	1:G:45:MET:HG2	2.18	0.44
1:H:409:ARG:NE	1:H:426:ALA:HA	2.31	0.44
1:D:61:LYS:HB2	1:D:303:PHE:HB2	2.00	0.44
1:F:313:ARG:HB3	1:F:314:PRO:HD3	2.00	0.44
1:B:60:TYR:CE1	1:B:302:VAL:HG11	2.52	0.44
1:C:22:ARG:O	1:C:25:PRO:HD2	2.17	0.44
1:F:384:VAL:HG13	1:F:390:VAL:HG21	1.98	0.44
1:H:575:GLU:OE2	1:H:588:LEU:N	2.42	0.44
1:A:131:PHE:O	1:A:135:ARG:HG2	2.17	0.44
1:F:105:PHE:CZ	1:F:159:LEU:HD12	2.53	0.44
1:G:102:ASN:OD1	1:G:160:PHE:HE2	2.01	0.44
1:G:351:ALA:HB3	1:G:429:THR:HG23	1.99	0.44
1:H:176:PHE:HA	1:H:180:PHE:HD2	1.82	0.44
1:C:123:ARG:HG2	1:C:339:ILE:HA	1.99	0.44
1:B:61:LYS:NZ	1:B:300:ASP:OD1	2.35	0.44
1:D:375:GLU:HG2	1:D:378:HIS:HD2	1.83	0.44
1:G:98:ASP:O	1:G:101:ARG:HG2	2.18	0.44
1:H:528:LEU:HD22	1:H:532:THR:HG21	2.00	0.44
1:E:313:ARG:HB3	1:E:314:PRO:HD3	1.99	0.43
1:G:258:ALA:O	1:G:262:GLU:HG2	2.18	0.43
1:B:41:GLY:O	1:B:45:MET:HG2	2.18	0.43
1:B:389:ARG:O	1:B:563:ASP:N	2.51	0.43
1:C:345:VAL:O	1:C:430:GLN:NE2	2.47	0.43
1:E:157:PHE:CD1	1:E:321:VAL:HG22	2.53	0.43
1:G:212:LYS:HG3	1:G:215:ARG:HH22	1.82	0.43
1:A:374:ARG:HH22	2:A:701:ADP:H1'	1.84	0.43
1:C:120:VAL:HG21	1:C:335:MET:SD	2.58	0.43
1:E:437:LEU:HD23	1:E:518:ILE:HB	1.99	0.43
1:B:22:ARG:O	1:B:25:PRO:HD2	2.18	0.43
1:C:105:PHE:CZ	1:C:159:LEU:HD12	2.53	0.43
1:F:334:GLU:O	1:F:338:LEU:HG	2.19	0.43
1:C:529:ASP:HA	1:D:554:HIS:CE1	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:154:MET:CE	1:F:329:LEU:HG	2.43	0.43
1:F:163:ALA:HB3	1:F:164:PRO:HD3	2.01	0.43
1:A:237:PHE:CD1	1:B:458:GLY:HA2	2.54	0.43
1:B:390:VAL:HG13	1:B:564:THR:HG23	1.99	0.43
1:E:154:MET:HB2	1:E:328:GLY:HA3	2.00	0.43
1:H:367:VAL:HB	1:H:415:GLU:HB2	2.00	0.43
1:D:566:LEU:HD23	1:D:576:GLN:HG3	1.99	0.43
1:D:26:TYR:N	1:D:26:TYR:CD2	2.87	0.43
1:D:358:ARG:HD2	1:D:358:ARG:HA	1.86	0.43
1:E:146:ARG:NH2	1:E:331:ASP:OD2	2.52	0.43
1:F:389:ARG:O	1:F:563:ASP:N	2.52	0.43
1:H:258:ALA:O	1:H:262:GLU:HG2	2.19	0.43
1:B:202:ILE:HB	1:B:268:LEU:HD13	2.00	0.42
1:E:495:GLY:O	1:F:135:ARG:NH2	2.46	0.42
1:A:566:LEU:HD23	1:A:576:GLN:HG3	2.01	0.42
1:B:42:ALA:O	1:B:46:VAL:HG23	2.19	0.42
1:B:206:ARG:NH1	1:B:265:LEU:HB2	2.33	0.42
1:D:42:ALA:O	1:D:46:VAL:HG23	2.20	0.42
1:D:519:LEU:HD13	1:D:547:ARG:HD3	2.01	0.42
1:E:42:ALA:O	1:E:46:VAL:HG23	2.18	0.42
1:F:154:MET:HE2	1:F:158:LEU:HD12	2.01	0.42
1:C:206:ARG:HG3	1:C:264:SER:OG	2.20	0.42
1:C:313:ARG:HB3	1:C:314:PRO:HD3	2.01	0.42
1:E:520:LEU:HD11	1:E:550:ILE:HD12	2.01	0.42
1:F:525:THR:HB	1:F:533:GLU:HG3	2.01	0.42
1:C:42:ALA:O	1:C:46:VAL:HG23	2.20	0.42
1:C:401:SER:OG	2:C:701:ADP:O2A	2.38	0.42
1:E:216:LEU:HD12	1:E:257:ALA:HB2	2.00	0.42
1:E:554:HIS:CE1	1:F:529:ASP:HB2	2.55	0.42
1:D:60:TYR:CE1	1:D:302:VAL:HG11	2.54	0.42
1:H:202:ILE:HB	1:H:268:LEU:HD13	2.02	0.42
1:C:437:LEU:HD23	1:C:518:ILE:HB	2.00	0.42
1:E:514:LYS:NZ	1:F:236:TYR:O	2.47	0.42
1:A:158:LEU:HG	1:A:325:ILE:HD12	2.02	0.42
1:A:450:THR:HA	1:A:490:GLU:HA	2.01	0.42
1:B:358:ARG:HA	1:B:358:ARG:HD2	1.82	0.42
1:E:181:GLY:O	1:E:182:LEU:HG	2.19	0.42
1:A:243:GLU:OE1	1:A:246:ARG:NH2	2.53	0.42
1:D:375:GLU:HG2	1:D:378:HIS:CD2	2.54	0.42
1:D:437:LEU:HD23	1:D:518:ILE:HB	2.02	0.42
1:E:397:GLY:HA2	2:E:701:ADP:H5'1	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:237:PHE:CD2	1:H:514:LYS:HD2	2.55	0.42
1:G:566:LEU:HD23	1:G:576:GLN:HG3	2.02	0.42
1:B:50:LYS:HD2	1:B:168:GLU:HB2	2.01	0.41
1:D:468:ASP:OD1	1:D:487:TYR:OH	2.30	0.41
1:E:221:LEU:HD11	1:F:148:THR:HG21	2.02	0.41
1:G:24:LEU:HD23	1:G:27:LEU:HD12	2.02	0.41
1:B:184:LEU:HD12	1:B:185:VAL:N	2.35	0.41
1:E:437:LEU:O	1:E:514:LYS:NZ	2.51	0.41
1:A:493:GLU:OE1	1:B:136:ARG:NH1	2.50	0.41
1:B:223:ARG:HD3	1:B:246:ARG:HG2	2.02	0.41
1:C:262:GLU:HG3	1:D:106:GLU:OE2	2.19	0.41
1:D:540:MET:HA	1:D:543:VAL:HG22	2.03	0.41
1:G:157:PHE:CD1	1:G:321:VAL:HG22	2.55	0.41
1:A:581:ASP:O	1:A:585:ARG:HG3	2.20	0.41
1:A:287:THR:HG21	1:A:301:LEU:HA	2.03	0.41
1:B:22:ARG:NH1	1:D:364:ASP:OD2	2.52	0.41
1:B:313:ARG:HB3	1:B:314:PRO:HD3	2.02	0.41
1:B:346:ALA:HB2	1:B:430:GLN:HE21	1.85	0.41
1:G:130:ARG:HG3	1:G:131:PHE:H	1.86	0.41
1:G:206:ARG:NH1	1:G:265:LEU:HB2	2.36	0.41
1:G:391:ALA:HB3	1:G:565:ILE:HG12	2.03	0.41
1:A:76:ALA:HA	1:A:79:VAL:HG22	2.03	0.41
1:B:61:LYS:HB2	1:B:303:PHE:HB2	2.01	0.41
1:C:224:ALA:HB2	1:C:247:TYR:CE1	2.56	0.41
1:E:106:GLU:OE2	1:F:262:GLU:HG3	2.20	0.41
1:F:566:LEU:HD23	1:F:576:GLN:HG3	2.03	0.41
1:G:145:GLU:CD	1:H:221:LEU:HD21	2.41	0.41
1:A:42:ALA:O	1:A:46:VAL:HG23	2.20	0.41
1:H:430:GLN:HB3	1:H:434:ARG:NH1	2.36	0.41
1:A:35:LEU:HD12	1:A:35:LEU:N	2.29	0.41
1:B:22:ARG:NE	1:D:417:ARG:HH21	2.19	0.41
1:B:157:PHE:HD1	1:B:157:PHE:HA	1.75	0.41
1:C:540:MET:HA	1:C:543:VAL:HG22	2.03	0.41
1:D:13:ARG:HA	1:D:13:ARG:HE	1.85	0.41
1:D:35:LEU:HD22	1:D:108:VAL:HG22	2.03	0.41
1:D:41:GLY:O	1:D:45:MET:HG2	2.21	0.41
1:D:446:LEU:HD11	1:D:503:LYS:HG2	2.03	0.41
1:F:54:LEU:O	1:F:57:PRO:HD2	2.21	0.41
1:F:213:MET:HA	1:F:257:ALA:HB1	2.03	0.41
1:F:520:LEU:HD11	1:F:550:ILE:HD12	2.03	0.41
1:G:473:GLY:O	1:G:539:THR:HG21	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:15:ASP:OD1	1:H:16:GLY:N	2.53	0.41
1:H:113:THR:HG21	1:H:152:ASP:OD1	2.20	0.41
1:H:401:SER:N	2:H:701:ADP:O1A	2.43	0.41
1:G:437:LEU:HD23	1:G:518:ILE:HB	2.03	0.41
1:B:454:ASN:HB3	1:B:510:ARG:HH21	1.86	0.40
1:F:98:ASP:O	1:F:101:ARG:HG2	2.21	0.40
1:C:95:VAL:HG11	1:D:273:ALA:HB2	2.02	0.40
1:C:129:LEU:HD22	1:C:410:PHE:CD2	2.57	0.40
1:C:354:LEU:HD12	1:C:423:GLN:OE1	2.21	0.40
1:C:596:GLN:HG2	1:D:530:THR:HG21	2.03	0.40
1:D:101:ARG:HG3	1:D:160:PHE:HE1	1.86	0.40
1:D:581:ASP:O	1:D:585:ARG:HG3	2.21	0.40
1:E:287:THR:HG21	1:E:301:LEU:HA	2.03	0.40
1:A:216:LEU:HD12	1:A:257:ALA:HB2	2.01	0.40
1:A:458:GLY:HA2	1:B:237:PHE:CD1	2.56	0.40
1:B:157:PHE:O	1:B:161:ASN:HB3	2.22	0.40
1:C:138:GLY:O	1:C:142:LYS:HG2	2.21	0.40
1:G:313:ARG:HB3	1:G:314:PRO:HD3	2.02	0.40
1:G:534:GLN:HG3	1:H:599:GLU:OE2	2.21	0.40
1:A:35:LEU:H	1:A:35:LEU:CD1	2.29	0.40
1:B:217:ASP:HB2	1:B:254:TYR:CE1	2.57	0.40
1:C:457:TYR:OH	1:D:234:VAL:HG22	2.22	0.40
1:E:223:ARG:HD3	1:E:246:ARG:HG2	2.03	0.40
1:G:120:VAL:O	1:G:124:LEU:HD23	2.22	0.40
1:H:42:ALA:O	1:H:46:VAL:HG23	2.21	0.40
1:A:437:LEU:O	1:A:514:LYS:NZ	2.48	0.40
1:G:229:LEU:HD11	1:H:137:THR:HG23	2.03	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	584/614 (95%)	572 (98%)	11 (2%)	1 (0%)	47	78
1	B	584/614 (95%)	565 (97%)	19 (3%)	0	100	100
1	C	588/614 (96%)	573 (97%)	14 (2%)	1 (0%)	47	78
1	D	584/614 (95%)	572 (98%)	11 (2%)	1 (0%)	47	78
1	E	587/614 (96%)	576 (98%)	11 (2%)	0	100	100
1	F	587/614 (96%)	574 (98%)	12 (2%)	1 (0%)	47	78
1	G	588/614 (96%)	581 (99%)	7 (1%)	0	100	100
1	H	588/614 (96%)	581 (99%)	7 (1%)	0	100	100
All	All	4690/4912 (96%)	4594 (98%)	92 (2%)	4 (0%)	51	83

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	34	VAL
1	C	182	LEU
1	D	182	LEU
1	F	182	LEU

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	469/492 (95%)	467 (100%)	2 (0%)	91	95
1	B	469/492 (95%)	466 (99%)	3 (1%)	86	93
1	C	472/492 (96%)	469 (99%)	3 (1%)	86	93
1	D	469/492 (95%)	468 (100%)	1 (0%)	93	97
1	E	471/492 (96%)	467 (99%)	4 (1%)	81	89
1	F	471/492 (96%)	469 (100%)	2 (0%)	91	95
1	G	472/492 (96%)	470 (100%)	2 (0%)	91	95
1	H	472/492 (96%)	470 (100%)	2 (0%)	91	95
All	All	3765/3936 (96%)	3746 (100%)	19 (0%)	88	94

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	108	VAL
1	A	153	THR
1	B	108	VAL
1	B	130	ARG
1	B	154	MET
1	C	13	ARG
1	C	154	MET
1	C	526	SER
1	D	26	TYR
1	E	26	TYR
1	E	132	HIS
1	E	154	MET
1	E	307	TYR
1	F	114	ARG
1	F	154	MET
1	G	125	HIS
1	G	307	TYR
1	H	206	ARG
1	H	307	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	596	GLN

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 16 ligands modelled in this entry, 8 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	ADP	H	701	3	24,29,29	0.94	1 (4%)	29,45,45	1.20	4 (13%)
2	ADP	A	701	3	24,29,29	0.97	1 (4%)	29,45,45	1.47	4 (13%)
2	ADP	F	701	3	24,29,29	0.92	1 (4%)	29,45,45	1.14	2 (6%)
2	ADP	E	701	3	24,29,29	0.95	1 (4%)	29,45,45	1.48	4 (13%)
2	ADP	D	701	3	24,29,29	0.95	1 (4%)	29,45,45	1.18	3 (10%)
2	ADP	B	701	3	24,29,29	0.96	1 (4%)	29,45,45	1.49	4 (13%)
2	ADP	C	701	3	24,29,29	0.96	1 (4%)	29,45,45	1.11	3 (10%)
2	ADP	G	701	3	24,29,29	0.94	1 (4%)	29,45,45	1.21	3 (10%)

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. '2' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	ADP	H	701	3	-	2/12/32/32	0/3/3/3
2	ADP	A	701	3	-	2/12/32/32	0/3/3/3
2	ADP	F	701	3	-	5/12/32/32	0/3/3/3
2	ADP	E	701	3	-	3/12/32/32	0/3/3/3
2	ADP	D	701	3	-	3/12/32/32	0/3/3/3
2	ADP	B	701	3	-	1/12/32/32	0/3/3/3
2	ADP	C	701	3	-	5/12/32/32	0/3/3/3
2	ADP	G	701	3	-	4/12/32/32	0/3/3/3

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	701	ADP	C5-C4	2.56	1.47	1.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	701	ADP	C5-C4	2.55	1.47	1.40
2	B	701	ADP	C5-C4	2.54	1.47	1.40
2	H	701	ADP	C5-C4	2.50	1.47	1.40
2	E	701	ADP	C5-C4	2.49	1.47	1.40
2	D	701	ADP	C5-C4	2.46	1.47	1.40
2	G	701	ADP	C5-C4	2.42	1.47	1.40
2	F	701	ADP	C5-C4	2.36	1.47	1.40

All (27) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	701	ADP	PA-O3A-PB	-3.62	120.39	132.83
2	E	701	ADP	PA-O3A-PB	-3.58	120.53	132.83
2	A	701	ADP	PA-O3A-PB	-3.35	121.31	132.83
2	B	701	ADP	C3'-C2'-C1'	3.30	105.94	100.98
2	E	701	ADP	C3'-C2'-C1'	3.27	105.91	100.98
2	A	701	ADP	C3'-C2'-C1'	3.26	105.88	100.98
2	E	701	ADP	N3-C2-N1	-3.21	123.66	128.68
2	B	701	ADP	N3-C2-N1	-3.17	123.72	128.68
2	A	701	ADP	N3-C2-N1	-3.11	123.81	128.68
2	H	701	ADP	PA-O3A-PB	-2.91	122.84	132.83
2	D	701	ADP	PA-O3A-PB	-2.73	123.44	132.83
2	G	701	ADP	PA-O3A-PB	-2.71	123.54	132.83
2	F	701	ADP	N3-C2-N1	-2.70	124.47	128.68
2	E	701	ADP	C4-C5-N7	-2.69	106.60	109.40
2	B	701	ADP	C4-C5-N7	-2.64	106.65	109.40
2	G	701	ADP	N3-C2-N1	-2.62	124.58	128.68
2	A	701	ADP	C4-C5-N7	-2.59	106.70	109.40
2	G	701	ADP	C4-C5-N7	-2.51	106.78	109.40
2	D	701	ADP	N3-C2-N1	-2.51	124.75	128.68
2	C	701	ADP	N3-C2-N1	-2.46	124.83	128.68
2	H	701	ADP	N3-C2-N1	-2.43	124.88	128.68
2	F	701	ADP	C4-C5-N7	-2.37	106.93	109.40
2	C	701	ADP	C4-C5-N7	-2.33	106.97	109.40
2	D	701	ADP	C4-C5-N7	-2.25	107.05	109.40
2	H	701	ADP	C4-C5-N7	-2.25	107.05	109.40
2	H	701	ADP	C3'-C2'-C1'	2.13	104.18	100.98
2	C	701	ADP	C3'-C2'-C1'	2.11	104.15	100.98

There are no chirality outliers.

All (25) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	C	701	ADP	PA-O3A-PB-O2B
2	C	701	ADP	PA-O3A-PB-O3B
2	C	701	ADP	C5'-O5'-PA-O1A
2	C	701	ADP	O4'-C4'-C5'-O5'
2	D	701	ADP	C5'-O5'-PA-O1A
2	D	701	ADP	C5'-O5'-PA-O2A
2	E	701	ADP	C5'-O5'-PA-O1A
2	E	701	ADP	C5'-O5'-PA-O2A
2	F	701	ADP	C5'-O5'-PA-O1A
2	F	701	ADP	C5'-O5'-PA-O2A
2	G	701	ADP	C5'-O5'-PA-O3A
2	F	701	ADP	C3'-C4'-C5'-O5'
2	G	701	ADP	O4'-C4'-C5'-O5'
2	F	701	ADP	O4'-C4'-C5'-O5'
2	G	701	ADP	C3'-C4'-C5'-O5'
2	D	701	ADP	C5'-O5'-PA-O3A
2	G	701	ADP	C5'-O5'-PA-O1A
2	B	701	ADP	O4'-C4'-C5'-O5'
2	A	701	ADP	O4'-C4'-C5'-O5'
2	C	701	ADP	PA-O3A-PB-O1B
2	E	701	ADP	C5'-O5'-PA-O3A
2	F	701	ADP	C5'-O5'-PA-O3A
2	H	701	ADP	O4'-C4'-C5'-O5'
2	A	701	ADP	C5'-O5'-PA-O1A
2	H	701	ADP	C5'-O5'-PA-O1A

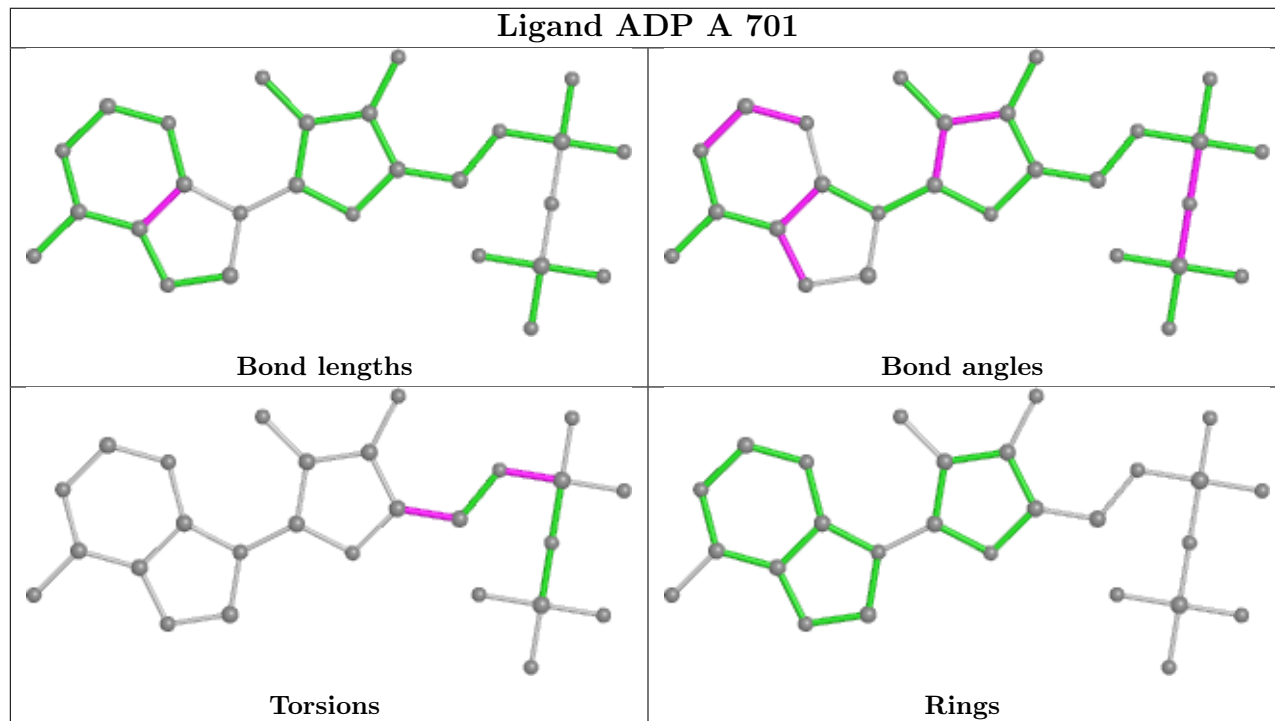
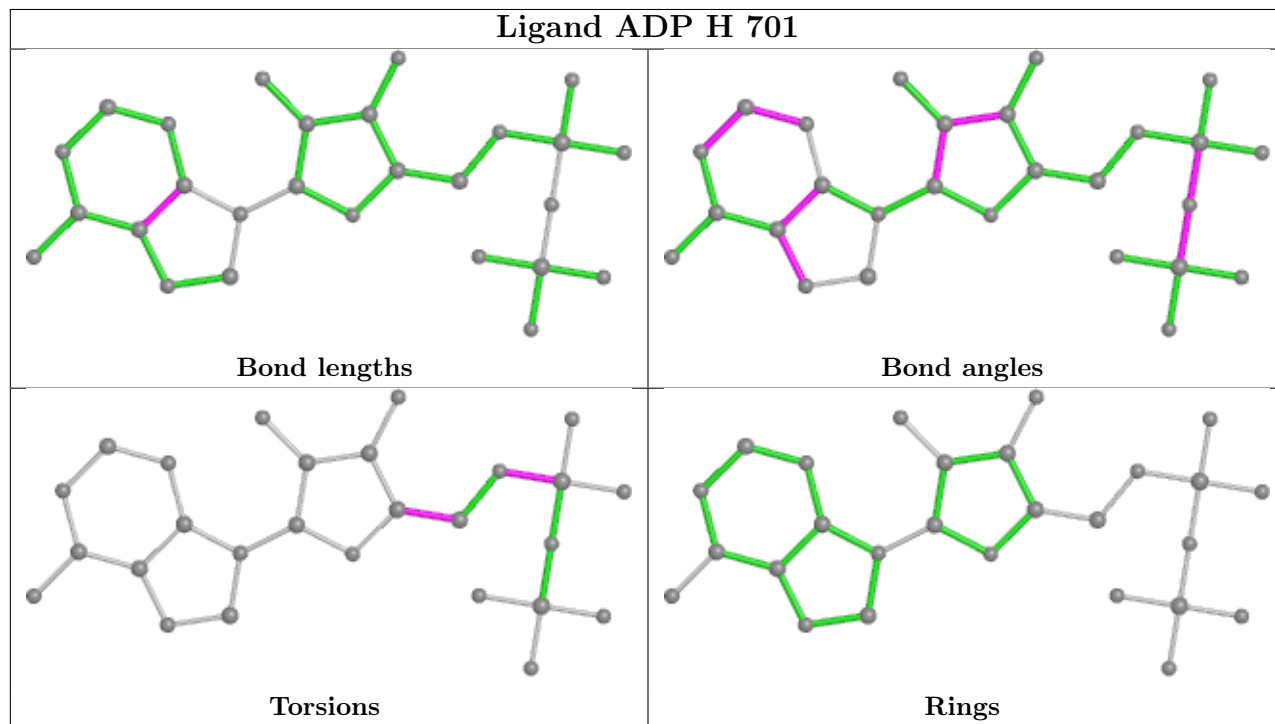
There are no ring outliers.

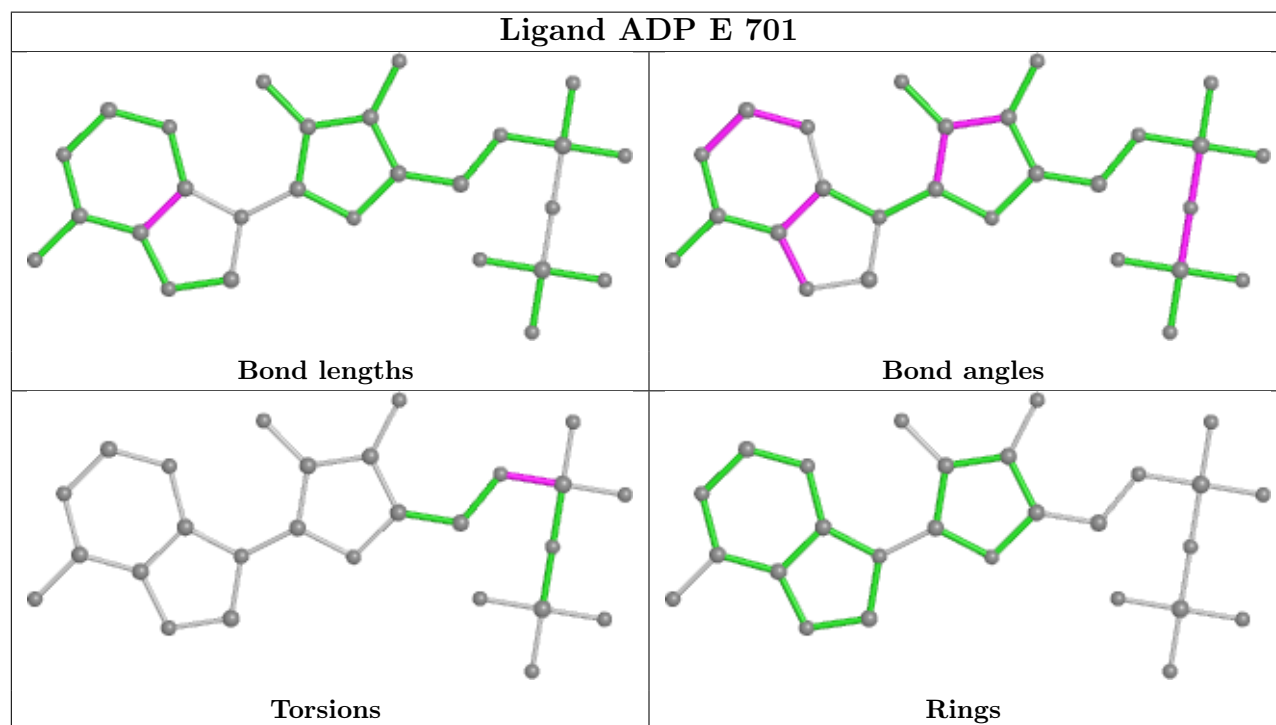
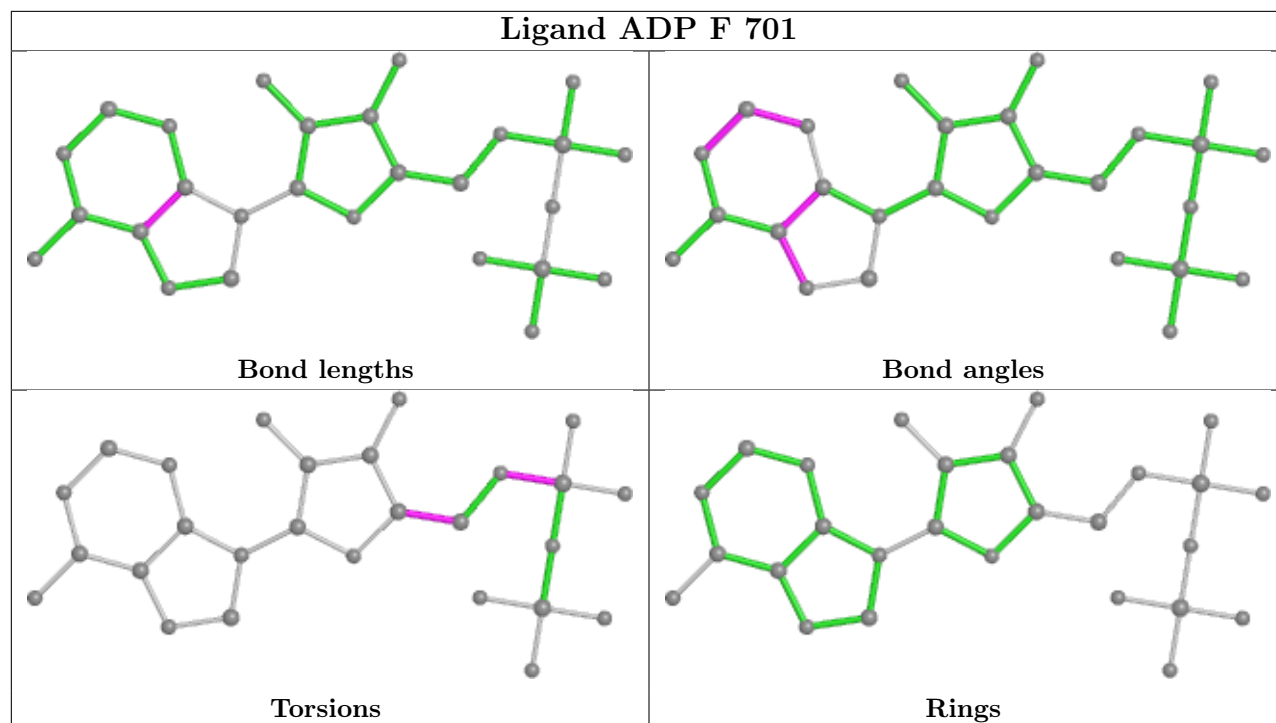
7 monomers are involved in 12 short contacts:

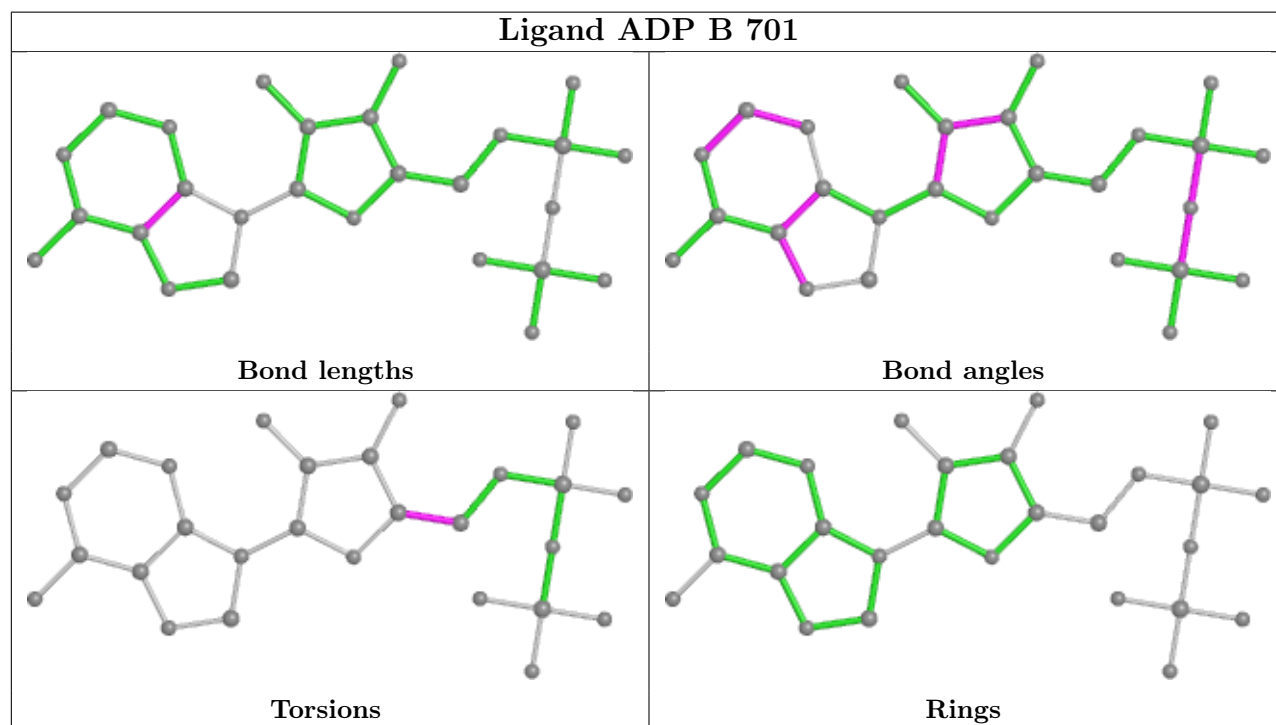
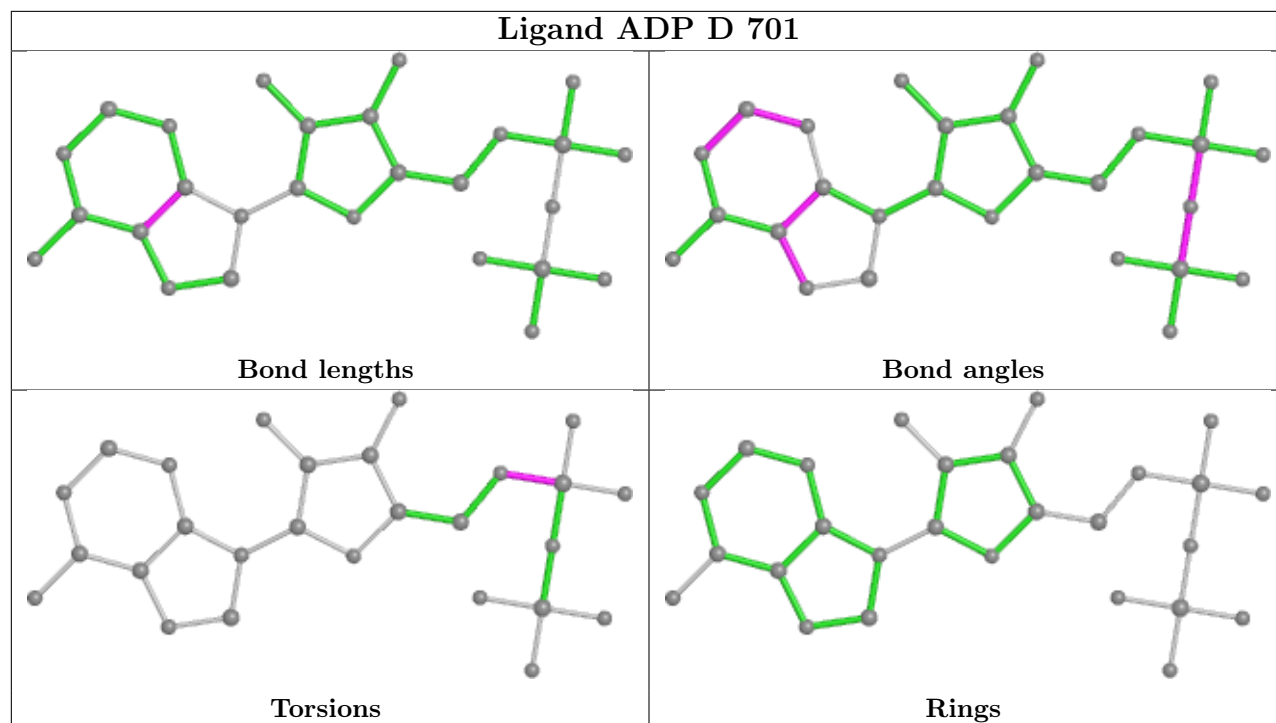
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	H	701	ADP	1	0
2	A	701	ADP	2	0
2	F	701	ADP	1	0
2	E	701	ADP	3	0
2	B	701	ADP	2	0
2	C	701	ADP	2	0
2	G	701	ADP	1	0

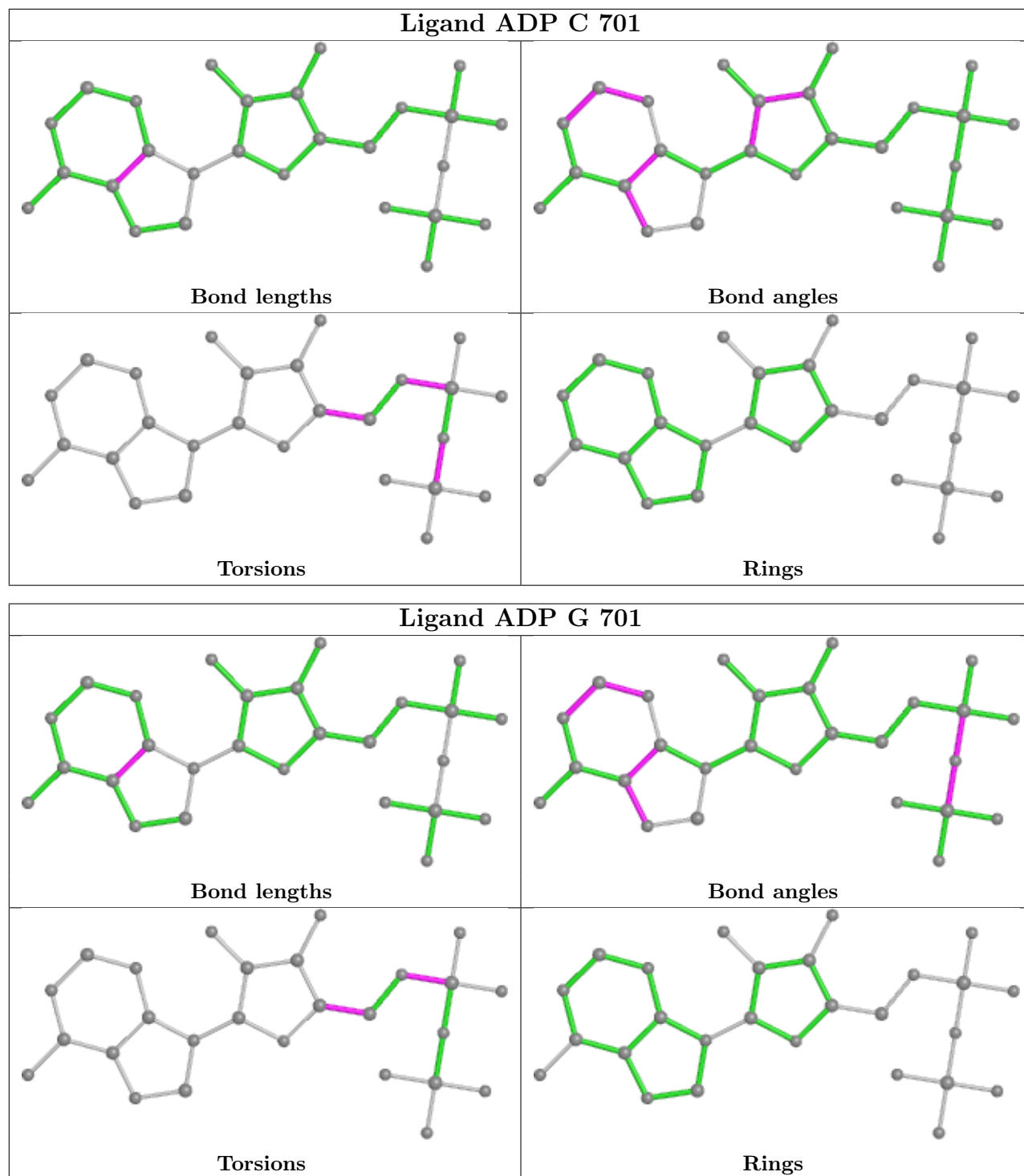
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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	586/614 (95%)	-0.34	5 (0%) 84 76	82, 131, 179, 338	0
1	B	586/614 (95%)	-0.28	7 (1%) 79 69	87, 138, 177, 227	0
1	C	590/614 (96%)	-0.32	10 (1%) 70 59	95, 136, 181, 240	0
1	D	586/614 (95%)	-0.20	19 (3%) 47 35	98, 142, 186, 400	0
1	E	589/614 (95%)	-0.04	33 (5%) 24 17	138, 210, 250, 271	0
1	F	589/614 (95%)	0.10	36 (6%) 21 14	136, 211, 256, 278	0
1	G	590/614 (96%)	0.34	79 (13%) 3 3	158, 224, 253, 262	0
1	H	590/614 (96%)	0.30	62 (10%) 6 5	179, 217, 251, 270	0
All	All	4706/4912 (95%)	-0.05	251 (5%) 26 20	82, 176, 245, 400	0

All (251) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	70	GLY	7.3
1	H	74	GLN	6.5
1	G	111	ASP	6.2
1	A	71	GLY	6.1
1	F	563	ASP	6.0
1	D	71	GLY	5.8
1	H	599	GLU	5.5
1	E	300	ASP	5.3
1	H	600	SER	5.3
1	H	349	PRO	5.3
1	G	352	PRO	5.2
1	H	589	TYR	5.2
1	F	81	LEU	5.0
1	D	70	GLY	5.0
1	G	178	LEU	5.0
1	G	581	ASP	4.9

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Mol	Chain	Res	Type	RSRZ
1	G	374	ARG	4.7
1	E	478	ASP	4.6
1	H	300	ASP	4.5
1	H	72	GLY	4.5
1	B	74	GLN	4.5
1	F	388	SER	4.3
1	F	231	TYR	4.3
1	G	259	VAL	4.3
1	G	427	HIS	4.3
1	H	457	TYR	4.3
1	E	448	ASN	4.3
1	D	72	GLY	4.3
1	F	599	GLU	4.3
1	H	73	ALA	4.2
1	G	488	ASP	4.2
1	F	82	ALA	4.2
1	H	298	VAL	4.2
1	F	62	LYS	4.2
1	D	73	ALA	4.2
1	F	71	GLY	4.1
1	E	494	ARG	4.1
1	H	560	ALA	4.1
1	G	484	PRO	4.0
1	C	293	GLN	4.0
1	G	353	ALA	4.0
1	G	576	GLN	4.0
1	G	132	HIS	3.9
1	H	388	SER	3.9
1	G	110	GLN	3.8
1	E	297	THR	3.8
1	G	31	ASP	3.8
1	F	389	ARG	3.8
1	F	72	GLY	3.8
1	E	71	GLY	3.8
1	E	289	TYR	3.8
1	G	485	GLN	3.8
1	D	135	ARG	3.7
1	G	58	PHE	3.7
1	G	584	ARG	3.7
1	E	498	LEU	3.7
1	G	483	LEU	3.7
1	E	86	ALA	3.7

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Mol	Chain	Res	Type	RSRZ
1	F	146	ARG	3.7
1	G	373	ASP	3.6
1	G	147	GLY	3.6
1	H	453	TYR	3.6
1	G	556	LEU	3.6
1	D	373	ASP	3.6
1	G	335	MET	3.6
1	F	145	GLU	3.5
1	E	89	LEU	3.5
1	H	137	THR	3.5
1	E	394	GLY	3.5
1	H	487	TYR	3.5
1	G	578	SER	3.5
1	G	585	ARG	3.4
1	H	593	TRP	3.4
1	H	77	LEU	3.3
1	F	35	LEU	3.3
1	H	588	LEU	3.3
1	G	114	ARG	3.3
1	H	348	VAL	3.3
1	D	375	GLU	3.3
1	C	264	SER	3.3
1	D	67	MET	3.3
1	G	587	GLY	3.3
1	E	72	GLY	3.3
1	H	78	THR	3.3
1	G	258	ALA	3.2
1	E	90	GLY	3.2
1	F	387	GLY	3.2
1	B	300	ASP	3.2
1	H	601	ALA	3.2
1	G	260	LYS	3.2
1	B	374	ARG	3.2
1	E	125	HIS	3.2
1	H	514	LYS	3.2
1	G	498	LEU	3.2
1	G	575	GLU	3.2
1	E	483	LEU	3.1
1	F	148	THR	3.1
1	G	579	HIS	3.1
1	C	598	ALA	3.1
1	H	543	VAL	3.1

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Mol	Chain	Res	Type	RSRZ
1	H	442	GLN	3.1
1	H	522	ASP	3.1
1	H	67	MET	3.0
1	F	593	TRP	3.0
1	H	443	ASP	3.0
1	C	295	LYS	3.0
1	G	602	GLU	3.0
1	H	586	ASP	3.0
1	E	480	ILE	3.0
1	E	482	ARG	3.0
1	H	484	PRO	3.0
1	D	374	ARG	3.0
1	B	295	LYS	3.0
1	E	569	ASP	3.0
1	G	174	VAL	2.9
1	C	498	LEU	2.9
1	C	599	GLU	2.9
1	H	389	ARG	2.9
1	H	563	ASP	2.9
1	G	378	HIS	2.9
1	B	316	ASP	2.9
1	G	455	ILE	2.9
1	H	146	ARG	2.9
1	E	476	ILE	2.9
1	F	59	ALA	2.9
1	H	598	ALA	2.8
1	H	488	ASP	2.8
1	H	602	GLU	2.8
1	F	298	VAL	2.8
1	H	75	PRO	2.8
1	F	110	GLN	2.8
1	H	177	TRP	2.8
1	G	137	THR	2.8
1	E	395	PRO	2.8
1	G	146	ARG	2.8
1	G	573	LEU	2.8
1	D	74	GLN	2.7
1	H	449	ASP	2.7
1	G	300	ASP	2.7
1	G	293	GLN	2.7
1	F	80	ALA	2.7
1	E	479	PHE	2.7

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Mol	Chain	Res	Type	RSRZ
1	G	577	GLY	2.7
1	A	69	LEU	2.7
1	G	376	ILE	2.7
1	H	375	GLU	2.6
1	G	30	ALA	2.6
1	H	526	SER	2.6
1	E	298	VAL	2.6
1	H	562	SER	2.6
1	F	79	VAL	2.6
1	H	485	GLN	2.6
1	G	586	ASP	2.6
1	D	137	THR	2.6
1	G	572	ARG	2.6
1	D	455	ILE	2.6
1	F	58	PHE	2.6
1	C	263	ASN	2.5
1	F	386	ALA	2.5
1	F	78	THR	2.5
1	G	177	TRP	2.5
1	H	590	ALA	2.5
1	G	520	LEU	2.5
1	G	285	ALA	2.5
1	G	506	VAL	2.5
1	G	559	ILE	2.5
1	H	63	ALA	2.5
1	C	494	ARG	2.5
1	F	313	ARG	2.4
1	F	562	SER	2.4
1	H	329	LEU	2.4
1	E	28	TRP	2.4
1	H	597	ALA	2.4
1	G	571	GLY	2.4
1	C	600	SER	2.4
1	G	574	ALA	2.4
1	G	170	THR	2.4
1	H	513	VAL	2.4
1	H	525	THR	2.4
1	H	136	ARG	2.4
1	A	67	MET	2.4
1	G	478	ASP	2.4
1	G	179	ASN	2.4
1	G	487	TYR	2.4

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Mol	Chain	Res	Type	RSRZ
1	D	570	GLN	2.3
1	F	208	HIS	2.3
1	G	208	HIS	2.3
1	F	373	ASP	2.3
1	E	67	MET	2.3
1	G	447	PHE	2.3
1	H	565	ILE	2.3
1	B	574	ALA	2.3
1	H	564	THR	2.3
1	F	498	LEU	2.3
1	G	286	TRP	2.3
1	D	598	ALA	2.3
1	H	347	ASP	2.3
1	G	108	VAL	2.3
1	E	252	ARG	2.3
1	F	61	LYS	2.3
1	H	445	VAL	2.3
1	E	130	ARG	2.3
1	E	222	ALA	2.3
1	G	570	GLN	2.3
1	G	176	PHE	2.3
1	H	490	GLU	2.3
1	G	486	GLY	2.3
1	G	503	LYS	2.3
1	G	583	LEU	2.3
1	G	521	PHE	2.2
1	G	569	ASP	2.2
1	E	58	PHE	2.2
1	E	430	GLN	2.2
1	B	373	ASP	2.2
1	F	447	PHE	2.2
1	G	32	ASN	2.2
1	C	292	SER	2.2
1	H	541	ARG	2.2
1	G	375	GLU	2.2
1	G	336	PHE	2.2
1	G	379	GLY	2.2
1	E	574	ALA	2.2
1	G	598	ALA	2.2
1	H	596	GLN	2.2
1	D	498	LEU	2.2
1	G	480	ILE	2.2

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Mol	Chain	Res	Type	RSRZ
1	H	62	LYS	2.2
1	E	396	SER	2.2
1	G	589	TYR	2.2
1	G	215	ARG	2.1
1	F	60	TYR	2.1
1	H	286	TRP	2.1
1	E	481	ALA	2.1
1	G	591	GLU	2.1
1	F	300	ASP	2.1
1	F	594	ALA	2.1
1	D	69	LEU	2.1
1	D	463	SER	2.1
1	F	416	GLY	2.1
1	G	263	ASN	2.1
1	D	79	VAL	2.0
1	F	586	ASP	2.0
1	A	73	ALA	2.0
1	G	283	ALA	2.0
1	D	371	ASP	2.0
1	E	575	GLU	2.0
1	H	31	ASP	2.0
1	H	575	GLU	2.0
1	G	332	MET	2.0
1	H	79	VAL	2.0
1	H	354	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](#)

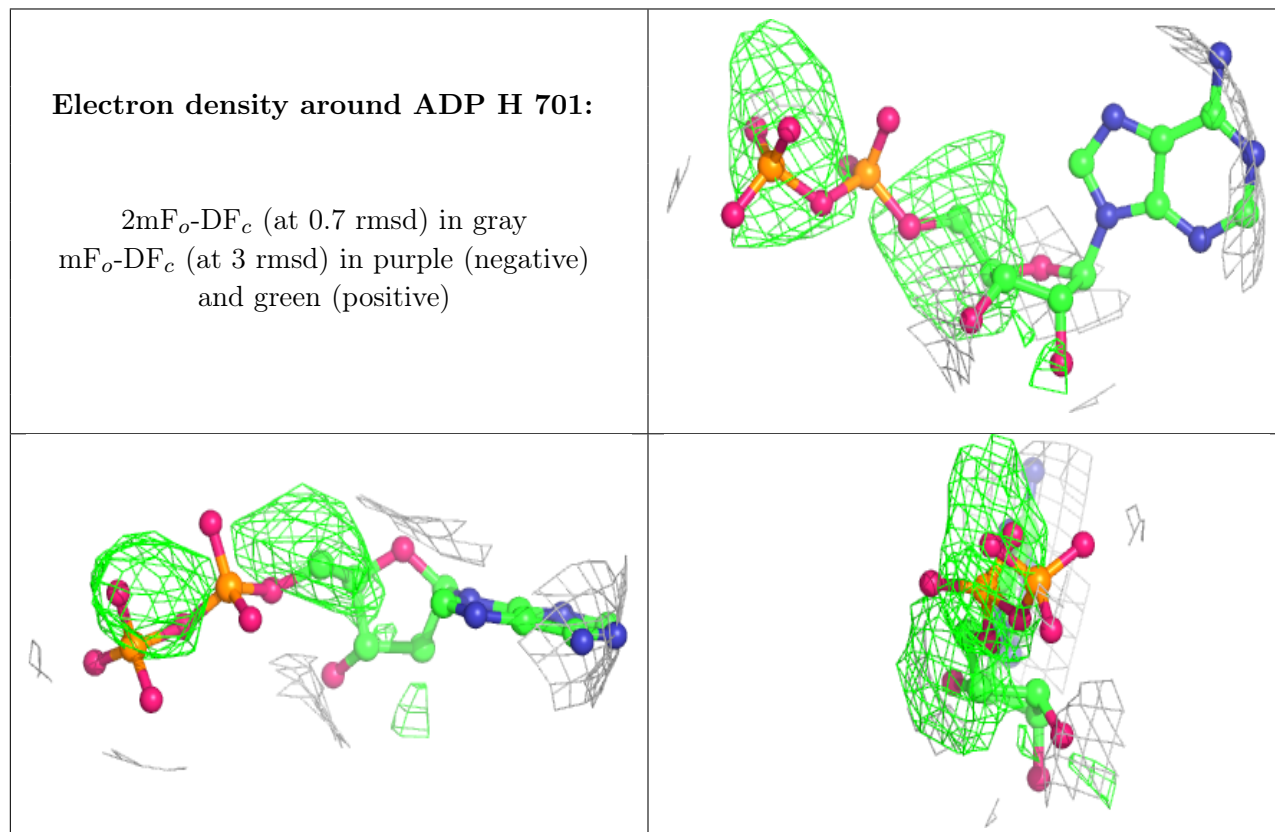
There are no monosaccharides in this entry.

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.

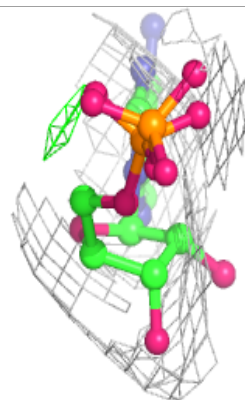
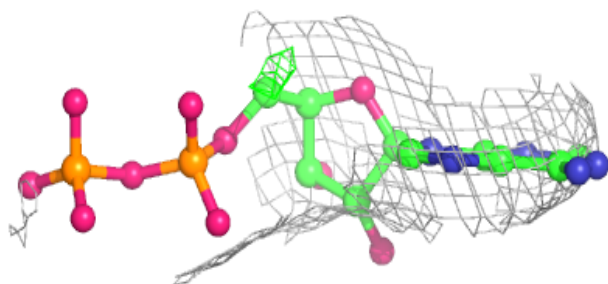
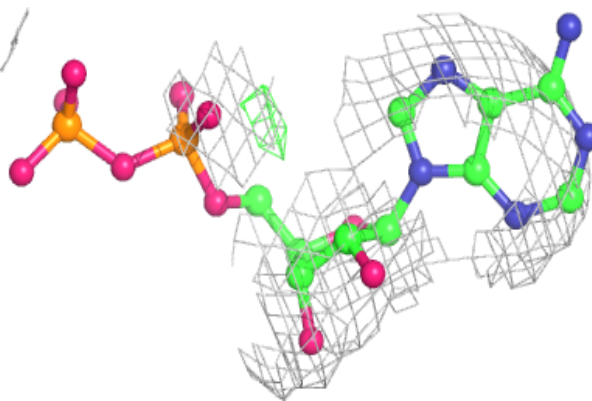
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	ADP	H	701	27/27	0.77	0.36	213,222,226,229	0
2	ADP	G	701	27/27	0.79	0.26	241,255,282,283	0
2	ADP	D	701	27/27	0.79	0.27	154,184,200,205	0
2	ADP	B	701	27/27	0.85	0.34	159,183,220,226	0
3	MG	G	702	1/1	0.85	0.84	151,151,151,151	0
2	ADP	F	701	27/27	0.88	0.37	196,203,210,212	0
3	MG	D	702	1/1	0.89	0.99	150,150,150,150	0
2	ADP	C	701	27/27	0.89	0.23	172,188,203,206	0
3	MG	E	702	1/1	0.91	0.58	99,99,99,99	0
2	ADP	A	701	27/27	0.93	0.25	123,144,170,175	0
2	ADP	E	701	27/27	0.93	0.24	174,183,194,197	0
3	MG	B	702	1/1	0.95	0.62	92,92,92,92	0
3	MG	F	702	1/1	0.97	0.44	120,120,120,120	0
3	MG	C	702	1/1	0.97	0.33	89,89,89,89	0
3	MG	A	702	1/1	0.98	0.29	74,74,74,74	0
3	MG	H	702	1/1	1.00	0.41	138,138,138,138	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.

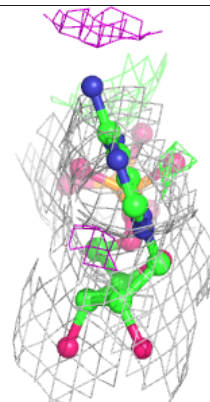
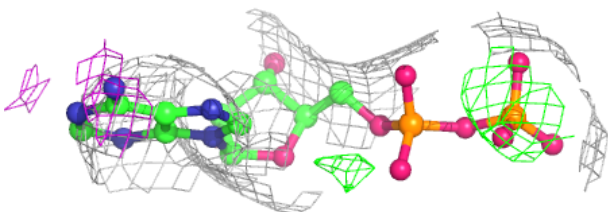
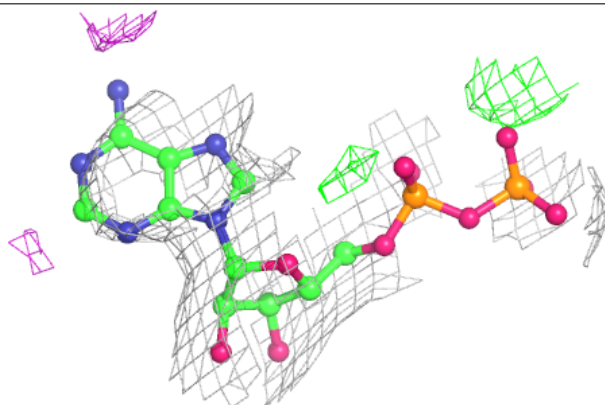


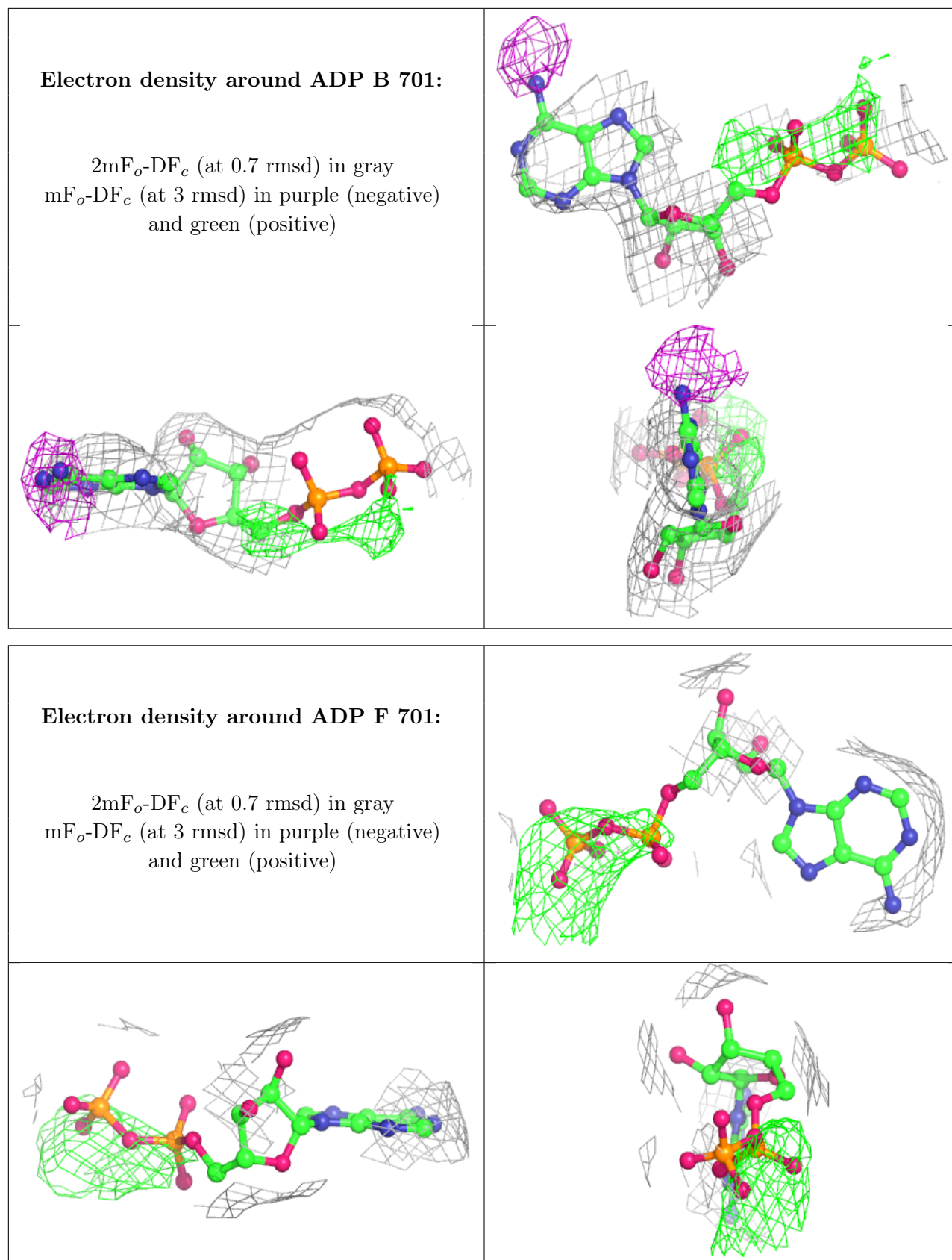
Electron density around ADP G 701:

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

**Electron density around ADP D 701:**

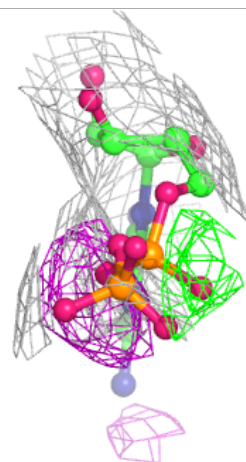
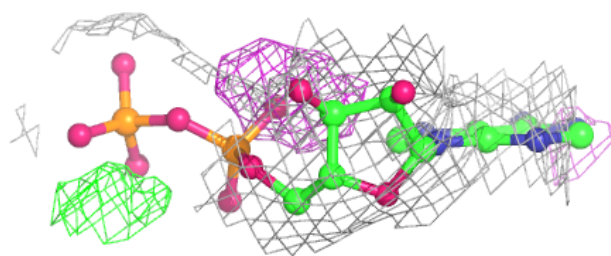
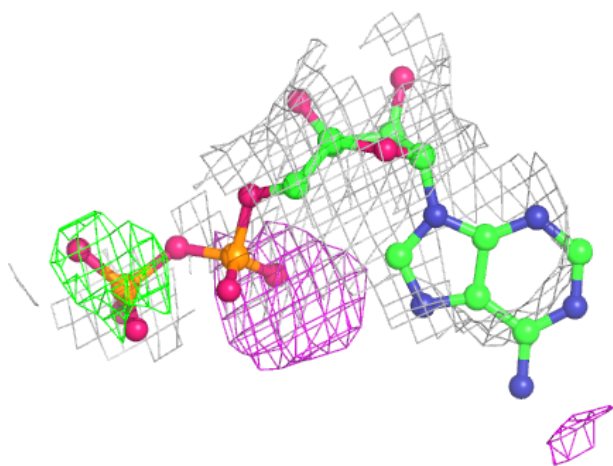
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





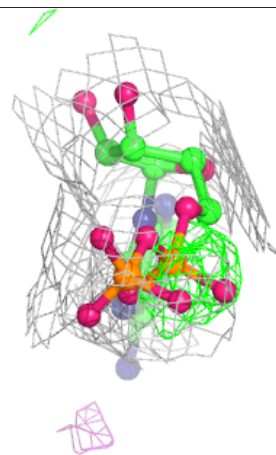
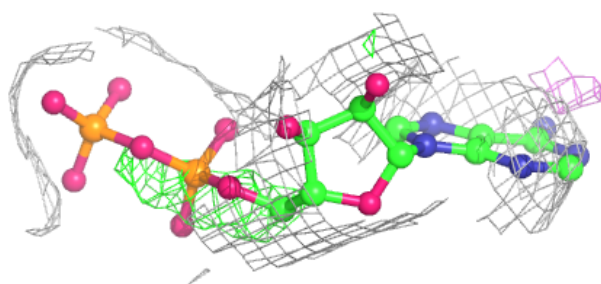
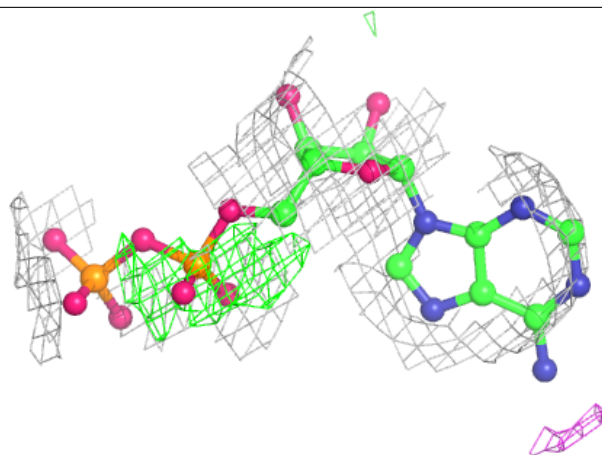
Electron density around ADP C 701:

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

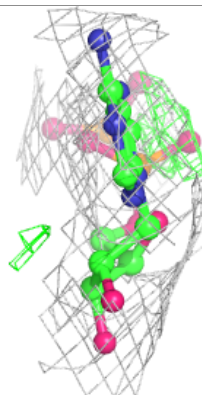
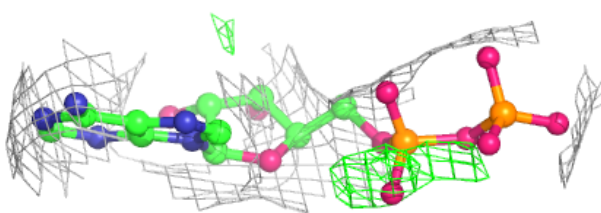
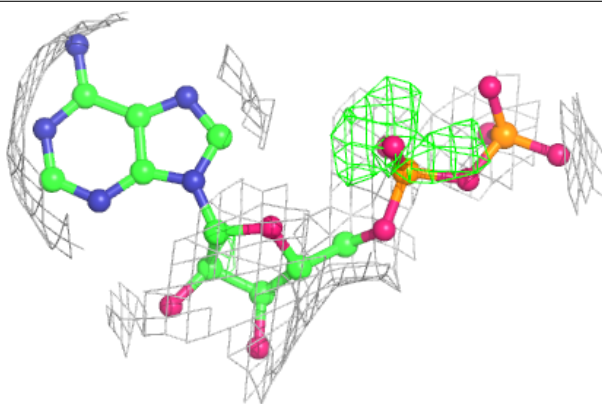


Electron density around ADP A 701:

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

**Electron density around ADP E 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.