



wwPDB X-ray Structure Validation Summary Report ⓘ

May 14, 2020 – 05:37 am BST

PDB ID : 1SVT
Title : Crystal structure of GroEL14-GroES7-(ADP-AlFx)7
Authors : Chaudhry, C.; Horwich, A.L.; Brunger, A.T.; Adams, P.D.
Deposited on : 2004-03-29
Resolution : 2.81 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The 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 : 2.11
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) : 2.11

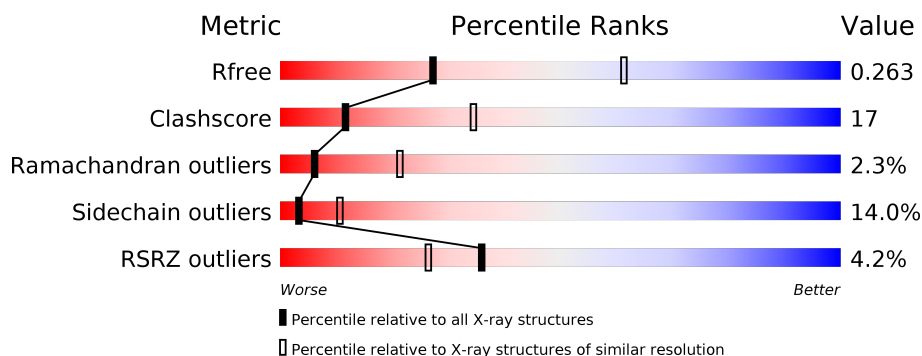
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.81 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	3140 (2.80-2.80)
Clashscore	141614	3569 (2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (2.80-2.80)
RSRZ outliers	127900	3078 (2.80-2.80)

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 on 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	524	<div> <div>4%</div> <div> <div>57%</div> <div>35%</div> <div>6%</div> </div> </div>
1	B	524	<div> <div>6%</div> <div> <div>62%</div> <div>31%</div> <div>6%</div> </div> </div>
1	C	524	<div> <div>5%</div> <div> <div>59%</div> <div>34%</div> <div>6%</div> </div> </div>
1	D	524	<div> <div>5%</div> <div> <div>60%</div> <div>33%</div> <div>6%</div> </div> </div>
1	E	524	<div> <div>7%</div> <div> <div>64%</div> <div>31%</div> <div>5%</div> </div> </div>
1	F	524	<div> <div>8%</div> <div> <div>65%</div> <div>30%</div> <div>5%</div> </div> </div>

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	G	524	
1	H	524	
1	I	524	
1	J	524	
1	K	524	
1	L	524	
1	M	524	
1	N	524	
2	O	97	
2	P	97	
2	Q	97	
2	R	97	
2	S	97	
2	T	97	
2	U	97	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
6	AF3	A	602	-	-	X	-
6	AF3	D	602	-	-	X	-
6	AF3	F	602	-	-	X	-

2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 59498 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 groEL protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	524	Total	C	N	O	S	0	0	0
			3855	2397	665	773	20			
1	B	524	Total	C	N	O	S	0	0	0
			3855	2397	665	773	20			
1	C	524	Total	C	N	O	S	0	0	0
			3855	2397	665	773	20			
1	D	524	Total	C	N	O	S	0	0	0
			3855	2397	665	773	20			
1	E	524	Total	C	N	O	S	0	0	0
			3855	2397	665	773	20			
1	F	524	Total	C	N	O	S	0	0	0
			3855	2397	665	773	20			
1	G	524	Total	C	N	O	S	0	0	0
			3855	2397	665	773	20			
1	H	524	Total	C	N	O	S	0	0	0
			3856	2397	665	774	20			
1	I	524	Total	C	N	O	S	0	0	0
			3856	2397	665	774	20			
1	J	524	Total	C	N	O	S	0	0	0
			3856	2397	665	774	20			
1	K	524	Total	C	N	O	S	0	0	0
			3856	2397	665	774	20			
1	L	524	Total	C	N	O	S	0	0	0
			3856	2397	665	774	20			
1	M	524	Total	C	N	O	S	0	0	0
			3856	2397	665	774	20			
1	N	524	Total	C	N	O	S	0	0	0
			3856	2397	665	774	20			

- Molecule 2 is a protein called groES protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	O	97	Total	C	N	O	S	0	0	0
			728	454	127	145	2			
2	P	97	Total	C	N	O	S	0	0	0
			728	454	127	145	2			
2	Q	97	Total	C	N	O	S	0	0	0
			728	454	127	145	2			
2	R	97	Total	C	N	O	S	0	0	0
			728	454	127	145	2			
2	S	97	Total	C	N	O	S	0	0	0
			728	454	127	145	2			
2	T	97	Total	C	N	O	S	0	0	0
			728	454	127	145	2			
2	U	97	Total	C	N	O	S	0	0	0
			728	454	127	145	2			

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

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

- Molecule 4 is POTASSIUM ION (three-letter code: K) (formula: K).

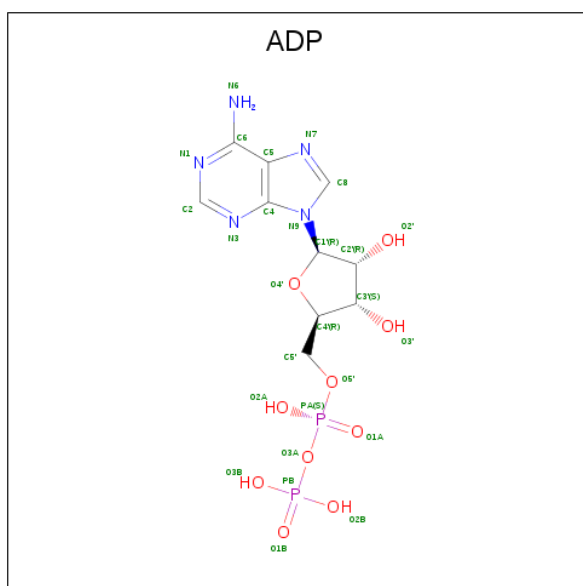
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	G	1	Total	K	0	0
			1	1		
4	D	1	Total	K	0	0
			1	1		
4	E	1	Total	K	0	0
			1	1		
4	B	1	Total	K	0	0
			1	1		

Continued on next page...

Continued from previous page...

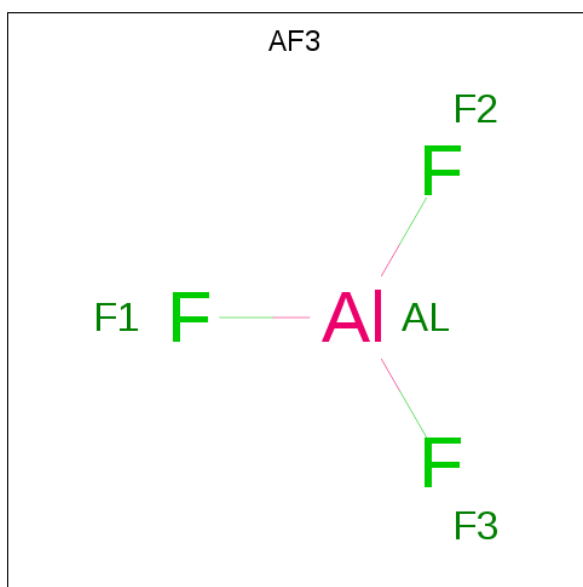
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	C	1	Total	K	0	0
			1	1		
4	A	1	Total	K	0	0
			1	1		
4	F	1	Total	K	0	0
			1	1		

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



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

- Molecule 6 is ALUMINUM FLUORIDE (three-letter code: AF3) (formula: AlF_3).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	Al	F	0	0
			4	1	3		
6	B	1	Total	Al	F	0	0
			4	1	3		
6	C	1	Total	Al	F	0	0
			4	1	3		
6	D	1	Total	Al	F	0	0
			4	1	3		
6	E	1	Total	Al	F	0	0
			4	1	3		
6	F	1	Total	Al	F	0	0
			4	1	3		
6	G	1	Total	Al	F	0	0
			4	1	3		

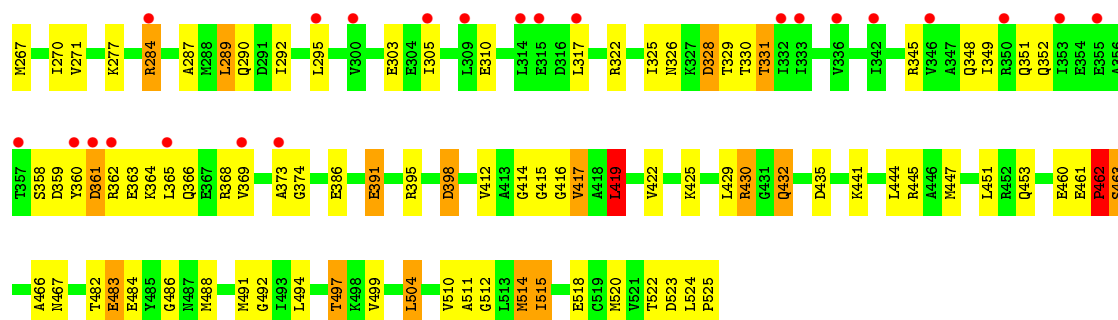
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	19	Total	O	0	0
			19	19		
7	B	10	Total	O	0	0
			10	10		
7	C	21	Total	O	0	0
			21	21		
7	D	14	Total	O	0	0
			14	14		
7	E	12	Total	O	0	0
			12	12		

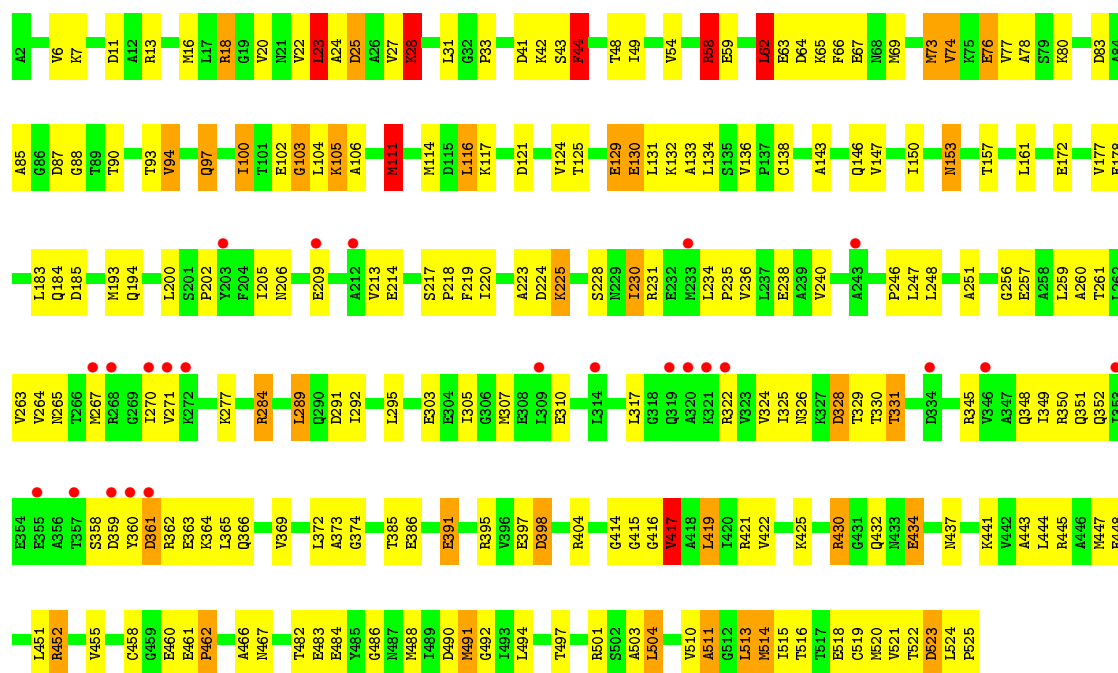
Continued on next page...

Continued from previous page...

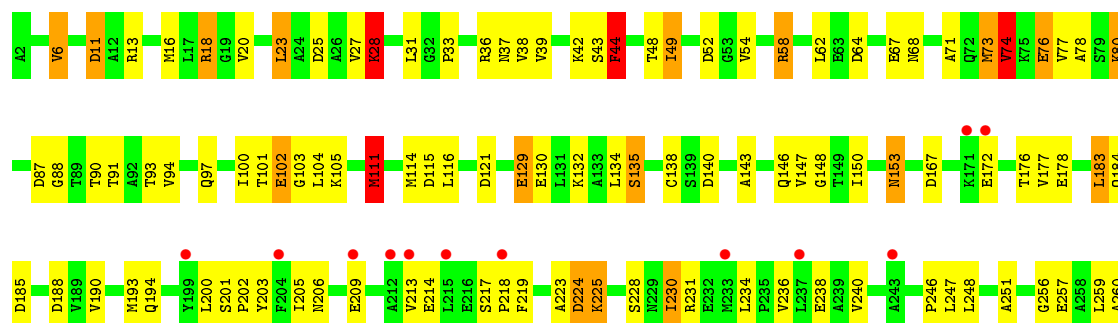
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	F	11	Total 11	O 11	0	0
7	G	20	Total 20	O 20	0	0
7	H	11	Total 11	O 11	0	0
7	I	17	Total 17	O 17	0	0
7	J	12	Total 12	O 12	0	0
7	K	14	Total 14	O 14	0	0
7	L	13	Total 13	O 13	0	0
7	M	10	Total 10	O 10	0	0
7	N	10	Total 10	O 10	0	0

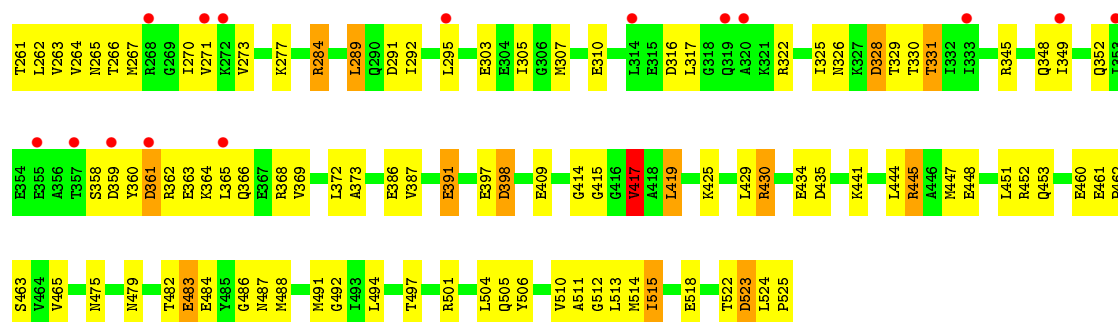


• Molecule 1: groEL protein

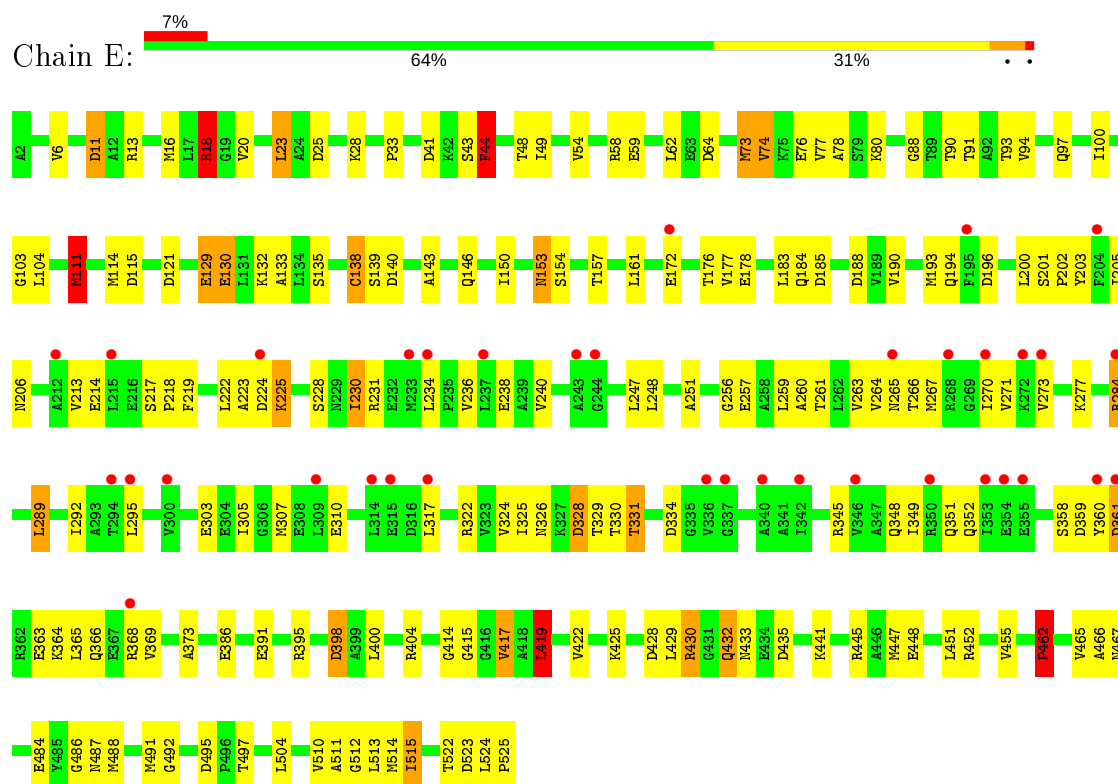


• Molecule 1: groEL protein

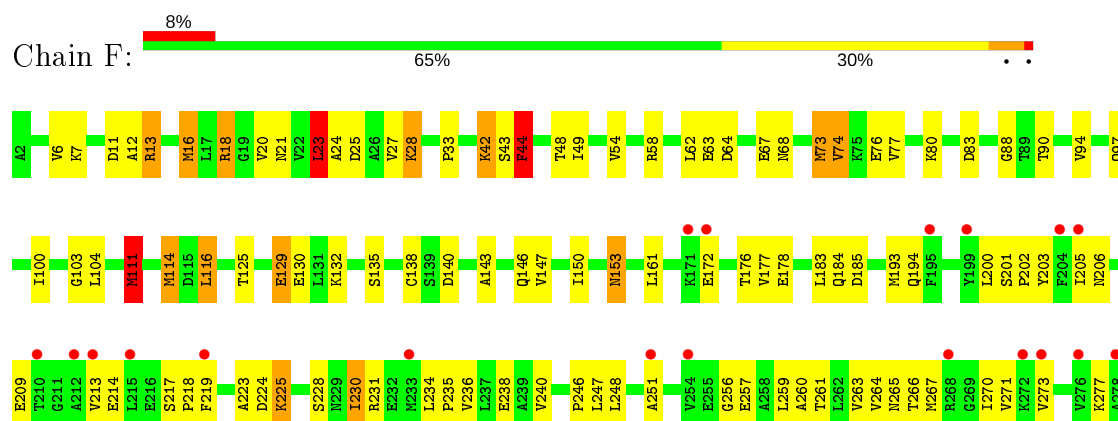


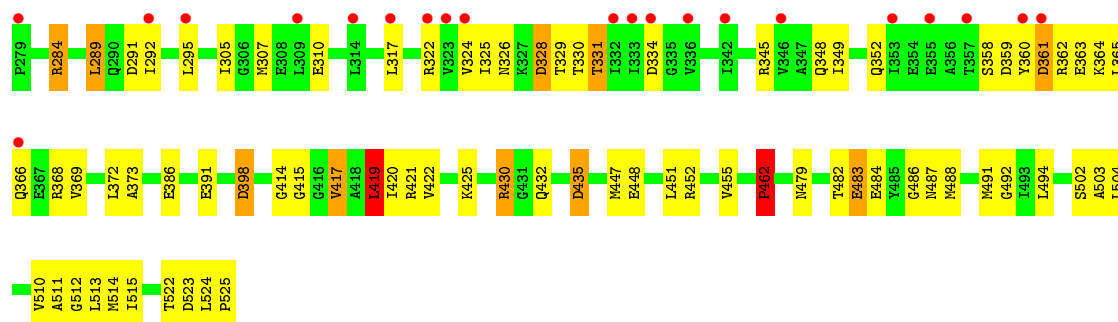


• Molecule 1: groEL protein

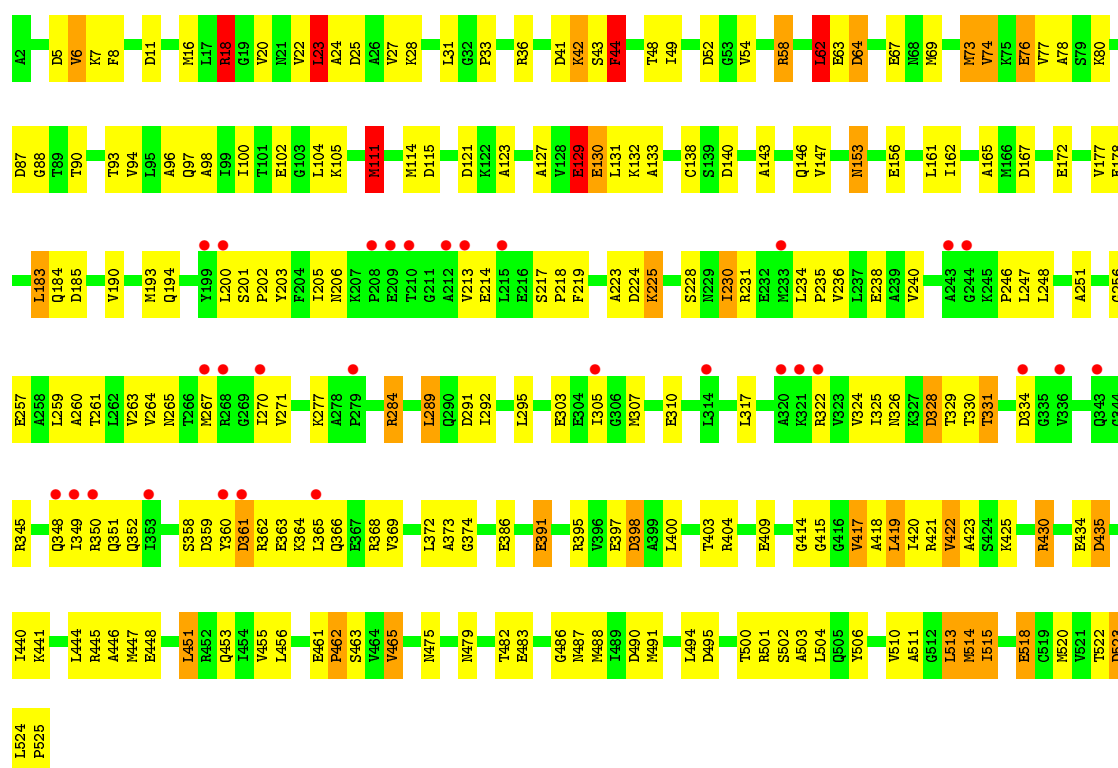


• Molecule 1: groEL protein

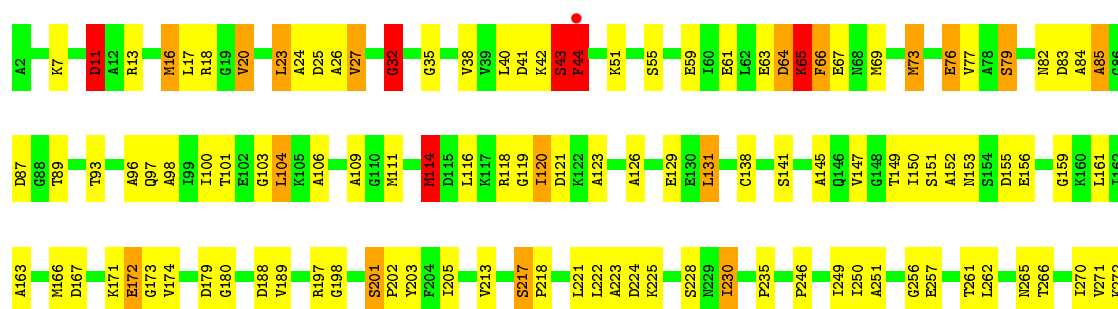


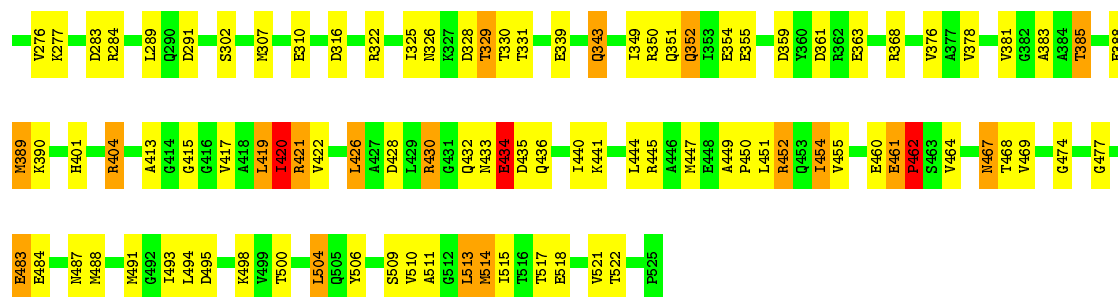


• Molecule 1: groEL protein

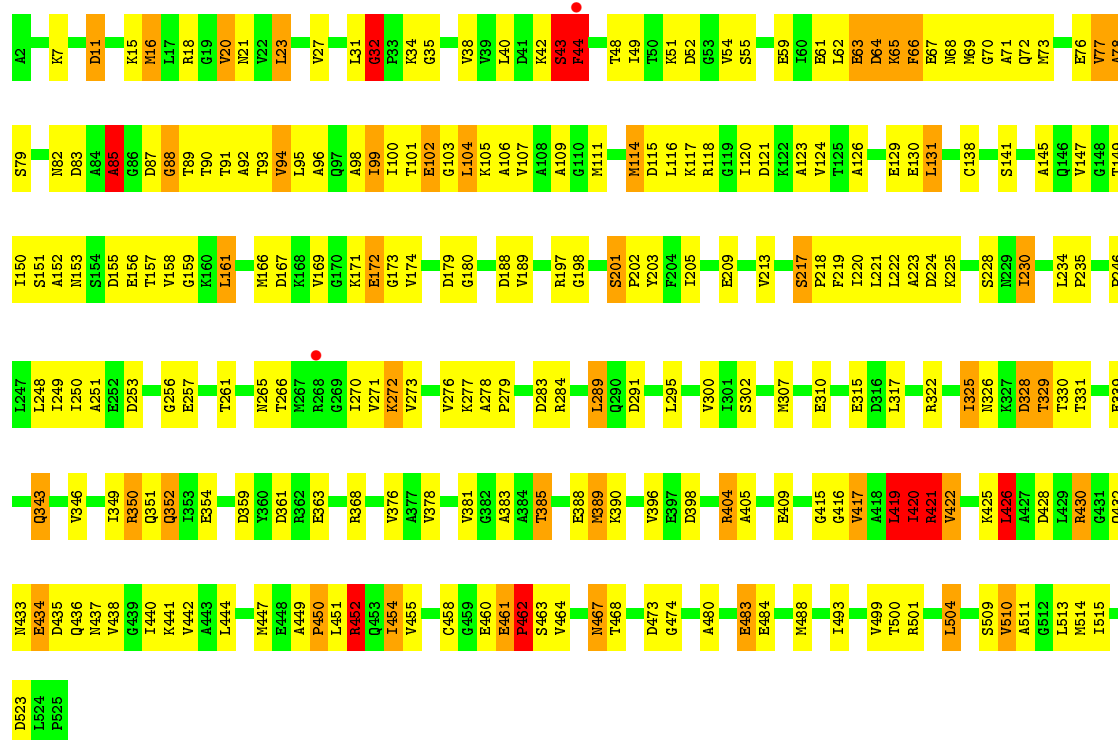


• Molecule 1: groEL protein

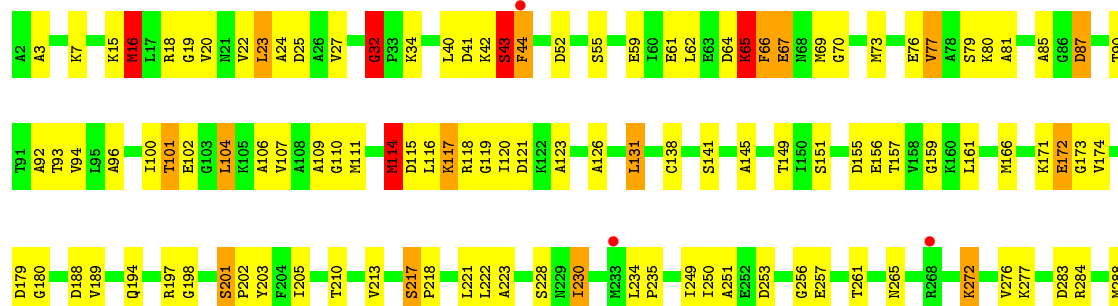


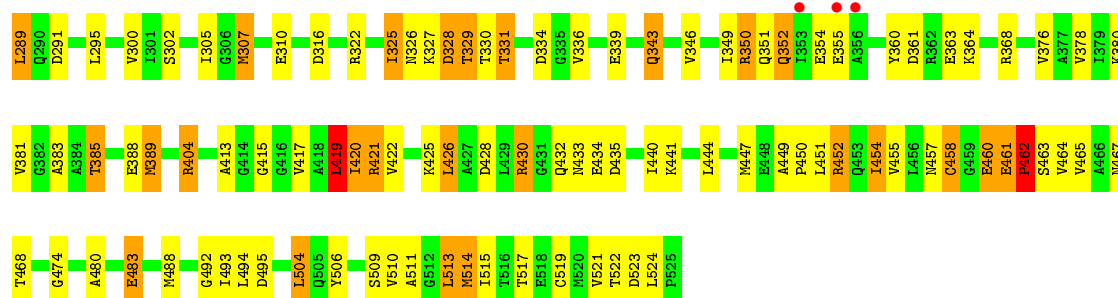


• Molecule 1: groEL protein

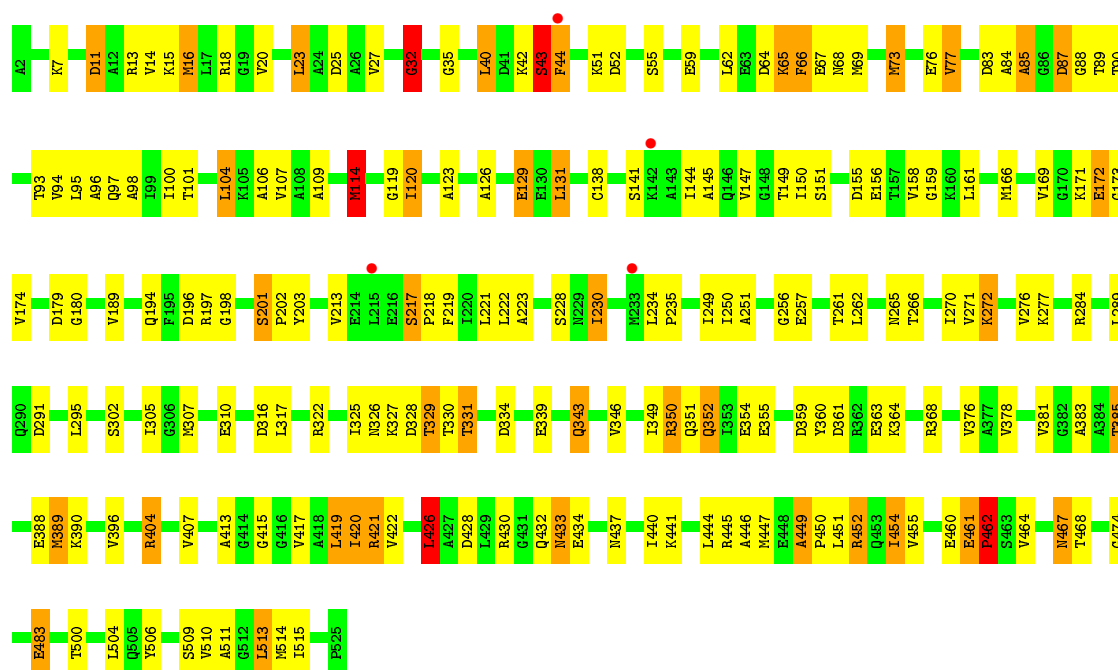


• Molecule 1: groEL protein

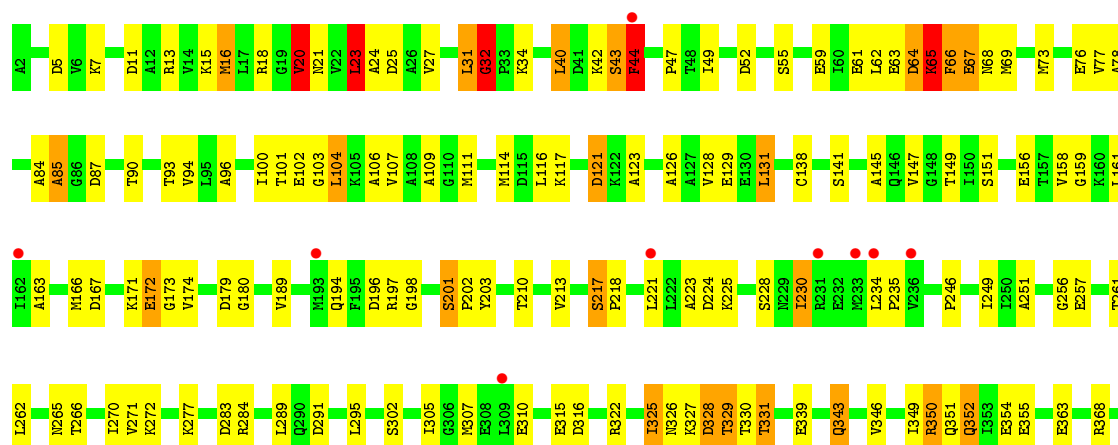


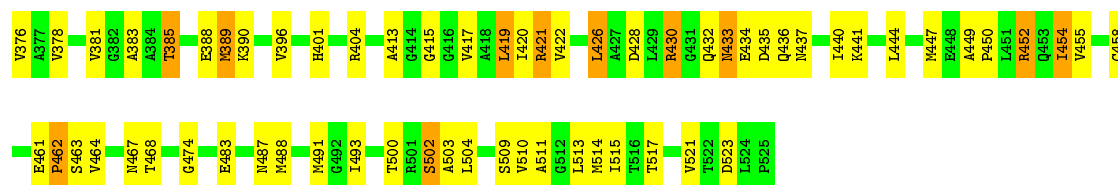


• Molecule 1: groEL protein

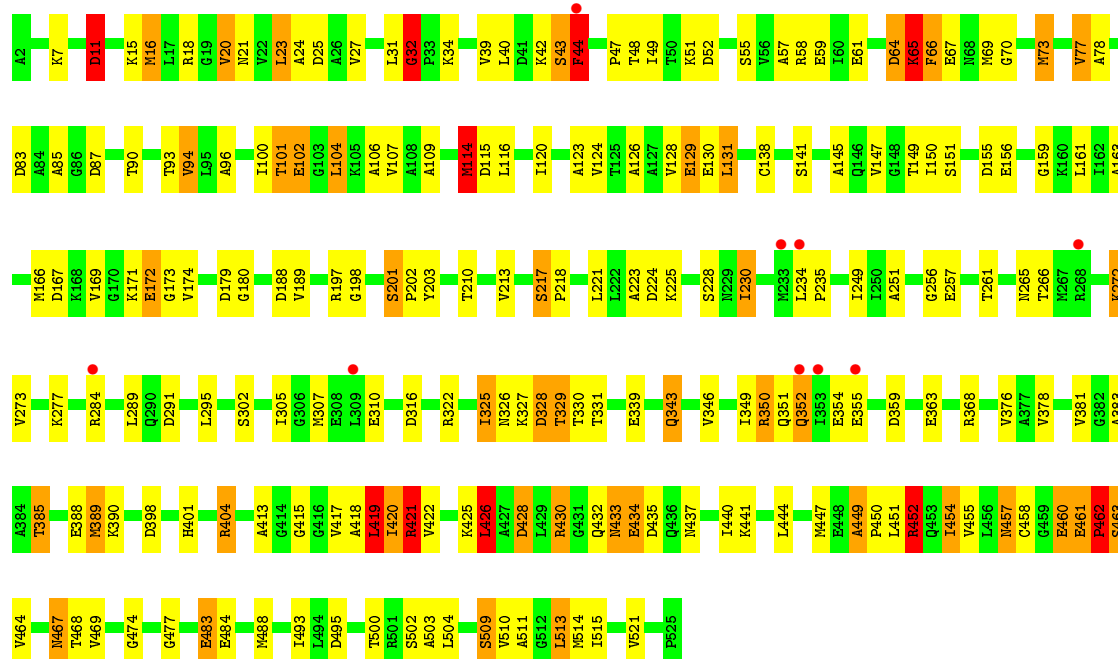


• Molecule 1: groEL protein

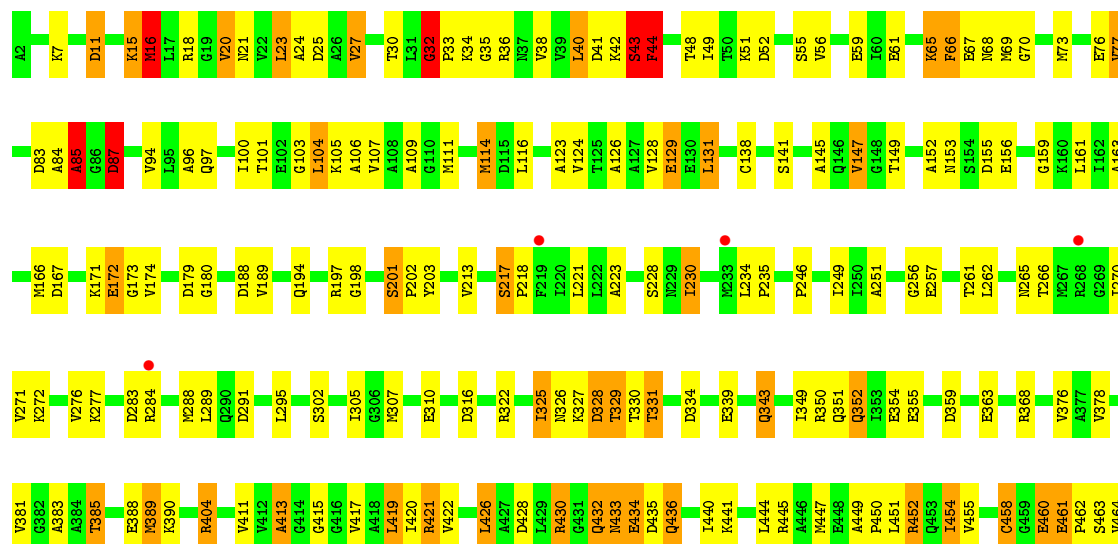


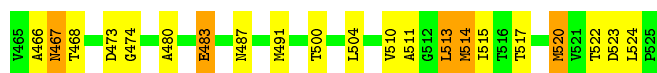


• Molecule 1: groEL protein



• Molecule 1: groEL protein

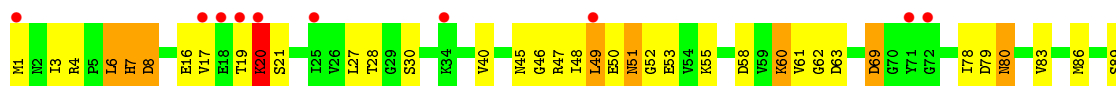




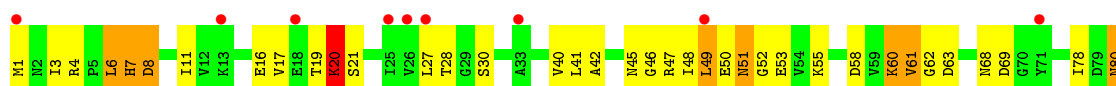
- Molecule 2: groES protein



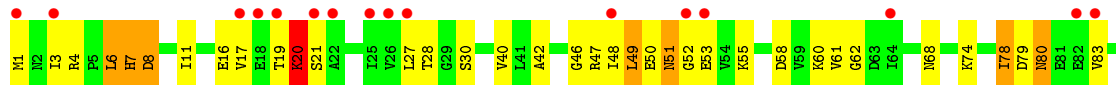
- Molecule 2: groES protein



- Molecule 2: groES protein

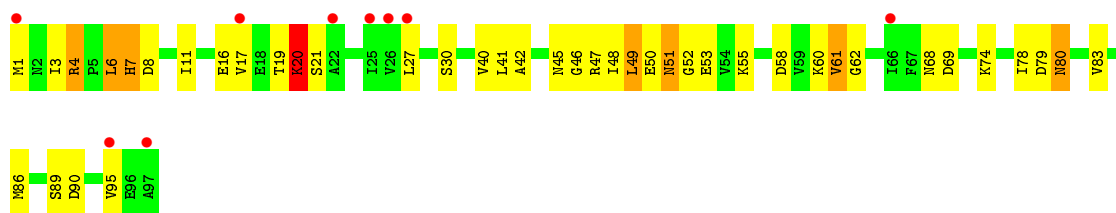


- Molecule 2: groES protein

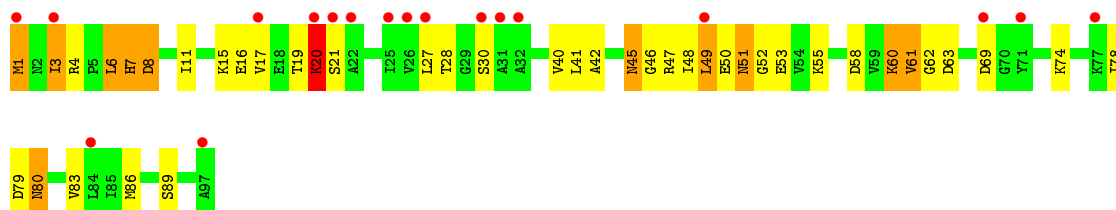


- Molecule 2: groES protein

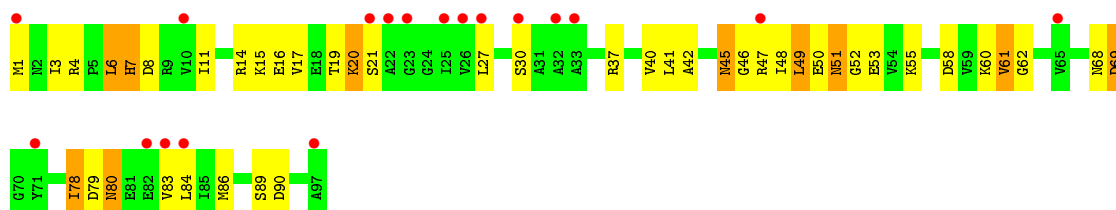




• Molecule 2: groES protein



• Molecule 2: groES protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	255.55Å 266.86Å 187.05Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.39 – 2.81 49.44 – 2.31	Depositor EDS
% Data completeness (in resolution range)	(Not available) (49.39-2.81) 60.7 (49.44-2.31)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.03 (at 2.32Å)	Xtriage
Refinement program	REFMAC refmac _5.1.19	Depositor
R, R_{free}	0.247 , 0.274 0.244 , 0.263	Depositor DCC
R_{free} test set	6710 reflections (1.94%)	wwPDB-VP
Wilson B-factor (Å ²)	43.9	Xtriage
Anisotropy	0.958	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 47.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	0.012 for k,h,-l	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	59498	wwPDB-VP
Average B, all atoms (Å ²)	2.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.16% 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 ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: K, MG, ADP, AF3

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	1.36	34/3883 (0.9%)	1.20	32/5243 (0.6%)
1	B	1.23	24/3883 (0.6%)	1.13	25/5243 (0.5%)
1	C	1.39	43/3883 (1.1%)	1.21	27/5243 (0.5%)
1	D	1.33	32/3883 (0.8%)	1.17	25/5243 (0.5%)
1	E	1.07	8/3883 (0.2%)	1.08	22/5243 (0.4%)
1	F	1.07	12/3883 (0.3%)	1.06	16/5243 (0.3%)
1	G	1.27	26/3883 (0.7%)	1.18	37/5243 (0.7%)
1	H	1.24	30/3884 (0.8%)	1.12	23/5243 (0.4%)
1	I	1.41	35/3884 (0.9%)	1.24	31/5243 (0.6%)
1	J	1.23	17/3884 (0.4%)	1.13	24/5243 (0.5%)
1	K	1.08	13/3884 (0.3%)	1.06	15/5243 (0.3%)
1	L	1.00	10/3884 (0.3%)	1.03	16/5243 (0.3%)
1	M	1.26	26/3884 (0.7%)	1.16	27/5243 (0.5%)
1	N	1.22	24/3884 (0.6%)	1.14	26/5243 (0.5%)
2	O	0.60	0/732	0.81	4/983 (0.4%)
2	P	0.59	0/732	0.83	6/983 (0.6%)
2	Q	0.57	0/732	0.83	4/983 (0.4%)
2	R	0.58	0/732	0.82	4/983 (0.4%)
2	S	0.55	0/732	0.82	4/983 (0.4%)
2	T	0.54	0/732	0.82	5/983 (0.5%)
2	U	0.58	0/732	0.82	4/983 (0.4%)
All	All	1.19	334/59493 (0.6%)	1.11	377/80283 (0.5%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	H	0	1

Continued on next page...

Continued from previous page...

Mol	Chain	#Chirality outliers	#Planarity outliers
1	I	0	1
1	J	0	1
1	K	0	1
1	L	0	1
1	M	0	1
1	N	0	1
All	All	0	8

The worst 5 of 334 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	I	461	GLU	CD-OE2	12.41	1.39	1.25
1	C	76	GLU	CD-OE1	11.87	1.38	1.25
1	I	483	GLU	CD-OE2	11.28	1.38	1.25
1	M	461	GLU	CD-OE2	11.22	1.38	1.25
1	G	76	GLU	CD-OE2	10.55	1.37	1.25

The worst 5 of 377 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	N	25	ASP	CB-CG-OD2	11.00	128.20	118.30
1	M	25	ASP	CB-CG-OD2	10.63	127.87	118.30
1	I	428	ASP	CB-CG-OD2	10.62	127.86	118.30
1	D	121	ASP	CB-CG-OD1	10.19	127.47	118.30
1	N	428	ASP	CB-CG-OD2	9.83	127.15	118.30

There are no chirality outliers.

5 of 8 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	43	SER	Peptide
1	H	32	GLY	Peptide
1	I	32	GLY	Peptide
1	J	32	GLY	Peptide
1	K	32	GLY	Peptide

5.2 Too-close contacts

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	3855	0	3974	158	0
1	B	3855	0	3976	151	0
1	C	3855	0	3975	155	0
1	D	3855	0	3976	145	0
1	E	3855	0	3975	122	0
1	F	3855	0	3976	133	0
1	G	3855	0	3974	158	0
1	H	3856	0	3976	129	0
1	I	3856	0	3976	174	0
1	J	3856	0	3976	143	0
1	K	3856	0	3976	130	0
1	L	3856	0	3976	135	0
1	M	3856	0	3976	144	0
1	N	3856	0	3976	143	0
2	O	728	0	762	26	0
2	P	728	0	762	22	0
2	Q	728	0	762	23	0
2	R	728	0	762	21	0
2	S	728	0	762	23	0
2	T	728	0	762	27	0
2	U	728	0	762	25	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
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
4	D	1	0	0	0	0
4	E	1	0	0	0	0
4	F	1	0	0	0	0
4	G	1	0	0	0	0
5	A	27	0	12	1	0
5	B	27	0	12	1	0
5	C	27	0	12	2	0
5	D	27	0	12	3	0
5	E	27	0	12	1	0
5	F	27	0	12	2	0
5	G	27	0	12	1	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	A	4	0	0	2	0
6	B	4	0	0	0	0
6	C	4	0	0	1	0
6	D	4	0	0	2	0
6	E	4	0	0	1	0
6	F	4	0	0	2	0
6	G	4	0	0	1	0
7	A	19	0	0	2	0
7	B	10	0	0	1	0
7	C	21	0	0	5	0
7	D	14	0	0	4	0
7	E	12	0	0	3	0
7	F	11	0	0	3	0
7	G	20	0	0	2	0
7	H	11	0	0	3	0
7	I	17	0	0	4	0
7	J	12	0	0	1	0
7	K	14	0	0	2	0
7	L	13	0	0	3	0
7	M	10	0	0	6	0
7	N	10	0	0	5	0
All	All	59498	0	61076	2099	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 17.

The worst 5 of 2099 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:N:288:MET:SD	1:N:288:MET:CE	2.01	1.46
1:F:114:MET:CE	1:F:114:MET:SD	2.02	1.46
1:I:447:MET:SD	1:I:447:MET:CE	2.05	1.45
1:K:16:MET:SD	1:K:16:MET:CE	2.05	1.45
1:J:288:MET:SD	1:J:288:MET:CE	2.04	1.45

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	522/524 (100%)	472 (90%)	44 (8%)	6 (1%)	14	41
1	B	522/524 (100%)	476 (91%)	39 (8%)	7 (1%)	12	36
1	C	522/524 (100%)	473 (91%)	37 (7%)	12 (2%)	6	21
1	D	522/524 (100%)	475 (91%)	41 (8%)	6 (1%)	14	41
1	E	522/524 (100%)	474 (91%)	42 (8%)	6 (1%)	14	41
1	F	522/524 (100%)	478 (92%)	38 (7%)	6 (1%)	14	41
1	G	522/524 (100%)	479 (92%)	37 (7%)	6 (1%)	14	41
1	H	522/524 (100%)	477 (91%)	36 (7%)	9 (2%)	9	29
1	I	522/524 (100%)	471 (90%)	43 (8%)	8 (2%)	10	33
1	J	522/524 (100%)	473 (91%)	40 (8%)	9 (2%)	9	29
1	K	522/524 (100%)	473 (91%)	41 (8%)	8 (2%)	10	33
1	L	522/524 (100%)	479 (92%)	34 (6%)	9 (2%)	9	29
1	M	522/524 (100%)	477 (91%)	35 (7%)	10 (2%)	8	26
1	N	522/524 (100%)	471 (90%)	44 (8%)	7 (1%)	12	36
2	O	95/97 (98%)	68 (72%)	17 (18%)	10 (10%)	0	1
2	P	95/97 (98%)	68 (72%)	16 (17%)	11 (12%)	0	1
2	Q	95/97 (98%)	68 (72%)	17 (18%)	10 (10%)	0	1
2	R	95/97 (98%)	68 (72%)	17 (18%)	10 (10%)	0	1
2	S	95/97 (98%)	70 (74%)	15 (16%)	10 (10%)	0	1
2	T	95/97 (98%)	69 (73%)	15 (16%)	11 (12%)	0	1
2	U	95/97 (98%)	68 (72%)	15 (16%)	12 (13%)	0	1
All	All	7973/8015 (100%)	7127 (89%)	663 (8%)	183 (2%)	6	21

5 of 183 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	44	PHE
1	B	44	PHE
1	C	44	PHE
1	D	44	PHE
1	E	44	PHE

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	404/404 (100%)	358 (89%)	46 (11%)	5	18
1	B	404/404 (100%)	356 (88%)	48 (12%)	5	16
1	C	404/404 (100%)	363 (90%)	41 (10%)	7	22
1	D	404/404 (100%)	360 (89%)	44 (11%)	6	19
1	E	404/404 (100%)	361 (89%)	43 (11%)	6	20
1	F	404/404 (100%)	360 (89%)	44 (11%)	6	19
1	G	404/404 (100%)	360 (89%)	44 (11%)	6	19
1	H	404/404 (100%)	336 (83%)	68 (17%)	2	6
1	I	404/404 (100%)	334 (83%)	70 (17%)	2	6
1	J	404/404 (100%)	337 (83%)	67 (17%)	2	7
1	K	404/404 (100%)	337 (83%)	67 (17%)	2	7
1	L	404/404 (100%)	337 (83%)	67 (17%)	2	7
1	M	404/404 (100%)	332 (82%)	72 (18%)	2	5
1	N	404/404 (100%)	337 (83%)	67 (17%)	2	7
2	O	80/80 (100%)	68 (85%)	12 (15%)	3	9
2	P	80/80 (100%)	68 (85%)	12 (15%)	3	9
2	Q	80/80 (100%)	68 (85%)	12 (15%)	3	9
2	R	80/80 (100%)	67 (84%)	13 (16%)	2	7
2	S	80/80 (100%)	69 (86%)	11 (14%)	3	11
2	T	80/80 (100%)	68 (85%)	12 (15%)	3	9

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	U	80/80 (100%)	67 (84%)	13 (16%)	2	7
All	All	6216/6216 (100%)	5343 (86%)	873 (14%)	3	11

5 of 873 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	I	104	LEU
1	J	331	THR
2	P	30	SER
1	I	201	SER
1	I	468	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 176 such sidechains are listed below:

Mol	Chain	Res	Type
1	G	348	GLN
1	I	97	GLN
2	P	45	ASN
1	G	453	GLN
1	H	265	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 28 ligands modelled in this entry, 14 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
5	ADP	E	600	3,4,6	24,29,29	1.40	3 (12%)	29,45,45	2.19	13 (44%)
6	AF3	B	602	1,3,5,4	0,3,3	0.00	-	-		
5	ADP	B	600	3,4,6	24,29,29	1.45	2 (8%)	29,45,45	2.21	13 (44%)
5	ADP	A	600	3,4,6	24,29,29	1.27	5 (20%)	29,45,45	1.78	7 (24%)
6	AF3	A	602	1,3,5,4	0,3,3	0.00	-	-		
5	ADP	C	600	3,4,6	24,29,29	1.33	4 (16%)	29,45,45	1.83	8 (27%)
6	AF3	G	602	1,3,5,4,7	0,3,3	0.00	-	-		
6	AF3	D	602	1,3,5,4	0,3,3	0.00	-	-		
6	AF3	E	602	1,3,5,4	0,3,3	0.00	-	-		
5	ADP	G	600	3,4,6	24,29,29	1.45	5 (20%)	29,45,45	1.83	8 (27%)
5	ADP	D	600	3,4,6	24,29,29	1.40	3 (12%)	29,45,45	1.77	6 (20%)
6	AF3	F	602	1,3,5,4	0,3,3	0.00	-	-		
6	AF3	C	602	1,3,5,4	0,3,3	0.00	-	-		
5	ADP	F	600	3,4,6	24,29,29	1.36	4 (16%)	29,45,45	1.89	7 (24%)

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
5	ADP	B	600	3,4,6	-	5/12/32/32	0/3/3/3
5	ADP	A	600	3,4,6	-	4/12/32/32	0/3/3/3
5	ADP	D	600	3,4,6	-	5/12/32/32	0/3/3/3
5	ADP	C	600	3,4,6	-	4/12/32/32	0/3/3/3
5	ADP	F	600	3,4,6	-	4/12/32/32	0/3/3/3
5	ADP	E	600	3,4,6	-	4/12/32/32	0/3/3/3
5	ADP	G	600	3,4,6	-	4/12/32/32	0/3/3/3

The worst 5 of 26 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	600	ADP	O4'-C1'	-3.74	1.35	1.41

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	G	600	ADP	C2'-C1'	-3.32	1.48	1.53
5	G	600	ADP	O4'-C4'	-3.23	1.37	1.45
5	C	600	ADP	C4-N3	-3.18	1.31	1.35
5	F	600	ADP	C2-N3	3.15	1.37	1.32

The worst 5 of 62 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	600	ADP	N3-C2-N1	-6.15	119.07	128.68
5	D	600	ADP	N3-C2-N1	-5.08	120.75	128.68
5	E	600	ADP	N3-C2-N1	-4.72	121.30	128.68
5	F	600	ADP	N3-C2-N1	-4.53	121.61	128.68
5	D	600	ADP	PA-O3A-PB	-4.29	118.10	132.83

There are no chirality outliers.

5 of 30 torsion outliers are listed below:

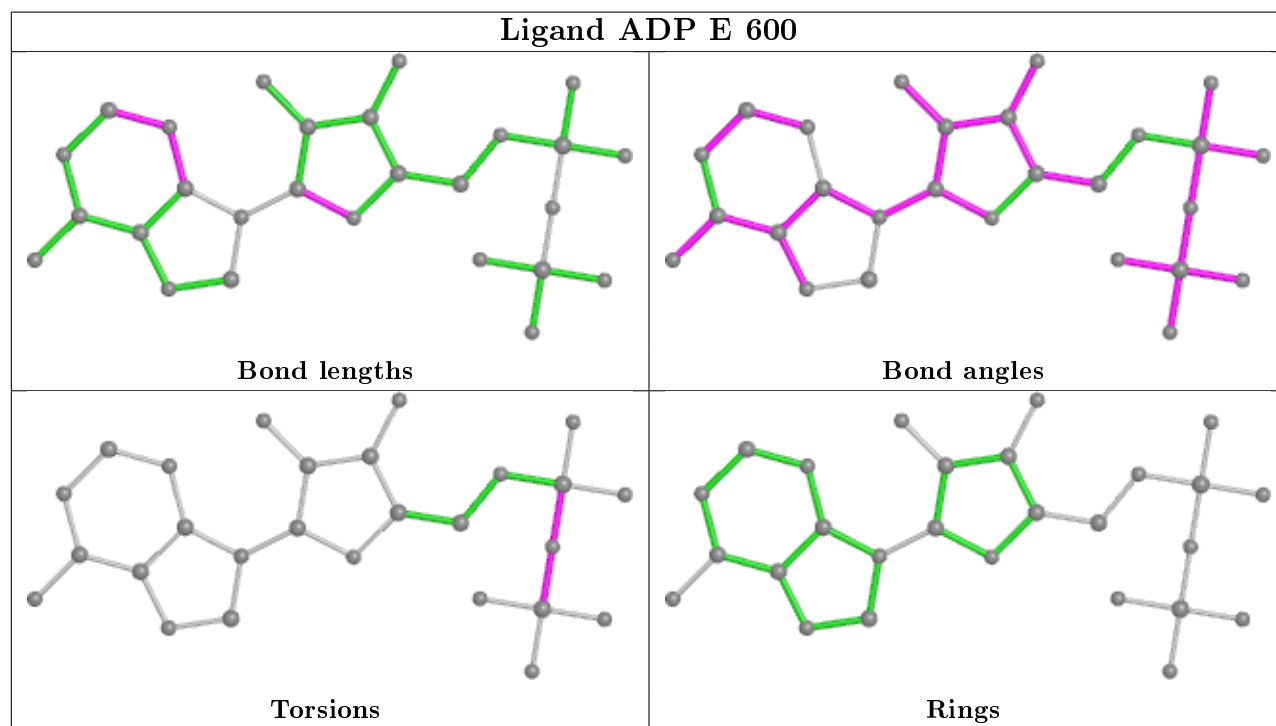
Mol	Chain	Res	Type	Atoms
5	G	600	ADP	PA-O3A-PB-O2B
5	D	600	ADP	PA-O3A-PB-O2B
5	C	600	ADP	PA-O3A-PB-O2B
5	F	600	ADP	PA-O3A-PB-O2B
5	E	600	ADP	PA-O3A-PB-O1B

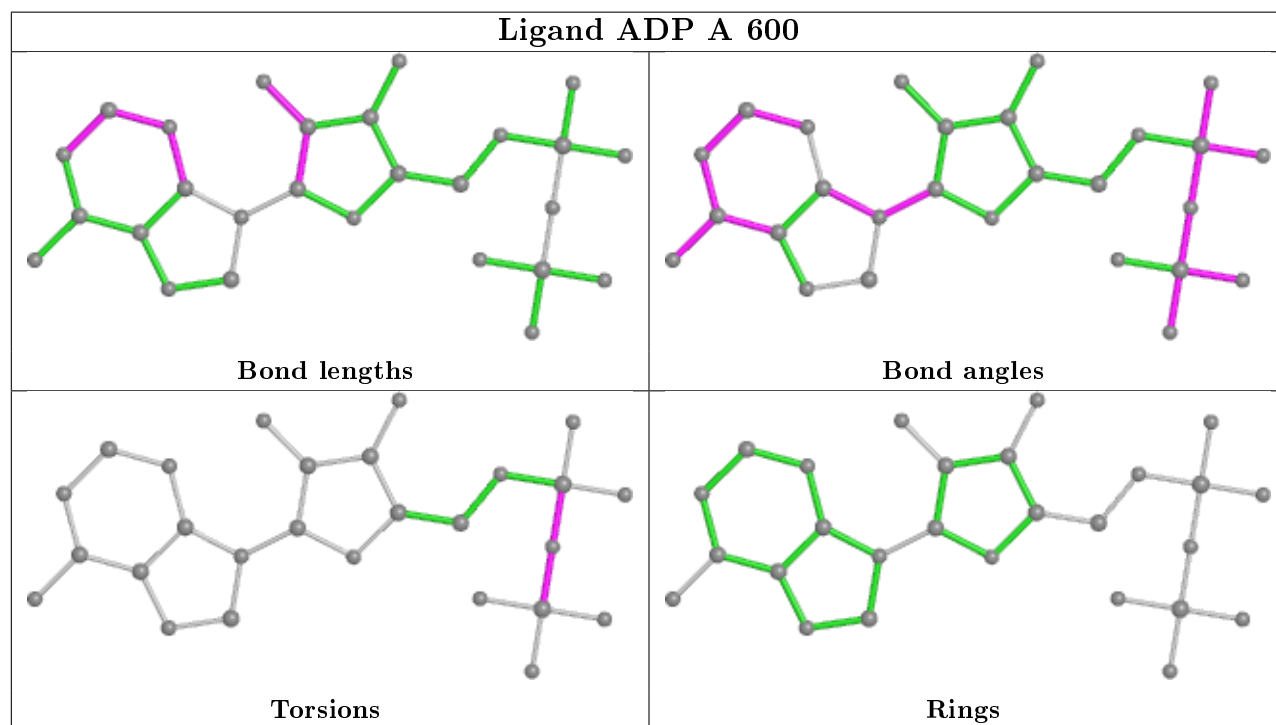
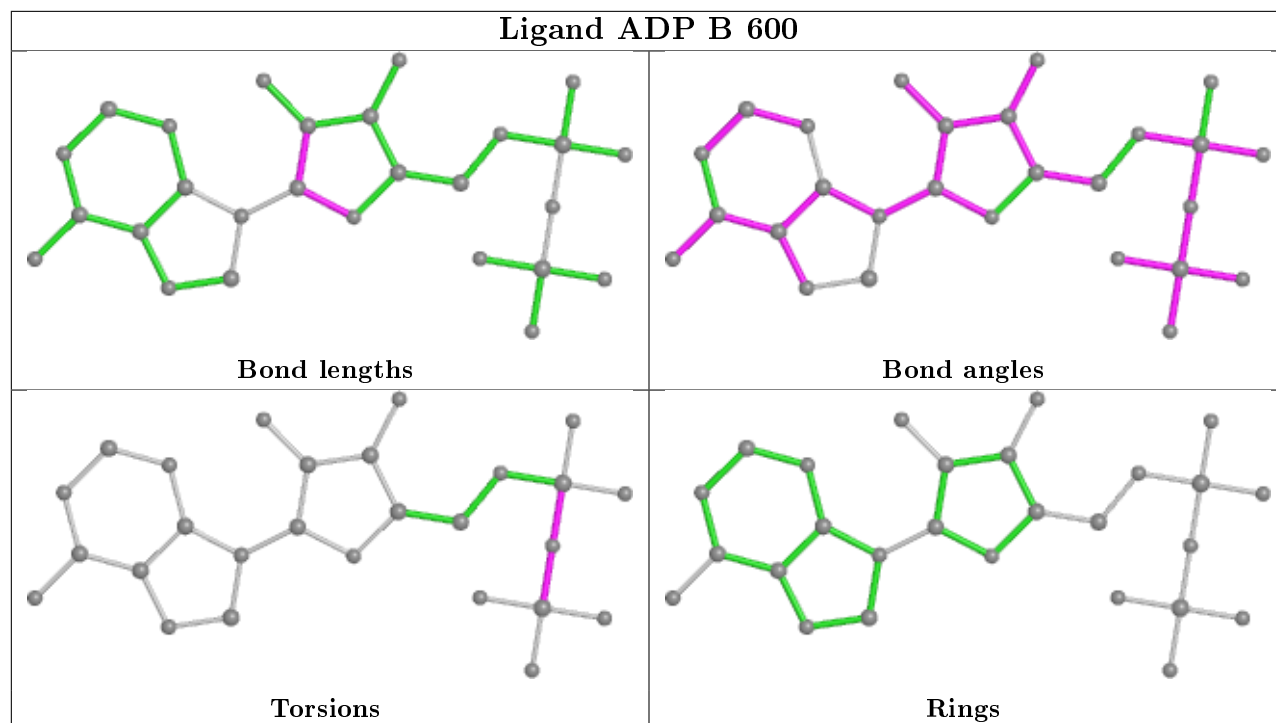
There are no ring outliers.

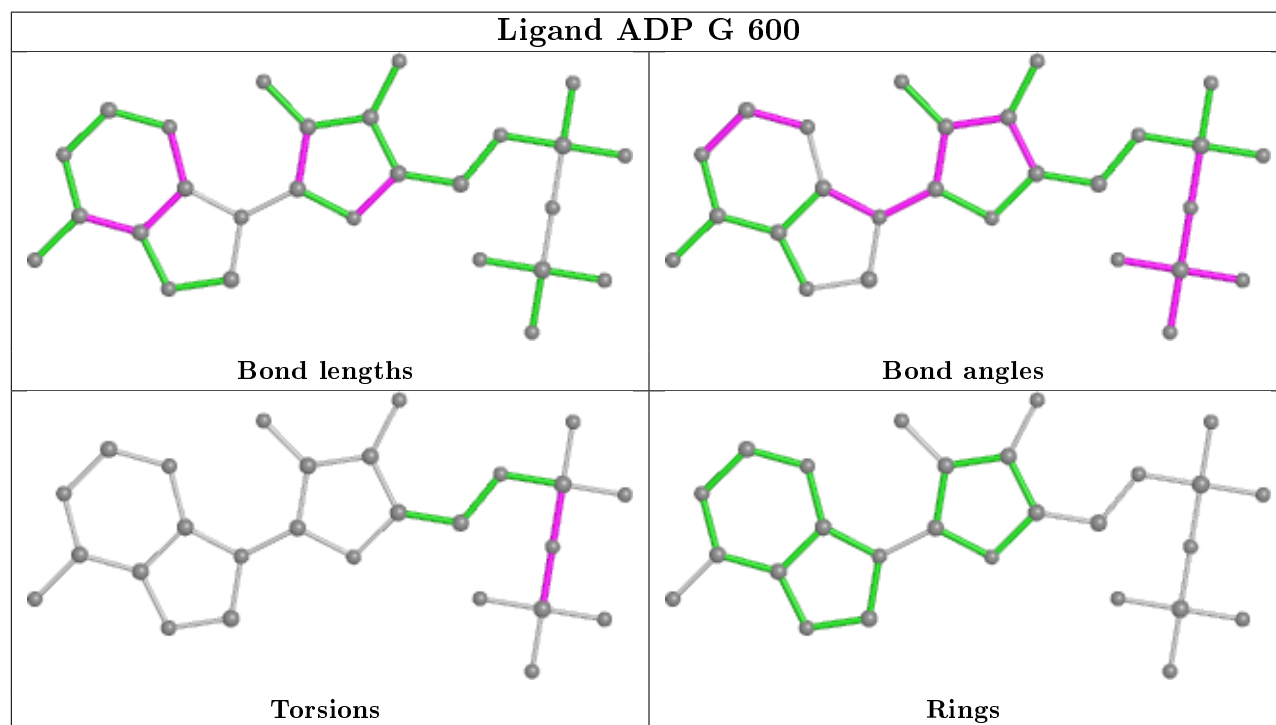
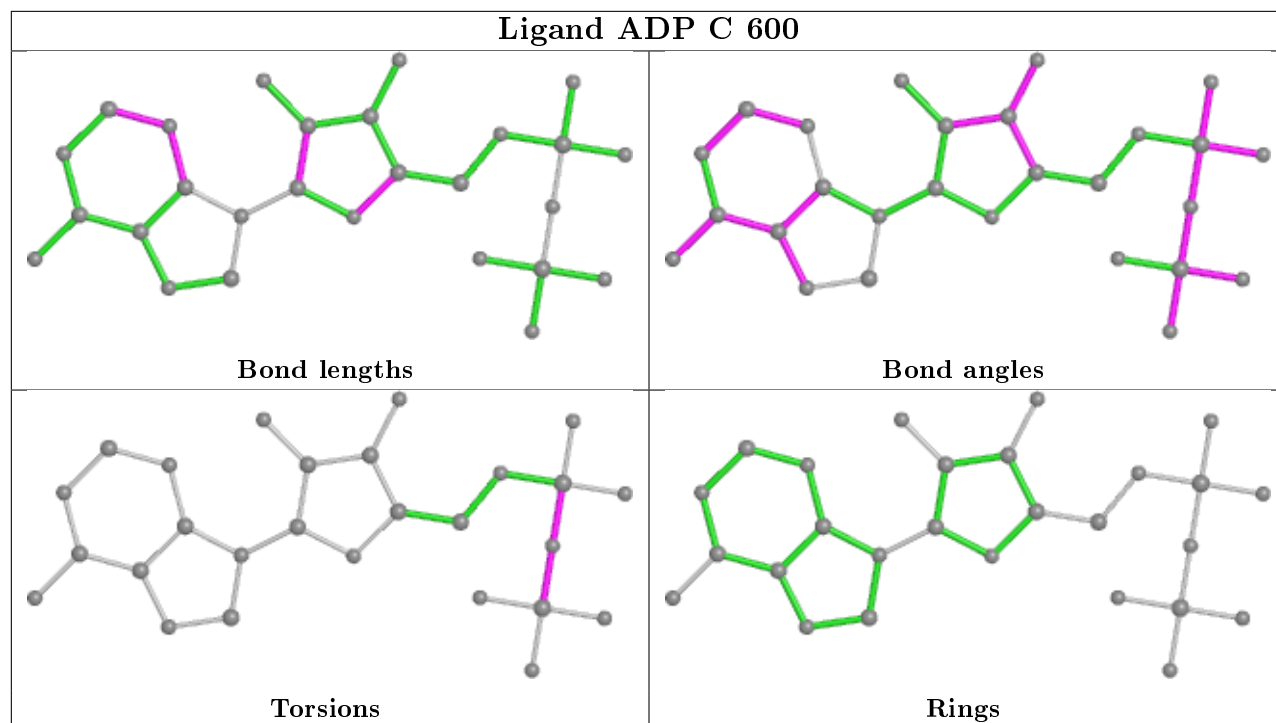
13 monomers are involved in 16 short contacts:

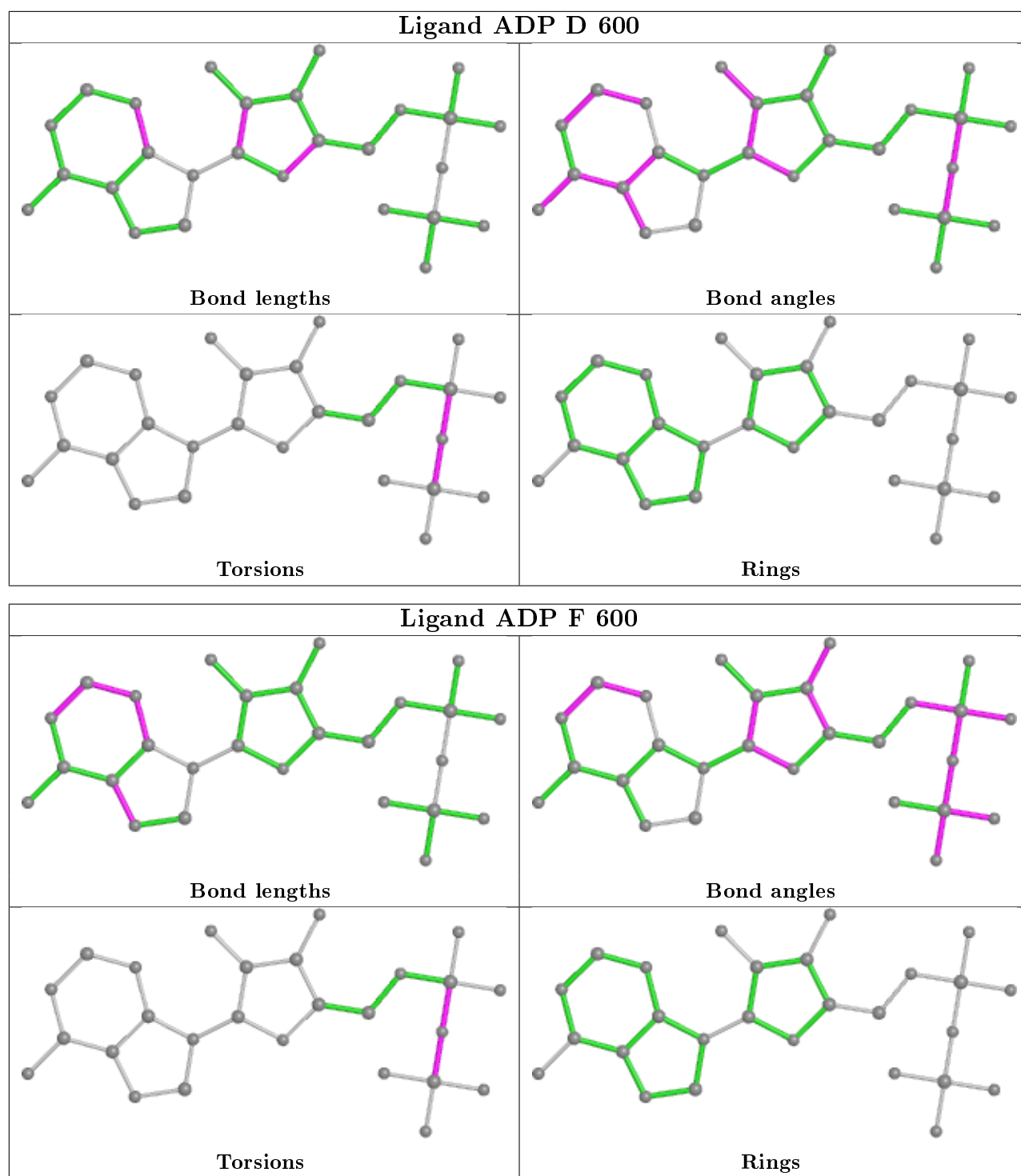
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	E	600	ADP	1	0
5	B	600	ADP	1	0
5	A	600	ADP	1	0
6	A	602	AF3	2	0
5	C	600	ADP	2	0
6	G	602	AF3	1	0
6	D	602	AF3	2	0
6	E	602	AF3	1	0
5	G	600	ADP	1	0
5	D	600	ADP	3	0
6	F	602	AF3	2	0
6	C	602	AF3	1	0
5	F	600	ADP	2	0

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 ⓘ

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	524/524 (100%)	-0.12	19 (3%) 42 32	2, 2, 4, 5	0
1	B	524/524 (100%)	-0.02	32 (6%) 21 13	2, 2, 4, 5	0
1	C	524/524 (100%)	-0.09	24 (4%) 32 22	2, 2, 4, 5	0
1	D	524/524 (100%)	-0.13	27 (5%) 27 18	2, 2, 4, 5	0
1	E	524/524 (100%)	0.00	36 (6%) 16 10	2, 2, 4, 5	0
1	F	524/524 (100%)	0.09	40 (7%) 13 7	2, 2, 4, 5	0
1	G	524/524 (100%)	-0.02	30 (5%) 23 15	2, 2, 4, 5	0
1	H	524/524 (100%)	-0.40	1 (0%) 95 94	2, 2, 4, 5	0
1	I	524/524 (100%)	-0.39	2 (0%) 92 91	2, 2, 4, 5	0
1	J	524/524 (100%)	-0.38	6 (1%) 80 75	2, 2, 4, 5	0
1	K	524/524 (100%)	-0.32	4 (0%) 86 81	2, 2, 4, 5	0
1	L	524/524 (100%)	-0.16	9 (1%) 70 63	2, 2, 3, 5	0
1	M	524/524 (100%)	-0.33	9 (1%) 70 63	2, 2, 4, 5	0
1	N	524/524 (100%)	-0.32	4 (0%) 86 81	2, 2, 4, 5	0
2	O	97/97 (100%)	0.80	15 (15%) 2 1	2, 2, 2, 2	0
2	P	97/97 (100%)	0.51	11 (11%) 5 3	2, 2, 2, 2	0
2	Q	97/97 (100%)	0.51	9 (9%) 8 4	2, 2, 2, 2	0
2	R	97/97 (100%)	0.87	17 (17%) 1 1	2, 2, 2, 2	0
2	S	97/97 (100%)	0.65	9 (9%) 8 4	2, 2, 2, 2	0
2	T	97/97 (100%)	0.85	18 (18%) 1 1	2, 2, 2, 2	0
2	U	97/97 (100%)	0.79	18 (18%) 1 1	2, 2, 2, 2	0
All	All	8015/8015 (100%)	-0.11	340 (4%) 36 26	2, 2, 4, 5	0

The worst 5 of 340 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	S	1	MET	8.7
2	T	22	ALA	7.7
1	B	314	LEU	7.5
2	T	25	ILE	7.2
1	F	215	LEU	7.1

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

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.

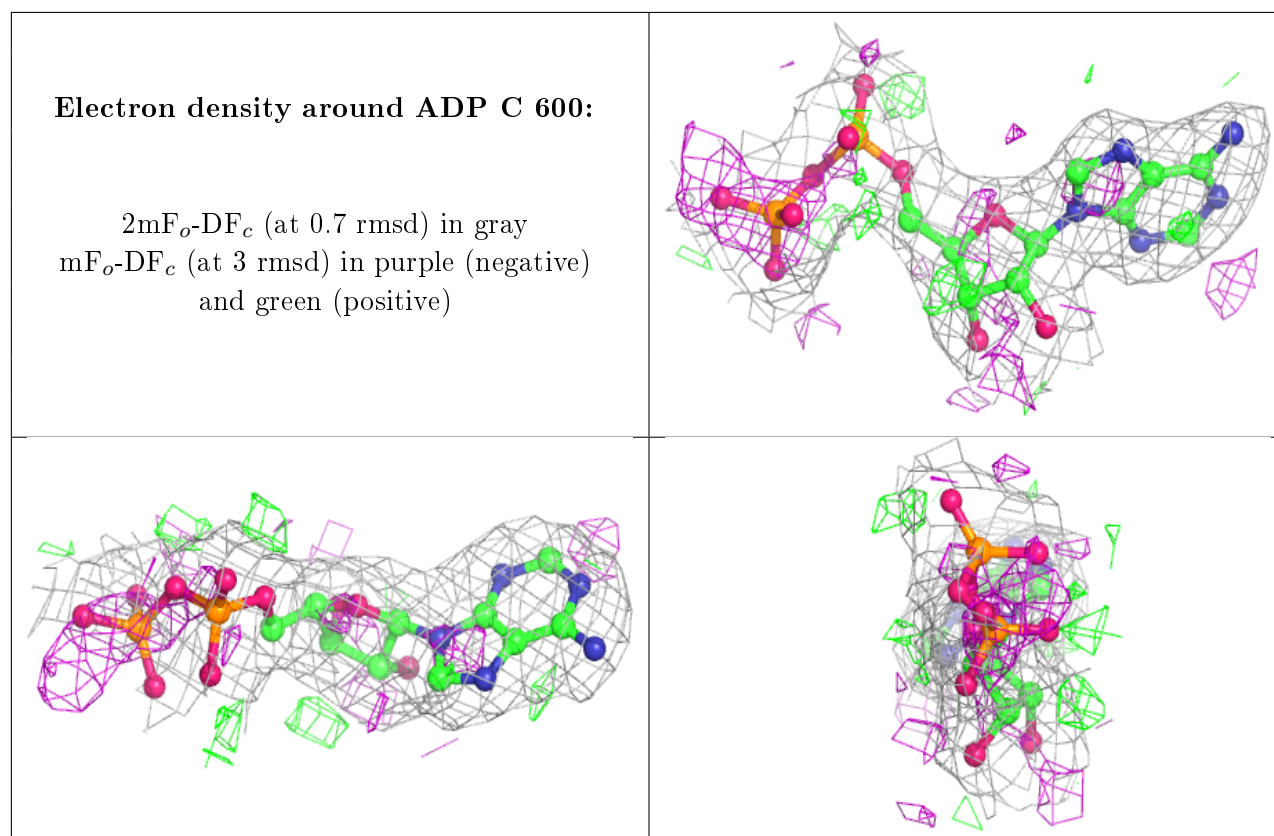
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
6	AF3	E	602	4/4	0.87	0.15	2,2,8,9	0
6	AF3	D	602	4/4	0.88	0.14	2,2,8,10	0
4	K	E	603	1/1	0.88	0.10	16,16,16,16	0
6	AF3	F	602	4/4	0.89	0.13	2,2,8,9	0
4	K	G	603	1/1	0.90	0.07	16,16,16,16	0
6	AF3	B	602	4/4	0.91	0.18	2,2,7,10	0
6	AF3	G	602	4/4	0.91	0.15	2,2,7,9	0
6	AF3	A	602	4/4	0.92	0.16	2,2,7,10	0
6	AF3	C	602	4/4	0.93	0.16	2,2,8,10	0
4	K	A	603	1/1	0.94	0.10	16,16,16,16	0
4	K	F	603	1/1	0.95	0.08	15,15,15,15	0
4	K	D	603	1/1	0.96	0.07	16,16,16,16	0
5	ADP	C	600	27/27	0.97	0.13	2,2,2,3	0
5	ADP	F	600	27/27	0.97	0.13	2,2,2,3	0
5	ADP	G	600	27/27	0.97	0.15	2,2,2,3	0
5	ADP	E	600	27/27	0.97	0.14	2,2,2,3	0
5	ADP	D	600	27/27	0.97	0.14	2,2,2,3	0
5	ADP	B	600	27/27	0.97	0.13	2,2,3,3	0
3	MG	E	601	1/1	0.98	0.20	2,2,2,2	0

Continued on next page...

Continued from previous page...

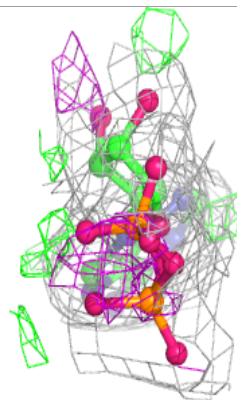
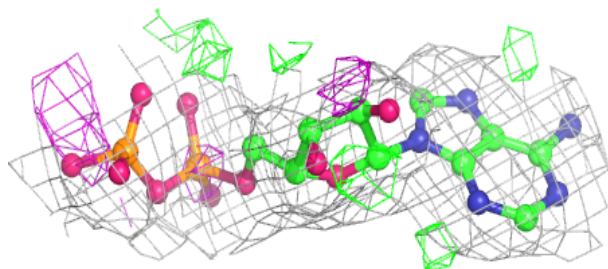
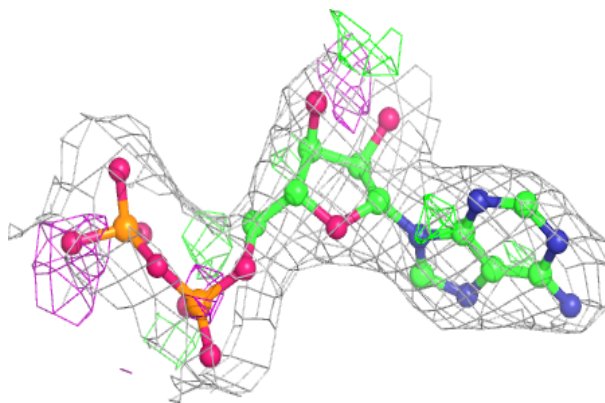
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	K	B	603	1/1	0.98	0.06	16,16,16,16	0
5	ADP	A	600	27/27	0.98	0.14	2,2,2,3	0
4	K	C	603	1/1	0.98	0.05	15,15,15,15	0
3	MG	C	601	1/1	0.98	0.22	2,2,2,2	0
3	MG	D	601	1/1	0.99	0.20	2,2,2,2	0
3	MG	F	601	1/1	0.99	0.23	2,2,2,2	0
3	MG	G	601	1/1	0.99	0.21	2,2,2,2	0
3	MG	A	601	1/1	0.99	0.22	2,2,2,2	0
3	MG	B	601	1/1	0.99	0.22	2,2,2,2	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.

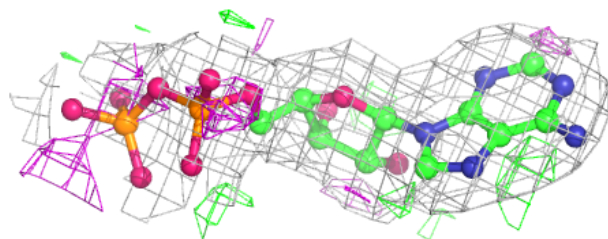
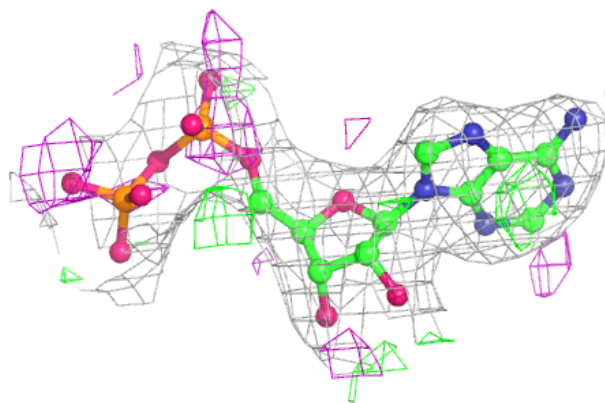


Electron density around ADP F 600:

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

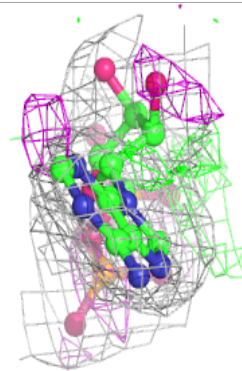
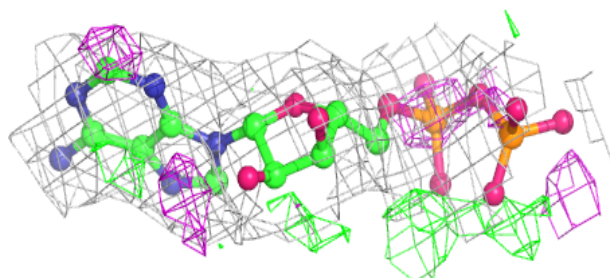
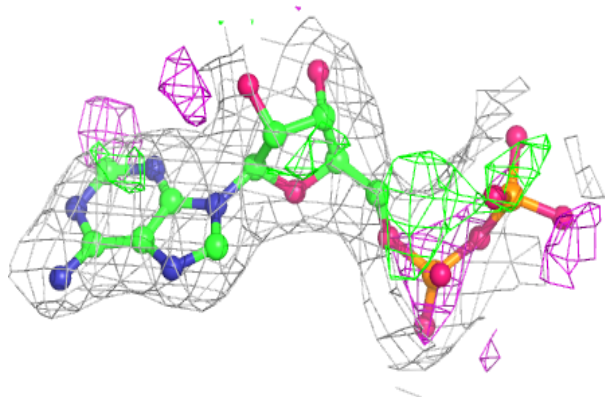
**Electron density around ADP G 600:**

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

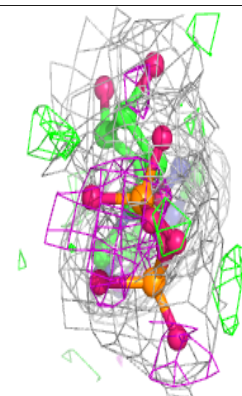
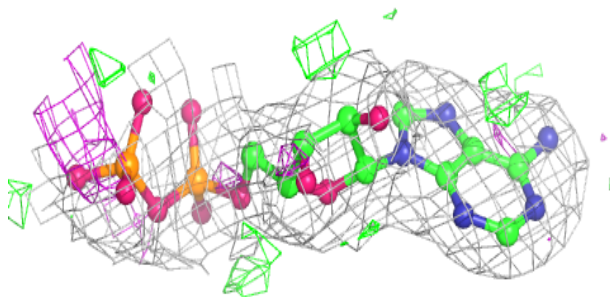
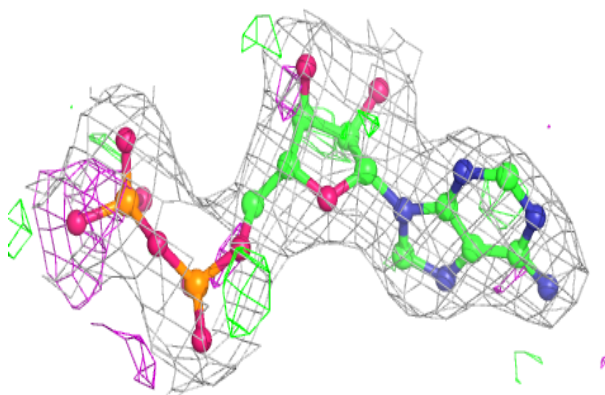


Electron density around ADP E 600:

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

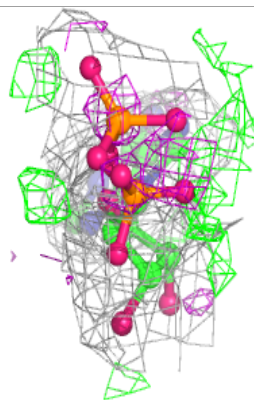
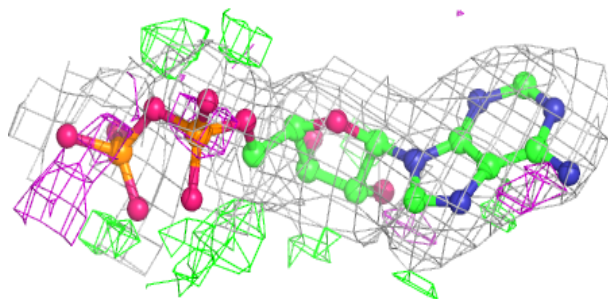
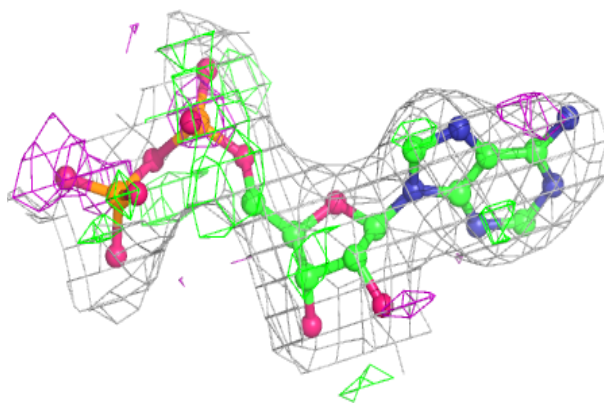
**Electron density around ADP D 600:**

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

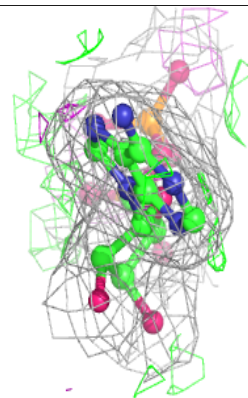
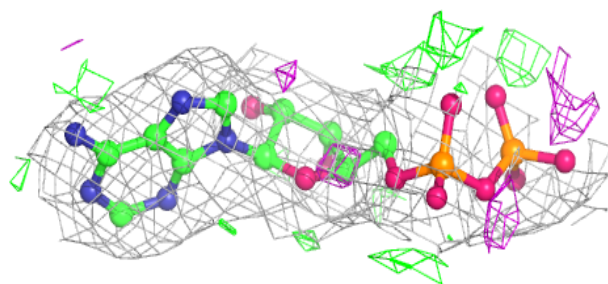
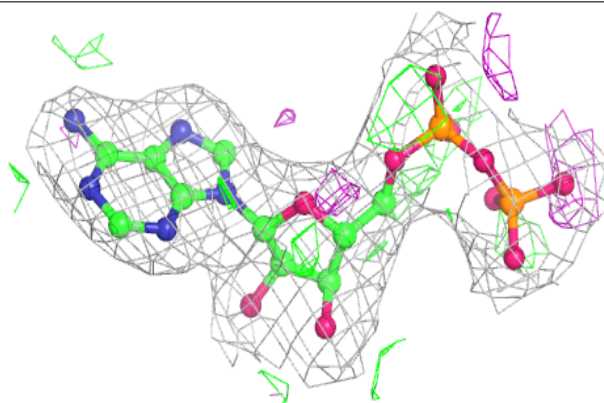


Electron density around ADP B 600:

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

**Electron density around ADP A 600:**

$2mF_o-DF_c$ (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.