Full wwPDB EM Validation Report ⓘ

Jun 1, 2024 – 10:40 AM EDT

PDB ID	:	7UJ0
EMDB ID	:	EMD-26559
Title	:	ClpAP complex bound to ClpS N-terminal extension, class IIIb
Authors	:	Kim, S.; Fei, X.; Sauer, R.T.; Baker, T.A.
Deposited on	:	2022-03-29
Resolution	:	3.26 Å(reported)

This is a Full wwPDB EM 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/EMValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

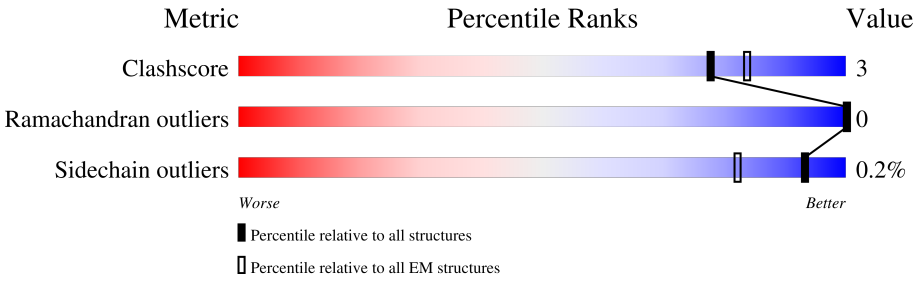
EMDB validation analysis	:	0.0.1.dev92
Mogul	:	1.8.5 (274361), CSD as541be (2020)
MolProbity	:	4.02b-467
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.26 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion < 40%). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	758	33% 70% 6% 24%
1	B	758	5% 71% 6% 23%
1	C	758	72% 23%
1	D	758	70% 6% 23%
1	E	758	11% 68% 8% 23%
1	F	758	37% 68% 8% 24%
2	S	106	9% 90%
3	H	201	88% 7% 5%

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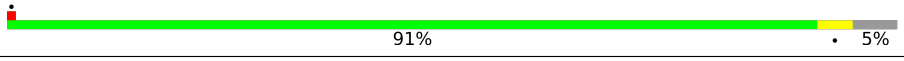
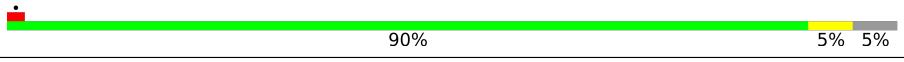
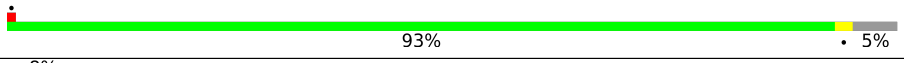
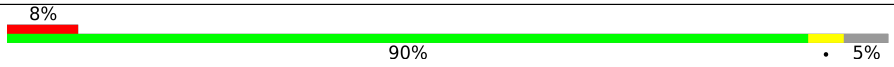
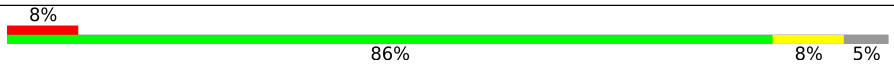
Mol	Chain	Length	Quality of chain
3	I	201	
3	J	201	
3	K	201	
3	L	201	
3	M	201	
3	N	201	

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 76458 atoms, of which 38452 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called ATP-dependent Clp protease ATP-binding subunit ClpA.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	577	Total	C	H	N	O	S	0	0
			9101	2835	4601	804	848	13		
1	B	580	Total	C	H	N	O	S	0	0
			9140	2847	4618	808	854	13		
1	C	581	Total	C	H	N	O	S	0	0
			9152	2851	4623	809	856	13		
1	D	580	Total	C	H	N	O	S	0	0
			9142	2848	4618	808	855	13		
1	E	580	Total	C	H	N	O	S	0	0
			9143	2848	4619	808	855	13		
1	F	579	Total	C	H	N	O	S	0	0
			9130	2844	4613	807	853	13		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	169	THR	MET	conflict	UNP A0A836NDF2
B	169	THR	MET	conflict	UNP A0A836NDF2
C	169	THR	MET	conflict	UNP A0A836NDF2
D	169	THR	MET	conflict	UNP A0A836NDF2
E	169	THR	MET	conflict	UNP A0A836NDF2
F	169	THR	MET	conflict	UNP A0A836NDF2

- Molecule 2 is a protein called ATP-dependent Clp protease adapter protein ClpS.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	S	11	Total	C	H	N	O	0	0
			179	54	93	16	16		

- Molecule 3 is a protein called ATP-dependent Clp protease proteolytic subunit.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	H	191	Total	C	H	N	O	S	0	0
			3002	943	1507	259	281	12		
3	I	191	Total	C	H	N	O	S	0	0
			3002	943	1507	259	281	12		
3	J	191	Total	C	H	N	O	S	0	0
			3002	943	1507	259	281	12		
3	K	191	Total	C	H	N	O	S	0	0
			3002	943	1507	259	281	12		
3	L	191	Total	C	H	N	O	S	0	0
			3002	943	1507	259	281	12		
3	M	190	Total	C	H	N	O	S	0	0
			2978	937	1494	255	280	12		
3	N	190	Total	C	H	N	O	S	0	0
			2978	937	1494	255	280	12		

There are 56 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
H	194	ARG	-	expression tag	UNP A0A0K4NM46
H	195	SER	-	expression tag	UNP A0A0K4NM46
H	196	HIS	-	expression tag	UNP A0A0K4NM46
H	197	HIS	-	expression tag	UNP A0A0K4NM46
H	198	HIS	-	expression tag	UNP A0A0K4NM46
H	199	HIS	-	expression tag	UNP A0A0K4NM46
H	200	HIS	-	expression tag	UNP A0A0K4NM46
H	201	HIS	-	expression tag	UNP A0A0K4NM46
I	194	ARG	-	expression tag	UNP A0A0K4NM46
I	195	SER	-	expression tag	UNP A0A0K4NM46
I	196	HIS	-	expression tag	UNP A0A0K4NM46
I	197	HIS	-	expression tag	UNP A0A0K4NM46
I	198	HIS	-	expression tag	UNP A0A0K4NM46
I	199	HIS	-	expression tag	UNP A0A0K4NM46
I	200	HIS	-	expression tag	UNP A0A0K4NM46
I	201	HIS	-	expression tag	UNP A0A0K4NM46
J	194	ARG	-	expression tag	UNP A0A0K4NM46
J	195	SER	-	expression tag	UNP A0A0K4NM46
J	196	HIS	-	expression tag	UNP A0A0K4NM46
J	197	HIS	-	expression tag	UNP A0A0K4NM46
J	198	HIS	-	expression tag	UNP A0A0K4NM46
J	199	HIS	-	expression tag	UNP A0A0K4NM46
J	200	HIS	-	expression tag	UNP A0A0K4NM46
J	201	HIS	-	expression tag	UNP A0A0K4NM46
K	194	ARG	-	expression tag	UNP A0A0K4NM46
K	195	SER	-	expression tag	UNP A0A0K4NM46

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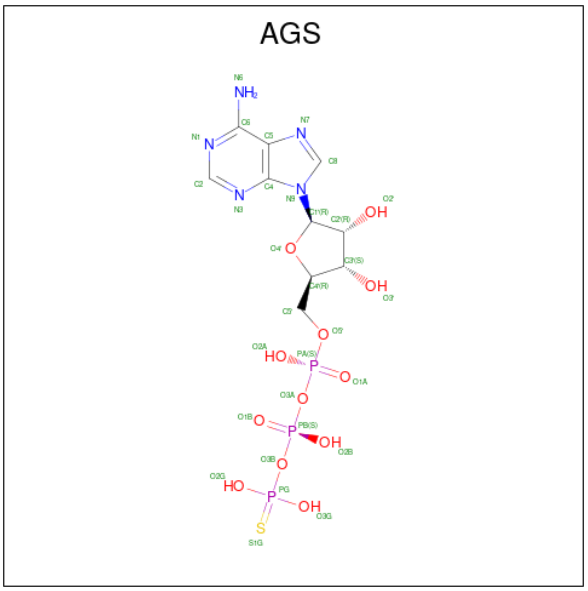
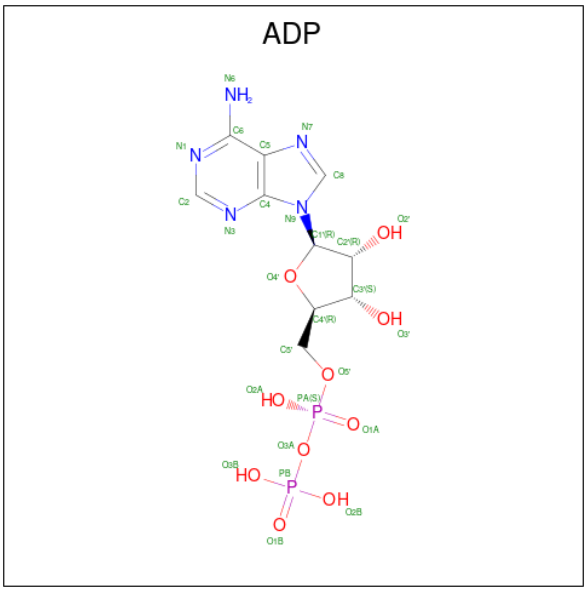
Chain	Residue	Modelled	Actual	Comment	Reference
K	196	HIS	-	expression tag	UNP A0A0K4NM46
K	197	HIS	-	expression tag	UNP A0A0K4NM46
K	198	HIS	-	expression tag	UNP A0A0K4NM46
K	199	HIS	-	expression tag	UNP A0A0K4NM46
K	200	HIS	-	expression tag	UNP A0A0K4NM46
K	201	HIS	-	expression tag	UNP A0A0K4NM46
L	194	ARG	-	expression tag	UNP A0A0K4NM46
L	195	SER	-	expression tag	UNP A0A0K4NM46
L	196	HIS	-	expression tag	UNP A0A0K4NM46
L	197	HIS	-	expression tag	UNP A0A0K4NM46
L	198	HIS	-	expression tag	UNP A0A0K4NM46
L	199	HIS	-	expression tag	UNP A0A0K4NM46
L	200	HIS	-	expression tag	UNP A0A0K4NM46
L	201	HIS	-	expression tag	UNP A0A0K4NM46
M	194	ARG	-	expression tag	UNP A0A0K4NM46
M	195	SER	-	expression tag	UNP A0A0K4NM46
M	196	HIS	-	expression tag	UNP A0A0K4NM46
M	197	HIS	-	expression tag	UNP A0A0K4NM46
M	198	HIS	-	expression tag	UNP A0A0K4NM46
M	199	HIS	-	expression tag	UNP A0A0K4NM46
M	200	HIS	-	expression tag	UNP A0A0K4NM46
M	201	HIS	-	expression tag	UNP A0A0K4NM46
N	194	ARG	-	expression tag	UNP A0A0K4NM46
N	195	SER	-	expression tag	UNP A0A0K4NM46
N	196	HIS	-	expression tag	UNP A0A0K4NM46
N	197	HIS	-	expression tag	UNP A0A0K4NM46
N	198	HIS	-	expression tag	UNP A0A0K4NM46
N	199	HIS	-	expression tag	UNP A0A0K4NM46
N	200	HIS	-	expression tag	UNP A0A0K4NM46
N	201	HIS	-	expression tag	UNP A0A0K4NM46

- Molecule 4 is PHOSPHOTHIOPHOSPHORIC ACID-ADENYLATE ESTER (three-letter code: AGS) (formula: $C_{10}H_{16}N_5O_{12}P_3S$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms							AltConf
4	A	1	Total	C	H	N	O	P	S	0
			43	10	12	5	12	3	1	
4	B	1	Total	C	H	N	O	P	S	0
			43	10	12	5	12	3	1	
4	B	1	Total	C	H	N	O	P	S	0
			43	10	12	5	12	3	1	
4	C	1	Total	C	H	N	O	P	S	0
			43	10	12	5	12	3	1	
4	C	1	Total	C	H	N	O	P	S	0
			43	10	12	5	12	3	1	
4	D	1	Total	C	H	N	O	P	S	0
			43	10	12	5	12	3	1	
4	D	1	Total	C	H	N	O	P	S	0
			43	10	12	5	12	3	1	

- Molecule 5 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms						AltConf
5	A	1	Total	C	H	N	O	P	0
			39	10	12	5	10	2	
5	E	1	Total	C	H	N	O	P	0
			39	10	12	5	10	2	
5	E	1	Total	C	H	N	O	P	0
			39	10	12	5	10	2	
5	F	1	Total	C	H	N	O	P	0
			39	10	12	5	10	2	
5	F	1	Total	C	H	N	O	P	0
			39	10	12	5	10	2	

- Molecule 6 is MAGNESIUM ION (three-letter code: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

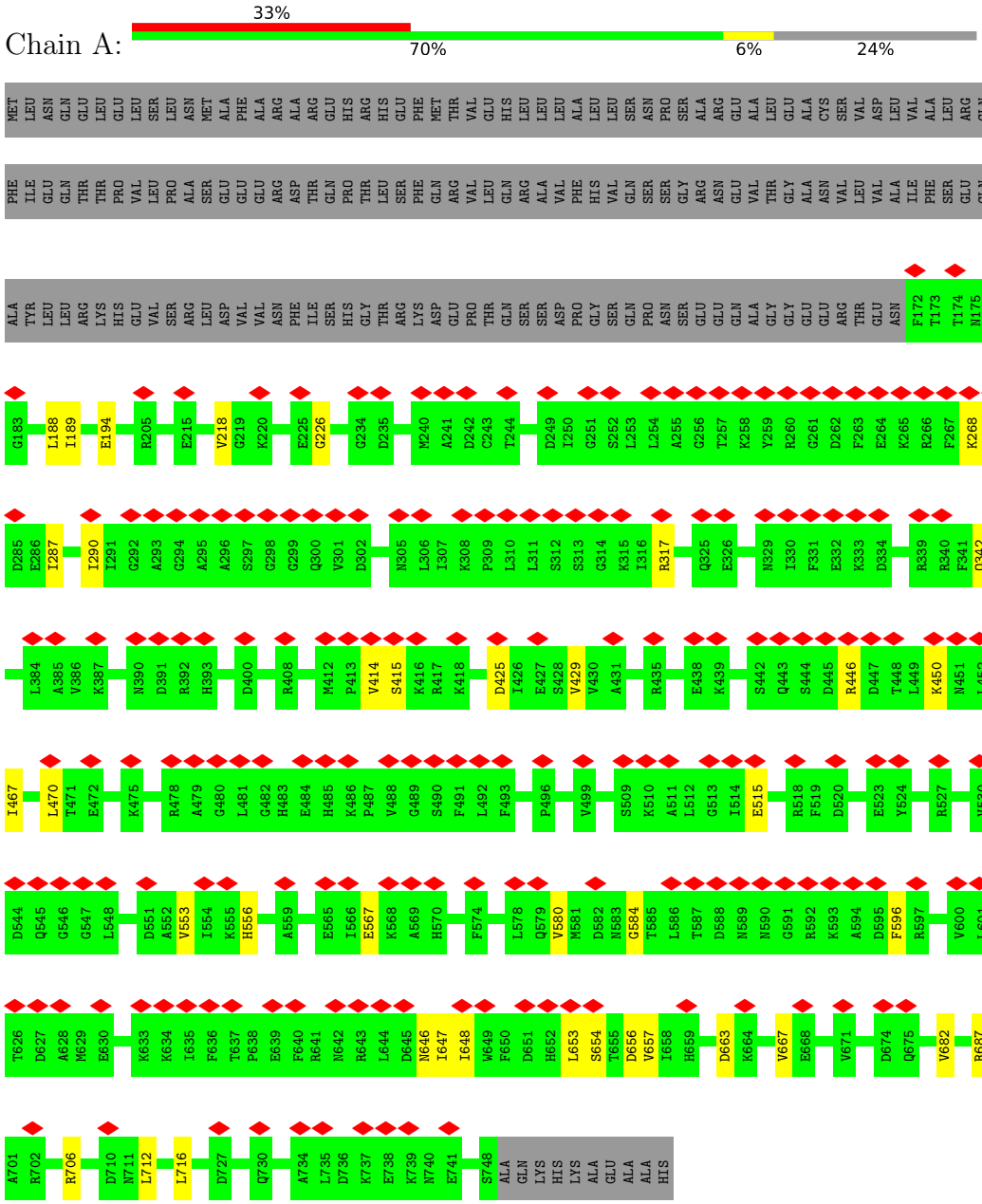
Mol	Chain	Residues	Atoms		AltConf
6	A	2	Total	Mg	0
			2	2	
6	B	2	Total	Mg	0
			2	2	
6	C	2	Total	Mg	0
			2	2	
6	D	2	Total	Mg	0
			2	2	
6	E	1	Total	Mg	0
			1	1	

3 Residue-property plots (i)

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 atom inclusion in map 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 diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). 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.

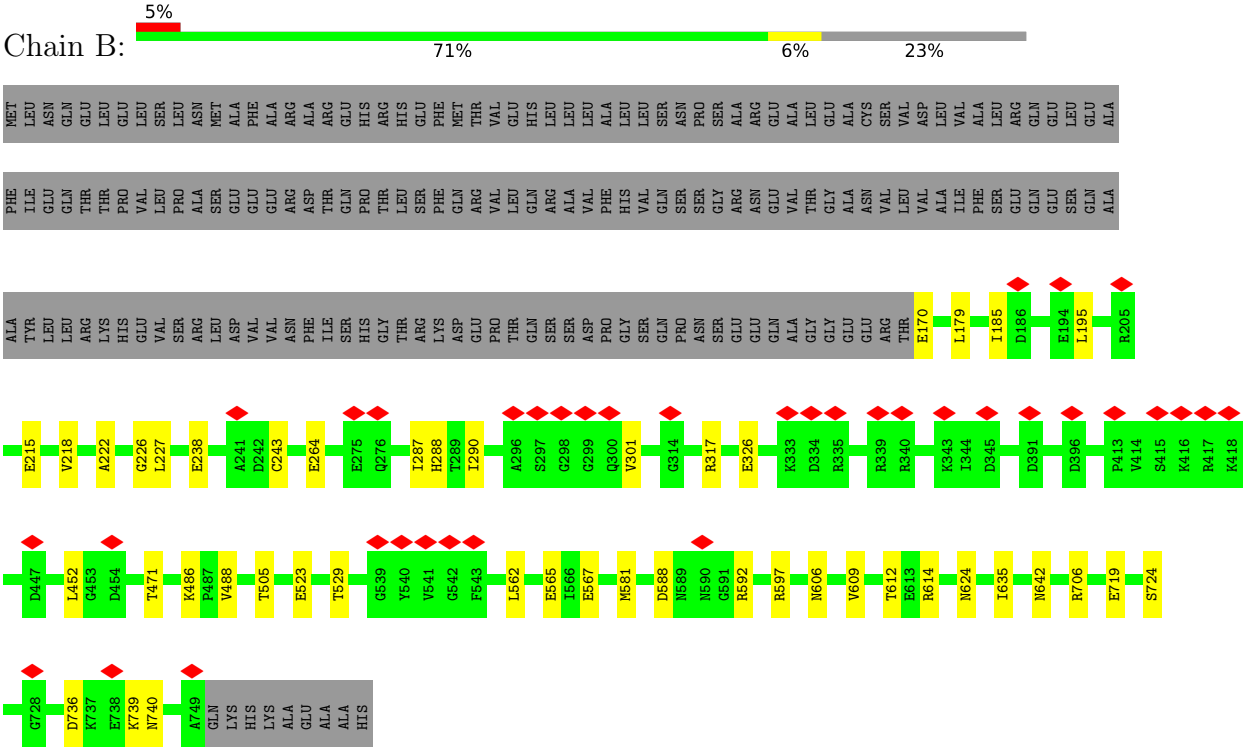
• Molecule 1: ATP-dependent Clp protease ATP-binding subunit ClpA

Chain A:



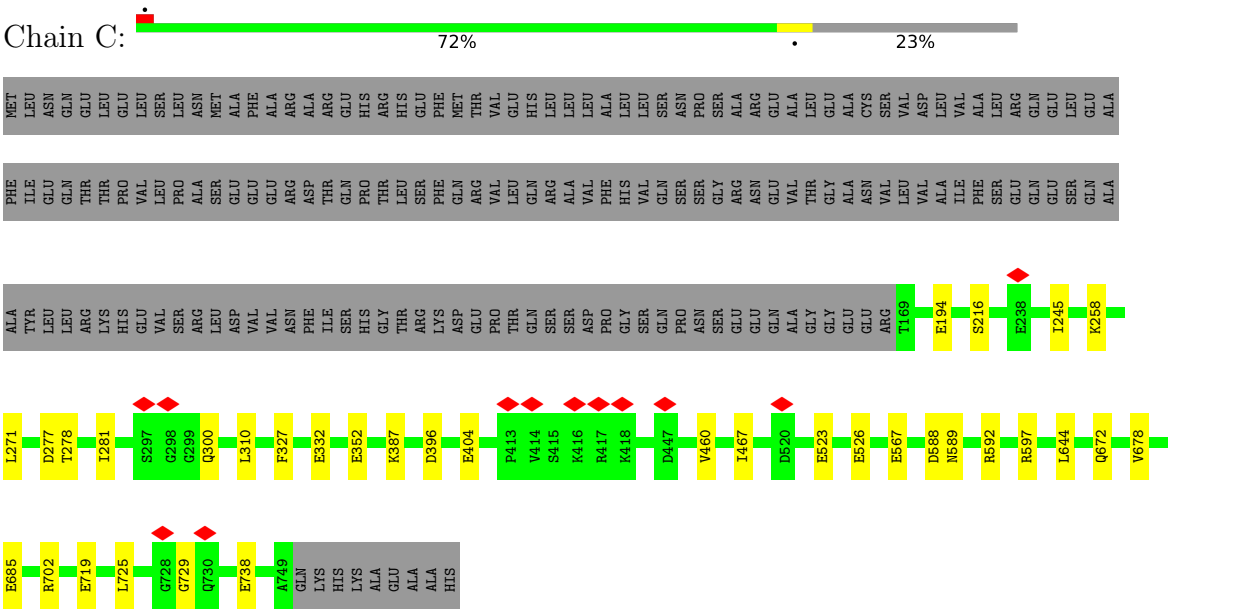
• Molecule 1: ATP-dependent Clp protease ATP-binding subunit ClpA

Chain B:



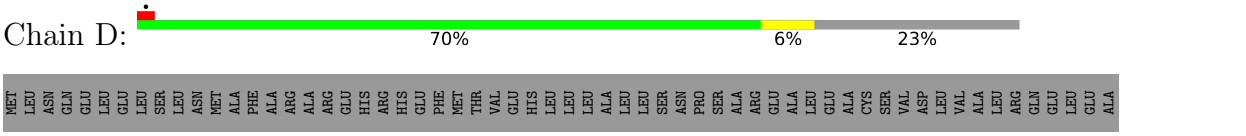
• Molecule 1: ATP-dependent Clp protease ATP-binding subunit ClpA

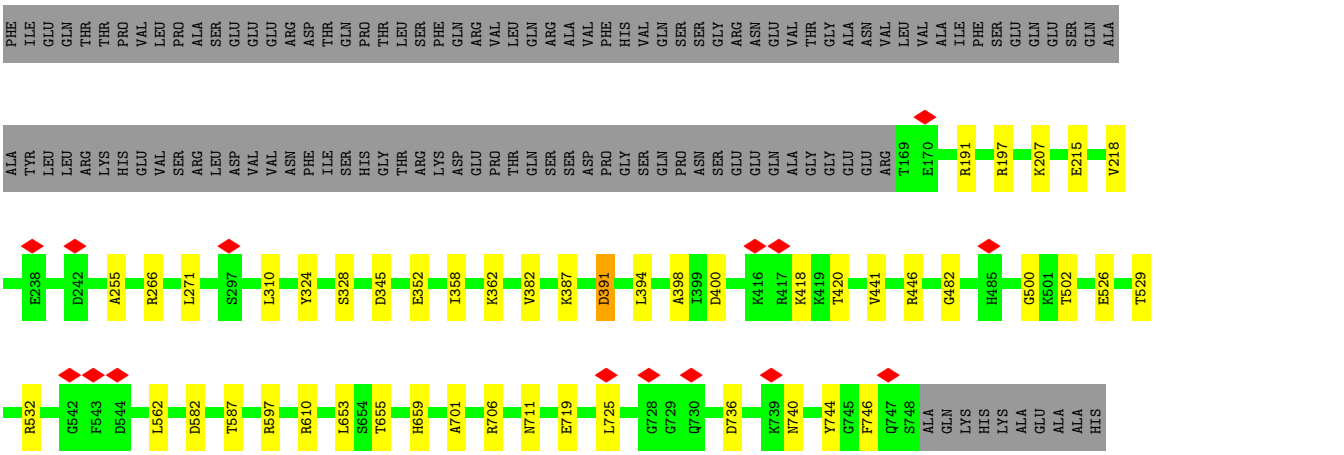
Chain C:



• Molecule 1: ATP-dependent Clp protease ATP-binding subunit ClpA

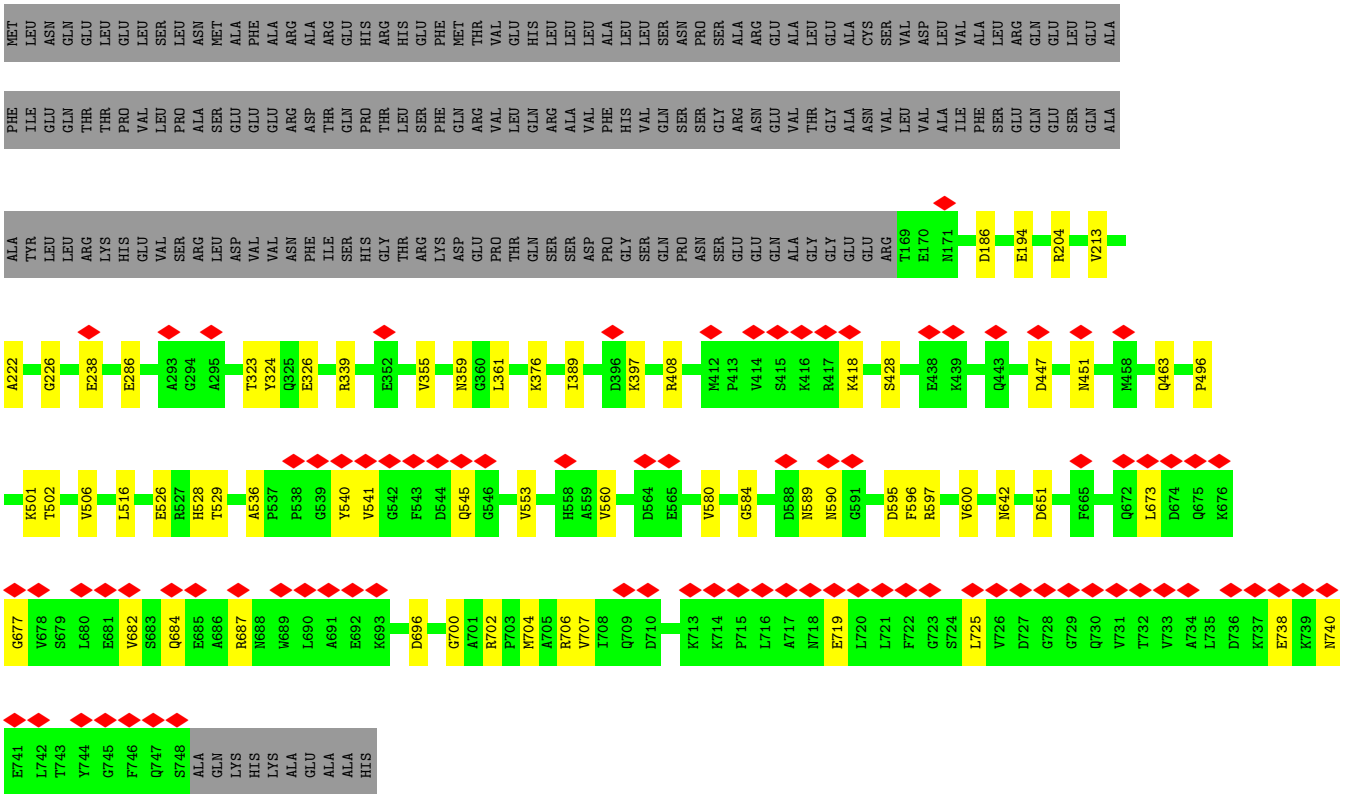
Chain D:





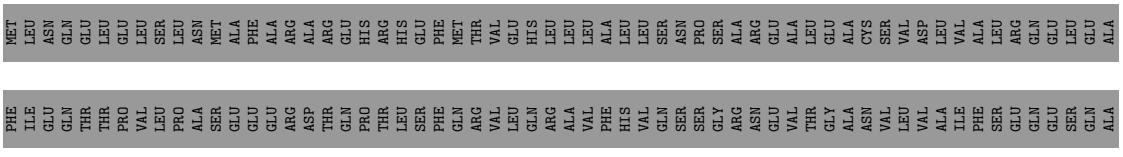
• Molecule 1: ATP-dependent Clp protease ATP-binding subunit ClpA

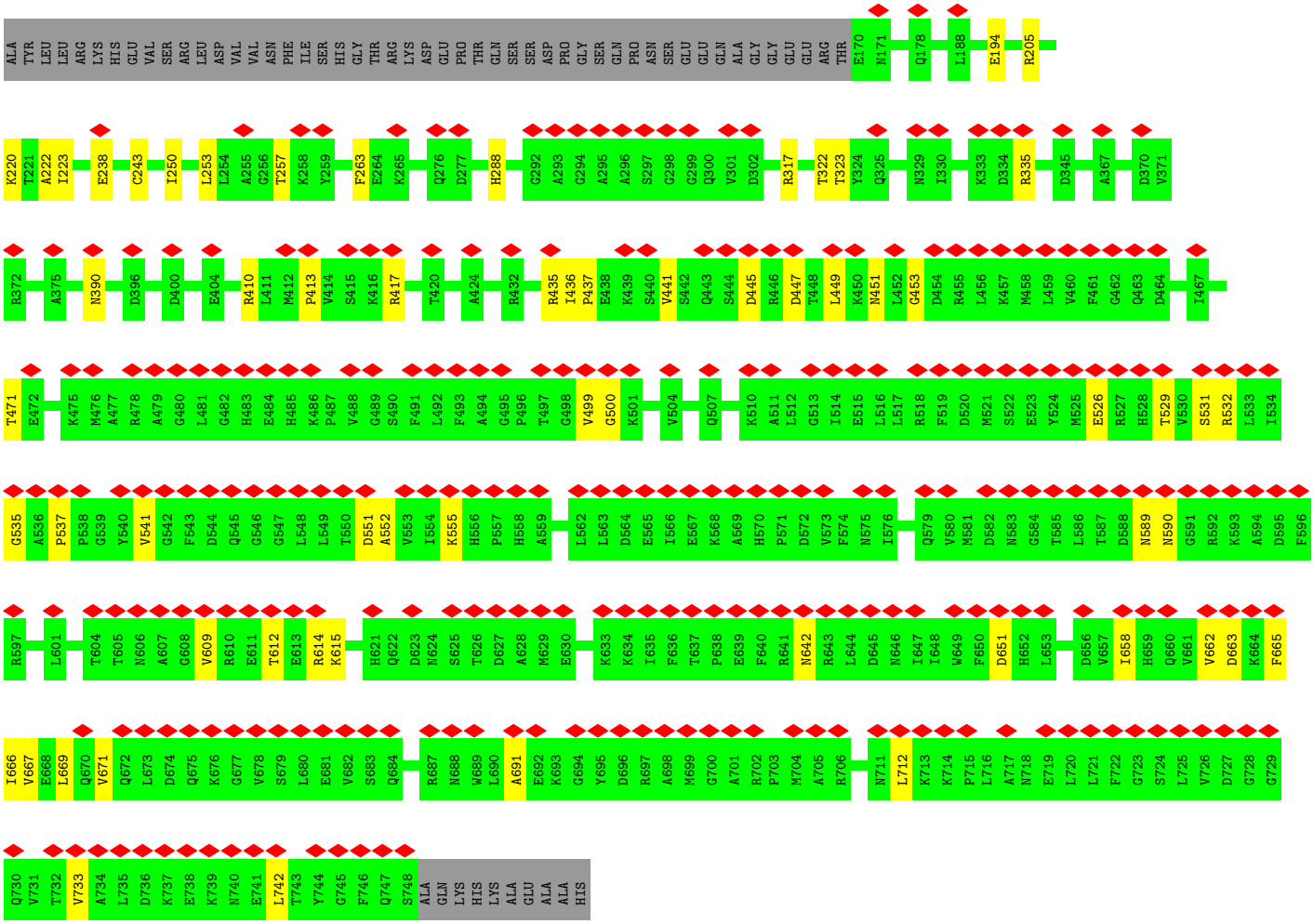
Chain E:



• Molecule 1: ATP-dependent Clp protease ATP-binding subunit ClpA

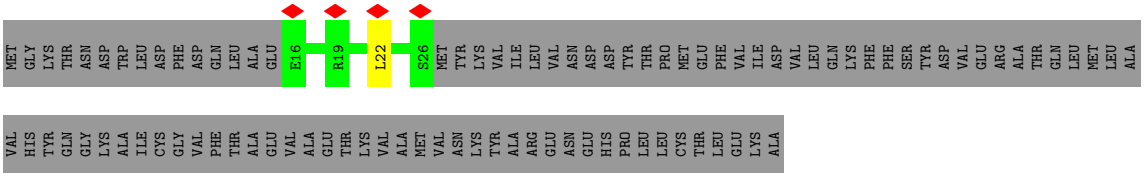
Chain F:





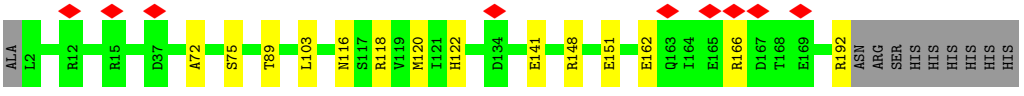
• Molecule 2: ATP-dependent Clp protease adapter protein ClpS

Chain S:



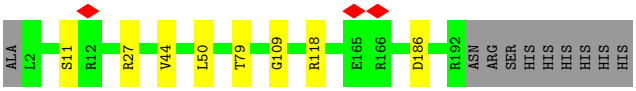
• Molecule 3: ATP-dependent Clp protease proteolytic subunit

Chain H:



• Molecule 3: ATP-dependent Clp protease proteolytic subunit

Chain I:

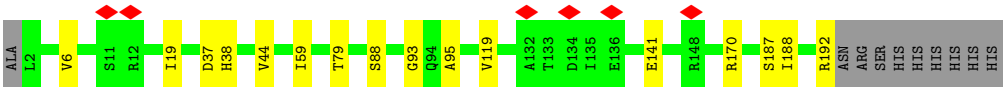


• Molecule 3: ATP-dependent Clp protease proteolytic subunit

Chain J:

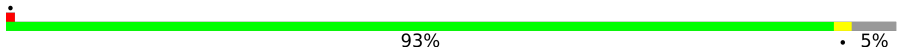
• Molecule 3: ATP-dependent Clp protease proteolytic subunit

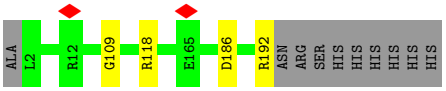
Chain K:



• Molecule 3: ATP-dependent Clp protease proteolytic subunit

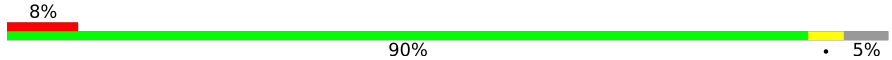
Chain L:

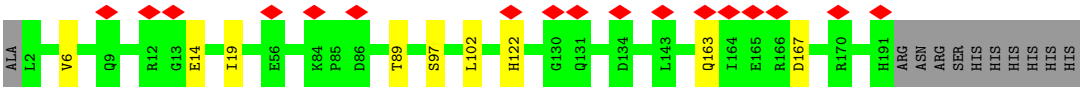




• Molecule 3: ATP-dependent Clp protease proteolytic subunit

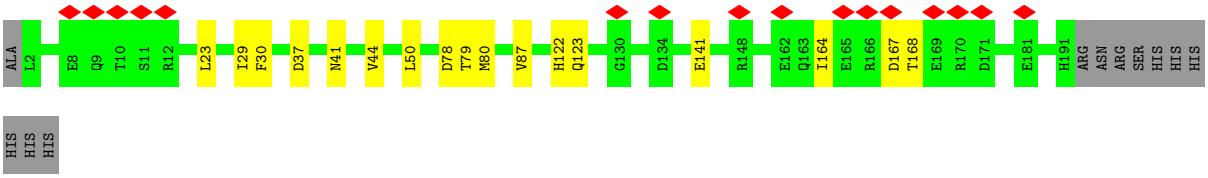
Chain M:





• Molecule 3: ATP-dependent Clp protease proteolytic subunit

Chain N:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	38006	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	34	Depositor
Minimum defocus (nm)	-500	Depositor
Maximum defocus (nm)	-2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	16.875	Depositor
Minimum map value	-6.958	Depositor
Average map value	0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	1.4	Depositor
Map size (Å)	150.51, 147.9, 186.18001	wwPDB
Map dimensions	214, 170, 173	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.86999995, 0.86999995, 0.87000006	Depositor

5 Model quality

5.1 Standard geometry

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

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	0.27	0/4566	0.53	0/6162
1	B	0.28	0/4588	0.53	0/6192
1	C	0.30	0/4595	0.52	0/6202
1	D	0.30	0/4590	0.54	1/6195 (0.0%)
1	E	0.28	0/4590	0.54	0/6195
1	F	0.27	0/4583	0.54	0/6185
2	S	0.28	0/87	0.64	0/116
3	H	0.29	0/1519	0.50	0/2047
3	I	0.30	0/1519	0.52	0/2047
3	J	0.31	0/1519	0.55	0/2047
3	K	0.31	0/1519	0.52	0/2047
3	L	0.30	0/1519	0.52	0/2047
3	M	0.29	0/1508	0.51	0/2033
3	N	0.29	0/1508	0.49	0/2033
All	All	0.29	0/38210	0.53	1/51548 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	D	391	ASP	CB-CG-OD1	6.90	124.51	118.30

There are no chirality outliers.

There are no planarity outliers.

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	4500	4601	4601	28	0
1	B	4522	4618	4617	28	0
1	C	4529	4623	4623	27	0
1	D	4524	4618	4618	33	0
1	E	4524	4619	4619	41	0
1	F	4517	4613	4613	42	0
2	S	86	93	92	1	0
3	H	1495	1507	1507	8	0
3	I	1495	1507	1507	5	0
3	J	1495	1507	1507	6	0
3	K	1495	1507	1507	9	0
3	L	1495	1507	1507	2	0
3	M	1484	1494	1494	6	0
3	N	1484	1494	1494	10	0
4	A	31	12	12	0	0
4	B	62	24	24	1	0
4	C	62	24	24	1	0
4	D	62	24	24	2	0
5	A	27	12	12	0	0
5	E	54	24	24	1	0
5	F	54	24	24	1	0
6	A	2	0	0	0	0
6	B	2	0	0	0	0
6	C	2	0	0	0	0
6	D	2	0	0	0	0
6	E	1	0	0	0	0
All	All	38006	38452	38450	222	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 3.

All (222) 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)
3:K:141:GLU:OE2	3:L:118:ARG:NH2	2.14	0.80
1:F:733:VAL:HG12	1:F:742:LEU:HD12	1.70	0.72
1:B:706:ARG:NH2	1:C:644:LEU:O	2.23	0.72
1:B:614:ARG:NH2	1:B:624:ASN:OD1	2.25	0.69
1:D:324:TYR:OH	1:D:345:ASP:OD1	2.10	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:I:44:VAL:HG13	3:I:79:THR:HG21	1.77	0.67
1:A:470:LEU:HD22	1:A:648:ILE:HD13	1.77	0.67
1:F:532:ARG:NH1	1:F:537:PRO:O	2.29	0.66
1:E:463:GLN:NE2	1:E:651:ASP:O	2.28	0.65
1:E:286:GLU:OE1	1:F:335:ARG:NH2	2.29	0.65
1:C:396:ASP:OD2	1:D:207:LYS:NZ	2.29	0.64
1:B:588:ASP:OD1	1:B:592:ARG:N	2.31	0.64
1:F:222:ALA:N	5:F:801:ADP:O2A	2.31	0.63
1:F:390:ASN:ND2	1:F:555:LYS:O	2.34	0.61
1:C:523:GLU:OE1	1:D:587:THR:OG1	2.19	0.59
1:C:216:SER:OG	4:C:801:AGS:S1G	2.57	0.59
1:F:253:LEU:O	1:F:257:THR:HG23	2.01	0.59
1:C:719:GLU:HB2	1:C:725:LEU:HD12	1.86	0.58
1:C:672:GLN:NE2	1:D:482:GLY:O	2.36	0.58
1:D:400:ASP:OD2	1:E:204:ARG:NH1	2.37	0.58
1:E:553:VAL:HG21	1:E:596:PHE:CD1	2.38	0.58
1:F:453:GLY:HA2	1:F:471:THR:HG21	1.86	0.58
1:C:460:VAL:HG23	1:C:467:ILE:HD11	1.86	0.58
1:E:389:ILE:O	1:E:397:LYS:NZ	2.25	0.57
1:F:658:ILE:HG22	1:F:691:ALA:HB1	1.86	0.57
1:F:435:ARG:O	1:F:436:ILE:HD13	2.05	0.57
1:F:322:THR:HG22	1:F:323:THR:H	1.69	0.57
3:N:80:MET:SD	3:N:87:VAL:HG21	2.44	0.57
3:K:44:VAL:HG13	3:K:79:THR:HG21	1.87	0.56
1:A:287:ILE:HD12	1:A:290:ILE:HD11	1.87	0.56
1:C:271:LEU:HD13	1:C:310:LEU:HD12	1.87	0.56
1:D:441:VAL:O	1:D:446:ARG:NH1	2.40	0.55
1:D:719:GLU:CB	1:D:725:LEU:HD12	2.36	0.55
1:A:464:ASP:HA	1:A:467:ILE:HD12	1.88	0.55
1:A:553:VAL:HG21	1:A:596:PHE:CZ	2.41	0.55
1:E:506:VAL:HG22	1:E:516:LEU:HD21	1.88	0.55
1:F:445:ASP:O	1:F:449:LEU:HD13	2.06	0.55
1:A:188:LEU:HD22	1:A:226:GLY:HA3	1.89	0.55
1:E:541:VAL:HG13	1:F:541:VAL:HG12	1.87	0.55
1:A:515:GLU:OE1	1:A:556:HIS:ND1	2.40	0.54
1:B:179:LEU:HD23	1:B:185:ILE:HD11	1.89	0.54
3:M:89:THR:HG21	3:M:102:LEU:O	2.08	0.54
1:E:696:ASP:O	1:E:700:GLY:N	2.40	0.54
3:J:113:CYS:SG	3:J:185:VAL:HG11	2.49	0.53
1:C:245:ILE:CD1	1:C:281:ILE:HD12	2.37	0.53
1:A:194:GLU:OE1	1:A:194:GLU:N	2.41	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:526:GLU:N	1:D:526:GLU:OE1	2.41	0.53
3:J:8:GLU:OE1	3:J:10:THR:OG1	2.26	0.53
1:E:506:VAL:HG22	1:E:516:LEU:CD2	2.39	0.53
1:B:486:LYS:NZ	1:B:581:MET:O	2.41	0.53
1:C:404:GLU:OE2	1:D:197:ARG:NH1	2.41	0.53
1:D:255:ALA:O	1:D:266:ARG:NH1	2.41	0.53
1:D:387:LYS:O	1:D:597:ARG:NH2	2.42	0.52
1:C:685:GLU:N	1:C:685:GLU:OE1	2.42	0.52
1:F:288:HIS:HB3	1:F:322:THR:HG23	1.92	0.52
1:E:496:PRO:O	1:E:501:LYS:NZ	2.43	0.52
3:J:77:TYR:OH	3:J:152:LEU:HD22	2.09	0.52
1:D:271:LEU:HD13	1:D:310:LEU:CD1	2.40	0.52
1:E:682:VAL:O	1:E:687:ARG:NH1	2.43	0.52
1:B:609:VAL:O	1:B:612:THR:OG1	2.22	0.52
1:B:523:GLU:O	1:B:529:THR:HG21	2.11	0.51
1:C:277:ASP:OD1	1:C:278:THR:N	2.43	0.51
3:M:6:VAL:HG11	3:M:19:ILE:HD12	1.91	0.51
1:E:326:GLU:N	1:E:326:GLU:OE1	2.43	0.51
1:F:410:ARG:O	1:F:417:ARG:NH1	2.44	0.51
1:B:170:GLU:OE1	1:B:170:GLU:N	2.44	0.51
1:C:738:GLU:N	1:C:738:GLU:OE1	2.43	0.51
1:A:706:ARG:NH2	1:B:642:ASN:O	2.43	0.51
3:N:29:ILE:HD11	3:N:50:LEU:HD12	1.92	0.51
1:F:662:VAL:HG12	1:F:666:ILE:HD12	1.93	0.50
1:C:352:GLU:N	1:C:352:GLU:OE1	2.45	0.50
1:D:358:ILE:HD11	1:D:398:ALA:HB1	1.93	0.50
1:B:606:ASN:ND2	4:B:802:AGS:S1G	2.85	0.50
1:F:257:THR:HG21	1:F:263:PHE:HB2	1.93	0.49
1:A:712:LEU:O	1:A:716:LEU:HD13	2.12	0.49
1:B:288:HIS:NE2	1:B:326:GLU:OE1	2.45	0.49
1:D:529:THR:OG1	1:D:532:ARG:NH2	2.46	0.49
1:A:653:LEU:HD13	1:A:657:VAL:HG11	1.93	0.49
1:C:387:LYS:O	1:C:597:ARG:NH1	2.45	0.49
4:D:801:AGS:O2B	1:E:339:ARG:NH2	2.44	0.49
1:F:614:ARG:NE	1:F:615:LYS:O	2.46	0.49
1:E:738:GLU:O	1:E:740:ASN:ND2	2.47	0.48
1:C:567:GLU:OE2	1:C:567:GLU:N	2.44	0.48
1:B:736:ASP:OD2	1:B:739:LYS:NZ	2.47	0.48
3:N:122:HIS:ND1	3:N:123:GLN:O	2.42	0.48
1:C:702:ARG:NH2	1:D:582:ASP:OD2	2.46	0.48
1:F:499:VAL:HG12	1:F:500:GLY:H	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:447:ASP:O	1:F:451:ASN:ND2	2.46	0.48
1:B:195:LEU:HD11	1:B:227:LEU:HD13	1.94	0.48
1:D:719:GLU:HB3	1:D:725:LEU:HD12	1.94	0.48
1:C:588:ASP:OD1	1:C:589:ASN:N	2.44	0.48
1:D:191:ARG:NH2	1:D:218:VAL:O	2.48	0.47
1:E:408:ARG:NH1	1:E:428:SER:OG	2.48	0.47
1:F:551:ASP:OD1	1:F:552:ALA:N	2.47	0.47
1:B:238:GLU:OE1	1:B:238:GLU:N	2.44	0.47
3:N:164:ILE:O	3:N:168:THR:OG1	2.22	0.47
1:F:194:GLU:OE1	1:F:194:GLU:N	2.44	0.47
1:E:447:ASP:O	1:E:451:ASN:ND2	2.48	0.47
3:K:187:SER:OG	3:K:188:ILE:N	2.48	0.47
1:A:287:ILE:CD1	1:A:290:ILE:HD11	2.44	0.47
3:J:23:LEU:HD13	3:J:30:PHE:CE1	2.50	0.47
1:A:278:THR:O	1:A:317:ARG:NH2	2.48	0.46
3:M:14:GLU:N	3:M:14:GLU:OE2	2.48	0.46
1:E:194:GLU:N	1:E:194:GLU:OE1	2.46	0.46
1:E:595:ASP:OD2	1:E:597:ARG:NH2	2.48	0.46
3:I:27:ARG:NH1	3:I:50:LEU:O	2.44	0.46
3:H:116:ASN:ND2	3:N:78:ASP:OD1	2.46	0.46
3:H:162:GLU:OE2	3:H:166:ARG:NE	2.44	0.46
1:D:352:GLU:OE1	1:D:352:GLU:N	2.48	0.46
1:B:264:GLU:OE2	1:B:301:VAL:HG21	2.16	0.46
1:F:526:GLU:O	1:F:529:THR:OG1	2.30	0.46
1:E:502:THR:O	1:E:506:VAL:HG23	2.16	0.46
1:B:452:LEU:HD23	1:B:452:LEU:O	2.16	0.46
1:B:243:CYS:SG	1:B:317:ARG:NH2	2.89	0.46
1:D:706:ARG:NH2	1:E:642:ASN:OD1	2.47	0.46
1:D:725:LEU:HD11	1:D:746:PHE:CE1	2.51	0.46
3:J:131:GLN:OE1	3:K:170:ARG:NH1	2.46	0.46
1:A:682:VAL:O	1:A:687:ARG:NH1	2.44	0.46
1:C:300:GLN:N	1:C:300:GLN:OE1	2.49	0.46
3:N:23:LEU:HD13	3:N:30:PHE:HE1	1.81	0.46
1:D:418:LYS:NZ	1:D:420:THR:O	2.41	0.45
1:F:609:VAL:O	1:F:612:THR:OG1	2.34	0.45
1:E:684:GLN:O	1:E:684:GLN:NE2	2.50	0.45
1:A:414:VAL:HG23	1:A:415:SER:H	1.81	0.45
1:C:194:GLU:OE1	1:C:194:GLU:N	2.49	0.45
1:C:678:VAL:HG21	1:C:725:LEU:HD22	1.99	0.45
1:B:488:VAL:HG13	1:B:597:ARG:O	2.17	0.45
1:E:222:ALA:O	1:E:226:GLY:N	2.48	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:706:ARG:NH1	1:F:642:ASN:O	2.49	0.45
1:A:189:ILE:HG21	1:A:356:GLN:HB2	1.99	0.45
1:A:553:VAL:HG21	1:A:596:PHE:CE2	2.50	0.45
1:F:531:SER:O	1:F:535:GLY:N	2.49	0.45
1:A:654:SER:OG	1:A:656:ASP:OD1	2.30	0.44
1:C:526:GLU:N	1:C:526:GLU:OE1	2.50	0.44
1:F:651:ASP:OD1	1:F:651:ASP:N	2.50	0.44
3:H:89:THR:HB	3:H:103:LEU:HD12	1.99	0.44
1:A:580:VAL:O	1:A:584:GLY:N	2.41	0.44
3:H:120:MET:SD	3:H:122:HIS:ND1	2.88	0.44
1:C:258:LYS:NZ	2:S:22:LEU:HD21	2.31	0.44
1:C:592:ARG:NH1	1:D:328:SER:OG	2.50	0.44
1:E:526:GLU:N	1:E:526:GLU:OE1	2.51	0.44
3:H:148:ARG:NH1	3:H:151:GLU:OE1	2.50	0.44
3:K:95:ALA:HB3	3:K:119:VAL:HG23	1.98	0.44
3:N:167:ASP:OD1	3:N:168:THR:HG23	2.16	0.44
3:K:6:VAL:HG11	3:K:19:ILE:HD12	1.99	0.44
1:E:186:ASP:HB3	1:E:361:LEU:HD22	1.99	0.44
1:A:605:THR:HG22	1:A:607:ALA:H	1.81	0.44
1:E:186:ASP:OD1	1:F:205:ARG:NH2	2.47	0.44
3:M:6:VAL:HG11	3:M:19:ILE:CD1	2.48	0.43
1:E:719:GLU:HB2	1:E:725:LEU:HD12	2.00	0.43
1:F:499:VAL:HG12	1:F:500:GLY:N	2.33	0.43
3:M:163:GLN:NE2	3:M:167:ASP:OD2	2.51	0.43
1:E:238:GLU:OE1	1:E:238:GLU:N	2.47	0.43
1:B:719:GLU:OE1	1:B:724:SER:N	2.51	0.43
1:E:213:VAL:HG12	1:E:324:TYR:CD1	2.53	0.43
1:D:653:LEU:CD1	1:D:701:ALA:HB2	2.48	0.43
1:B:565:GLU:OE2	1:B:606:ASN:ND2	2.51	0.43
1:D:215:GLU:O	1:D:218:VAL:HG22	2.19	0.43
1:D:655:THR:O	1:D:659:HIS:ND1	2.49	0.43
1:F:663:ASP:O	1:F:667:VAL:HG23	2.19	0.43
3:J:71:THR:OG1	3:K:93:GLY:O	2.36	0.43
1:D:610:ARG:NE	3:I:11:SER:OG	2.48	0.43
1:D:271:LEU:HD13	1:D:310:LEU:HD13	2.01	0.43
1:F:220:LYS:O	1:F:223:ILE:HG22	2.19	0.43
1:F:238:GLU:OE1	1:F:238:GLU:N	2.47	0.43
1:B:452:LEU:CD2	1:B:471:THR:HG22	2.49	0.42
1:D:711:ASN:O	1:D:744:TYR:OH	2.30	0.42
1:E:528:HIS:CE1	1:E:529:THR:HG23	2.54	0.42
3:I:109:GLY:N	3:I:186:ASP:OD2	2.50	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:673:LEU:O	1:E:677:GLY:N	2.52	0.42
1:F:250:ILE:HD12	1:F:250:ILE:H	1.84	0.42
1:A:425:ASP:O	1:A:429:VAL:HG23	2.20	0.42
1:A:567:GLU:OE1	1:A:567:GLU:N	2.48	0.42
1:A:646:ASN:OD1	1:A:647:ILE:N	2.53	0.42
1:F:667:VAL:O	1:F:671:VAL:HG23	2.20	0.42
3:L:109:GLY:N	3:L:186:ASP:OD2	2.52	0.42
1:A:446:ARG:O	1:A:450:LYS:NZ	2.51	0.42
1:A:342:GLN:O	1:A:344:ILE:HD12	2.19	0.42
1:E:355:VAL:O	1:E:359:ASN:ND2	2.47	0.42
1:F:413:PRO:O	1:F:417:ARG:NH1	2.52	0.42
3:H:118:ARG:NE	3:N:141:GLU:OE2	2.44	0.42
1:A:690:LEU:O	1:A:694:GLY:N	2.46	0.42
1:E:540:TYR:OH	1:F:590:ASN:OD1	2.36	0.42
1:E:589:ASN:OD1	1:E:590:ASN:N	2.52	0.42
3:H:72:ALA:O	3:H:75:SER:OG	2.33	0.42
1:E:580:VAL:O	1:E:584:GLY:N	2.50	0.42
1:D:736:ASP:O	1:D:740:ASN:N	2.51	0.42
1:E:323:THR:HG22	1:E:324:TYR:N	2.35	0.42
1:E:704:MET:HA	1:E:707:VAL:HG22	2.02	0.42
1:B:222:ALA:O	1:B:226:GLY:N	2.46	0.42
3:K:37:ASP:OD1	3:K:38:HIS:N	2.53	0.42
1:D:382:VAL:HG13	1:D:394:LEU:HD11	2.02	0.41
1:F:712:LEU:HD23	1:F:712:LEU:H	1.85	0.41
1:C:460:VAL:CG2	1:C:467:ILE:HD11	2.49	0.41
1:E:541:VAL:HG13	1:F:541:VAL:CG1	2.49	0.41
1:D:358:ILE:O	1:D:362:LYS:N	2.53	0.41
1:D:500:GLY:N	4:D:802:AGS:N7	2.69	0.41
1:F:665:PHE:O	1:F:669:LEU:HD23	2.20	0.41
1:B:215:GLU:O	1:B:218:VAL:HG22	2.20	0.41
1:D:502:THR:HG23	1:D:562:LEU:HD21	2.03	0.41
1:A:218:VAL:HG12	1:A:218:VAL:O	2.21	0.41
1:F:243:CYS:SG	1:F:317:ARG:NH2	2.93	0.41
1:F:662:VAL:CG2	1:F:691:ALA:HB2	2.51	0.41
1:A:277:ASP:O	1:A:280:SER:OG	2.32	0.41
1:A:663:ASP:O	1:A:667:VAL:HG23	2.20	0.41
1:B:736:ASP:O	1:B:740:ASN:N	2.55	0.41
1:C:678:VAL:HG23	1:C:729:GLY:O	2.21	0.41
3:M:97:SER:OG	3:M:122:HIS:O	2.39	0.41
1:B:287:ILE:HD11	1:B:290:ILE:HD11	2.03	0.40
3:K:59:ILE:O	3:K:88:SER:N	2.49	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:567:GLU:HG3	1:B:635:ILE:HD13	2.03	0.40
1:E:560:VAL:HG13	1:E:600:VAL:HG13	2.03	0.40
1:E:702:ARG:NH2	5:E:802:ADP:O1B	2.54	0.40
1:F:589:ASN:OD1	1:F:590:ASN:N	2.54	0.40
3:N:37:ASP:O	3:N:41:ASN:ND2	2.47	0.40
3:N:44:VAL:HG13	3:N:79:THR:HG21	2.03	0.40
1:E:536:ALA:HB2	1:E:545:GLN:HE22	1.85	0.40
1:F:437:PRO:O	1:F:441:VAL:HG23	2.21	0.40
1:C:327:PHE:O	1:C:332:GLU:N	2.52	0.40
3:H:141:GLU:OE2	3:I:118:ARG:NH1	2.52	0.40
1:B:301:VAL:HG23	1:B:301:VAL:O	2.21	0.40
1:B:505:THR:HG21	1:B:562:LEU:HD13	2.04	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	575/758 (76%)	572 (100%)	3 (0%)	0	100	100
1	B	578/758 (76%)	576 (100%)	2 (0%)	0	100	100
1	C	579/758 (76%)	570 (98%)	9 (2%)	0	100	100
1	D	578/758 (76%)	576 (100%)	2 (0%)	0	100	100
1	E	578/758 (76%)	576 (100%)	2 (0%)	0	100	100
1	F	577/758 (76%)	573 (99%)	4 (1%)	0	100	100
2	S	9/106 (8%)	9 (100%)	0	0	100	100
3	H	189/201 (94%)	189 (100%)	0	0	100	100
3	I	189/201 (94%)	188 (100%)	1 (0%)	0	100	100
3	J	189/201 (94%)	189 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	K	189/201 (94%)	189 (100%)	0	0	100	100
3	L	189/201 (94%)	189 (100%)	0	0	100	100
3	M	188/201 (94%)	188 (100%)	0	0	100	100
3	N	188/201 (94%)	187 (100%)	1 (0%)	0	100	100
All	All	4795/6061 (79%)	4771 (100%)	24 (0%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	484/639 (76%)	483 (100%)	1 (0%)	93	96
1	B	486/639 (76%)	486 (100%)	0	100	100
1	C	487/639 (76%)	487 (100%)	0	100	100
1	D	487/639 (76%)	486 (100%)	1 (0%)	93	96
1	E	487/639 (76%)	485 (100%)	2 (0%)	91	94
1	F	486/639 (76%)	486 (100%)	0	100	100
2	S	10/93 (11%)	10 (100%)	0	100	100
3	H	162/171 (95%)	161 (99%)	1 (1%)	86	91
3	I	162/171 (95%)	162 (100%)	0	100	100
3	J	162/171 (95%)	162 (100%)	0	100	100
3	K	162/171 (95%)	161 (99%)	1 (1%)	86	91
3	L	162/171 (95%)	161 (99%)	1 (1%)	86	91
3	M	161/171 (94%)	161 (100%)	0	100	100
3	N	161/171 (94%)	161 (100%)	0	100	100
All	All	4059/5124 (79%)	4052 (100%)	7 (0%)	93	96

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	268	LYS
1	D	391	ASP
1	E	376	LYS
1	E	418	LYS
3	H	192	ARG
3	K	192	ARG
3	L	192	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	606	ASN
1	D	325	GLN
1	D	329	ASN
1	D	730	GLN
1	E	233	GLN
1	E	545	GLN
1	E	684	GLN
1	E	740	ASN
1	F	711	ASN
3	H	41	ASN
3	L	41	ASN
3	N	191	HIS

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 21 ligands modelled in this entry, 9 are monoatomic - leaving 12 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
4	AGS	C	801	6	26,33,33	0.81	0	26,52,52	0.87	1 (3%)
5	ADP	A	802	-	24,29,29	0.67	0	29,45,45	0.85	2 (6%)
4	AGS	A	801	6	26,33,33	0.82	1 (3%)	26,52,52	0.93	2 (7%)
5	ADP	F	802	-	24,29,29	0.65	0	29,45,45	0.76	1 (3%)
5	ADP	E	802	-	24,29,29	0.68	0	29,45,45	0.74	1 (3%)
4	AGS	B	802	6	26,33,33	0.83	1 (3%)	26,52,52	0.91	1 (3%)
4	AGS	D	802	6	26,33,33	0.83	1 (3%)	26,52,52	0.88	1 (3%)
4	AGS	C	802	6	26,33,33	0.82	1 (3%)	26,52,52	0.81	1 (3%)
5	ADP	E	801	6	24,29,29	0.69	0	29,45,45	0.79	1 (3%)
5	ADP	F	801	-	24,29,29	0.67	0	29,45,45	0.83	1 (3%)
4	AGS	D	801	6	26,33,33	0.84	1 (3%)	26,52,52	0.96	1 (3%)
4	AGS	B	801	6	26,33,33	0.81	1 (3%)	26,52,52	0.85	1 (3%)

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
4	AGS	C	801	6	-	3/17/38/38	0/3/3/3
5	ADP	A	802	-	-	1/12/32/32	0/3/3/3
4	AGS	A	801	6	-	5/17/38/38	0/3/3/3
5	ADP	F	802	-	-	4/12/32/32	0/3/3/3
5	ADP	E	802	-	-	0/12/32/32	0/3/3/3
4	AGS	B	802	6	-	1/17/38/38	0/3/3/3
4	AGS	D	802	6	-	4/17/38/38	0/3/3/3
4	AGS	C	802	6	-	2/17/38/38	0/3/3/3
5	ADP	E	801	6	-	2/12/32/32	0/3/3/3
5	ADP	F	801	-	-	0/12/32/32	0/3/3/3
4	AGS	D	801	6	-	3/17/38/38	0/3/3/3
4	AGS	B	801	6	-	1/17/38/38	0/3/3/3

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	801	AGS	PG-S1G	2.13	1.95	1.90
4	D	801	AGS	PG-S1G	2.13	1.95	1.90
4	D	802	AGS	PG-S1G	2.12	1.95	1.90
4	B	801	AGS	PG-S1G	2.10	1.95	1.90
4	B	802	AGS	PG-S1G	2.04	1.95	1.90
4	C	802	AGS	PG-S1G	2.00	1.95	1.90

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	A	801	AGS	O4'-C1'-C2'	-2.38	103.45	106.93
5	F	802	ADP	C5-C6-N6	2.31	123.86	120.35
5	A	802	ADP	C5-C6-N6	2.26	123.78	120.35
4	C	801	AGS	C5-C6-N6	2.22	123.73	120.35
4	B	801	AGS	C5-C6-N6	2.22	123.72	120.35
5	F	801	ADP	C5-C6-N6	2.20	123.70	120.35
5	E	801	ADP	C5-C6-N6	2.15	123.62	120.35
4	C	802	AGS	C5-C6-N6	2.14	123.61	120.35
4	D	801	AGS	C5-C6-N6	2.14	123.60	120.35
4	D	802	AGS	C5-C6-N6	2.13	123.59	120.35
5	A	802	ADP	O4'-C1'-C2'	-2.10	103.85	106.93
4	B	802	AGS	C5-C6-N6	2.10	123.54	120.35
5	E	802	ADP	C5-C6-N6	2.07	123.50	120.35
4	A	801	AGS	C5-C6-N6	2.01	123.40	120.35

There are no chirality outliers.

All (26) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	801	AGS	C5'-O5'-PA-O2A
4	A	801	AGS	C5'-O5'-PA-O3A
4	A	801	AGS	C4'-C5'-O5'-PA
4	C	801	AGS	C5'-O5'-PA-O3A
4	C	802	AGS	C5'-O5'-PA-O1A
4	C	802	AGS	C5'-O5'-PA-O3A
4	D	802	AGS	C5'-O5'-PA-O1A
4	D	802	AGS	O4'-C4'-C5'-O5'
5	E	801	ADP	C3'-C4'-C5'-O5'
5	F	802	ADP	C4'-C5'-O5'-PA
5	F	802	ADP	O4'-C4'-C5'-O5'
4	D	802	AGS	C3'-C4'-C5'-O5'

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Mol	Chain	Res	Type	Atoms
5	E	801	ADP	O4'-C4'-C5'-O5'
5	F	802	ADP	C3'-C4'-C5'-O5'
4	D	802	AGS	C4'-C5'-O5'-PA
4	A	801	AGS	O4'-C4'-C5'-O5'
4	C	801	AGS	C4'-C5'-O5'-PA
4	D	801	AGS	C4'-C5'-O5'-PA
4	D	801	AGS	PB-O3A-PA-O5'
4	B	801	AGS	C4'-C5'-O5'-PA
4	C	801	AGS	C5'-O5'-PA-O1A
4	A	801	AGS	C3'-C4'-C5'-O5'
4	B	802	AGS	PG-O3B-PB-O1B
5	F	802	ADP	C5'-O5'-PA-O3A
5	A	802	ADP	O4'-C4'-C5'-O5'
4	D	801	AGS	C5'-O5'-PA-O1A

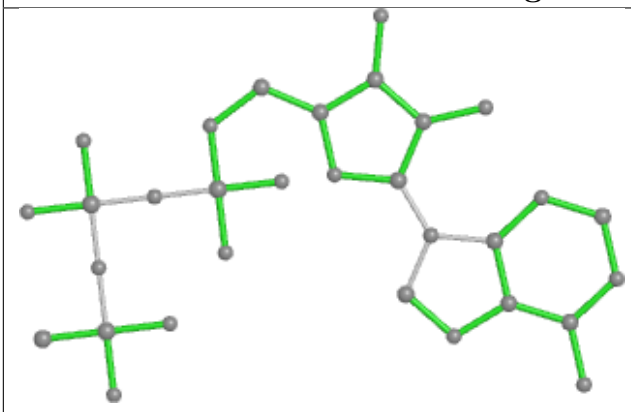
There are no ring outliers.

6 monomers are involved in 6 short contacts:

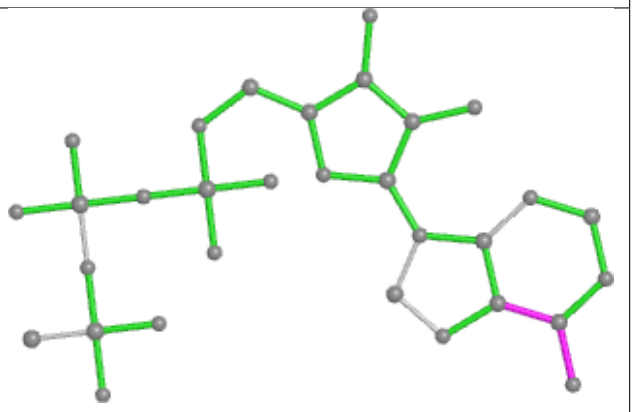
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	C	801	AGS	1	0
5	E	802	ADP	1	0
4	B	802	AGS	1	0
4	D	802	AGS	1	0
5	F	801	ADP	1	0
4	D	801	AGS	1	0

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 then 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.

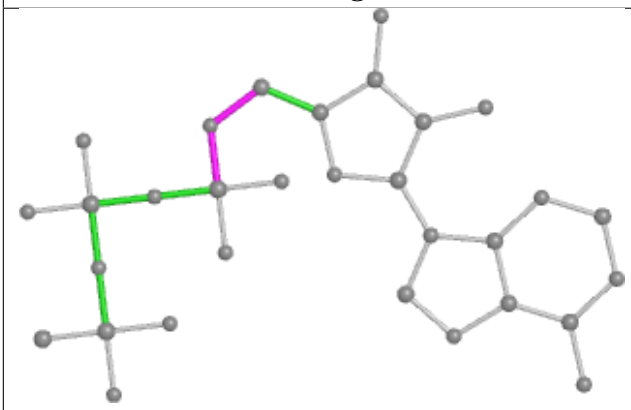
Ligand AGS C 801



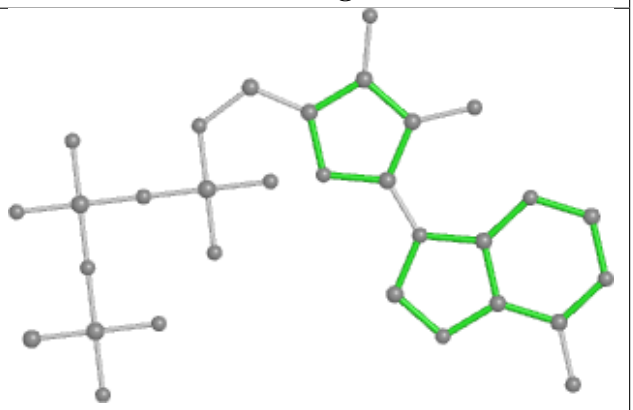
Bond lengths



Bond angles

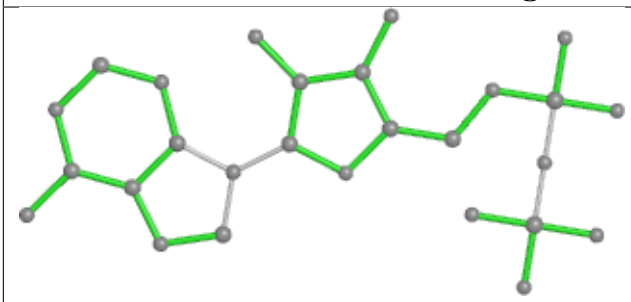


Torsions



Rings

Ligand ADP A 802



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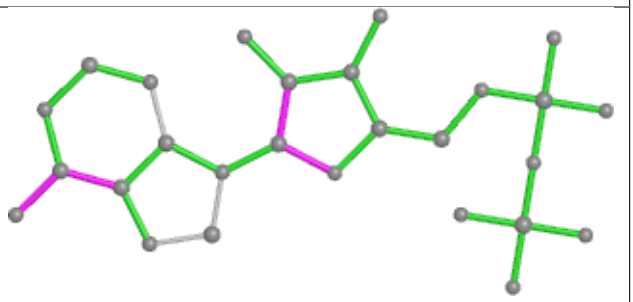

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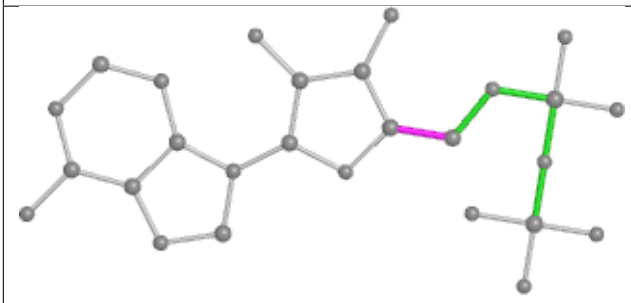

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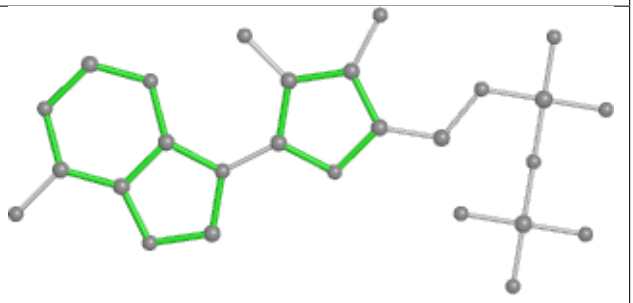
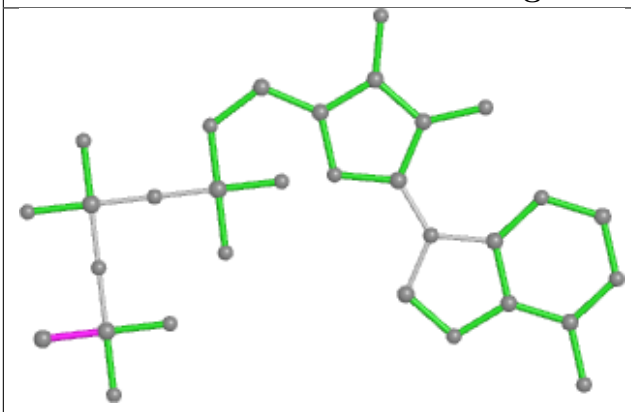


Rings

Ligand AGS A 801



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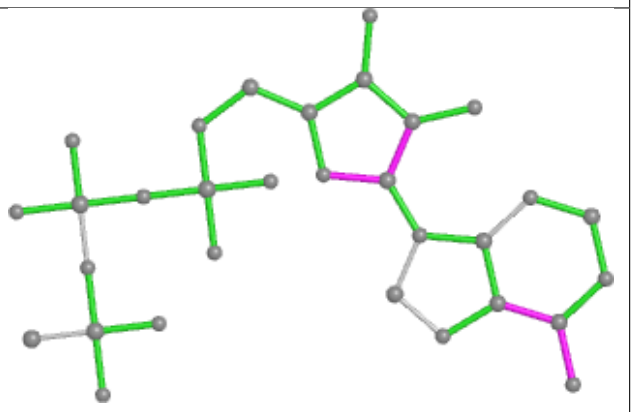

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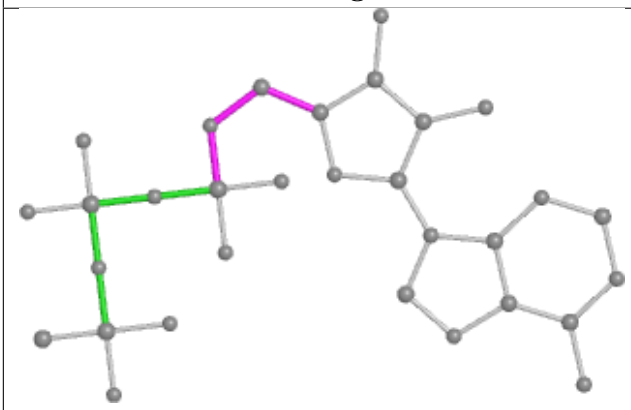

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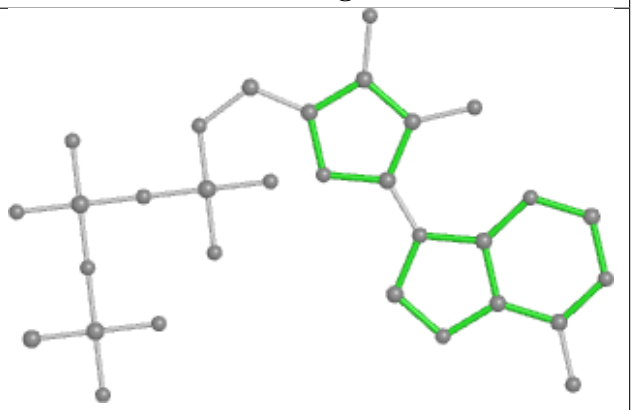
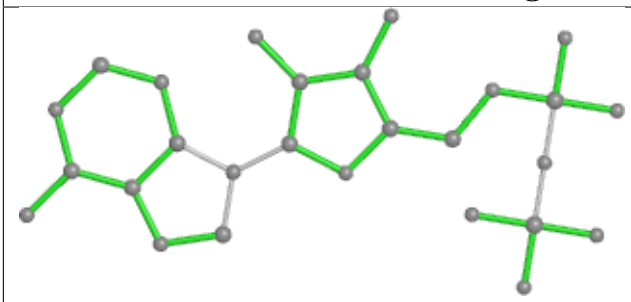


Rings

Ligand ADP F 802



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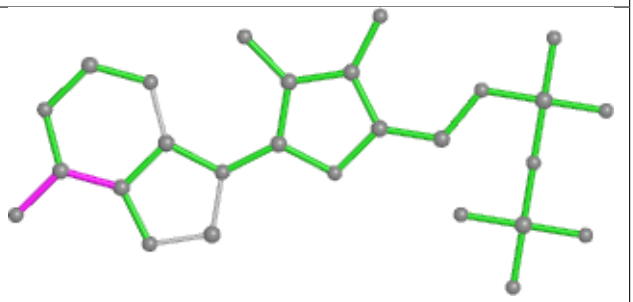

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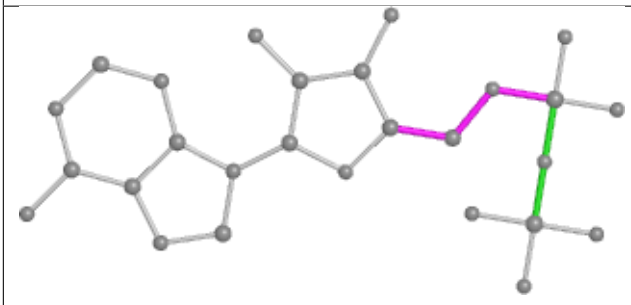

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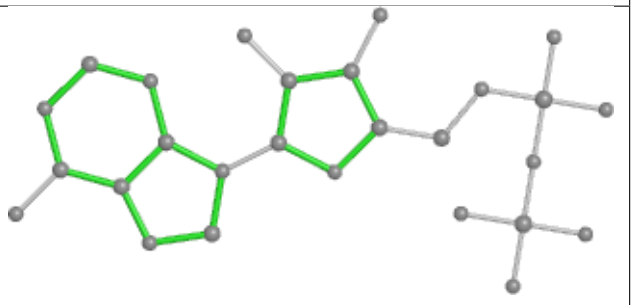
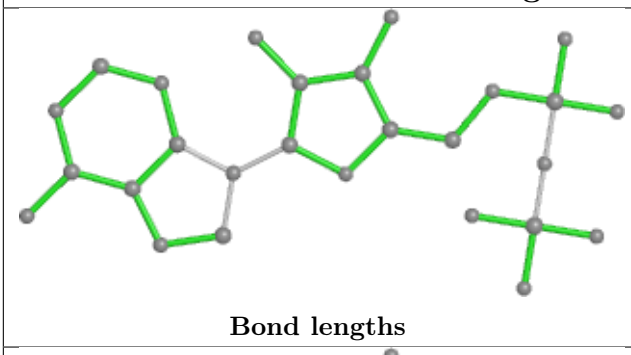


Rings

Ligand ADP E 802



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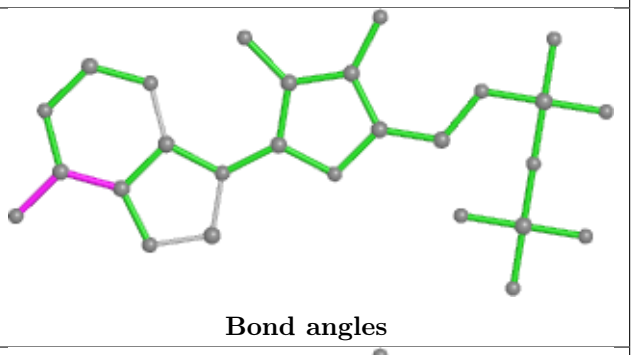

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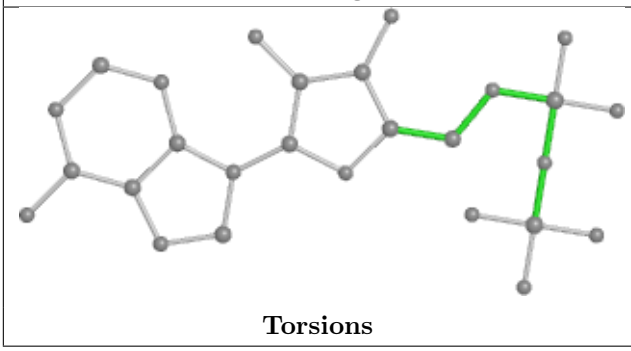

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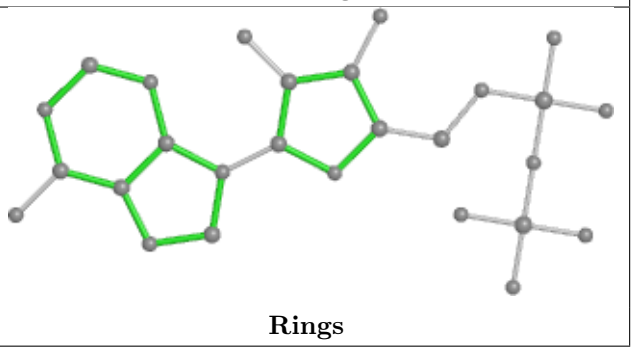
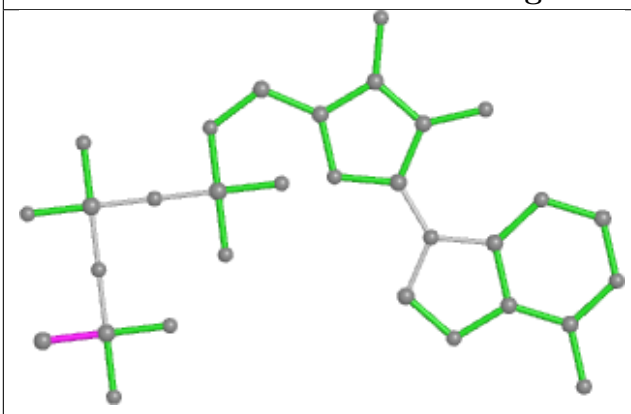
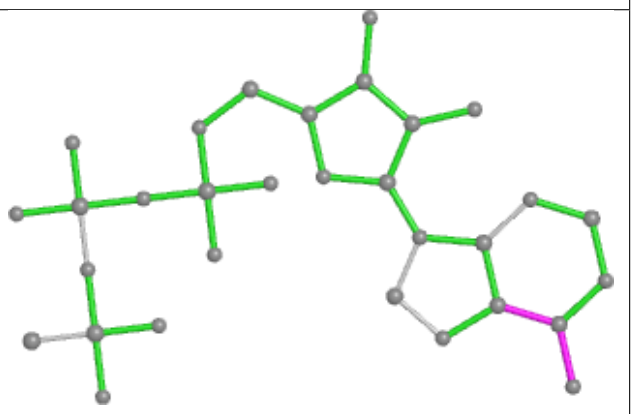


Rings

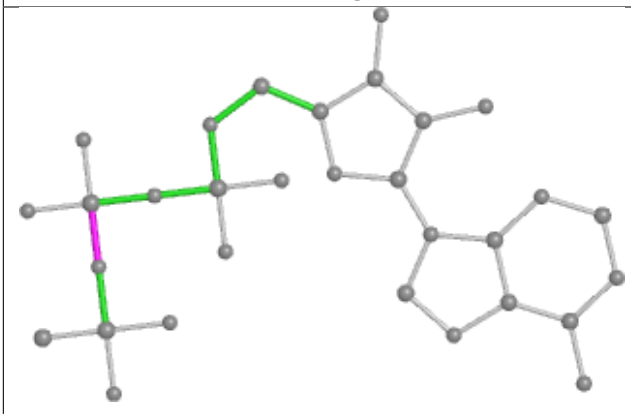
Ligand AGS B 802



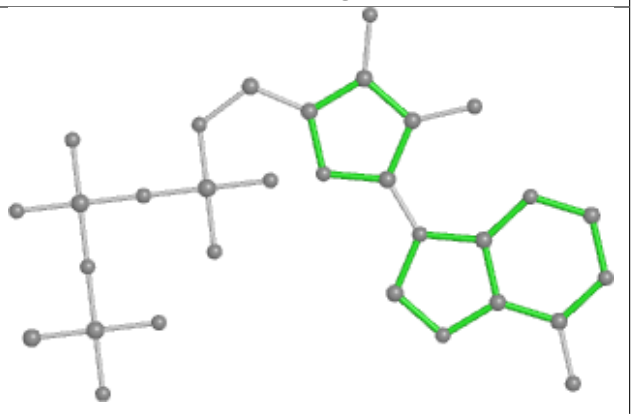
Bond lengths



Bond angles

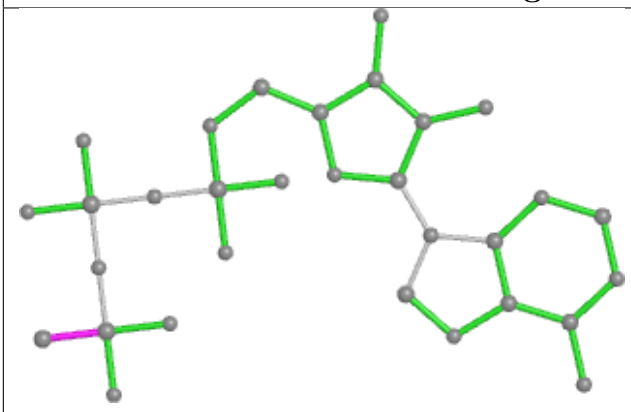


Torsions

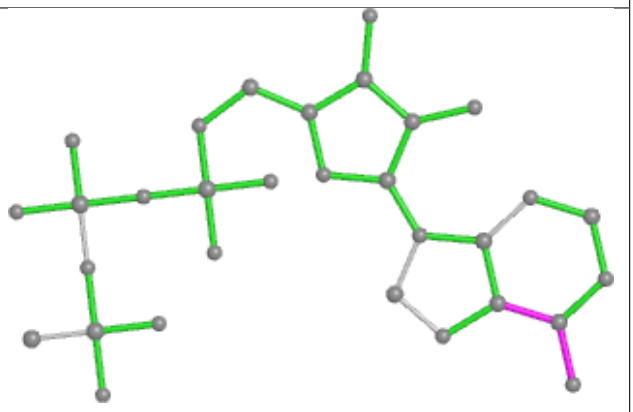


Rings

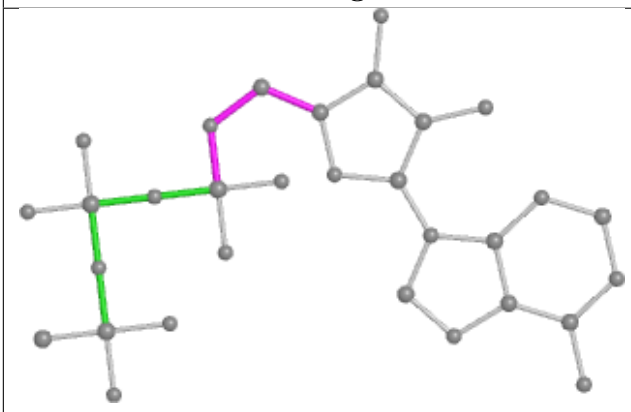
Ligand AGS D 802



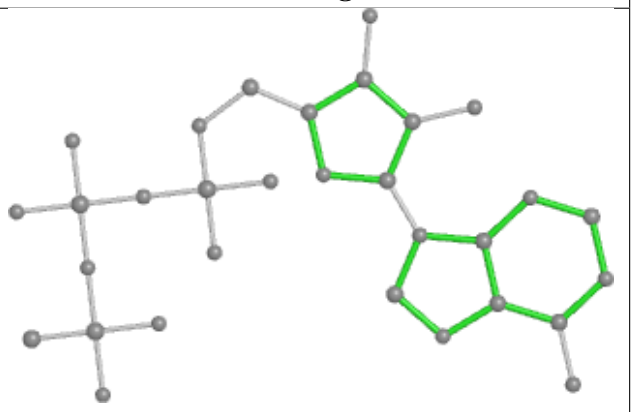
Bond lengths



Bond angles

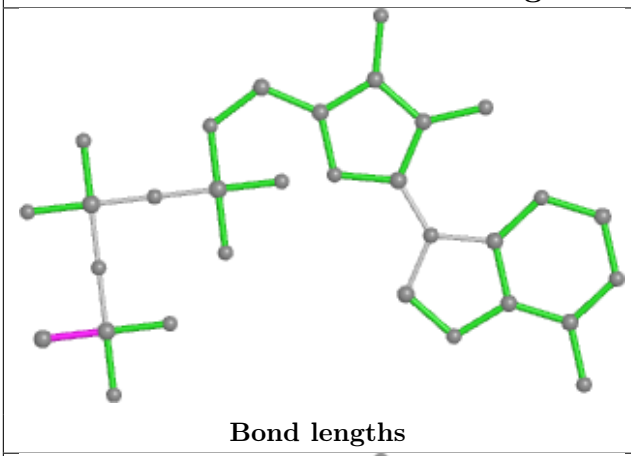


Torsions

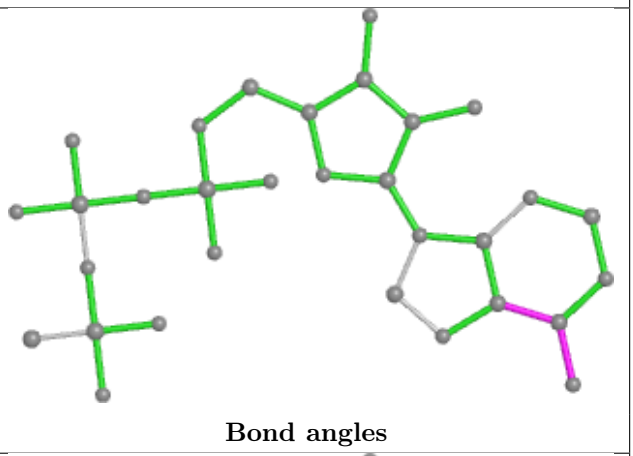


Rings

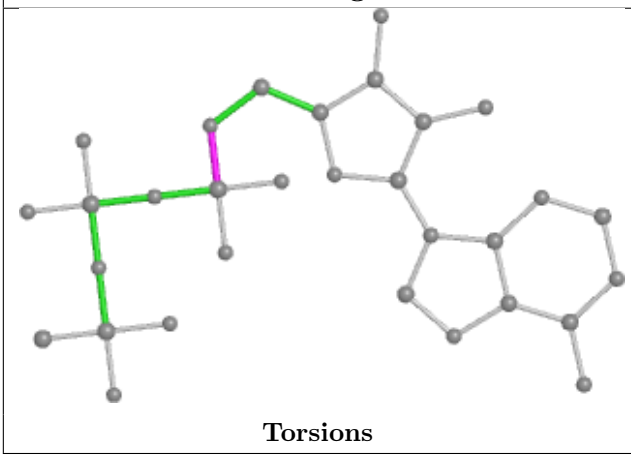
Ligand AGS C 802



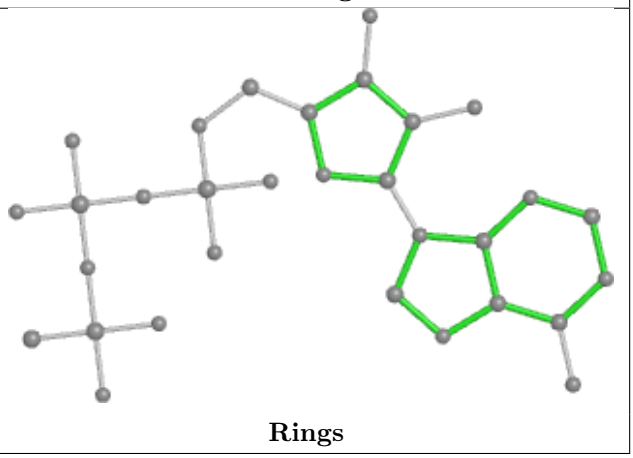
Bond lengths



Bond angles

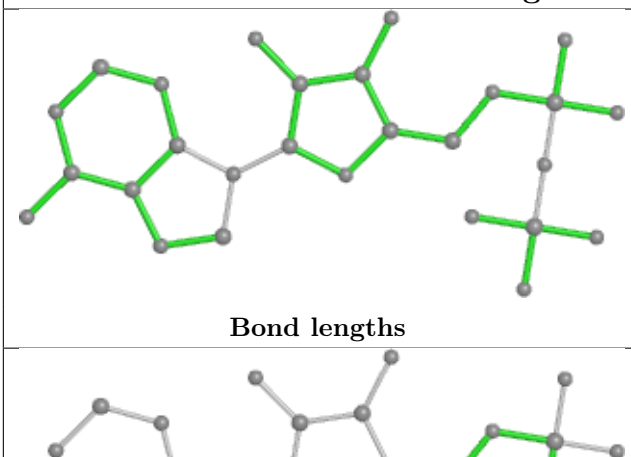


Torsions

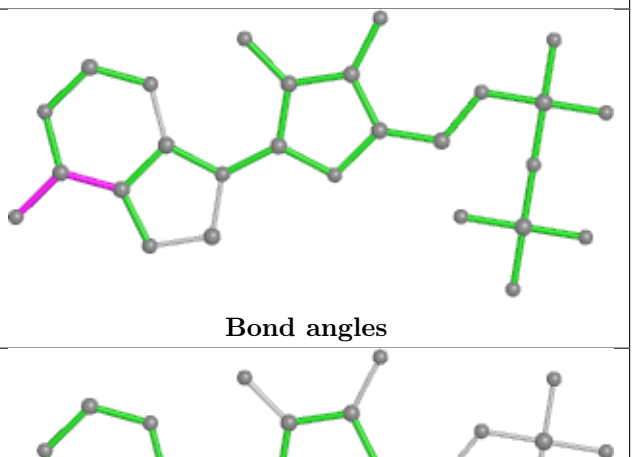


Rings

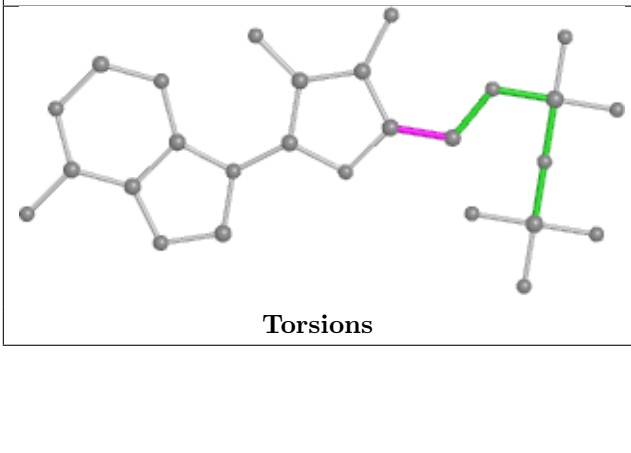
Ligand ADP E 801



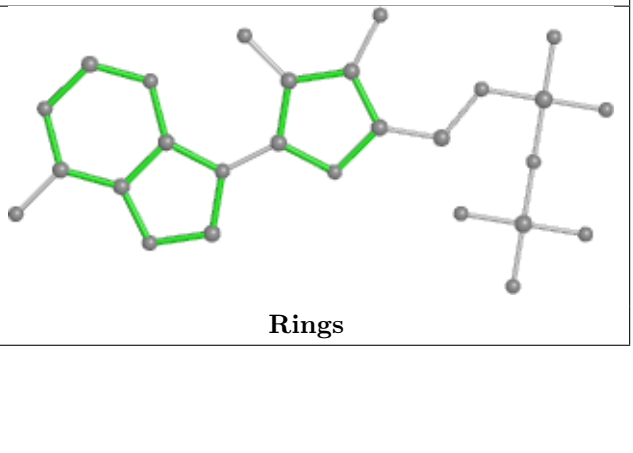
Bond lengths



Bond angles

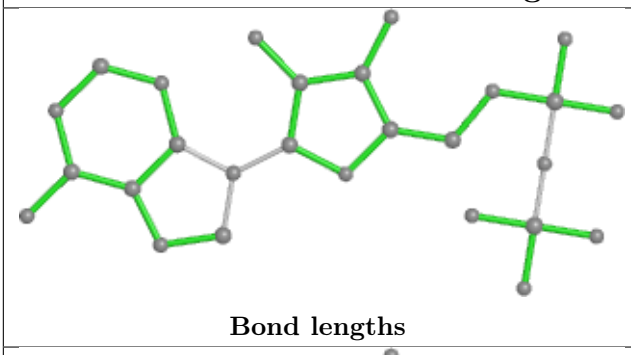


Torsions

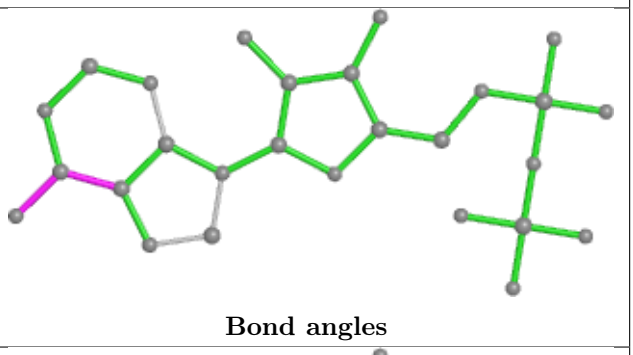


Rings

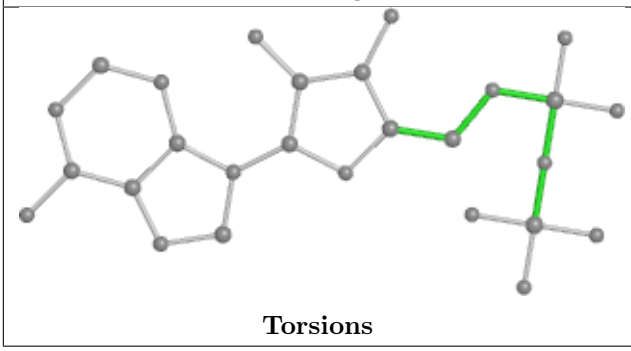
Ligand ADP F 801



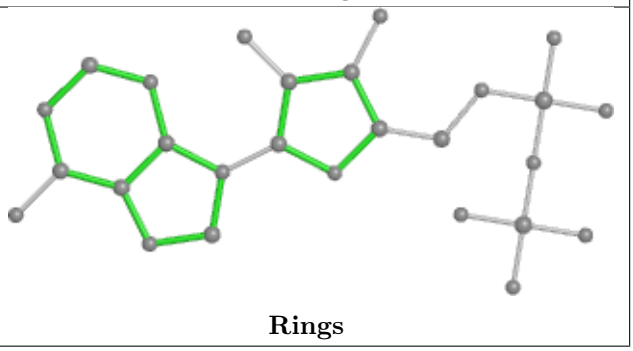
Bond lengths



Bond angles

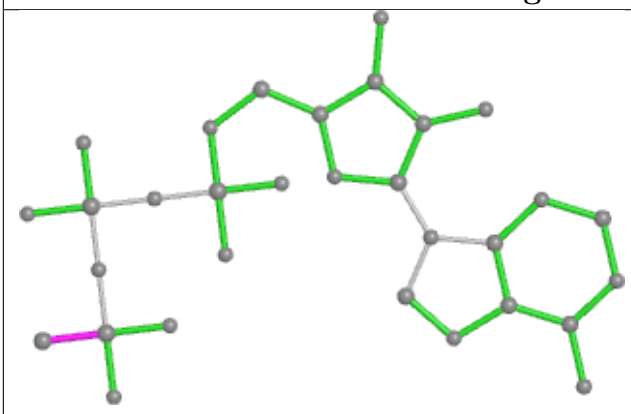


Torsions

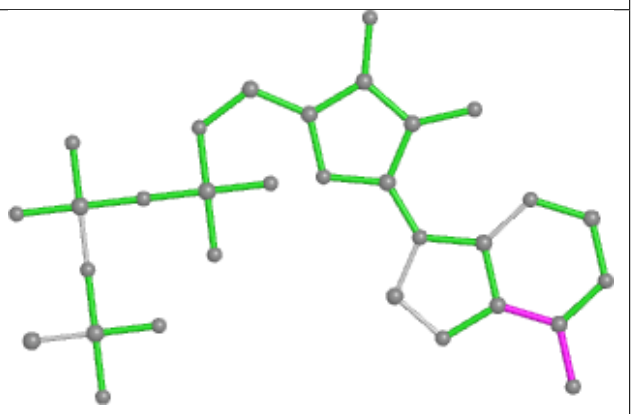


Rings

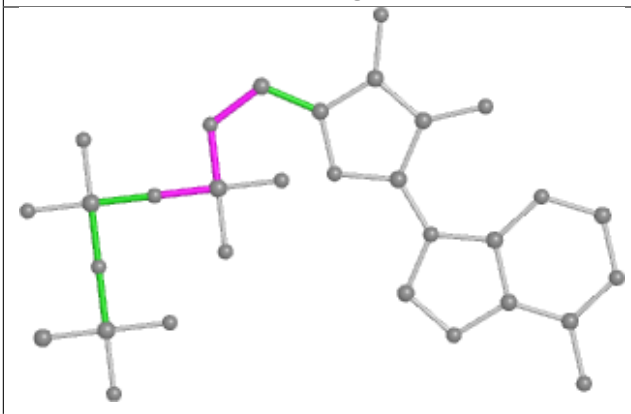
Ligand AGS D 801



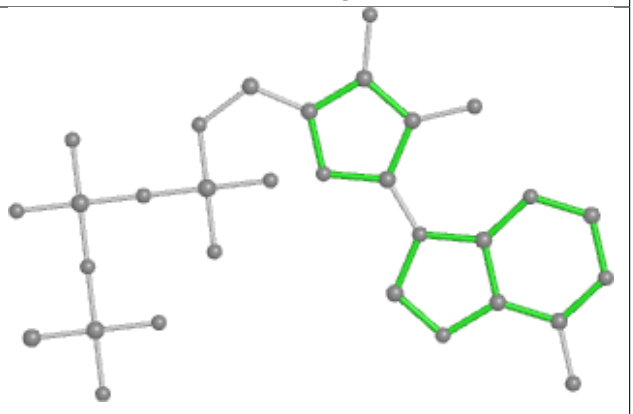
Bond lengths



Bond angles

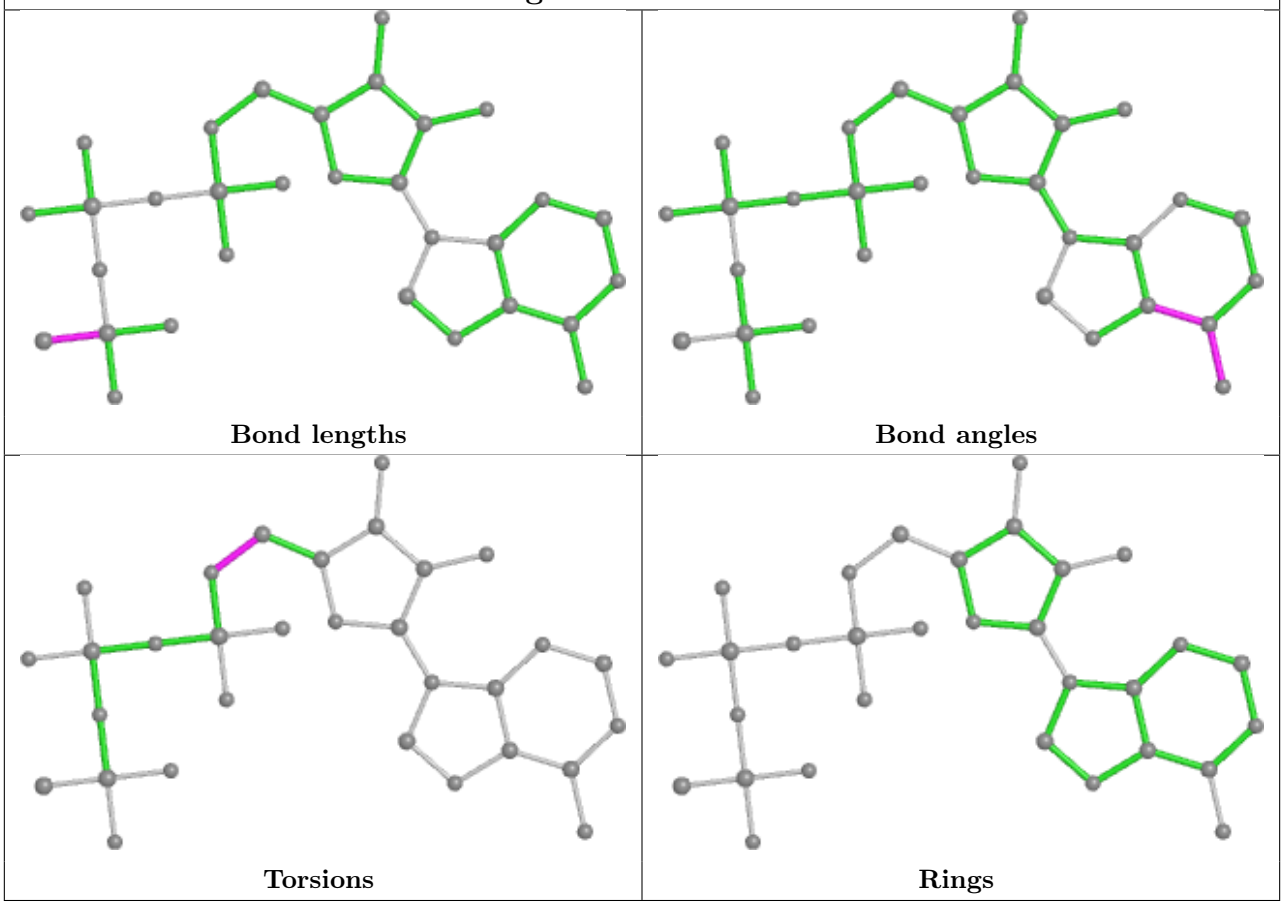


Torsions



Rings

Ligand AGS B 801



5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

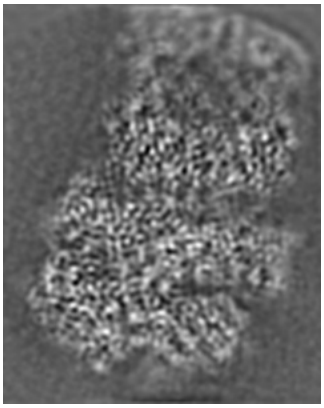
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-26559. These allow visual inspection of the internal detail of the map and identification of artifacts.

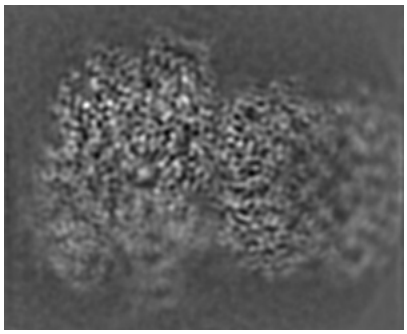
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

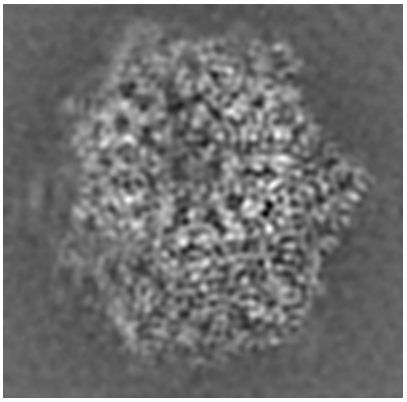
6.1.1 Primary map



X



Y

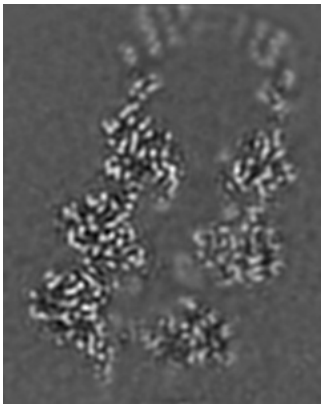


Z

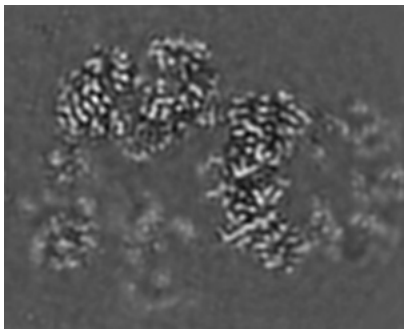
The images above show the map projected in three orthogonal directions.

6.2 Central slices

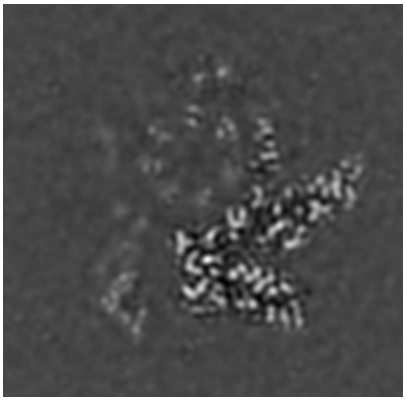
6.2.1 Primary map



X Index: 86



Y Index: 85

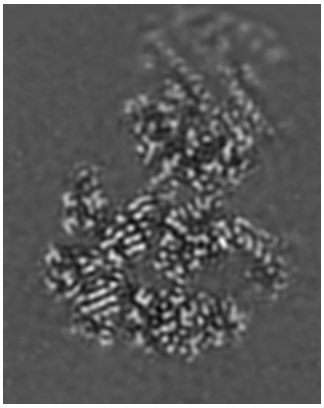


Z Index: 107

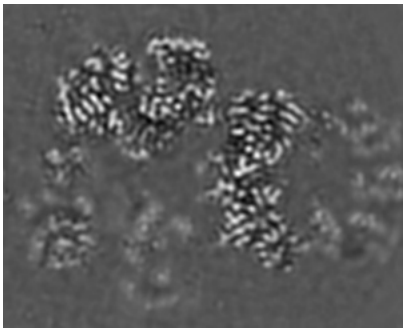
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

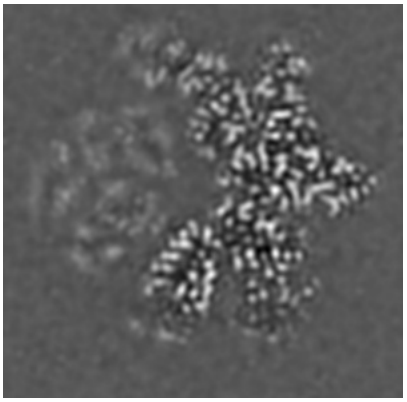
6.3.1 Primary map



X Index: 115



Y Index: 86

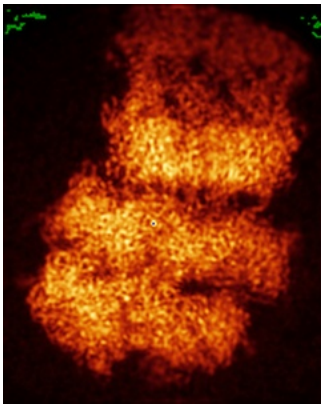


Z Index: 84

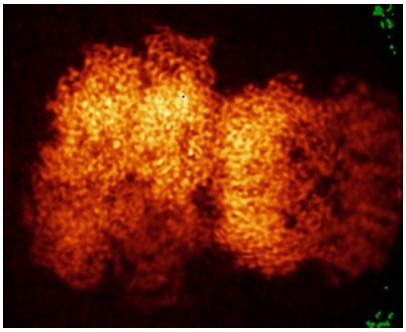
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

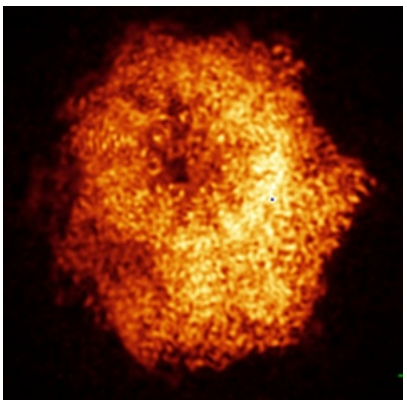
6.4.1 Primary map



X



Y

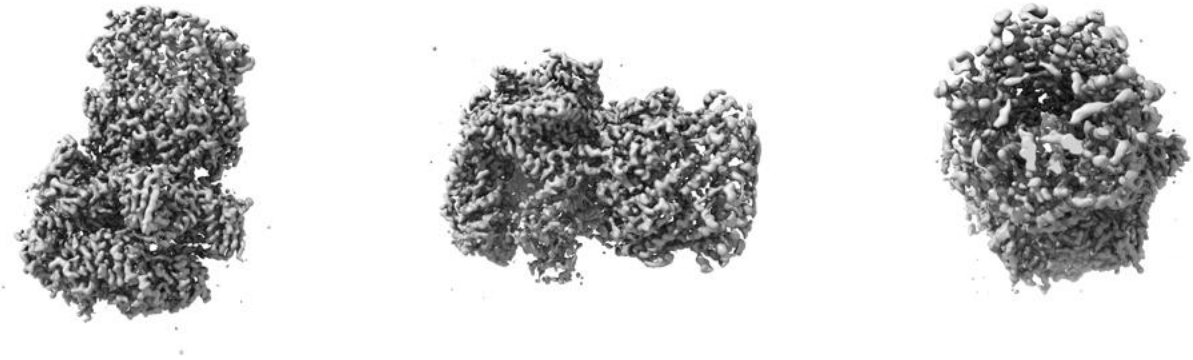


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views (i)

6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 1.4. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

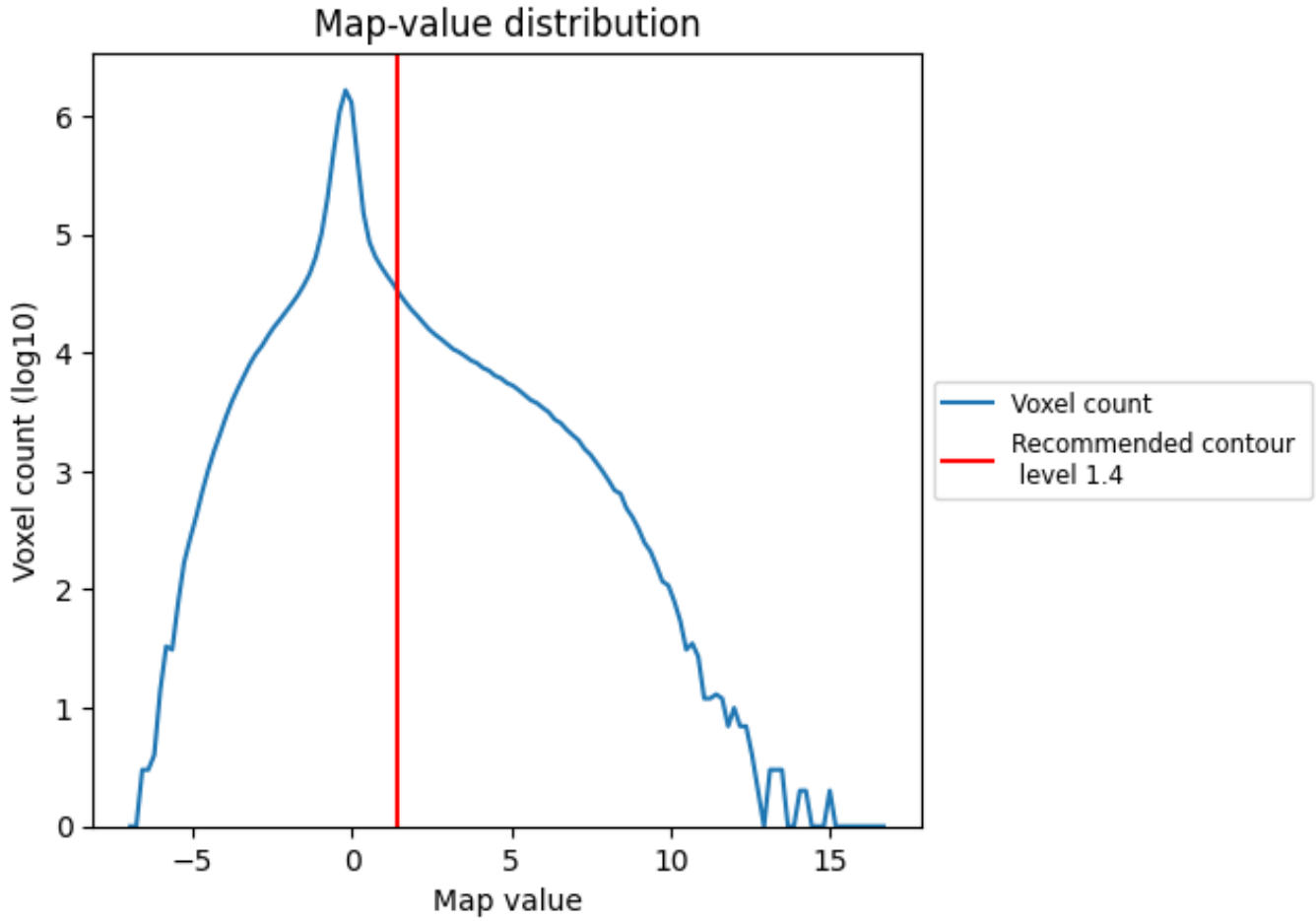
6.6 Mask visualisation (i)

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

7 Map analysis

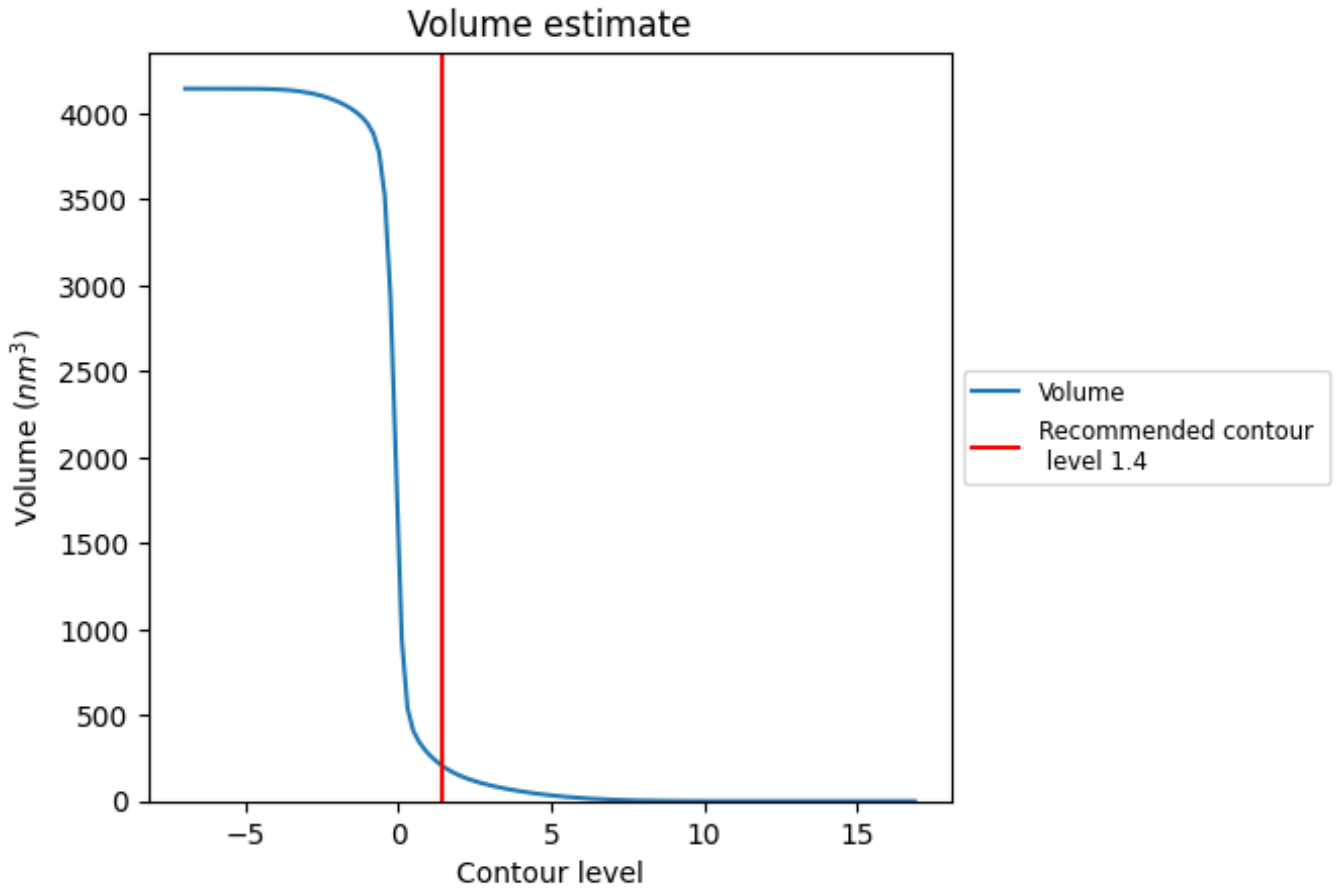
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

7.2 Volume estimate (i)



The volume at the recommended contour level is 210 nm^3; this corresponds to an approximate mass of 190 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum (i)

This section was not generated. The rotationally averaged power spectrum is only generated for cubic maps.

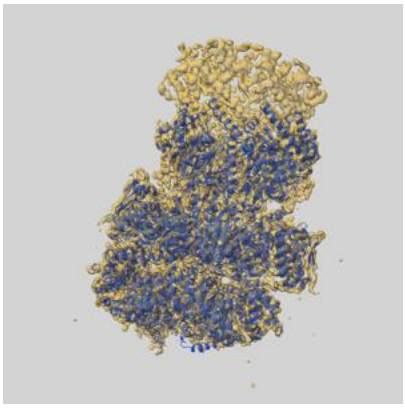
8 Fourier-Shell correlation

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

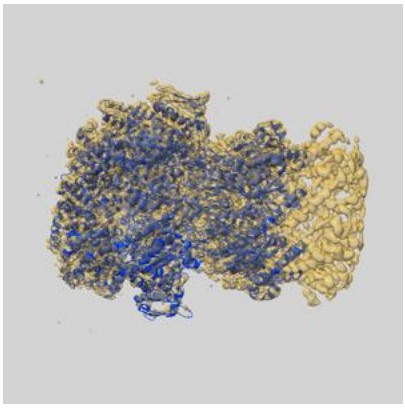
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-26559 and PDB model 7UJ0. Per-residue inclusion information can be found in section 3 on page 9.

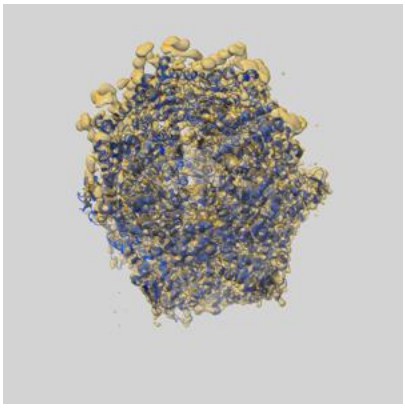
9.1 Map-model overlay



X



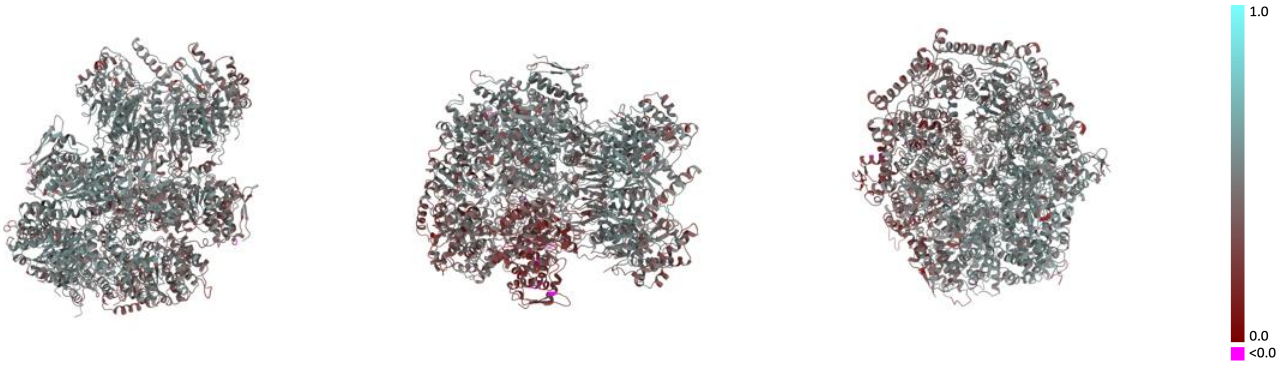
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 1.4 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

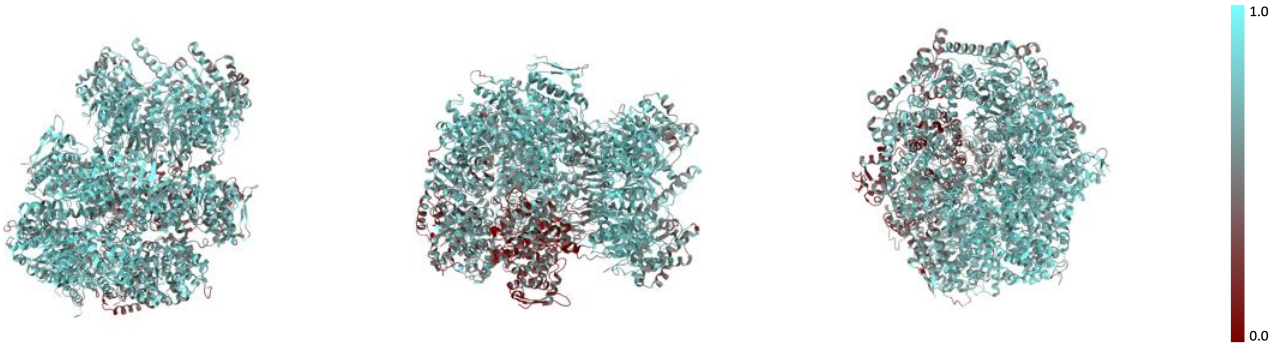
9.2 Q-score mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

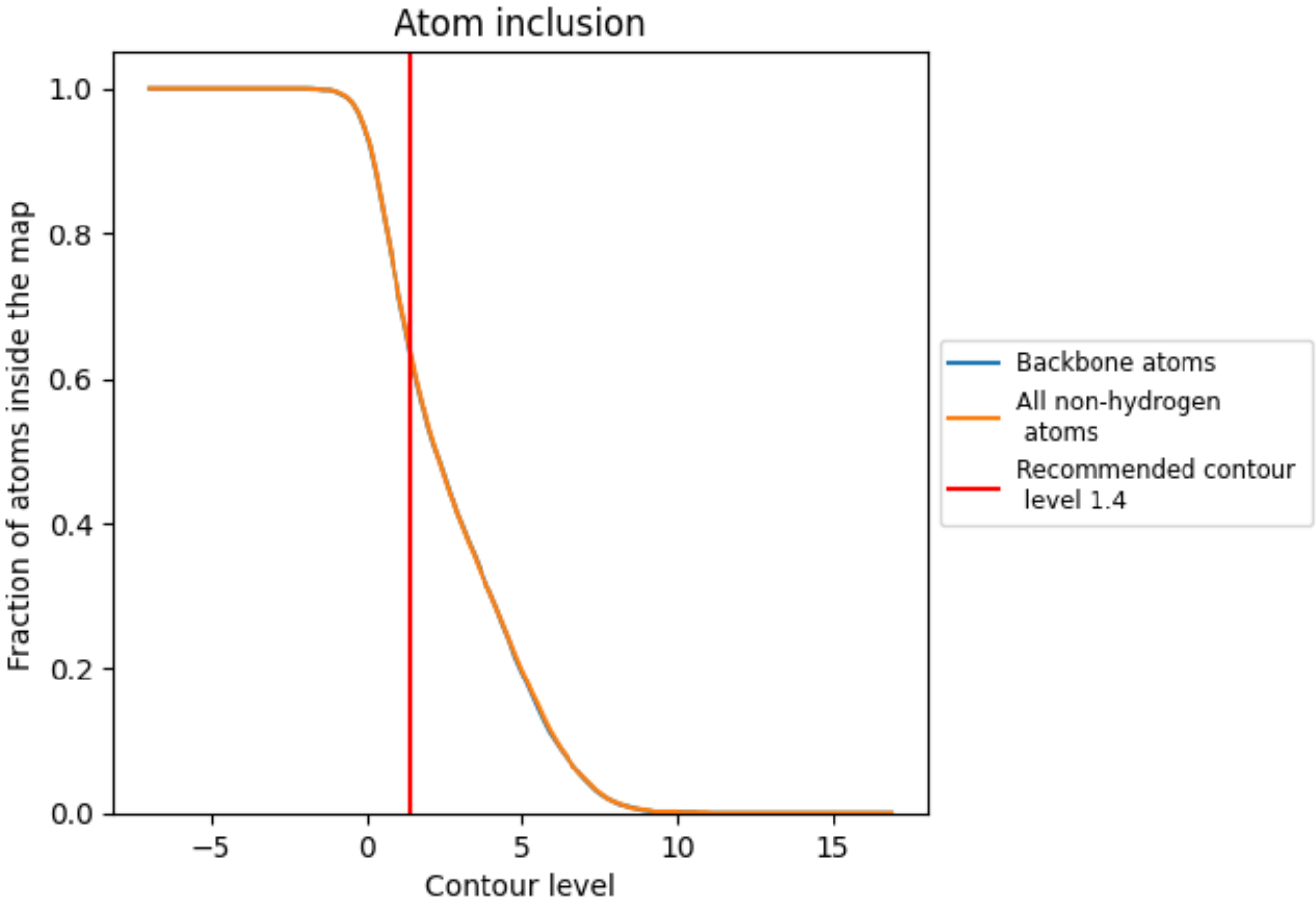
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (1.4).

9.4 Atom inclusion (i)



At the recommended contour level, 64% of all backbone atoms, 64% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (1.4) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6390	0.4450
A	0.4400	0.3370
B	0.7160	0.4800
C	0.7750	0.5140
D	0.7660	0.5050
E	0.6500	0.4440
F	0.4110	0.3220
H	0.7030	0.4750
I	0.7320	0.4890
J	0.7280	0.4920
K	0.7370	0.4940
L	0.7180	0.4710
M	0.6680	0.4360
N	0.6630	0.4530
S	0.4880	0.4520