



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 01:39 AM UTC

PDB ID : 7JY8 / pdb_00007jy8
EMDB ID : EMD-22524
Title : Analysis of a strand exchange reaction with a mini filament of 9-RecA, 27-mer ssDNA, partially-homologous 67 bp dsDNA and ATPgammaS
Authors : Pavletich, N.P.
Deposited on : 2020-08-29
Resolution : 2.40 Å(reported)
Based on initial model : 3CMW

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:

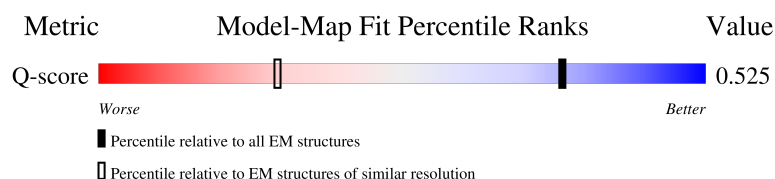
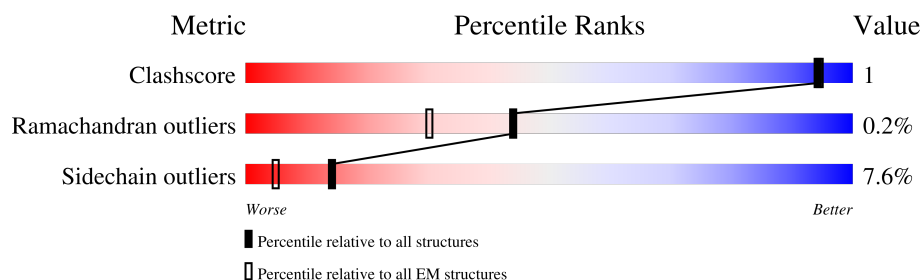
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

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

The reported resolution of this entry is 2.40 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.



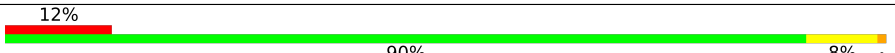
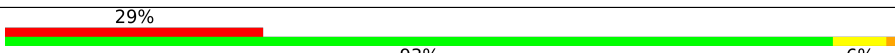
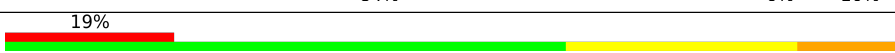
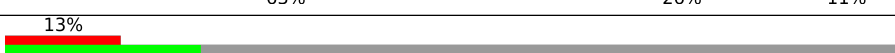
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	5628 (1.90 - 2.90)

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 $\leq 5\%$. 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	334	74% 87% 12%
1	B	334	22% 94% 5%
1	C	334	11% 90% 9%
1	D	334	7% 91% 7%

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Mol	Chain	Length	Quality of chain
1	E	334	
1	F	334	
1	G	334	
1	H	334	
1	I	334	
2	S	27	
3	T	45	

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 46845 atoms, of which 23485 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 Protein RecA.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	333	Total	C	H	N	O	S	0	0
			5085	1575	2577	435	486	12		
1	B	333	Total	C	H	N	O	S	0	0
			5085	1575	2577	435	486	12		
1	C	333	Total	C	H	N	O	S	0	0
			5085	1575	2577	435	486	12		
1	D	333	Total	C	H	N	O	S	0	0
			5085	1575	2577	435	486	12		
1	E	333	Total	C	H	N	O	S	0	0
			5085	1575	2577	435	486	12		
1	F	333	Total	C	H	N	O	S	0	0
			5085	1575	2577	435	486	12		
1	G	333	Total	C	H	N	O	S	0	0
			5085	1575	2577	435	486	12		
1	H	333	Total	C	H	N	O	S	0	0
			5085	1575	2577	435	486	12		
1	I	300	Total	C	H	N	O	S	0	0
			4575	1421	2317	388	438	11		

- Molecule 2 is a DNA chain called DNA (27-MER).

Mol	Chain	Residues	Atoms						AltConf	Trace
2	S	27	Total	C	H	N	O	P	0	0
			865	270	325	54	189	27		

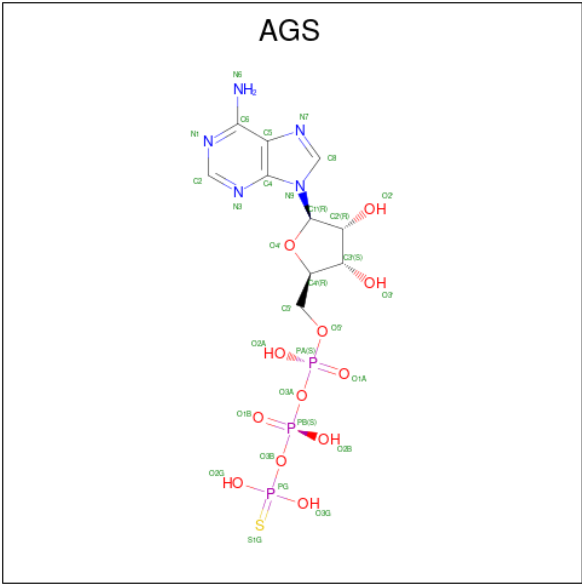
- Molecule 3 is a DNA chain called DNA (5'-D(P*AP*AP*AP*AP*AP*AP*AP*AP*A)-3').

Mol	Chain	Residues	Atoms						AltConf	Trace
3	T	10	Total	C	H	N	O	P	0	0
			320	100	110	50	50	10		

- Molecule 4 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

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

- Molecule 5 is PHOSPHOTHIOPHOSPHORIC ACID-ADENYLATE ESTER (CCD ID: AGS) (formula: C₁₀H₁₆N₅O₁₂P₃S).

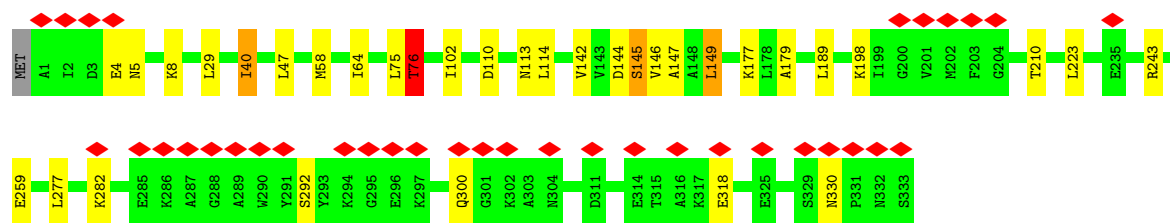


Mol	Chain	Residues	Atoms							AltConf
5	A	1	Total	C	H	N	O	P	S	0
			44	10	13	5	12	3	1	
5	B	1	Total	C	H	N	O	P	S	0
			44	10	13	5	12	3	1	

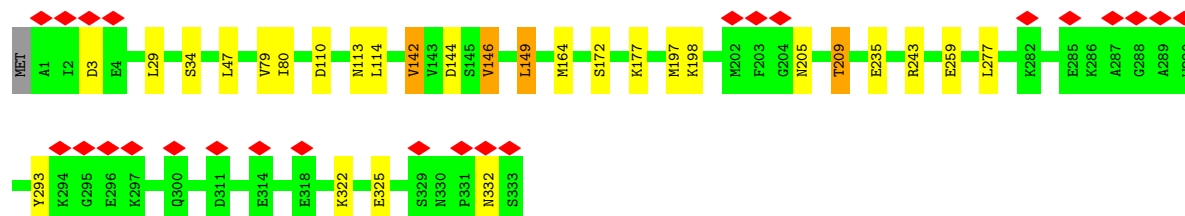
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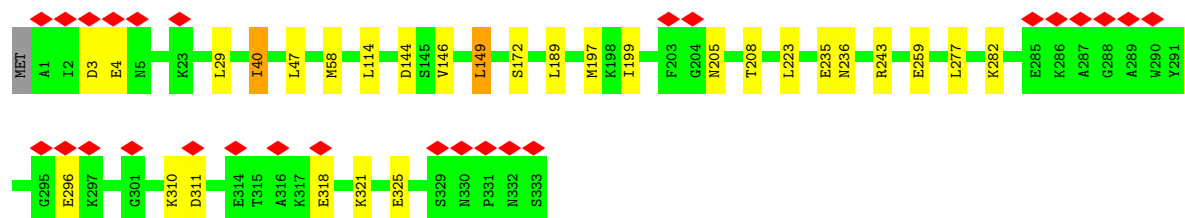
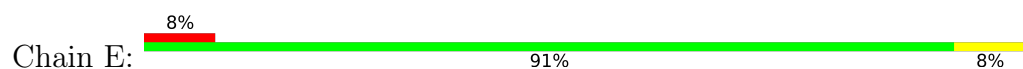
Mol	Chain	Residues	Atoms							AltConf
5	C	1	Total	C	H	N	O	P	S	0
			44	10	13	5	12	3	1	
5	D	1	Total	C	H	N	O	P	S	0
			44	10	13	5	12	3	1	
5	E	1	Total	C	H	N	O	P	S	0
			44	10	13	5	12	3	1	
5	F	1	Total	C	H	N	O	P	S	0
			44	10	13	5	12	3	1	
5	G	1	Total	C	H	N	O	P	S	0
			44	10	13	5	12	3	1	
5	H	1	Total	C	H	N	O	P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



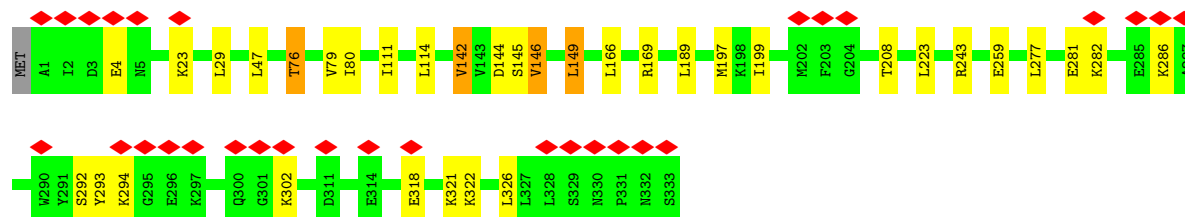
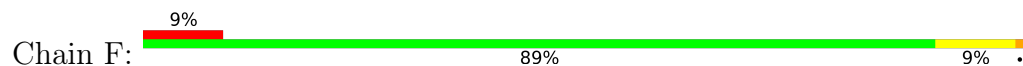
• Molecule 1: Protein RecA



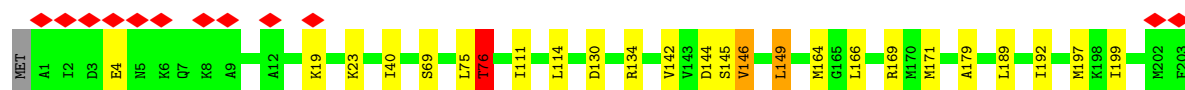
• Molecule 1: Protein RecA

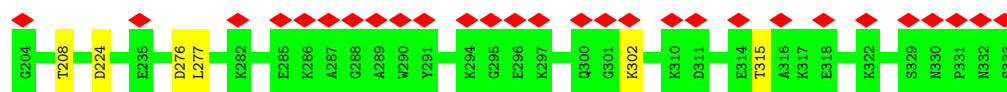


• Molecule 1: Protein RecA

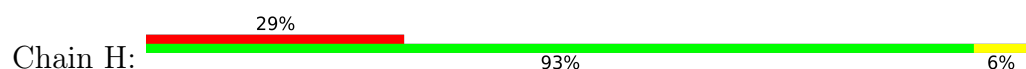


• Molecule 1: Protein RecA

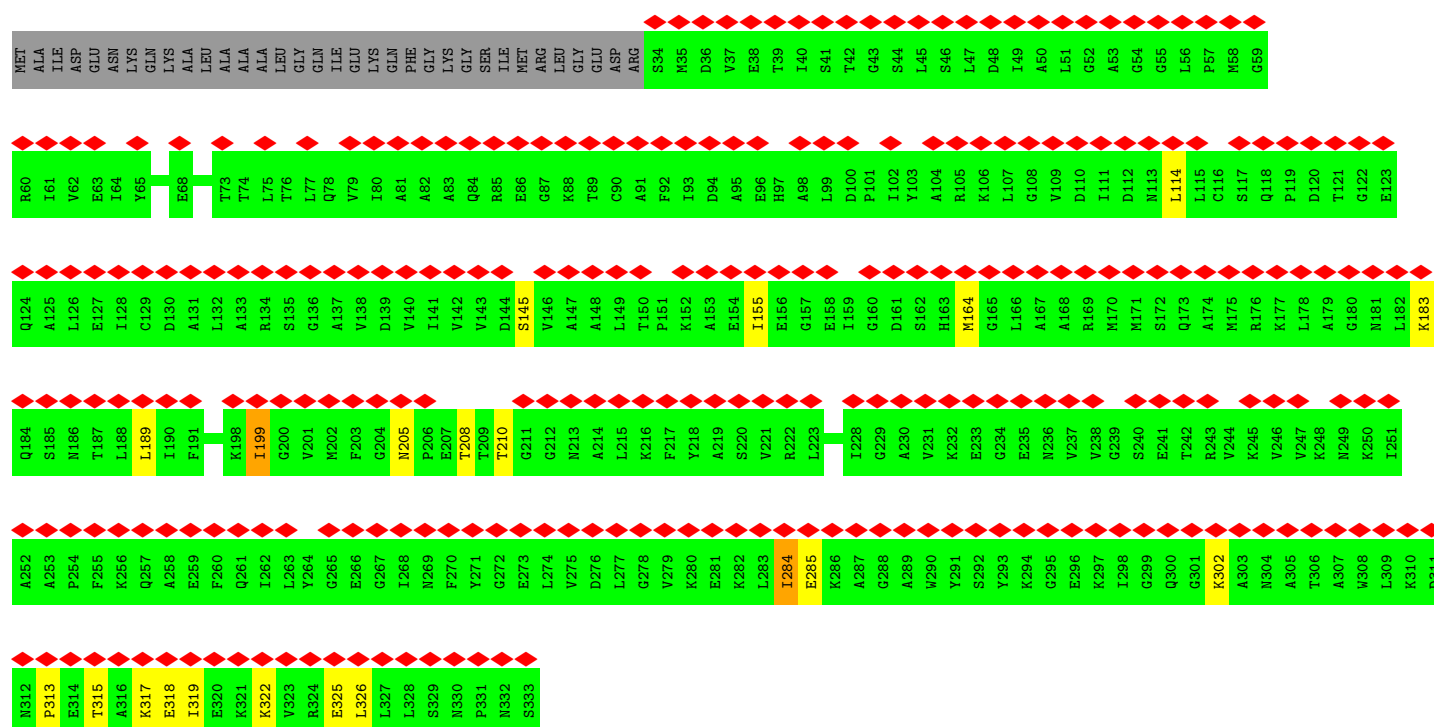
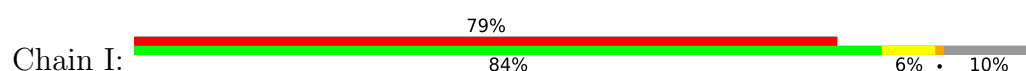




• Molecule 1: Protein RecA

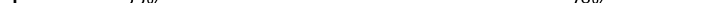


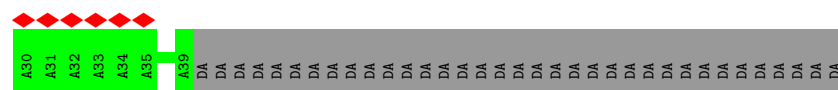
• Molecule 1: Protein RecA



• Molecule 2: DNA (27-MER)



- Chain T: 



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	1697726	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	52	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.527	Depositor
Minimum map value	-0.220	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.028	Depositor
Map size ($\text{\AA}$)	275.968, 275.968, 275.968	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.078, 1.078, 1.078	Depositor

5 Model quality

5.1 Standard geometry

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

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	A	1.09	0/2537	1.57	3/3413 (0.1%)
1	B	1.06	0/2537	1.52	3/3413 (0.1%)
1	C	1.04	0/2537	1.51	5/3413 (0.1%)
1	D	1.04	0/2537	1.50	3/3413 (0.1%)
1	E	1.03	0/2537	1.51	3/3413 (0.1%)
1	F	1.04	0/2537	1.52	2/3413 (0.1%)
1	G	1.04	0/2537	1.51	6/3413 (0.2%)
1	H	1.03	0/2537	1.50	3/3413 (0.1%)
1	I	1.10	0/2286	1.54	0/3081
2	S	0.52	0/593	1.38	7/914 (0.8%)
3	T	0.28	0/239	0.58	0/366
All	All	1.04	0/23414	1.51	35/31665 (0.1%)

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	B	0	1
1	C	0	1
1	H	0	1
All	All	0	3

There are no bond length outliers.

All (35) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	144	ASP	CA-C-N	7.63	136.12	121.54
1	G	144	ASP	C-N-CA	7.63	136.12	121.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	144	ASP	CA-C-N	7.25	135.38	121.54
1	F	144	ASP	C-N-CA	7.25	135.38	121.54
1	C	144	ASP	CA-C-N	6.34	133.66	121.54
1	C	144	ASP	C-N-CA	6.34	133.66	121.54
2	S	8	DT	C4'-C3'-O3'	-6.33	100.50	110.00
1	E	144	ASP	CA-C-N	6.31	133.59	121.54
1	E	144	ASP	C-N-CA	6.31	133.59	121.54
1	H	144	ASP	CA-C-N	6.02	133.03	121.54
1	H	144	ASP	C-N-CA	6.02	133.03	121.54
1	G	76	THR	CB-CA-C	5.98	122.14	110.67
1	D	209	THR	CB-CA-C	5.87	121.64	109.38
2	S	9	DT	C2'-C3'-O3'	5.79	120.18	111.50
1	D	144	ASP	CA-C-N	5.71	132.44	121.54
1	D	144	ASP	C-N-CA	5.71	132.44	121.54
1	C	76	THR	CB-CA-C	5.54	121.31	110.67
2	S	9	DT	C4'-C3'-O3'	-5.51	101.74	110.00
1	A	22	GLY	CA-C-O	-5.50	118.35	122.37
2	S	18	DT	C2'-C3'-O3'	5.45	119.68	111.50
1	E	311	ASP	CA-CB-CG	5.35	117.95	112.60
1	A	104	ALA	CA-C-N	5.25	127.62	120.54
1	A	104	ALA	C-N-CA	5.25	127.62	120.54
2	S	12	DT	C2'-C3'-O3'	5.20	119.29	111.50
2	S	6	DT	C2'-C3'-O3'	5.18	119.28	111.50
1	B	209	THR	CB-CA-C	5.17	119.69	109.66
1	B	144	ASP	CA-C-N	5.13	131.33	121.54
1	B	144	ASP	C-N-CA	5.13	131.33	121.54
2	S	14	DT	C4'-C3'-O3'	-5.12	102.31	110.00
1	H	209	THR	CB-CA-C	5.12	120.08	109.38
1	G	224	ASP	CA-CB-CG	5.03	117.63	112.60
1	C	179	ALA	CA-C-N	5.03	125.42	119.94
1	C	179	ALA	C-N-CA	5.03	125.42	119.94
1	G	179	ALA	CA-C-N	5.00	125.49	119.94
1	G	179	ALA	C-N-CA	5.00	125.49	119.94

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	145	SER	Peptide
1	C	145	SER	Peptide
1	H	145	SER	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	2508	2577	2576	7	0
1	B	2508	2577	2576	4	0
1	C	2508	2577	2576	8	0
1	D	2508	2577	2576	7	0
1	E	2508	2577	2576	6	0
1	F	2508	2577	2576	10	0
1	G	2508	2577	2576	10	0
1	H	2508	2577	2576	5	0
1	I	2258	2317	2313	3	0
2	S	540	325	325	8	0
3	T	210	110	111	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
4	H	1	0	0	0	0
4	I	1	0	0	0	0
5	A	31	13	12	0	0
5	B	31	13	12	0	0
5	C	31	13	12	0	0
5	D	31	13	12	0	0
5	E	31	13	12	0	0
5	F	31	13	12	0	0
5	G	31	13	12	0	0
5	H	31	13	12	0	0
5	I	31	13	12	0	0
All	All	23360	23485	23465	54	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 1.

All (54) 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:E:243:ARG:NH1	1:E:259:GLU:OE2	2.30	0.64
1:F:146:VAL:HA	1:F:149:LEU:HD22	1.80	0.63
1:A:169:ARG:NH1	2:S:24:DT:O2	2.34	0.60
1:E:40:ILE:HD11	1:E:58:MET:SD	2.41	0.60
1:A:76:THR:HG21	1:A:142:VAL:HG21	1.84	0.57
1:C:40:ILE:HD11	1:C:58:MET:SD	2.44	0.57
1:C:198:LYS:HA	2:S:21:DT:H73	1.86	0.57
1:H:164:MET:HB3	1:I:199:ILE:HD11	1.88	0.55
1:D:146:VAL:HA	1:D:149:LEU:HD22	1.89	0.54
1:G:146:VAL:HA	1:G:149:LEU:HD22	1.88	0.54
1:D:243:ARG:NH1	1:D:259:GLU:OE2	2.42	0.53
1:A:76:THR:CG2	1:A:142:VAL:HG21	2.38	0.53
1:D:198:LYS:HA	2:S:18:DT:H73	1.91	0.53
1:B:169:ARG:NH1	2:S:21:DT:O2	2.41	0.52
1:G:149:LEU:HD23	1:G:171:MET:HE3	1.93	0.51
1:C:147:ALA:HA	1:C:210:THR:HG21	1.92	0.49
1:C:146:VAL:HA	1:C:149:LEU:HD22	1.95	0.48
1:I:313:PRO:O	1:I:317:LYS:HG3	2.13	0.48
1:D:110:ASP:OD2	1:D:113:ASN:ND2	2.44	0.48
1:F:76:THR:CG2	1:F:142:VAL:HG21	2.43	0.48
1:F:76:THR:HG21	1:F:142:VAL:HG21	1.95	0.48
1:A:300:GLN:C	1:A:304:ASN:HD21	2.22	0.48
1:D:293:TYR:OH	1:D:322:LYS:NZ	2.47	0.48
1:D:164:MET:HB3	1:E:199:ILE:HD12	1.97	0.47
1:D:80:ILE:HD11	1:D:142:VAL:CG1	2.45	0.46
1:G:169:ARG:NH1	2:S:6:DT:O2	2.48	0.46
1:E:146:VAL:HA	1:E:149:LEU:HD22	1.97	0.46
1:F:29:LEU:HD23	1:G:111:ILE:HD12	1.98	0.46
1:C:243:ARG:NH1	1:C:259:GLU:OE2	2.49	0.46
1:C:64:ILE:HD13	1:C:75:LEU:HD23	1.98	0.45
1:G:164:MET:HB3	1:H:199:ILE:HD12	1.99	0.45
1:G:199:ILE:HG22	2:S:10:DT:C5	2.52	0.44
1:G:276:ASP:OD1	1:G:302:LYS:NZ	2.51	0.44
1:C:76:THR:CG2	1:C:142:VAL:HG11	2.48	0.43
1:H:243:ARG:NH1	1:H:259:GLU:OE2	2.51	0.43
1:E:29:LEU:HD23	1:F:111:ILE:HD12	1.99	0.43
1:A:205:ASN:H	1:A:205:ASN:HD22	1.65	0.43
1:G:76:THR:CG2	1:G:142:VAL:HG11	2.48	0.43
1:F:199:ILE:HG22	2:S:13:DT:C5	2.54	0.43
1:G:76:THR:HG21	1:G:192:ILE:HD11	2.01	0.43
1:F:243:ARG:NH1	1:F:259:GLU:OE2	2.51	0.42
1:G:130:ASP:OD2	1:G:134:ARG:NH1	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:169:ARG:NH1	2:S:9:DT:O2	2.42	0.42
1:H:76:THR:HG21	1:H:192:ILE:HD11	2.02	0.42
1:B:76:THR:HG21	1:B:192:ILE:HD11	2.01	0.42
1:C:110:ASP:OD1	1:C:113:ASN:ND2	2.50	0.42
1:F:293:TYR:CE2	1:F:294:LYS:HE2	2.55	0.42
1:E:321:LYS:O	1:E:325:GLU:HG2	2.20	0.41
1:I:284:ILE:HD11	1:I:319:ILE:HD13	2.02	0.41
1:B:96:GLU:HG3	1:B:145:SER:HB2	2.01	0.41
1:A:243:ARG:NH1	1:A:259:GLU:OE2	2.53	0.41
1:A:29:LEU:HB3	1:B:111:ILE:HG23	2.03	0.40
1:F:80:ILE:HD11	1:F:142:VAL:CG1	2.51	0.40
1:H:146:VAL:HA	1:H:149:LEU:HD22	2.03	0.40

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 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	331/334 (99%)	323 (98%)	7 (2%)	1 (0%)	36	50
1	B	331/334 (99%)	321 (97%)	10 (3%)	0	100	100
1	C	331/334 (99%)	320 (97%)	10 (3%)	1 (0%)	36	50
1	D	331/334 (99%)	315 (95%)	16 (5%)	0	100	100
1	E	331/334 (99%)	319 (96%)	12 (4%)	0	100	100
1	F	331/334 (99%)	320 (97%)	10 (3%)	1 (0%)	36	50
1	G	331/334 (99%)	318 (96%)	12 (4%)	1 (0%)	36	50
1	H	331/334 (99%)	320 (97%)	11 (3%)	0	100	100
1	I	298/334 (89%)	293 (98%)	4 (1%)	1 (0%)	36	50
All	All	2946/3006 (98%)	2849 (97%)	92 (3%)	5 (0%)	44	58

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	145	SER
1	G	145	SER
1	A	145	SER
1	F	145	SER
1	I	145	SER

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 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	262/263 (100%)	225 (86%)	37 (14%)	3	4
1	B	262/263 (100%)	250 (95%)	12 (5%)	24	41
1	C	262/263 (100%)	243 (93%)	19 (7%)	13	22
1	D	262/263 (100%)	244 (93%)	18 (7%)	14	24
1	E	262/263 (100%)	242 (92%)	20 (8%)	12	21
1	F	262/263 (100%)	238 (91%)	24 (9%)	8	14
1	G	262/263 (100%)	246 (94%)	16 (6%)	17	30
1	H	262/263 (100%)	248 (95%)	14 (5%)	20	36
1	I	238/263 (90%)	221 (93%)	17 (7%)	13	23
All	All	2334/2367 (99%)	2157 (92%)	177 (8%)	14	21

All (177) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	ILE
1	A	3	ASP
1	A	29	LEU
1	A	68	GLU
1	A	76	THR
1	A	100	ASP
1	A	102	ILE
1	A	106	LYS

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Mol	Chain	Res	Type
1	A	112	ASP
1	A	114	LEU
1	A	118	GLN
1	A	120	ASP
1	A	142	VAL
1	A	146	VAL
1	A	156	GLU
1	A	171	MET
1	A	177	LYS
1	A	184	GLN
1	A	189	LEU
1	A	199	ILE
1	A	205	ASN
1	A	208	THR
1	A	209	THR
1	A	227	ARG
1	A	232	LYS
1	A	235	GLU
1	A	237	VAL
1	A	268	ILE
1	A	277	LEU
1	A	282	LYS
1	A	292	SER
1	A	294	LYS
1	A	304	ASN
1	A	310	LYS
1	A	314	GLU
1	A	317	LYS
1	A	321	LYS
1	B	2	ILE
1	B	3	ASP
1	B	4	GLU
1	B	29	LEU
1	B	189	LEU
1	B	208	THR
1	B	209	THR
1	B	223	LEU
1	B	292	SER
1	B	310	LYS
1	B	317	LYS
1	B	318	GLU
1	C	4	GLU

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Mol	Chain	Res	Type
1	C	5	ASN
1	C	8	LYS
1	C	29	LEU
1	C	40	ILE
1	C	47	LEU
1	C	76	THR
1	C	102	ILE
1	C	114	LEU
1	C	149	LEU
1	C	177	LYS
1	C	189	LEU
1	C	223	LEU
1	C	277	LEU
1	C	282	LYS
1	C	292	SER
1	C	300	GLN
1	C	318	GLU
1	C	330	ASN
1	D	3	ASP
1	D	29	LEU
1	D	34	SER
1	D	47	LEU
1	D	79	VAL
1	D	114	LEU
1	D	142	VAL
1	D	146	VAL
1	D	149	LEU
1	D	172	SER
1	D	177	LYS
1	D	197	MET
1	D	205	ASN
1	D	209	THR
1	D	235	GLU
1	D	277	LEU
1	D	325	GLU
1	D	332	ASN
1	E	3	ASP
1	E	4	GLU
1	E	40	ILE
1	E	47	LEU
1	E	114	LEU
1	E	149	LEU

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Mol	Chain	Res	Type
1	E	172	SER
1	E	189	LEU
1	E	197	MET
1	E	205	ASN
1	E	208	THR
1	E	223	LEU
1	E	235	GLU
1	E	236	ASN
1	E	277	LEU
1	E	282	LYS
1	E	292	SER
1	E	296	GLU
1	E	310	LYS
1	E	318	GLU
1	F	4	GLU
1	F	23	LYS
1	F	47	LEU
1	F	76	THR
1	F	79	VAL
1	F	114	LEU
1	F	142	VAL
1	F	146	VAL
1	F	149	LEU
1	F	166	LEU
1	F	189	LEU
1	F	197	MET
1	F	208	THR
1	F	223	LEU
1	F	277	LEU
1	F	281	GLU
1	F	282	LYS
1	F	286	LYS
1	F	292	SER
1	F	302	LYS
1	F	318	GLU
1	F	321	LYS
1	F	322	LYS
1	F	326	LEU
1	G	4	GLU
1	G	19	LYS
1	G	23	LYS
1	G	40	ILE

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Mol	Chain	Res	Type
1	G	69	SER
1	G	75	LEU
1	G	76	THR
1	G	114	LEU
1	G	146	VAL
1	G	149	LEU
1	G	166	LEU
1	G	189	LEU
1	G	197	MET
1	G	208	THR
1	G	277	LEU
1	G	315	THR
1	H	19	LYS
1	H	25	SER
1	H	29	LEU
1	H	149	LEU
1	H	171	MET
1	H	177	LYS
1	H	189	LEU
1	H	197	MET
1	H	205	ASN
1	H	209	THR
1	H	223	LEU
1	H	277	LEU
1	H	292	SER
1	H	314	GLU
1	I	114	LEU
1	I	155	ILE
1	I	164	MET
1	I	183	LYS
1	I	189	LEU
1	I	199	ILE
1	I	205	ASN
1	I	208	THR
1	I	210	THR
1	I	284	ILE
1	I	285	GLU
1	I	302	LYS
1	I	315	THR
1	I	318	GLU
1	I	322	LYS
1	I	325	GLU

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Mol	Chain	Res	Type
1	I	326	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (34) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	20	GLN
1	A	184	GLN
1	A	205	ASN
1	A	213	ASN
1	A	257	GLN
1	A	304	ASN
1	B	20	GLN
1	B	97	HIS
1	B	124	GLN
1	B	213	ASN
1	B	236	ASN
1	C	257	GLN
1	C	300	GLN
1	C	332	ASN
1	D	20	GLN
1	D	97	HIS
1	D	205	ASN
1	D	332	ASN
1	E	20	GLN
1	E	124	GLN
1	E	205	ASN
1	F	5	ASN
1	F	97	HIS
1	F	184	GLN
1	F	236	ASN
1	F	312	ASN
1	G	5	ASN
1	G	20	GLN
1	H	205	ASN
1	H	257	GLN
1	I	186	ASN
1	I	205	ASN
1	I	213	ASN
1	I	257	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 18 ligands modelled in this entry, 9 are monoatomic - leaving 9 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	AGS	C	402	4	32,33,33	1.79	7 (21%)	45,52,52	1.93	12 (26%)
5	AGS	F	402	4	32,33,33	1.71	7 (21%)	45,52,52	1.90	13 (28%)
5	AGS	B	402	4	32,33,33	1.98	10 (31%)	45,52,52	1.87	12 (26%)
5	AGS	I	402	4	32,33,33	1.98	9 (28%)	45,52,52	1.95	13 (28%)
5	AGS	G	402	4	32,33,33	1.93	8 (25%)	45,52,52	1.97	11 (24%)
5	AGS	H	402	4	32,33,33	1.84	7 (21%)	45,52,52	1.92	11 (24%)
5	AGS	D	402	4	32,33,33	1.72	6 (18%)	45,52,52	2.01	12 (26%)
5	AGS	E	402	4	32,33,33	1.72	6 (18%)	45,52,52	2.03	11 (24%)
5	AGS	A	402	4	32,33,33	2.17	8 (25%)	45,52,52	1.97	13 (28%)

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	AGS	C	402	4	-	2/21/38/38	0/3/3/3
5	AGS	F	402	4	-	3/21/38/38	0/3/3/3
5	AGS	B	402	4	-	2/21/38/38	0/3/3/3
5	AGS	I	402	4	-	2/21/38/38	0/3/3/3
5	AGS	G	402	4	-	1/21/38/38	0/3/3/3
5	AGS	H	402	4	-	2/21/38/38	0/3/3/3
5	AGS	D	402	4	-	2/21/38/38	0/3/3/3
5	AGS	E	402	4	-	2/21/38/38	0/3/3/3
5	AGS	A	402	4	-	1/21/38/38	0/3/3/3

All (68) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	402	AGS	PG-S1G	8.36	2.08	1.90
5	B	402	AGS	PG-S1G	6.68	2.05	1.90
5	I	402	AGS	PG-S1G	6.51	2.04	1.90
5	C	402	AGS	PG-S1G	5.73	2.03	1.90
5	D	402	AGS	PG-S1G	5.51	2.02	1.90
5	H	402	AGS	PG-S1G	5.48	2.02	1.90
5	A	402	AGS	C5-C4	5.06	1.48	1.39
5	E	402	AGS	PG-S1G	5.05	2.01	1.90
5	I	402	AGS	C5-C4	5.02	1.48	1.39
5	B	402	AGS	C5-C4	4.91	1.47	1.39
5	H	402	AGS	C5-C4	4.68	1.47	1.39
5	F	402	AGS	C5-C4	4.50	1.47	1.39
5	G	402	AGS	PG-O3G	-4.43	1.40	1.54
5	G	402	AGS	PG-S1G	4.42	2.00	1.90
5	G	402	AGS	C5-C4	4.38	1.46	1.39
5	C	402	AGS	C5-C4	4.33	1.46	1.39
5	D	402	AGS	C5-C4	4.15	1.46	1.39
5	F	402	AGS	PG-S1G	4.03	1.99	1.90
5	E	402	AGS	C5-C4	4.01	1.46	1.39
5	H	402	AGS	PG-O3G	-3.78	1.42	1.54
5	D	402	AGS	PG-O3G	-3.68	1.42	1.54
5	E	402	AGS	PG-O3G	-3.49	1.43	1.54
5	C	402	AGS	PG-O3G	-3.49	1.43	1.54
5	F	402	AGS	PG-O3G	-3.48	1.43	1.54
5	G	402	AGS	C5-N7	-3.45	1.32	1.39
5	F	402	AGS	C5-N7	-3.17	1.33	1.39
5	A	402	AGS	C5-C6	3.05	1.49	1.41
5	H	402	AGS	C5-N7	-3.04	1.33	1.39
5	G	402	AGS	PB-O3A	-2.99	1.56	1.59

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	E	402	AGS	C5-N7	-2.92	1.33	1.39
5	B	402	AGS	C8-N7	2.73	1.36	1.31
5	G	402	AGS	C4-N9	-2.67	1.32	1.37
5	B	402	AGS	PB-O3B	2.64	1.62	1.59
5	I	402	AGS	C5-C6	2.64	1.48	1.41
5	D	402	AGS	C5-N7	-2.64	1.34	1.39
5	I	402	AGS	PA-O3A	2.62	1.62	1.59
5	B	402	AGS	C5-C6	2.57	1.48	1.41
5	A	402	AGS	C8-N7	2.57	1.36	1.31
5	I	402	AGS	C8-N7	2.55	1.36	1.31
5	F	402	AGS	C8-N7	2.53	1.36	1.31
5	C	402	AGS	C8-N7	2.50	1.36	1.31
5	B	402	AGS	C5-N7	-2.46	1.34	1.39
5	I	402	AGS	PB-O3A	2.41	1.62	1.59
5	H	402	AGS	C4-N9	-2.39	1.32	1.37
5	C	402	AGS	C4-N9	-2.39	1.32	1.37
5	A	402	AGS	PB-O3B	2.37	1.62	1.59
5	G	402	AGS	PB-O2B	-2.35	1.44	1.55
5	I	402	AGS	PG-O3G	-2.35	1.47	1.54
5	I	402	AGS	C5-N7	-2.31	1.34	1.39
5	H	402	AGS	PB-O2B	-2.30	1.44	1.55
5	B	402	AGS	PG-O3G	-2.30	1.47	1.54
5	I	402	AGS	PB-O3B	2.24	1.61	1.59
5	D	402	AGS	C4-N9	-2.21	1.33	1.37
5	F	402	AGS	C4-N9	-2.21	1.33	1.37
5	A	402	AGS	PG-O2G	2.21	1.61	1.54
5	E	402	AGS	C4-N9	-2.19	1.33	1.37
5	D	402	AGS	C8-N7	2.17	1.35	1.31
5	A	402	AGS	C5-N7	-2.17	1.35	1.39
5	C	402	AGS	C5-N7	-2.14	1.35	1.39
5	G	402	AGS	PB-O3B	2.14	1.61	1.59
5	F	402	AGS	PB-O2B	-2.12	1.45	1.55
5	C	402	AGS	C5-C6	2.10	1.46	1.41
5	A	402	AGS	PB-O3A	2.08	1.61	1.59
5	B	402	AGS	PB-O3A	2.06	1.61	1.59
5	H	402	AGS	C8-N7	2.04	1.35	1.31
5	E	402	AGS	C8-N7	2.04	1.35	1.31
5	B	402	AGS	PA-O3A	2.01	1.61	1.59
5	B	402	AGS	C4-N9	-2.01	1.33	1.37

All (108) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	E	402	AGS	C5-C4-N3	-5.93	118.56	126.72
5	A	402	AGS	C5-C4-N3	-5.92	118.56	126.72
5	G	402	AGS	C5-C4-N3	-5.69	118.88	126.72
5	I	402	AGS	C5-C4-N3	-5.66	118.92	126.72
5	F	402	AGS	C5-C4-N3	-5.56	119.06	126.72
5	B	402	AGS	C5-C4-N3	-5.44	119.22	126.72
5	C	402	AGS	C5-C4-N3	-5.39	119.30	126.72
5	H	402	AGS	C5-C4-N3	-5.36	119.34	126.72
5	D	402	AGS	C5-C4-N3	-5.24	119.50	126.72
5	E	402	AGS	N3-C4-N9	5.03	135.72	127.17
5	D	402	AGS	N3-C4-N9	4.92	135.53	127.17
5	G	402	AGS	N3-C4-N9	4.92	135.53	127.17
5	F	402	AGS	N3-C4-N9	4.86	135.44	127.17
5	H	402	AGS	N3-C4-N9	4.70	135.17	127.17
5	C	402	AGS	N3-C4-N9	4.70	135.16	127.17
5	I	402	AGS	N3-C4-N9	4.69	135.14	127.17
5	A	402	AGS	N3-C4-N9	4.58	134.95	127.17
5	B	402	AGS	N3-C4-N9	4.46	134.75	127.17
5	D	402	AGS	C4-N9-C8	4.24	110.19	105.74
5	A	402	AGS	C2-N3-C4	4.03	121.68	111.83
5	I	402	AGS	O4'-C1'-N9	3.98	115.74	108.09
5	A	402	AGS	N3-C2-N1	-3.92	122.64	128.58
5	C	402	AGS	C4-N9-C8	3.90	109.83	105.74
5	C	402	AGS	N3-C2-N1	-3.87	122.73	128.58
5	A	402	AGS	C4-C5-N7	-3.85	106.18	110.58
5	B	402	AGS	N3-C2-N1	-3.85	122.76	128.58
5	I	402	AGS	N3-C2-N1	-3.84	122.77	128.58
5	I	402	AGS	C2-N3-C4	3.83	121.19	111.83
5	E	402	AGS	C4-N9-C8	3.78	109.71	105.74
5	D	402	AGS	N3-C2-N1	-3.75	122.90	128.58
5	B	402	AGS	C2-N3-C4	3.72	120.92	111.83
5	E	402	AGS	C2-N3-C4	3.67	120.80	111.83
5	H	402	AGS	O4'-C1'-N9	3.65	115.11	108.09
5	G	402	AGS	C2-N3-C4	3.58	120.58	111.83
5	C	402	AGS	C2-N3-C4	3.58	120.56	111.83
5	G	402	AGS	N3-C2-N1	-3.52	123.25	128.58
5	D	402	AGS	C2-N3-C4	3.52	120.42	111.83
5	E	402	AGS	N3-C2-N1	-3.51	123.27	128.58
5	E	402	AGS	C4-C5-N7	-3.49	106.59	110.58
5	H	402	AGS	C4-N9-C8	3.46	109.37	105.74
5	G	402	AGS	C4-N9-C8	3.42	109.33	105.74
5	G	402	AGS	C4-C5-N7	-3.38	106.72	110.58
5	F	402	AGS	N3-C2-N1	-3.36	123.50	128.58

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	F	402	AGS	C4-N9-C8	3.36	109.27	105.74
5	F	402	AGS	C2-N3-C4	3.33	119.96	111.83
5	H	402	AGS	N3-C2-N1	-3.21	123.72	128.58
5	H	402	AGS	C2-N3-C4	3.21	119.67	111.83
5	D	402	AGS	N9-C8-N7	-3.18	109.43	113.94
5	E	402	AGS	C5-N7-C8	3.16	108.41	103.45
5	B	402	AGS	O4'-C1'-N9	3.15	114.14	108.09
5	D	402	AGS	O4'-C1'-N9	3.13	114.09	108.09
5	I	402	AGS	C4-C5-N7	-3.07	107.07	110.58
5	E	402	AGS	N9-C8-N7	-3.07	109.58	113.94
5	G	402	AGS	C5-N7-C8	3.04	108.22	103.45
5	B	402	AGS	C4-C5-N7	-3.03	107.11	110.58
5	B	402	AGS	O2G-PG-O3B	3.02	114.73	104.64
5	B	402	AGS	C4-N9-C8	3.00	108.89	105.74
5	H	402	AGS	C4-C5-N7	-2.96	107.19	110.58
5	D	402	AGS	C2'-C1'-N9	-2.95	105.97	113.30
5	F	402	AGS	O2G-PG-O3B	2.93	114.42	104.64
5	A	402	AGS	C5-N7-C8	2.91	108.03	103.45
5	H	402	AGS	C2'-C1'-N9	-2.90	106.11	113.30
5	A	402	AGS	PB-O3B-PG	-2.89	122.59	133.17
5	I	402	AGS	C4-N9-C8	2.84	108.72	105.74
5	C	402	AGS	N9-C8-N7	-2.81	109.95	113.94
5	G	402	AGS	C2'-C1'-N9	-2.79	106.37	113.30
5	H	402	AGS	C5-N7-C8	2.76	107.79	103.45
5	D	402	AGS	C5-N7-C8	2.74	107.76	103.45
5	C	402	AGS	O2G-PG-O3B	2.74	113.79	104.64
5	C	402	AGS	C4-C5-N7	-2.69	107.50	110.58
5	G	402	AGS	N9-C8-N7	-2.68	110.14	113.94
5	C	402	AGS	O4'-C1'-N9	2.68	113.23	108.09
5	G	402	AGS	O4'-C1'-N9	2.67	113.22	108.09
5	F	402	AGS	C4-C5-N7	-2.67	107.53	110.58
5	A	402	AGS	C4-N9-C8	2.65	108.53	105.74
5	H	402	AGS	N9-C8-N7	-2.65	110.18	113.94
5	E	402	AGS	O4'-C1'-N9	2.64	113.16	108.09
5	F	402	AGS	O4'-C1'-N9	2.62	113.11	108.09
5	E	402	AGS	C2'-C1'-N9	-2.59	106.86	113.30
5	I	402	AGS	O2G-PG-O3B	2.59	113.28	104.64
5	D	402	AGS	C4-C5-N7	-2.57	107.64	110.58
5	F	402	AGS	N9-C8-N7	-2.53	110.35	113.94
5	C	402	AGS	C2'-C1'-N9	-2.52	107.04	113.30
5	F	402	AGS	C5-N7-C8	2.48	107.35	103.45
5	B	402	AGS	C5-N7-C8	2.48	107.34	103.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	E	402	AGS	O2G-PG-O3B	2.47	112.90	104.64
5	A	402	AGS	C3'-C2'-C1'	2.47	106.14	101.46
5	A	402	AGS	C6-C5-N7	2.45	136.82	132.09
5	I	402	AGS	C5-N7-C8	2.44	107.29	103.45
5	C	402	AGS	C5-N7-C8	2.36	107.15	103.45
5	B	402	AGS	N9-C8-N7	-2.33	110.62	113.94
5	F	402	AGS	C2'-C1'-N9	-2.30	107.59	113.30
5	A	402	AGS	O4'-C1'-N9	2.24	112.39	108.09
5	I	402	AGS	C2'-C1'-N9	-2.23	107.76	113.30
5	A	402	AGS	N9-C8-N7	-2.22	110.79	113.94
5	H	402	AGS	O2G-PG-O3B	2.19	111.96	104.64
5	A	402	AGS	C2-N1-C6	2.16	122.28	118.73
5	D	402	AGS	N6-C6-N1	2.14	123.14	118.38
5	G	402	AGS	O2G-PG-O3B	2.12	111.73	104.64
5	F	402	AGS	N6-C6-N1	2.12	123.11	118.38
5	D	402	AGS	O2G-PG-O3B	2.12	111.72	104.64
5	I	402	AGS	N9-C8-N7	-2.08	110.98	113.94
5	B	402	AGS	C2-N1-C6	2.07	122.12	118.73
5	I	402	AGS	C6-C5-N7	2.04	136.02	132.09
5	B	402	AGS	C6-C5-N7	2.02	135.99	132.09
5	I	402	AGS	PB-O3B-PG	-2.02	125.78	133.17
5	F	402	AGS	C5-C6-N6	-2.00	118.33	123.29
5	C	402	AGS	C6-C5-N7	2.00	135.95	132.09

There are no chirality outliers.

All (17) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	B	402	AGS	PB-O3B-PG-O2G
5	B	402	AGS	PB-O3B-PG-O3G
5	C	402	AGS	PB-O3B-PG-O2G
5	C	402	AGS	PB-O3B-PG-O3G
5	D	402	AGS	PB-O3B-PG-O2G
5	D	402	AGS	PB-O3B-PG-O3G
5	E	402	AGS	PB-O3B-PG-O3G
5	F	402	AGS	PB-O3B-PG-O2G
5	F	402	AGS	PB-O3B-PG-O3G
5	G	402	AGS	PB-O3B-PG-O3G
5	H	402	AGS	PB-O3B-PG-O3G
5	I	402	AGS	PB-O3B-PG-O2G
5	I	402	AGS	PB-O3B-PG-O3G
5	E	402	AGS	PB-O3B-PG-O2G

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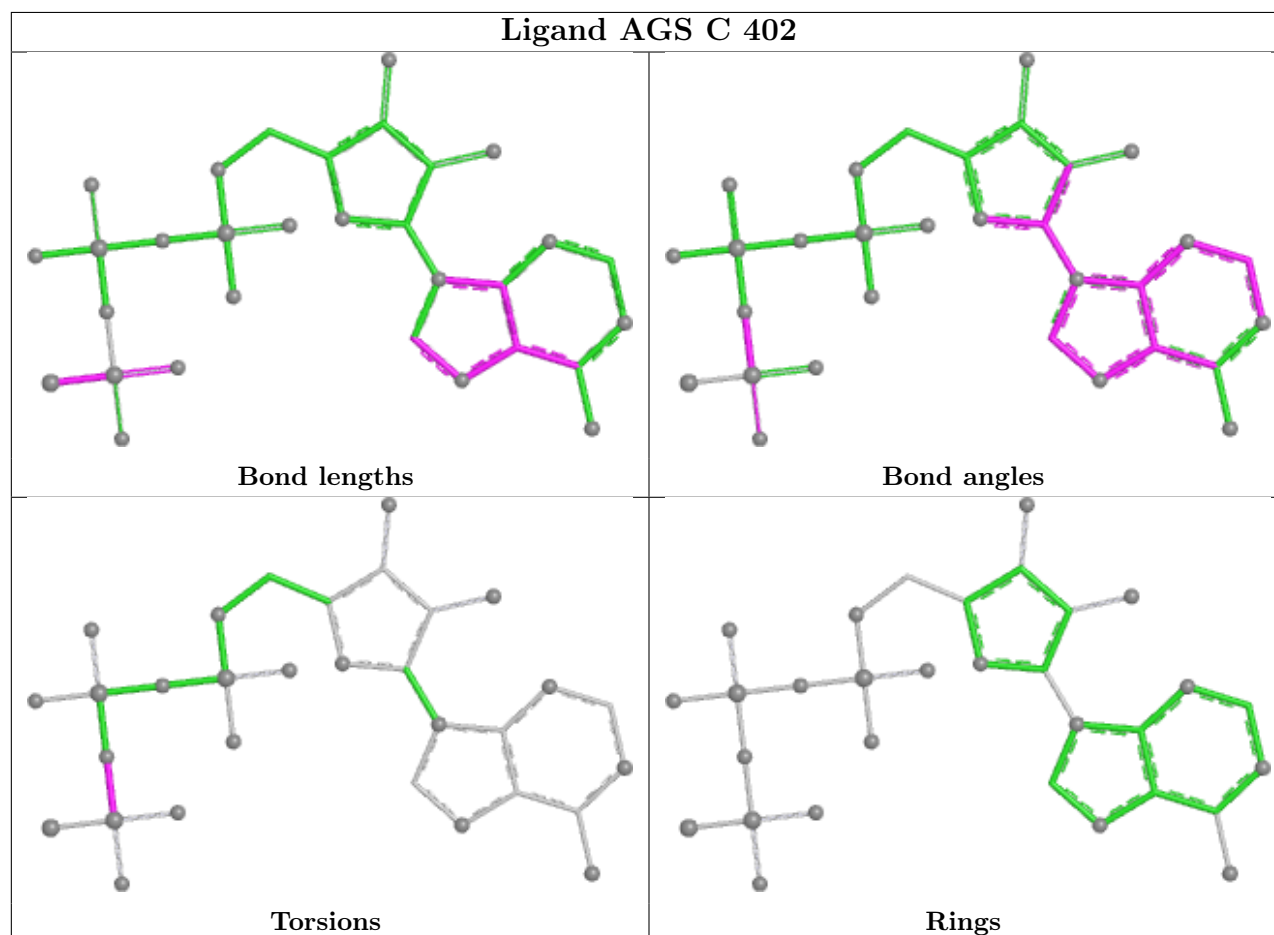
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Mol	Chain	Res	Type	Atoms
5	H	402	AGS	PB-O3B-PG-O2G
5	A	402	AGS	PG-O3B-PB-O2B
5	F	402	AGS	PG-O3B-PB-O2B

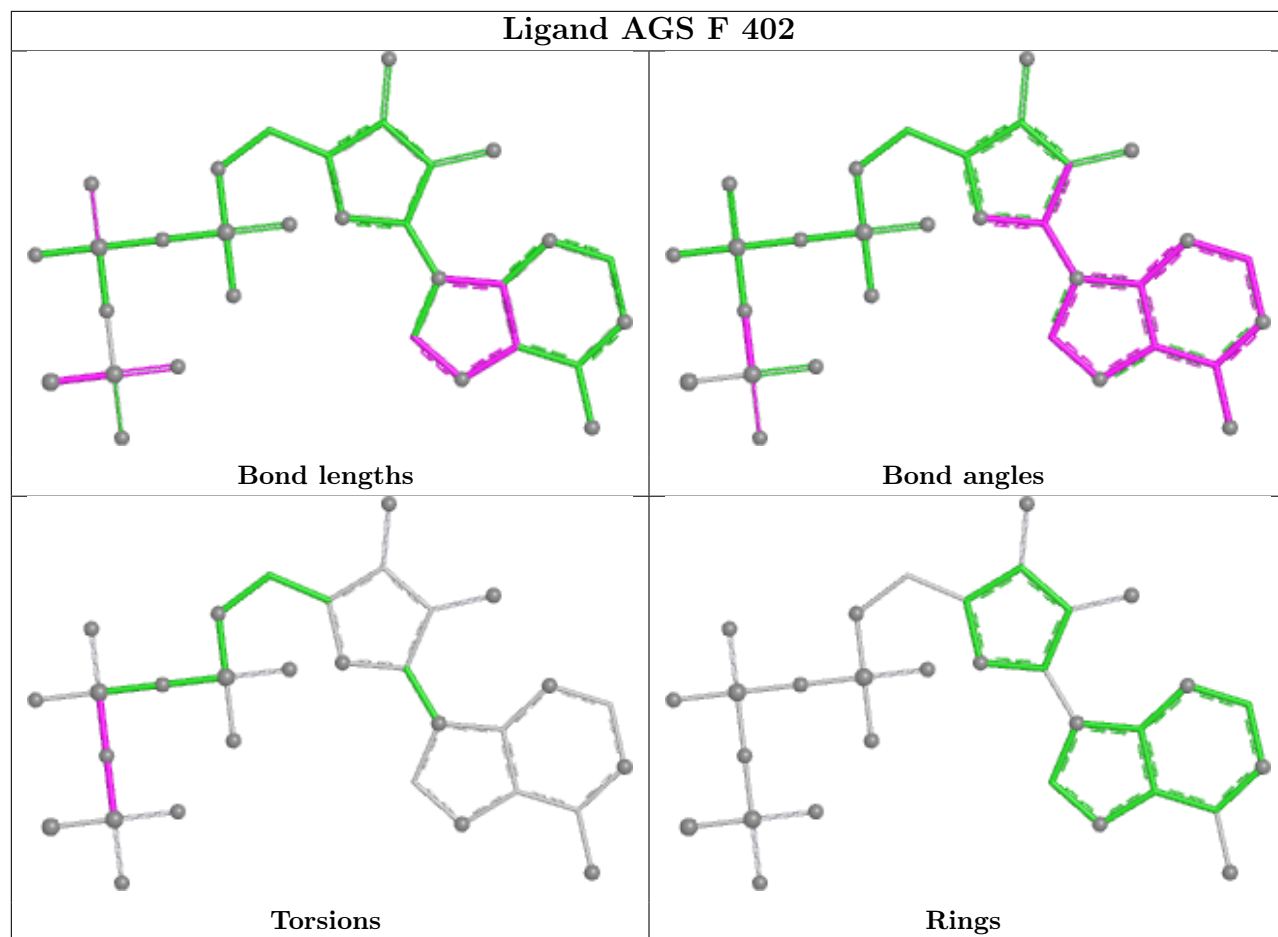
There are no ring outliers.

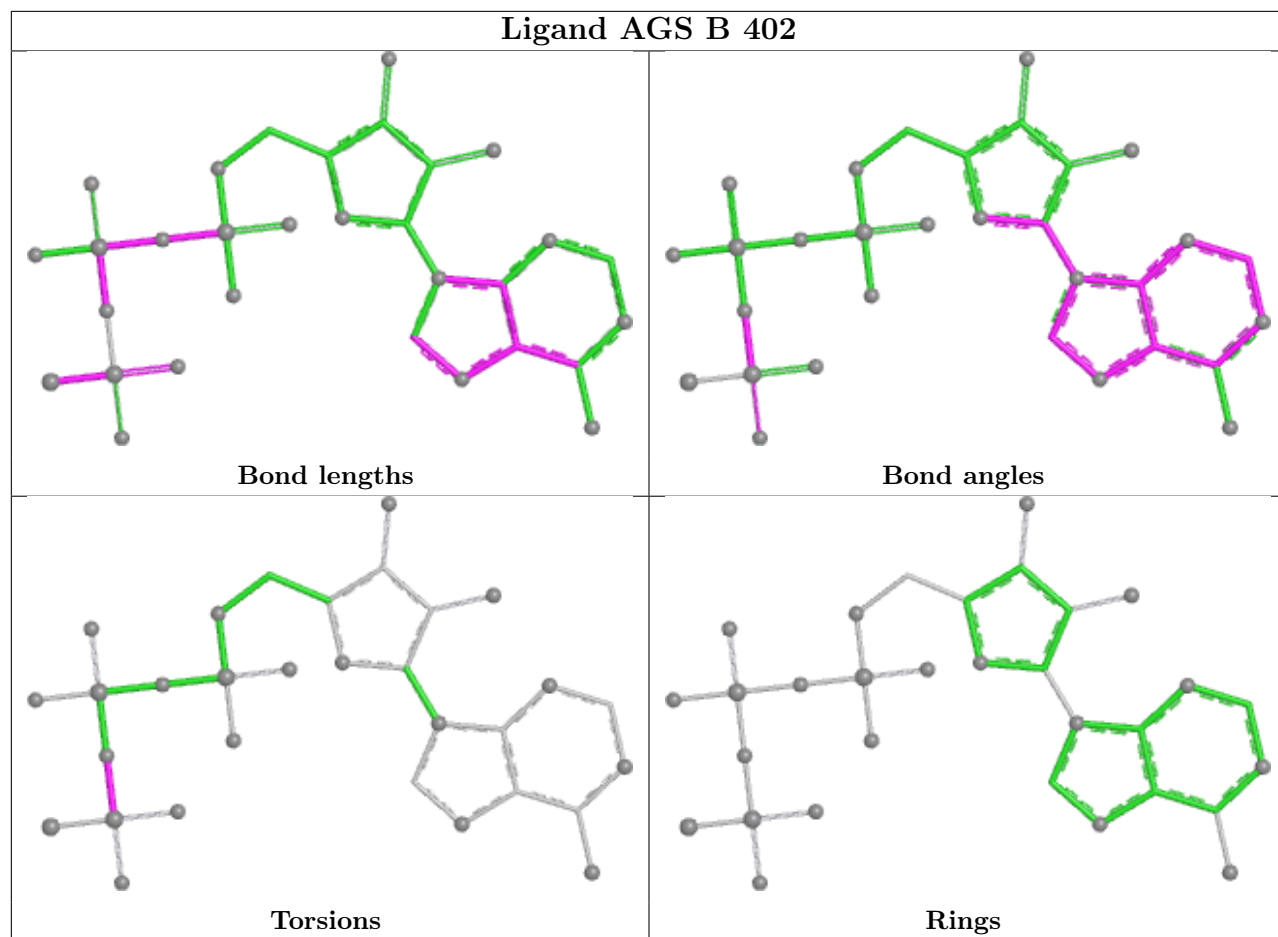
No monomer is involved in short contacts.

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.

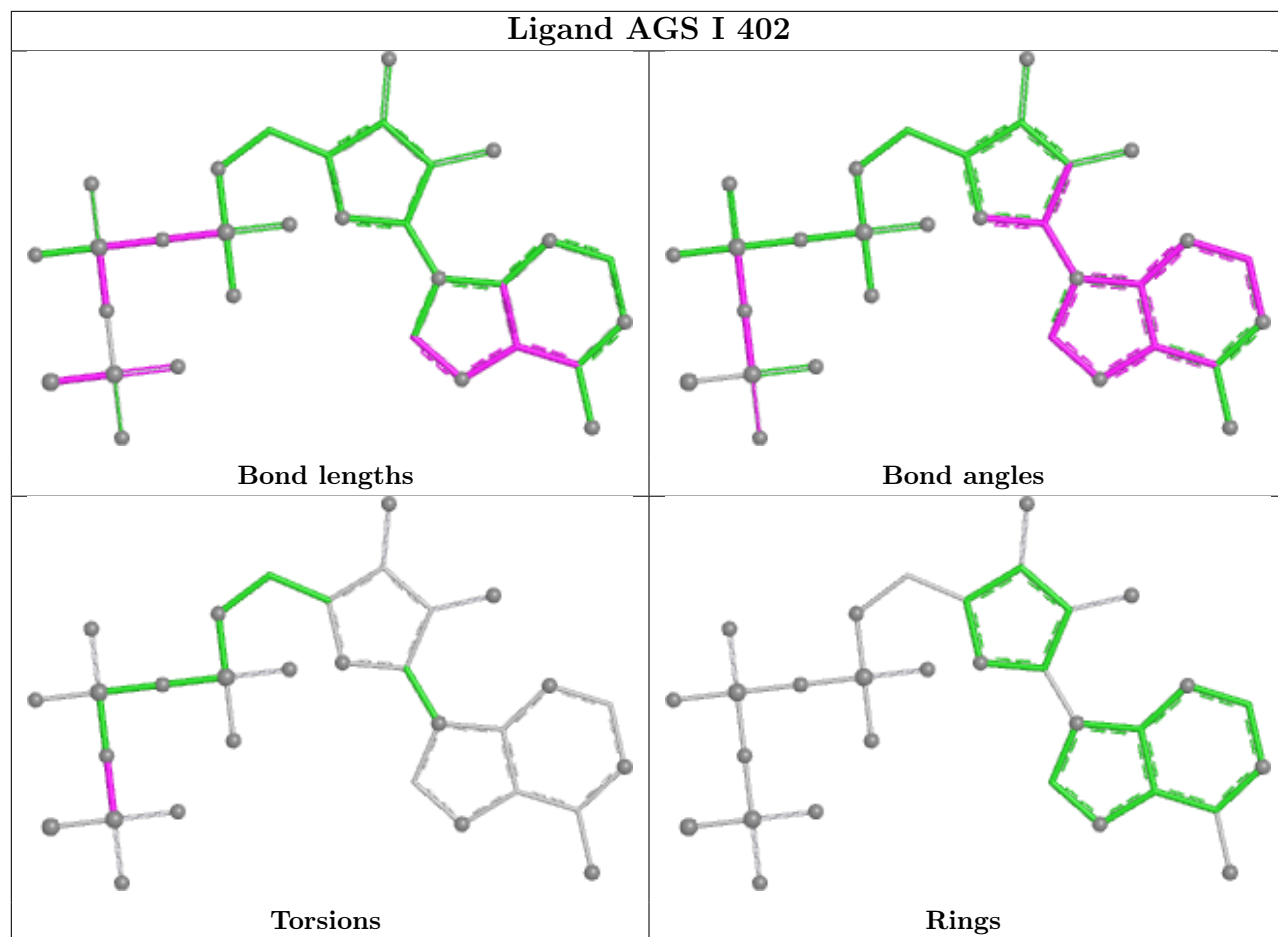


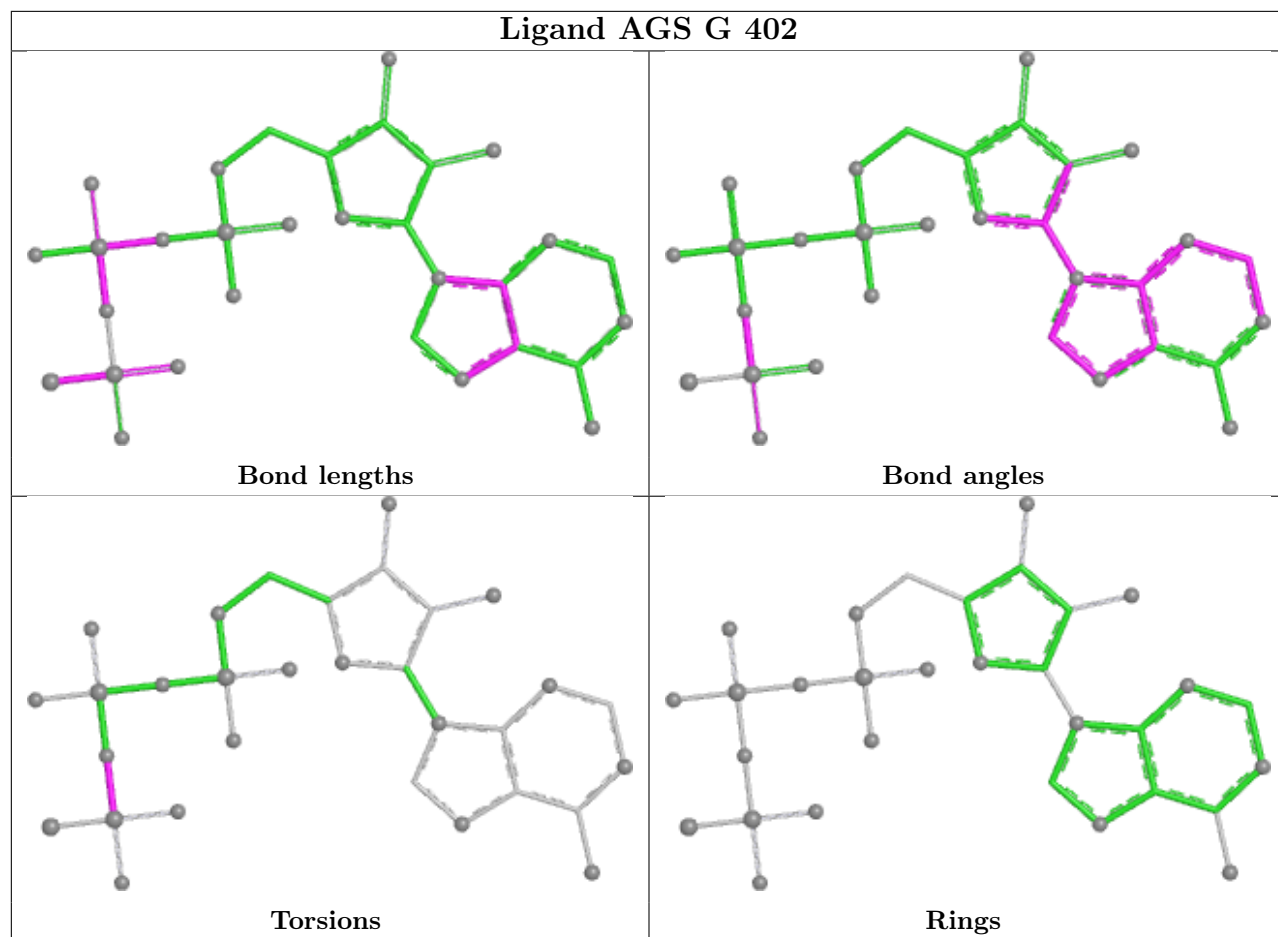
Ligand AGS F 402

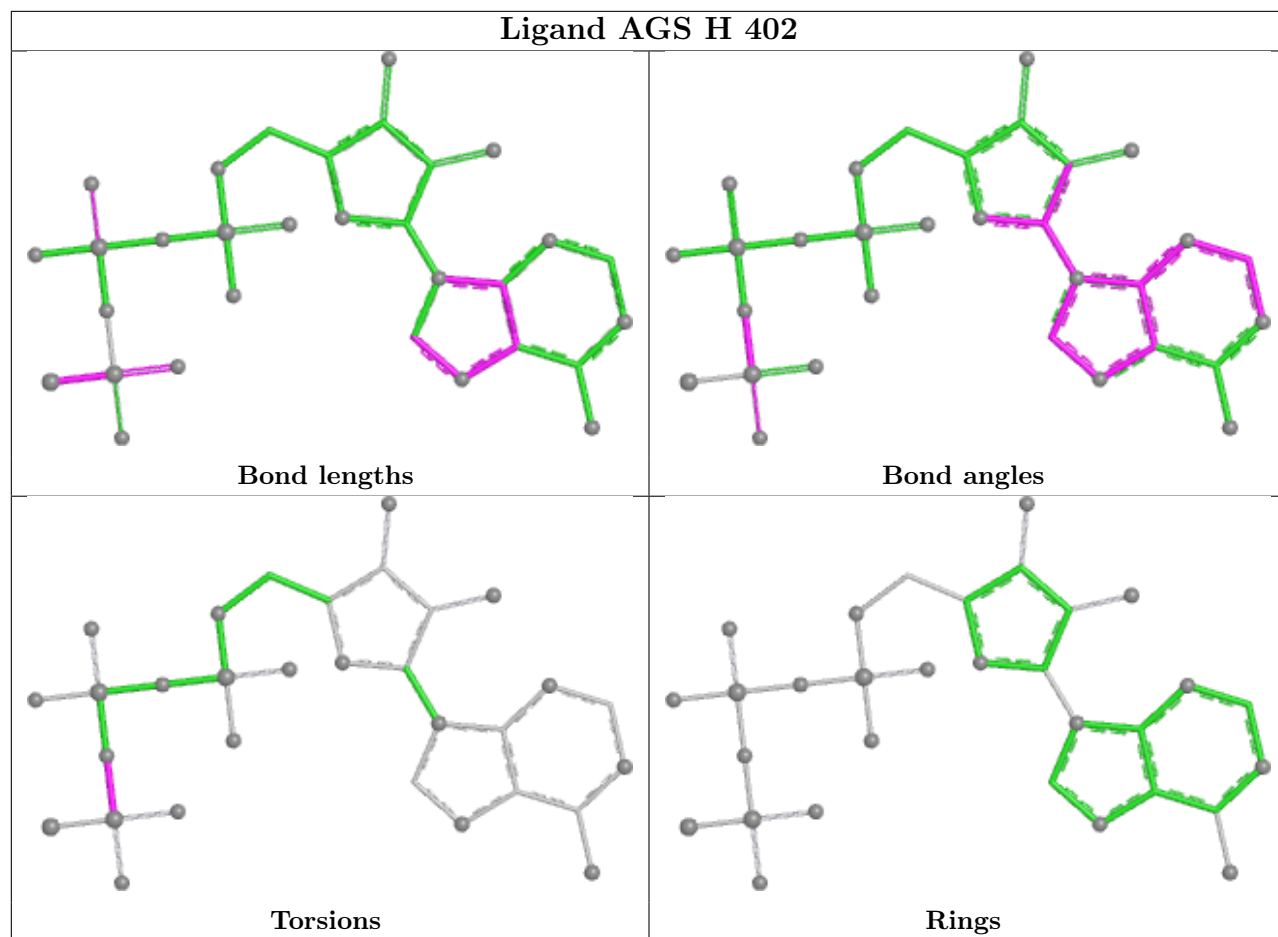


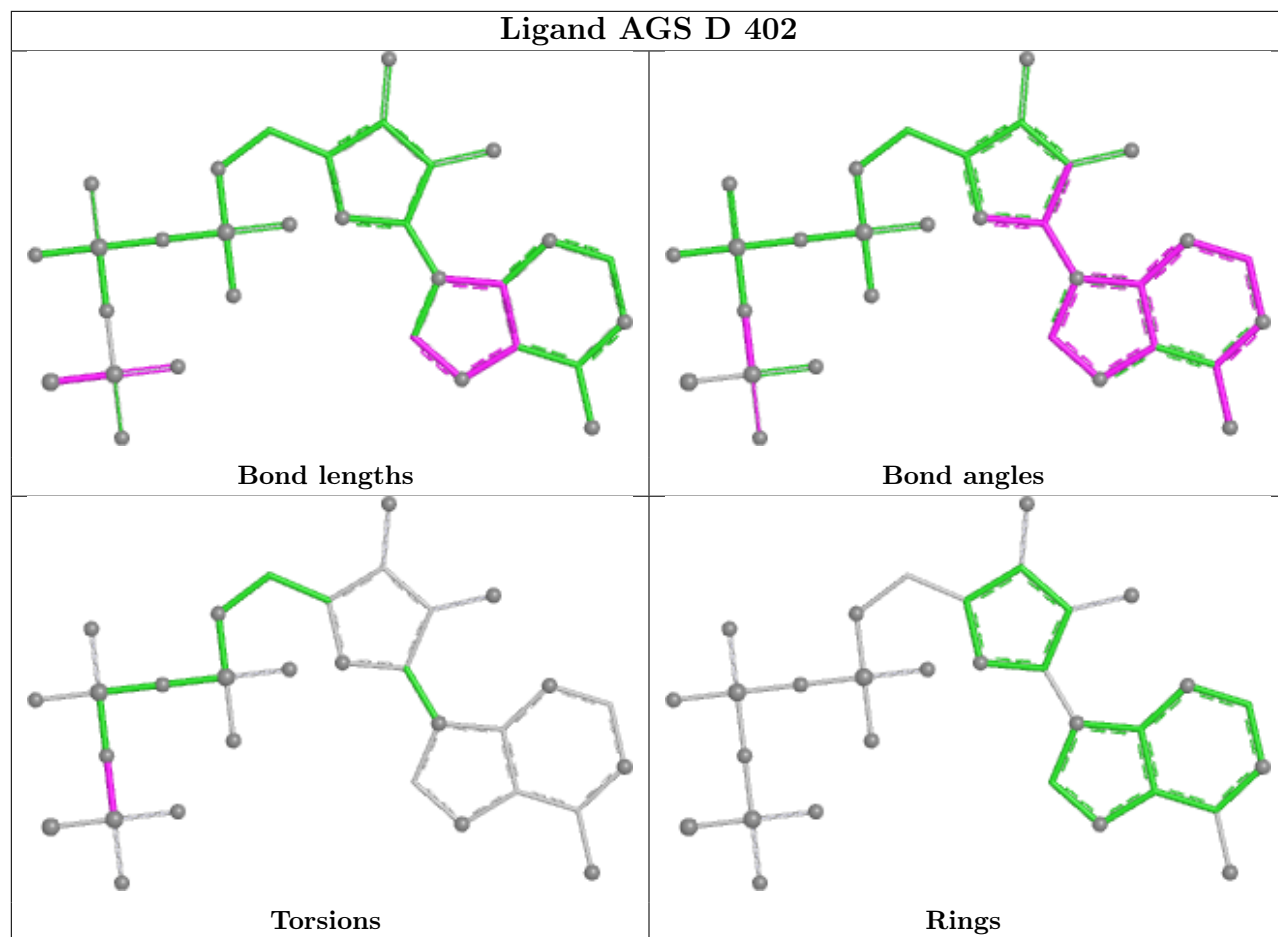


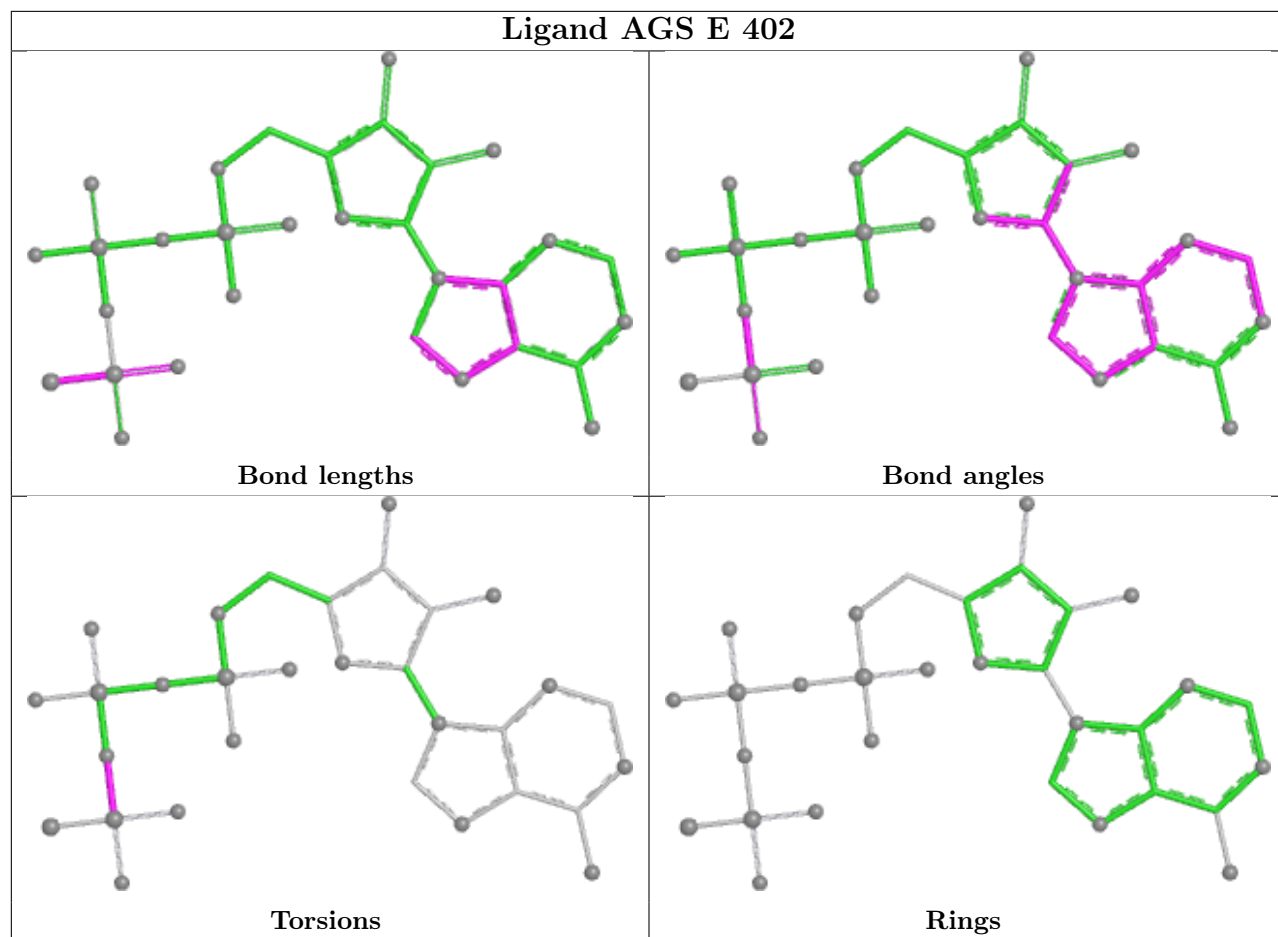
Ligand AGS I 402

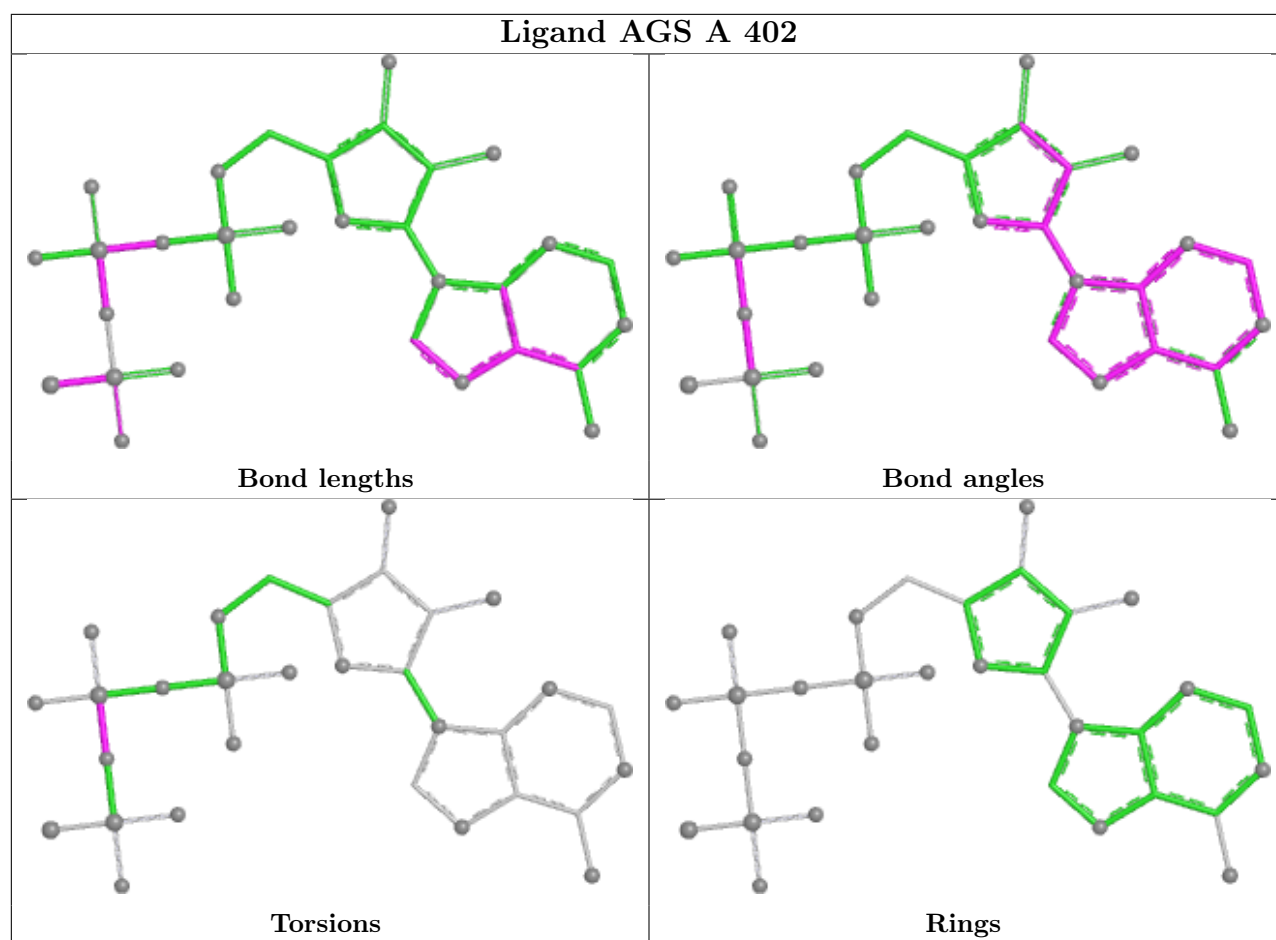












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

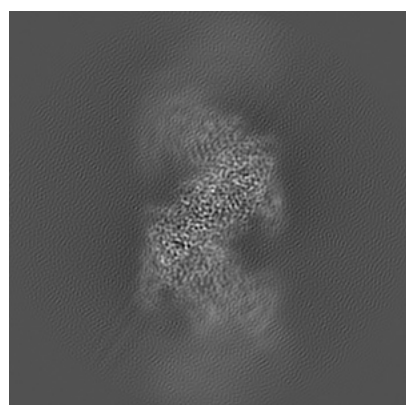
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-22524. These allow visual inspection of the internal detail of the map and identification of artifacts.

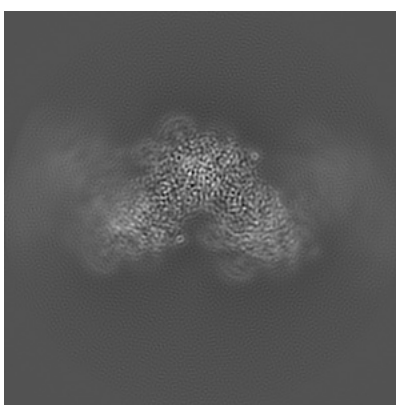
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

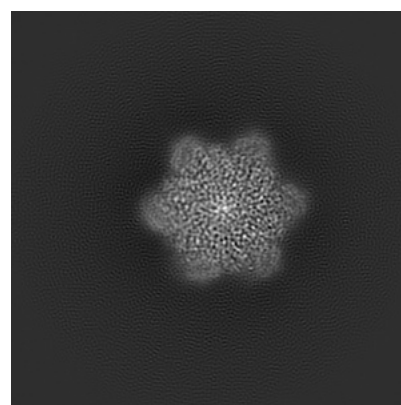
6.1.1 Primary map



X



Y

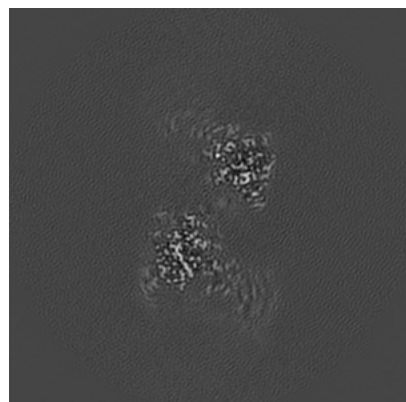


Z

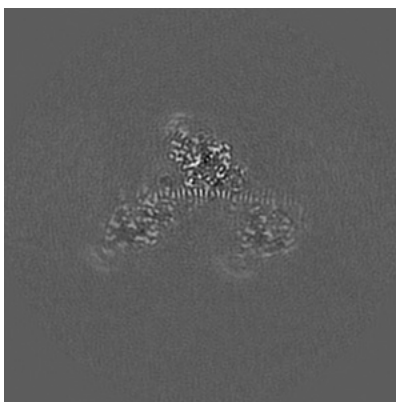
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

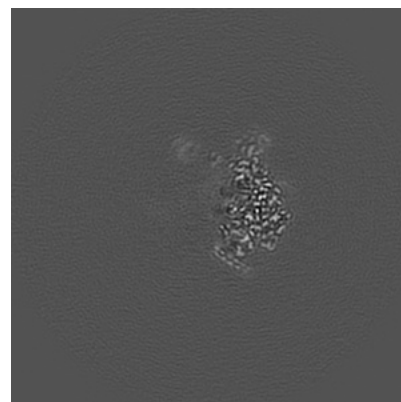
6.2.1 Primary map



X Index: 128



Y Index: 128

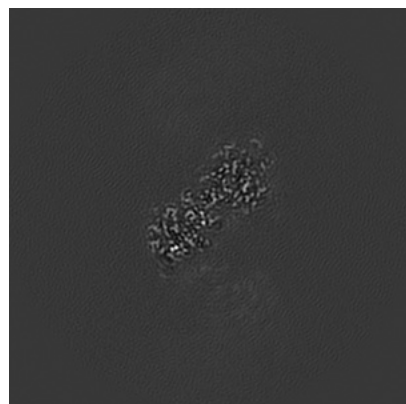


Z Index: 128

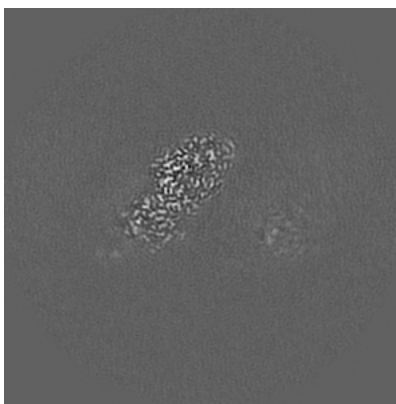
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

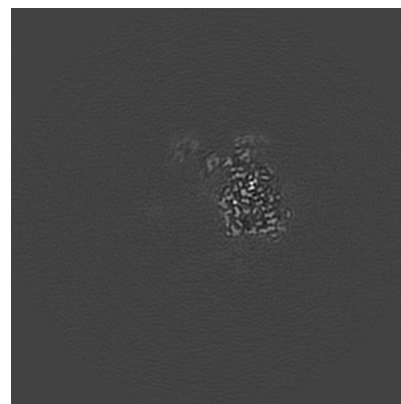
6.3.1 Primary map



X Index: 142



Y Index: 113

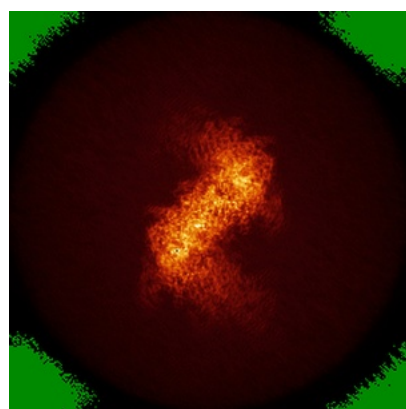


Z Index: 133

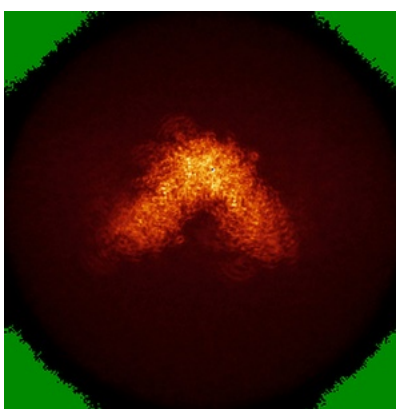
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

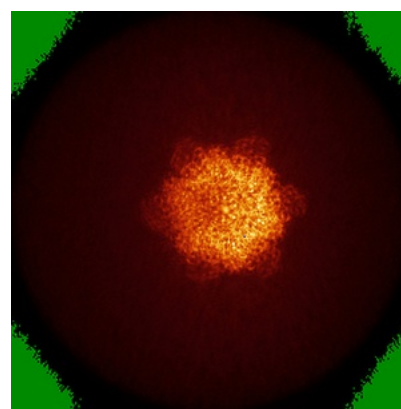
6.4.1 Primary map



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

This section was not generated.

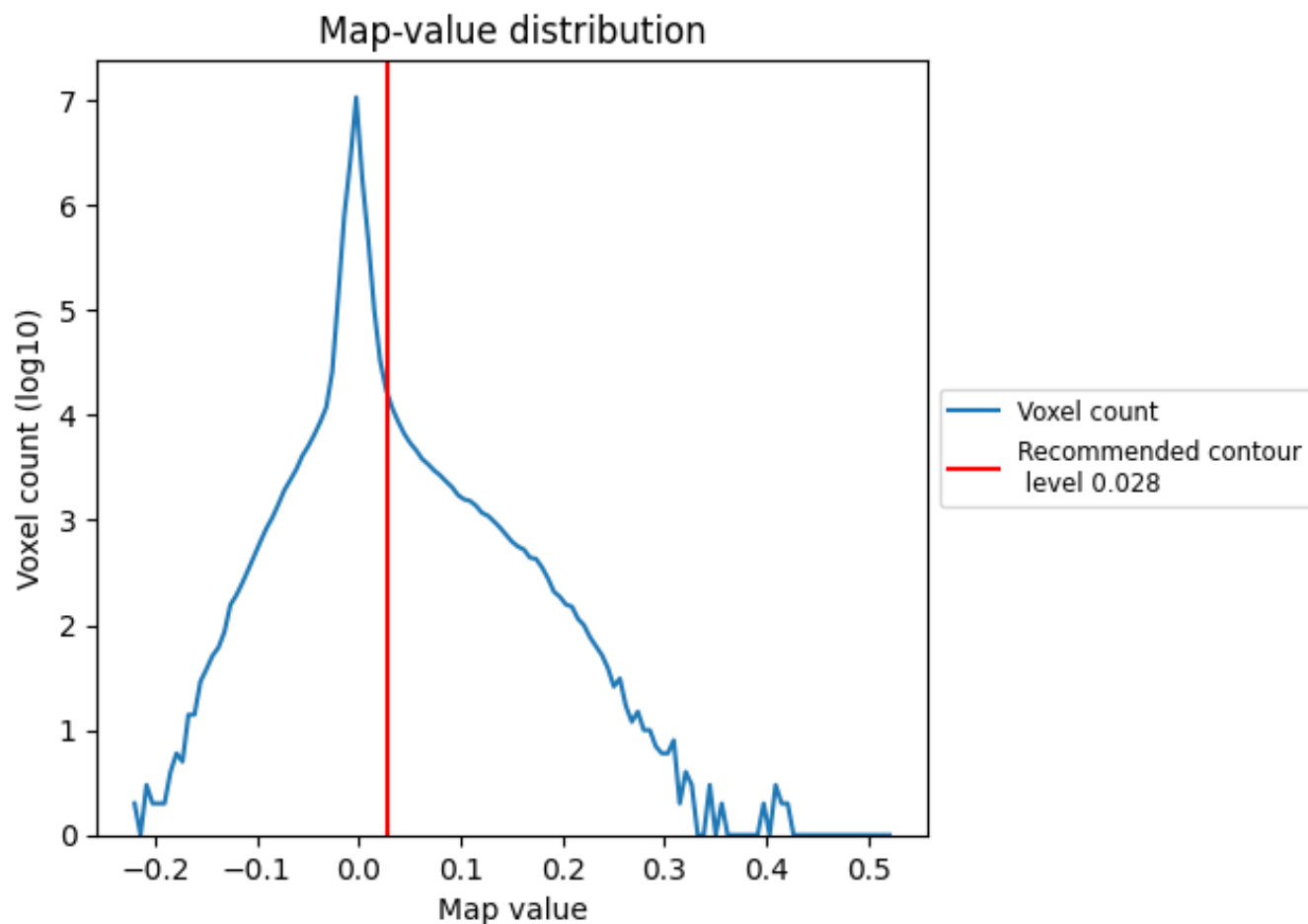
6.6 Mask visualisation

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

7 Map analysis [i](#)

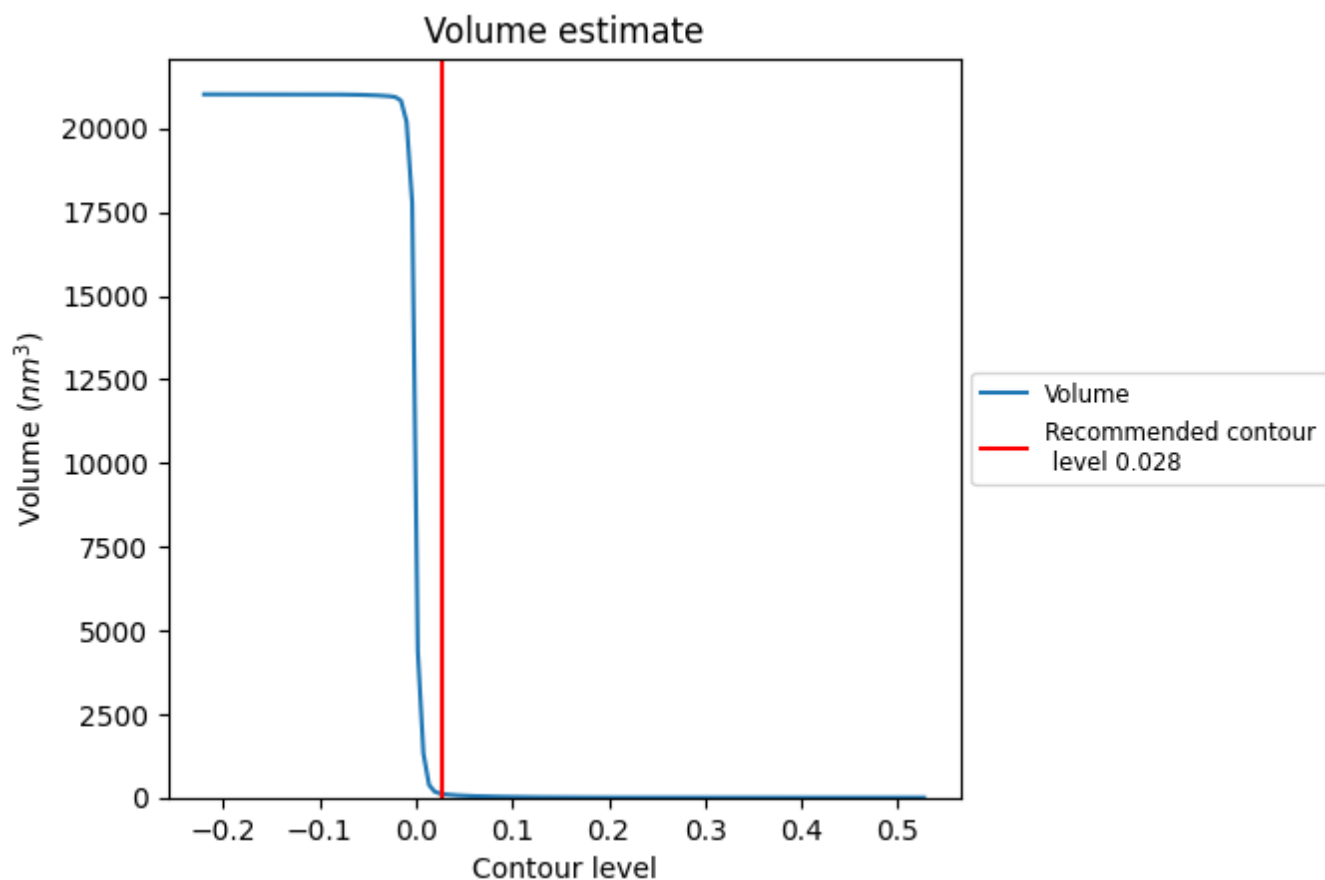
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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.

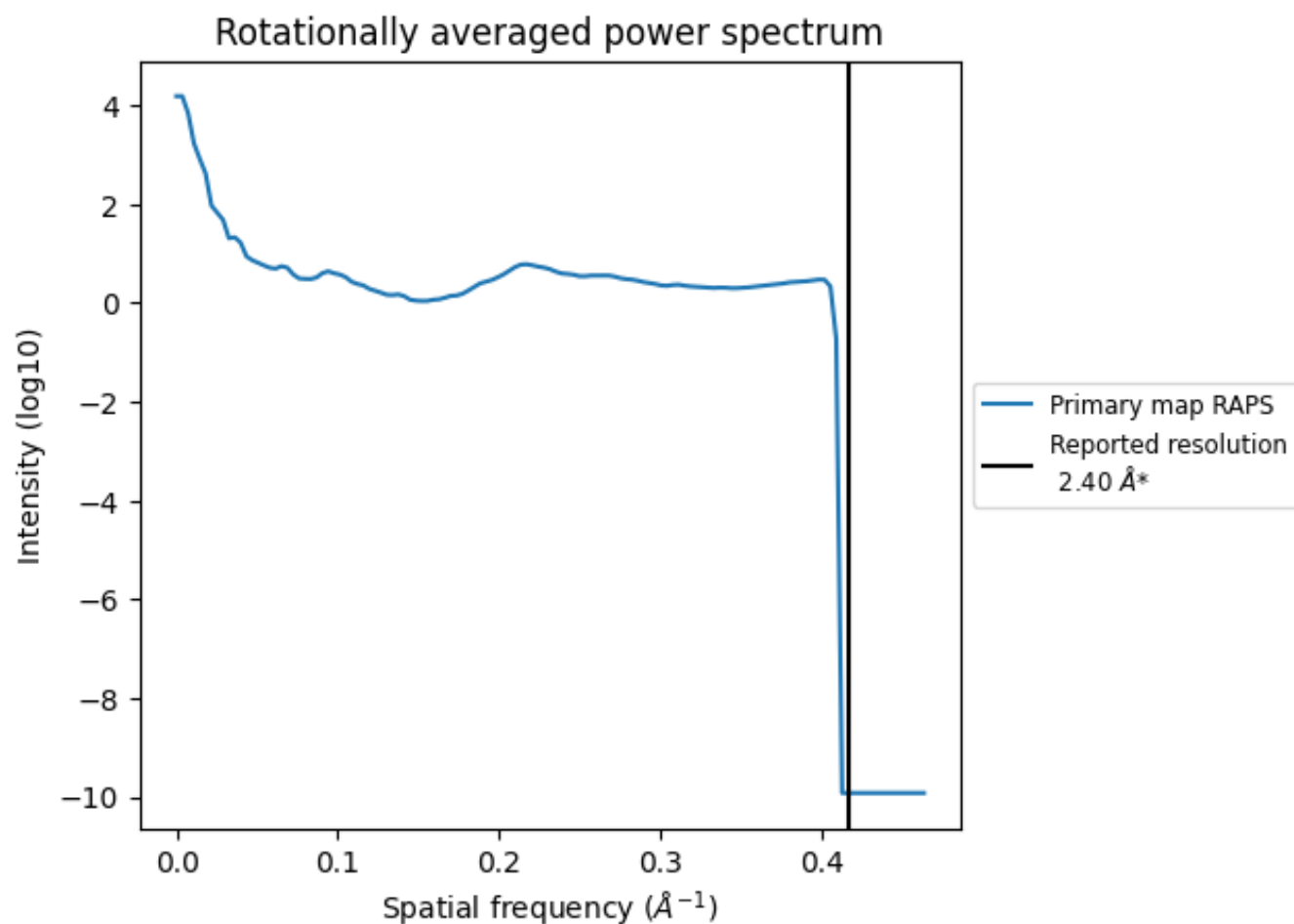
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 107 nm^3 ; this corresponds to an approximate mass of 97 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 ⓘ



*Reported resolution corresponds to spatial frequency of 0.417 Å⁻¹

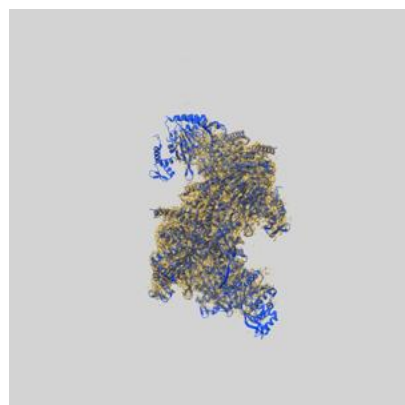
8 Fourier-Shell correlation

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

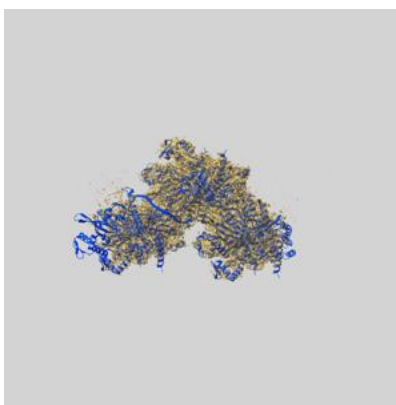
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-22524 and PDB model 7JY8. Per-residue inclusion information can be found in [section 3](#) on [page 7](#).

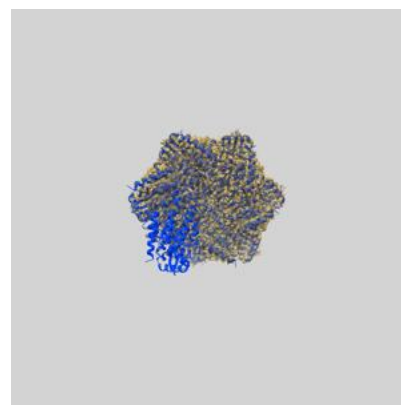
9.1 Map-model overlay [i](#)



X



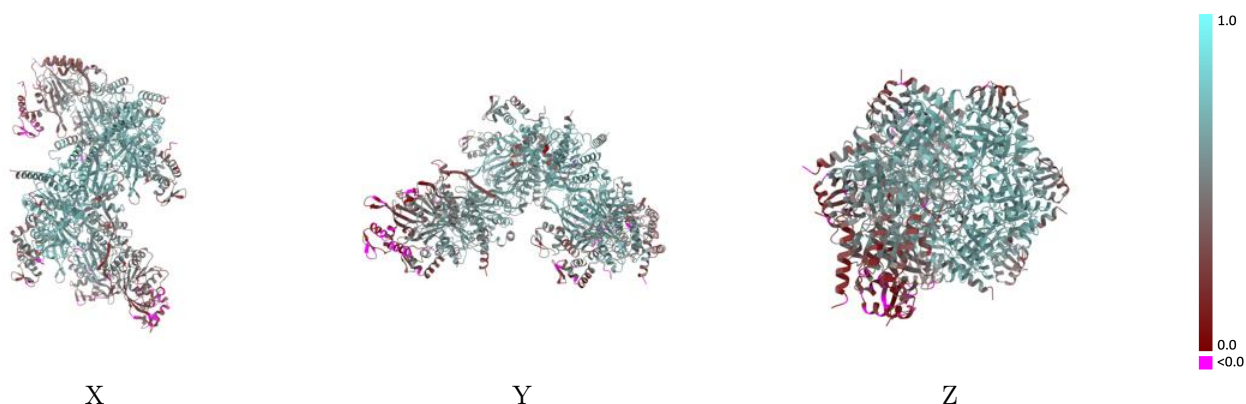
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.028 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](#)

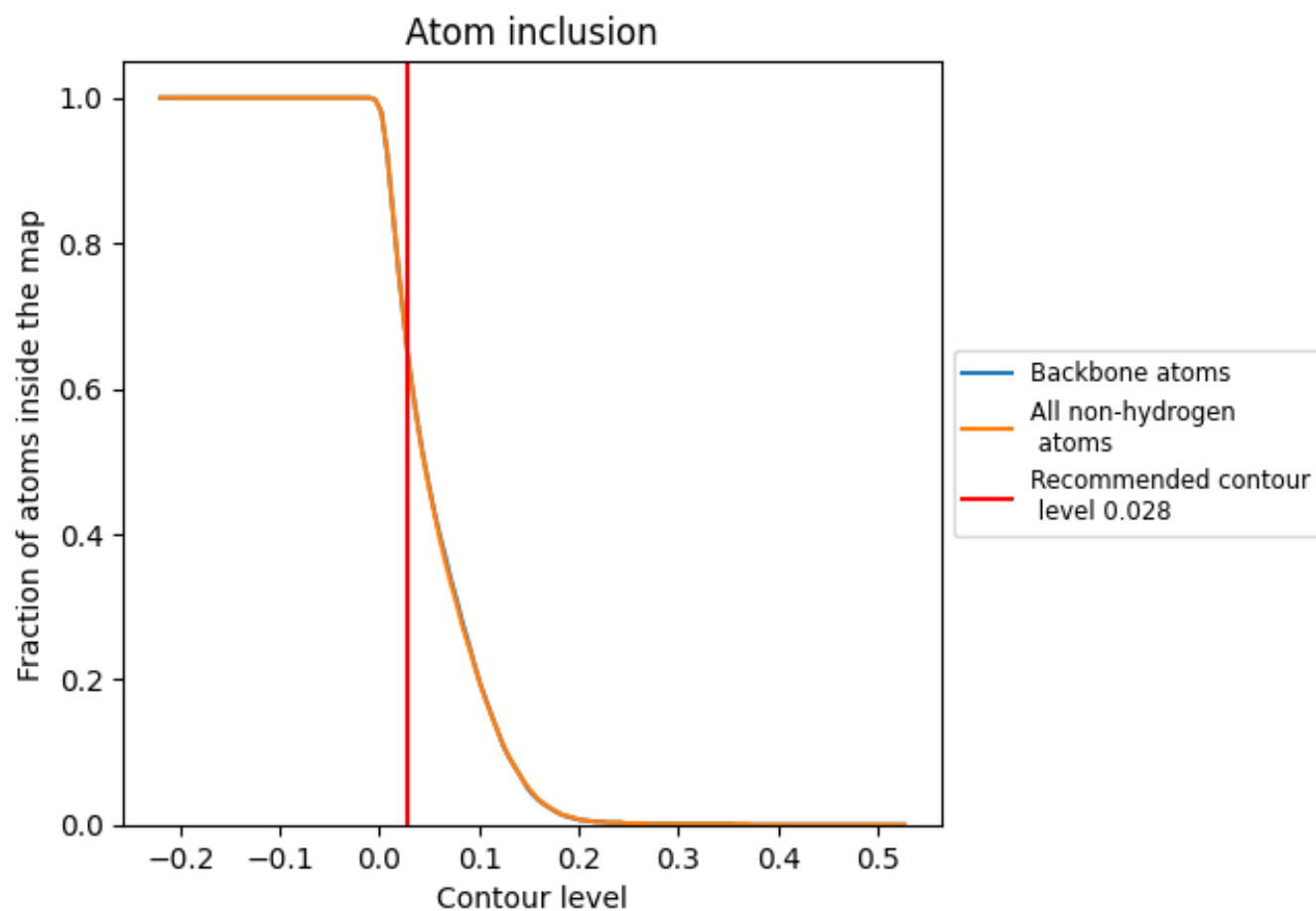


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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](#)

This section was not generated.

9.4 Atom inclusion ⓘ



At the recommended contour level, 65% of all backbone atoms, 65% 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 (0.028) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6510	0.5250
A	0.2330	0.3240
B	0.6660	0.5290
C	0.8170	0.5950
D	0.8550	0.6200
E	0.8610	0.6330
F	0.8470	0.6080
G	0.8070	0.5910
H	0.6200	0.4990
I	0.1450	0.3170
S	0.7720	0.5370
T	0.2380	0.3650

1.0

0.0

<0.0