



Full wwPDB EM Validation Report ⓘ

Jun 16, 2025 – 01:32 PM EDT

PDB ID : 9BP7 / pdb_00009bp7
EMDB ID : EMD-44763
Title : Cryo-EM structure of human heteromeric Glycine Receptor alpha3S346E-beta
in presence of glycine and 2,6-DTBP
Authors : Liu, X.; Wang, W.
Deposited on : 2024-05-07
Resolution : 3.60 Å(reported)
Based on initial model : 8DN2

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.dev118
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0rc1
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.44

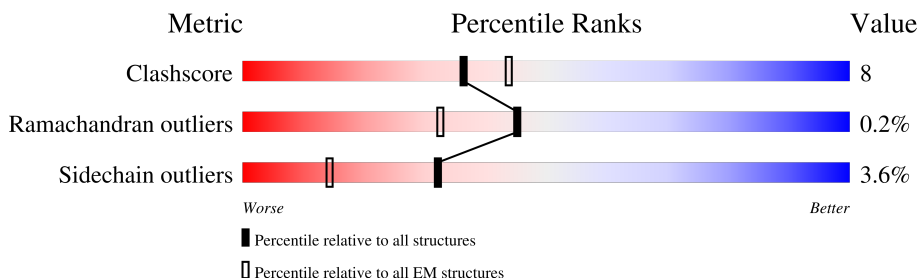
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.60 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	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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	422	<div> <div>56%</div> <div>65%</div> <div>15%</div> <div>19%</div> </div>
1	B	422	<div> <div>54%</div> <div>68%</div> <div>12%</div> <div>19%</div> </div>
1	C	422	<div> <div>54%</div> <div>66%</div> <div>14%</div> <div>19%</div> </div>
1	D	422	<div> <div>55%</div> <div>68%</div> <div>13%</div> <div>18%</div> </div>
2	E	680	<div> <div>32%</div> <div>39%</div> <div>9%</div> <div>51%</div> </div>

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	GLY	C	502	-	X	-	-

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 13731 atoms, of which 0 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 Glycine receptor subunit alpha-3.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	343	Total	C	N	O	S	1	0
			2760	1797	446	498	19		
1	B	340	Total	C	N	O	S	0	0
			2734	1787	441	487	19		
1	C	340	Total	C	N	O	S	0	0
			2728	1784	436	488	20		
1	D	344	Total	C	N	O	S	0	0
			2765	1806	445	494	20		

There are 40 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	ALA	deletion	UNP O75311
A	?	-	LEU	deletion	UNP O75311
A	?	-	GLU	deletion	UNP O75311
A	?	-	LYS	deletion	UNP O75311
A	?	-	PHE	deletion	UNP O75311
A	?	-	TYR	deletion	UNP O75311
A	?	-	ARG	deletion	UNP O75311
A	?	-	PHE	deletion	UNP O75311
A	?	-	SER	deletion	UNP O75311
A	346	GLU	SER	conflict	UNP O75311
B	?	-	ALA	deletion	UNP O75311
B	?	-	LEU	deletion	UNP O75311
B	?	-	GLU	deletion	UNP O75311
B	?	-	LYS	deletion	UNP O75311
B	?	-	PHE	deletion	UNP O75311
B	?	-	TYR	deletion	UNP O75311
B	?	-	ARG	deletion	UNP O75311
B	?	-	PHE	deletion	UNP O75311
B	?	-	SER	deletion	UNP O75311
B	346	GLU	SER	conflict	UNP O75311
C	?	-	ALA	deletion	UNP O75311
C	?	-	LEU	deletion	UNP O75311

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Chain	Residue	Modelled	Actual	Comment	Reference
C	?	-	GLU	deletion	UNP O75311
C	?	-	LYS	deletion	UNP O75311
C	?	-	PHE	deletion	UNP O75311
C	?	-	TYR	deletion	UNP O75311
C	?	-	ARG	deletion	UNP O75311
C	?	-	PHE	deletion	UNP O75311
C	?	-	SER	deletion	UNP O75311
C	346	GLU	SER	conflict	UNP O75311
D	?	-	ALA	deletion	UNP O75311
D	?	-	LEU	deletion	UNP O75311
D	?	-	GLU	deletion	UNP O75311
D	?	-	LYS	deletion	UNP O75311
D	?	-	PHE	deletion	UNP O75311
D	?	-	TYR	deletion	UNP O75311
D	?	-	ARG	deletion	UNP O75311
D	?	-	PHE	deletion	UNP O75311
D	?	-	SER	deletion	UNP O75311
D	346	GLU	SER	conflict	UNP O75311

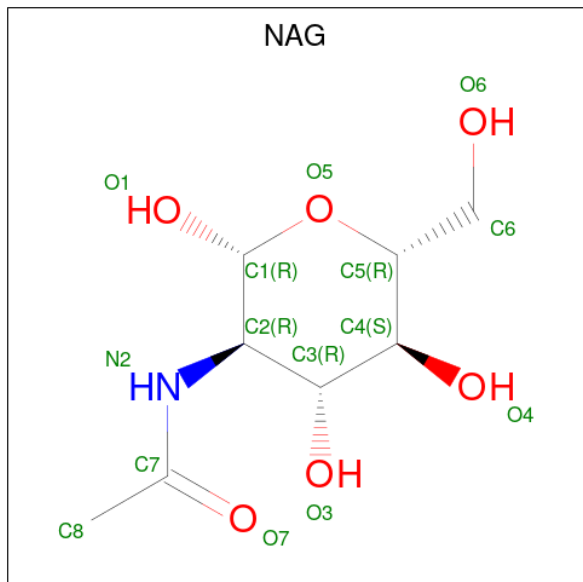
- Molecule 2 is a protein called Glycine receptor subunit beta, Green fluorescent protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	E	336	Total	C	N	O	S	0	0
			2659	1746	420	478	15		

There are 14 discrepancies between the modelled and reference sequences:

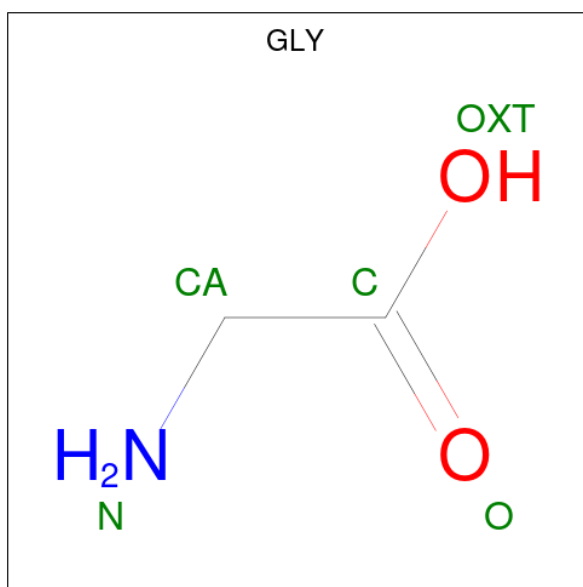
Chain	Residue	Modelled	Actual	Comment	Reference
E	333A	GLY	-	linker	UNP P48167
E	333B	GLY	-	linker	UNP P48167
E	333C	SER	-	linker	UNP P48167
E	333D	SER	-	linker	UNP P48167
E	333E	ALA	-	linker	UNP P48167
E	333F	ALA	-	linker	UNP P48167
E	333G	ALA	-	linker	UNP P48167
E	335S	PHE	LEU	conflict	UNP A0A9X4KGN5
E	335T	SER	THR	conflict	UNP A0A9X4KGN5
E	342D	HIS	LEU	conflict	UNP A0A9X4KGN5
E	342N	SER	-	linker	UNP A0A9X4KGN5
E	342O	GLY	-	linker	UNP A0A9X4KGN5
E	342P	SER	-	linker	UNP A0A9X4KGN5
E	342Q	GLY	-	linker	UNP A0A9X4KGN5

- Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$) (labeled as "Ligand of Interest" by depositor).

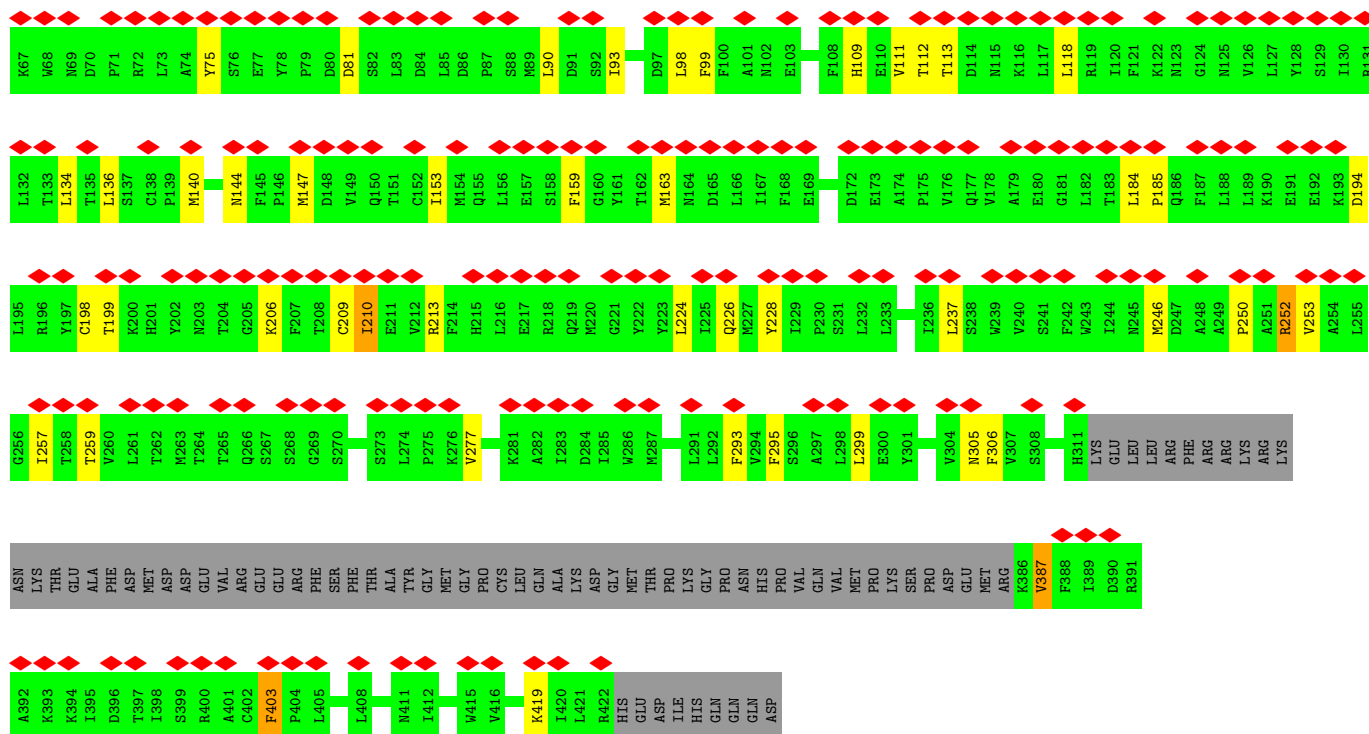


Mol	Chain	Residues	Atoms				AltConf
3	A	1	Total	C	N	O	0
			14	8	1	5	
3	B	1	Total	C	N	O	0
			14	8	1	5	
3	C	1	Total	C	N	O	0
			14	8	1	5	
3	D	1	Total	C	N	O	0
			14	8	1	5	
3	E	1	Total	C	N	O	0
			14	8	1	5	

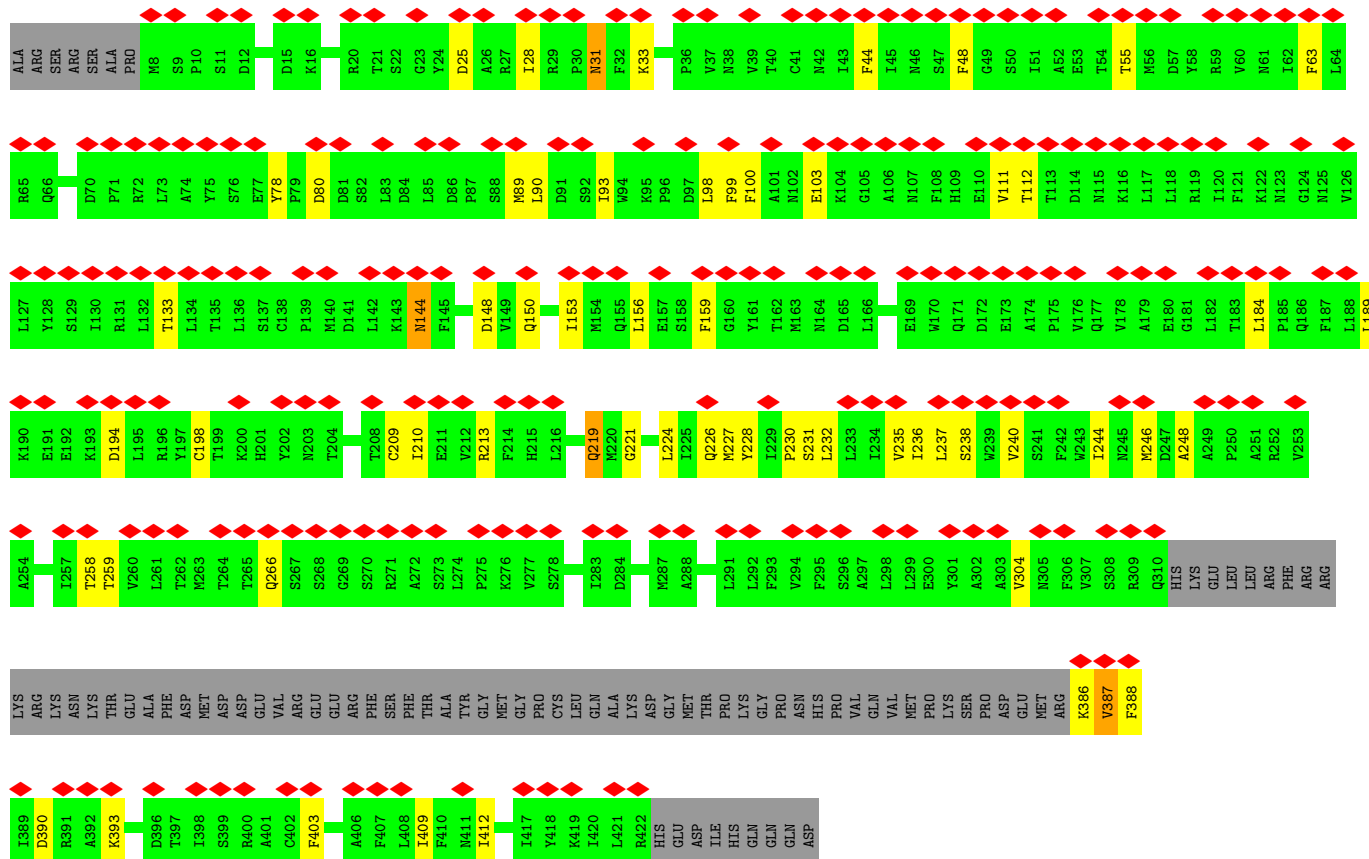
- Molecule 4 is GLYCINE (CCD ID: GLY) (formula: $C_2H_5NO_2$) (labeled as "Ligand of Interest" by depositor).



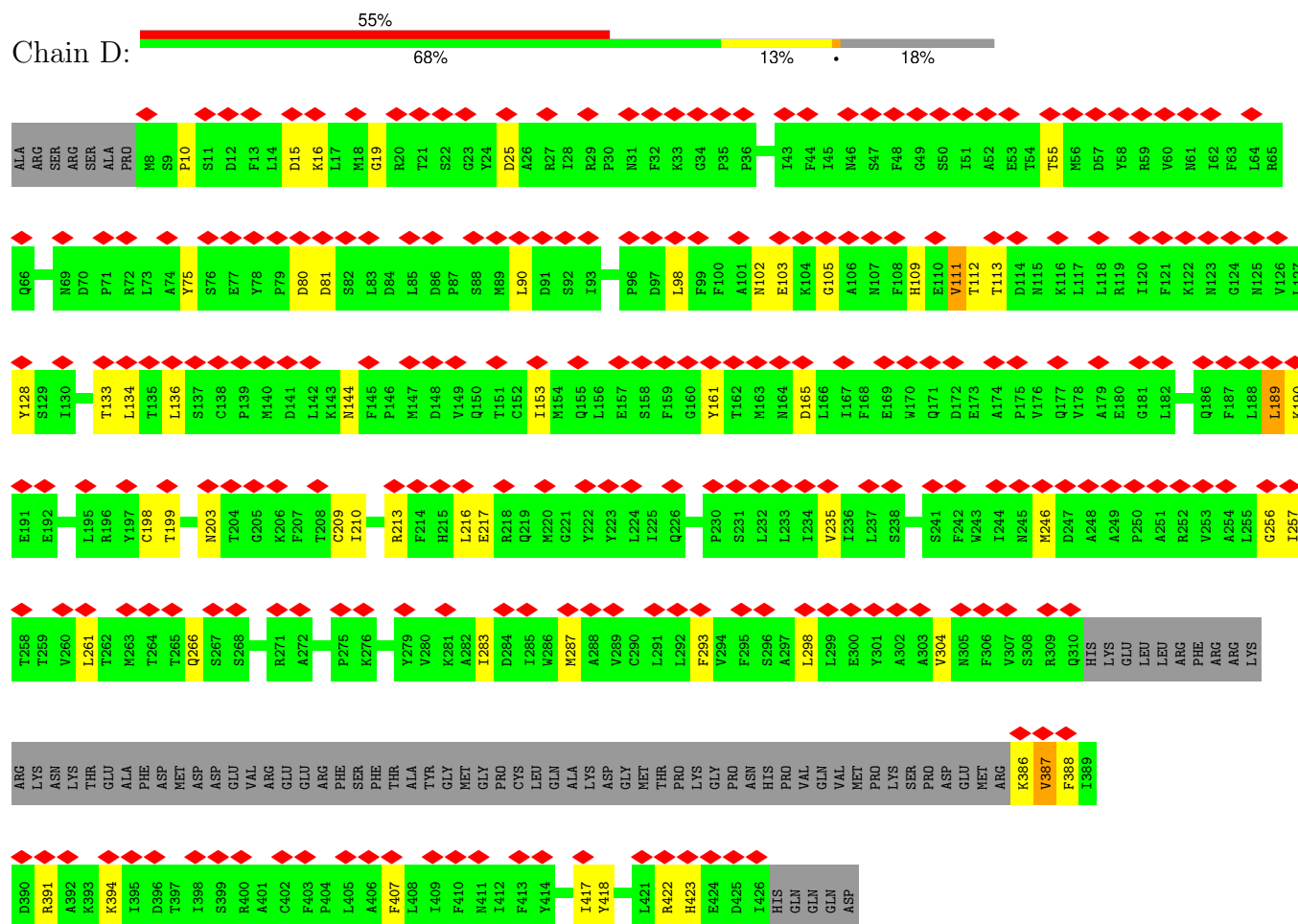
Mol	Chain	Residues	Atoms				AltConf
4	A	1	Total	C	N	O	0
			5	2	1	2	
4	C	1	Total	C	N	O	0
			5	2	1	2	
4	E	1	Total	C	N	O	0
			5	2	1	2	



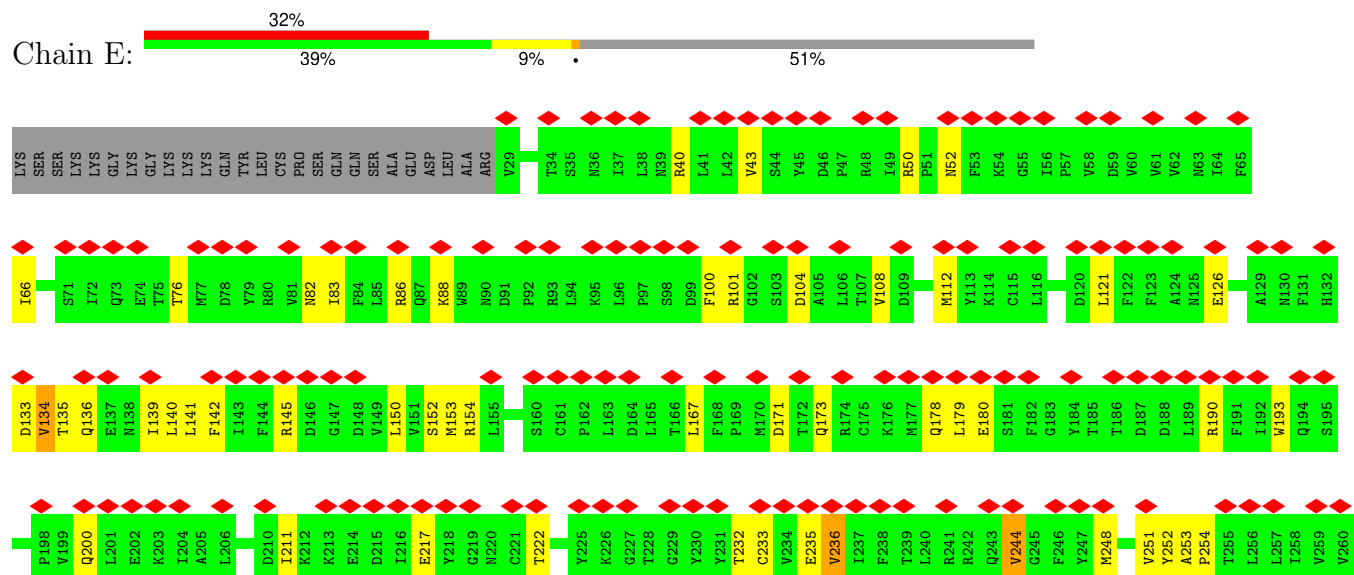
• Molecule 1: Glycine receptor subunit alpha-3



Chain D:



Chain E:



GLY	THR	VAL	ASN	LEU	E324	L261
LYS	ALA	THR	PHE	LYS	Y325	S262
PRO	ALA	ALA	LYS	PHE	A326	V263
ILE	GLY	ILE	ILE	ILE	V327	L264
GLY	THR	THR	ARG	THR	V328	S265
VAL	ILE	THR	HIS	THR	Q329	F266
ASN	HIS	THR	ASN	ALA	V330	
ASN	HIS	THR	ASN	ALA	M331	N269
GLY	THR	THR	GLY	LEU	V332	P270
LYS	THR	THR	GLY	PRO	L333	
GLY	THR	THR	VAL	VAL	M333	S273
LYS	THR	THR	GLN	PRO	GLY	GLY
GLN	LYS	LYS	LEU	TRP	A274	A275
ALA	SER	SER	ALA	THR	SER	R276
ASN	GLY	GLY	ASP	LEU	SER	V277
ASN	GLY	GLY	ASN	VAL	ALA	O278
LYS	GLY	GLY	HIS	VAL	ALA	P278
LYS	GLY	GLY	THR	THR	ALA	L279
PRO	GLY	GLY	GLN	THR	VAL	
PRO	GLY	VAL	ASN	PHE	SER	G280
PRO	GLY	GLY	THR	SER	LYS	
ALA	GLY	THR	THR	TYR	GLY	I281
LYS	THR	THR	ILE	GLY	GLY	F282
PRO	ARG	THR	ILE	VAL	GLU	S283
VAL	CYS	ARG	ASP	GLN	GLU	V284
VAL	CYS	CYS	PHE	CYS	LEU	L285
ILE	LYS	LYS	LYS	PHE	PHE	S286
P445	LYS	LYS	PRO	GLU	THR	
T446	VAL	VAL	ASP	ASP	GLY	L287
A447	CYS	CYS	VAL	GLY	VAL	A288
	THR	THR	LEU	THR	VAL	S289
	THR	THR	LEU	PRO	PRO	E290
R450	LYS	LYS	PRO	ASP	ILE	C291
I451	LYS	ASP	LYS	HIS	LEU	
D452	ASP	ASP	HIS	MET	VAL	T292
L453	LEU	THR	LYS	LYN	GLU	T293
Y454	ARG	ARG	LEU	HIS	LEU	L294
A455	SER	SER	LEU	LYS	ASP	A295
R456	ASN	ASN	THR	PHE	GLY	A296
	ASP	ASP	GLN	PHE	ASP	E297
A457	PHE	PHE	SER	TYR	VAL	L298
L458	SER	ILE	ALA	SER	ASN	P299
F459	ILE	VAL	LEU	ALA	GLY	HIS
P460	VAL	VAL	SER	MET	HIS	K300
F461	GLY	GLY	LYS	PRO	LYS	V301
	SER	SER	ASP	GLU	PHE	S302
	LEU	LEU	PRO	GLY	THR	S303
L464	PRO	PRO	ASN	TYR	VAL	V304
F465	ARG	ARG	GLU	VAL	GLY	K305
F466	ASP	ASP	LYS	GLN	GLY	A306
M467	PHE	GLU	ASP	ARG	GLY	L307
V468	LEU	SER	HIS	GLN	GLY	D308
I469	SER	LEU	LYS	LYS	THR	V309
	ASN	VAL	MET	ILE	ALA	M310
	THR	THR	LEU	GLY	THR	T311
S472	ASP	ASP	LEU	LYS	LYS	L312
I473	CYS	THR	GLU	ASP	GLY	A313
Y474	TYR	TYR	PHE	VAL	LEU	
L475					THR	
						L316
						F317
						G318
						F319
						A320
						S321
						L322
						V223

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	22755	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 ($e^-/\text{\AA}^2$)	69.6	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	3.173	Depositor
Minimum map value	-2.638	Depositor
Average map value	0.010	Depositor
Map value standard deviation	0.105	Depositor
Recommended contour level	0.36	Depositor
Map size (\AA)	239.04, 239.04, 239.04	wwPDB
Map dimensions	288, 288, 288	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	0.83, 0.83, 0.83	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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	0.15	0/2831	0.30	0/3849
1	B	0.13	0/2805	0.29	0/3812
1	C	0.12	0/2798	0.29	0/3803
1	D	0.11	0/2836	0.28	0/3854
2	E	0.14	0/2730	0.29	0/3727
All	All	0.13	0/14000	0.29	0/19045

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2760	0	2707	50	0
1	B	2734	0	2702	35	0
1	C	2728	0	2698	47	0
1	D	2765	0	2733	43	0
2	E	2659	0	2601	66	0
3	A	14	0	13	0	0
3	B	14	0	13	0	0
3	C	14	0	13	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	D	14	0	13	0	0
3	E	14	0	13	0	0
4	A	5	0	2	0	0
4	C	5	0	2	0	0
4	E	5	0	2	1	0
All	All	13731	0	13512	205	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 8.

All (205) 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:C:246:MET:HE2	1:C:304:VAL:CG1	1.35	1.55
1:A:255:LEU:CD1	2:E:281:ILE:HD11	1.37	1.49
1:C:246:MET:CE	1:C:304:VAL:HG11	1.39	1.47
1:A:255:LEU:CD1	2:E:281:ILE:CD1	1.98	1.39
2:E:278:PRO:O	2:E:282:PHE:HD2	1.15	1.24
2:E:278:PRO:O	2:E:282:PHE:CD2	1.92	1.20
1:A:255:LEU:HD11	2:E:281:ILE:CD1	1.64	1.20
1:C:246:MET:CE	1:C:304:VAL:CG1	2.08	1.15
1:A:255:LEU:HD12	2:E:281:ILE:CD1	1.73	1.13
1:D:257:ILE:HD13	2:E:282:PHE:CD2	1.94	1.02
2:E:278:PRO:HB3	2:E:282:PHE:HE2	1.33	0.91
1:C:246:MET:HE1	1:C:304:VAL:HG11	1.54	0.89
1:C:246:MET:HE2	1:C:304:VAL:HG12	1.57	0.85
1:A:255:LEU:CG	2:E:281:ILE:HD11	2.10	0.82
1:A:255:LEU:HD12	2:E:281:ILE:HD13	1.61	0.81
1:C:246:MET:CE	1:C:304:VAL:HG12	2.06	0.80
1:D:257:ILE:HD11	2:E:279:LEU:HD23	1.63	0.80
1:A:255:LEU:CD1	2:E:281:ILE:HD13	2.13	0.79
1:A:255:LEU:HD11	2:E:281:ILE:HD11	0.80	0.78
1:A:238:SER:HB2	1:A:259:THR:HG21	1.68	0.75
1:C:246:MET:HE2	1:C:304:VAL:HG11	0.76	0.74
2:E:278:PRO:C	2:E:282:PHE:HD2	1.98	0.70
2:E:180:GLU:HG3	2:E:233:CYS:HB3	1.76	0.68
2:E:278:PRO:CB	2:E:282:PHE:HE2	2.05	0.67
1:C:246:MET:HE1	1:C:304:VAL:CG1	2.16	0.66
1:B:134:LEU:HD23	1:B:136:LEU:HD21	1.75	0.66
1:D:109:HIS:NE2	1:D:133:THR:OG1	2.28	0.66
1:D:257:ILE:CD1	2:E:282:PHE:CD2	2.77	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:254:ALA:O	1:A:258:THR:OG1	2.13	0.65
2:E:278:PRO:C	2:E:282:PHE:CD2	2.75	0.64
2:E:100:PHE:O	2:E:145:ARG:NH1	2.31	0.63
1:D:199:THR:H	1:D:209:CYS:HB3	1.63	0.63
2:E:278:PRO:HB3	2:E:282:PHE:CE2	2.25	0.63
1:A:255:LEU:CD1	2:E:281:ILE:HD12	2.23	0.62
1:A:255:LEU:CG	2:E:281:ILE:CD1	2.73	0.61
1:A:112:THR:OG1	2:E:121:LEU:O	2.15	0.61
1:D:134:LEU:HD23	1:D:136:LEU:HD21	1.82	0.61
1:B:147:MET:HG2	1:B:419:LYS:HZ3	1.64	0.60
1:B:257:ILE:HG23	1:C:258:THR:HG22	1.84	0.60
1:B:98:LEU:O	1:C:112:THR:OG1	2.21	0.59
1:A:218:ARG:HD3	1:A:223:TYR:HE2	1.68	0.58
2:E:248:MET:HA	2:E:252:TYR:HD2	1.68	0.58
1:C:144:ASN:OD1	1:C:144:ASN:N	2.37	0.57
1:A:271:ARG:NH2	1:B:226:GLN:OE1	2.38	0.57
2:E:291:CYS:HA	2:E:311:LEU:HD13	1.85	0.57
1:D:257:ILE:HG21	2:E:282:PHE:CZ	2.40	0.57
1:A:109:HIS:HE2	1:A:133:THR:HG1	1.53	0.56
1:D:257:ILE:HG21	2:E:282:PHE:CE1	2.40	0.56
2:E:142:PHE:HB2	2:E:150:LEU:HB3	1.88	0.56
2:E:171:ASP:OD2	2:E:173:GLN:NE2	2.35	0.56
1:A:134:LEU:HD23	1:A:136:LEU:HD21	1.87	0.56
1:B:299:LEU:HD11	1:C:240:VAL:HG11	1.88	0.55
2:E:104:ASP:N	2:E:104:ASP:OD1	2.39	0.55
2:E:217:GLU:OE1	2:E:217:GLU:N	2.40	0.55
1:B:199:THR:H	1:B:209:CYS:HB3	1.72	0.54
1:C:44:PHE:HB3	1:C:63:PHE:HB2	1.90	0.54
1:A:246:MET:SD	1:A:246:MET:N	2.76	0.54
1:D:256:GLY:HA3	1:D:298:LEU:HD13	1.90	0.54
1:A:255:LEU:HD12	2:E:281:ILE:HD12	1.79	0.54
1:D:283:ILE:HD11	1:D:287:MET:HE2	1.88	0.54
1:D:417:ILE:HG12	1:D:422:ARG:HB3	1.89	0.54
2:E:108:VAL:HB	2:E:141:LEU:HD23	1.90	0.54
2:E:66:ILE:HD13	2:E:83:ILE:HG22	1.90	0.54
1:A:199:THR:H	1:A:209:CYS:HB3	1.73	0.54
2:E:139:ILE:HG12	2:E:153:MET:HG2	1.90	0.53
1:B:17:LEU:HG	1:B:18:MET:HG3	1.89	0.53
1:C:238:SER:HB3	1:C:259:THR:HG21	1.90	0.53
1:C:390:ASP:HA	1:C:393:LYS:HE3	1.89	0.53
1:D:111:VAL:O	1:D:112:THR:OG1	2.27	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:148:ASP:OD2	1:C:150:GLN:NE2	2.42	0.52
1:B:75:TYR:OH	1:B:81:ASP:O	2.28	0.52
1:D:266:GLN:HE21	1:D:287:MET:HE1	1.75	0.52
2:E:190:ARG:HA	2:E:232:THR:HG21	1.92	0.51
1:A:44:PHE:HD1	1:A:177:GLN:HG3	1.74	0.51
1:B:224:LEU:HD23	1:B:228:TYR:HD2	1.74	0.51
1:C:100:PHE:HB2	1:C:103:GLU:HG2	1.92	0.51
1:C:226:GLN:HG3	1:C:227:MET:HE3	1.92	0.51
2:E:82:ASN:OD1	2:E:154:ARG:NH1	2.44	0.50
1:C:219:GLN:HG2	1:C:221:GLY:H	1.76	0.50
1:C:386:LYS:C	1:C:388:PHE:H	2.19	0.50
2:E:101:ARG:HA	2:E:145:ARG:HH12	1.76	0.50
1:A:250:PRO:HA	1:A:253:VAL:HG12	1.93	0.50
1:B:27:ARG:HE	1:C:89:MET:HE1	1.77	0.49
2:E:244:VAL:HG22	2:E:248:MET:HB2	1.92	0.49
1:A:249:ALA:N	1:A:250:PRO:HD2	2.28	0.49
1:B:246:MET:N	1:B:246:MET:SD	2.85	0.49
1:D:144:ASN:N	1:D:144:ASN:OD1	2.45	0.49
1:B:111:VAL:HG12	1:B:112:THR:HG23	1.95	0.49
1:D:190:LYS:HE3	1:D:217:GLU:HG2	1.94	0.49
1:A:53:GLU:OE2	1:A:218:ARG:NH1	2.34	0.48
1:A:175:PRO:HG3	1:A:195:LEU:HD11	1.94	0.48
2:E:140:LEU:HB3	2:E:152:SER:OG	2.13	0.48
1:B:153:ILE:HG12	1:B:213:ARG:HD3	1.95	0.48
1:D:75:TYR:OH	1:D:81:ASP:O	2.31	0.48
1:C:48:PHE:HD1	1:C:184:LEU:HD11	1.78	0.48
1:A:15:ASP:HA	1:A:19:GLY:HA3	1.95	0.48
1:C:230:PRO:HB3	1:C:266:GLN:HE22	1.78	0.48
1:B:53:GLU:HG3	1:B:140:MET:HE1	1.96	0.48
1:D:257:ILE:HG21	2:E:282:PHE:CD1	2.49	0.47
2:E:121:LEU:HD11	2:E:179:LEU:HD23	1.97	0.47
1:D:90:LEU:HD13	1:D:128:TYR:HE1	1.80	0.47
1:A:75:TYR:OH	1:A:81:ASP:O	2.31	0.47
1:D:257:ILE:HG21	2:E:282:PHE:CE2	2.49	0.47
1:A:111:VAL:O	1:A:112:THR:OG1	2.33	0.47
1:A:111:VAL:HG12	1:A:112:THR:HG23	1.97	0.47
1:C:194:ASP:HB2	1:C:213:ARG:HB2	1.96	0.47
1:D:386:LYS:C	1:D:388:PHE:H	2.23	0.47
1:D:422:ARG:HG3	1:D:423:HIS:ND1	2.30	0.47
1:A:231:SER:OG	1:A:290:CYS:SG	2.73	0.47
1:C:111:VAL:HG12	1:C:112:THR:HG23	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:153:ILE:HG12	1:D:213:ARG:HD3	1.97	0.46
1:C:153:ILE:HG12	1:C:213:ARG:HD3	1.96	0.46
2:E:248:MET:O	2:E:252:TYR:HB2	2.15	0.46
1:A:255:LEU:HG	2:E:281:ILE:CD1	2.44	0.46
1:A:386:LYS:C	1:A:388:PHE:H	2.23	0.46
1:D:161:TYR:HB3	1:D:165:ASP:HB2	1.97	0.46
1:D:25:ASP:OD1	1:D:25:ASP:N	2.48	0.46
1:D:189:LEU:HD12	1:D:216:LEU:HD21	1.98	0.46
1:D:257:ILE:O	1:D:261:LEU:HG	2.16	0.46
1:A:144:ASN:N	1:A:144:ASN:OD1	2.49	0.45
1:C:98:LEU:O	1:D:112:THR:OG1	2.35	0.45
2:E:193:TRP:CZ2	2:E:236:VAL:HG23	2.51	0.45
1:A:234:ILE:HG21	1:A:263:MET:HG2	1.98	0.45
1:D:15:ASP:HA	1:D:19:GLY:HA3	1.98	0.45
2:E:133:ASP:N	2:E:133:ASP:OD1	2.49	0.45
2:E:50:ARG:NH1	2:E:52:ASN:O	2.49	0.45
2:E:171:ASP:OD1	2:E:171:ASP:N	2.50	0.45
1:C:228:TYR:O	1:C:231:SER:OG	2.29	0.45
1:D:98:LEU:O	2:E:135:THR:OG1	2.34	0.45
1:A:256:GLY:HA3	1:A:298:LEU:HD13	1.98	0.45
1:A:257:ILE:O	1:A:261:LEU:HG	2.17	0.45
2:E:253:ALA:HB3	2:E:254:PRO:HD3	1.99	0.45
2:E:298:LEU:H	2:E:298:LEU:HD12	1.82	0.44
1:C:98:LEU:HD21	1:C:156:LEU:HD23	2.00	0.44
1:C:90:LEU:HD23	1:C:93:ILE:HD11	2.00	0.44
1:A:87:PRO:HB3	1:A:116:LYS:HB2	1.99	0.44
1:B:252:ARG:HE	1:B:252:ARG:HB3	1.70	0.44
1:A:24:TYR:HE2	1:A:93:ILE:HA	1.83	0.44
1:A:98:LEU:O	1:B:112:THR:OG1	2.35	0.44
1:A:210:ILE:HD13	1:A:210:ILE:HA	1.85	0.44
1:B:295:PHE:CZ	1:C:237:LEU:HD22	2.53	0.44
1:C:111:VAL:O	1:C:112:THR:OG1	2.31	0.44
1:D:391:ARG:O	1:D:394:LYS:HG2	2.18	0.44
2:E:86:ARG:NE	4:E:502:GLY:OXT	2.39	0.44
1:B:305:ASN:OD1	1:C:248:ALA:HB1	2.17	0.44
1:C:409:ILE:HA	1:C:412:ILE:HG22	1.99	0.44
1:A:90:LEU:HD21	1:A:118:LEU:HB2	2.00	0.43
1:B:210:ILE:HD13	1:B:210:ILE:HA	1.88	0.43
1:B:111:VAL:O	1:B:112:THR:OG1	2.28	0.43
1:B:99:PHE:CD1	1:B:159:PHE:HB2	2.54	0.43
1:C:31:ASN:OD1	1:C:31:ASN:N	2.50	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:90:LEU:HD21	1:B:118:LEU:HD13	2.00	0.43
1:D:102:ASN:ND2	1:D:153:ILE:O	2.51	0.43
2:E:134:VAL:C	2:E:136:GLN:H	2.27	0.43
1:D:257:ILE:CG2	2:E:282:PHE:CD1	3.02	0.43
2:E:298:LEU:HD22	2:E:305:LYS:HE3	2.00	0.43
1:C:28:ILE:HD13	1:D:10:PRO:HG2	2.01	0.43
2:E:108:VAL:HG11	2:E:112:MET:HE2	2.01	0.43
1:D:246:MET:HE3	1:D:304:VAL:HG12	1.99	0.42
2:E:275:ALA:C	2:E:278:PRO:HD2	2.43	0.42
2:E:277:VAL:HG22	2:E:325:TYR:CE2	2.53	0.42
1:D:235:VAL:HG11	1:D:407:PHE:CZ	2.55	0.42
1:C:209:CYS:SG	1:C:210:ILE:N	2.93	0.42
1:C:78:TYR:HB3	1:C:80:ASP:OD1	2.20	0.42
2:E:320:ALA:HA	2:E:323:VAL:HG12	2.02	0.42
1:B:194:ASP:HB2	1:B:213:ARG:HB2	2.02	0.42
1:B:306:PHE:HB2	1:C:244:ILE:HG23	2.02	0.42
2:E:178:GLN:HA	2:E:235:GLU:HA	2.01	0.42
1:A:403:PHE:HD1	1:A:403:PHE:HA	1.69	0.42
1:C:224:LEU:HD12	1:C:228:TYR:HD2	1.83	0.42
1:D:16:LYS:HE3	1:D:16:LYS:HB3	1.87	0.42
1:D:203:ASN:ND2	2:E:200:GLN:HE22	2.18	0.42
1:D:111:VAL:C	1:D:113:THR:H	2.27	0.41
2:E:222:THR:N	2:E:233:CYS:SG	2.92	0.41
1:A:232:LEU:O	1:A:236:ILE:HG12	2.20	0.41
1:B:111:VAL:C	1:B:113:THR:H	2.28	0.41
1:C:25:ASP:OD1	1:C:25:ASP:N	2.50	0.41
1:D:199:THR:N	1:D:209:CYS:HB3	2.32	0.41
1:A:220:MET:SD	1:A:220:MET:N	2.81	0.41
1:B:250:PRO:HA	1:B:253:VAL:HG12	2.02	0.41
1:B:295:PHE:CE2	1:C:237:LEU:HD22	2.55	0.41
1:A:227:MET:SD	1:A:270:SER:OG	2.67	0.41
1:C:210:ILE:HD13	1:C:210:ILE:HA	1.88	0.41
2:E:278:PRO:CB	2:E:282:PHE:CE2	2.95	0.41
1:A:29:ARG:NH1	1:A:31:ASN:O	2.53	0.41
1:D:210:ILE:HD13	1:D:210:ILE:HA	1.92	0.41
1:C:232:LEU:O	1:C:235:VAL:HG12	2.20	0.41
1:A:80:ASP:N	1:A:80:ASP:OD1	2.52	0.41
1:B:257:ILE:H	1:B:257:ILE:HG13	1.61	0.41
1:C:99:PHE:CD1	1:C:159:PHE:HB2	2.56	0.41
1:C:236:ILE:O	1:C:240:VAL:HG23	2.21	0.41
1:D:103:GLU:HG2	1:D:105:GLY:H	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:40:ARG:H	2:E:43:VAL:HG12	1.85	0.41
1:B:163:MET:SD	1:B:206:LYS:HE2	2.61	0.40
1:B:163:MET:HE2	1:B:163:MET:HB3	1.97	0.40
1:B:184:LEU:HD13	1:B:185:PRO:HD2	2.02	0.40
1:C:33:LYS:HE3	1:D:80:ASP:OD2	2.21	0.40
1:A:239:TRP:CH2	1:A:404:PRO:HA	2.57	0.40
1:D:417:ILE:HG12	1:D:422:ARG:HD2	2.04	0.40
1:A:30:PRO:HB3	1:A:70:ASP:HB2	2.02	0.40
1:A:293:PHE:HE2	1:A:407:PHE:HA	1.86	0.40
1:B:199:THR:N	1:B:209:CYS:HB3	2.35	0.40
2:E:88:LYS:HE3	2:E:88:LYS:HB2	1.91	0.40
1:B:24:TYR:HE2	1:B:93:ILE:HA	1.86	0.40
1:B:403:PHE:HD1	1:B:403:PHE:HA	1.75	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	340/422 (81%)	330 (97%)	9 (3%)	1 (0%)	37	67
1	B	336/422 (80%)	325 (97%)	10 (3%)	1 (0%)	37	67
1	C	336/422 (80%)	327 (97%)	8 (2%)	1 (0%)	37	67
1	D	340/422 (81%)	329 (97%)	10 (3%)	1 (0%)	37	67
2	E	332/680 (49%)	312 (94%)	20 (6%)	0	100	100
All	All	1684/2368 (71%)	1623 (96%)	57 (3%)	4 (0%)	45	73

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	387	VAL

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Mol	Chain	Res	Type
1	B	387	VAL
1	C	387	VAL
1	D	387	VAL

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	302/381 (79%)	292 (97%)	10 (3%)	33	61
1	B	299/381 (78%)	286 (96%)	13 (4%)	25	54
1	C	299/381 (78%)	290 (97%)	9 (3%)	36	63
1	D	303/381 (80%)	296 (98%)	7 (2%)	45	68
2	E	289/598 (48%)	275 (95%)	14 (5%)	21	51
All	All	1492/2122 (70%)	1439 (96%)	53 (4%)	32	59

All (53) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	37	VAL
1	A	55	THR
1	A	90	LEU
1	A	188	LEU
1	A	198	CYS
1	A	210	ILE
1	A	258	THR
1	A	387	VAL
1	A	403	PHE
1	A	418	TYR
1	B	37	VAL
1	B	55	THR
1	B	109	HIS
1	B	144	ASN
1	B	198	CYS
1	B	210	ILE

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Mol	Chain	Res	Type
1	B	237	LEU
1	B	252	ARG
1	B	259	THR
1	B	277	VAL
1	B	293	PHE
1	B	387	VAL
1	B	403	PHE
1	C	31	ASN
1	C	55	THR
1	C	133	THR
1	C	144	ASN
1	C	189	LEU
1	C	198	CYS
1	C	219	GLN
1	C	387	VAL
1	C	403	PHE
1	D	55	THR
1	D	111	VAL
1	D	189	LEU
1	D	198	CYS
1	D	293	PHE
1	D	387	VAL
1	D	418	TYR
2	E	76	THR
2	E	126	GLU
2	E	134	VAL
2	E	167	LEU
2	E	211	ILE
2	E	236	VAL
2	E	244	VAL
2	E	251	VAL
2	E	277	VAL
2	E	298	LEU
2	E	304	VAL
2	E	317	PHE
2	E	324	GLU
2	E	459	PHE

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

Mol	Chain	Res	Type
1	A	171	GLN

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Mol	Chain	Res	Type
1	B	144	ASN
1	C	201	HIS
1	C	203	ASN
1	D	177	GLN
1	D	186	GLN
2	E	200	GLN
2	E	467	ASN

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 ⓘ

8 ligands are modelled in this entry.

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	$\# Z > 2$
3	NAG	B	501	1	14,14,15	0.69	0	17,19,21	1.94	3 (17%)
3	NAG	D	501	1	14,14,15	0.68	0	17,19,21	1.68	3 (17%)
3	NAG	A	501	1	14,14,15	0.67	0	17,19,21	1.75	2 (11%)
4	GLY	A	502	-	4,4,4	1.18	1 (25%)	3,4,4	1.67	1 (33%)
4	GLY	E	502	-	4,4,4	1.19	1 (25%)	3,4,4	1.61	1 (33%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	NAG	C	501	1	14,14,15	0.69	0	17,19,21	1.97	2 (11%)
4	GLY	C	502	-	4,4,4	1.18	1 (25%)	3,4,4	1.62	1 (33%)
3	NAG	E	501	2	14,14,15	0.70	0	17,19,21	0.96	1 (5%)

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
3	NAG	B	501	1	-	2/6/23/26	0/1/1/1
3	NAG	D	501	1	-	2/6/23/26	0/1/1/1
3	NAG	A	501	1	-	2/6/23/26	0/1/1/1
4	GLY	A	502	-	-	0/2/2/2	-
4	GLY	E	502	-	-	0/2/2/2	-
3	NAG	C	501	1	-	2/6/23/26	0/1/1/1
4	GLY	C	502	-	-	2/2/2/2	-
3	NAG	E	501	2	-	1/6/23/26	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	E	502	GLY	OXT-C	-2.27	1.23	1.30
4	C	502	GLY	OXT-C	-2.25	1.23	1.30
4	A	502	GLY	OXT-C	-2.24	1.23	1.30

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	501	NAG	C2-N2-C7	6.70	131.88	122.90
3	B	501	NAG	C2-N2-C7	6.34	131.39	122.90
3	A	501	NAG	C2-N2-C7	5.54	130.33	122.90
3	D	501	NAG	C2-N2-C7	5.16	129.81	122.90
3	E	501	NAG	O5-C1-C2	-2.77	107.00	111.29
3	C	501	NAG	O7-C7-N2	2.55	126.49	121.98
3	B	501	NAG	O7-C7-N2	2.50	126.40	121.98
3	D	501	NAG	O5-C1-C2	-2.27	107.78	111.29
3	B	501	NAG	C1-O5-C5	2.27	115.22	112.19
3	A	501	NAG	O7-C7-N2	2.20	125.86	121.98
4	A	502	GLY	OXT-C-O	-2.14	117.83	123.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	501	NAG	O7-C7-N2	2.10	125.68	121.98
4	C	502	GLY	OXT-C-O	-2.07	118.02	123.33
4	E	502	GLY	OXT-C-O	-2.06	118.04	123.33

There are no chirality outliers.

All (11) torsion outliers are listed below:

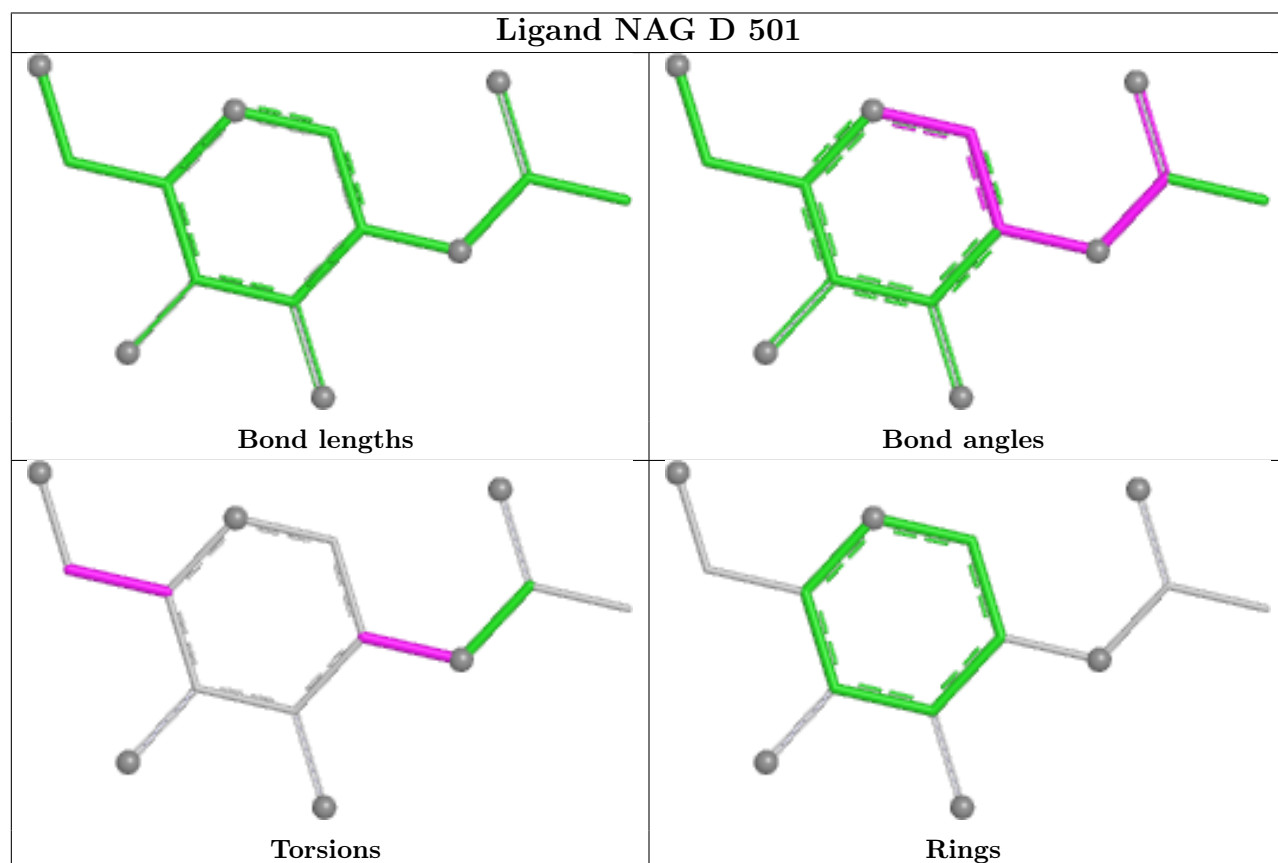
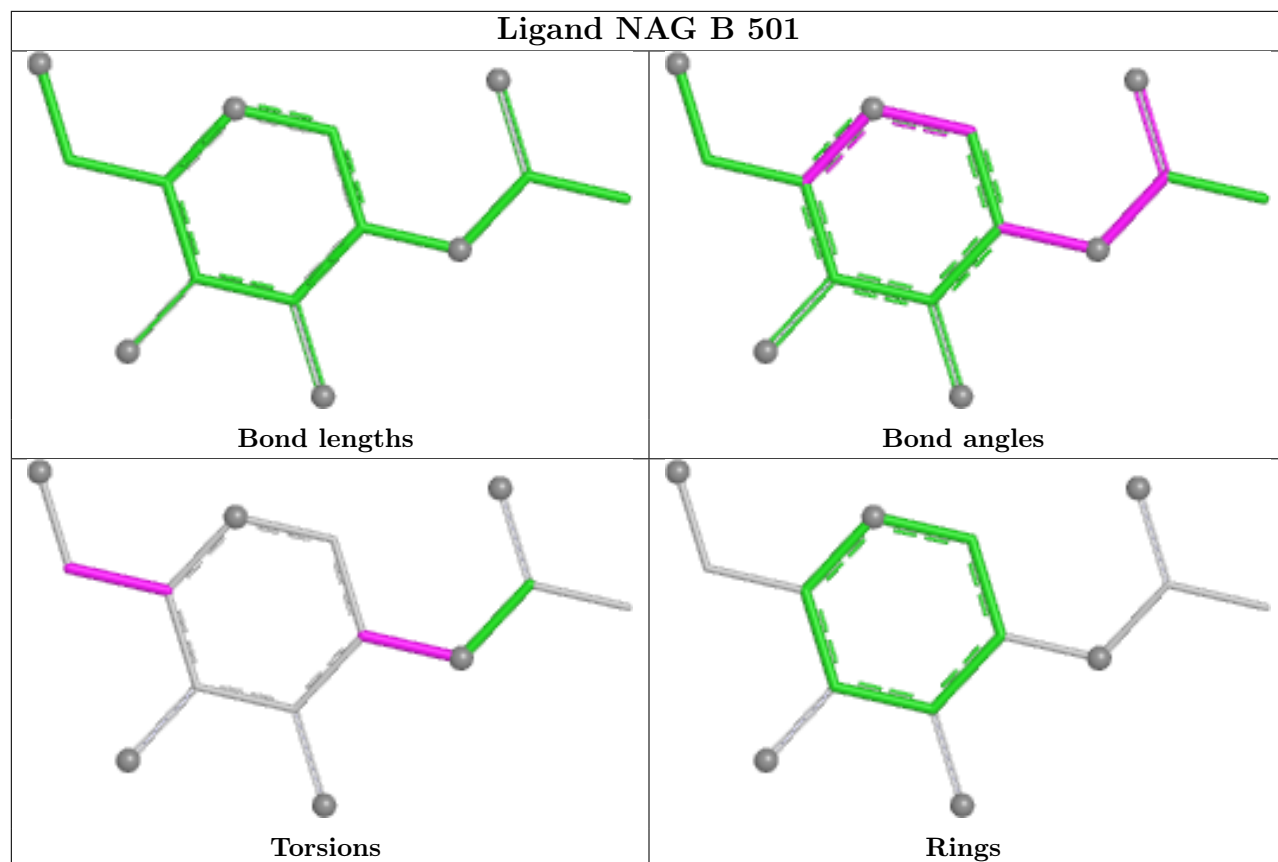
Mol	Chain	Res	Type	Atoms
3	A	501	NAG	C3-C2-N2-C7
3	B	501	NAG	C3-C2-N2-C7
3	C	501	NAG	C3-C2-N2-C7
3	D	501	NAG	C3-C2-N2-C7
3	E	501	NAG	O5-C5-C6-O6
3	A	501	NAG	O5-C5-C6-O6
3	D	501	NAG	O5-C5-C6-O6
3	B	501	NAG	O5-C5-C6-O6
3	C	501	NAG	O5-C5-C6-O6
4	C	502	GLY	OXT-C-CA-N
4	C	502	GLY	O-C-CA-N

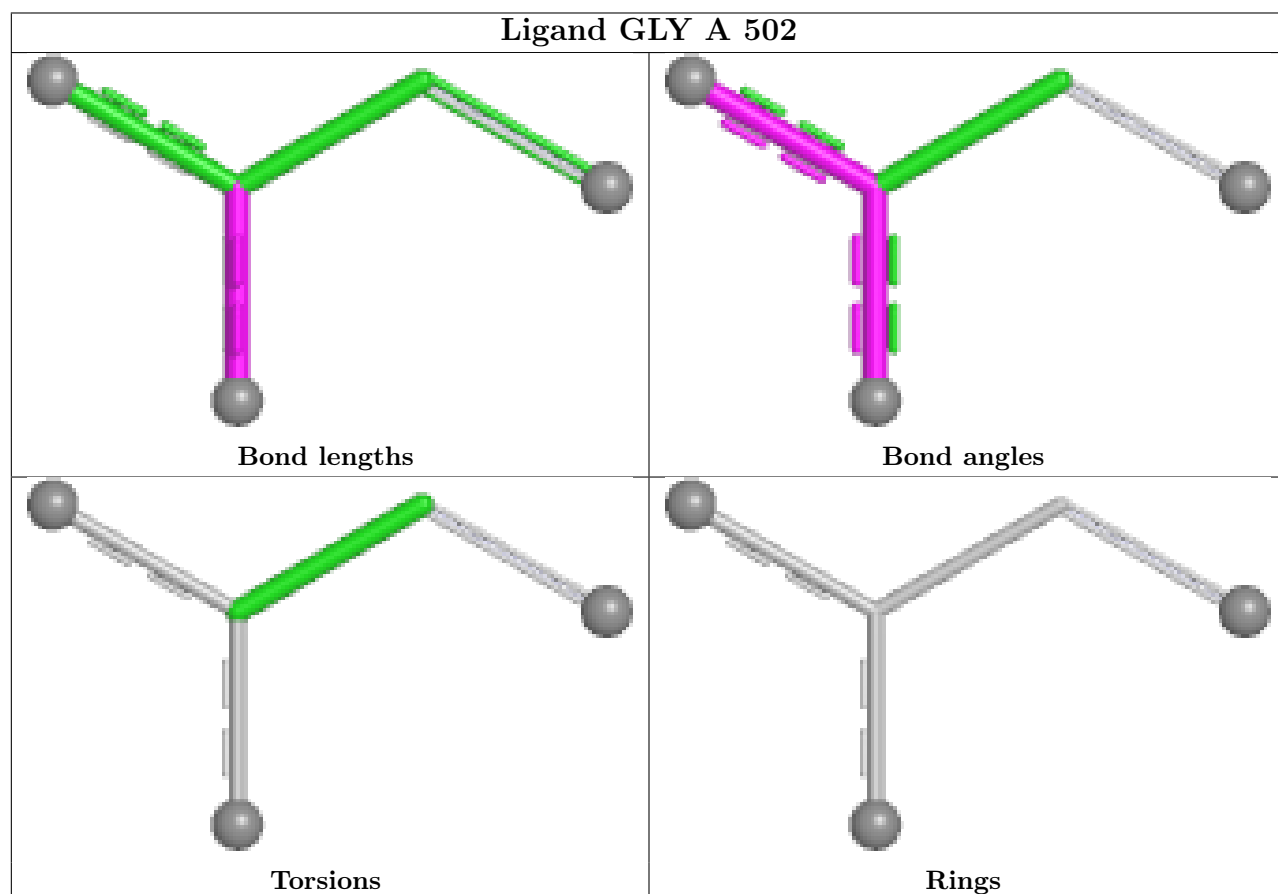
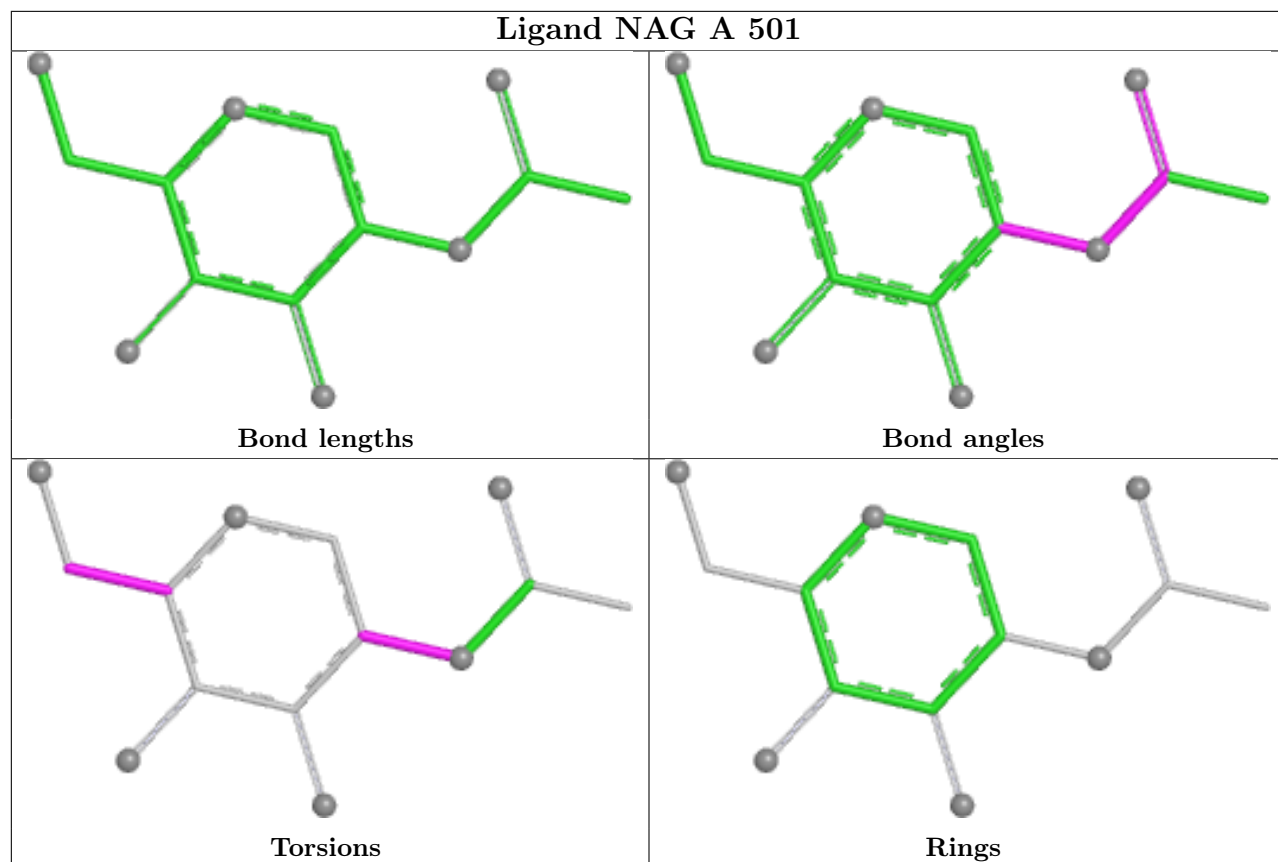
There are no ring outliers.

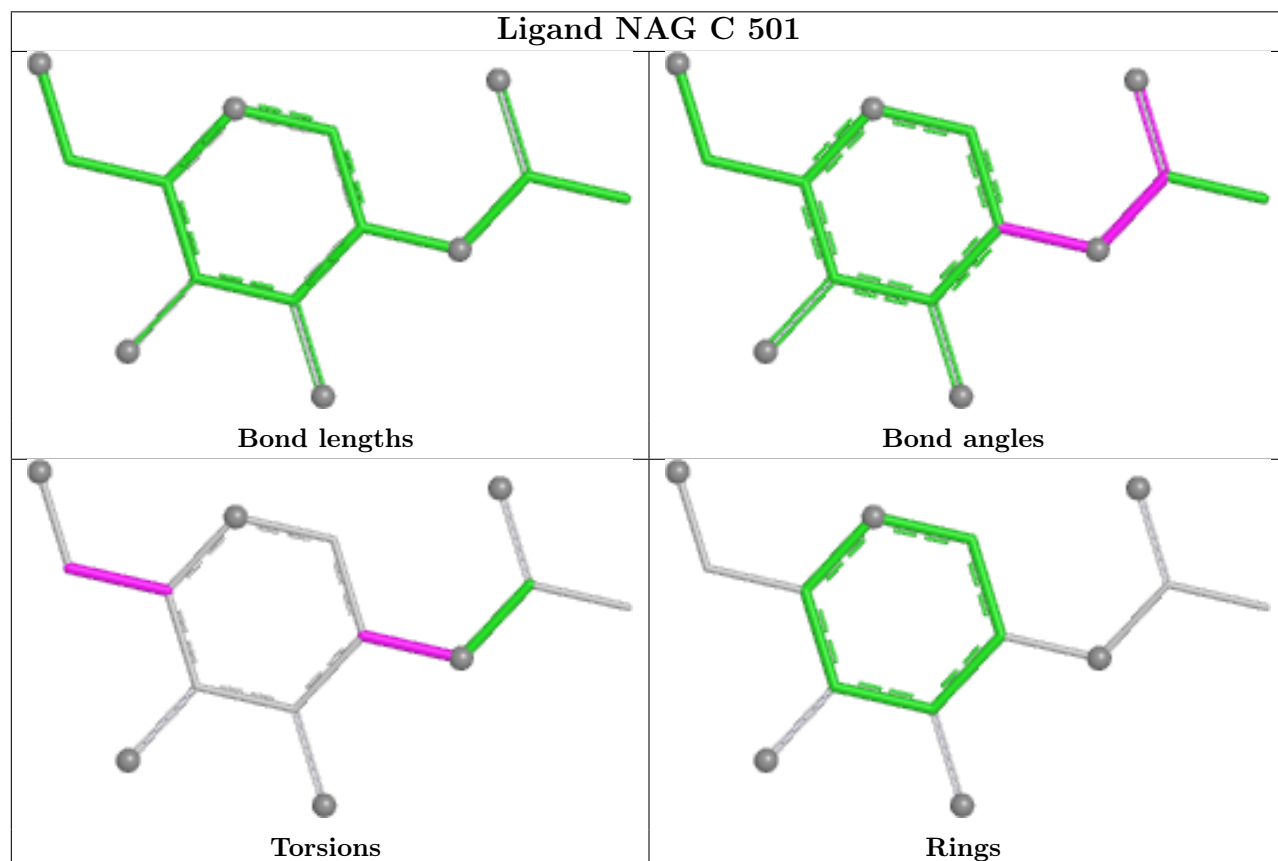
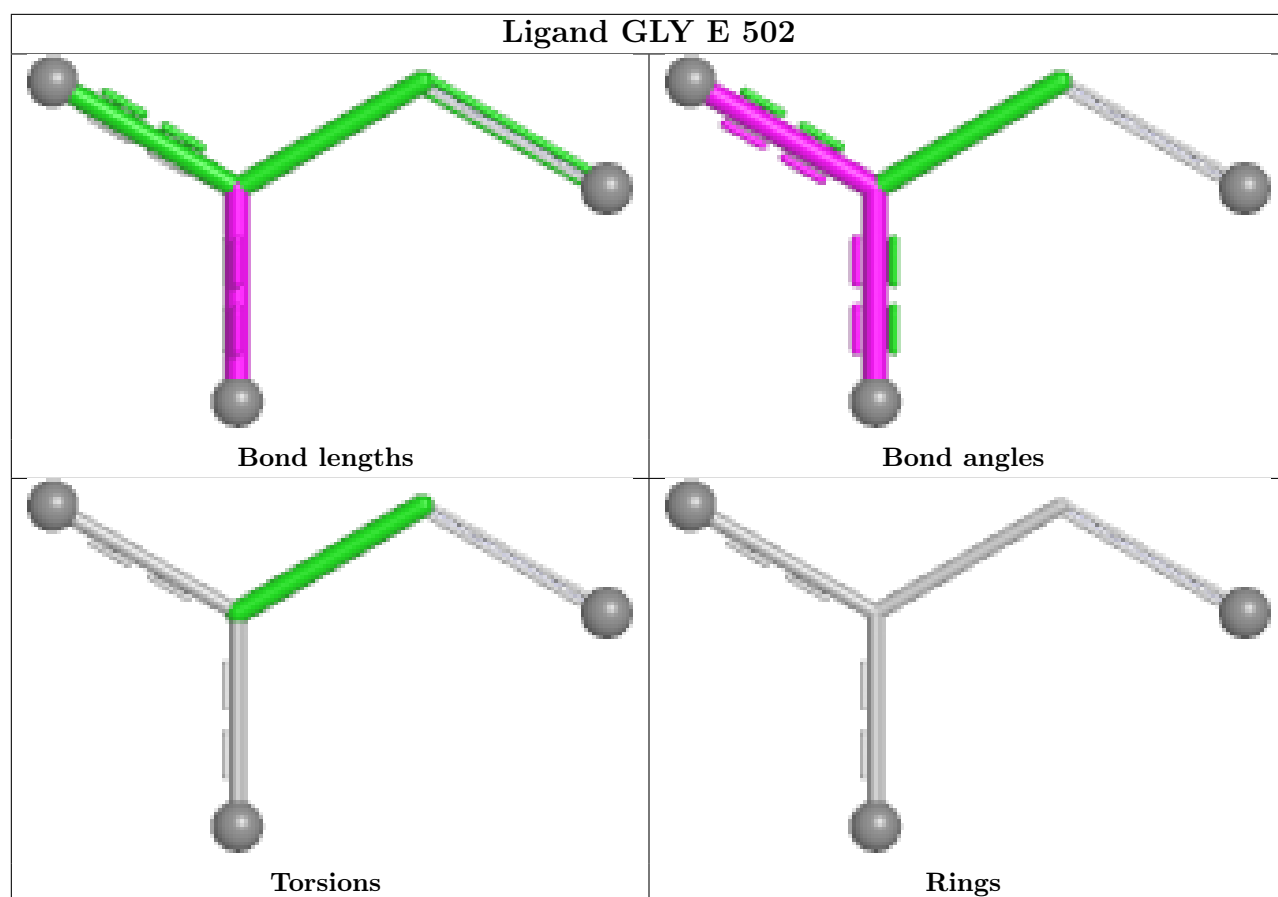
1 monomer is involved in 1 short contact:

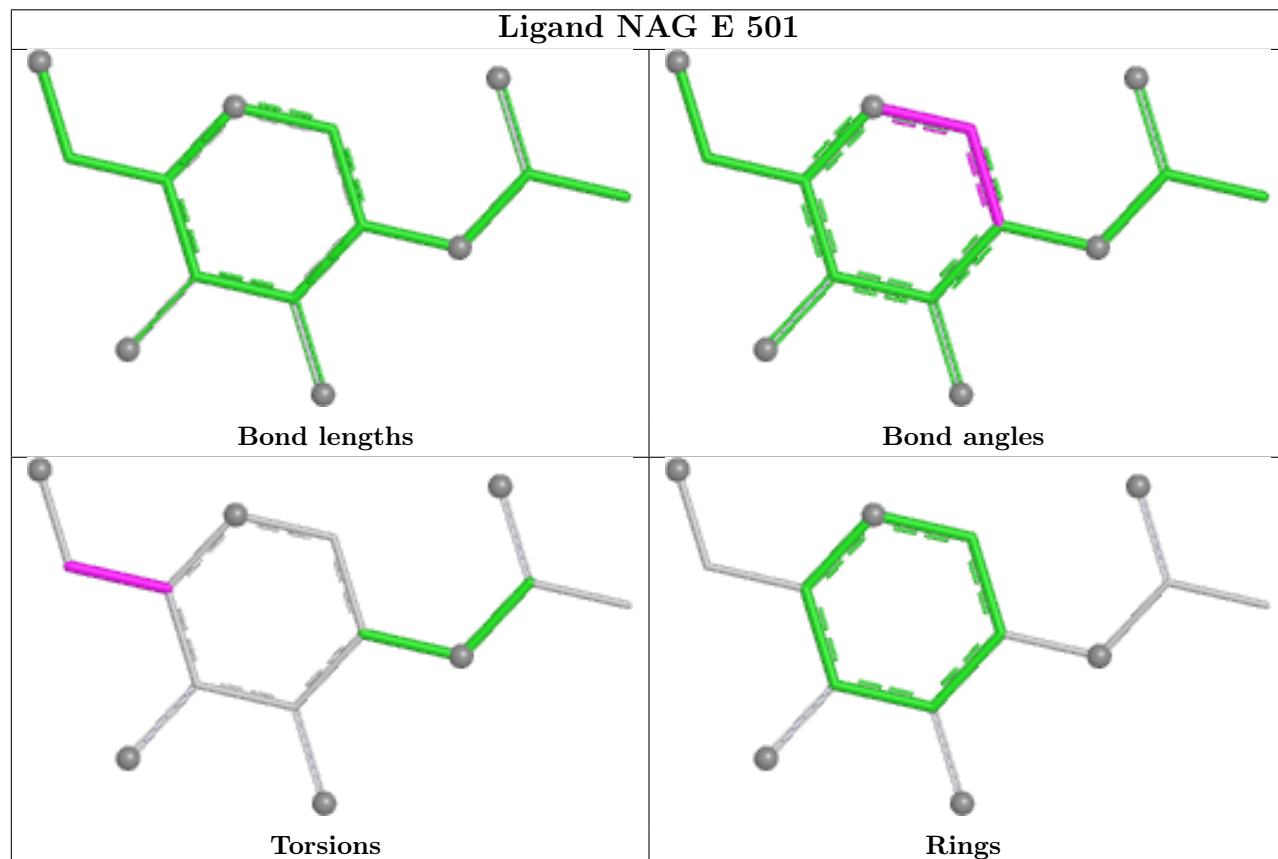
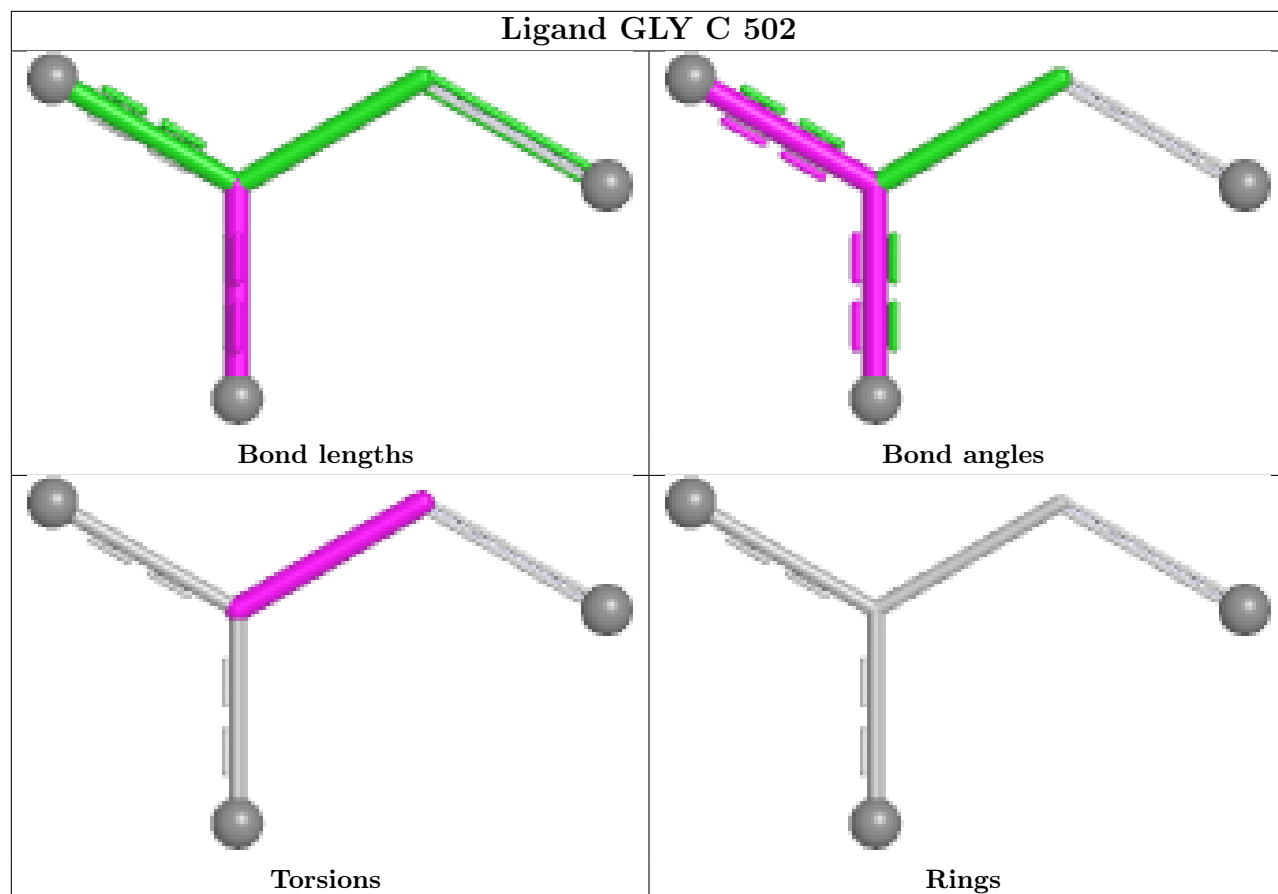
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	E	502	GLY	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.









5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

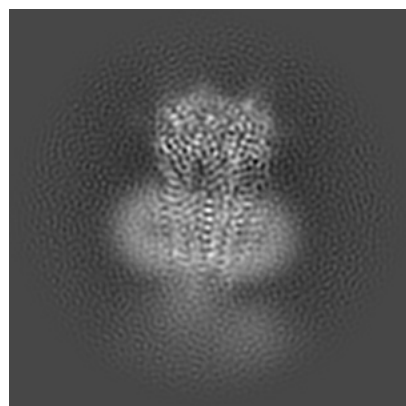
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-44763. These allow visual inspection of the internal detail of the map and identification of artifacts.

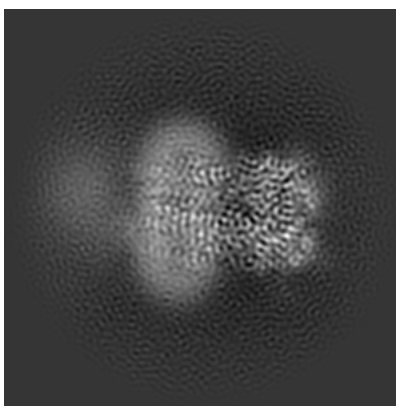
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

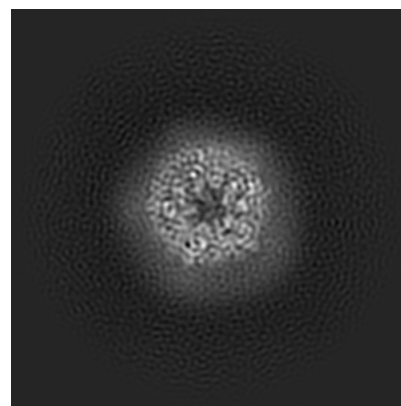
6.1.1 Primary map



X

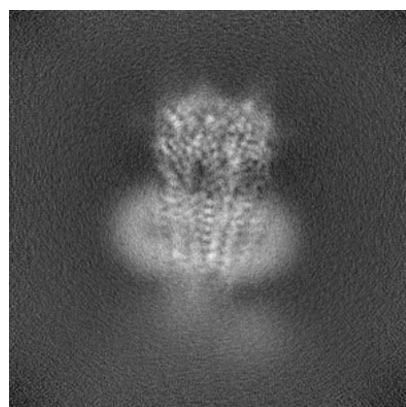


Y

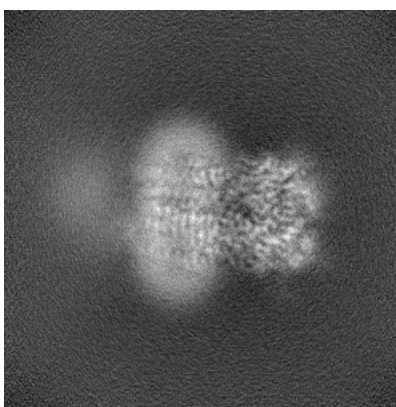


Z

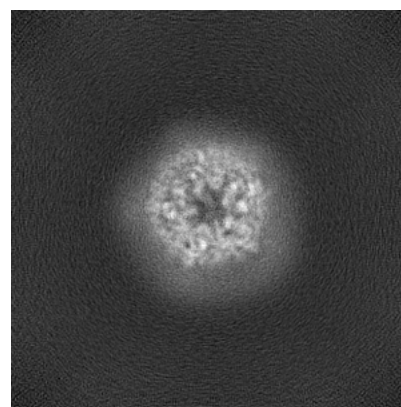
6.1.2 Raw map



X



Y

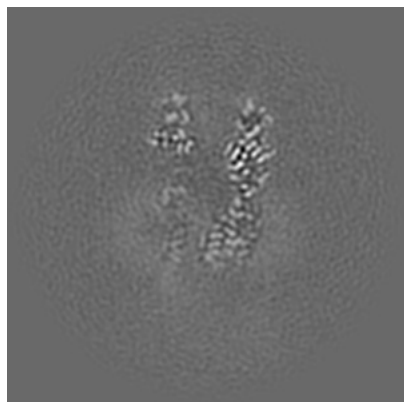


Z

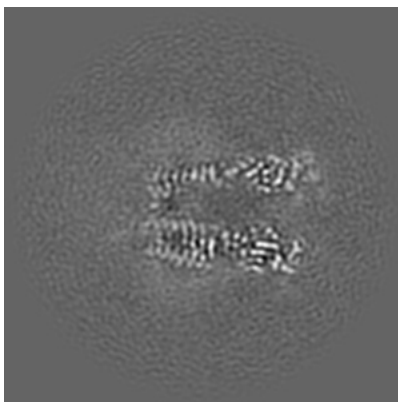
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

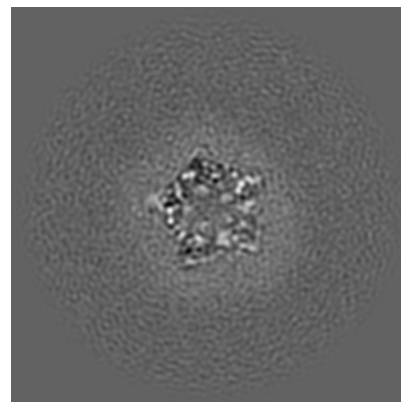
6.2.1 Primary map



X Index: 144

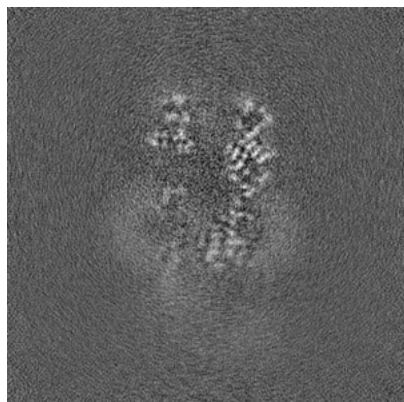


Y Index: 144

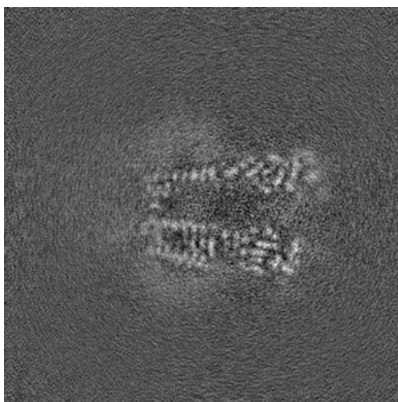


Z Index: 144

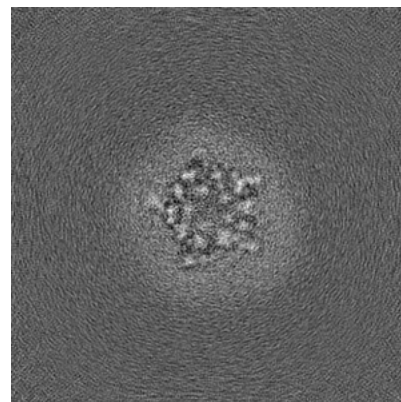
6.2.2 Raw map



X Index: 144



Y Index: 144

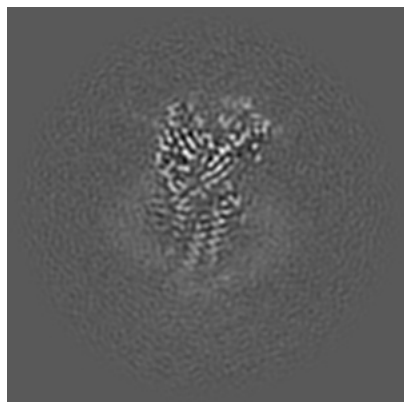


Z Index: 144

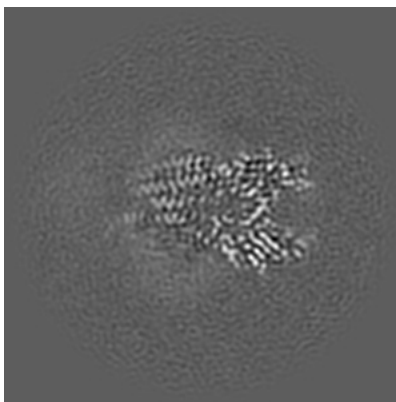
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

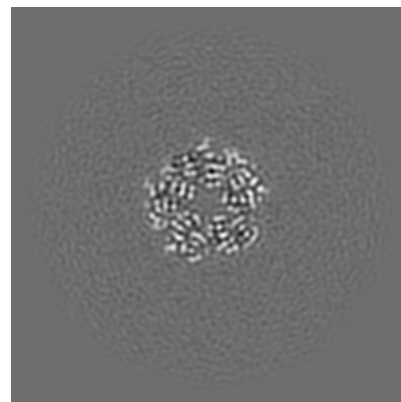
6.3.1 Primary map



X Index: 123

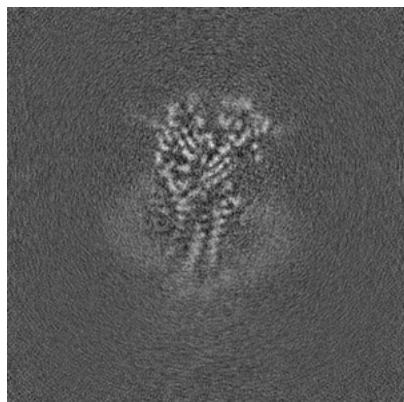


Y Index: 159

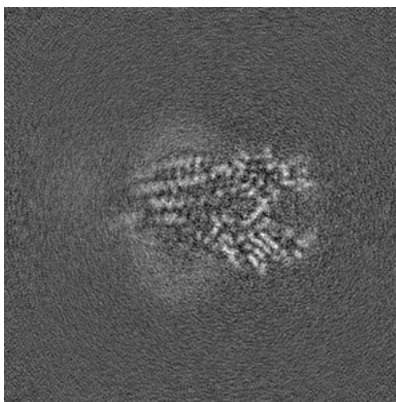


Z Index: 185

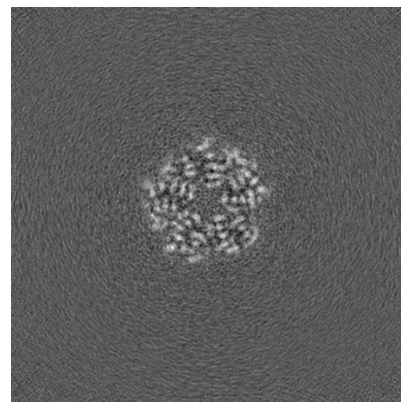
6.3.2 Raw map



X Index: 123



Y Index: 159

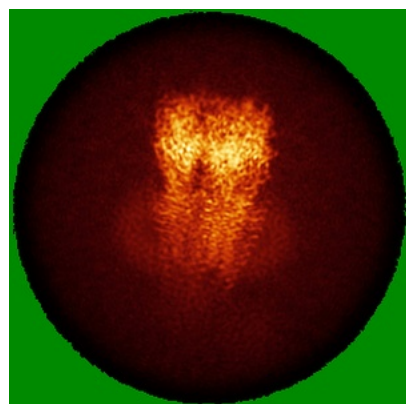


Z Index: 185

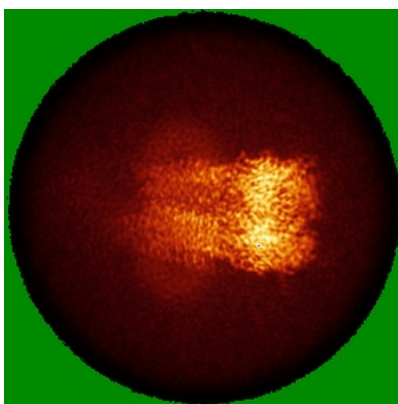
The images above show the largest variance slices of the map in three orthogonal directions.

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

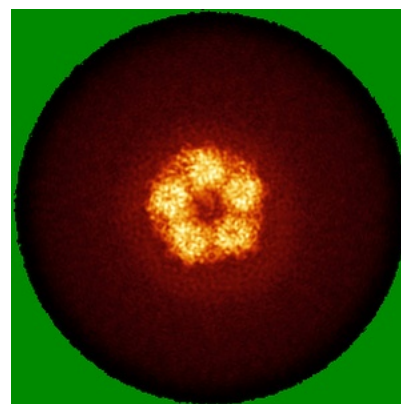
6.4.1 Primary map



X

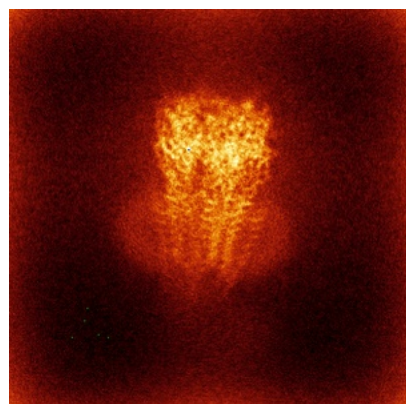


Y

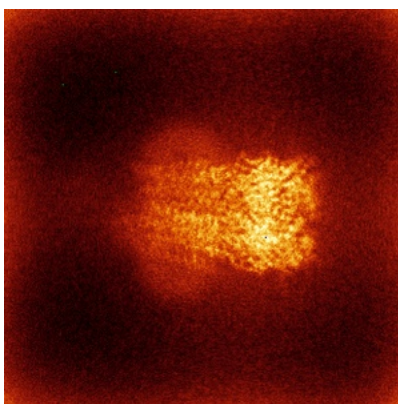


Z

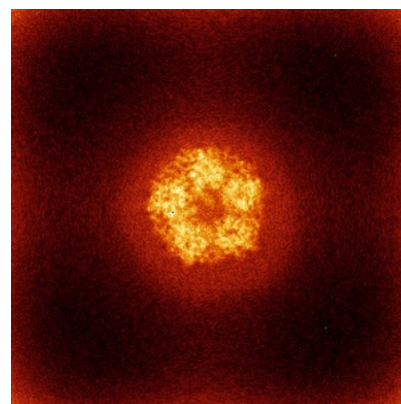
6.4.2 Raw map



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.

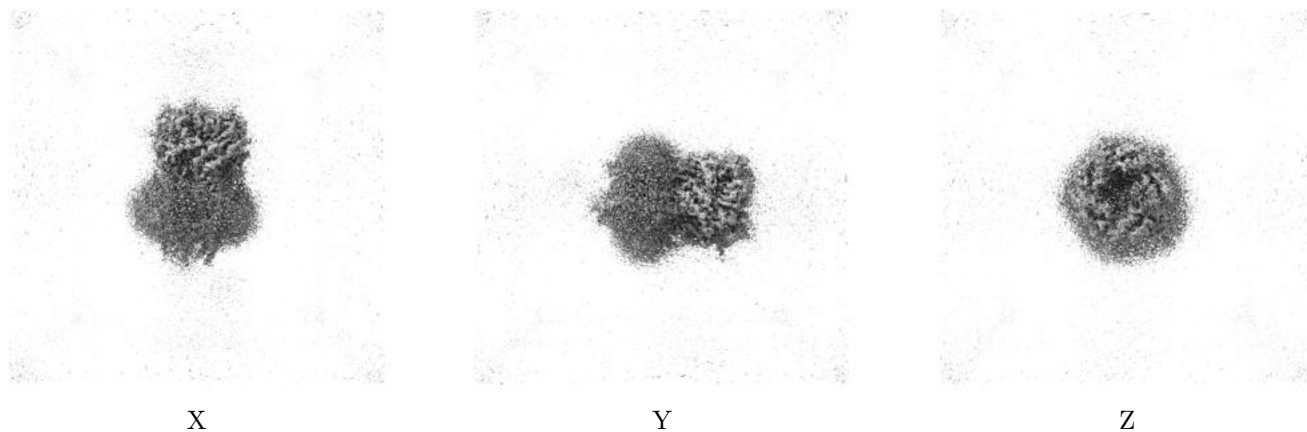
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.36. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

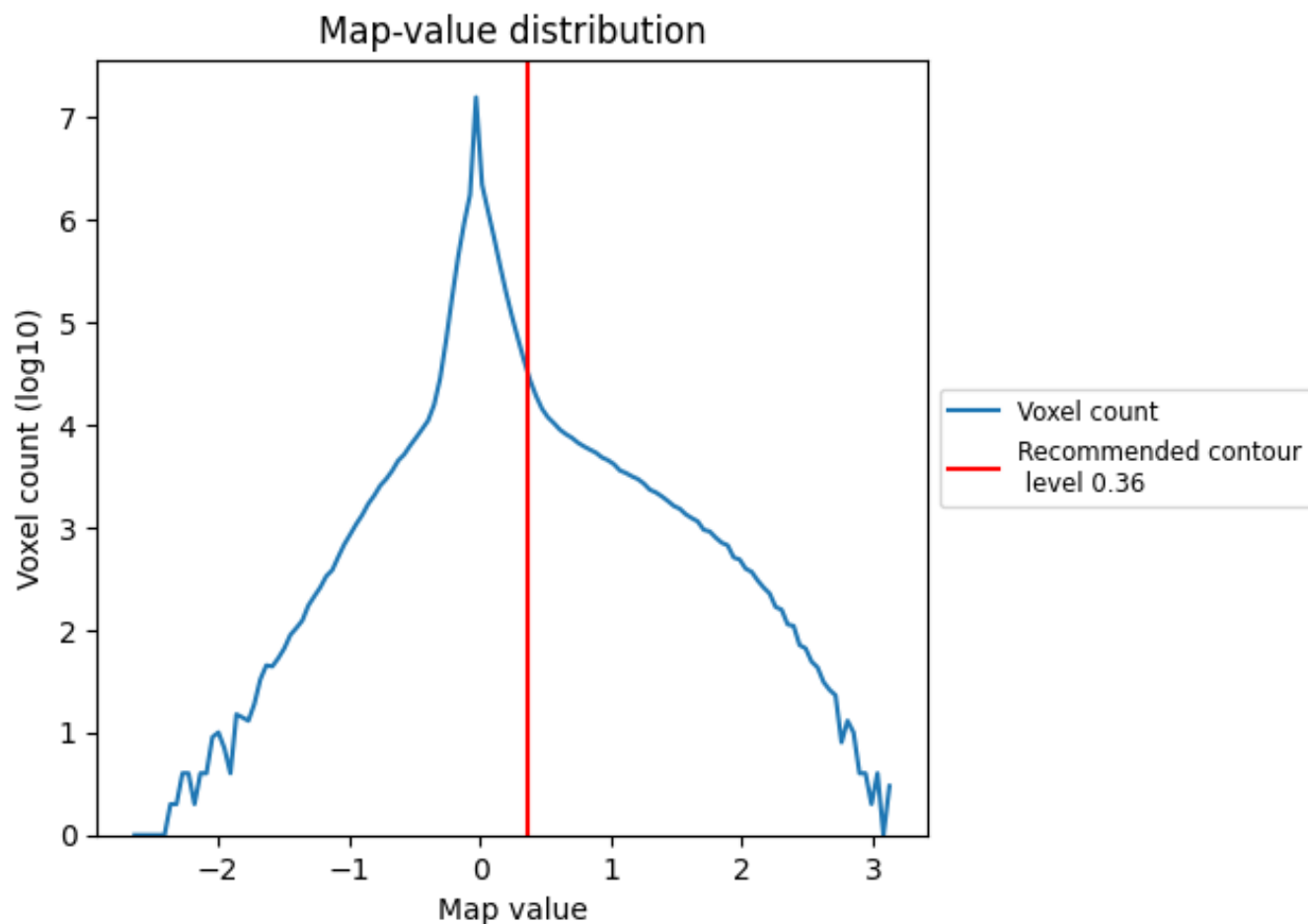
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

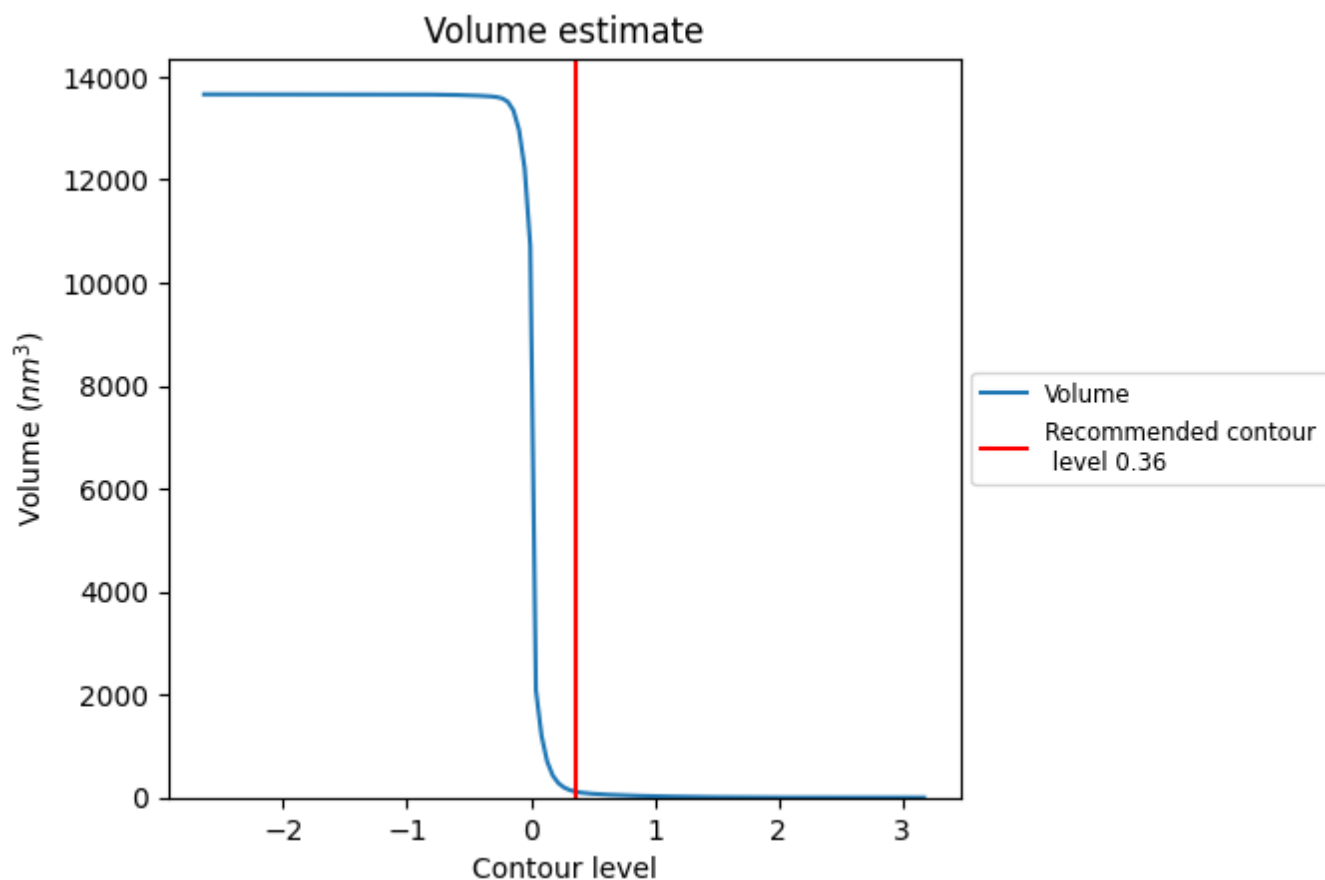
This section contains the results of statistical analysis of the map.

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.

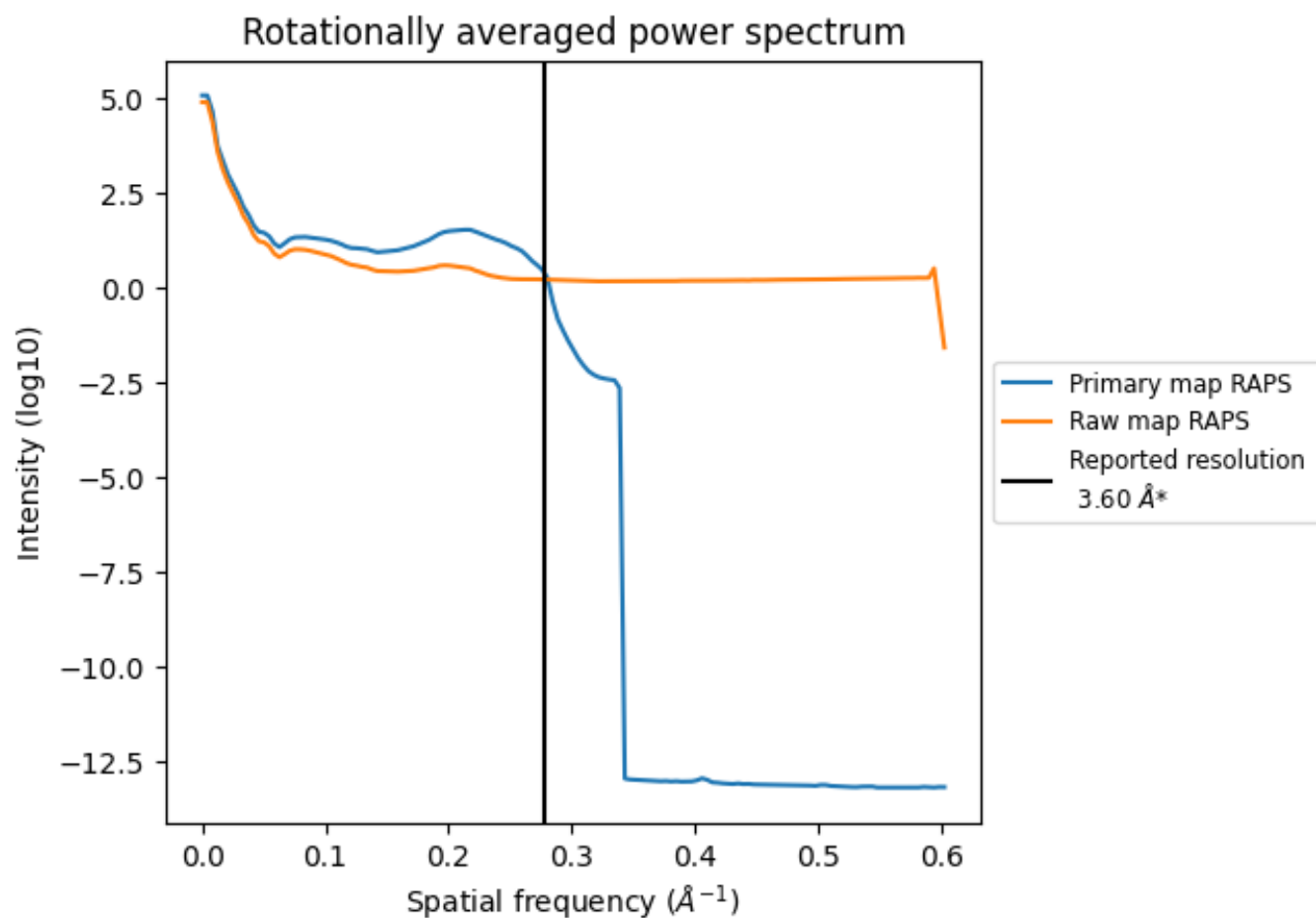
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 115 nm³; this corresponds to an approximate mass of 104 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 ⓘ

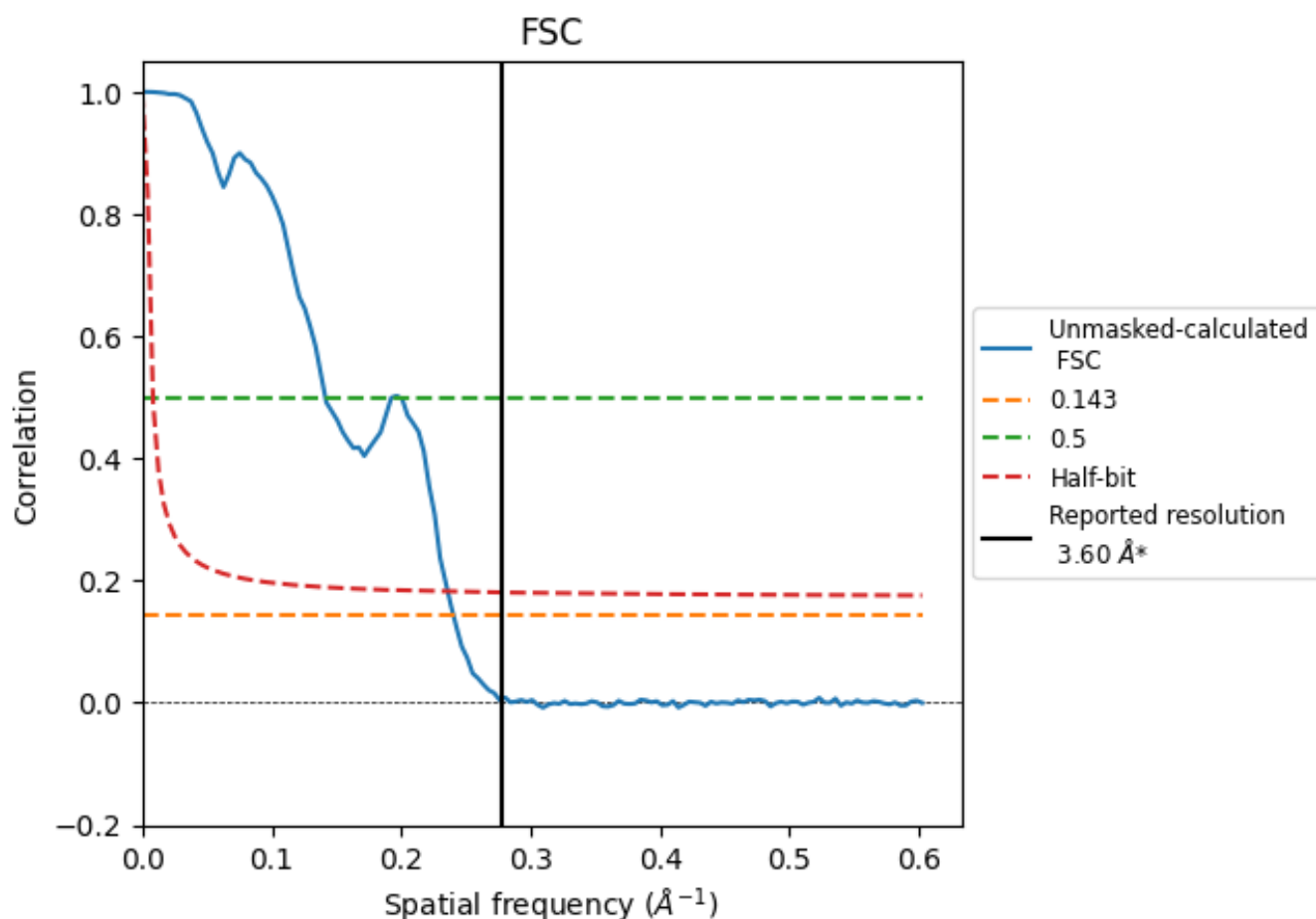


*Reported resolution corresponds to spatial frequency of 0.278 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.278 \AA^{-1}

8.2 Resolution estimates [i](#)

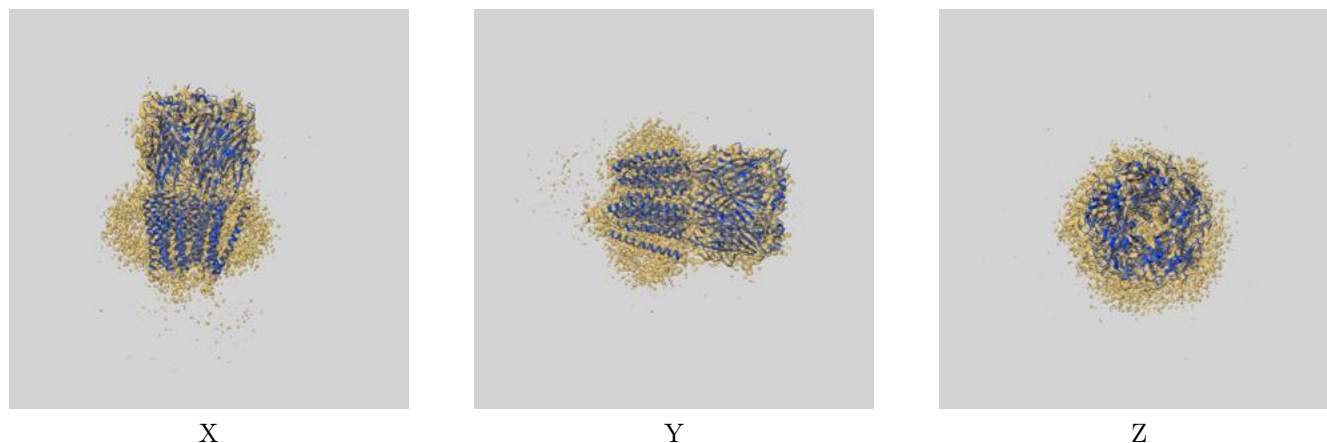
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.60	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.16	7.07	4.24

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.16 differs from the reported value 3.6 by more than 10 %

9 Map-model fit [i](#)

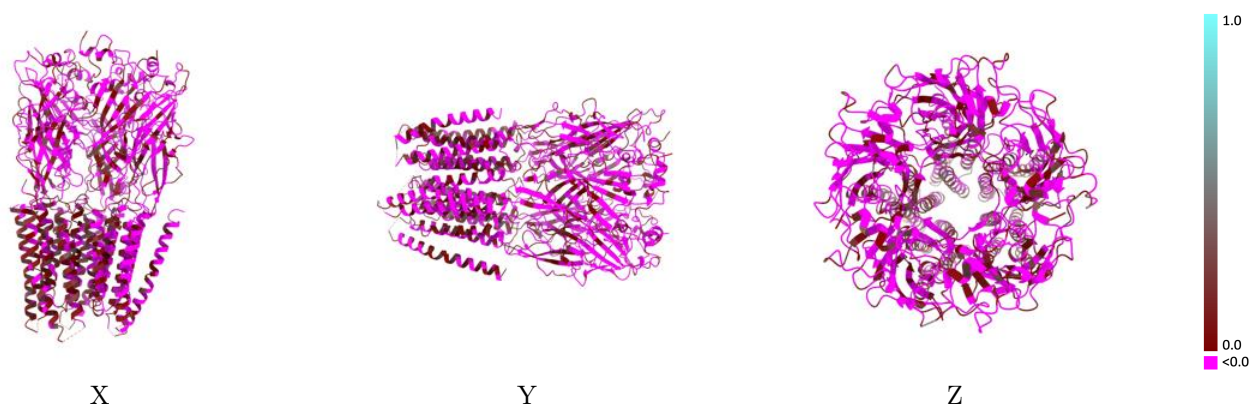
This section contains information regarding the fit between EMDB map EMD-44763 and PDB model 9BP7. Per-residue inclusion information can be found in section [3](#) on page [8](#).

9.1 Map-model overlay [i](#)



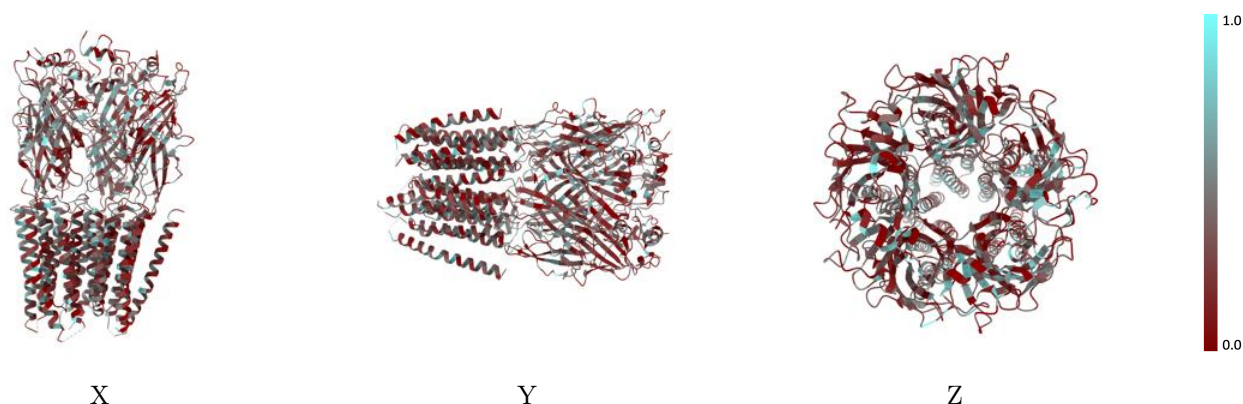
The images above show the 3D surface view of the map at the recommended contour level 0.36 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



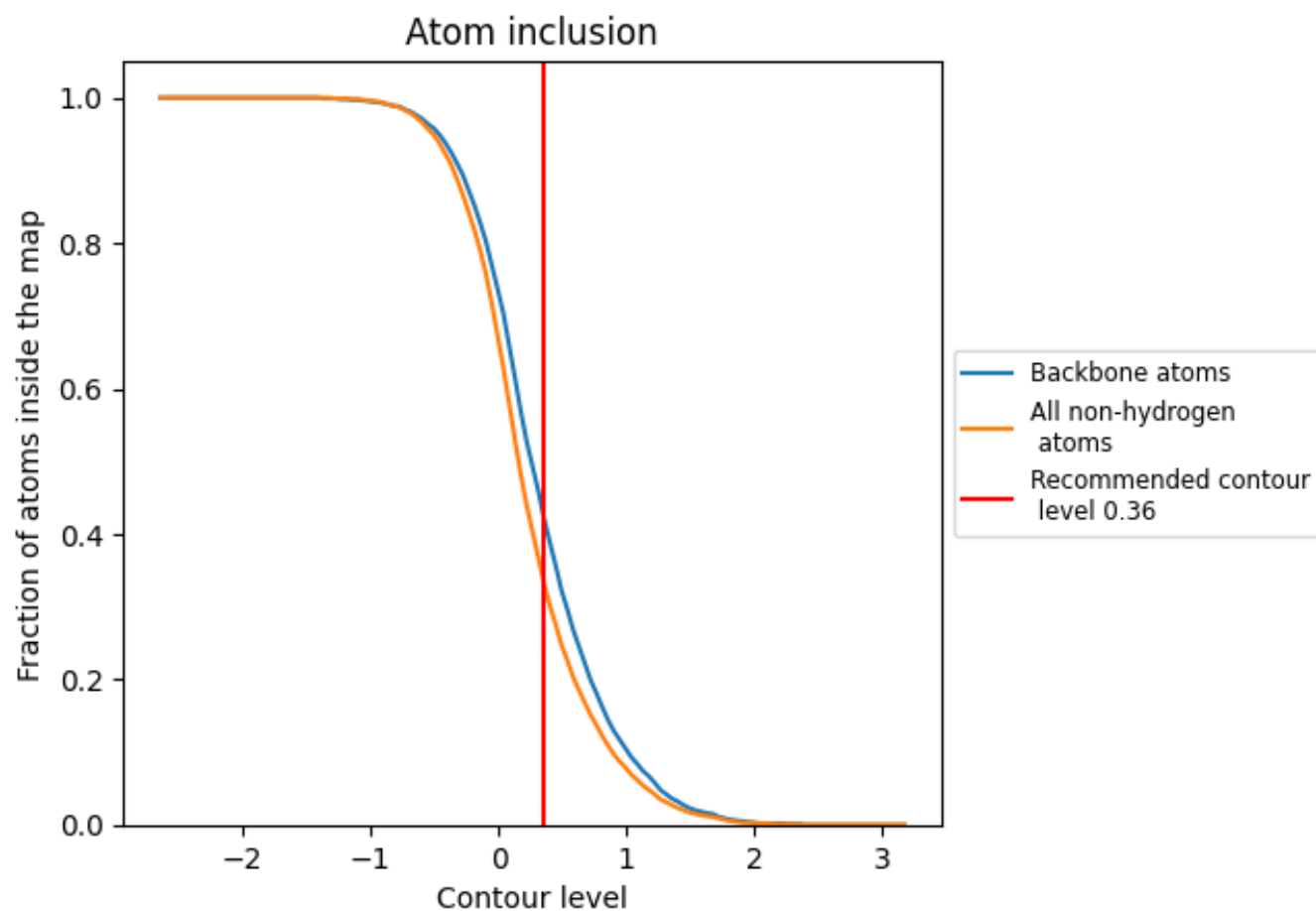
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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



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 (0.36).

9.4 Atom inclusion [i](#)



At the recommended contour level, 42% of all backbone atoms, 33% 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 (0.36) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.3300	<div></div> -0.0290
A	<div></div> 0.3260	<div></div> -0.0520
B	<div></div> 0.3300	<div></div> -0.0440
C	<div></div> 0.3310	<div></div> -0.0100
D	<div></div> 0.3280	<div></div> -0.0070
E	<div></div> 0.3360	<div></div> -0.0350

