



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 08:15 PM UTC

PDB ID : 8WPU / pdb_00008wpu
EMDB ID : EMD-37724
Title : Human calcium-sensing receptor(CaSR) bound to cinacalcet in complex with Gq protein
Authors : Ling, S.L.; Meng, X.Y.; Tian, C.L.
Deposited on : 2023-10-10
Resolution : 3.10 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

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

A user guide is available at

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

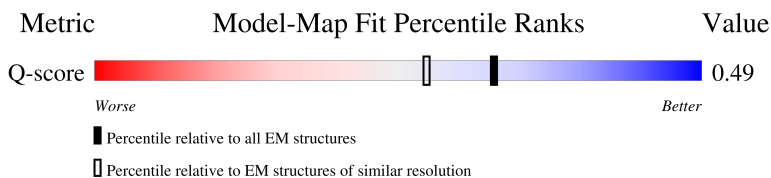
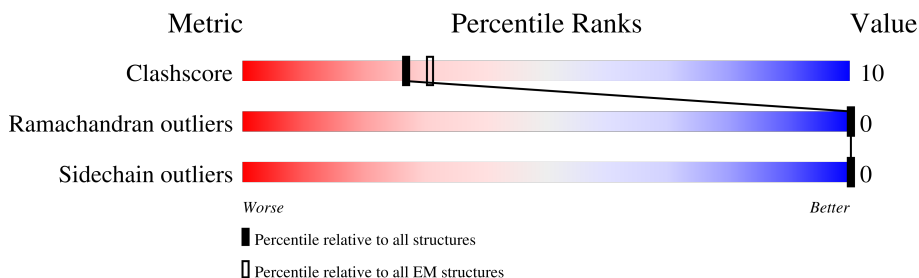
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.10 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.



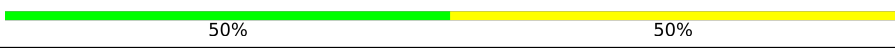
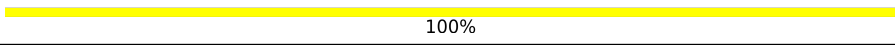
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	14724 (2.60 - 3.60)

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	1076	
1	B	1076	
2	G	246	
3	C	376	

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Mol	Chain	Length	Quality of chain
4	D	71	
5	E	297	
6	F	2	
6	H	2	

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
11	PO4	A	1109	-	-	X	-

2 Entry composition

There are 12 unique types of molecules in this entry. The entry contains 18794 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 Extracellular calcium-sensing receptor,calcium-sensing receptor.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	B	808	Total	C	N	O	S	0	0
			6178	4023	1015	1106	34		
1	A	803	Total	C	N	O	S	0	0
			6169	4013	1009	1115	32		

There are 60 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-10	MET	-	initiating methionine	UNP P41180
B	-9	LYS	-	expression tag	UNP P41180
B	-8	THR	-	expression tag	UNP P41180
B	-7	ILE	-	expression tag	UNP P41180
B	-6	ILE	-	expression tag	UNP P41180
B	-5	ALA	-	expression tag	UNP P41180
B	-4	LEU	-	expression tag	UNP P41180
B	-3	SER	-	expression tag	UNP P41180
B	-2	TYR	-	expression tag	UNP P41180
B	-1	ILE	-	expression tag	UNP P41180
B	0	PHE	-	expression tag	UNP P41180
B	1	CYS	-	expression tag	UNP P41180
B	2	LEU	-	expression tag	UNP P41180
B	3	VAL	-	expression tag	UNP P41180
B	4	PHE	-	expression tag	UNP P41180
B	5	ALA	-	expression tag	UNP P41180
B	6	ASP	-	expression tag	UNP P41180
B	7	TYR	-	expression tag	UNP P41180
B	8	LYS	-	expression tag	UNP P41180
B	9	ASP	-	expression tag	UNP P41180
B	10	ASP	-	expression tag	UNP P41180
B	11	ASP	-	expression tag	UNP P41180
B	12	ASP	-	expression tag	UNP P41180
B	13	GLU	-	expression tag	UNP P41180
B	14	ASN	-	expression tag	UNP P41180
B	15	LEU	-	expression tag	UNP P41180

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Chain	Residue	Modelled	Actual	Comment	Reference
B	16	TYR	-	expression tag	UNP P41180
B	17	PHE	-	expression tag	UNP P41180
B	18	GLN	-	expression tag	UNP P41180
B	19	GLY	-	expression tag	UNP P41180
A	-10	MET	-	initiating methionine	UNP P41180
A	-9	LYS	-	expression tag	UNP P41180
A	-8	THR	-	expression tag	UNP P41180
A	-7	ILE	-	expression tag	UNP P41180
A	-6	ILE	-	expression tag	UNP P41180
A	-5	ALA	-	expression tag	UNP P41180
A	-4	LEU	-	expression tag	UNP P41180
A	-3	SER	-	expression tag	UNP P41180
A	-2	TYR	-	expression tag	UNP P41180
A	-1	ILE	-	expression tag	UNP P41180
A	0	PHE	-	expression tag	UNP P41180
A	1	CYS	-	expression tag	UNP P41180
A	2	LEU	-	expression tag	UNP P41180
A	3	VAL	-	expression tag	UNP P41180
A	4	PHE	-	expression tag	UNP P41180
A	5	ALA	-	expression tag	UNP P41180
A	6	ASP	-	expression tag	UNP P41180
A	7	TYR	-	expression tag	UNP P41180
A	8	LYS	-	expression tag	UNP P41180
A	9	ASP	-	expression tag	UNP P41180
A	10	ASP	-	expression tag	UNP P41180
A	11	ASP	-	expression tag	UNP P41180
A	12	ASP	-	expression tag	UNP P41180
A	13	GLU	-	expression tag	UNP P41180
A	14	ASN	-	expression tag	UNP P41180
A	15	LEU	-	expression tag	UNP P41180
A	16	TYR	-	expression tag	UNP P41180
A	17	PHE	-	expression tag	UNP P41180
A	18	GLN	-	expression tag	UNP P41180
A	19	GLY	-	expression tag	UNP P41180

- Molecule 2 is a protein called G subunit q (Gi2-mini-Gq chimeric).

Mol	Chain	Residues	Atoms					AltConf	Trace
2	G	217	Total	C	N	O	S	0	0
			1619	1036	290	286	7		

- Molecule 3 is a protein called Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	341	Total	C	N	O	S	0	0
			2523	1563	451	490	19		

There are 37 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	-9	HIS	-	expression tag	UNP P62873
C	-8	HIS	-	expression tag	UNP P62873
C	-7	HIS	-	expression tag	UNP P62873
C	-6	HIS	-	expression tag	UNP P62873
C	-5	HIS	-	expression tag	UNP P62873
C	-4	HIS	-	expression tag	UNP P62873
C	-3	GLY	-	expression tag	UNP P62873
C	-2	SER	-	expression tag	UNP P62873
C	-1	LEU	-	expression tag	UNP P62873
C	0	LEU	-	expression tag	UNP P62873
C	1	GLN	-	expression tag	UNP P62873
C	341	GLY	-	expression tag	UNP P62873
C	342	SER	-	expression tag	UNP P62873
C	343	SER	-	expression tag	UNP P62873
C	344	GLY	-	expression tag	UNP P62873
C	345	GLY	-	expression tag	UNP P62873
C	346	GLY	-	expression tag	UNP P62873
C	347	GLY	-	expression tag	UNP P62873
C	348	SER	-	expression tag	UNP P62873
C	349	GLY	-	expression tag	UNP P62873
C	350	GLY	-	expression tag	UNP P62873
C	351	GLY	-	expression tag	UNP P62873
C	352	GLY	-	expression tag	UNP P62873
C	353	SER	-	expression tag	UNP P62873
C	354	SER	-	expression tag	UNP P62873
C	355	GLY	-	expression tag	UNP P62873
C	356	VAL	-	expression tag	UNP P62873
C	357	SER	-	expression tag	UNP P62873
C	358	GLY	-	expression tag	UNP P62873
C	359	TRP	-	expression tag	UNP P62873
C	360	ARG	-	expression tag	UNP P62873
C	361	LEU	-	expression tag	UNP P62873
C	362	PHE	-	expression tag	UNP P62873
C	363	LYS	-	expression tag	UNP P62873
C	364	LYS	-	expression tag	UNP P62873
C	365	ILE	-	expression tag	UNP P62873
C	366	SER	-	expression tag	UNP P62873

- Molecule 4 is a protein called Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	55	Total	C	N	O	S	0	0
			356	223	65	66	2		

- Molecule 5 is a protein called ScFv16.

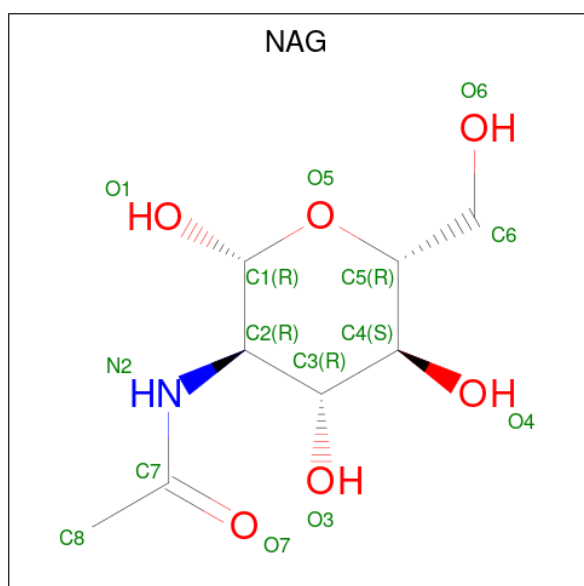
Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	229	Total	C	N	O	S	0	0
			1643	1052	275	309	7		

- Molecule 6 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



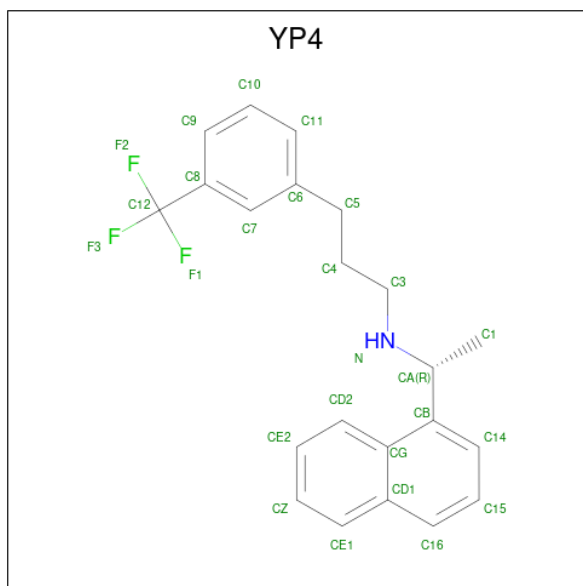
Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	2	Total	C	N	O		0	0
			28	16	2	10			
6	H	2	Total	C	N	O		0	0
			28	16	2	10			

- Molecule 7 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



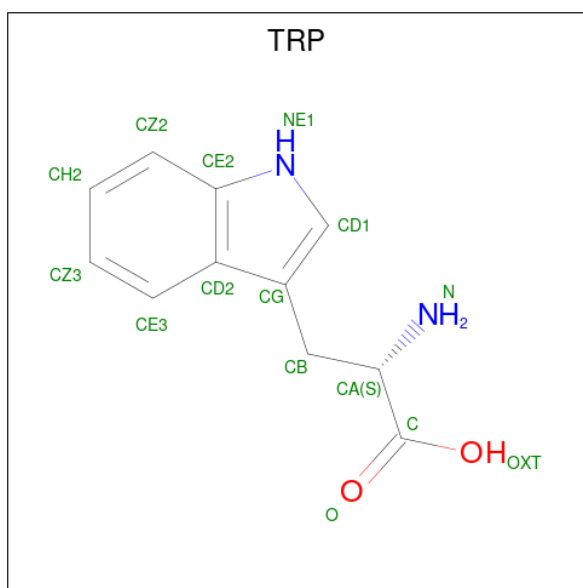
Mol	Chain	Residues	Atoms				AltConf
7	B	1	Total	C	N	O	0
			14	8	1	5	
7	B	1	Total	C	N	O	0
			14	8	1	5	
7	B	1	Total	C	N	O	0
			14	8	1	5	
7	B	1	Total	C	N	O	0
			14	8	1	5	
7	A	1	Total	C	N	O	0
			14	8	1	5	
7	A	1	Total	C	N	O	0
			14	8	1	5	
7	A	1	Total	C	N	O	0
			14	8	1	5	
7	A	1	Total	C	N	O	0
			14	8	1	5	

- Molecule 8 is N-[(1R)-1-(naphthalen-1-yl)ethyl]-3-[3-(trifluoromethyl)phenyl]propan-1-amine (CCD ID: YP4) (formula: C₂₂H₂₂F₃N) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				AltConf
8	B	1	Total	C	F	N	0
			26	22	3	1	
8	A	1	Total	C	F	N	0
			26	22	3	1	

- Molecule 9 is TRYPTOPHAN (CCD ID: TRP) (formula: $C_{11}H_{12}N_2O_2$).

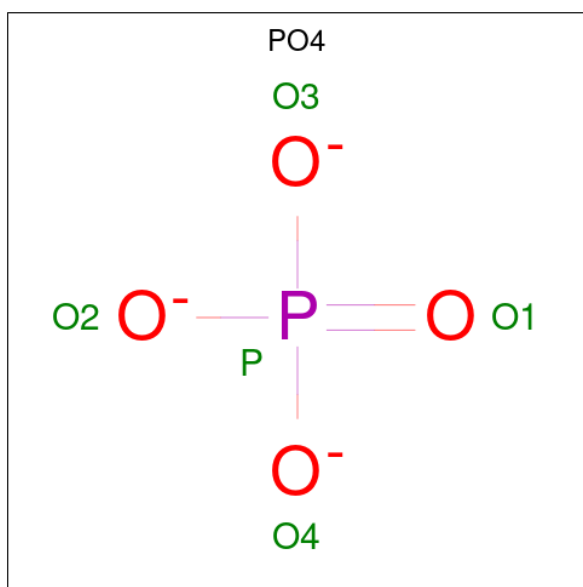


Mol	Chain	Residues	Atoms				AltConf
9	B	1	Total	C	N	O	0
			15	11	2	2	
9	A	1	Total	C	N	O	0
			15	11	2	2	

- Molecule 10 is CALCIUM ION (CCD ID: CA) (formula: Ca).

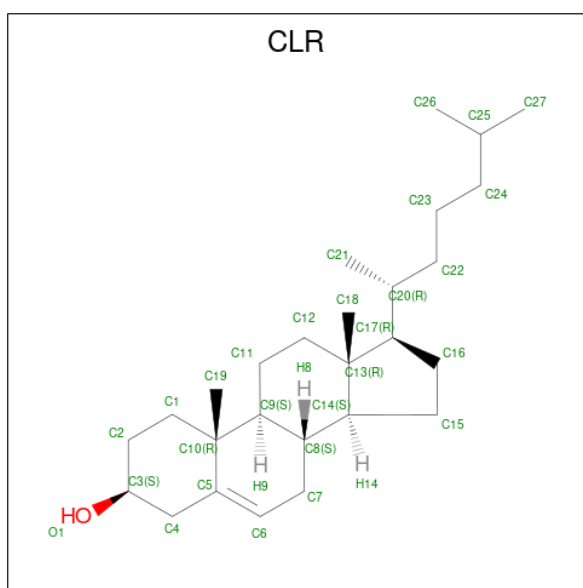
Mol	Chain	Residues	Atoms		AltConf
10	B	2	Total	Ca	0
			2	2	
10	A	2	Total	Ca	0
			2	2	

- Molecule 11 is PHOSPHATE ION (CCD ID: PO4) (formula: O_4P).



Mol	Chain	Residues	Atoms			AltConf
11	B	1	Total	O	P	0
			5	4	1	
11	A	1	Total	O	P	0
			5	4	1	

- Molecule 12 is CHOLESTEROL (CCD ID: CLR) (formula: $C_{27}H_{46}O$).

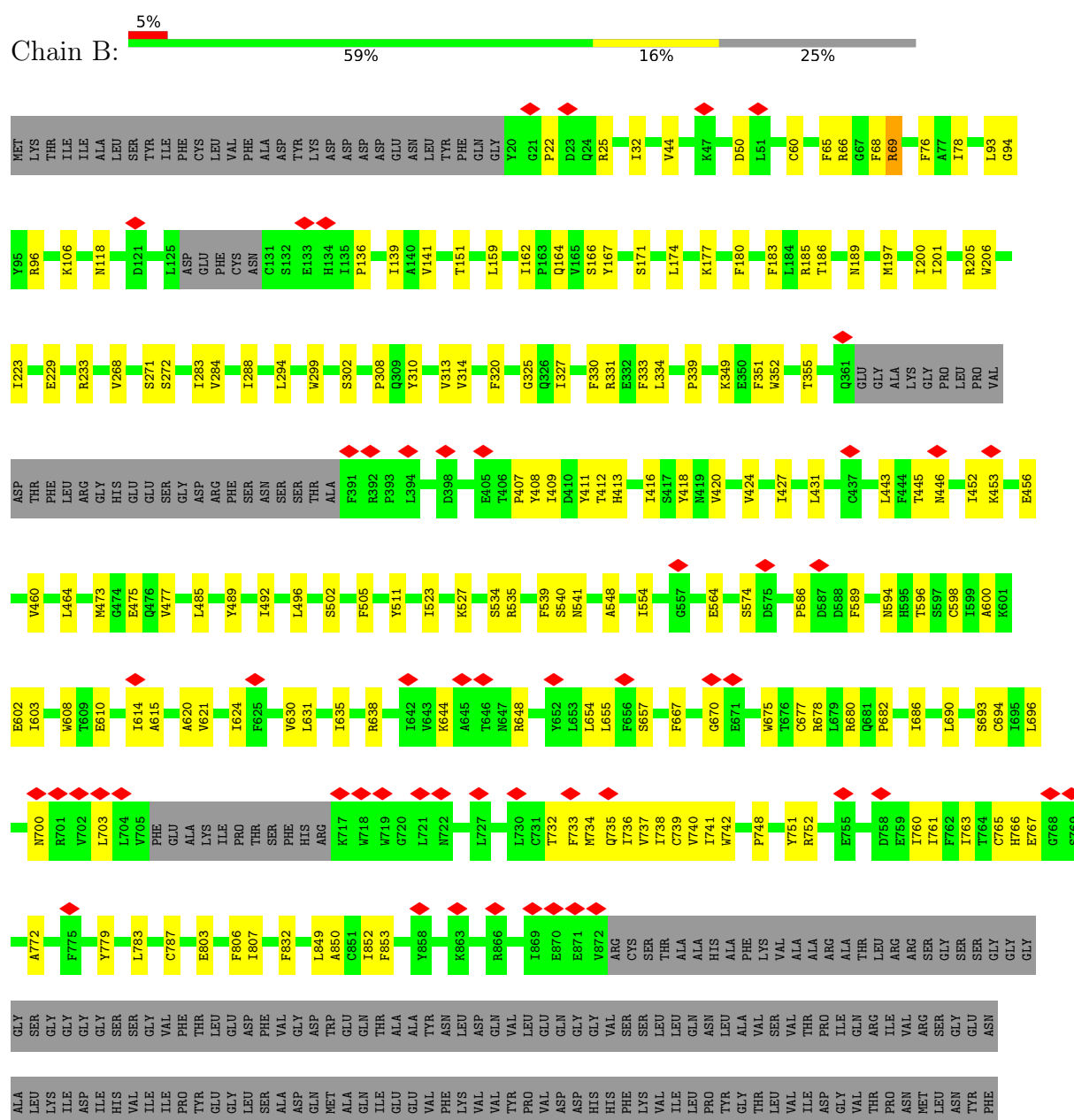


Mol	Chain	Residues	Atoms			AltConf
12	B	1	Total	C	O	0
			28	27	1	

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.

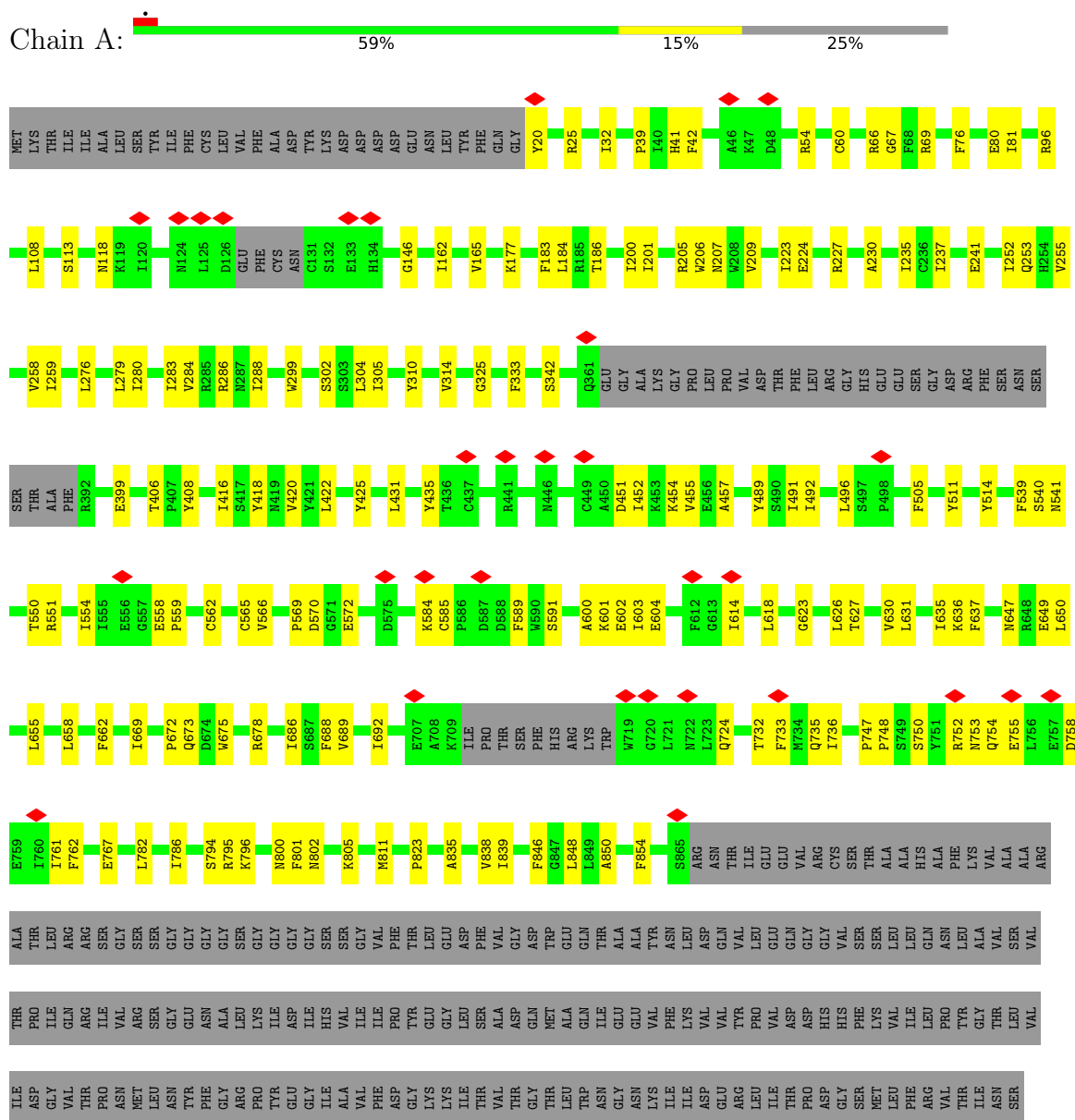
- Molecule 1: Extracellular calcium-sensing receptor,calcium-sensing receptor



GLY
ARG
PRO
TYR
GLU
GLY
ILE
ALA
VAL
PHE
ASP
GLY
LYS
LYS
ILE
THR
GLY
THR
TRP
ASP
ASN
GLY
ASN
LYS
ILE
ILE
GLN
GLU
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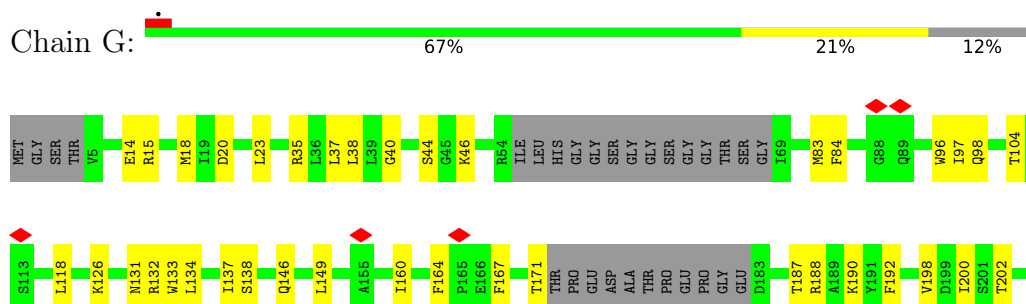
- Molecule 1: Extracellular calcium-sensing receptor,calcium-sensing receptor

Chain A:



- Molecule 2: G subunit q (Gi2-mini-Gq chimeric)

Chain G:



- Molecule 6: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain H:  100%

MAG1
MAG2

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	239610	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 ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	1300	Depositor
Maximum defocus (nm)	1700	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	3.892	Depositor
Minimum map value	-0.308	Depositor
Average map value	0.007	Depositor
Map value standard deviation	0.041	Depositor
Recommended contour level	0.4	Depositor
Map size ($\text{\AA}$)	428.00003, 430.14, 483.64	wwPDB
Map dimensions	400, 402, 452	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.07, 1.07, 1.07	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: CLR, YP4, PO4, CA, 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	0.21	1/6326 (0.0%)	0.29	0/8613
1	B	0.20	2/6338 (0.0%)	0.35	1/8634 (0.0%)
2	G	0.13	0/1646	0.34	0/2230
3	C	0.19	0/2570	0.33	0/3500
4	D	0.13	0/362	0.29	0/499
5	E	0.14	0/1687	0.37	0/2302
All	All	0.19	3/18929 (0.0%)	0.33	1/25778 (0.0%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	69	ARG	N-CA	-6.46	1.38	1.46
1	A	805	LYS	CA-C	-6.16	1.45	1.52
1	B	69	ARG	CA-C	-5.28	1.46	1.52

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	69	ARG	N-CA-C	-7.49	102.81	110.97

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	6169	0	5895	117	0
1	B	6178	0	5880	127	0
2	G	1619	0	1517	33	0
3	C	2523	0	2341	51	0
4	D	356	0	308	4	0
5	E	1643	0	1464	35	0
6	F	28	0	25	1	0
6	H	28	0	25	4	0
7	A	70	0	65	2	0
7	B	56	0	52	0	0
8	A	26	0	0	0	0
8	B	26	0	0	0	0
9	A	15	0	9	1	0
9	B	15	0	9	0	0
10	A	2	0	0	0	0
10	B	2	0	0	0	0
11	A	5	0	0	2	0
11	B	5	0	0	0	0
12	B	28	0	46	2	0
All	All	18794	0	17636	359	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 10.

The worst 5 of 359 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:B:65:PHE:O	1:B:69:ARG:HG3	1.84	0.78
1:A:603:ILE:HA	1:A:761:ILE:HG23	1.72	0.72
1:B:69:ARG:HH22	1:B:411:TYR:CB	2.03	0.72
1:A:589:PHE:HA	1:A:600:ALA:HA	1.74	0.70
1:B:69:ARG:NH2	1:B:411:TYR:HB3	2.07	0.69

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	795/1076 (74%)	773 (97%)	22 (3%)	0	100	100
1	B	800/1076 (74%)	768 (96%)	32 (4%)	0	100	100
2	G	211/246 (86%)	202 (96%)	9 (4%)	0	100	100
3	C	339/376 (90%)	316 (93%)	23 (7%)	0	100	100
4	D	53/71 (75%)	49 (92%)	4 (8%)	0	100	100
5	E	225/297 (76%)	204 (91%)	21 (9%)	0	100	100
All	All	2423/3142 (77%)	2312 (95%)	111 (5%)	0	100	100

There are no Ramachandran outliers to report.

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	639/926 (69%)	639 (100%)	0	100	100
1	B	632/926 (68%)	632 (100%)	0	100	100
2	G	151/213 (71%)	151 (100%)	0	100	100
3	C	254/307 (83%)	254 (100%)	0	100	100
4	D	27/58 (47%)	27 (100%)	0	100	100
5	E	155/239 (65%)	155 (100%)	0	100	100
All	All	1858/2669 (70%)	1858 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 19 such sidechains are listed below:

Mol	Chain	Res	Type
3	C	32	GLN
4	D	18	GLN

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Mol	Chain	Res	Type
5	E	82	GLN
3	C	311	HIS
1	A	27	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 ⓘ

4 monosaccharides 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	$\# Z > 2$
6	NAG	F	1	6,1	14,14,15	0.28	0	17,19,21	0.43	0
6	NAG	F	2	6	14,14,15	0.22	0	17,19,21	0.49	0
6	NAG	H	1	6,1	14,14,15	0.25	0	17,19,21	0.47	0
6	NAG	H	2	6	14,14,15	0.26	0	17,19,21	0.45	0

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
6	NAG	F	1	6,1	-	4/6/23/26	0/1/1/1
6	NAG	F	2	6	-	0/6/23/26	0/1/1/1
6	NAG	H	1	6,1	-	0/6/23/26	0/1/1/1
6	NAG	H	2	6	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

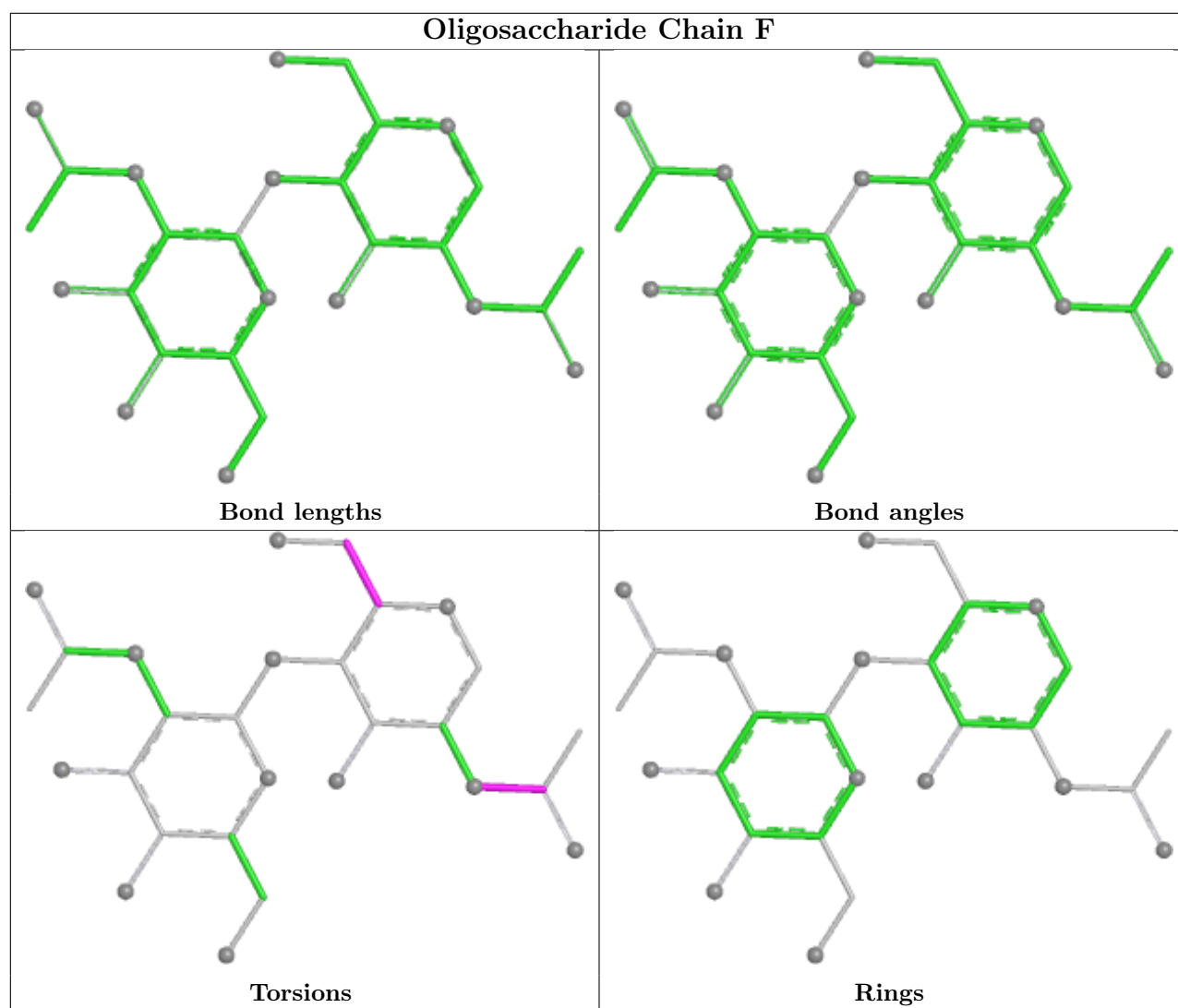
Mol	Chain	Res	Type	Atoms
6	H	2	NAG	O5-C5-C6-O6
6	F	1	NAG	O5-C5-C6-O6
6	H	2	NAG	C4-C5-C6-O6
6	F	1	NAG	C4-C5-C6-O6
6	F	1	NAG	C8-C7-N2-C2

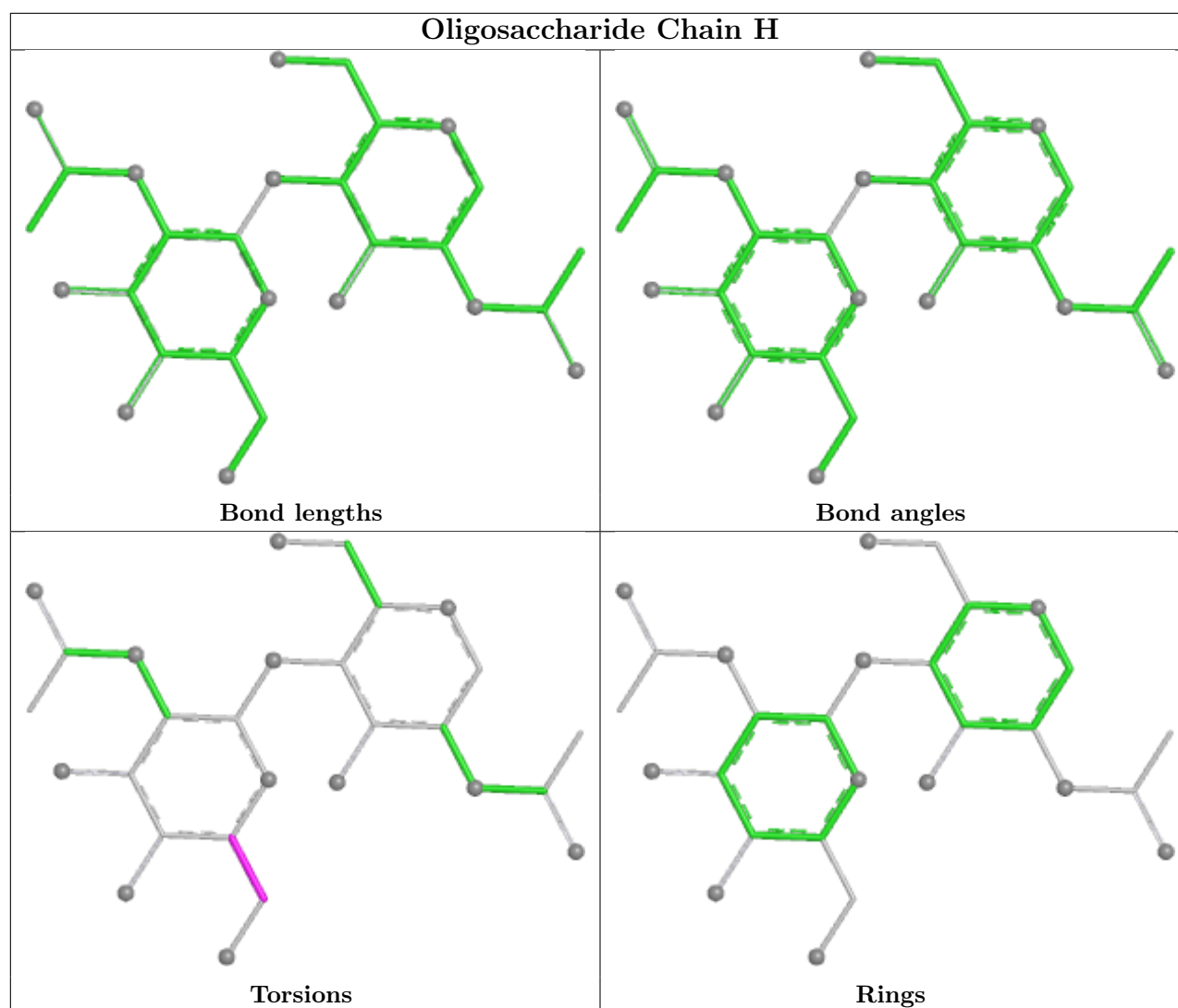
There are no ring outliers.

3 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	H	1	NAG	4	0
6	H	2	NAG	2	0
6	F	1	NAG	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 oligosaccharide.





5.6 Ligand geometry [i](#)

Of 20 ligands modelled in this entry, 4 are monoatomic - leaving 16 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	$\# Z > 2$
7	NAG	A	1105	1	14,14,15	0.19	0	17,19,21	0.45	0
12	CLR	B	1110	-	31,31,31	0.38	0	48,48,48	0.96	5 (10%)
7	NAG	A	1102	1	14,14,15	0.25	0	17,19,21	0.57	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
7	NAG	A	1106	1	14,14,15	0.68	1 (7%)	17,19,21	0.82	0
8	YP4	B	1105	-	28,28,28	0.65	0	39,39,39	0.79	1 (2%)
7	NAG	B	1102	1	14,14,15	0.22	0	17,19,21	0.43	0
9	TRP	A	1107	-	15,16,16	0.76	1 (6%)	18,22,22	0.76	1 (5%)
7	NAG	B	1104	1	14,14,15	0.92	1 (7%)	17,19,21	1.24	1 (5%)
11	PO4	B	1109	-	4,4,4	1.02	0	6,6,6	0.44	0
8	YP4	A	1110	-	28,28,28	0.64	0	39,39,39	0.77	0
11	PO4	A	1109	-	4,4,4	1.01	0	6,6,6	0.46	0
7	NAG	B	1103	1	14,14,15	0.23	0	17,19,21	0.45	0
7	NAG	A	1103	1	14,14,15	0.21	0	17,19,21	0.42	0
7	NAG	A	1104	1	14,14,15	0.26	0	17,19,21	0.50	0
9	TRP	B	1106	-	15,16,16	0.75	1 (6%)	18,22,22	0.77	1 (5%)
7	NAG	B	1101	1	14,14,15	0.21	0	17,19,21	0.46	0

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
7	NAG	A	1105	1	-	2/6/23/26	0/1/1/1
12	CLR	B	1110	-	-	9/10/68/68	0/4/4/4
7	NAG	A	1102	1	-	2/6/23/26	0/1/1/1
7	NAG	A	1106	1	-	3/6/23/26	0/1/1/1
8	YP4	B	1105	-	-	6/17/17/17	0/3/3/3
7	NAG	B	1102	1	-	1/6/23/26	0/1/1/1
9	TRP	A	1107	-	-	2/8/8/8	0/2/2/2
7	NAG	B	1104	1	-	4/6/23/26	0/1/1/1
8	YP4	A	1110	-	-	4/17/17/17	0/3/3/3
7	NAG	B	1103	1	-	2/6/23/26	0/1/1/1
7	NAG	A	1103	1	-	1/6/23/26	0/1/1/1
7	NAG	A	1104	1	-	0/6/23/26	0/1/1/1
9	TRP	B	1106	-	-	4/8/8/8	0/2/2/2
7	NAG	B	1101	1	-	0/6/23/26	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	B	1104	NAG	O5-C1	3.17	1.49	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	A	1107	TRP	OXT-C	-2.40	1.23	1.30
7	A	1106	NAG	O5-C1	-2.33	1.39	1.43
9	B	1106	TRP	OXT-C	-2.29	1.23	1.30

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	B	1104	NAG	C1-O5-C5	4.86	118.70	112.19
12	B	1110	CLR	C16-C17-C13	-2.87	100.47	103.84
9	B	1106	TRP	OXT-C-O	-2.70	117.95	124.08
9	A	1107	TRP	OXT-C-O	-2.69	117.98	124.08
12	B	1110	CLR	C14-C8-C9	2.48	112.32	109.09

There are no chirality outliers.

5 of 40 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
8	B	1105	YP4	C1-CA-N-C3
8	B	1105	YP4	CB-CA-N-C3
8	A	1110	YP4	C4-C3-N-CA
8	A	1110	YP4	C1-CA-N-C3
8	A	1110	YP4	CB-CA-N-C3

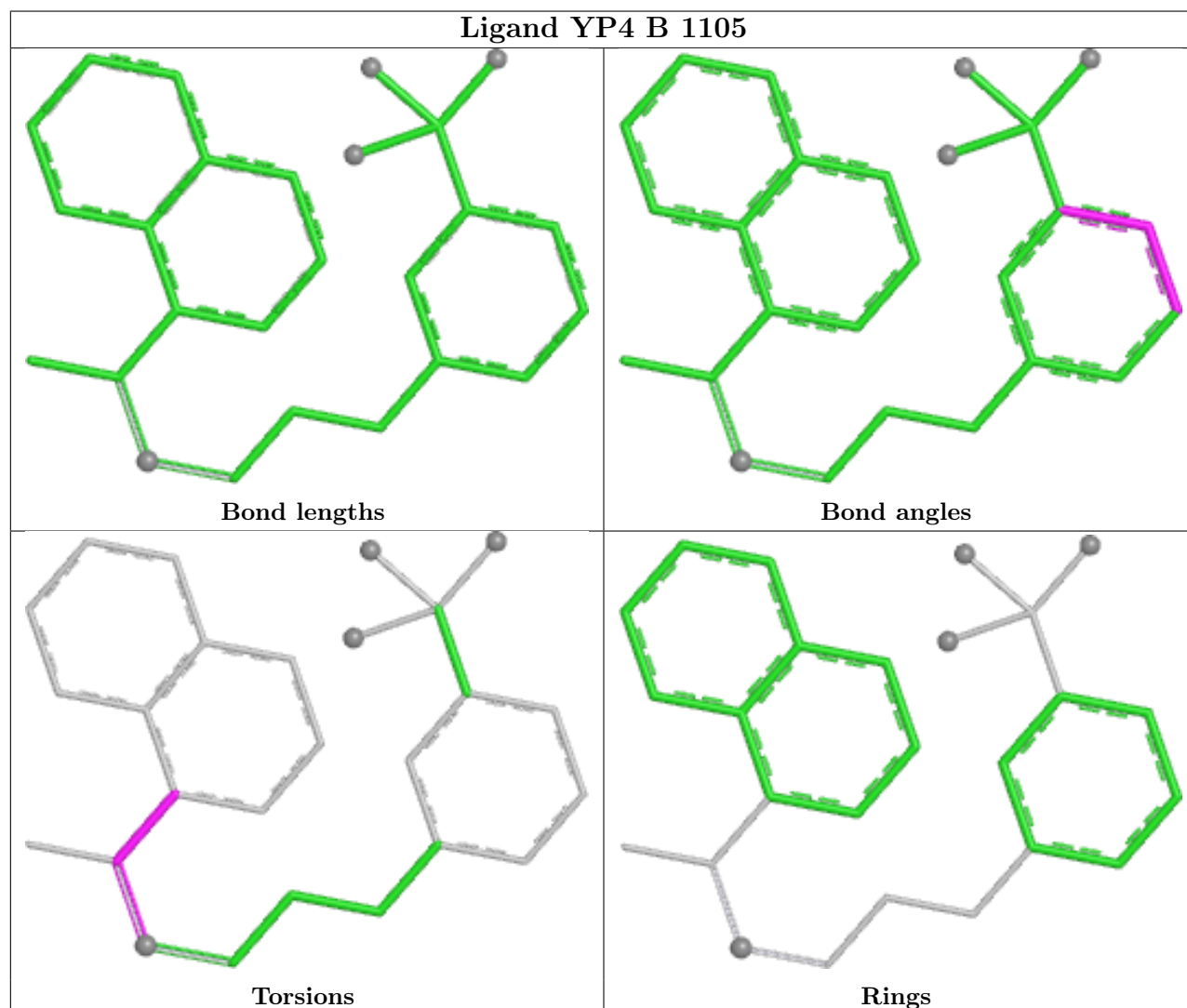
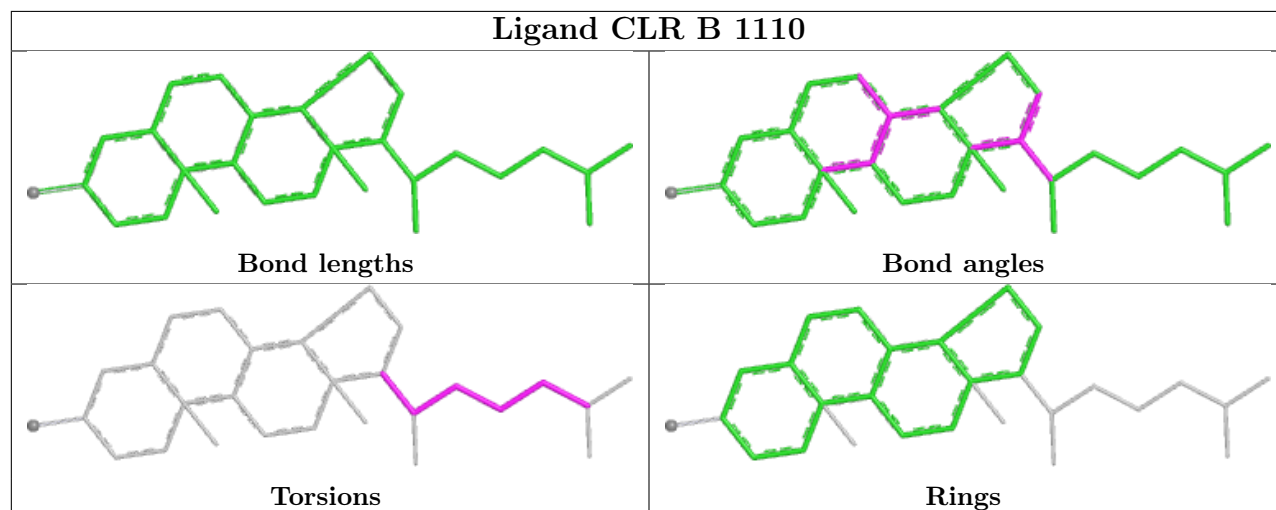
There are no ring outliers.

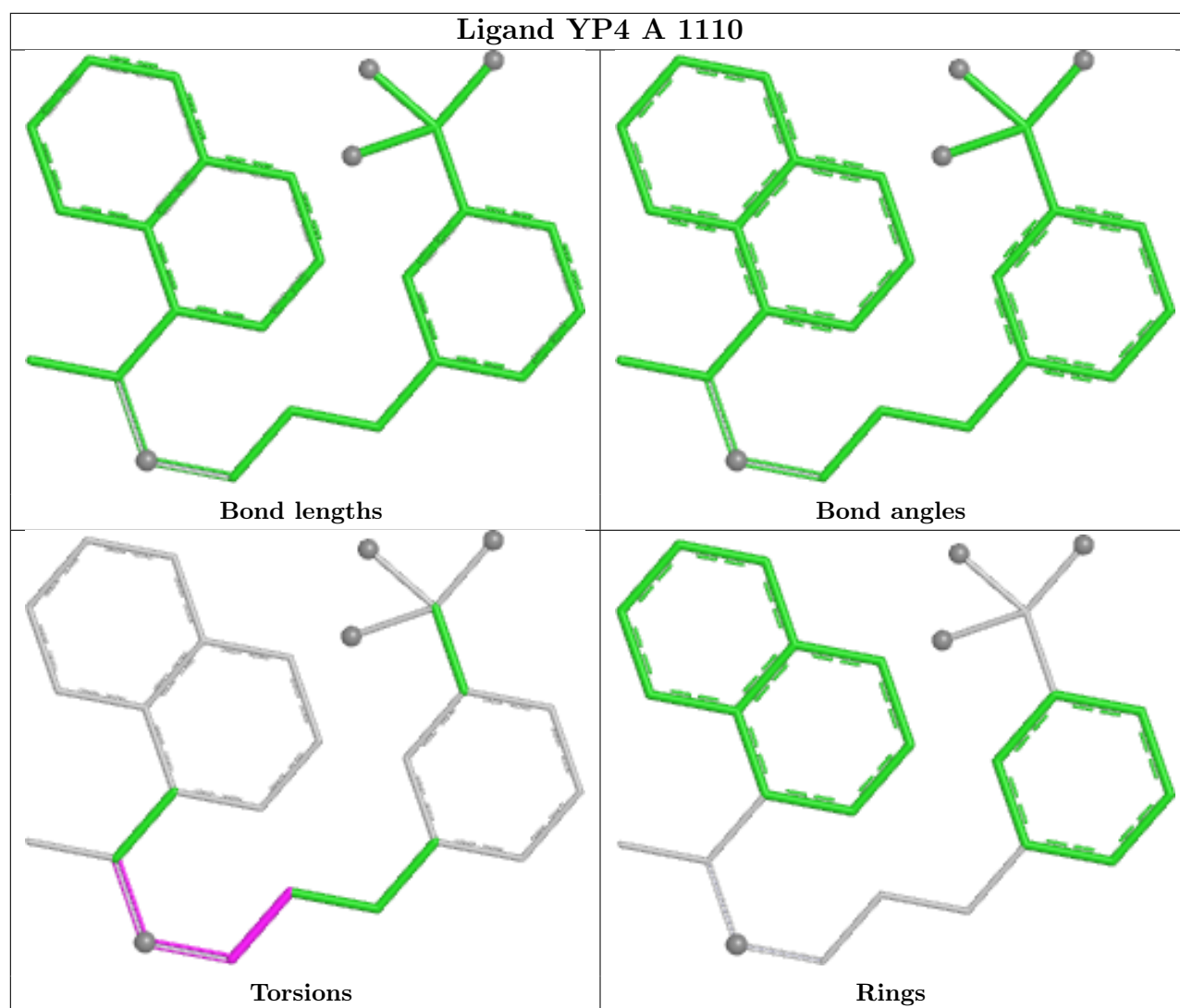
5 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
12	B	1110	CLR	2	0
7	A	1106	NAG	1	0
9	A	1107	TRP	1	0
11	A	1109	PO4	2	0
7	A	1104	NAG	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.

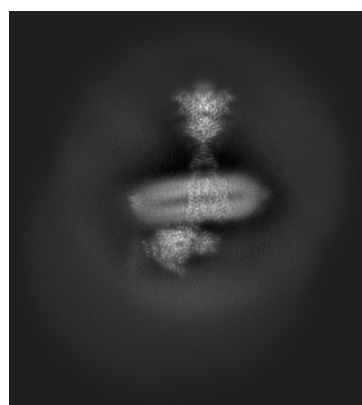
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-37724. These allow visual inspection of the internal detail of the map and identification of artifacts.

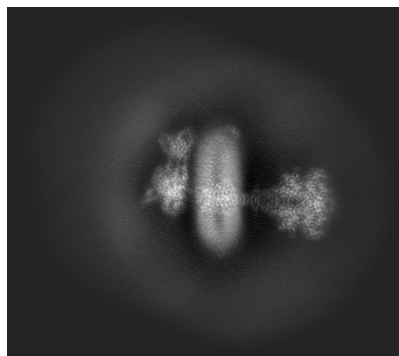
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

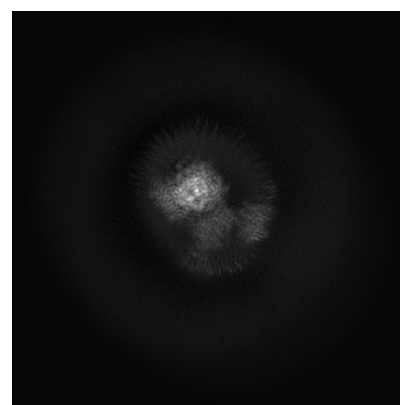
6.1.1 Primary map



X



Y

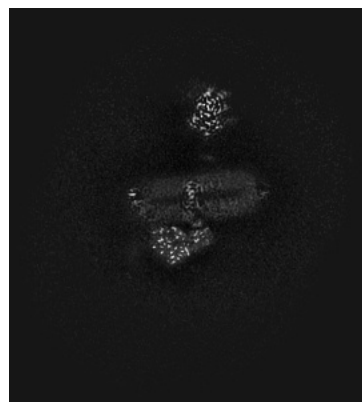


Z

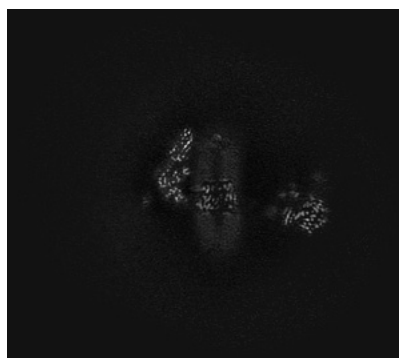
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

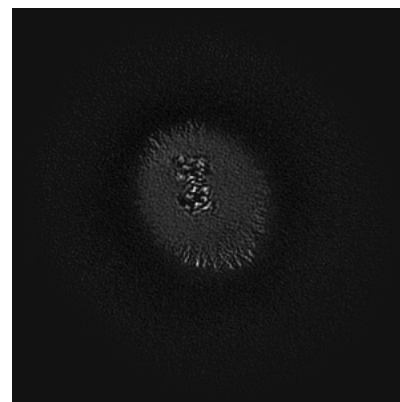
6.2.1 Primary map



X Index: 200



Y Index: 201



Z Index: 226

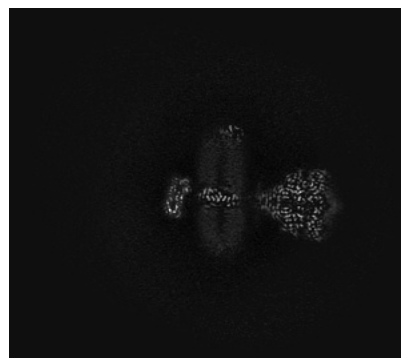
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

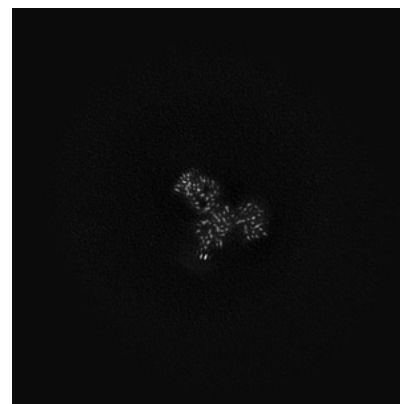
6.3.1 Primary map



X Index: 186



Y Index: 220



Z Index: 190

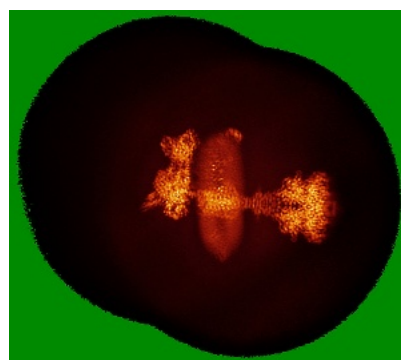
The images above show the largest variance slices of the map in three orthogonal directions.

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

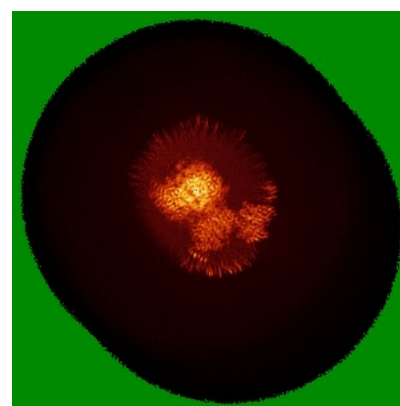
6.4.1 Primary map



X



Y

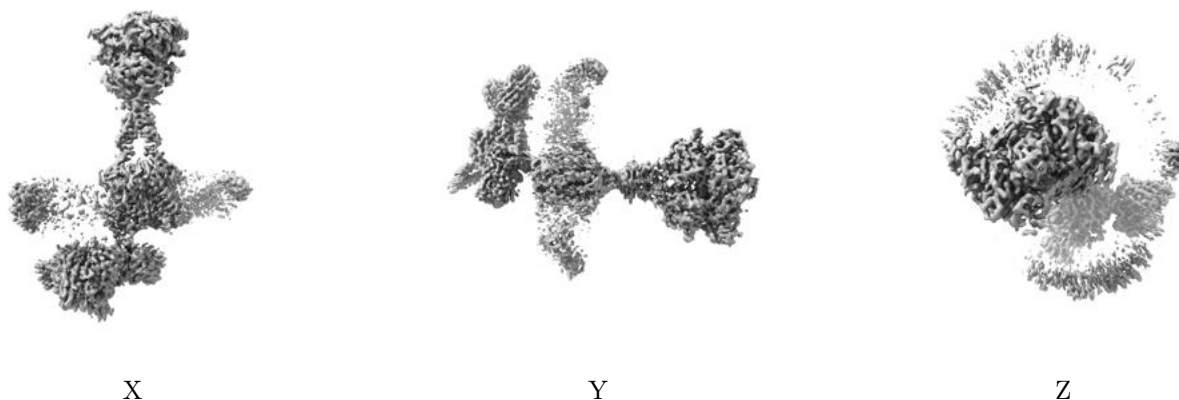


Z

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



The images above show the 3D surface view of the map at the recommended contour level 0.4. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

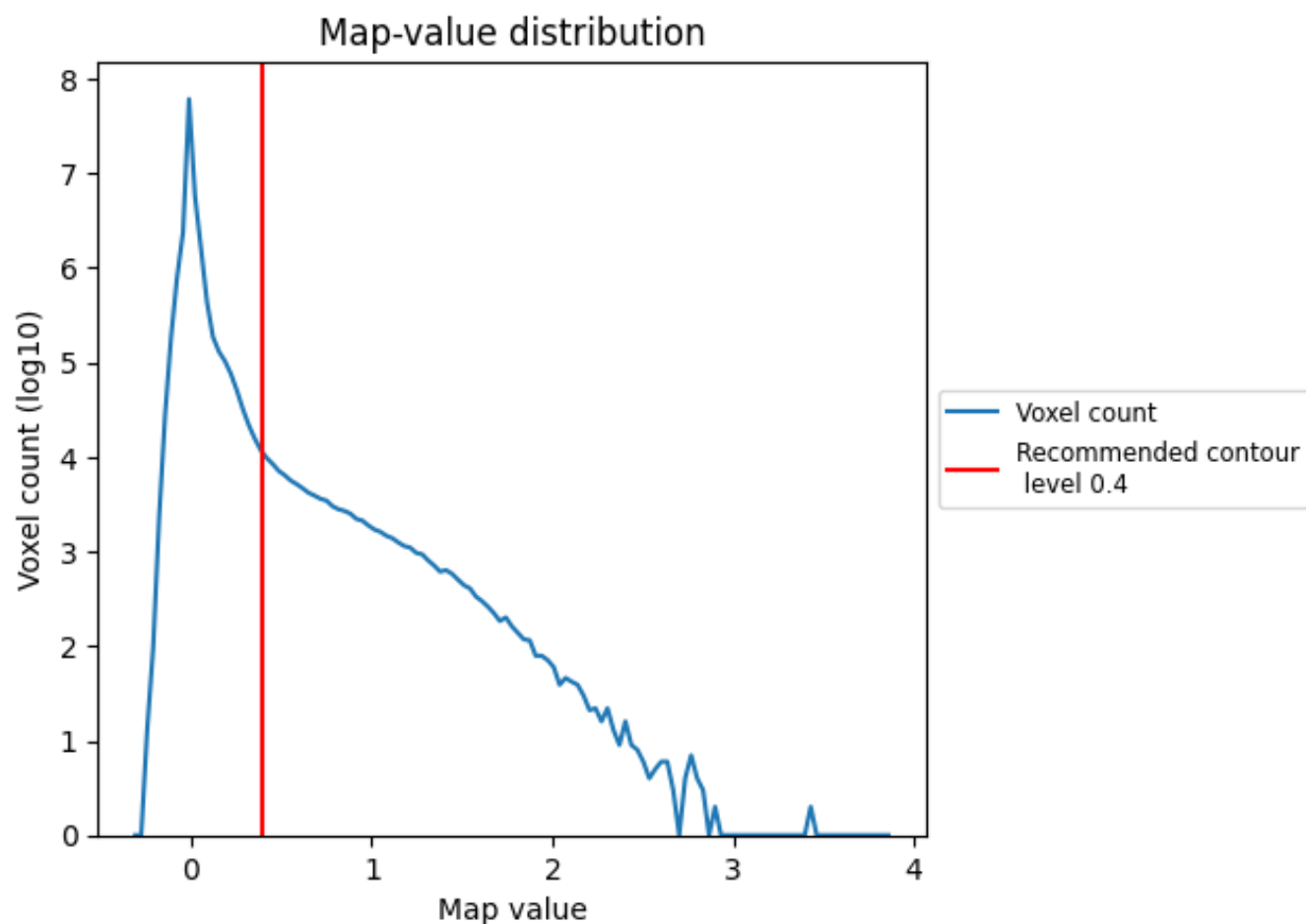
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

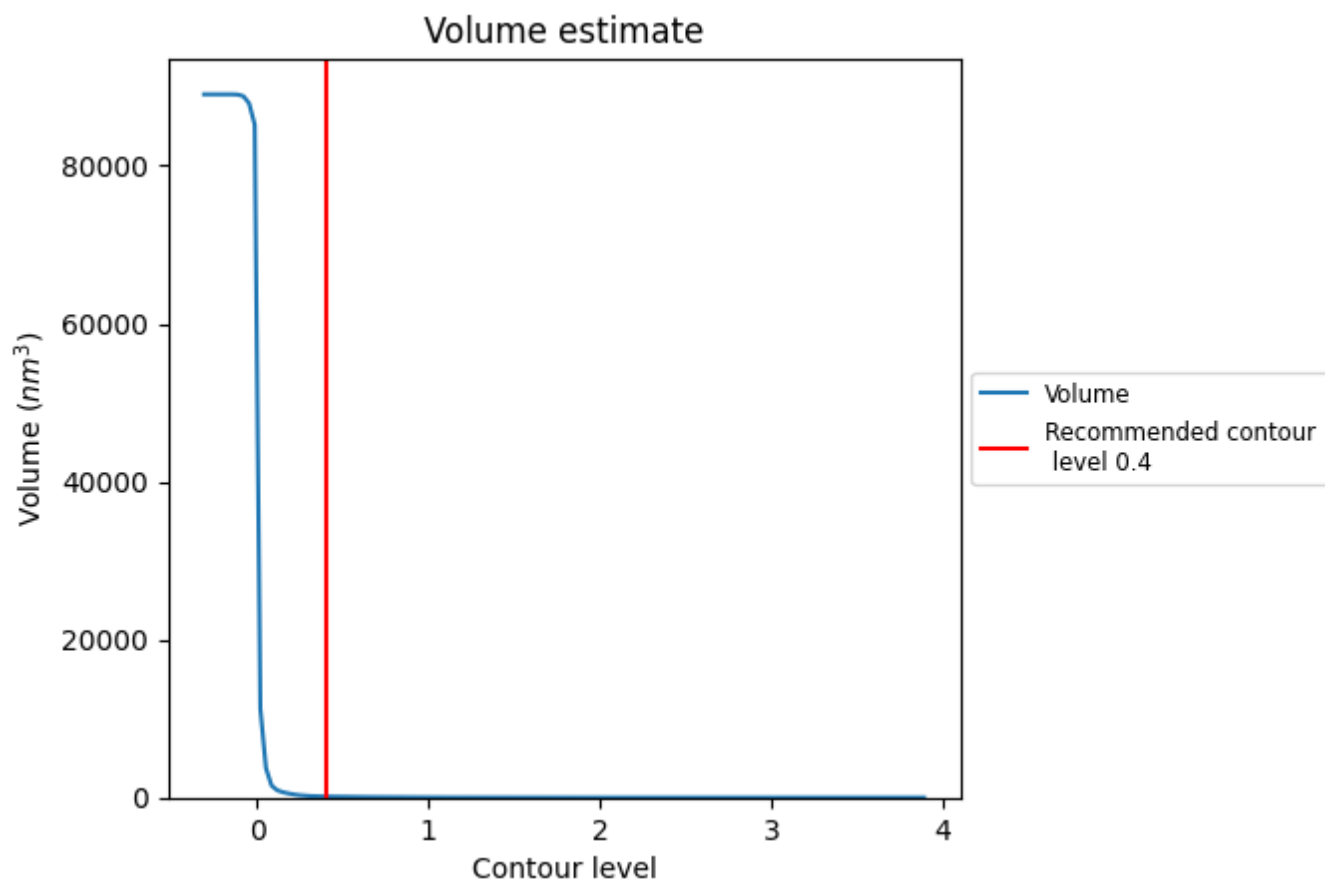
This section contains the results of statistical analysis of the map.

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 129 nm³; this corresponds to an approximate mass of 117 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.

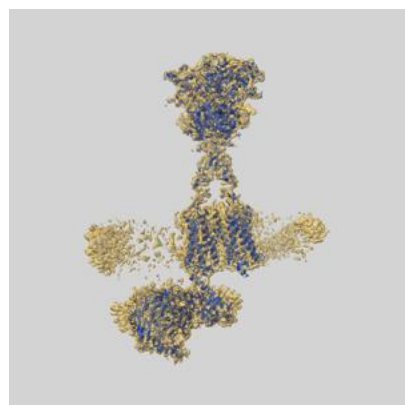
8 Fourier-Shell correlation

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

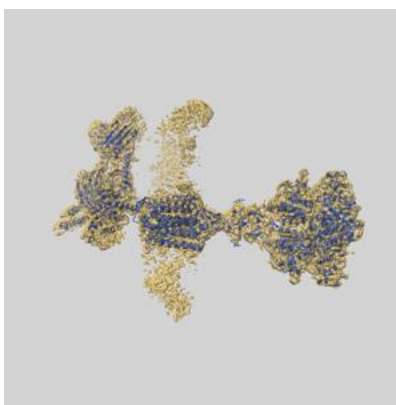
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-37724 and PDB model 8WPU. Per-residue inclusion information can be found in section [3](#) on page [11](#).

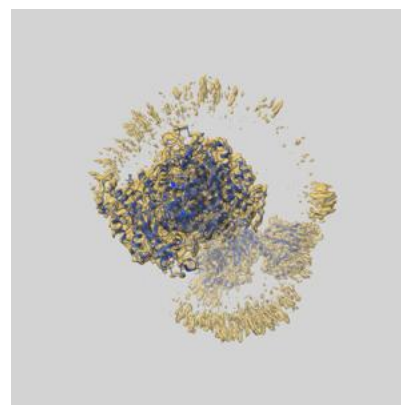
9.1 Map-model overlay [i](#)



X



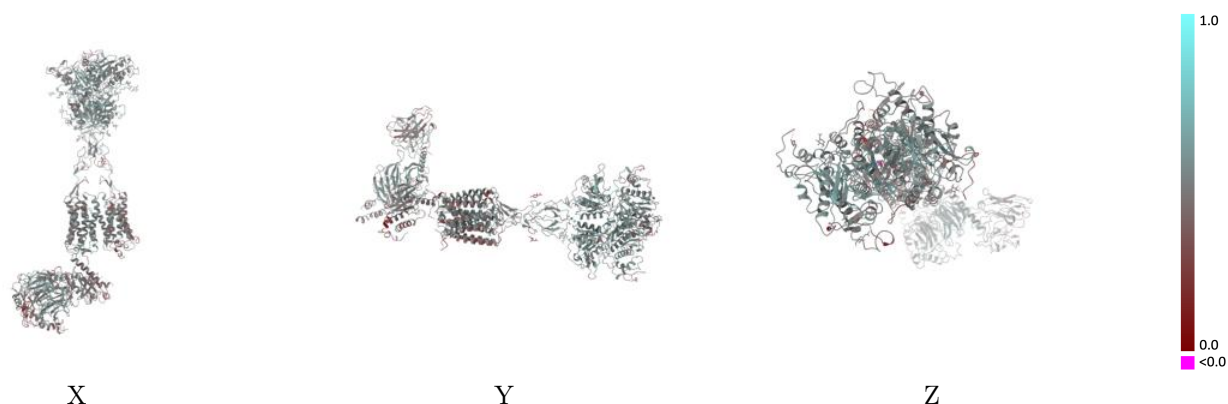
Y



Z

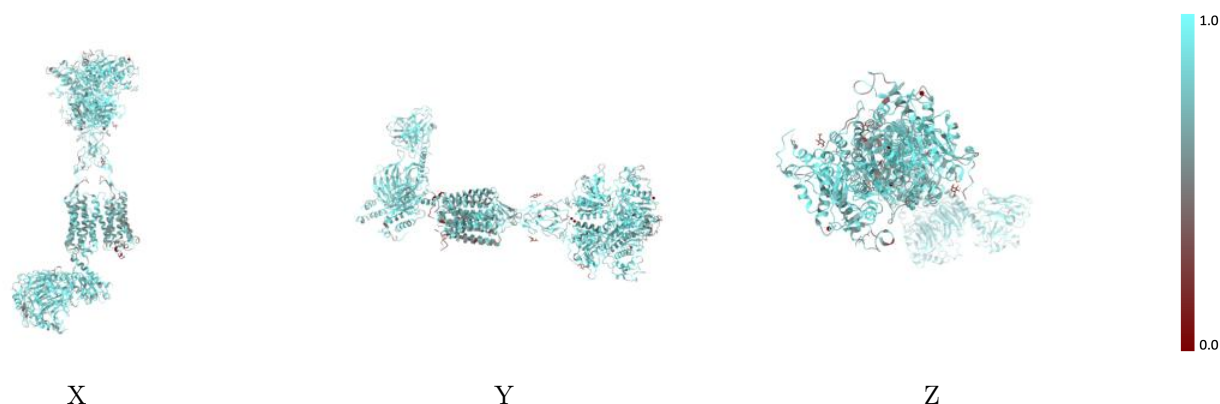
The images above show the 3D surface view of the map at the recommended contour level 0.4 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



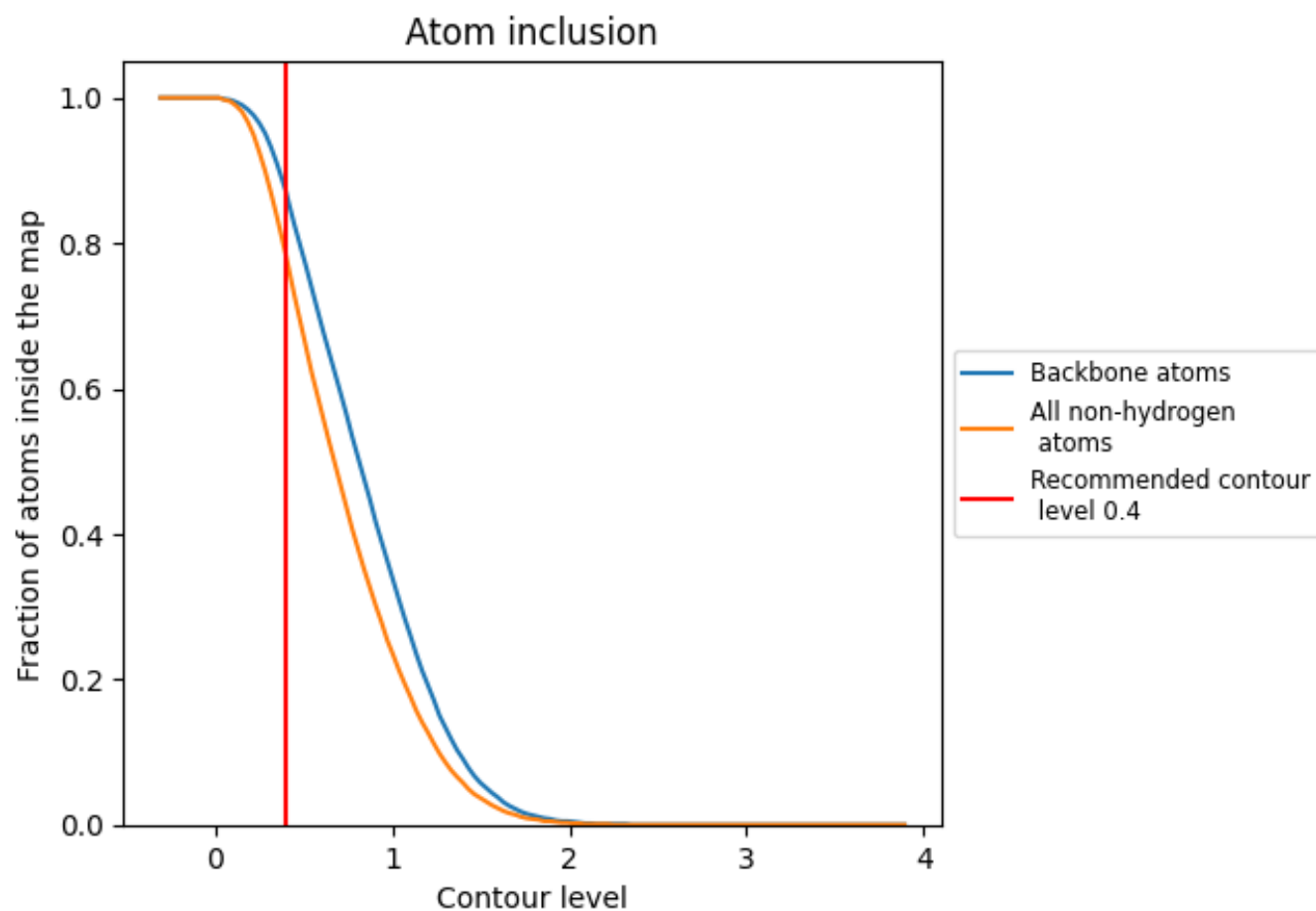
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.4).

9.4 Atom inclusion [i](#)



At the recommended contour level, 87% of all backbone atoms, 78% 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 (0.4) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7830	0.4900
A	0.7890	0.5090
B	0.7600	0.4870
C	0.8240	0.5050
D	0.7790	0.4710
E	0.8000	0.4590
F	0.6430	0.4860
G	0.7720	0.4340
H	0.6790	0.4560

1.0

0.0

<0.0