



Full wwPDB EM Validation Report ⓘ

Nov 13, 2022 – 06:39 AM EST

PDB ID : 6VEC
EMDB ID : EMD-21155
Title : Cryo-EM structure of F-actin/Plastin2-ABD2 complex
Authors : Zheng, W.; Kudryashov, D.S.; Egelman, E.H.
Deposited on : 2019-12-31
Resolution : 3.90 Å(reported)
Based on initial model : 5ONV

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.dev43
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2

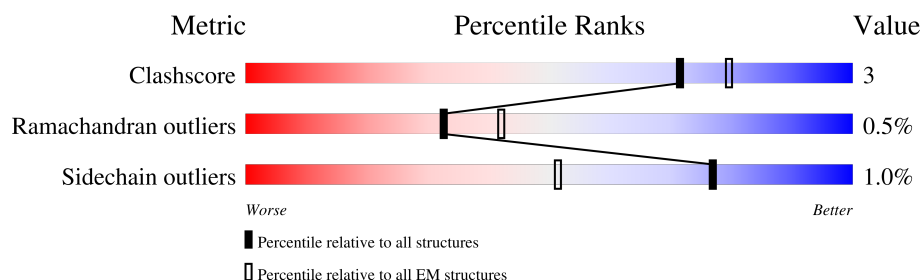
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.90 Å.

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



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

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. 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	377	
1	B	377	
1	C	377	
1	D	377	
1	E	377	
1	F	377	
1	G	377	
1	H	377	

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Mol	Chain	Length	Quality of chain
1	I	377	
1	J	377	
1	K	377	
2	a	422	
2	b	422	
2	c	422	
2	d	422	
2	e	422	
2	f	422	
2	g	422	
2	h	422	
2	i	422	
2	j	422	
2	k	422	

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 53064 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 Actin, alpha skeletal muscle.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	370	Total	C	N	O	S	0	0
			2887	1827	488	551	21		
1	B	370	Total	C	N	O	S	0	0
			2887	1827	488	551	21		
1	C	370	Total	C	N	O	S	0	0
			2887	1827	488	551	21		
1	D	370	Total	C	N	O	S	0	0
			2887	1827	488	551	21		
1	E	370	Total	C	N	O	S	0	0
			2887	1827	488	551	21		
1	F	370	Total	C	N	O	S	0	0
			2887	1827	488	551	21		
1	G	370	Total	C	N	O	S	0	0
			2887	1827	488	551	21		
1	H	370	Total	C	N	O	S	0	0
			2887	1827	488	551	21		
1	I	370	Total	C	N	O	S	0	0
			2887	1827	488	551	21		
1	J	370	Total	C	N	O	S	0	0
			2887	1827	488	551	21		
1	K	370	Total	C	N	O	S	0	0
			2887	1827	488	551	21		

- Molecule 2 is a protein called LCP1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	a	241	Total	C	N	O	S	0	0
			1909	1210	328	361	10		
2	b	241	Total	C	N	O	S	0	0
			1909	1210	328	361	10		
2	c	241	Total	C	N	O	S	0	0
			1909	1210	328	361	10		
2	d	241	Total	C	N	O	S	0	0
			1909	1210	328	361	10		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	e	241	Total 1909	C 1210	N 328	O 361	S 10	0	0
2	f	241	Total 1909	C 1210	N 328	O 361	S 10	0	0
2	g	241	Total 1909	C 1210	N 328	O 361	S 10	0	0
2	h	241	Total 1909	C 1210	N 328	O 361	S 10	0	0
2	i	241	Total 1909	C 1210	N 328	O 361	S 10	0	0
2	j	241	Total 1909	C 1210	N 328	O 361	S 10	0	0
2	k	241	Total 1909	C 1210	N 328	O 361	S 10	0	0

There are 352 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
a	206	MET	-	expression tag	UNP V9HWJ7
a	207	ASN	-	expression tag	UNP V9HWJ7
a	208	HIS	-	expression tag	UNP V9HWJ7
a	209	LYS	-	expression tag	UNP V9HWJ7
a	210	VAL	-	expression tag	UNP V9HWJ7
a	211	HIS	-	expression tag	UNP V9HWJ7
a	212	HIS	-	expression tag	UNP V9HWJ7
a	213	HIS	-	expression tag	UNP V9HWJ7
a	214	HIS	-	expression tag	UNP V9HWJ7
a	215	HIS	-	expression tag	UNP V9HWJ7
a	216	HIS	-	expression tag	UNP V9HWJ7
a	217	ILE	-	expression tag	UNP V9HWJ7
a	218	GLU	-	expression tag	UNP V9HWJ7
a	219	GLY	-	expression tag	UNP V9HWJ7
a	220	ARG	-	expression tag	UNP V9HWJ7
a	221	HIS	-	expression tag	UNP V9HWJ7
a	222	MET	-	expression tag	UNP V9HWJ7
a	223	GLU	-	expression tag	UNP V9HWJ7
a	224	LEU	-	expression tag	UNP V9HWJ7
a	225	GLY	-	expression tag	UNP V9HWJ7
a	226	THR	-	expression tag	UNP V9HWJ7
a	227	LEU	-	expression tag	UNP V9HWJ7
a	228	GLU	-	expression tag	UNP V9HWJ7
a	229	GLU	-	expression tag	UNP V9HWJ7
a	230	ASN	-	expression tag	UNP V9HWJ7

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Chain	Residue	Modelled	Actual	Comment	Reference
a	231	LEU	-	expression tag	UNP V9HWJ7
a	232	TYR	-	expression tag	UNP V9HWJ7
a	233	PHE	-	expression tag	UNP V9HWJ7
a	234	GLN	-	expression tag	UNP V9HWJ7
a	235	GLY	-	expression tag	UNP V9HWJ7
a	236	GLU	-	expression tag	UNP V9HWJ7
a	237	LEU	-	expression tag	UNP V9HWJ7
b	206	MET	-	expression tag	UNP V9HWJ7
b	207	ASN	-	expression tag	UNP V9HWJ7
b	208	HIS	-	expression tag	UNP V9HWJ7
b	209	LYS	-	expression tag	UNP V9HWJ7
b	210	VAL	-	expression tag	UNP V9HWJ7
b	211	HIS	-	expression tag	UNP V9HWJ7
b	212	HIS	-	expression tag	UNP V9HWJ7
b	213	HIS	-	expression tag	UNP V9HWJ7
b	214	HIS	-	expression tag	UNP V9HWJ7
b	215	HIS	-	expression tag	UNP V9HWJ7
b	216	HIS	-	expression tag	UNP V9HWJ7
b	217	ILE	-	expression tag	UNP V9HWJ7
b	218	GLU	-	expression tag	UNP V9HWJ7
b	219	GLY	-	expression tag	UNP V9HWJ7
b	220	ARG	-	expression tag	UNP V9HWJ7
b	221	HIS	-	expression tag	UNP V9HWJ7
b	222	MET	-	expression tag	UNP V9HWJ7
b	223	GLU	-	expression tag	UNP V9HWJ7
b	224	LEU	-	expression tag	UNP V9HWJ7
b	225	GLY	-	expression tag	UNP V9HWJ7
b	226	THR	-	expression tag	UNP V9HWJ7
b	227	LEU	-	expression tag	UNP V9HWJ7
b	228	GLU	-	expression tag	UNP V9HWJ7
b	229	GLU	-	expression tag	UNP V9HWJ7
b	230	ASN	-	expression tag	UNP V9HWJ7
b	231	LEU	-	expression tag	UNP V9HWJ7
b	232	TYR	-	expression tag	UNP V9HWJ7
b	233	PHE	-	expression tag	UNP V9HWJ7
b	234	GLN	-	expression tag	UNP V9HWJ7
b	235	GLY	-	expression tag	UNP V9HWJ7
b	236	GLU	-	expression tag	UNP V9HWJ7
b	237	LEU	-	expression tag	UNP V9HWJ7
c	206	MET	-	expression tag	UNP V9HWJ7
c	207	ASN	-	expression tag	UNP V9HWJ7
c	208	HIS	-	expression tag	UNP V9HWJ7

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Chain	Residue	Modelled	Actual	Comment	Reference
c	209	LYS	-	expression tag	UNP V9HWJ7
c	210	VAL	-	expression tag	UNP V9HWJ7
c	211	HIS	-	expression tag	UNP V9HWJ7
c	212	HIS	-	expression tag	UNP V9HWJ7
c	213	HIS	-	expression tag	UNP V9HWJ7
c	214	HIS	-	expression tag	UNP V9HWJ7
c	215	HIS	-	expression tag	UNP V9HWJ7
c	216	HIS	-	expression tag	UNP V9HWJ7
c	217	ILE	-	expression tag	UNP V9HWJ7
c	218	GLU	-	expression tag	UNP V9HWJ7
c	219	GLY	-	expression tag	UNP V9HWJ7
c	220	ARG	-	expression tag	UNP V9HWJ7
c	221	HIS	-	expression tag	UNP V9HWJ7
c	222	MET	-	expression tag	UNP V9HWJ7
c	223	GLU	-	expression tag	UNP V9HWJ7
c	224	LEU	-	expression tag	UNP V9HWJ7
c	225	GLY	-	expression tag	UNP V9HWJ7
c	226	THR	-	expression tag	UNP V9HWJ7
c	227	LEU	-	expression tag	UNP V9HWJ7
c	228	GLU	-	expression tag	UNP V9HWJ7
c	229	GLU	-	expression tag	UNP V9HWJ7
c	230	ASN	-	expression tag	UNP V9HWJ7
c	231	LEU	-	expression tag	UNP V9HWJ7
c	232	TYR	-	expression tag	UNP V9HWJ7
c	233	PHE	-	expression tag	UNP V9HWJ7
c	234	GLN	-	expression tag	UNP V9HWJ7
c	235	GLY	-	expression tag	UNP V9HWJ7
c	236	GLU	-	expression tag	UNP V9HWJ7
c	237	LEU	-	expression tag	UNP V9HWJ7
d	206	MET	-	expression tag	UNP V9HWJ7
d	207	ASN	-	expression tag	UNP V9HWJ7
d	208	HIS	-	expression tag	UNP V9HWJ7
d	209	LYS	-	expression tag	UNP V9HWJ7
d	210	VAL	-	expression tag	UNP V9HWJ7
d	211	HIS	-	expression tag	UNP V9HWJ7
d	212	HIS	-	expression tag	UNP V9HWJ7
d	213	HIS	-	expression tag	UNP V9HWJ7
d	214	HIS	-	expression tag	UNP V9HWJ7
d	215	HIS	-	expression tag	UNP V9HWJ7
d	216	HIS	-	expression tag	UNP V9HWJ7
d	217	ILE	-	expression tag	UNP V9HWJ7
d	218	GLU	-	expression tag	UNP V9HWJ7

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Chain	Residue	Modelled	Actual	Comment	Reference
d	219	GLY	-	expression tag	UNP V9HWJ7
d	220	ARG	-	expression tag	UNP V9HWJ7
d	221	HIS	-	expression tag	UNP V9HWJ7
d	222	MET	-	expression tag	UNP V9HWJ7
d	223	GLU	-	expression tag	UNP V9HWJ7
d	224	LEU	-	expression tag	UNP V9HWJ7
d	225	GLY	-	expression tag	UNP V9HWJ7
d	226	THR	-	expression tag	UNP V9HWJ7
d	227	LEU	-	expression tag	UNP V9HWJ7
d	228	GLU	-	expression tag	UNP V9HWJ7
d	229	GLU	-	expression tag	UNP V9HWJ7
d	230	ASN	-	expression tag	UNP V9HWJ7
d	231	LEU	-	expression tag	UNP V9HWJ7
d	232	TYR	-	expression tag	UNP V9HWJ7
d	233	PHE	-	expression tag	UNP V9HWJ7
d	234	GLN	-	expression tag	UNP V9HWJ7
d	235	GLY	-	expression tag	UNP V9HWJ7
d	236	GLU	-	expression tag	UNP V9HWJ7
d	237	LEU	-	expression tag	UNP V9HWJ7
e	206	MET	-	expression tag	UNP V9HWJ7
e	207	ASN	-	expression tag	UNP V9HWJ7
e	208	HIS	-	expression tag	UNP V9HWJ7
e	209	LYS	-	expression tag	UNP V9HWJ7
e	210	VAL	-	expression tag	UNP V9HWJ7
e	211	HIS	-	expression tag	UNP V9HWJ7
e	212	HIS	-	expression tag	UNP V9HWJ7
e	213	HIS	-	expression tag	UNP V9HWJ7
e	214	HIS	-	expression tag	UNP V9HWJ7
e	215	HIS	-	expression tag	UNP V9HWJ7
e	216	HIS	-	expression tag	UNP V9HWJ7
e	217	ILE	-	expression tag	UNP V9HWJ7
e	218	GLU	-	expression tag	UNP V9HWJ7
e	219	GLY	-	expression tag	UNP V9HWJ7
e	220	ARG	-	expression tag	UNP V9HWJ7
e	221	HIS	-	expression tag	UNP V9HWJ7
e	222	MET	-	expression tag	UNP V9HWJ7
e	223	GLU	-	expression tag	UNP V9HWJ7
e	224	LEU	-	expression tag	UNP V9HWJ7
e	225	GLY	-	expression tag	UNP V9HWJ7
e	226	THR	-	expression tag	UNP V9HWJ7
e	227	LEU	-	expression tag	UNP V9HWJ7
e	228	GLU	-	expression tag	UNP V9HWJ7

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Chain	Residue	Modelled	Actual	Comment	Reference
e	229	GLU	-	expression tag	UNP V9HWJ7
e	230	ASN	-	expression tag	UNP V9HWJ7
e	231	LEU	-	expression tag	UNP V9HWJ7
e	232	TYR	-	expression tag	UNP V9HWJ7
e	233	PHE	-	expression tag	UNP V9HWJ7
e	234	GLN	-	expression tag	UNP V9HWJ7
e	235	GLY	-	expression tag	UNP V9HWJ7
e	236	GLU	-	expression tag	UNP V9HWJ7
e	237	LEU	-	expression tag	UNP V9HWJ7
f	206	MET	-	expression tag	UNP V9HWJ7
f	207	ASN	-	expression tag	UNP V9HWJ7
f	208	HIS	-	expression tag	UNP V9HWJ7
f	209	LYS	-	expression tag	UNP V9HWJ7
f	210	VAL	-	expression tag	UNP V9HWJ7
f	211	HIS	-	expression tag	UNP V9HWJ7
f	212	HIS	-	expression tag	UNP V9HWJ7
f	213	HIS	-	expression tag	UNP V9HWJ7
f	214	HIS	-	expression tag	UNP V9HWJ7
f	215	HIS	-	expression tag	UNP V9HWJ7
f	216	HIS	-	expression tag	UNP V9HWJ7
f	217	ILE	-	expression tag	UNP V9HWJ7
f	218	GLU	-	expression tag	UNP V9HWJ7
f	219	GLY	-	expression tag	UNP V9HWJ7
f	220	ARG	-	expression tag	UNP V9HWJ7
f	221	HIS	-	expression tag	UNP V9HWJ7
f	222	MET	-	expression tag	UNP V9HWJ7
f	223	GLU	-	expression tag	UNP V9HWJ7
f	224	LEU	-	expression tag	UNP V9HWJ7
f	225	GLY	-	expression tag	UNP V9HWJ7
f	226	THR	-	expression tag	UNP V9HWJ7
f	227	LEU	-	expression tag	UNP V9HWJ7
f	228	GLU	-	expression tag	UNP V9HWJ7
f	229	GLU	-	expression tag	UNP V9HWJ7
f	230	ASN	-	expression tag	UNP V9HWJ7
f	231	LEU	-	expression tag	UNP V9HWJ7
f	232	TYR	-	expression tag	UNP V9HWJ7
f	233	PHE	-	expression tag	UNP V9HWJ7
f	234	GLN	-	expression tag	UNP V9HWJ7
f	235	GLY	-	expression tag	UNP V9HWJ7
f	236	GLU	-	expression tag	UNP V9HWJ7
f	237	LEU	-	expression tag	UNP V9HWJ7
g	206	MET	-	expression tag	UNP V9HWJ7

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Chain	Residue	Modelled	Actual	Comment	Reference
g	207	ASN	-	expression tag	UNP V9HWJ7
g	208	HIS	-	expression tag	UNP V9HWJ7
g	209	LYS	-	expression tag	UNP V9HWJ7
g	210	VAL	-	expression tag	UNP V9HWJ7
g	211	HIS	-	expression tag	UNP V9HWJ7
g	212	HIS	-	expression tag	UNP V9HWJ7
g	213	HIS	-	expression tag	UNP V9HWJ7
g	214	HIS	-	expression tag	UNP V9HWJ7
g	215	HIS	-	expression tag	UNP V9HWJ7
g	216	HIS	-	expression tag	UNP V9HWJ7
g	217	ILE	-	expression tag	UNP V9HWJ7
g	218	GLU	-	expression tag	UNP V9HWJ7
g	219	GLY	-	expression tag	UNP V9HWJ7
g	220	ARG	-	expression tag	UNP V9HWJ7
g	221	HIS	-	expression tag	UNP V9HWJ7
g	222	MET	-	expression tag	UNP V9HWJ7
g	223	GLU	-	expression tag	UNP V9HWJ7
g	224	LEU	-	expression tag	UNP V9HWJ7
g	225	GLY	-	expression tag	UNP V9HWJ7
g	226	THR	-	expression tag	UNP V9HWJ7
g	227	LEU	-	expression tag	UNP V9HWJ7
g	228	GLU	-	expression tag	UNP V9HWJ7
g	229	GLU	-	expression tag	UNP V9HWJ7
g	230	ASN	-	expression tag	UNP V9HWJ7
g	231	LEU	-	expression tag	UNP V9HWJ7
g	232	TYR	-	expression tag	UNP V9HWJ7
g	233	PHE	-	expression tag	UNP V9HWJ7
g	234	GLN	-	expression tag	UNP V9HWJ7
g	235	GLY	-	expression tag	UNP V9HWJ7
g	236	GLU	-	expression tag	UNP V9HWJ7
g	237	LEU	-	expression tag	UNP V9HWJ7
h	206	MET	-	expression tag	UNP V9HWJ7
h	207	ASN	-	expression tag	UNP V9HWJ7
h	208	HIS	-	expression tag	UNP V9HWJ7
h	209	LYS	-	expression tag	UNP V9HWJ7
h	210	VAL	-	expression tag	UNP V9HWJ7
h	211	HIS	-	expression tag	UNP V9HWJ7
h	212	HIS	-	expression tag	UNP V9HWJ7
h	213	HIS	-	expression tag	UNP V9HWJ7
h	214	HIS	-	expression tag	UNP V9HWJ7
h	215	HIS	-	expression tag	UNP V9HWJ7
h	216	HIS	-	expression tag	UNP V9HWJ7

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Chain	Residue	Modelled	Actual	Comment	Reference
h	217	ILE	-	expression tag	UNP V9HWJ7
h	218	GLU	-	expression tag	UNP V9HWJ7
h	219	GLY	-	expression tag	UNP V9HWJ7
h	220	ARG	-	expression tag	UNP V9HWJ7
h	221	HIS	-	expression tag	UNP V9HWJ7
h	222	MET	-	expression tag	UNP V9HWJ7
h	223	GLU	-	expression tag	UNP V9HWJ7
h	224	LEU	-	expression tag	UNP V9HWJ7
h	225	GLY	-	expression tag	UNP V9HWJ7
h	226	THR	-	expression tag	UNP V9HWJ7
h	227	LEU	-	expression tag	UNP V9HWJ7
h	228	GLU	-	expression tag	UNP V9HWJ7
h	229	GLU	-	expression tag	UNP V9HWJ7
h	230	ASN	-	expression tag	UNP V9HWJ7
h	231	LEU	-	expression tag	UNP V9HWJ7
h	232	TYR	-	expression tag	UNP V9HWJ7
h	233	PHE	-	expression tag	UNP V9HWJ7
h	234	GLN	-	expression tag	UNP V9HWJ7
h	235	GLY	-	expression tag	UNP V9HWJ7
h	236	GLU	-	expression tag	UNP V9HWJ7
h	237	LEU	-	expression tag	UNP V9HWJ7
i	206	MET	-	expression tag	UNP V9HWJ7
i	207	ASN	-	expression tag	UNP V9HWJ7
i	208	HIS	-	expression tag	UNP V9HWJ7
i	209	LYS	-	expression tag	UNP V9HWJ7
i	210	VAL	-	expression tag	UNP V9HWJ7
i	211	HIS	-	expression tag	UNP V9HWJ7
i	212	HIS	-	expression tag	UNP V9HWJ7
i	213	HIS	-	expression tag	UNP V9HWJ7
i	214	HIS	-	expression tag	UNP V9HWJ7
i	215	HIS	-	expression tag	UNP V9HWJ7
i	216	HIS	-	expression tag	UNP V9HWJ7
i	217	ILE	-	expression tag	UNP V9HWJ7
i	218	GLU	-	expression tag	UNP V9HWJ7
i	219	GLY	-	expression tag	UNP V9HWJ7
i	220	ARG	-	expression tag	UNP V9HWJ7
i	221	HIS	-	expression tag	UNP V9HWJ7
i	222	MET	-	expression tag	UNP V9HWJ7
i	223	GLU	-	expression tag	UNP V9HWJ7
i	224	LEU	-	expression tag	UNP V9HWJ7
i	225	GLY	-	expression tag	UNP V9HWJ7
i	226	THR	-	expression tag	UNP V9HWJ7

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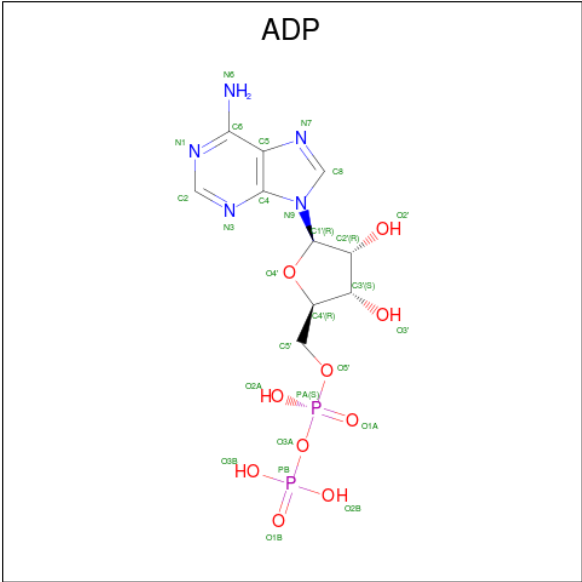
Chain	Residue	Modelled	Actual	Comment	Reference
i	227	LEU	-	expression tag	UNP V9HWJ7
i	228	GLU	-	expression tag	UNP V9HWJ7
i	229	GLU	-	expression tag	UNP V9HWJ7
i	230	ASN	-	expression tag	UNP V9HWJ7
i	231	LEU	-	expression tag	UNP V9HWJ7
i	232	TYR	-	expression tag	UNP V9HWJ7
i	233	PHE	-	expression tag	UNP V9HWJ7
i	234	GLN	-	expression tag	UNP V9HWJ7
i	235	GLY	-	expression tag	UNP V9HWJ7
i	236	GLU	-	expression tag	UNP V9HWJ7
i	237	LEU	-	expression tag	UNP V9HWJ7
j	206	MET	-	expression tag	UNP V9HWJ7
j	207	ASN	-	expression tag	UNP V9HWJ7
j	208	HIS	-	expression tag	UNP V9HWJ7
j	209	LYS	-	expression tag	UNP V9HWJ7
j	210	VAL	-	expression tag	UNP V9HWJ7
j	211	HIS	-	expression tag	UNP V9HWJ7
j	212	HIS	-	expression tag	UNP V9HWJ7
j	213	HIS	-	expression tag	UNP V9HWJ7
j	214	HIS	-	expression tag	UNP V9HWJ7
j	215	HIS	-	expression tag	UNP V9HWJ7
j	216	HIS	-	expression tag	UNP V9HWJ7
j	217	ILE	-	expression tag	UNP V9HWJ7
j	218	GLU	-	expression tag	UNP V9HWJ7
j	219	GLY	-	expression tag	UNP V9HWJ7
j	220	ARG	-	expression tag	UNP V9HWJ7
j	221	HIS	-	expression tag	UNP V9HWJ7
j	222	MET	-	expression tag	UNP V9HWJ7
j	223	GLU	-	expression tag	UNP V9HWJ7
j	224	LEU	-	expression tag	UNP V9HWJ7
j	225	GLY	-	expression tag	UNP V9HWJ7
j	226	THR	-	expression tag	UNP V9HWJ7
j	227	LEU	-	expression tag	UNP V9HWJ7
j	228	GLU	-	expression tag	UNP V9HWJ7
j	229	GLU	-	expression tag	UNP V9HWJ7
j	230	ASN	-	expression tag	UNP V9HWJ7
j	231	LEU	-	expression tag	UNP V9HWJ7
j	232	TYR	-	expression tag	UNP V9HWJ7
j	233	PHE	-	expression tag	UNP V9HWJ7
j	234	GLN	-	expression tag	UNP V9HWJ7
j	235	GLY	-	expression tag	UNP V9HWJ7
j	236	GLU	-	expression tag	UNP V9HWJ7

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Chain	Residue	Modelled	Actual	Comment	Reference
j	237	LEU	-	expression tag	UNP V9HWJ7
k	206	MET	-	expression tag	UNP V9HWJ7
k	207	ASN	-	expression tag	UNP V9HWJ7
k	208	HIS	-	expression tag	UNP V9HWJ7
k	209	LYS	-	expression tag	UNP V9HWJ7
k	210	VAL	-	expression tag	UNP V9HWJ7
k	211	HIS	-	expression tag	UNP V9HWJ7
k	212	HIS	-	expression tag	UNP V9HWJ7
k	213	HIS	-	expression tag	UNP V9HWJ7
k	214	HIS	-	expression tag	UNP V9HWJ7
k	215	HIS	-	expression tag	UNP V9HWJ7
k	216	HIS	-	expression tag	UNP V9HWJ7
k	217	ILE	-	expression tag	UNP V9HWJ7
k	218	GLU	-	expression tag	UNP V9HWJ7
k	219	GLY	-	expression tag	UNP V9HWJ7
k	220	ARG	-	expression tag	UNP V9HWJ7
k	221	HIS	-	expression tag	UNP V9HWJ7
k	222	MET	-	expression tag	UNP V9HWJ7
k	223	GLU	-	expression tag	UNP V9HWJ7
k	224	LEU	-	expression tag	UNP V9HWJ7
k	225	GLY	-	expression tag	UNP V9HWJ7
k	226	THR	-	expression tag	UNP V9HWJ7
k	227	LEU	-	expression tag	UNP V9HWJ7
k	228	GLU	-	expression tag	UNP V9HWJ7
k	229	GLU	-	expression tag	UNP V9HWJ7
k	230	ASN	-	expression tag	UNP V9HWJ7
k	231	LEU	-	expression tag	UNP V9HWJ7
k	232	TYR	-	expression tag	UNP V9HWJ7
k	233	PHE	-	expression tag	UNP V9HWJ7
k	234	GLN	-	expression tag	UNP V9HWJ7
k	235	GLY	-	expression tag	UNP V9HWJ7
k	236	GLU	-	expression tag	UNP V9HWJ7
k	237	LEU	-	expression tag	UNP V9HWJ7

- Molecule 3 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula: C₁₀H₁₅N₅O₁₀P₂).



Mol	Chain	Residues	Atoms					AltConf
3	A	1	Total	C	N	O	P	0
			27	10	5	10	2	
3	B	1	Total	C	N	O	P	0
			27	10	5	10	2	
3	C	1	Total	C	N	O	P	0
			27	10	5	10	2	
3	D	1	Total	C	N	O	P	0
			27	10	5	10	2	
3	E	1	Total	C	N	O	P	0
			27	10	5	10	2	
3	F	1	Total	C	N	O	P	0
			27	10	5	10	2	
3	G	1	Total	C	N	O	P	0
			27	10	5	10	2	
3	H	1	Total	C	N	O	P	0
			27	10	5	10	2	
3	I	1	Total	C	N	O	P	0
			27	10	5	10	2	
3	J	1	Total	C	N	O	P	0
			27	10	5	10	2	
3	K	1	Total	C	N	O	P	0
			27	10	5	10	2	

- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
4	A	1	Total	Mg	0
			1	1	

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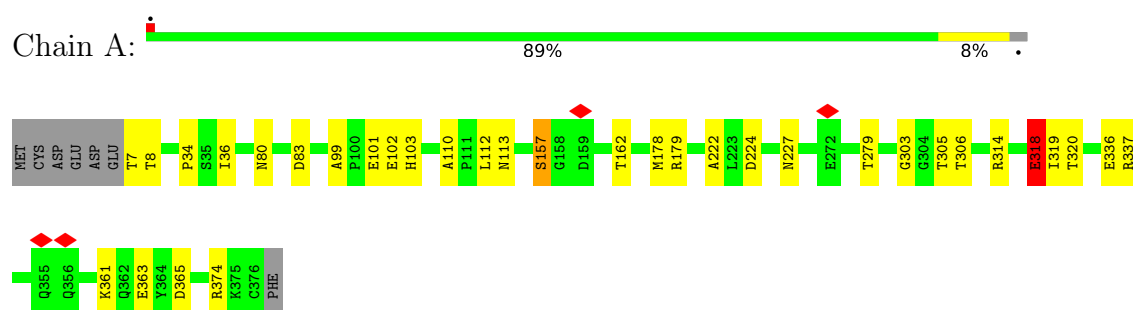
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Mol	Chain	Residues	Atoms		AltConf
4	B	1	Total 1	Mg 1	0
4	C	1	Total 1	Mg 1	0
4	D	1	Total 1	Mg 1	0
4	E	1	Total 1	Mg 1	0
4	F	1	Total 1	Mg 1	0
4	G	1	Total 1	Mg 1	0
4	H	1	Total 1	Mg 1	0
4	I	1	Total 1	Mg 1	0
4	J	1	Total 1	Mg 1	0
4	K	1	Total 1	Mg 1	0

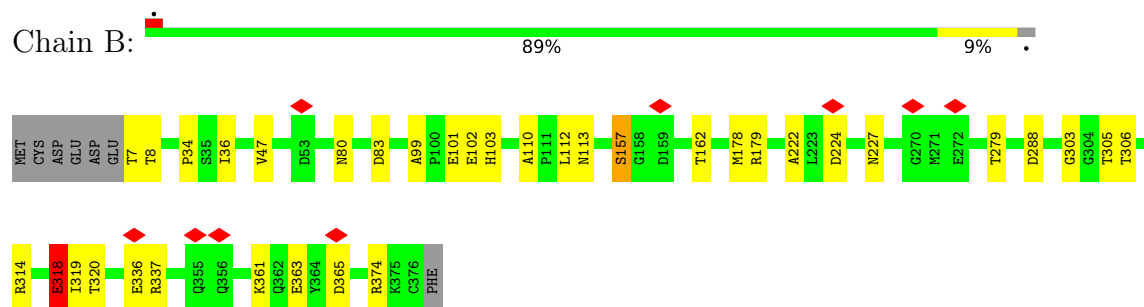
3 Residue-property plots [i](#)

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.

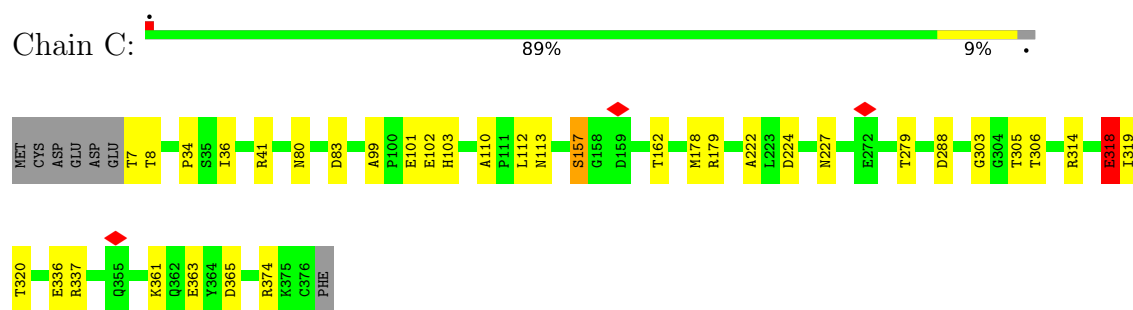
- Molecule 1: Actin, alpha skeletal muscle



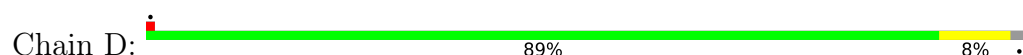
- Molecule 1: Actin, alpha skeletal muscle

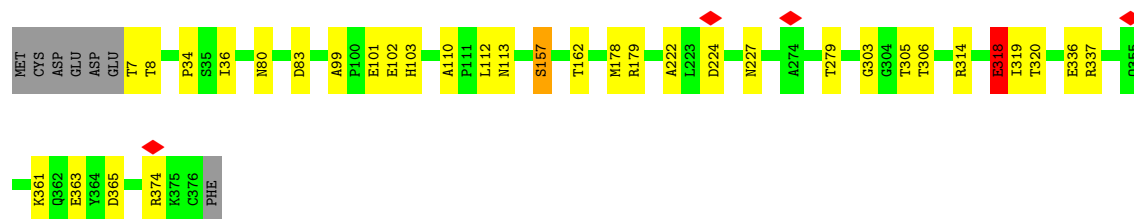


- Molecule 1: Actin, alpha skeletal muscle

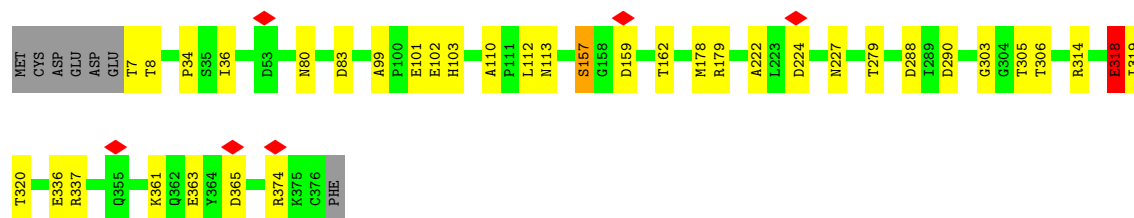
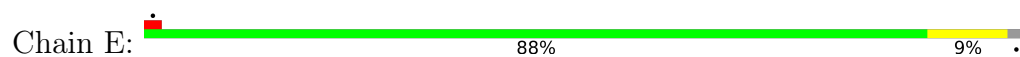


- Molecule 1: Actin, alpha skeletal muscle

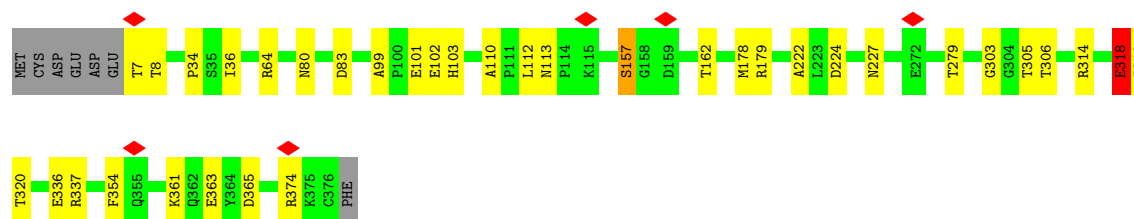
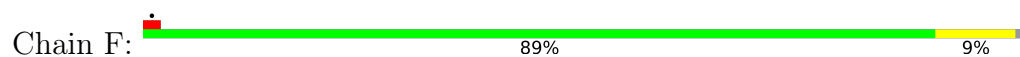




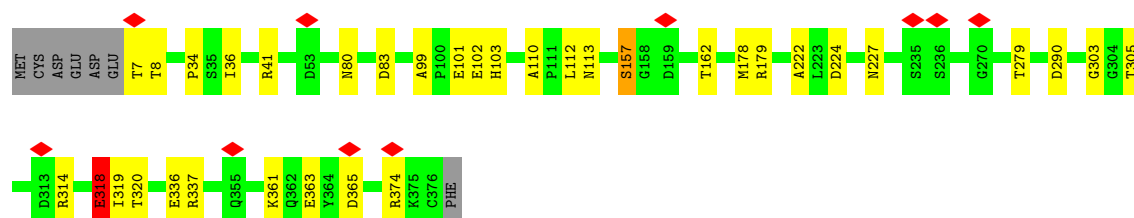
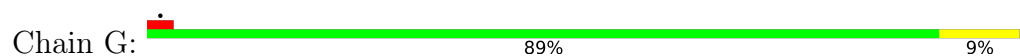
- Molecule 1: Actin, alpha skeletal muscle



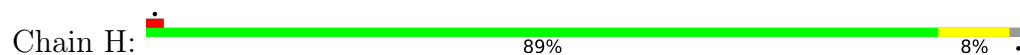
- Molecule 1: Actin, alpha skeletal muscle

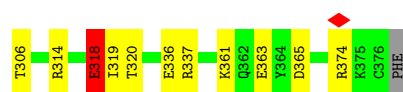


- Molecule 1: Actin, alpha skeletal muscle

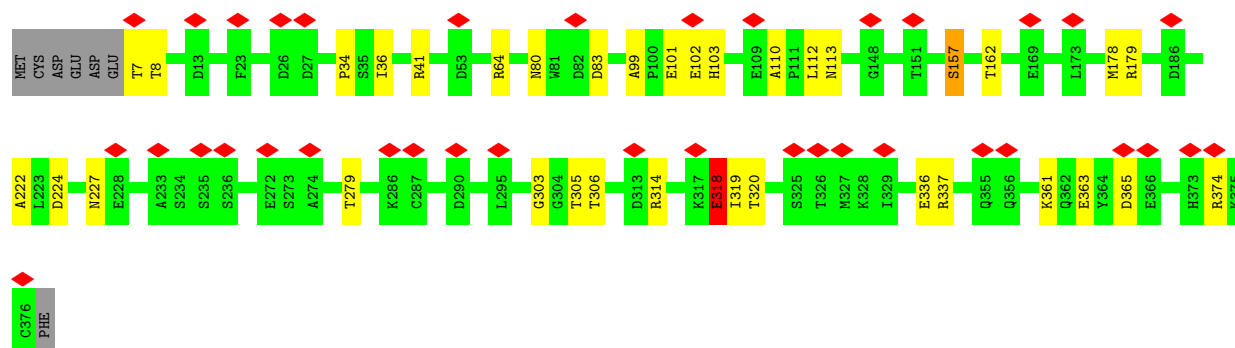
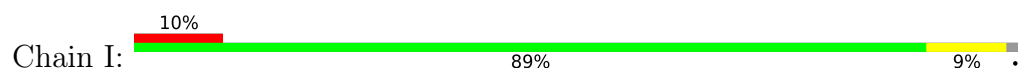


- Molecule 1: Actin, alpha skeletal muscle

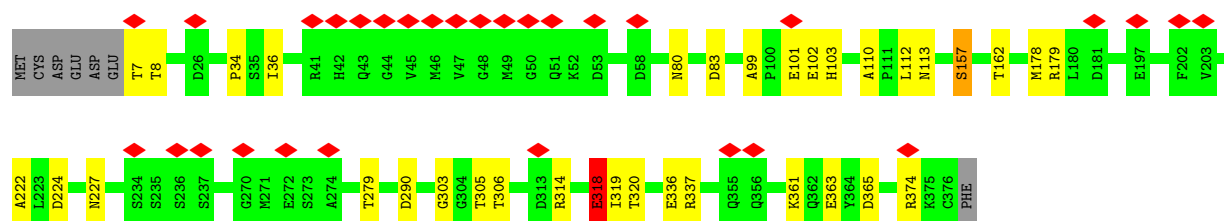
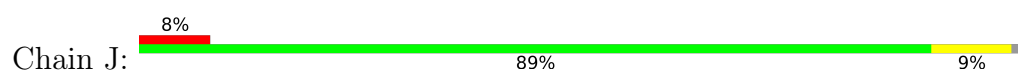




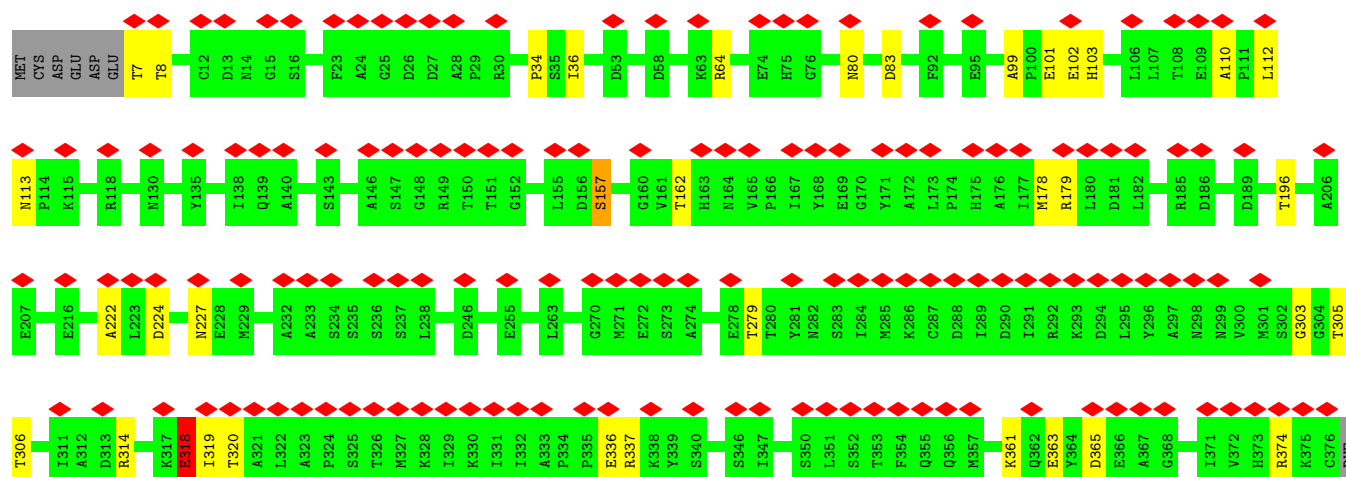
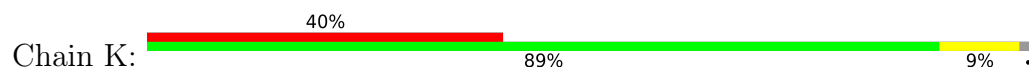
- Molecule 1: Actin, alpha skeletal muscle



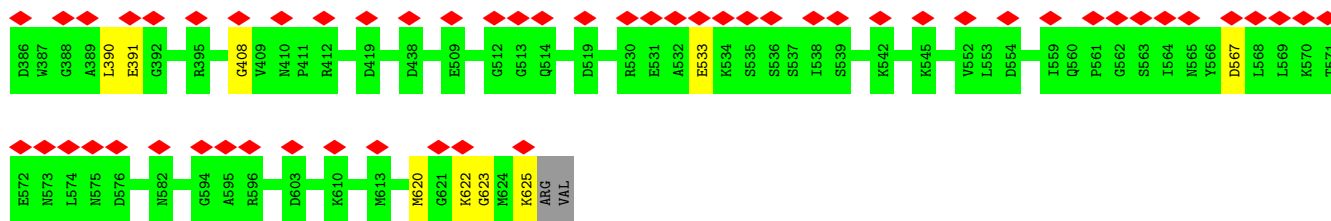
- Molecule 1: Actin, alpha skeletal muscle



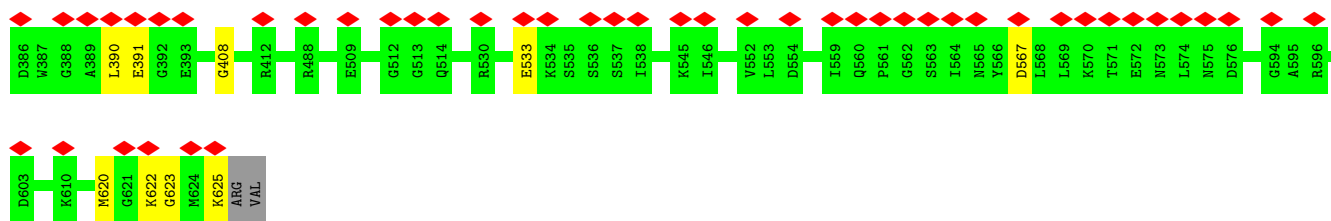
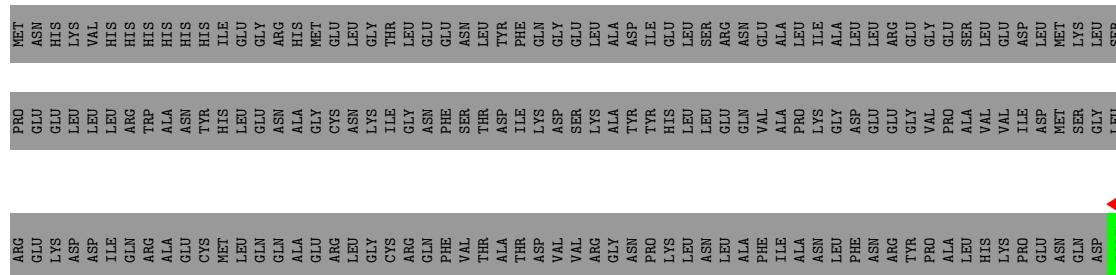
- Molecule 1: Actin, alpha skeletal muscle



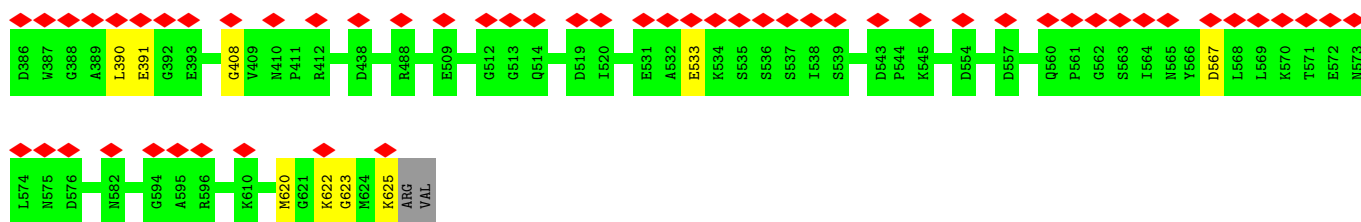
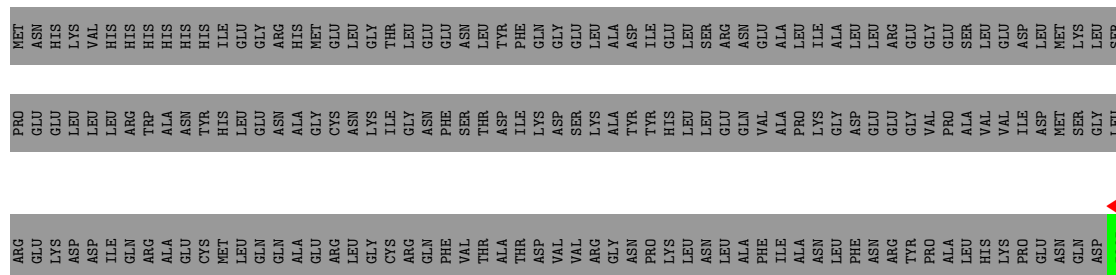
- Molecule 2: LCP1



• Molecule 2: LCP1

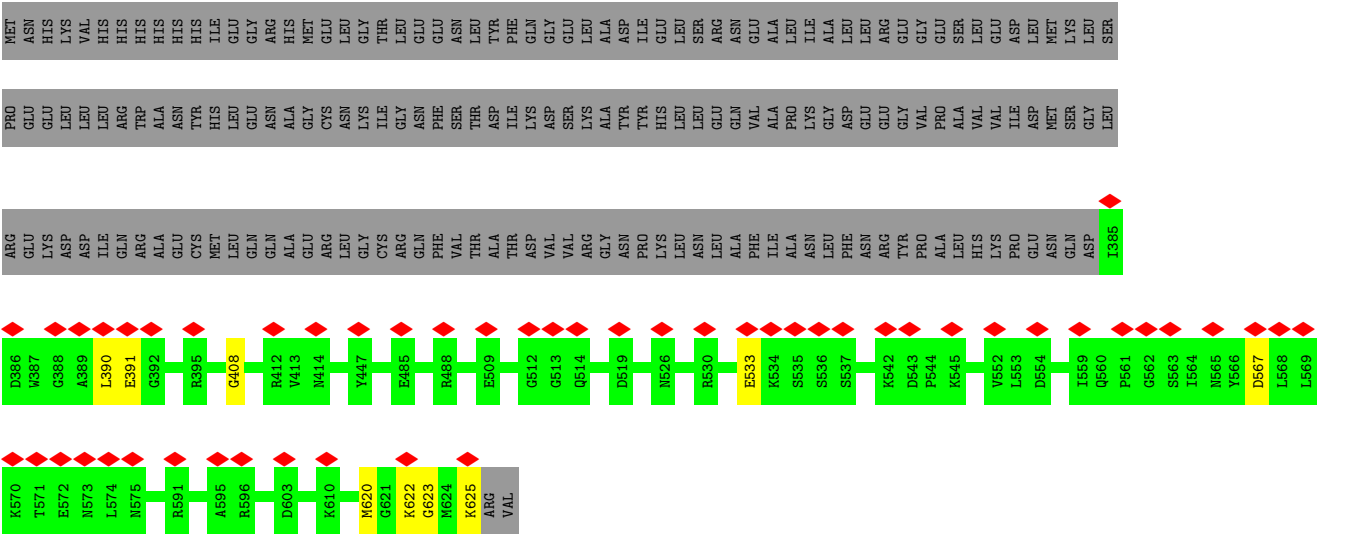


• Molecule 2: LCP1

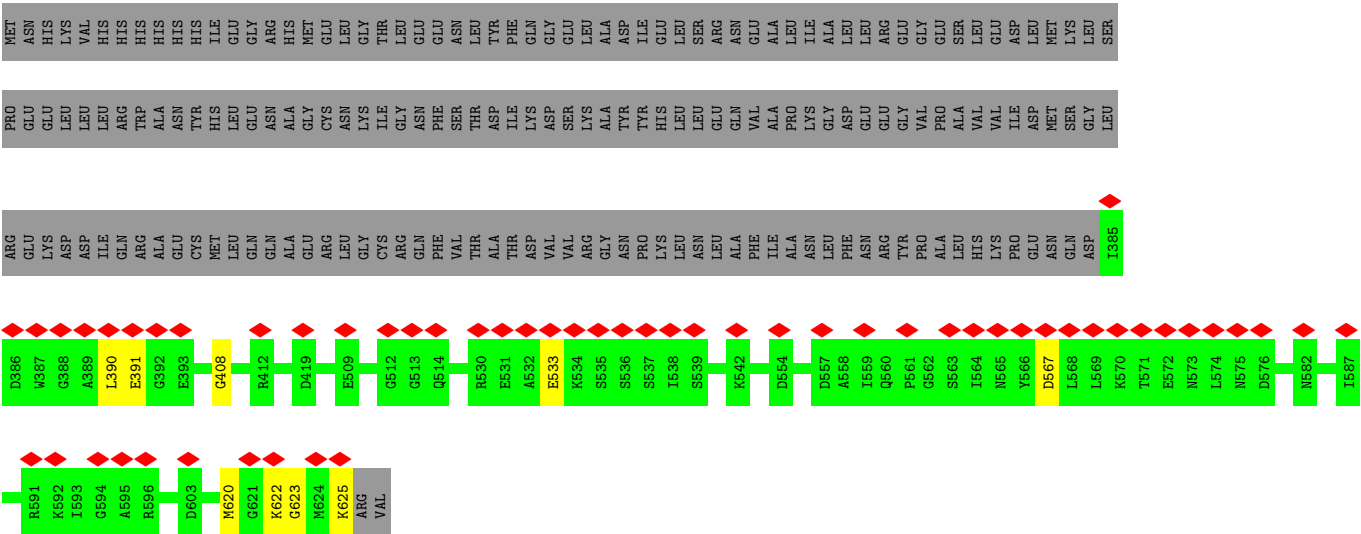


• Molecule 2: LCP1

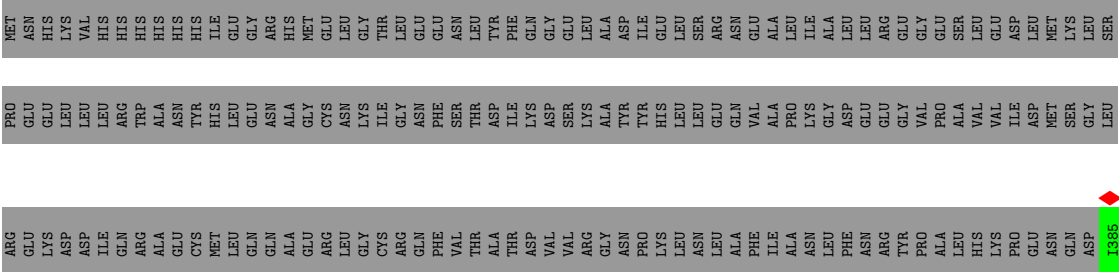


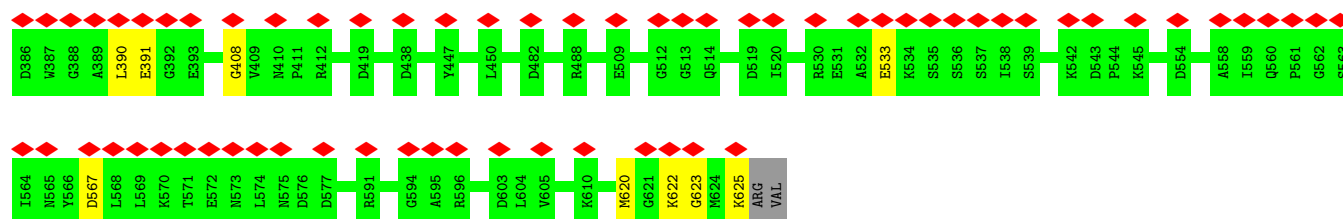


• Molecule 2: LCP1

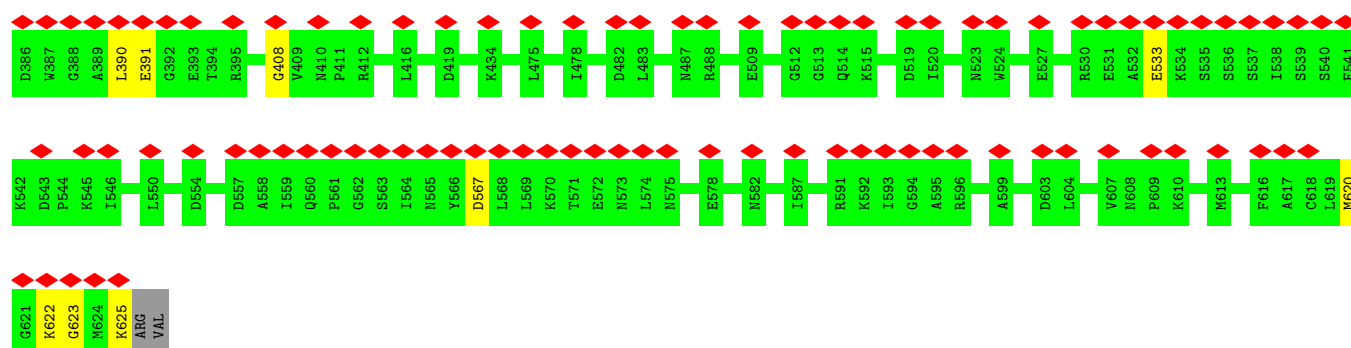
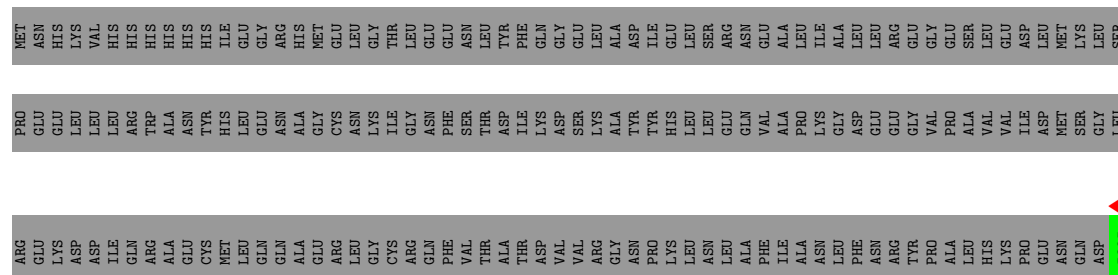


• Molecule 2: LCP1

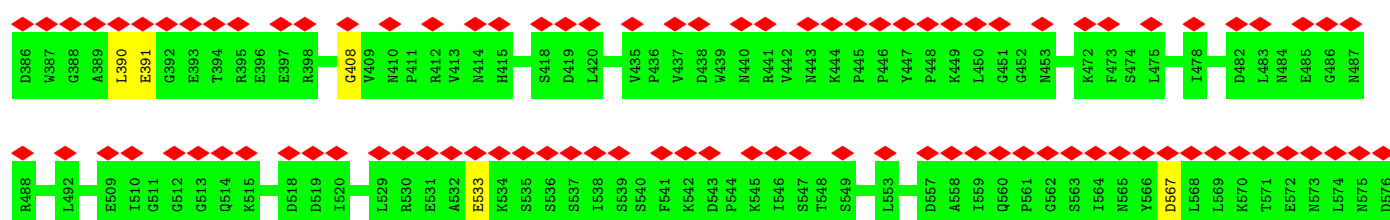
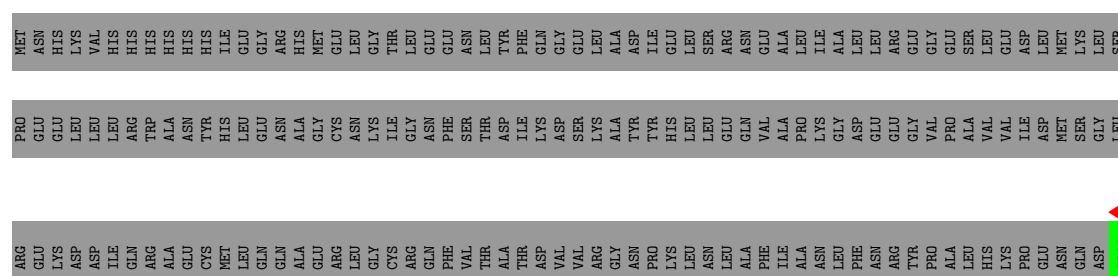




• Molecule 2: LCP1



• Molecule 2: LCP1



4 Experimental information

Property	Value	Source
EM reconstruction method	HELICAL	Depositor
Imposed symmetry	HELICAL, twist=-166.5°, rise=28.0 Å, axial sym=C1	Depositor
Number of segments used	124092	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 ($e^-/\text{Å}^2$)	20	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.261	Depositor
Minimum map value	-0.086	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.011	Depositor
Recommended contour level	0.0611	Depositor
Map size (Å)	358.4, 358.4, 358.4	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.4, 1.4, 1.4	Depositor

5 Model quality

5.1 Standard geometry

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

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	0.40	0/2949	0.57	0/3996
1	B	0.40	0/2949	0.57	0/3996
1	C	0.40	0/2949	0.57	0/3996
1	D	0.40	0/2949	0.57	0/3996
1	E	0.40	0/2949	0.57	0/3996
1	F	0.40	0/2949	0.57	0/3996
1	G	0.40	0/2949	0.57	0/3996
1	H	0.40	0/2949	0.57	0/3996
1	I	0.40	0/2949	0.57	0/3996
1	J	0.40	0/2949	0.57	0/3996
1	K	0.40	0/2949	0.57	0/3996
2	a	0.40	0/1942	0.68	3/2626 (0.1%)
2	b	0.40	0/1942	0.68	3/2626 (0.1%)
2	c	0.40	0/1942	0.68	3/2626 (0.1%)
2	d	0.40	0/1942	0.68	3/2626 (0.1%)
2	e	0.40	0/1942	0.68	3/2626 (0.1%)
2	f	0.40	0/1942	0.68	3/2626 (0.1%)
2	g	0.40	0/1942	0.68	3/2626 (0.1%)
2	h	0.40	0/1942	0.68	3/2626 (0.1%)
2	i	0.40	0/1942	0.68	3/2626 (0.1%)
2	j	0.40	0/1942	0.68	3/2626 (0.1%)
2	k	0.40	0/1942	0.68	3/2626 (0.1%)
All	All	0.40	0/53801	0.62	33/72842 (0.0%)

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

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

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Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	1
1	C	0	1
1	D	0	1
1	E	0	1
1	F	0	1
1	G	0	1
1	H	0	1
1	I	0	1
1	J	0	1
1	K	0	1
2	a	0	1
2	b	0	1
2	c	0	1
2	d	0	1
2	e	0	1
2	f	0	1
2	g	0	1
2	h	0	1
2	i	0	1
2	j	0	1
2	k	0	1
All	All	0	22

There are no bond length outliers.

All (33) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	d	622	LYS	CB-CG-CD	7.60	131.37	111.60
2	a	622	LYS	CB-CG-CD	7.60	131.36	111.60
2	h	622	LYS	CB-CG-CD	7.59	131.34	111.60
2	g	622	LYS	CB-CG-CD	7.59	131.34	111.60
2	e	622	LYS	CB-CG-CD	7.59	131.32	111.60
2	i	622	LYS	CB-CG-CD	7.59	131.32	111.60
2	k	622	LYS	CB-CG-CD	7.59	131.33	111.60
2	b	622	LYS	CB-CG-CD	7.58	131.32	111.60
2	j	622	LYS	CB-CG-CD	7.58	131.32	111.60
2	f	622	LYS	CB-CG-CD	7.58	131.31	111.60
2	c	622	LYS	CB-CG-CD	7.58	131.30	111.60
2	c	390	LEU	C-N-CA	7.21	139.72	121.70
2	h	390	LEU	C-N-CA	7.21	139.72	121.70
2	j	390	LEU	C-N-CA	7.21	139.71	121.70
2	d	390	LEU	C-N-CA	7.21	139.71	121.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	f	390	LEU	C-N-CA	7.21	139.71	121.70
2	e	390	LEU	C-N-CA	7.20	139.71	121.70
2	a	390	LEU	C-N-CA	7.20	139.70	121.70
2	b	390	LEU	C-N-CA	7.20	139.70	121.70
2	i	390	LEU	C-N-CA	7.20	139.70	121.70
2	g	390	LEU	C-N-CA	7.19	139.68	121.70
2	k	390	LEU	C-N-CA	7.18	139.64	121.70
2	b	623	GLY	C-N-CA	5.69	135.93	121.70
2	e	623	GLY	C-N-CA	5.69	135.92	121.70
2	c	623	GLY	C-N-CA	5.69	135.91	121.70
2	i	623	GLY	C-N-CA	5.69	135.91	121.70
2	h	623	GLY	C-N-CA	5.68	135.91	121.70
2	k	623	GLY	C-N-CA	5.68	135.91	121.70
2	f	623	GLY	C-N-CA	5.68	135.90	121.70
2	a	623	GLY	C-N-CA	5.68	135.89	121.70
2	d	623	GLY	C-N-CA	5.68	135.89	121.70
2	g	623	GLY	C-N-CA	5.66	135.85	121.70
2	j	623	GLY	C-N-CA	5.66	135.85	121.70

There are no chirality outliers.

All (22) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	318	GLU	Peptide
1	B	318	GLU	Peptide
1	C	318	GLU	Peptide
1	D	318	GLU	Peptide
1	E	318	GLU	Peptide
1	F	318	GLU	Peptide
1	G	318	GLU	Peptide
1	H	318	GLU	Peptide
1	I	318	GLU	Peptide
1	J	318	GLU	Peptide
1	K	318	GLU	Peptide
2	a	620	MET	Peptide
2	b	620	MET	Peptide
2	c	620	MET	Peptide
2	d	620	MET	Peptide
2	e	620	MET	Peptide
2	f	620	MET	Peptide
2	g	620	MET	Peptide
2	h	620	MET	Peptide

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Mol	Chain	Res	Type	Group
2	i	620	MET	Peptide
2	j	620	MET	Peptide
2	k	620	MET	Peptide

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	2887	0	2862	18	0
1	B	2887	0	2862	22	0
1	C	2887	0	2862	21	0
1	D	2887	0	2862	20	0
1	E	2887	0	2862	22	0
1	F	2887	0	2862	22	0
1	G	2887	0	2862	21	0
1	H	2887	0	2862	20	0
1	I	2887	0	2862	22	0
1	J	2887	0	2862	20	0
1	K	2887	0	2862	22	0
2	a	1909	0	1934	0	0
2	b	1909	0	1934	0	0
2	c	1909	0	1934	0	0
2	d	1909	0	1934	0	0
2	e	1909	0	1934	0	0
2	f	1909	0	1934	0	0
2	g	1909	0	1934	0	0
2	h	1909	0	1934	0	0
2	i	1909	0	1934	0	0
2	j	1909	0	1934	0	0
2	k	1909	0	1934	0	0
3	A	27	0	12	0	0
3	B	27	0	12	0	0
3	C	27	0	12	0	0
3	D	27	0	12	0	0
3	E	27	0	12	1	0
3	F	27	0	12	0	0
3	G	27	0	12	0	0
3	H	27	0	12	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	I	27	0	12	0	0
3	J	27	0	12	0	0
3	K	27	0	12	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
4	J	1	0	0	0	0
4	K	1	0	0	0	0
All	All	53064	0	52888	222	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 3.

All (222) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:157:SER:HG	1:J:305:THR:HG1	1.01	0.91
1:B:157:SER:HG	1:B:305:THR:HG1	1.05	0.88
1:F:157:SER:HG	1:F:305:THR:HG1	1.04	0.86
1:K:157:SER:HG	1:K:305:THR:HG1	1.01	0.83
1:H:157:SER:HG	1:H:305:THR:HG1	1.01	0.82
1:E:157:SER:HG	1:E:305:THR:HG1	1.02	0.79
1:D:157:SER:HG	1:D:305:THR:HG1	1.01	0.77
1:C:157:SER:HG	1:C:305:THR:HG1	1.01	0.76
1:I:112:LEU:O	1:I:179:ARG:NH1	2.22	0.73
1:B:112:LEU:O	1:B:179:ARG:NH1	2.22	0.73
1:D:112:LEU:O	1:D:179:ARG:NH1	2.22	0.73
1:G:112:LEU:O	1:G:179:ARG:NH1	2.22	0.73
1:F:112:LEU:O	1:F:179:ARG:NH1	2.22	0.72
1:K:112:LEU:O	1:K:179:ARG:NH1	2.22	0.72
1:C:112:LEU:O	1:C:179:ARG:NH1	2.22	0.72
1:F:306:THR:O	1:F:337:ARG:NH1	2.23	0.72
1:H:112:LEU:O	1:H:179:ARG:NH1	2.22	0.72
1:A:112:LEU:O	1:A:179:ARG:NH1	2.22	0.72
1:E:112:LEU:O	1:E:179:ARG:NH1	2.22	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:306:THR:O	1:J:337:ARG:NH1	2.23	0.72
1:D:306:THR:O	1:D:337:ARG:NH1	2.23	0.72
1:H:306:THR:O	1:H:337:ARG:NH1	2.23	0.72
1:A:306:THR:O	1:A:337:ARG:NH1	2.23	0.72
1:B:306:THR:O	1:B:337:ARG:NH1	2.23	0.72
1:K:306:THR:O	1:K:337:ARG:NH1	2.23	0.72
1:G:110:ALA:O	1:G:113:ASN:ND2	2.24	0.71
1:E:306:THR:O	1:E:337:ARG:NH1	2.23	0.71
1:G:306:THR:O	1:G:337:ARG:NH1	2.23	0.71
1:D:110:ALA:O	1:D:113:ASN:ND2	2.24	0.71
1:J:112:LEU:O	1:J:179:ARG:NH1	2.22	0.71
1:H:110:ALA:O	1:H:113:ASN:ND2	2.24	0.71
1:B:110:ALA:O	1:B:113:ASN:ND2	2.23	0.71
1:C:110:ALA:O	1:C:113:ASN:ND2	2.24	0.71
1:I:110:ALA:O	1:I:113:ASN:ND2	2.24	0.71
1:I:306:THR:O	1:I:337:ARG:NH1	2.23	0.71
1:C:306:THR:O	1:C:337:ARG:NH1	2.23	0.71
1:F:110:ALA:O	1:F:113:ASN:ND2	2.24	0.71
1:J:110:ALA:O	1:J:113:ASN:ND2	2.24	0.71
1:E:110:ALA:O	1:E:113:ASN:ND2	2.24	0.71
1:K:110:ALA:O	1:K:113:ASN:ND2	2.24	0.70
1:A:110:ALA:O	1:A:113:ASN:ND2	2.23	0.70
1:D:224:ASP:OD2	1:D:227:ASN:ND2	2.26	0.69
1:F:224:ASP:OD2	1:F:227:ASN:ND2	2.26	0.69
1:K:224:ASP:OD2	1:K:227:ASN:ND2	2.26	0.69
1:I:80:ASN:ND2	1:I:83:ASP:OD2	2.26	0.69
1:D:80:ASN:ND2	1:D:83:ASP:OD2	2.26	0.69
1:E:80:ASN:ND2	1:E:83:ASP:OD2	2.26	0.69
1:G:80:ASN:ND2	1:G:83:ASP:OD2	2.26	0.69
1:G:224:ASP:OD2	1:G:227:ASN:ND2	2.26	0.69
1:A:224:ASP:OD2	1:A:227:ASN:ND2	2.26	0.69
1:B:224:ASP:OD2	1:B:227:ASN:ND2	2.26	0.68
1:C:80:ASN:ND2	1:C:83:ASP:OD2	2.26	0.68
1:B:80:ASN:ND2	1:B:83:ASP:OD2	2.26	0.68
1:H:80:ASN:ND2	1:H:83:ASP:OD2	2.26	0.68
1:J:80:ASN:ND2	1:J:83:ASP:OD2	2.26	0.68
1:K:80:ASN:ND2	1:K:83:ASP:OD2	2.26	0.68
1:C:224:ASP:OD2	1:C:227:ASN:ND2	2.26	0.68
1:I:224:ASP:OD2	1:I:227:ASN:ND2	2.26	0.68
1:F:80:ASN:ND2	1:F:83:ASP:OD2	2.26	0.68
1:E:224:ASP:OD2	1:E:227:ASN:ND2	2.26	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:224:ASP:OD2	1:J:227:ASN:ND2	2.26	0.68
1:A:80:ASN:ND2	1:A:83:ASP:OD2	2.26	0.68
1:H:224:ASP:OD2	1:H:227:ASN:ND2	2.26	0.68
1:C:157:SER:O	1:C:305:THR:OG1	2.13	0.66
1:G:157:SER:O	1:G:305:THR:OG1	2.13	0.66
1:B:157:SER:O	1:B:305:THR:OG1	2.13	0.66
1:K:157:SER:O	1:K:305:THR:OG1	2.13	0.66
1:A:318:GLU:O	1:A:320:THR:N	2.29	0.66
1:D:363:GLU:OE2	1:D:374:ARG:NH2	2.29	0.66
1:E:157:SER:O	1:E:305:THR:OG1	2.13	0.66
1:I:157:SER:O	1:I:305:THR:OG1	2.13	0.66
1:F:157:SER:O	1:F:305:THR:OG1	2.13	0.66
1:H:363:GLU:OE2	1:H:374:ARG:NH2	2.29	0.66
1:A:363:GLU:OE2	1:A:374:ARG:NH2	2.29	0.65
1:E:318:GLU:O	1:E:320:THR:N	2.29	0.65
1:A:157:SER:O	1:A:305:THR:OG1	2.13	0.65
1:C:318:GLU:O	1:C:320:THR:N	2.29	0.65
1:G:318:GLU:O	1:G:320:THR:N	2.29	0.65
1:I:363:GLU:OE2	1:I:374:ARG:NH2	2.29	0.65
1:D:157:SER:O	1:D:305:THR:OG1	2.13	0.65
1:D:318:GLU:O	1:D:320:THR:N	2.29	0.65
1:H:157:SER:O	1:H:305:THR:OG1	2.13	0.65
1:J:318:GLU:O	1:J:320:THR:N	2.29	0.65
1:K:363:GLU:OE2	1:K:374:ARG:NH2	2.29	0.65
1:B:318:GLU:O	1:B:320:THR:N	2.29	0.65
1:J:157:SER:O	1:J:305:THR:OG1	2.13	0.65
1:K:318:GLU:O	1:K:320:THR:N	2.29	0.65
1:C:363:GLU:OE2	1:C:374:ARG:NH2	2.29	0.65
1:E:363:GLU:OE2	1:E:374:ARG:NH2	2.29	0.65
1:F:363:GLU:OE2	1:F:374:ARG:NH2	2.29	0.65
1:G:363:GLU:OE2	1:G:374:ARG:NH2	2.29	0.64
1:I:318:GLU:O	1:I:320:THR:N	2.29	0.64
1:J:363:GLU:OE2	1:J:374:ARG:NH2	2.29	0.64
1:F:318:GLU:O	1:F:320:THR:N	2.29	0.64
1:H:318:GLU:O	1:H:320:THR:N	2.29	0.64
1:B:363:GLU:OE2	1:B:374:ARG:NH2	2.29	0.64
1:J:303:GLY:O	1:J:306:THR:OG1	2.16	0.63
1:B:288:ASP:OD2	1:C:41:ARG:NH2	2.32	0.62
1:C:303:GLY:O	1:C:306:THR:OG1	2.16	0.62
1:I:157:SER:OG	1:I:305:THR:OG1	1.93	0.62
1:A:303:GLY:O	1:A:306:THR:OG1	2.16	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:303:GLY:O	1:D:306:THR:OG1	2.16	0.61
1:E:303:GLY:O	1:E:306:THR:OG1	2.16	0.61
1:F:303:GLY:O	1:F:306:THR:OG1	2.16	0.61
1:H:303:GLY:O	1:H:306:THR:OG1	2.16	0.61
1:B:303:GLY:O	1:B:306:THR:OG1	2.16	0.60
1:I:303:GLY:O	1:I:306:THR:OG1	2.16	0.60
1:E:290:ASP:OD2	1:I:64:ARG:NE	2.35	0.59
1:H:102:GLU:OE2	1:H:103:HIS:NE2	2.37	0.58
1:J:102:GLU:OE2	1:J:103:HIS:NE2	2.37	0.58
1:A:102:GLU:OE2	1:A:103:HIS:NE2	2.37	0.58
1:F:102:GLU:OE2	1:F:103:HIS:NE2	2.37	0.58
1:K:102:GLU:OE2	1:K:103:HIS:NE2	2.37	0.57
1:B:102:GLU:OE2	1:B:103:HIS:NE2	2.37	0.57
1:D:102:GLU:OE2	1:D:103:HIS:NE2	2.37	0.57
1:G:102:GLU:OE2	1:G:103:HIS:NE2	2.37	0.57
1:I:102:GLU:OE2	1:I:103:HIS:NE2	2.37	0.57
1:E:102:GLU:OE2	1:E:103:HIS:NE2	2.37	0.57
1:G:303:GLY:O	1:G:306:THR:OG1	2.16	0.57
1:C:102:GLU:OE2	1:C:103:HIS:NE2	2.37	0.57
1:K:303:GLY:O	1:K:306:THR:OG1	2.16	0.54
1:C:99:ALA:HB1	1:C:101:GLU:OE1	2.08	0.54
1:B:99:ALA:HB1	1:B:101:GLU:OE1	2.08	0.54
1:F:99:ALA:HB1	1:F:101:GLU:OE1	2.08	0.54
1:E:99:ALA:HB1	1:E:101:GLU:OE1	2.08	0.54
1:A:99:ALA:HB1	1:A:101:GLU:OE1	2.08	0.54
1:D:99:ALA:HB1	1:D:101:GLU:OE1	2.08	0.54
1:E:159:ASP:OD1	3:E:401:ADP:O3'	2.25	0.54
1:G:99:ALA:HB1	1:G:101:GLU:OE1	2.08	0.54
1:H:99:ALA:HB1	1:H:101:GLU:OE1	2.08	0.54
1:J:99:ALA:HB1	1:J:101:GLU:OE1	2.08	0.53
1:A:34:PRO:HG2	1:A:36:ILE:HD12	1.91	0.53
1:I:99:ALA:HB1	1:I:101:GLU:OE1	2.08	0.53
1:I:34:PRO:HG2	1:I:36:ILE:HD12	1.91	0.53
1:K:99:ALA:HB1	1:K:101:GLU:OE1	2.08	0.53
1:K:34:PRO:HG2	1:K:36:ILE:HD12	1.91	0.53
1:D:34:PRO:HG2	1:D:36:ILE:HD12	1.91	0.52
1:A:178:MET:SD	1:A:279:THR:OG1	2.68	0.52
1:H:34:PRO:HG2	1:H:36:ILE:HD12	1.91	0.52
1:F:178:MET:SD	1:F:279:THR:OG1	2.68	0.52
1:C:34:PRO:HG2	1:C:36:ILE:HD12	1.91	0.52
1:E:178:MET:SD	1:E:279:THR:OG1	2.68	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:178:MET:SD	1:J:279:THR:OG1	2.68	0.52
1:B:34:PRO:HG2	1:B:36:ILE:HD12	1.91	0.52
1:D:178:MET:SD	1:D:279:THR:OG1	2.68	0.52
1:G:34:PRO:HG2	1:G:36:ILE:HD12	1.91	0.52
1:J:34:PRO:HG2	1:J:36:ILE:HD12	1.91	0.52
1:E:34:PRO:HG2	1:E:36:ILE:HD12	1.91	0.51
1:C:178:MET:SD	1:C:279:THR:OG1	2.68	0.51
1:I:178:MET:SD	1:I:279:THR:OG1	2.68	0.51
1:F:34:PRO:HG2	1:F:36:ILE:HD12	1.91	0.51
1:K:178:MET:SD	1:K:279:THR:OG1	2.68	0.51
1:B:178:MET:SD	1:B:279:THR:OG1	2.68	0.50
1:A:336:GLU:N	1:A:336:GLU:OE1	2.45	0.50
1:D:336:GLU:OE1	1:D:336:GLU:N	2.45	0.50
1:E:336:GLU:N	1:E:336:GLU:OE1	2.45	0.50
1:H:336:GLU:N	1:H:336:GLU:OE1	2.45	0.50
1:K:336:GLU:OE1	1:K:336:GLU:N	2.45	0.50
1:I:336:GLU:OE1	1:I:336:GLU:N	2.45	0.50
1:H:178:MET:SD	1:H:279:THR:OG1	2.68	0.50
1:G:336:GLU:N	1:G:336:GLU:OE1	2.45	0.49
1:C:288:ASP:OD2	1:G:41:ARG:NH2	2.45	0.49
1:F:361:LYS:NZ	1:F:365:ASP:OD1	2.46	0.49
1:C:336:GLU:N	1:C:336:GLU:OE1	2.45	0.49
1:B:336:GLU:N	1:B:336:GLU:OE1	2.45	0.49
1:G:361:LYS:NZ	1:G:365:ASP:OD1	2.46	0.48
1:J:361:LYS:NZ	1:J:365:ASP:OD1	2.46	0.48
1:C:361:LYS:NZ	1:C:365:ASP:OD1	2.46	0.48
1:E:361:LYS:NZ	1:E:365:ASP:OD1	2.46	0.48
1:G:178:MET:SD	1:G:279:THR:OG1	2.68	0.48
1:F:336:GLU:OE1	1:F:336:GLU:N	2.45	0.48
1:J:336:GLU:N	1:J:336:GLU:OE1	2.45	0.48
1:D:361:LYS:NZ	1:D:365:ASP:OD1	2.46	0.48
1:A:361:LYS:NZ	1:A:365:ASP:OD1	2.46	0.47
1:F:64:ARG:NE	1:J:290:ASP:OD2	2.47	0.47
1:H:361:LYS:NZ	1:H:365:ASP:OD1	2.46	0.47
1:K:361:LYS:NZ	1:K:365:ASP:OD1	2.46	0.47
1:B:361:LYS:NZ	1:B:365:ASP:OD1	2.46	0.47
1:I:361:LYS:NZ	1:I:365:ASP:OD1	2.46	0.46
1:G:290:ASP:OD2	1:K:64:ARG:NE	2.49	0.46
1:K:157:SER:OG	1:K:305:THR:OG1	1.92	0.44
1:F:7:THR:OG1	1:F:8:THR:N	2.51	0.44
1:G:7:THR:OG1	1:G:8:THR:N	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:7:THR:OG1	1:B:8:THR:N	2.50	0.44
1:C:7:THR:OG1	1:C:8:THR:N	2.50	0.44
1:G:157:SER:OG	1:G:305:THR:OG1	1.92	0.44
1:H:7:THR:OG1	1:H:8:THR:N	2.51	0.44
1:B:157:SER:OG	1:B:305:THR:OG1	1.92	0.44
1:J:7:THR:OG1	1:J:8:THR:N	2.51	0.44
1:K:7:THR:OG1	1:K:8:THR:N	2.51	0.44
1:E:288:ASP:OD2	1:I:41:ARG:NH2	2.50	0.43
1:I:112:LEU:HB3	1:K:196:THR:HG21	2.00	0.43
1:E:7:THR:OG1	1:E:8:THR:N	2.51	0.43
1:A:7:THR:OG1	1:A:8:THR:N	2.50	0.42
1:D:7:THR:OG1	1:D:8:THR:N	2.51	0.42
1:H:222:ALA:O	1:H:314:ARG:NH1	2.53	0.42
1:K:222:ALA:O	1:K:314:ARG:NH1	2.53	0.42
1:H:157:SER:OG	1:H:305:THR:OG1	1.92	0.42
1:A:222:ALA:O	1:A:314:ARG:NH1	2.53	0.42
1:E:222:ALA:O	1:E:314:ARG:NH1	2.53	0.42
1:I:7:THR:OG1	1:I:8:THR:N	2.50	0.42
1:A:157:SER:HB2	1:A:162:THR:HG23	2.02	0.42
1:D:157:SER:HB2	1:D:162:THR:HG23	2.02	0.42
1:I:222:ALA:O	1:I:314:ARG:NH1	2.53	0.42
1:C:222:ALA:O	1:C:314:ARG:NH1	2.53	0.41
1:G:157:SER:HB2	1:G:162:THR:HG23	2.03	0.41
1:H:157:SER:HB2	1:H:162:THR:HG23	2.02	0.41
1:K:157:SER:HB2	1:K:162:THR:HG23	2.02	0.41
1:D:222:ALA:O	1:D:314:ARG:NH1	2.53	0.41
1:B:222:ALA:O	1:B:314:ARG:NH1	2.53	0.41
1:E:157:SER:HB2	1:E:162:THR:HG23	2.02	0.41
1:C:157:SER:HB2	1:C:162:THR:HG23	2.02	0.41
1:B:157:SER:HB2	1:B:162:THR:HG23	2.02	0.41
1:I:157:SER:HB2	1:I:162:THR:HG23	2.02	0.41
1:F:157:SER:HB2	1:F:162:THR:HG23	2.02	0.41
1:F:222:ALA:O	1:F:314:ARG:NH1	2.53	0.41
1:J:157:SER:HB2	1:J:162:THR:HG23	2.02	0.41
1:J:222:ALA:O	1:J:314:ARG:NH1	2.53	0.41
1:F:157:SER:OG	1:F:305:THR:OG1	1.92	0.40
1:D:157:SER:OG	1:D:305:THR:OG1	1.92	0.40
1:G:222:ALA:O	1:G:314:ARG:NH1	2.53	0.40
1:B:47:VAL:HG21	1:F:354:PHE:CZ	2.57	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	368/377 (98%)	350 (95%)	16 (4%)	2 (0%)	29	67
1	B	368/377 (98%)	350 (95%)	16 (4%)	2 (0%)	29	67
1	C	368/377 (98%)	350 (95%)	16 (4%)	2 (0%)	29	67
1	D	368/377 (98%)	350 (95%)	16 (4%)	2 (0%)	29	67
1	E	368/377 (98%)	350 (95%)	16 (4%)	2 (0%)	29	67
1	F	368/377 (98%)	350 (95%)	16 (4%)	2 (0%)	29	67
1	G	368/377 (98%)	350 (95%)	16 (4%)	2 (0%)	29	67
1	H	368/377 (98%)	350 (95%)	16 (4%)	2 (0%)	29	67
1	I	368/377 (98%)	350 (95%)	16 (4%)	2 (0%)	29	67
1	J	368/377 (98%)	350 (95%)	16 (4%)	2 (0%)	29	67
1	K	368/377 (98%)	350 (95%)	16 (4%)	2 (0%)	29	67
2	a	239/422 (57%)	210 (88%)	28 (12%)	1 (0%)	34	71
2	b	239/422 (57%)	211 (88%)	27 (11%)	1 (0%)	34	71
2	c	239/422 (57%)	210 (88%)	28 (12%)	1 (0%)	34	71
2	d	239/422 (57%)	210 (88%)	28 (12%)	1 (0%)	34	71
2	e	239/422 (57%)	211 (88%)	27 (11%)	1 (0%)	34	71
2	f	239/422 (57%)	210 (88%)	28 (12%)	1 (0%)	34	71
2	g	239/422 (57%)	210 (88%)	28 (12%)	1 (0%)	34	71
2	h	239/422 (57%)	211 (88%)	27 (11%)	1 (0%)	34	71
2	i	239/422 (57%)	211 (88%)	27 (11%)	1 (0%)	34	71
2	j	239/422 (57%)	210 (88%)	28 (12%)	1 (0%)	34	71
2	k	239/422 (57%)	211 (88%)	27 (11%)	1 (0%)	34	71
All	All	6677/8789 (76%)	6165 (92%)	479 (7%)	33 (0%)	32	67

All (33) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	319	ILE
1	B	319	ILE
1	C	319	ILE
1	D	319	ILE
1	E	319	ILE
1	F	319	ILE
1	G	319	ILE
1	H	319	ILE
1	I	319	ILE
1	J	319	ILE
1	K	319	ILE
1	A	318	GLU
1	B	318	GLU
1	C	318	GLU
1	D	318	GLU
1	E	318	GLU
1	F	318	GLU
1	G	318	GLU
1	H	318	GLU
1	I	318	GLU
1	J	318	GLU
1	K	318	GLU
2	a	408	GLY
2	b	408	GLY
2	c	408	GLY
2	e	408	GLY
2	f	408	GLY
2	g	408	GLY
2	h	408	GLY
2	i	408	GLY
2	k	408	GLY
2	d	408	GLY
2	j	408	GLY

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	313/320 (98%)	312 (100%)	1 (0%)	92	95
1	B	313/320 (98%)	312 (100%)	1 (0%)	92	95
1	C	313/320 (98%)	312 (100%)	1 (0%)	92	95
1	D	313/320 (98%)	312 (100%)	1 (0%)	92	95
1	E	313/320 (98%)	312 (100%)	1 (0%)	92	95
1	F	313/320 (98%)	312 (100%)	1 (0%)	92	95
1	G	313/320 (98%)	312 (100%)	1 (0%)	92	95
1	H	313/320 (98%)	312 (100%)	1 (0%)	92	95
1	I	313/320 (98%)	312 (100%)	1 (0%)	92	95
1	J	313/320 (98%)	312 (100%)	1 (0%)	92	95
1	K	313/320 (98%)	312 (100%)	1 (0%)	92	95
2	a	211/367 (58%)	207 (98%)	4 (2%)	57	75
2	b	211/367 (58%)	207 (98%)	4 (2%)	57	75
2	c	211/367 (58%)	207 (98%)	4 (2%)	57	75
2	d	211/367 (58%)	207 (98%)	4 (2%)	57	75
2	e	211/367 (58%)	207 (98%)	4 (2%)	57	75
2	f	211/367 (58%)	207 (98%)	4 (2%)	57	75
2	g	211/367 (58%)	207 (98%)	4 (2%)	57	75
2	h	211/367 (58%)	207 (98%)	4 (2%)	57	75
2	i	211/367 (58%)	207 (98%)	4 (2%)	57	75
2	j	211/367 (58%)	207 (98%)	4 (2%)	57	75
2	k	211/367 (58%)	207 (98%)	4 (2%)	57	75
All	All	5764/7557 (76%)	5709 (99%)	55 (1%)	77	86

All (55) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	157	SER
1	B	157	SER
1	C	157	SER
1	D	157	SER
1	E	157	SER
1	F	157	SER
1	G	157	SER
1	H	157	SER

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Mol	Chain	Res	Type
1	I	157	SER
1	J	157	SER
1	K	157	SER
2	a	391	GLU
2	a	533	GLU
2	a	567	ASP
2	a	625	LYS
2	b	391	GLU
2	b	533	GLU
2	b	567	ASP
2	b	625	LYS
2	c	391	GLU
2	c	533	GLU
2	c	567	ASP
2	c	625	LYS
2	d	391	GLU
2	d	533	GLU
2	d	567	ASP
2	d	625	LYS
2	e	391	GLU
2	e	533	GLU
2	e	567	ASP
2	e	625	LYS
2	f	391	GLU
2	f	533	GLU
2	f	567	ASP
2	f	625	LYS
2	g	391	GLU
2	g	533	GLU
2	g	567	ASP
2	g	625	LYS
2	h	391	GLU
2	h	533	GLU
2	h	567	ASP
2	h	625	LYS
2	i	391	GLU
2	i	533	GLU
2	i	567	ASP
2	i	625	LYS
2	j	391	GLU
2	j	533	GLU
2	j	567	ASP

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Mol	Chain	Res	Type
2	j	625	LYS
2	k	391	GLU
2	k	533	GLU
2	k	567	ASP
2	k	625	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (21) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	113	ASN
1	B	14	ASN
1	B	113	ASN
1	C	14	ASN
1	C	113	ASN
1	D	113	ASN
1	E	113	ASN
1	F	113	ASN
1	G	14	ASN
1	G	113	ASN
1	H	113	ASN
1	I	113	ASN
1	J	113	ASN
1	K	14	ASN
1	K	113	ASN
2	a	523	ASN
2	c	523	ASN
2	e	523	ASN
2	i	523	ASN
2	j	523	ASN
2	k	523	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 [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 22 ligands modelled in this entry, 11 are monoatomic - leaving 11 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
3	ADP	C	401	4	24,29,29	0.89	1 (4%)	29,45,45	1.60	5 (17%)
3	ADP	B	401	4	24,29,29	0.89	1 (4%)	29,45,45	1.59	5 (17%)
3	ADP	J	401	4	24,29,29	0.90	1 (4%)	29,45,45	1.59	5 (17%)
3	ADP	F	401	4	24,29,29	0.90	1 (4%)	29,45,45	1.59	5 (17%)
3	ADP	E	401	4	24,29,29	0.90	1 (4%)	29,45,45	1.60	5 (17%)
3	ADP	A	401	4	24,29,29	0.90	1 (4%)	29,45,45	1.59	6 (20%)
3	ADP	I	401	4	24,29,29	0.90	1 (4%)	29,45,45	1.59	6 (20%)
3	ADP	H	401	4	24,29,29	0.90	1 (4%)	29,45,45	1.59	5 (17%)
3	ADP	D	401	4	24,29,29	0.89	1 (4%)	29,45,45	1.59	5 (17%)
3	ADP	K	401	4	24,29,29	0.90	1 (4%)	29,45,45	1.59	5 (17%)
3	ADP	G	401	4	24,29,29	0.90	1 (4%)	29,45,45	1.59	5 (17%)

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	ADP	C	401	4	-	1/12/32/32	0/3/3/3
3	ADP	B	401	4	-	1/12/32/32	0/3/3/3
3	ADP	J	401	4	-	1/12/32/32	0/3/3/3
3	ADP	F	401	4	-	1/12/32/32	0/3/3/3
3	ADP	E	401	4	-	1/12/32/32	0/3/3/3
3	ADP	A	401	4	-	1/12/32/32	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	ADP	I	401	4	-	1/12/32/32	0/3/3/3
3	ADP	H	401	4	-	1/12/32/32	0/3/3/3
3	ADP	D	401	4	-	1/12/32/32	0/3/3/3
3	ADP	K	401	4	-	1/12/32/32	0/3/3/3
3	ADP	G	401	4	-	1/12/32/32	0/3/3/3

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	I	401	ADP	C5-C4	2.20	1.46	1.40
3	H	401	ADP	C5-C4	2.20	1.46	1.40
3	A	401	ADP	C5-C4	2.20	1.46	1.40
3	J	401	ADP	C5-C4	2.20	1.46	1.40
3	F	401	ADP	C5-C4	2.19	1.46	1.40
3	B	401	ADP	C5-C4	2.18	1.46	1.40
3	K	401	ADP	C5-C4	2.18	1.46	1.40
3	G	401	ADP	C5-C4	2.17	1.46	1.40
3	D	401	ADP	C5-C4	2.16	1.46	1.40
3	C	401	ADP	C5-C4	2.16	1.46	1.40
3	E	401	ADP	C5-C4	2.15	1.46	1.40

All (57) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	401	ADP	PA-O3A-PB	-4.34	117.93	132.83
3	B	401	ADP	PA-O3A-PB	-4.34	117.95	132.83
3	E	401	ADP	PA-O3A-PB	-4.33	117.96	132.83
3	G	401	ADP	PA-O3A-PB	-4.33	117.96	132.83
3	H	401	ADP	PA-O3A-PB	-4.33	117.97	132.83
3	C	401	ADP	PA-O3A-PB	-4.33	117.98	132.83
3	I	401	ADP	PA-O3A-PB	-4.32	117.99	132.83
3	A	401	ADP	PA-O3A-PB	-4.32	117.99	132.83
3	F	401	ADP	PA-O3A-PB	-4.32	117.99	132.83
3	K	401	ADP	PA-O3A-PB	-4.32	118.00	132.83
3	J	401	ADP	PA-O3A-PB	-4.32	118.01	132.83
3	E	401	ADP	N3-C2-N1	-3.52	123.17	128.68
3	K	401	ADP	N3-C2-N1	-3.50	123.21	128.68
3	C	401	ADP	N3-C2-N1	-3.50	123.21	128.68
3	A	401	ADP	N3-C2-N1	-3.49	123.22	128.68
3	D	401	ADP	N3-C2-N1	-3.49	123.23	128.68
3	F	401	ADP	N3-C2-N1	-3.48	123.24	128.68
3	J	401	ADP	N3-C2-N1	-3.48	123.25	128.68

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	401	ADP	N3-C2-N1	-3.47	123.26	128.68
3	H	401	ADP	N3-C2-N1	-3.46	123.27	128.68
3	G	401	ADP	N3-C2-N1	-3.46	123.27	128.68
3	I	401	ADP	N3-C2-N1	-3.44	123.30	128.68
3	C	401	ADP	C3'-C2'-C1'	2.82	105.22	100.98
3	B	401	ADP	C3'-C2'-C1'	2.81	105.21	100.98
3	K	401	ADP	C3'-C2'-C1'	2.80	105.20	100.98
3	E	401	ADP	C3'-C2'-C1'	2.79	105.19	100.98
3	I	401	ADP	C3'-C2'-C1'	2.79	105.18	100.98
3	A	401	ADP	C3'-C2'-C1'	2.79	105.18	100.98
3	F	401	ADP	C3'-C2'-C1'	2.78	105.17	100.98
3	J	401	ADP	C3'-C2'-C1'	2.78	105.17	100.98
3	H	401	ADP	C3'-C2'-C1'	2.78	105.16	100.98
3	D	401	ADP	C3'-C2'-C1'	2.77	105.16	100.98
3	G	401	ADP	C3'-C2'-C1'	2.77	105.14	100.98
3	F	401	ADP	C4-C5-N7	-2.54	106.75	109.40
3	A	401	ADP	C4-C5-N7	-2.54	106.75	109.40
3	B	401	ADP	C4-C5-N7	-2.53	106.76	109.40
3	I	401	ADP	C4-C5-N7	-2.53	106.76	109.40
3	C	401	ADP	C4-C5-N7	-2.53	106.77	109.40
3	J	401	ADP	C4-C5-N7	-2.52	106.78	109.40
3	D	401	ADP	C4-C5-N7	-2.51	106.78	109.40
3	E	401	ADP	C4-C5-N7	-2.51	106.78	109.40
3	G	401	ADP	C4-C5-N7	-2.51	106.78	109.40
3	H	401	ADP	C4-C5-N7	-2.51	106.78	109.40
3	K	401	ADP	C4-C5-N7	-2.50	106.80	109.40
3	E	401	ADP	C2'-C3'-C4'	2.14	106.81	102.64
3	D	401	ADP	C2'-C3'-C4'	2.14	106.80	102.64
3	G	401	ADP	C2'-C3'-C4'	2.14	106.79	102.64
3	F	401	ADP	C2'-C3'-C4'	2.13	106.79	102.64
3	K	401	ADP	C2'-C3'-C4'	2.13	106.78	102.64
3	H	401	ADP	C2'-C3'-C4'	2.13	106.77	102.64
3	J	401	ADP	C2'-C3'-C4'	2.12	106.77	102.64
3	A	401	ADP	C2'-C3'-C4'	2.12	106.77	102.64
3	I	401	ADP	C2'-C3'-C4'	2.12	106.75	102.64
3	B	401	ADP	C2'-C3'-C4'	2.10	106.73	102.64
3	C	401	ADP	C2'-C3'-C4'	2.10	106.72	102.64
3	A	401	ADP	O3B-PB-O2B	2.01	115.31	107.64
3	I	401	ADP	O3B-PB-O2B	2.00	115.29	107.64

There are no chirality outliers.

All (11) torsion outliers are listed below:

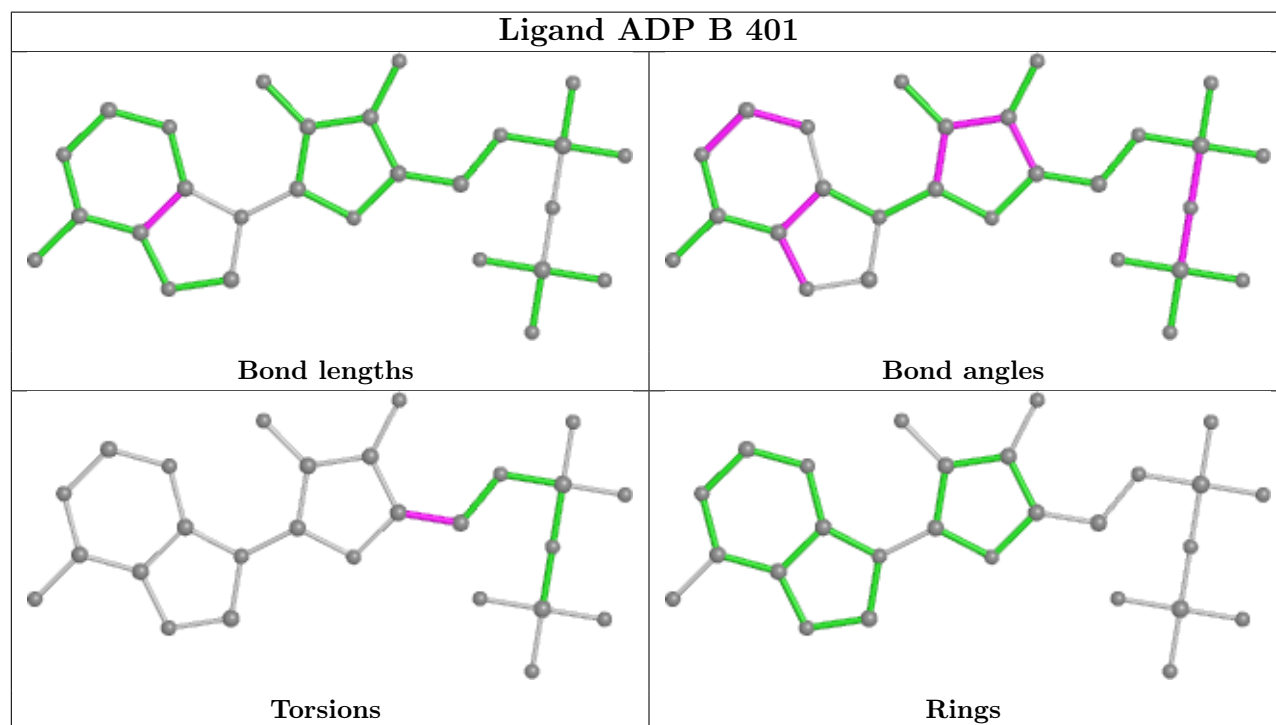
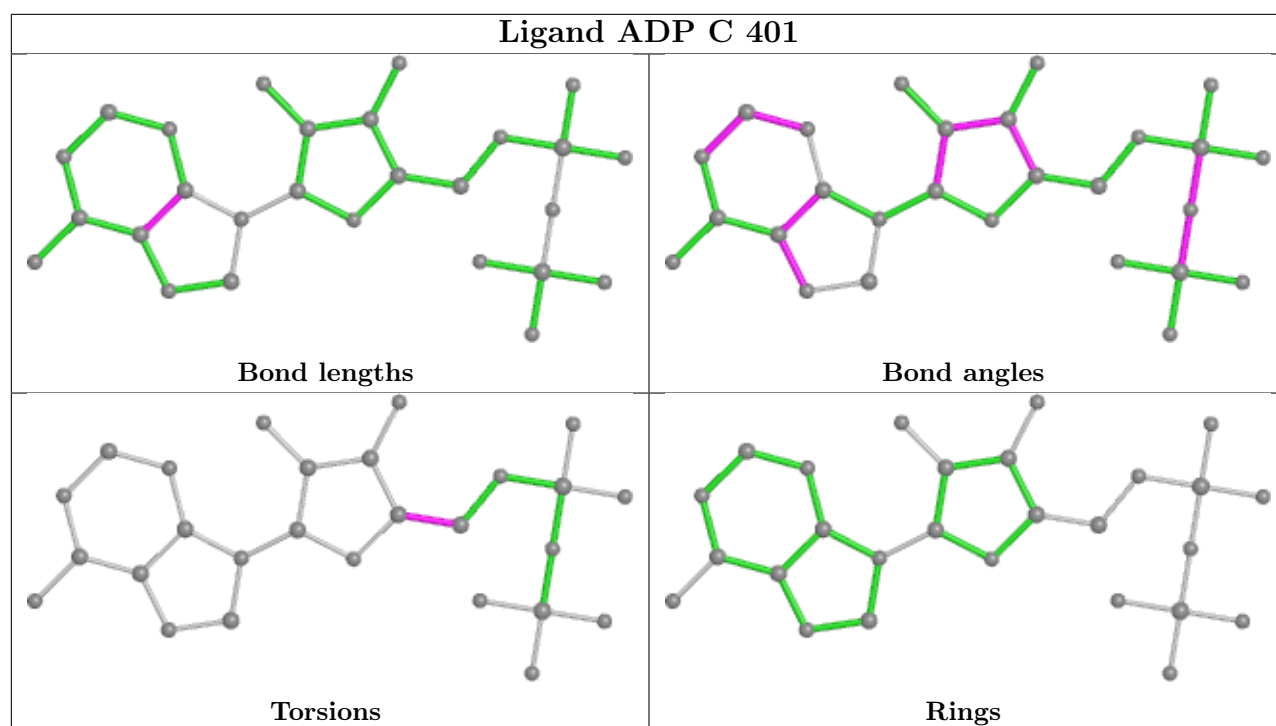
Mol	Chain	Res	Type	Atoms
3	A	401	ADP	C3'-C4'-C5'-O5'
3	B	401	ADP	C3'-C4'-C5'-O5'
3	C	401	ADP	C3'-C4'-C5'-O5'
3	E	401	ADP	C3'-C4'-C5'-O5'
3	G	401	ADP	C3'-C4'-C5'-O5'
3	H	401	ADP	C3'-C4'-C5'-O5'
3	I	401	ADP	C3'-C4'-C5'-O5'
3	J	401	ADP	C3'-C4'-C5'-O5'
3	D	401	ADP	C3'-C4'-C5'-O5'
3	F	401	ADP	C3'-C4'-C5'-O5'
3	K	401	ADP	C3'-C4'-C5'-O5'

There are no ring outliers.

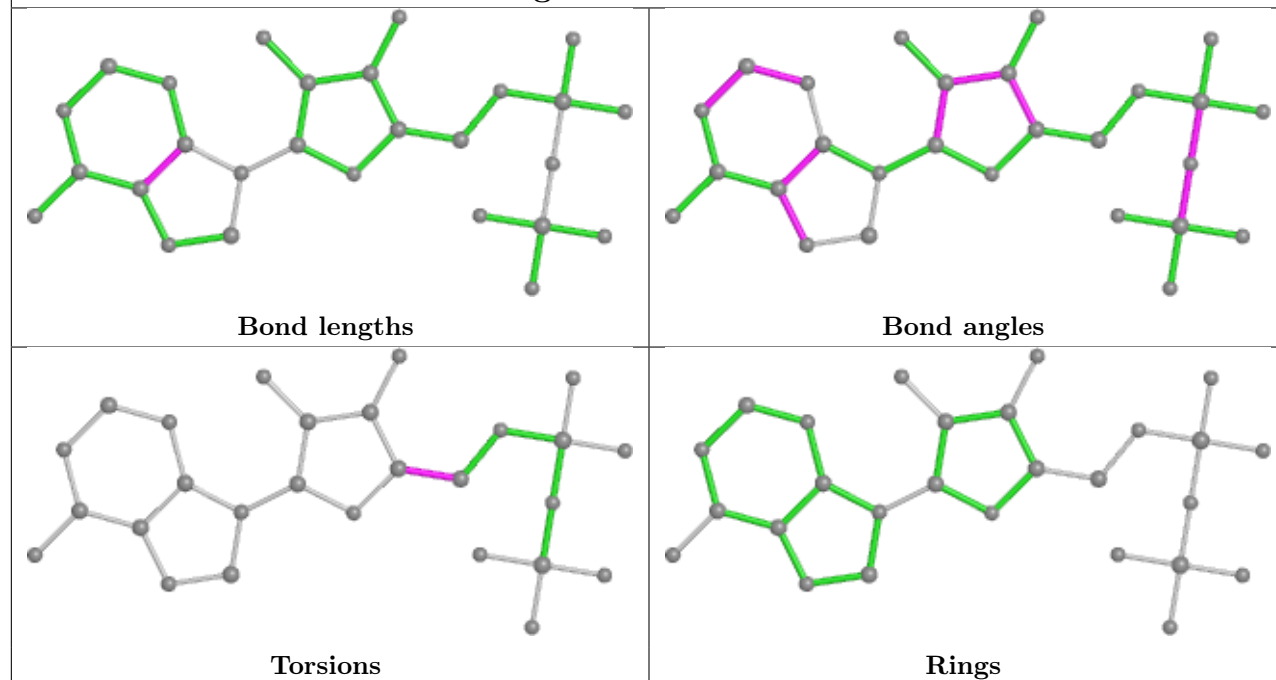
1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	E	401	ADP	1	0

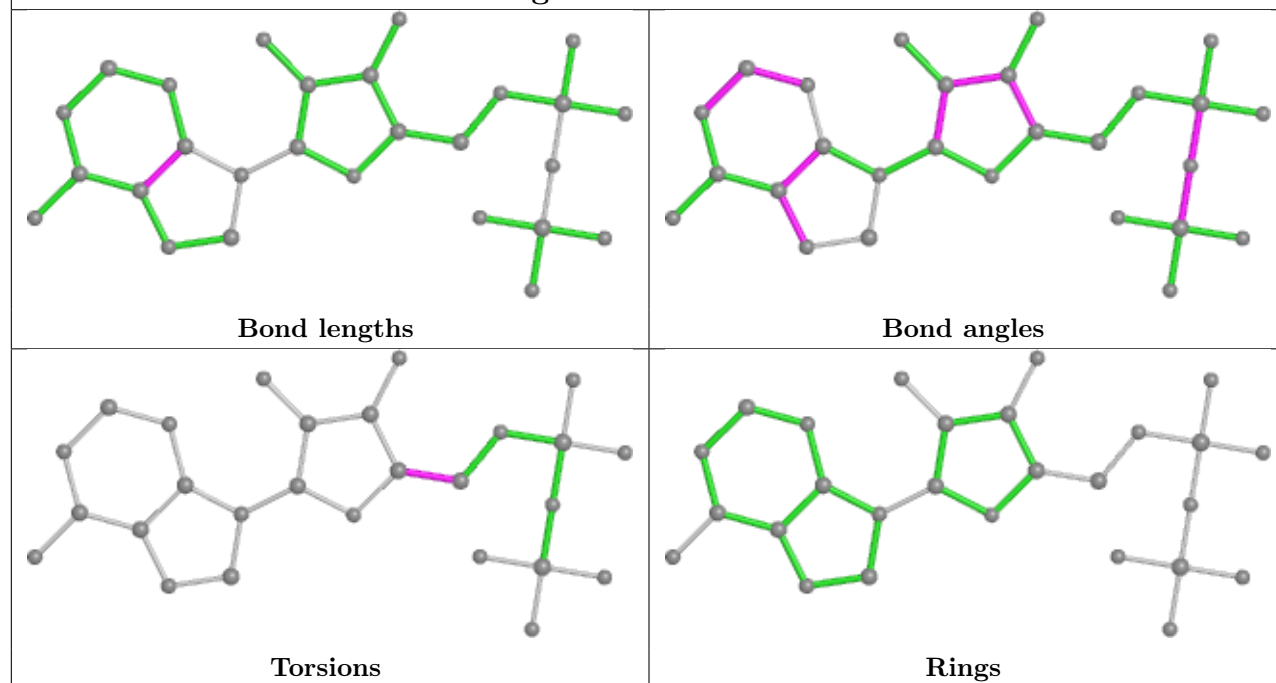
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.

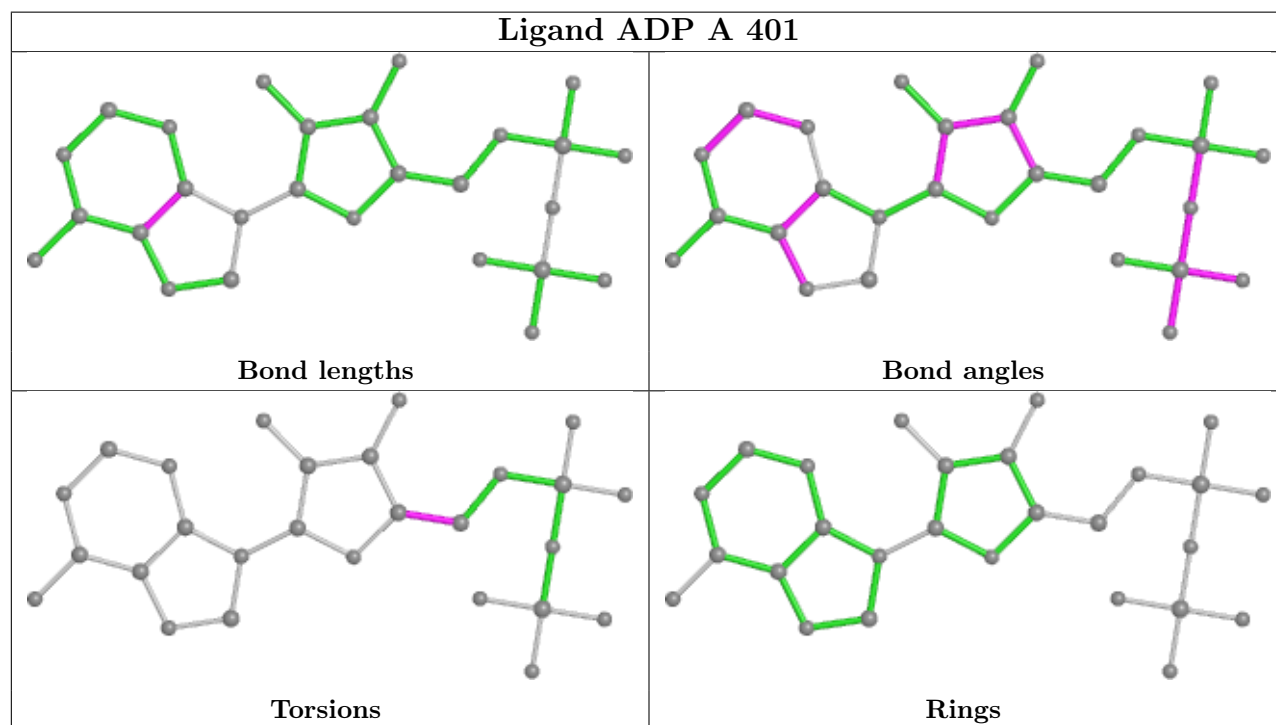
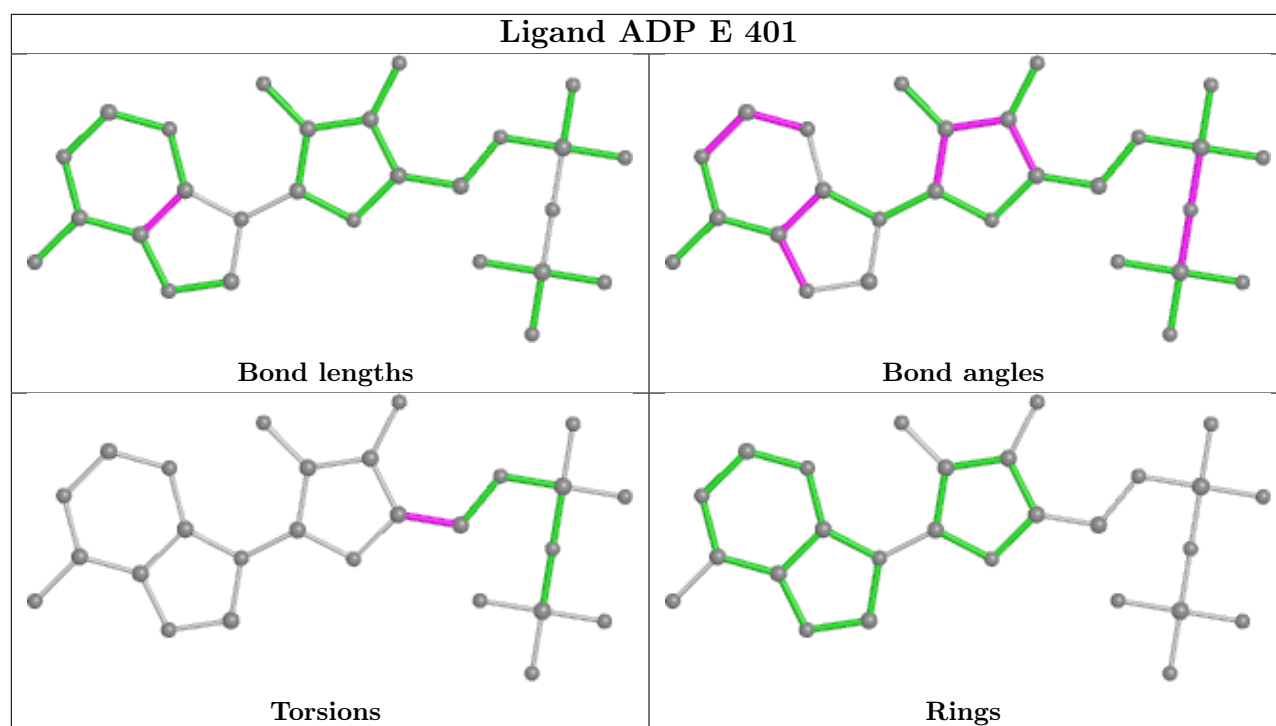


Ligand ADP J 401

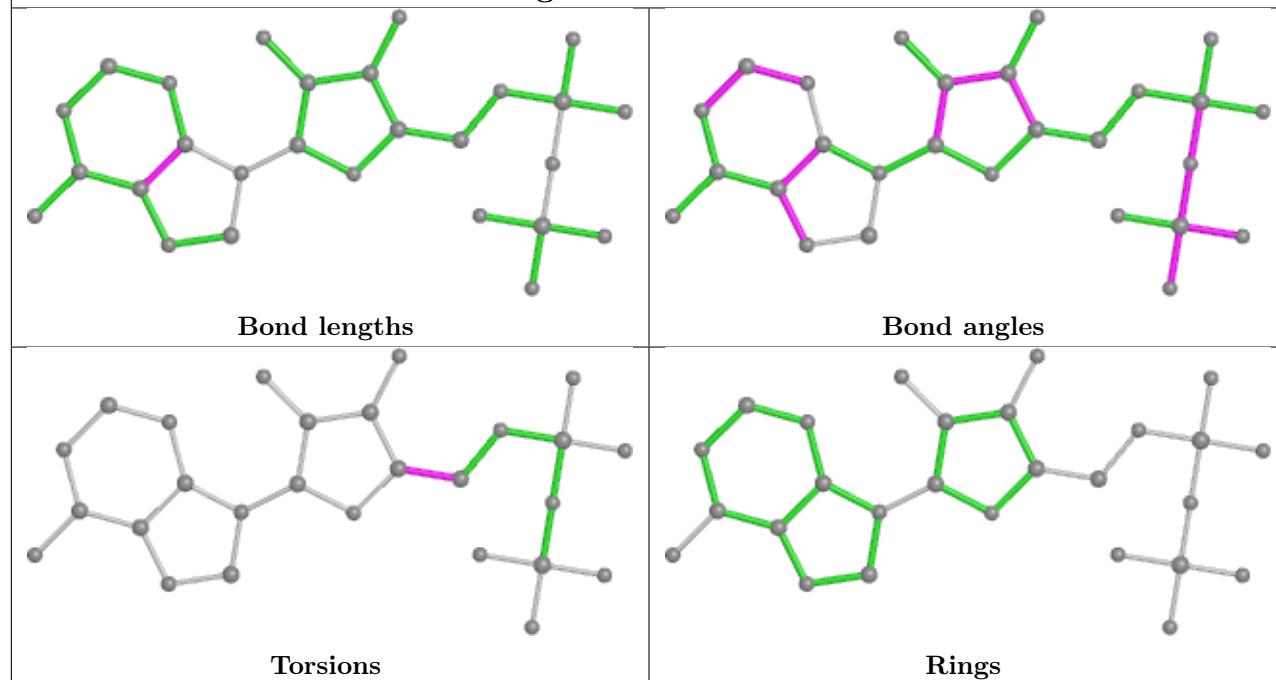


Ligand ADP F 401

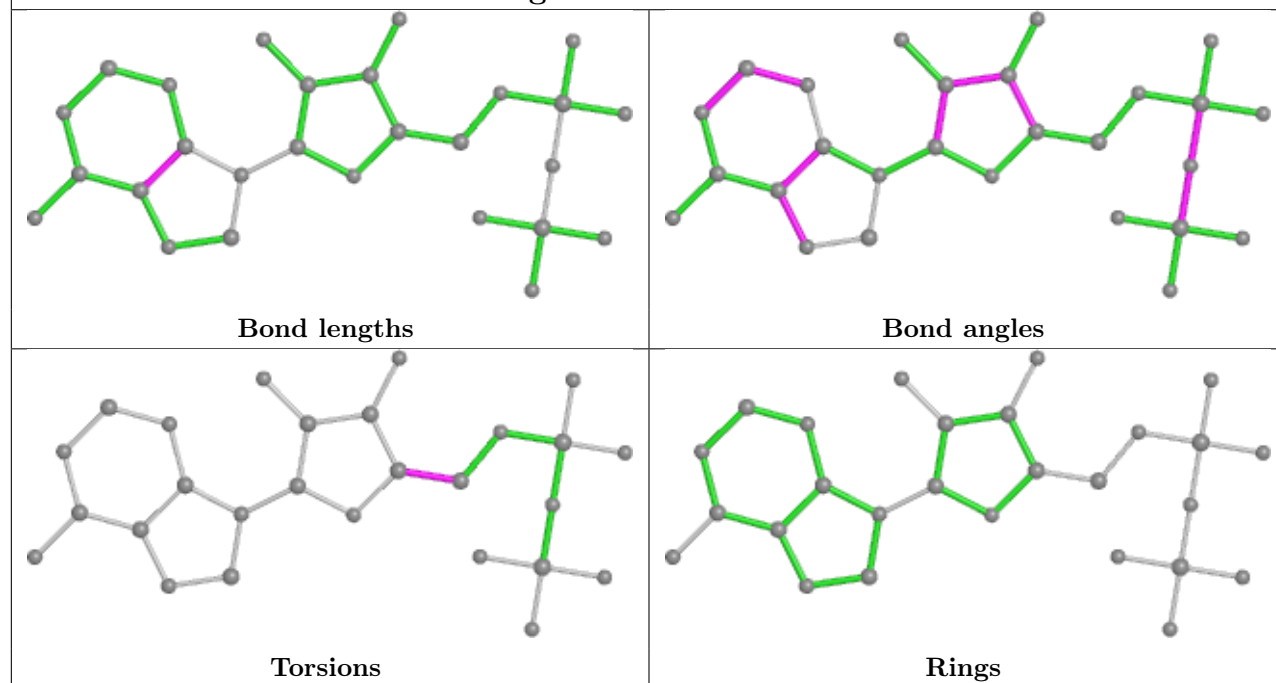


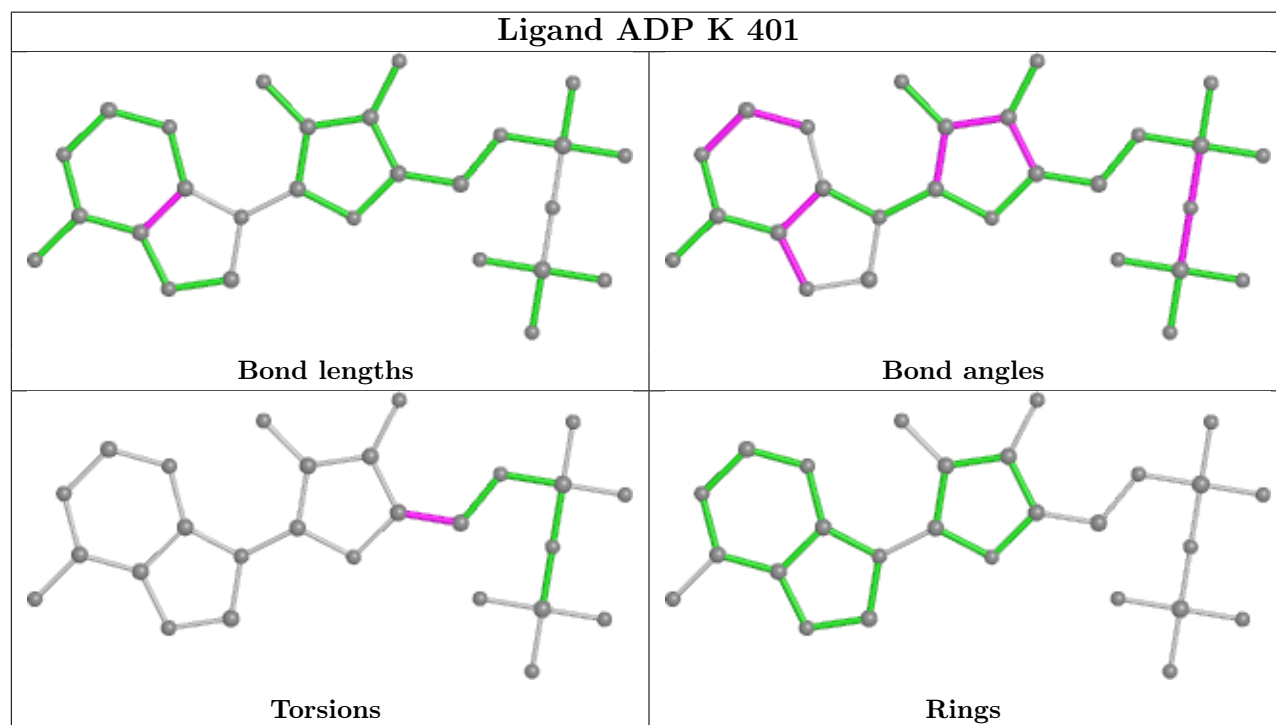
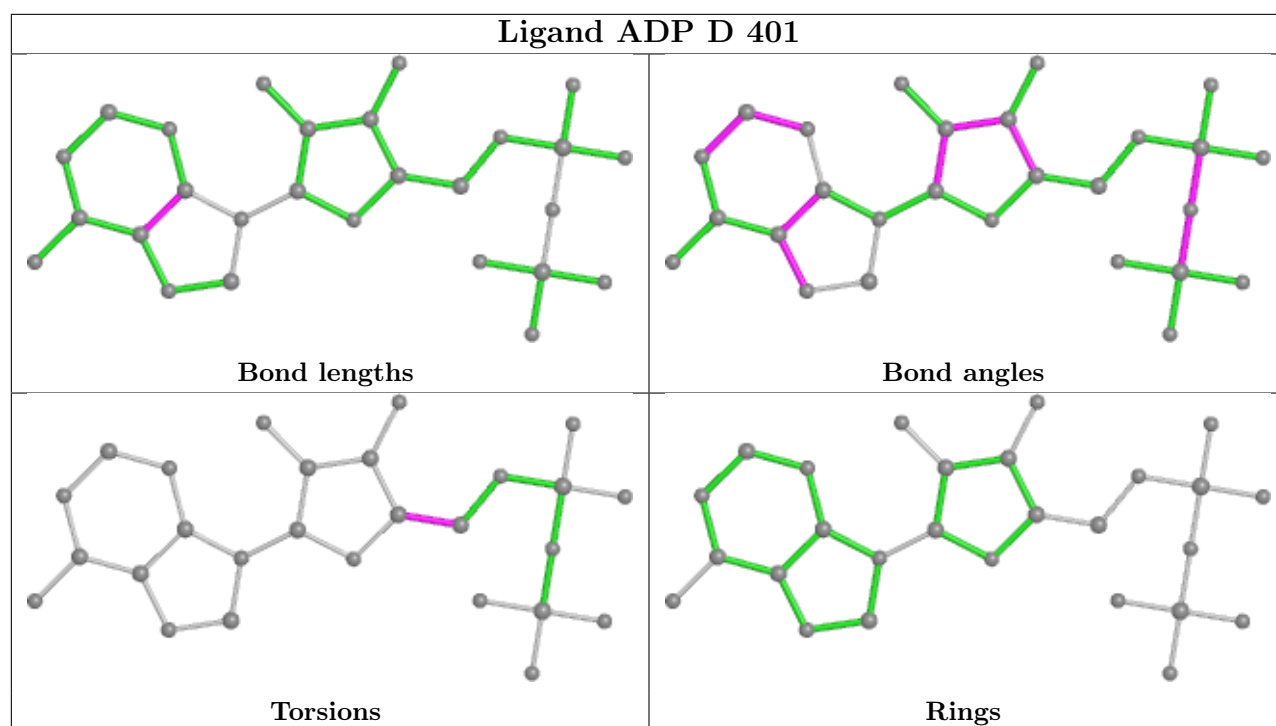


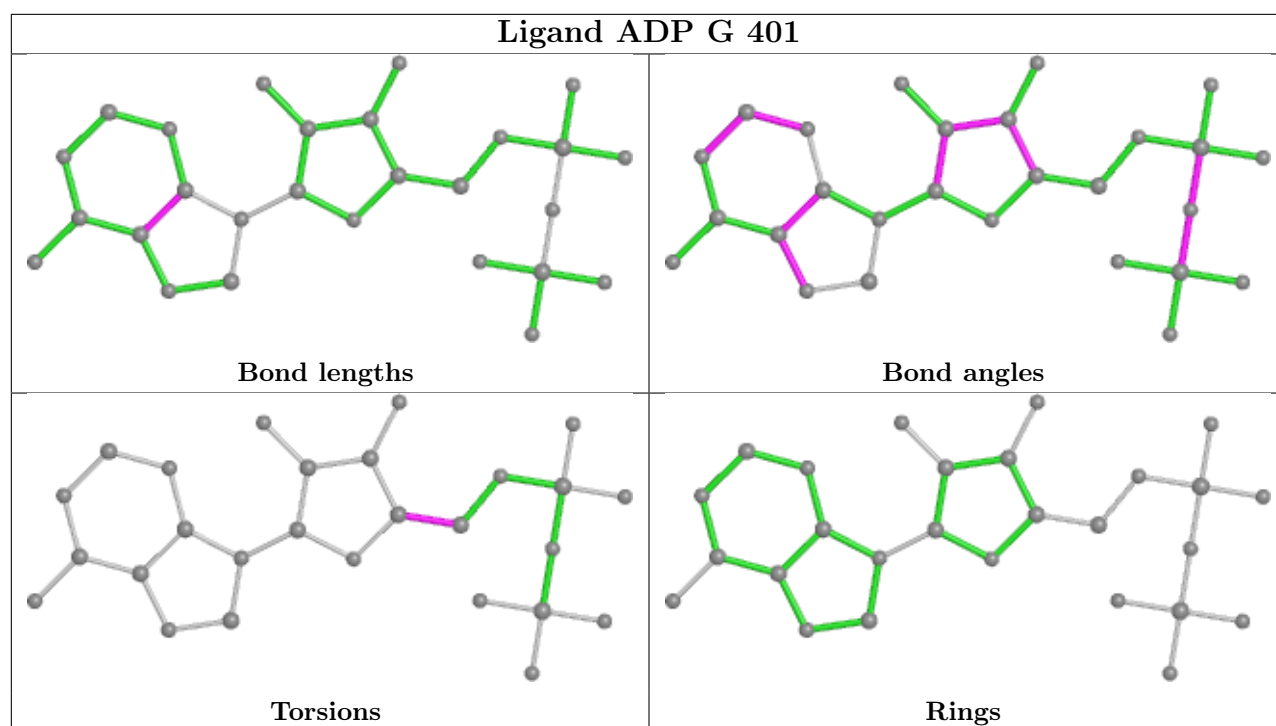
Ligand ADP I 401



Ligand ADP H 401







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.

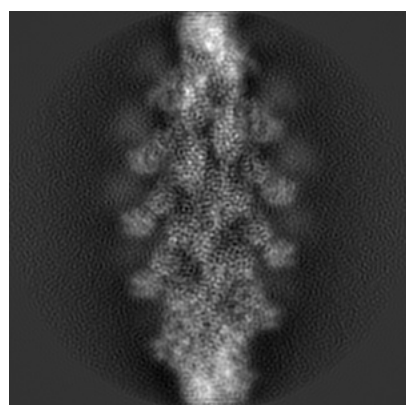
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-21155. These allow visual inspection of the internal detail of the map and identification of artifacts.

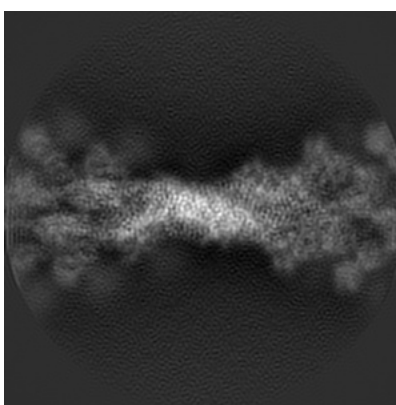
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

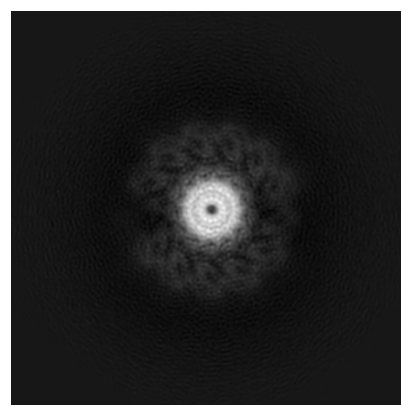
6.1.1 Primary map



X



Y

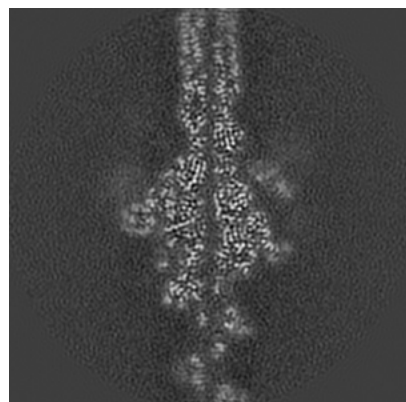


Z

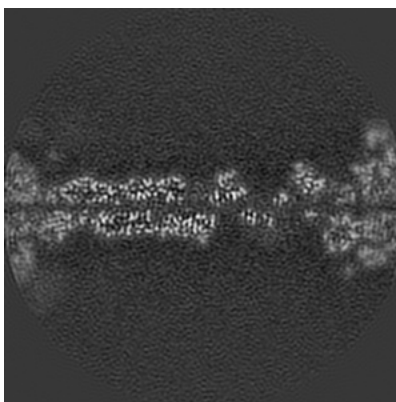
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

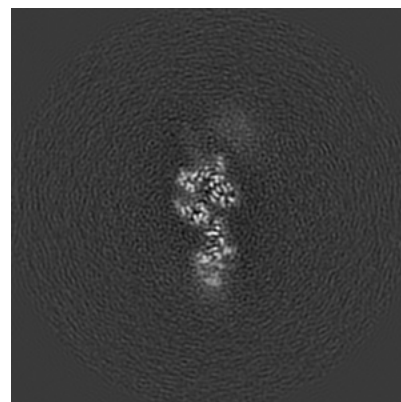
6.2.1 Primary map



X Index: 128



Y Index: 128

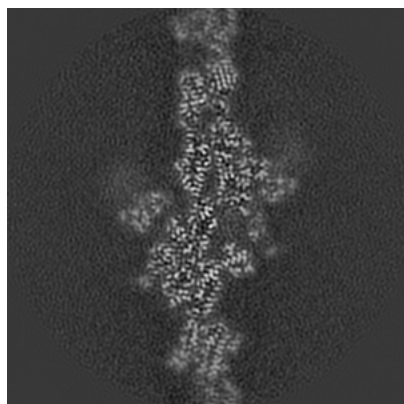


Z Index: 128

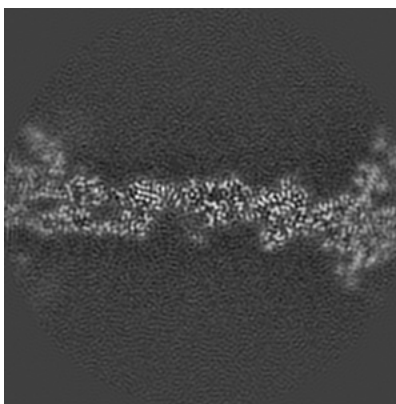
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

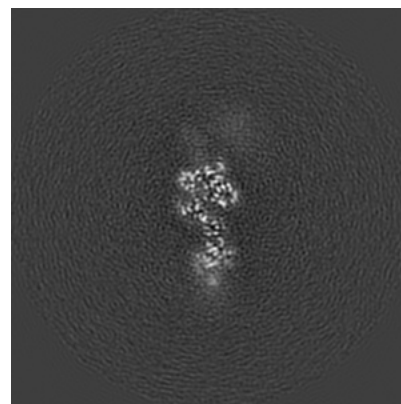
6.3.1 Primary map



X Index: 122



Y Index: 135



Z Index: 129

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

6.4 Orthogonal surface views [i](#)

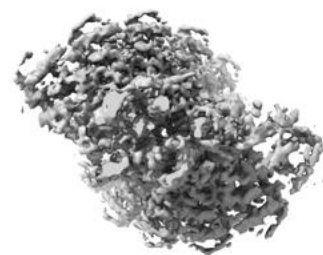
6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0611. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

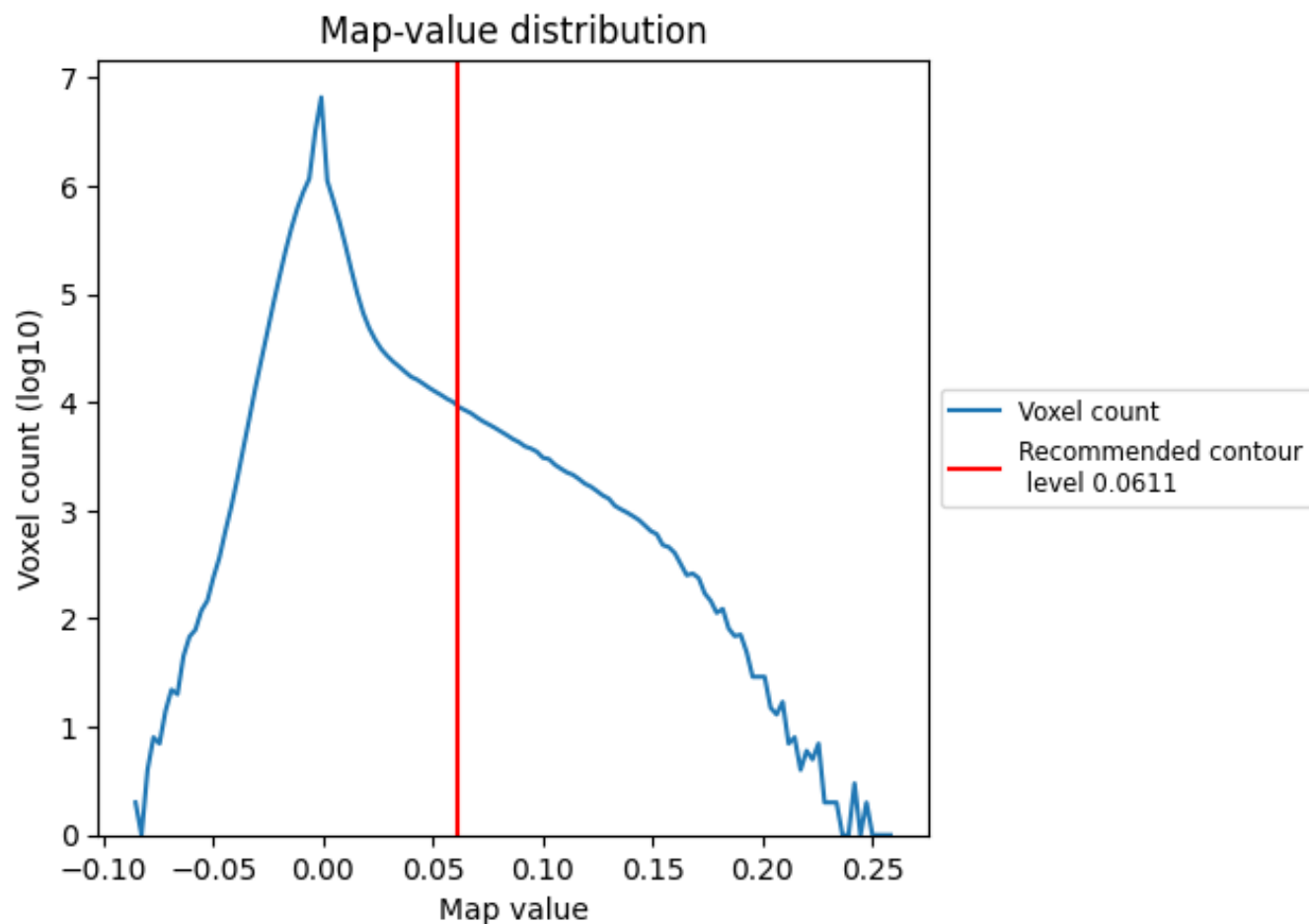
6.5 Mask visualisation

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

7 Map analysis [i](#)

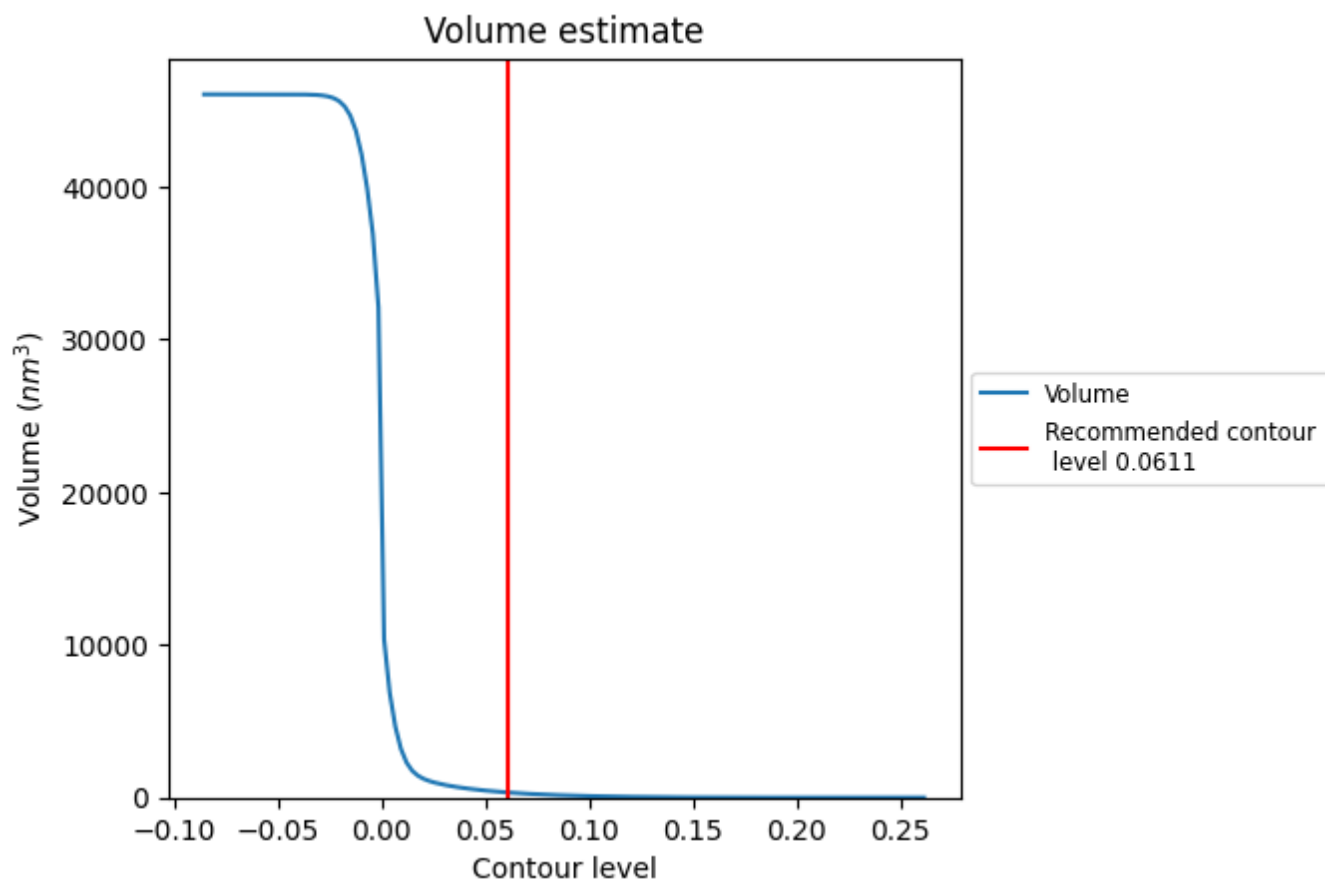
This section contains the results of statistical analysis of the map.

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.

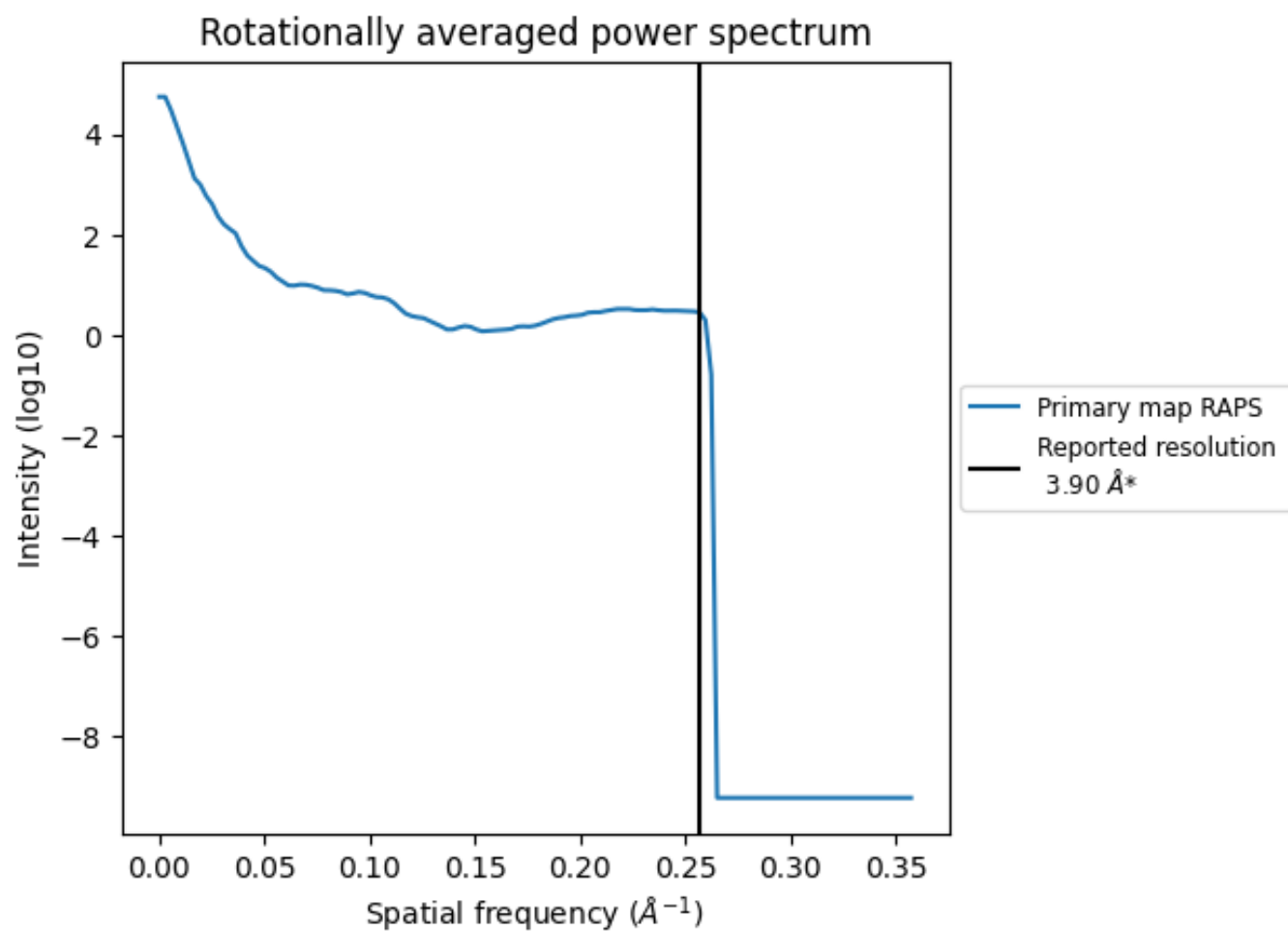
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 328 nm³; this corresponds to an approximate mass of 296 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 0.256 Å⁻¹

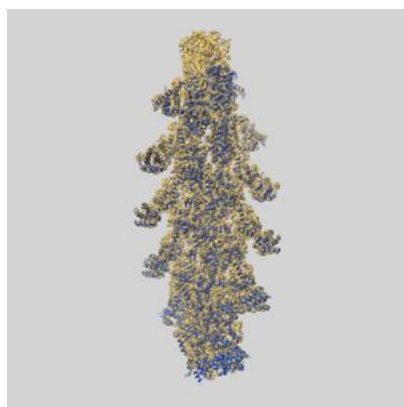
8 Fourier-Shell correlation ⓘ

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

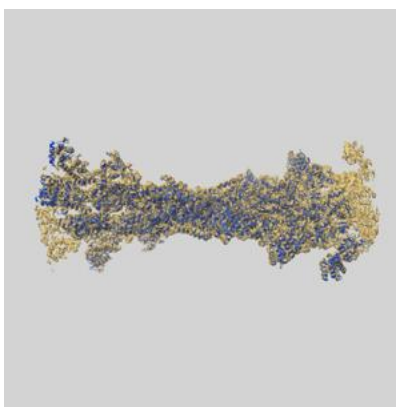
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-21155 and PDB model 6VEC. Per-residue inclusion information can be found in section 3 on page 16.

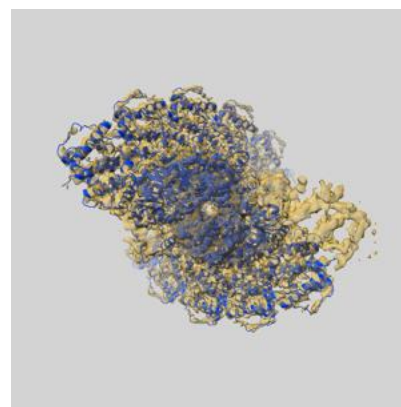
9.1 Map-model overlay [i](#)



X



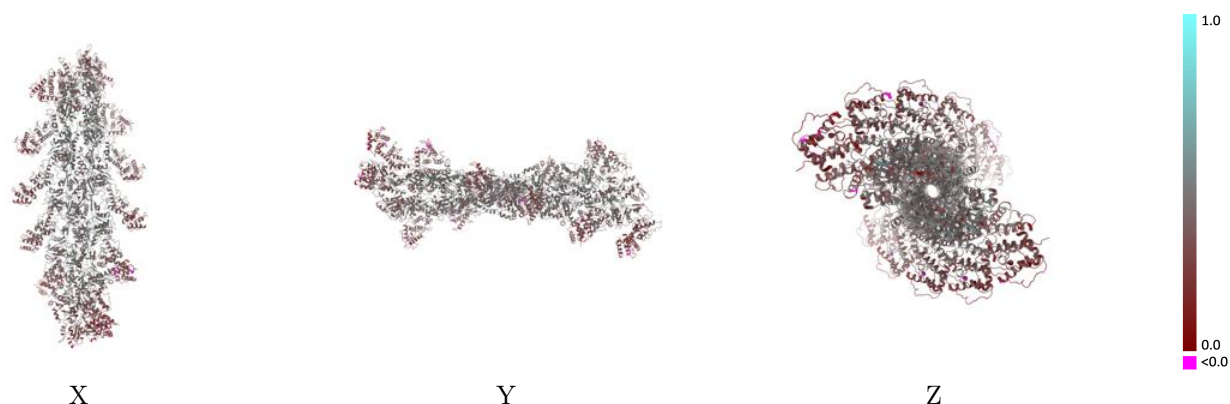
Y



Z

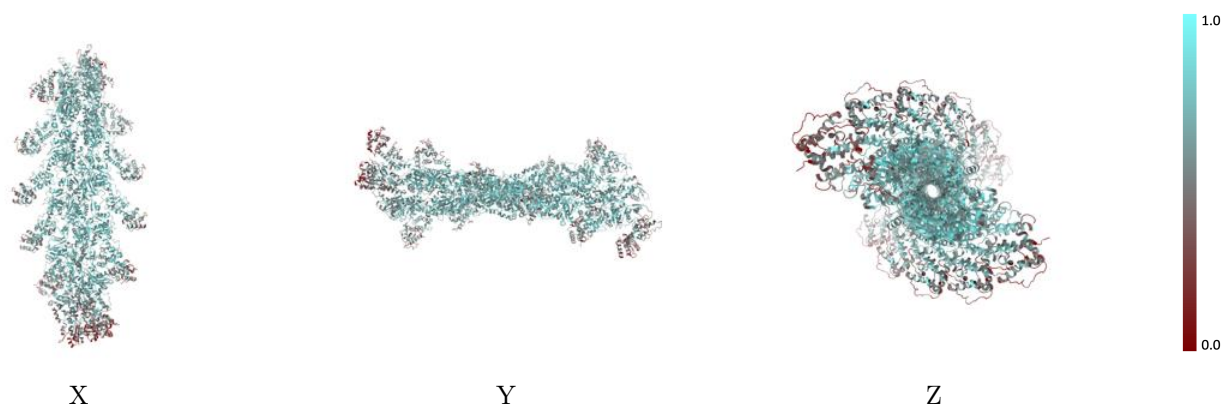
The images above show the 3D surface view of the map at the recommended contour level 0.0611 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



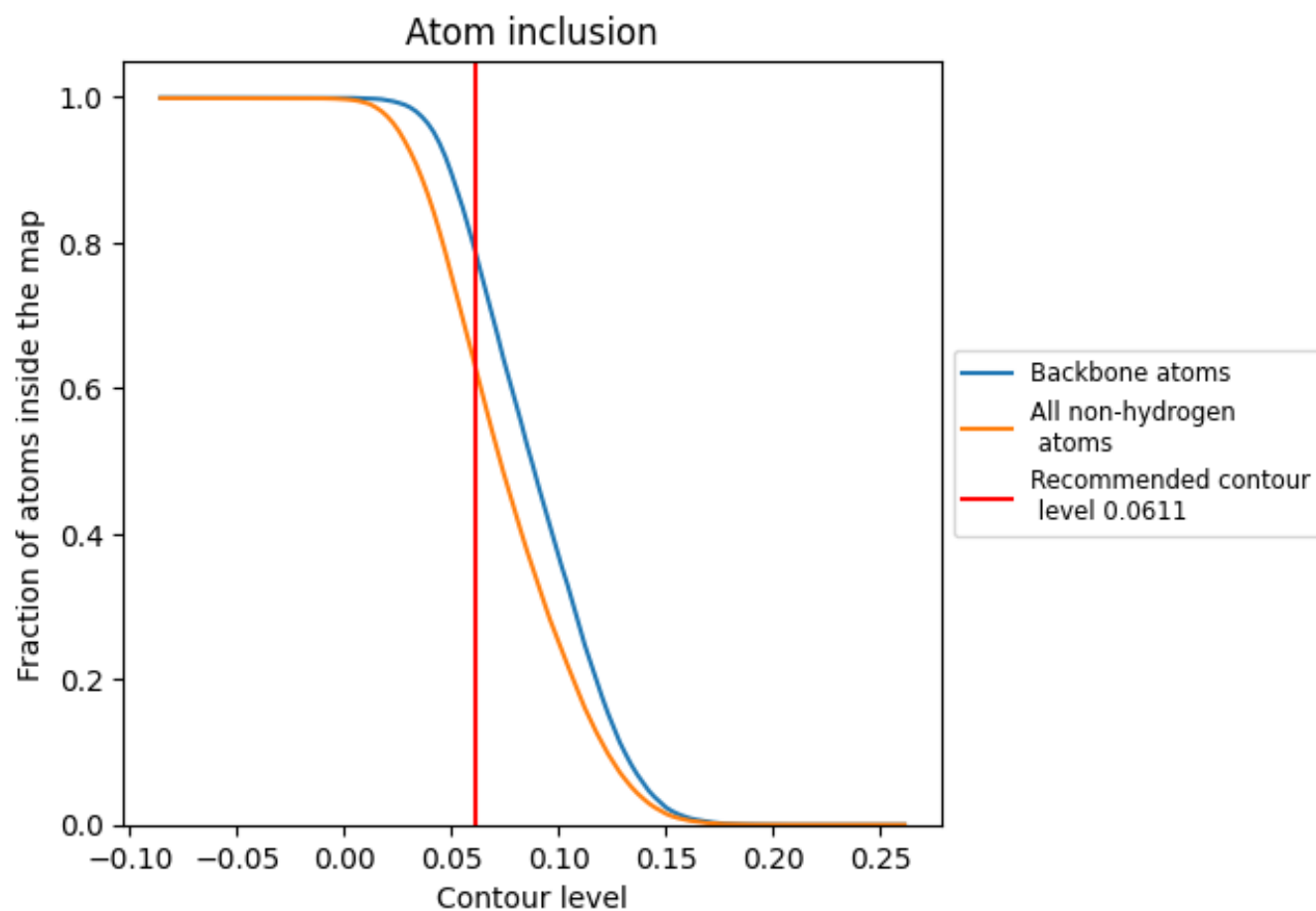
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0611).















































9.4 Atom inclusion [i](#)



At the recommended contour level, 79% of all backbone atoms, 63% 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 (0.0611) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6284	 0.3850
A	 0.7366	 0.4510
B	 0.7405	 0.4540
C	 0.7433	 0.4520
D	 0.7391	 0.4550
E	 0.7314	 0.4500
F	 0.7338	 0.4560
G	 0.7142	 0.4370
H	 0.7097	 0.4400
I	 0.6362	 0.3970
J	 0.6506	 0.4100
K	 0.4624	 0.3330
a	 0.5854	 0.3400
b	 0.5961	 0.3480
c	 0.5880	 0.3390
d	 0.5870	 0.3390
e	 0.5694	 0.3220
f	 0.5635	 0.3400
g	 0.5635	 0.3330
h	 0.5155	 0.3100
i	 0.4829	 0.2790
j	 0.4029	 0.2640
k	 0.4120	 0.2640

